



UNIVERSITAT DE
BARCELONA

Role of conjugated sterols homeostasis in plant development and stress response

Joan Manel Lopez Tubau

ADVERTIMENT. La consulta d'aquesta tesi queda condicionada a l'acceptació de les següents condicions d'ús: La difusió d'aquesta tesi per mitjà del servei TDX (www.tdx.cat) i a través del Dipòsit Digital de la UB (diposit.ub.edu) ha estat autoritzada pels titulars dels drets de propietat intel·lectual únicament per a usos privats emmarcats en activitats d'investigació i docència. No s'autoritza la seva reproducció amb finalitats de lucre ni la seva difusió i posada a disposició des d'un lloc aliè al servei TDX ni al Dipòsit Digital de la UB. No s'autoritza la presentació del seu contingut en una finestra o marc aliè a TDX o al Dipòsit Digital de la UB (framing). Aquesta reserva de drets afecta tant al resum de presentació de la tesi com als seus continguts. En la utilització o cita de parts de la tesi és obligat indicar el nom de la persona autora.

ADVERTENCIA. La consulta de esta tesis queda condicionada a la aceptación de las siguientes condiciones de uso: La difusión de esta tesis por medio del servicio TDR (www.tdx.cat) y a través del Repositorio Digital de la UB (diposit.ub.edu) ha sido autorizada por los titulares de los derechos de propiedad intelectual únicamente para usos privados enmarcados en actividades de investigación y docencia. No se autoriza su reproducción con finalidades de lucro ni su difusión y puesta a disposición desde un sitio ajeno al servicio TDR o al Repositorio Digital de la UB. No se autoriza la presentación de su contenido en una ventana o marco ajeno a TDR o al Repositorio Digital de la UB (framing). Esta reserva de derechos afecta tanto al resumen de presentación de la tesis como a sus contenidos. En la utilización o cita de partes de la tesis es obligado indicar el nombre de la persona autora.

WARNING. On having consulted this thesis you're accepting the following use conditions: Spreading this thesis by the TDX (www.tdx.cat) service and by the UB Digital Repository (diposit.ub.edu) has been authorized by the titular of the intellectual property rights only for private uses placed in investigation and teaching activities. Reproduction with lucrative aims is not authorized nor its spreading and availability from a site foreign to the TDX service or to the UB Digital Repository. Introducing its content in a window or frame foreign to the TDX service or to the UB Digital Repository is not authorized (framing). Those rights affect to the presentation summary of the thesis as well as to its contents. In the using or citation of parts of the thesis it's obliged to indicate the name of the author.



UNIVERSITAT DE
BARCELONA

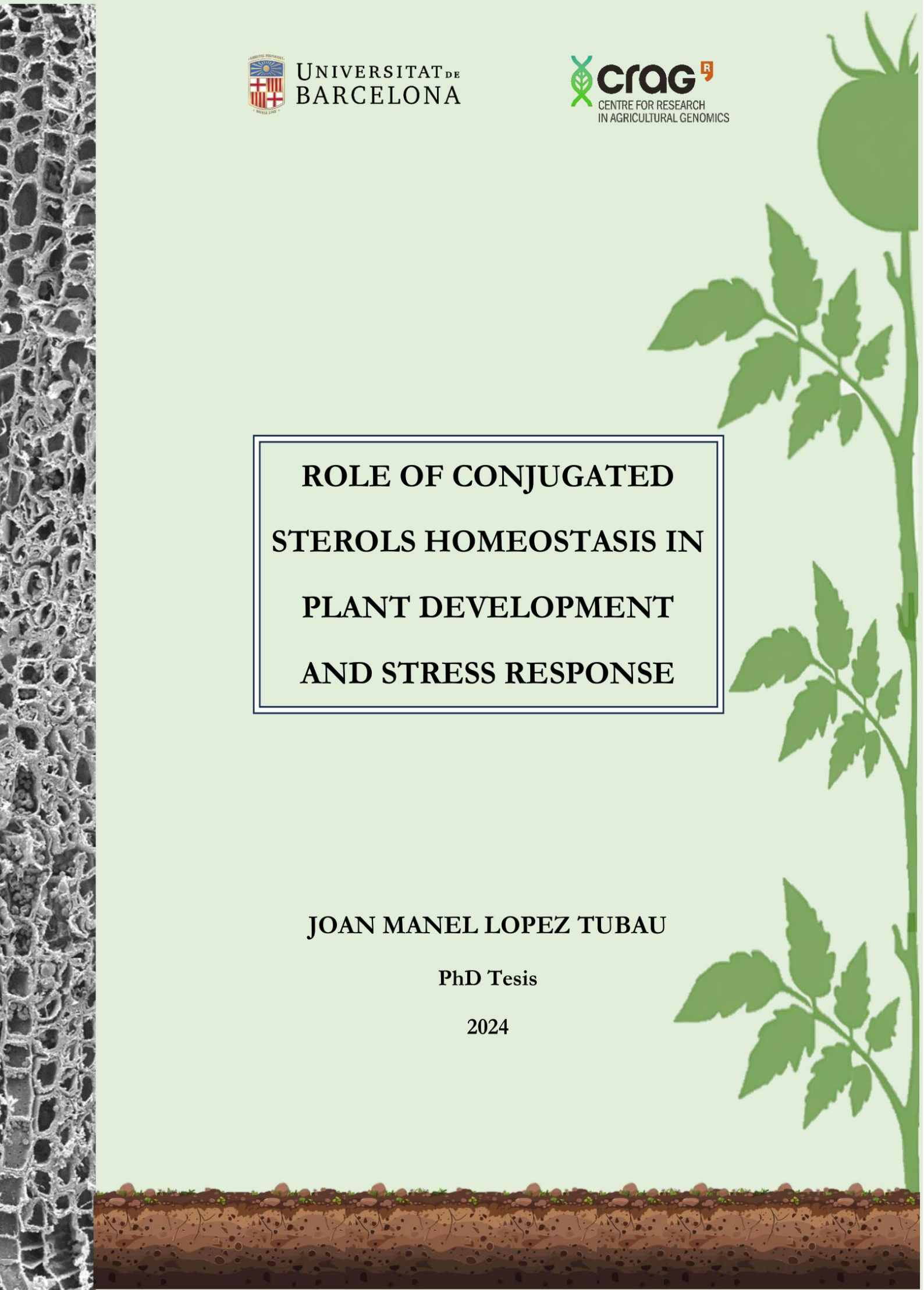


ROLE OF CONJUGATED STEROLS HOMEOSTASIS IN PLANT DEVELOPMENT AND STRESS RESPONSE

JOAN MANEL LOPEZ TUBAU

PhD Thesis

2024





UNIVERSITAT DE BARCELONA

FACULTAT DE FARMÀCIA I CIÈNCIES DE L'ALIMENTACIÓ

ROLE OF CONJUGATED STEROLS HOMEOSTASIS IN PLANT DEVELOPMENT
AND STRESS RESPONSE

Joan Manel Lopez Tubau | 2024

UNIVERSITAT DE BARCELONA

FACULTAT DE FARMÀCIA I CIÈNCIES DE L'ALIMENTACIÓ

PROGRAMA DE DOCTORAT: BIOTECNOLOGIA

ROLE OF CONJUGATED STEROLS HOMEOSTASIS IN PLANT DEVELOPMENT
AND STRESS RESPONSE

Memòria presentada per Joan Manel Lopez Tubau per optar al títol de doctor per la
universitat de Barcelona

Dr. Albert Ferrer i Prats
Director i Tutor

Dr. Teresa Altabella Artigas
Directora

Joan Manel Lopez Tubau
Doctorand

"Somewhere, something incredible is waiting to be known."

— **Carl Sagan**

Agraïments

El destí em tenia reservada una “bona nova” que mai hagués imaginat. No volies ser cuiner? No volies inventar coses? No volies aprendre i explicar tot el que sabies i molt més a qualsevol persona? – Si que ho volia, però pogués viatjar al passat i veure el petit Joanet que estava creixent, no li donaria cap detall de tot el que passaria. Totes les coses s’han alineat perquè acabes escrivint una tesi sobre tomàquets, mentre un virus mundial es propagaria i que ames, viuria un temps a Barcelona per fer la carrera, després aniria a viure a Manresa per establir la meva nova base familiar i emprendre el meravellós regal de fer una tesis doctoral, i mentrestant, viuria uns mesos a Múrcia i Estrasburg. Fer el que t’apassiona no te preu però no sols és fer-ho, sinó veure qui t’acompanya i quines persones han fet d’aquests 5 anys un temps memorable, per això vull dedicar aquestes paraules a totes aquestes persones.

Primerament, vull agrair als meus directors de tesi, el Dr. Albert Ferrer i la Dra. Teresa Altabella. Encara recordo quan vaig començar amb ells sent estudiant de grau i vaig fer tot el possible per fer el màxim de hores practiques en el seu grup. I quan vaig pensar que l’aventura s’acabava vaig rebre un correu meravellós dient que hi havia una plaça de predoc al seu grup, i va ser aquí on va començar tota aquesta meravella. Aquesta tesis així com tot el meu aprenentatge, no hauria estat possible sense la seva tutela, la seva orientació, consells i tots aquells moments d’exigència que tot i fer venir maldecap a vegades, han estat per donar bons fruits. Agraeixo la confiança i el suport en tots els aspectes, a vegades fora dels terme purament de la tesi que han demostrat que a part de directors de tesis han estat un pilar un acompanyament imprescindible per mi.

També agraeixo a la Dra. Micaela Carvajal i al Dr. Hubert Schaller tot el suport i escalf que van donar-me en les estades fora del CRAG i que vam permetre’m créixer i aprendre un pilot sota el paraigües d’excel·lents científics i meravelloses persones. “Muchas gracias Mica por la cena del primer día y por todo el buen rollo y apoyo que me diste durante mi estancia” i “Je tiens à remercier Hubert pour l'excellent stage de formation à Strasbourg et pour avoir organisé une excursion en canoë. Ce fut une expérience absolument merveilleuse.

Moltes gràcies a la meva família del 203, ha set un enorme i gegant meravella que ha maximitzat tots els meus èxits i ha escoltat totes les meves desgracies. A l’Alma Burciaga, qui va tutelar la meva estada com estudiant i qui va demostrar-me que amb esforç i resiliència les coses es tiren endavant i que si amés es fa amb bona actitud, tot resulta mes favorable. A Laura Gutiérrez, qui a part de ser una “senyora” a qui li he de regalar Chupa Chups, has estat una bona consellera i una excel·lent organitzadora del laboratori (1000 gracies per tots els

estocs i llistes que vas fer i que seguim utilitzant gràcies al teu esforç). A l'Àngel de Jesús, qui tot i tenir una pandèmia de per mig va ajudar-me i donar-me suport durant tot el seu temps al CRAG. A en Kostadin, qui tot i estar sempre revolucionat aïllant endòfits i seqüenciant-los sempre tenia una estoneta pel cafè i descansar el cap quan les coses no sortien com jo volia. A la Cuiyun Deng, una noia que va arribar i era molt vergonyosa, amb qui al inici gairebé ni ens enteníem; Recordo encara pensar que treballava amb llavors de Labitorsi de Colòmbia, però no, era Arabidopsis i era Col-0. Qui ho diria que persones tan diferents farien l'esforç tots plegats de generar un ambient tan maco i que aniríem a dinar i sopar junts, a fer bubble tea, a fer cafès, etc i sobretot a ajudar-nos mútuament amb la feina. No he conegut mai algú tan generós com tu Cuiyun 谢谢崔云!

A la Fernanda i la Chen a qui els hi desitjo el millor i els hi dono molts ànims per acabar la tesis. A la Jacqueline Freire que tot i no ser del 203, vam adoptar-la un bon temps. Una amiga amb totes les paraules amb qui hem rigut molt junts, ens hem donat suport en els mals moments i ho hem tirat tot endavant! Ànims amb la portulaca i sobretot "Que chévere haberte conocido". Agrair també a tots els del grup de l'Ivan per la pinya que fèiem. A tots i totes les estudiants que han passat pel laboratori, gràcies a l'Elena, Elisabetta, Carmen, Clàudia, Maria, Susana, Sergi, Amaia, per la vostra dedicació i esforç. També agraeixo al personal del CRAG que han col·laborat activament en tot aquesta feina. A la Pilar i Eva per l'obtenció de plantes, a la Montse Amenós pels 100000 consells en confocal, a la Joana Ribes per la seva simpatia i disposició sempre a ajudar quan es necessitava fer una RT-qPCR, a la Natalie per tot el suport amb la metabolòmica i sobretot a la Natalia Berbis, amb qui fem un equip genial!

A tots els qui m'heu donat suport fora del laboratori, a la mama Pilar i el papa Santi, a la meva germana Irene, al cunyat Sergi i el millor nebot de l'univers, l'Axel, no se que hauria fet sense la vostra aprovació i la bona actitud que heu tingut sempre envers a mi. Al Ruben, per tenir la santa paciència de suportar-me a casa (i el que li queda) i voler compartir tota la vida a mi. A la Julia i la Mireia per alegrar-me sempre la vida des de els primers dies d'universitat. A la Judit Santacana qui va animar-me a anar al CRAG i a en Pau i en Lluís que s'han convertit en un suport esplèndid en tot aquest procés! Segur que em deixo a algú per no existeixen suficients paraules per agrair tot l'amor i el suport. Per fi! Ja ho hem fet!

Summary

Phytosterols are a family of triterpenoid compounds that occur in free form (FS) or conjugated as sterol esters (SE), sterol glycosides (SG) and acylated sterol glycosides (ASG). Free sterols and their glycosylated derivatives are structural components of the cell membranes that play a key role in maintaining their fluidity and permeability, while SE are stored in cytoplasmic lipid droplets, where they serve as a reservoir of sterols that can be accumulated or mobilized depending on the cellular needs. In SG, the C3 hydroxyl group of the sterol backbone is linked through a glycosidic bond to a sugar moiety, which may have a long-chain fatty acid esterified to the hydroxyl group at position C6 leading to ASG. The hydroxyl group of FS can also be esterified to a long-chain fatty acid producing SE. FS are the common precursors of SG and SE, which are synthesized by the UDP-glucose:sterol glycosyltransferases (SGT) and the acyl-CoA/phospholipid:sterol acyltransferases (ASAT/PSAT), respectively. These enzymes have been cloned and characterized in different plants, including tomato, where our group has characterized SlASAT1, SlPSAT1 and the four SGTs (SlSGT1-SlSGT4). However, the specific role of these enzymes in the conjugated sterol metabolism is still not well understood. To investigate the biological function of conjugated sterols, in this thesis we have used tomato CRISPR/Cas9 *slpsat1*, *slasat1* and *slpsat1xslasat1* knock-out mutants, and SlSGT3 overexpressing plants (SlSGT3-ox) to investigate how changes in the profile of conjugated sterols may affect tomato growth and development and its response to biotic stress.

The characterization of *slpsat1* and *slasat1* single and double knock-out mutants revealed that SlPSAT1 has a predominant role in tomato SE biosynthesis while SlASAT1 would mainly regulate the flux of the sterol pathway. The strong reduction of SE levels in the leaves, fruits and seeds associated to PSAT1 and ASAT1 inactivation affect in different ways several important cellular and physiological processes, leading to reduced leaf number of lipid droplets, enhanced seed germination speed, early leaf senescence, reduction of the overall plant size, and increased resistance of fruits to *Botrytis cinerea* infection. Analysis of the overall profile of free and conjugated sterols in fruits and seeds of the *slpsat31 x slasat34* mutant revealed also different qualitative and quantitative effects on the composition of free and glycosylated sterols. While in fruits impaired SE biosynthesis resulted in higher levels of FS and SG and lower levels of ASG compared to the WT, no changes were observed in seed FS levels while those of SG and ASG increased drastically. Moreover, the impact of the changes in sterol composition on the metabolome of fruit and seeds has been studied, and the results have shown a differential impact on fruit and seed metabolomes, although in both

cases disruption of the free and conjugated sterol balance in the *slpsat31* x *slasat34* mutant induces autophagy in both organs.

SISGT3-ox plants show a significant increase in SG levels, accompanied by a marked reduction in SE in both leaves and fruits. This resulted in a strong vegetative phenotype characterized by a clear dwarfism and thickening of the internodes, while fruits are firmer than WT fruits and show a marked delay in ripening, which is most likely due to a delay in the peak of ethylene production. These results, along with the triple response to ethylene observed in SISGT3-ox seedlings, suggests a relationship between SG and the synthesis and/or perception-sensitivity to this hormone. To gain some insight about the molecular mechanisms underlying these physiological effects, we performed a transcriptomic analysis of SISGT3-ox seedlings. The results showed a misregulation, among others, of genes involved in developmental processes, cell wall biogenesis, cytoskeleton and organelle organization, detoxification and responses to different stimuli, that might help to explain some of the observed phenotypes.

To obtain fruits equivalent to those in SISGT3-ox plants, but avoiding the observed alterations in plant development, plants overexpressing SISGT3 under E8 fruit specific ethylene responsive promoter have been generated and preliminary characterized.

Finally, a method for isolating lipid rafts from leaves and roots has been set up. This will allow the study of the effects of altered levels of sterols on the lipid and protein composition of these plasma membrane subdomains, which have been reported to be involved in a variety of plant cell biological processes. To gain further insight on the intracellular localization of sterols some preliminary analysis of the spatial distribution of sterols have been carried out using MALDI-MSI analysis.

Altogether, the results obtained in this work demonstrate that conjugated sterols play an important role in the growth and development of tomato plants and fruits, as well as in the plant response to biotic stress. The results of this thesis project have set the basis for further studies aimed at deciphering the molecular mechanisms underlying the perturbations observed in these physiological processes.

Resum

Els fitosterols són una família de compostos triterpenoides que es troben en forma lliure (FS) o conjugada com a esteril èsters (SE), esteril glucòsids (SG) i acil esteril glucòsids (ASG). Els esterols lliures i els seus derivats glicosilats són components estructurals de les membranes cel·lulars que juguen un paper clau en el manteniment de la seva fluïdesa i permeabilitat, mentre que els SE es guarden en gotes lipídiques citoplasmàtiques, on actuen com a reservori que es poden acumular o mobilitzar segons les necessitats cel·lulars. En els SG, el grup hidroxil C3 de l'esquelet està unit mitjançant un enllaç glicosídic a un grup de sucre, que pot tenir un àcid gras de cadena llarga esterificat al grup hidroxil en la posició C6, formant així un ASG. El grup hidroxil dels FS també es pot esterificar amb un àcid gras de cadena llarga, produint SE. Els FS són els precursors comuns dels SG i SE, que es sintetitzen mitjançant les UDP-glucosa glicosiltransferases (SGT) i les acil-CoA/fosfolípid aciltransferases (ASAT/PSAT), respectivament.

Aquests enzims s'han clonat i caracteritzat en diferents plantes, incloent el tomàquet, on el nostre grup ha caracteritzat SLASAT1, SIPSAT1 i les quatre SGT (SISGT1-SISGT4). No obstant això, el paper específic d'aquests enzims en el metabolisme d'esterols conjugats encara no es comprèn bé. Per investigar la funció biològica dels esterols conjugats, en aquesta tesi hem utilitzat mutants knock-out de tomàquet CRISPR/Cas9 *slpsat1*, *slasat1* i *slpsat31* $\times$ *slasat34*, així com plantes sobreexpresores de SISGT3 (SISGT3-ox) per investigar com els canvis en el perfil d'estèrils conjugats poden afectar el creixement i desenvolupament del tomàquet i la seva resposta a l'estrès biòtic.

La caracterització dels mutants knock-out individuals i dobles de *slpsat1* i *slasat1* ha revelat que SIPSAT1 té un paper predominant en la biosíntesi de SE al tomàquet, mentre que SLASAT1 regula principalment el flux de la via d'esterols. La reducció important dels nivells de SE en les fulles, fruits i llavors associada a la inactivació de PSAT1 i ASAT1 afecta de diferents maneres diversos processos cel·lulars i fisiològics importants, conduint a una reducció del nombre de gotes lipídiques a les fulles, una velocitat de germinació de llavors augmentada, una senescència foliar prematura, una reducció de la mida global de la planta i una major resistència dels fruits a la infecció per *Botrytis cinerea*. L'anàlisi del perfil global d'esterols lliures i conjugats en fruits i llavors del mutant *slpsat31* $\times$ *slasat34* també ha revelat diferents efectes qualitius i quantitius en la composició d'estèrils lliures i glicosilats. Mentre que en els fruits la biosíntesi deteriorada de SE resulta en nivells més alts de FS i SG i nivells més baixos d'ASG en comparació amb el WT, no s'han observat canvis en els nivells

de FS a les llavors, mentre que els nivells de SG i ASG han augmentat dràsticament. A més, l'impacte dels canvis en la composició d'estèrils en el metabolisme dels fruits i llavors ha estat estudiat, i els resultats han mostrat un impacte diferencial en el metabolisme de fruits i llavors, tot i que en ambdós casos la alteració de l'equilibri d'estèrils lliures i conjugats en el mutant *slpsat31 x slasat34* indueix autofàgia en ambdós òrgans.

Les plantes *SlSGT3-ox* mostren un augment significatiu en els nivells de SG, acompanyat d'una reducció marcada en SE tant a les fulles com als fruits. Això resulta en un fenotip vegetatiu fortament caracteritzat per un nanisme clar i un engruiximent dels entrenusos, mentre que els fruits són més fermes que els fruits WT i mostren un retard marcat en la maduració, que probablement es deu a un retard en el pic de producció d'etilè. Aquests resultats, juntament amb la resposta triple al etilè observada en les plàntules *SlSGT3-ox*, suggereixen una relació entre SG i la síntesi i/o percepció-sensibilitat a aquesta hormona. Per obtenir informació sobre els mecanismes moleculars subjacents a aquests efectes fisiològics, vam realitzar una anàlisi transcriptòmica de les plàntules *SlSGT3-ox*. Els resultats van mostrar una desregulació, entre d'altres, de gens implicats en processos de desenvolupament, biogènesi de la paret cel·lular, organització del citoesquelet i orgànuls, desintoxicació i respostes a diferents estímuls, cosa que podria ajudar a explicar alguns dels fenotips observats.

Per obtenir fruits equivalents als de les plantes *SlSGT3-ox*, però evitant les alteracions observades en el desenvolupament de la planta, s'han generat i caracteritzat preliminarment plantes amb sobreexpressió de *SlSGT3* sota un promotor específic de fruites E8 sensible al etilè.

Finalment, s'ha establert un mètode per aïllar rafts lipídics de fulles i arrels. Això permetrà l'estudi dels efectes de nivells alterats d'estèrils sobre la composició lipídica i proteica d'aquests subdominis de la membrana plasmàtica, els quals s'han informat com a implicats en diversos processos biològics cel·lulars de plantes. Per obtenir més informació sobre la localització intracel·lular dels estèrils, s'han realitzat algunes anàlisis preliminars de la distribució espacial dels estèrils utilitzant l'anàlisi MALDI-MSI.

En conjunt, els resultats obtinguts en aquest treball demostren que els esterols conjugats juguen un paper important en el creixement i desenvolupament de les plantes i fruits de tomàquet, així com en la resposta de la planta a l'estrès biòtic. Els resultats d'aquest projecte de tesi han establert les bases per a futurs estudis encaminats a desxifrar els mecanismes moleculars subjacents a les alteracions observades en aquests processos fisiològics.

Contents

1.	INTRODUCTION	1
1.1.	Structure and function of sterols	1
1.2.	Biosynthesis of phytosterols.....	5
1.3.	Conjugated sterols in plants	9
1.4.	Steryl glycosides	10
1.5.	Sterol glycosyltransferases	12
1.6.	Steryl esters	14
1.7.	Sterol acyltransferases	16
1.8.	Role of sterols in plant growth and development.....	18
1.9.	Sterols and plant response to stress	20
1.10.	Tomato, agronomic crop and research plant model	23
2.	OBJECTIVES.....	25
2.1.	General Objective.....	25
2.2.	Detailed objectives.....	25
3.	RESULTS	27
3.1.	CHAPTER I.....	27
	Role of steryl ester biosynthesis on plant growth and developmental processes	27
3.1.1.	Generation of tomato <i>slpsat31</i> $\times$ <i>slasat34</i> double knock-out mutants	27
3.1.2.	Effect of SIPSAT1 and SIASAT1 inactivation on the sterol profile of tomato leaves.....	29
3.1.3.	Effect of SIPSAT1 and SIASAT1 inactivation on lipid droplet abundance in tomato leaves.....	32
3.1.4.	Knock-out mutants <i>slpsat1</i> and <i>slpsat31</i> $\times$ <i>slasat34</i> exhibit reduced size and early leaf senescence	34
3.1.5.	Effect of SIPSAT1 and SIASAT1 inactivation on the sterol profile of tomato seeds	38
3.1.6.	Tomato SIPSAT1 and SIASAT1 gene mutations increase the germination speed	41
3.1.7.	Effect of SIPSAT1 and SIASAT1 inactivation on the sterol profile of tomato mature fruit	43
3.1.8.	Effect of impaired steryl ester biosynthesis on tomato fruit quality	47
3.1.9.	Altered sterol levels cause organ specific metabolic perturbations in fruits and seed... ..	50
3.2.	CHAPTER II	61
	From germination to fruit: Unraveling the role of SISGT3 on tomato (<i>Solanum lycopersicum</i> cv MicroTom) plant growth and development	61
3.2.1.	Generation of tomato plants expressing the GUS reporter gene under native <i>SISGT3</i> promoter	61

3.2.2.	Histochemical assay of GUS enzyme activity in proSlSGT3::GUS transgenic tomato lines	63
3.2.3.	Generation of tomato (<i>Solanum lycopersicum</i> cv MicroTom) plants overexpressing sterol glucosyltransferase 3 (SGT3)	65
3.2.4.	Characterization of SlSGT3-ox plants.....	67
3.2.4.1.	Expression analysis of SlSGT3 in leaves of SlSGT3-ox plants.....	67
3.2.4.2.	Sterol profile in leaves of SlSGT3-ox plants.....	68
3.2.4.3.	Effect of SlSGT3 overexpression on tomato vegetative development..	71
3.2.4.4.	Expression analysis of SlSGT3 in red fruits of SlSGT3-ox plants	74
3.2.4.5.	Sterol profile in red fruits of SlSGT3-ox plants	75
3.2.4.6.	Effect of SlSGT3 overexpression on tomato fruit size.....	78
3.2.4.7.	Overexpression of SlSGT3 affects seed germination and viability.....	80
3.2.4.8.	Ethylene triple response in transgenic tomato seedlings.....	82
3.2.4.9.	Transcriptional profiling of SlSGT3-ox seedlings.....	84
3.2.4.10.	Altered sterol levels cause metabolic perturbations in fruits.....	91
3.2.5.	Generation of E8::SlSGT3 tomato plants.....	96
3.2.6.	Expression analysis of SlSGT3 mRNA in fruits of proE8::SlSGT3 plants	97
3.2.7.	Characterization of the phenotype of pE8::SlSGT3 plants.....	98
3.3.	CHAPTER III.....	101
	Characterization of sterol spatial distribution in tomato plants: a focus on detergent-resistant membranes and histological 27-Alkyne Cholesterol Detection.....	101
3.3.1.	Characterization of lipid rafts (LR) in tomato leaves and roots	101
3.3.2.	Isolation of PM, DRM and DSF Fractions	101
3.3.3.	Determination of sterol profiles in leaves and roots of tomato plants.....	103
3.3.4.	Ultrastructural analysis of tomato leaves and roots PM and DRM.....	106
3.3.5.	Cellular imaging of phytosterols.....	109
3.3.5.1.	In situ location of sterols and derivative compounds on tomato plants	109
3.3.5.2.	Subcellular localization of 27-Alkynecholesterol-Azide adduct on tomato stems	112
4.	DISCUSSION.....	115
4.1.	Chapter I	115
4.1.1.	Generation and sterol profiling of tomato <i>slpsat31</i> x <i>slasat34</i> double knock-out mutant.....	115
4.1.2.	<i>Slpsat1</i> and <i>slpsat31</i> x <i>slasat34</i> knock-out mutants exhibit reduced size an early leaf senescence phenotype	119
4.1.3.	SE levels lead to divergent patterns of LD formation in tomato leaves ...	120
4.1.4.	Tomato <i>slpsat1</i> and <i>slasat1</i> mutations increase the germination speed.....	121
4.1.5.	Altered sterol levels cause organ specific metabolic perturbations in fruits and seeds..	123

4.1.6.	Fruits of the <i>slsat31</i> x <i>slpsat34</i> mutant show enhanced resistance to <i>B. cinerea</i> infection	126
4.2.	Chapter II.....	127
4.2.1.	Overexpression of SLSGT3 affects tomato plant growth and development	127
4.2.2.	Overexpression of SLSGT3 results in an increase of SG levels shifting specie composition in red tomato fruits negatively affecting fruit size and seed set.	131
4.2.3.	Overexpression of SLSGT3 results in delayed fruit ripening and differential ethylene-sensing	136
4.3.	Chapter III	139
4.3.1.	Characterization of LR in tomato leaves and roots	139
4.3.2.	Sterol localization in tomato plants tissues	144
5.	CONCLUSIONS.....	146
6.	MATERIALS AND METHODS.....	150
6.1.	Microbiological material.....	150
6.1.1.	Bacterial strains.	150
6.1.2.	Culture media	150
6.1.3.	Bacterial strains transformation.....	151
6.2.	Tomato (<i>Solanum lycopersicum</i>) cv. Micro-Tom cultivation	152
6.2.1.	Soil	152
6.2.2.	Hydroponic conditions	152
6.2.3.	Axenic culture	153
6.3.	Molecular methods and analysis	154
6.3.1.	Genomic DNA extraction.....	154
6.3.2.	Miniprep extraction for plasmid DNA.....	155
6.3.3.	Amplification of DNA fragments by polymerase chain reaction (PCR)...	155
6.3.4.	Analysis of recombinant clones by colony PCR	157
6.3.5.	Gene expression analysis by RT-qPCR.....	157
6.3.6.	Gene copy number analysis by qPCR.....	158
6.4.	Generation of transgenic tomato lines	160
6.4.1.	Generation of transgenic plants carrying the pSLSGT3::GUS transgene.	160
6.4.2.	Generation of transgenic plants carrying the CaMV35S::SGT3 transgene.	160
6.4.3.	Generation of transgenic plants carrying the pE8::SGT3 transgene.	161
6.5.	Generation of tomato <i>slpsat31</i> x <i>slsat34</i> double knock-out mutant	163
6.5.1.	Detection of CRISPR/Cas9-induced mutations in cross-pollinated <i>slpsat31</i> x <i>slsat34</i> mutant plants.....	163
6.6.	Tomato transformation.....	164
6.7.	Whole genome expression analysis by RNA-Seq	165

6.8.	Embryo analysis	166
6.9.	Lipid body staining	166
6.10.	Sterol Analysis	167
6.11.	Lipid raft isolation	169
6.11.1.	MF, PM, DRM and DSF fractions obtention	169
6.12.	ATPase activity.....	171
6.13.	Western blot analysis.....	173
6.14.	Matrix-Assisted Laser Desorption/Ionization Mass Spectrometry Imaging (MALDI-MSI imaging).....	175
6.14.1.	Tomato cv MicroTom feeding for sterol MSI imaging	175
6.14.2.	Cryosectioning for MALDI-MSI imaging	176
6.14.3.	MSI acquisition	176
6.15.	Tissue Fixation and Embedding.....	178
6.16.	Metabolite Extraction and Quantification.	180
6.16.1.	Procedure.....	180
6.16.2.	Data Processing and Compound Annotation and Analysis.	181
7.	Bibliography.....	182
8.	Supplemental material	221

LIST OF FIGURES

INTRODUCTION

Figure 1. Sterol basic chemical structure..	1
Figure 2. Chemical structure of the main phytosterols..	2
Figure 3. Distribution of sterols in the PM..	4
Figure 4. Simplified phytosterol biosynthesis pathway..	8
Figure 5. Biosynthesis of conjugated sterols from free sterols.....	9
Figure 6. <i>Botrytis cinerea</i> infection diagram. Physical/Chemical and hormonal responses of tomato plant response against fungi.....	22
Figure 7. Tomato fruit development.....	24

CHAPTER I

Figure 8. Electrophoresis gel.....	27
Figure 9. Total levels of SE and FS in leaves of <i>slpsat1</i> , <i>slasat1</i> , and <i>slpsat31</i> x <i>slasat34</i> mutants.	30
Figure 10. Intracellular presence of lipid droplets in leaf epidermal cells of WT, <i>slpsat28</i> , <i>slpsat31</i> , <i>slasat34</i> , <i>slasat35</i> and <i>slpsat31</i> x <i>slasat34</i> knock-out mutants.....	30
Figure 11. Phenotypic characterization of <i>slpsat28</i> , <i>slpsat31</i> , <i>slasat34</i> , <i>slasat35</i> and <i>slpsat31</i> x <i>slasat34</i> mutant plants..	35
Figure 12. Induced senescence assay using detached leaves maintained in darkness.	36
Figure 13. Total levels of free and conjugated sterols in seeds of <i>slpsat1</i> , <i>slasat1</i> , and <i>slpsat31</i> x <i>slasat34</i> mutants.	39
Figure 14. Germination rate of seeds from <i>slpsat1</i> , <i>slasat1</i> , and <i>slpsat31</i> x <i>slasat34</i> knock-out mutants.	42
Figure 15. Total levels of free and conjugated sterols in fruits of <i>slpsat1</i> , <i>slasat1</i> , and <i>slpsat31</i> x <i>slasat34</i> mutants.....	45
Figure 16. Physiological characteristics of red tomato fruit and seeds.	47
Figure 17. The <i>slpsat31</i> x <i>slasat34</i> fruits show enhanced resistance to <i>B. cinerea</i> infection....	48
Figure 18. Metabolic profile distribution in WT and <i>slpsat31</i> x <i>slasat34</i> tissue.....	50
Figure 19. Highlighted lipid abundance and distribution in <i>slpsat31</i> x <i>slasat34</i> and WT tissues.	52

Figure 20. Highlighted lipid abundance and distribution in <i>slpsat31</i> x <i>slsat34</i> and WT tissues.	53
Figure 21. Highlighted dipeptide abundance and distribution in <i>slpsat31</i> x <i>slsat34</i> and WT tissues.	54
Figure 22. Highlighted phenylpropanoid abundance and distribution in <i>slpsat31</i> x <i>slsat34</i> and WT tissues.	55
Figure 23. Differential metabolite abundance in <i>slpsat31</i> x <i>slsat34</i> versus WT in different tissues.	57
Figure 24. Differential metabolite pathways in <i>slpsat31</i> x <i>slsat34</i> versus WT in different tissues.	59

CHAPTER II

Figure 25. SLSGT3 promoter amplification and proSLSGT3::GUS transgene analysis.	62
Figure 26. Representative images showing histochemical detection of GUS enzyme activity in proSLSGT3::GUS tomato fruits at the indicated developmental stages.	63
Figure 27. Representative images showing histochemical detection of GUS enzyme activity of the proSLSGT3::GUS (line 42) tomato flowers and seeds.	64
Figure 28. Identification of 35SCaMV:SLSGT3:Tnos transgene insertion in transformed tomato plants	65
Figure 29. Expression levels of SLSGT3 in homozygous single transgene copy lines.	67
Figure 30. Content of free and conjugated sterol in leaves of WT and SLSGT3-ox lines.	68
Figure 31. Content of the main sterol species in leaves of tomato WT and SLSGT3 overexpressing lines.	69
Figure 32. Phenotype of plants overexpressing SLSGT3.	70
Figure 33. Morphometric analysis of SLSGT3-ox plants	73
Figure 34. Expression levels of SLSGT3 in red fruits of WT and SLSGT3-ox lines.	74
Figure 35. Content of free and conjugated sterol in red fruits of WT and SLSGT3-ox lines.	75
Figure 36. Content of the main sterol species in free and conjugated fractions in red fruits of from WT and SLSGT3-ox lines.	76
Figure 37. Phenotypic characterization of WT and SLSGT3-ox fruits.	78
Figure 38. Representative images of red matured fruits.	79
Figure 39. Phenotype and germination rate of seeds from SLSGT3-ox plants.	80

Figure 40. Seedling growth in darkness.	83
Figure 41. RNAseq results for tomato seedlings.....	84
Figure 42. Venn diagrams from log2 fold change (fc) ≥ 2 and ≤ 2 genes down and upregulated in seedlings of the SLSGT3-ox lines.....	88
Figure 43. Genes downregulated in seedlings of SLSGT3-ox considering a log2 fold change (fc) ≤ 2	89
Figure 44. Genes upregulated in seedling of the SLSGT3-ox considering a log2 fold change (fc) ≥ 2	90
Figure 45. Metabolic profile distribution in WT and SLSGT3-ox red tomato fruit pericarp.	91
Figure 46. Highlighted lipid abundance in SLSGT3-ox lines and WT tissues.	92
Figure 47. Highlighted metabolites abundance in pSLSGT3-ox lines and WT tissues.....	93
Figure 48. Identification of <i>E8::SLSGT3:Tnos</i> transgene insertion in transformed tomato plants.....	96
Figure 49. Expression levels of <i>SLSGT3 mRNA</i> in <i>E8::SLSGT3</i> homozygous transgenic lines.	97
Figure 50. Phenotype of Micro-Tom plants expressing SLSGT3 under control of the E8 promoter.....	98

CHAPTER III

Figure 51. H ⁺ ATPase western blot analysis.	102
Figure 52. Sterol composition from four isolated fractions.	103
Figure 53. Sterol composition from PM and DRM from leaves and roots.	105
Figure 54. Ultrastructural analysis of tomato leaves and roots PM and DRM.....	107
Figure 55. Distribution of plant metabolites annotated in <i>Solanum lycopersicum</i> cv MicroTom grown in hydroponic culture (control) and supplemented with 27-alkinecholesterol (27-ALK treated).....	109
Figure 56. High-performance thin-layer chromatography.....	113
Figure 57. Tomato stem confocal microscopy.....	114
Figure 58. Tomato seed and plant manipulation for 27-alkinecholesterol feeding.....	175

LIST OF TABLES

CHAPTER I

Table 1. FS and SE quantification in leaves of WT, <i>slasat34</i> , <i>slasat35</i> , <i>slpsat28</i> , <i>slpsat31</i> , and <i>slpsat31</i> x <i>slasat34</i> mutants.	31
Table 2. FS, SE, SG and ASG quantification in seeds of WT, <i>slasat34</i> , <i>slasat35</i> , <i>slpsat28</i> , <i>slpsat31</i> and <i>slpsat31</i> x <i>slasat34</i> mutants.....	40
Table 3. FS, SE, SG and ASG quantification in fruits of WT, <i>slasat1</i> , <i>slpsat1</i> and <i>slpsat31</i> x <i>slasat34</i> mutants.	46

CHAPTER II

Table 4. Internode length.	71
Table 5. Quantification of diameter and cell area in WT and line 9.....	83

CHAPTER III

Table 6. Number of days to reach the indicated fruit developmental stages, and the average number of seeds per fruit.....	99
Table 7. Protein concentration ($\mu\text{g/g}$ FW) in MF, PM, DRM and DSF from tomato leaves and roots.....	102
Table 8. PM and DRM vesicles size from tomato leaves and roots.....	108
Table 9. Standard detection ($10\mu\text{g/mL}$) performed by MALDI-MSI using different matrix composition.	111
Table 10. Mixture composition for in vitro alkyne-azide adduct formation.	113
Table 11. Antibiotics and supplements used in the preparation of media for bacterial cultures.	150
Table 12. Composition, stock concentration, and added volume of macronutrients and micronutrients in the Hoagland nutrient solution for hydroponic cultivation.....	152
Table 13. CTAB Composition and final concentration of CTAB buffer for DNA extraction	155
Table 14. Composition of the PCR mixture for plant genotyping.....	156
Table 15. Composition of the PCR mixture for DNA fragment amplification	156
Table 16. Composition of the PCR mixture for RT-qPCR DNA fragment amplification	157

Table 17. Primers used for genotyping and transgene copy number quantification in transgenic tomato plants and RT-qPCR.....	158
Table 18. Primers used to generate the different constructs into Gateway plasmids.	162
Table 19. Primers used to check the CRISPR/Cas9 mutations in the <i>shpsat31xslasat34</i> double knock-out mutants.....	164
Table 20. .Lipid raft buffers and enrichment separation phases composition.....	170
Table 21. Composition and concentration of the compounds used to generate the Pi slope	171
Table 22. Composition and concentration of the ATPase assay buffer.	172
Table 23. Composition and concentration of the loading buffer.	173
Table 24. Standards tested for MSI.....	177
Table 25. Composition, volume and concentration of the fixation buffer.	178

LIST OF ABBREVIATIONS

PM	Plasma membrane
ER	Endoplasmic reticulum
IPP	Isopentenyl diphosphate
DRM	Detergent-resistant membranes
DSF	Sterol-depleted detergent-soluble
DMAPP	Dimethylallyl diphosphate
MVA	Mevalonate pathway
MEP	Methylerythritol 4-phosphate pathway
HMG-CoA	3-hydroxy-3-methylglutaryl coenzyme A
AATC	Acetoacetyl-CoA thiolase
HMGS	3-hydroxi-3-methylglutaryl-CoA synthase
HMGR	3-hydroxy-3 methylglutaryl-CoA reductase
MVK	MVA kinase
PMK	Phospho-MVA kinase
MVAPP	MVA 5-diphosphate
MVD	MVAPP decarboxylase
IDI	IPP isomerase
FPS	Farnesyl diphosphate synthase
FPP	Farnesyl diphosphate
SQS	Squalene synthase
OS	2,3 oxidosqualene
SQE	Squalene epoxidase
CAS	Cycloartenol synthase
SSR2	Sterol side-chain reductase 2
SMT1/2/3	Sterol-methyltransferase 1, 2 and 3
FS	Free sterols
SE	Steryl esters
SG	Steryl glycosides
ASG	Acyl steryl glycosides
LD	Lipid droplet
ASAT	Acyl-CoA sterol acyltransferases
PSAT	Phospholipid:sterol acyltransferases
SGT	UDP-glucose:sterol glycosyltransferases

SGAT Sterol glycoside acyltransferase
JA Jasmonic acid
SA Salicylic acid
WT Wild-type
FPKM Fragments per Kilobase Million
FDR False discovery rate
GO gene ontology
DEGs differentially expressed genes
fc Fold change
TF transcription factors
TAG Triacylglycerols
MGDG monogalactosyldiacylglycerols
DGDG digalactosyldiacylglycerols
DAG diacylglycerols
lysoPC lysophosphatidylcholine
lysoPE lysophosphatidylethanolamine
SEM scanning electron microscope

1. INTRODUCTION

1.1. Structure and function of sterols

Sterols are isoprenoid-derived lipids present in all eukaryotic organisms, including higher plants. Their chemical structure is characterized by a cyclopentanoperhydrophenanthrene ring system, consisting of four rigid rings, with methyl substituents at positions C4, C10, C13 and C14 in some cases, a hydroxyl group at C3, and an aliphatic side chain of 8-10 carbon atoms attached to C17 (Ferrer et al., 2017) (Figure 1).

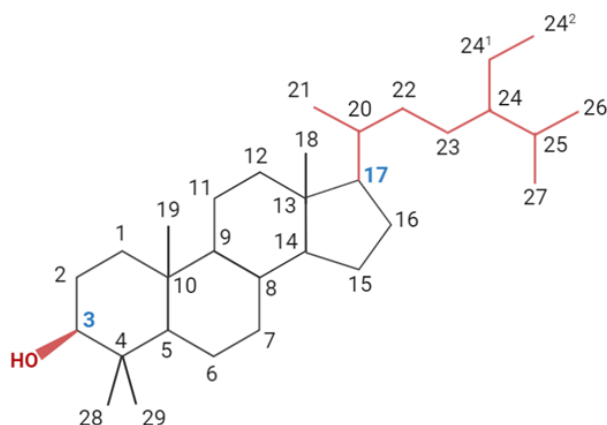


Figure 1. Sterol basic chemical structure. Carbon atoms are numbered according to IUPAC nomenclature 1989 (Moreau et al., 2018). The aliphatic side chain at C17 position is shown in red.

Animals produce only cholesterol as a predominant sterol, while fungi and plants exhibit a more diverse sterol composition (Desmond & Gribaldo, 2009). Fungi produce at least five different sterols, being ergosterol and fungisterol the major ones. In contrast, plants synthesize over 250 different sterols known as phytosterols (Darnet et al., 2021), which mainly differ in the nature of the C17 aliphatic lateral chain and the number and position of double bonds in the side chain and the ring skeleton, being β -sitosterol, stigmasterol and campesterol the most abundant species (Figure 2) (Nes, 2011; Ferrer et al., 2017; Zhang et al., 2020). Cholesterol is typically found in low amounts in plants, usually comprising less than 1% of the total sterols. However, certain plant families, such as the Solanaceae,

accumulate higher levels of cholesterol (Andersson et al., 2004; Kortner et al., 2014; Jaceldo-Siegl et al., 2017).

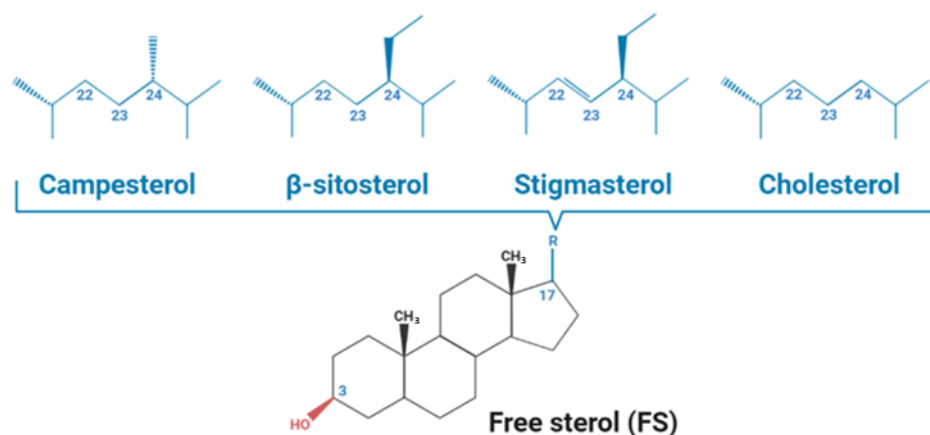


Figure 2. Chemical structure of the main phytosterols. Structural nucleus of free sterols (below) and aliphatic side chains (R) attached to position C17 (above) in the four major phytosterols: campesterol, β -sitosterol, stigmasterol and cholesterol (Adapted from Ferrer et al., 2017).

Phytosterols can also differ in the number of methyl substituents at the C4 position, leading to their classification as 4-desmethyl, 4-monomethyl, and 4,4-dimethyl sterols, being 4-desmethyl sterols the most abundant (Plat & Mensink, 2002). The structural diversity of plant sterols is further enhanced by alkylation at the C24 position of the aliphatic side chain attached to C17. Ethylation is more common (>70% of sterols) than methylation (>30% of sterols) (Field et al., 2004). Based on these structural variations, plant sterol can be categorized into three main groups: (1) 24-demethylsterols, which lack a C24 substitution, such as cholesterol (27 carbon atoms), (2) 24-methylesterols, containing a methyl group at the C24 position, as seen in campesterol (28 carbon atoms), and (3) 24-ethylsterols, with an ethyl group at C24, as it is the case of β -sitosterol and stigmasterol (29 carbon atoms) (Valitova et al., 2016). Additionally, the presence of double bonds in the side chain, usually between C22 and C23, contributes to the diversity of sterol species found in plant cells (Belin et al., 2018). This structural variability not only impacts membrane properties but also plays a crucial role in various cellular processes and plant signalling pathways (Ghosh, 2017). Phytosterols, along with glycerolipids (primarily phospholipids) and sphingolipids, are essential constituents of the plant cell plasma membrane (PM), where they interact with the hydrophobic fatty acid chains of other lipids, restricting their movement, a phenomenon known as the ordering effect (Dufourc., 2008). Consequently, the composition of sterols and their relative proportions play an important role in determining the biophysical properties of cell membranes, such as permeability, fluidity, and flexibility. Therefore, small alterations in

the sterol profile or arrangement can lead to significant variations in the mechanical properties of membranes, which can modulate the activity of membrane-linked proteins, including enzymes, transport channels, receptors, and other components involved in signal transduction pathways (Schaller, 2003; Hodzic et al., 2008). The crucial role of sterols in determining the physiochemical properties of cell membranes makes them important players in the adaptive responses of plants to abiotic (Roche et al., 2008; Chaturvedi et al., 2011; Dupont et al., 2011; Du et al., 2022; Warnecke et al., 1999) and biotic stresses (Wang et al., 2012; Kopischke et al., 2013; Castillo et al., 2019).

Sterols are not homogeneously distributed within the PM. Their interaction with other membrane lipids, particularly sphingolipids, and specific membrane proteins that do not diffuse freely through the lipid bilayer, but are laterally segregated into dynamic nanoclusters, leads to the formation of specialized microdomains known as lipid rafts (Figure 3) (Malinsky et al., 2013; Garcia-Parajo et al., 2014; Tapken and Murphy., 2015; Sezgin et al., 2017; Jaillais & Ott et al., 2019). These microdomains are also known as detergent-resistant membranes (DRM) because they have low solubility in ionic detergents like Triton X-100 (Schayek, 2003; Wachtler et al., 2003). Proteomic analysis of plant DRM has revealed differential protein composition when compared to the overall PM proteome, which suggests a role in several biological processes such as cell-to-cell interactions, membrane transport, protein trafficking, signal transduction, stress responses, and polarized growth (Figure 3) (Zhang et al., 2016; Zhou et al., 2017; Sartorel et al., 2018; Platre et al., 2019; Lange et al., 2020; Dedo et al., 2021). The presence of anionic lipids, such as phosphatidylserine, in these microdomains also affect their signalling properties. In tomato the presence of proteins, like GRAIN SETTING DEFECT1 and REMORINS in lipid rafts and plasmodesmata affects callose homeostasis and modulate plant development and defense responses (Ediriweera et al., 2020; Mongrand et al., 2004).

The biological functions of phytosterols vary among different sterol species. For example, β -sitosterol and stigmasterol are primarily maintaining the structure and stability of the PM, while campesterol serves as a precursor for brassinosteroids, which are essential plant hormones that regulate growth, development, and stress responses (Tjellström et al., 2009; Ovečka et al., 2010). Additionally, cholesterol not only is a structural membrane component, as in animals, but also acts as a precursor for specialized triterpenoid metabolites like saponins and steroidal glycoalkaloids, which have potential pharmacological activity and/or toxicity in animals (Milner et al., 2011; Silvestro et al., 2013; Sonawane et al., 2016).

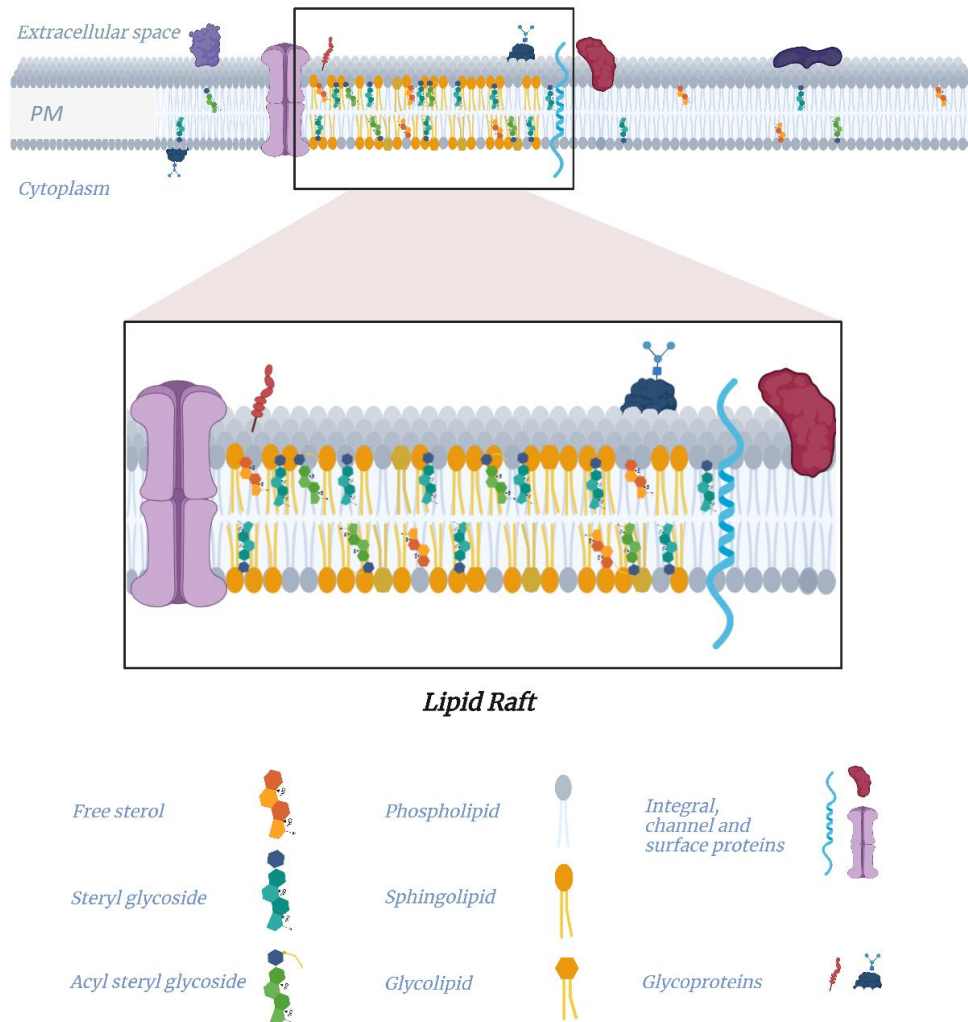


Figure 3. Distribution of sterols in the PM. Representation of free sterols, steryl glucosides and acyl steryl glucosides in lipid rafts, which are highly dynamic specialized domains on the PM enriched on sphingolipids, glycolipids and sterols.

1.2. Biosynthesis of phytosterols

As previously mentioned, sterols are isoprenoid-derived lipids and, consequently, are synthesized from isopentenyl diphosphate (IPP) and dimethylallyl diphosphate (DMAPP), which are the common precursors for all terpenoids (Kuzuyama, 2017). In plants, these isomers are produced through two distinct metabolic pathways: the mevalonate pathway (MVA) that take place in the cytosol/endoplasmic reticulum (ER), and the methylerythritol 4-phosphate pathway (MEP) that operates in plastids (Rodríguez-Concepción and Boronat, 2002). Despite their spatial separation, there are some interactions between both pathways at molecular and metabolic levels, and some exchange of IPP and DMAPP between them can occurs in some circumstances, likely to facilitate the coordinated synthesis of a wide array of terpenoids from a single common substrate (Boronat, 2010). The precursors for plastid isoprenoids, including chlorophylls and carotenoids, are synthesized through the MEP pathway, highlighting its importance in plant metabolism (Carretero-Paulet et al., 2006).

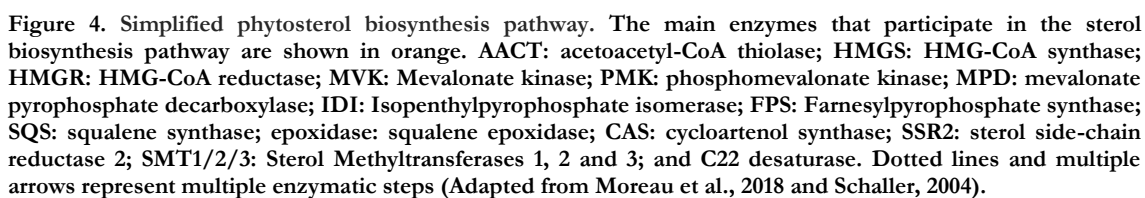
Sterols are synthesized from precursors derived from the mevalonate (MVA) pathway (Aboobucker and Suza, 2019). The biosynthesis of IPP begins with the condensation of three acetyl-CoA molecules to form 3-hydroxy-3-methylglutaryl coenzyme A (HMG-CoA), which is catalyzed by acetoacetyl-CoA thiolase (AATC) and 3-hydroxy-3-methylglutaryl-CoA synthase (HMGS) in the cytosol (Bach and Benveniste, 1997). HMG-CoA is subsequently converted into MVA in a NADPH-dependent reaction mediated by the rate-limiting enzyme 3-hydroxy-3-methylglutaryl-CoA reductase (HMGR), thereby regulating the synthesis of isoprenoid end-products such as sterols. HMGR is anchored to the ER membrane, which is important to modulate its activity, mediated by the catalytic domain facing the cytosol (Pulido et al., 2012; Vranová et al., 2013; Tholl, 2015). Finally, MVA is transformed into IPP through a series of enzymatic reactions: MVA kinase (MVK) and phospho-MVA kinase (PMK) catalyze two phosphorylation steps to yield MVA 5-diphosphate (MVAPP), which through an ATP-dependent decarboxylation mediated by MVAPP decarboxylase (MVD) generates IPP, which is isomerized into DMAPP by IPP isomerase (IDI).

The sequential condensation of one molecule of DMAPP with two units of IPP by farnesyl diphosphate synthase (FPS) leads to the production of farnesyl diphosphate (FPP) in the cytosol. FPP acts as a precursor for various branches of the cytosol-ER isoprenoid pathway, resulting in the formation of a diverse array of end products, including sesquiterpenes such as sesquiterpenoid phytoalexins, long-chain prenyl-diphosphates like dolichols and polyprenols, and triterpenes like sterols and brassinosteroids Furthermore, FPP also acts as

a substrate for protein prenylation. The condensation of two FPP units by squalene synthase (SQS) results in the synthesis of squalene, a polyunsaturated aliphatic C₃₀ hydrocarbon that is the initial committed precursor of the sterol triterpene biosynthetic pathway. Squalene oxidation produces 2,3 oxidosqualene (OS) in a reaction catalyzed by squalene epoxidase (SQE), which is the first oxygenation step in the sterol biosynthesis pathway. The enzymatic reactions leading to OS from acetyl-CoA are common to all eukaryotic organisms. However, from OS the plant sterol biosynthetic pathway diverges from those of fungi or mammals and is mediated by specific steps restricted to plants (Benveniste, 2002; Vranová et al., 2013; Piironen et al., 2000; Aboobucker and Suza, 2019). Thus, cycloartenol synthase (CAS) catalyzes the cyclization of OS to produce cycloartenol instead of lanosterol, which is the first cyclic intermediate in fungal and mammalian sterol biosynthesis (Hartmann, 1998; Schaller, 2003). The flux regulation of the different branched pathways leading to the main sterol end-products is controlled at specific steps (Figure 4). Cycloartenol is the first metabolite susceptible to be converted in two different compounds by the action of sterol side-chain reductase 2 (SSR2) and sterol methyltransferase 1 (SMT1). SSR2 converts cycloartenol to cycloartanol and directs the flux of the precursors towards the cholesterol branch, which involves unique but also shared enzymes with other branches of the sterol pathway. On the other hand, SMT1 catalyzes the alkylation of cycloartenol to 24-methylenecycloartanol, generating precursors for the synthesis of plant-specific sterols, like β -sitosterol, stigmasterol and campesterol (Sonawane et al., 2016; Benveniste, 2002). Reactions downstream SMT1 proceed linearly until the formation of 24-methylenelophenol, where another branching point is found. The 24-methylenelophenol could be considered a specific precursor of campesterol biosynthesis, while the sterol-methyltransferases 2 and 3 (SMT2/3) convert it to 24-ethylidenelophenol, directing carbon flux towards β -sitosterol and stigmasterol biosynthesis, and allows plants to produce 24-ethyl sterols as the major molecular species (Figure 4) (Benveniste, 2002; Schaller, 2003; Carland et al., 2010). β -Sitosterol is converted to stigmasterol in a reaction catalyzed by C22 desaturase, which is the final step in this branch of the phytosterol biosynthesis pathway (Schaller, 2004). This last reaction is essential for maintaining PM structure, since β -sitosterol and stigmasterol play important roles in regulating its dynamic properties (Schuler et al., 1991). Moreover, the balance between 24-methyl and 24-ethyl sterols has been reported to impact plant growth and development (Valitova et al., 2016).

Most of the reactions involved in the sterol biosynthetic pathway occur in the ER. However, sterols predominantly accumulate in the PM, which suggest the existence of a transport

mechanism between these two membranous systems. In fact, compared with other cell endomembranes, the PM exhibits the highest sterol content relative to the corresponding levels of proteins and phospholipids (Yamauchi et al., 2007).



1.3. Conjugated sterols in plants

In plants, sterols are present not only as free sterols (FS) with a β -hydroxyl group at the C3 position of the sterol backbone, but also in conjugated forms such as steryl esters (SE), steryl glycosides (SG) and acyl steryl glycosides (ASG) (Silvestro et al., 2013). SE have the hydroxyl group at the C3 position esterified with a fatty acid, while in SG and ASG, the hydroxyl group at C3 is linked to a sugar through a β -glycosidic bond. ASG are derivatives of SG where the C6 position in the sugar moiety is esterified with a fatty acid (Figure 5) (Silvestro et al., 2013). These different forms of sterols play distinct roles in the plant cell, while FS, SG, and ASG are structural components of the PM, SE are located in storage cytosolic compartments known as lipid droplets (LD) (Ferrer et al., 2017).

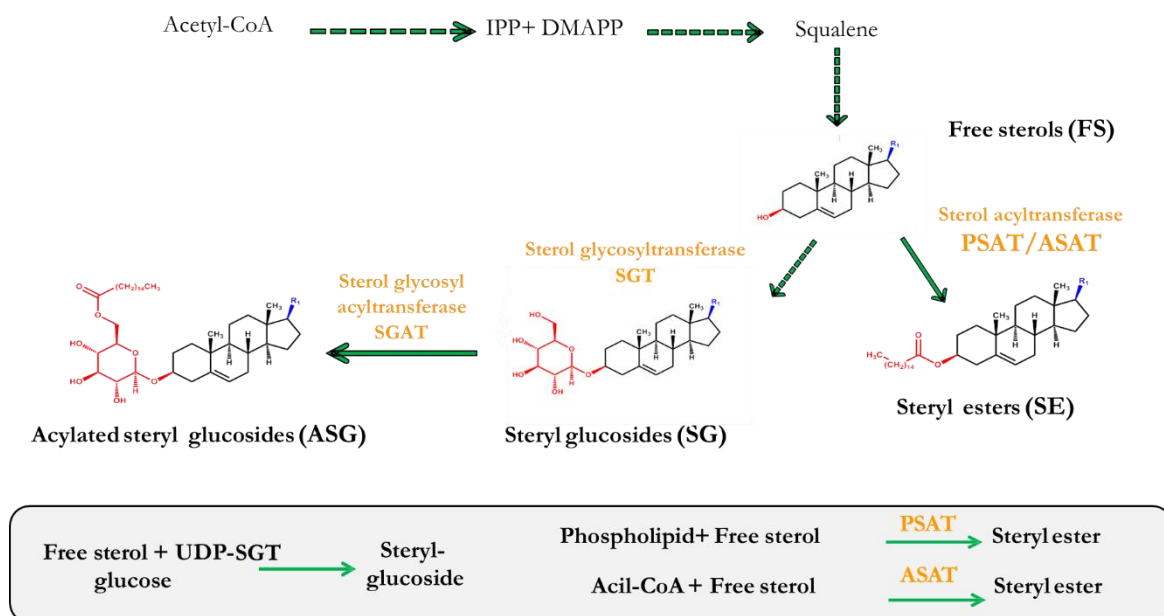


Figure 5. Biosynthesis of conjugated sterols from free sterols. Enzymes involved in the synthesis of conjugated sterols are shown in orange. SGT: UDP-glucose: sterol glucosyltransferase; SGAT: steryl glucoside acyltransferase; ASAT: acyl-CoA: sterol acyltransferase; PSAT: phospholipid: sterol acyltransferase. At the bottom, a summary of the main glycosylation and acylation reactions (Adapted from Ferrer et al., 2017).

1.4. Steryl glycosides

Glycosylated sterols (SG and ASG) are widely distributed in plants, but display variability in total content and relative proportions among different plant species, tissues, and in response to various developmental and environmental factors (Ferrer *et al.*, 2017). Moreover, the sterol profile of glycosylated sterols not always reflect the total sterol composition in the same plant tissue, indicating a preferential glycosylation of specific sterol species (Potocka & Zimowski, 2008). In most plant species SG and ASG are minor components, constituting approximately 10-30% of the total sterol content (Moreau *et al.*, 2002; Nyström *et al.*, 2012). However, plants of the genus *Solanum* are an exception due to the very high content of glycosylated sterols (Choi *et al.*, 2014), which in the case of tomato accounts for more than 85% of the total sterols in leaves and fruits (Moreau & Hicks., 2004). Furthermore, important changes in the quantity and profile of FS and conjugated sterols have been reported during tomato fruit ripening, chilling, and re-warming (Whitaker., 1994). The biological significance of the high content of glycosylated sterols in *Solanum* species is still not completely understood. It has been suggested that these compounds may contribute to maintaining cell membrane integrity against disruptive effects of the high levels of SGAs present in these plant species (Nyström *et al.*, 2007). In the case of tomato, the high levels of glycosylated sterols may explain why tomato tissues are able to withstand the high concentration of α -tomatine (Steel and Drysdale., 1988), a bioactive SGA found in all tomato organs, but especially abundant in the peel of green fruits (Barkai-Golan., 2001; Friedman., 2002; Iijima *et al.*, 2013).

Glycosylation serves to modify several compounds, including hormones, specialized metabolites, biotic and abiotic chemicals and environmental toxins, to maintain their cellular homeostasis (Guo *et al.*, 2023). This process not only helps to stabilize the target compounds but also influences their physiological activities and intracellular distribution (Lim & Bowler., 2004). Concerning sterols, the addition of a sugar moiety in SG reduces their hydrophobicity compared to FS, and potentially impact on their localization within cell membranes (Behr *et al.*, 2020). It has been proposed that the steroid nucleus of SG is embedded in the hydrophobic core of cell membranes, while the sugar moiety faces the polar head groups of the lipid bilayer oriented to the hydrophilic surface. In the case of ASG, both the sterol moiety and the fatty acid chain could be immersed in the hydrophobic phase of the membrane, with the sugar portion oriented towards the hydrophilic surface (Wewer *et al.*, 2014).

In addition to their structural role, glycosylated sterols have been suggested to function as glucose transporters and/or signaling molecules in plants (Nyström *et al.*, 2012). SG may

also serve as primers for ceramide glycosylation, indicating their involvement in lipid metabolism pathways (Itkin et al., 2011). Furthermore, glycosylated sterols have been reported to be essential for pollen viability in *Arabidopsis*, where they contribute to pollen coat maturation (McClements & Öztürk., 2021). On the other hand, an important amount of glycosylated sterols, mainly cholesterol and its glycosylated derivative, has been found in the phloem, although their precise biological role in this context remains unclear (Shiva et al., 2020).

1.5. Sterol glycosyltransferases

Sterol glycosides are synthesized by UDP-glucose:sterol glycosyltransferases (SGT), which attach sugar residues to the sterol backbone at the C3 position through a glycosidic bond (Figure 5). Although UDP-glucose is the major sugar donor for plant SGTs, other sugars like galactose, xylose, or mannose can also be used for FS glycosylation (Ferrer *et al.*, 2017). SG can be further modified to form ASG through the esterification of the hydroxyl group at the C6 of the sugar moiety with a long-chain fatty acid, a reaction catalysed by sterol glycoside acyltransferase (SGAT) (Figure 5) (Bouvier-Navé *et al.*, 2010). This enzyme activity has been reported in various plant species such as potato, tobacco, eggplant, *Calendula officinalis*, and carrot (Wojciechowski and Zimowski, 1975), but no genes encoding for SGATs have yet been identified in plants, animals, algae, fungi nor bacteria (Ferrer *et al.*, 2017).

The presence of SGT activity has been detected in several higher plants, and the reaction has been suggested to occur associated primarily with cell membranes, although soluble cytosolic SGTs have also been identified (Ramirez-Estrada *et al.*, 2017). However, SGTs have been cloned and functionally characterized in a few number of higher plants, including two in *Arabidopsis thaliana* (Warnecke *et al.*, 1997; DeBolt *et al.*, 2009), four in *Withania somnifera* (Madina *et al.*, 2007; Chaturvedi *et al.*, 2012), one in *Avena sativa* (Warnecke *et al.*, 1997), two in *Gossypium hirsutum* (Li *et al.*, 2014), one in *Gymnea sylvestre* (Tiwari *et al.*, 2014), and four in *Solanum lycopersicum* (Ramirez-Estrada *et al.*, 2017).

These studies have unveiled that most plant species contain small gene families encoding SGT isozymes, which can perform specialized functions. For instance, in *Arabidopsis*, the differential expression of the two genes encoding SGTs (*UGT80A2* and *UGT80B1*) has been associated with distinct substrate preferences towards the major phytosterols (Stucky *et al.*, 2015). In cotton, the two *GbSGT* genes show different expression pattern under heat shock stress, and the encoded isozymes also display different biochemical properties and subcellular localization (Li *et al.*, 2014). The four members of the *W. somnifera* SGT gene family are also differentially induced by heat and cold stress, and treatment with jasmonic acid (JA) and salicylic acid (SA) (Chaturvedi *et al.*, 2012). In line with these observations, the four tomato *SlSGT* genes (*SlSGT1* - *SlSGT4*) were differentially expressed in different plant organs and throughout the different stages of fruit development and ripening. *SlSGT1* was the more highly expressed gene in the different tomato organs. In contrast, *SlSGT4* expression was extremely low. In fruits, the expression of *SlSGT1* and *SlSGT2* expression decreased along ripening, while *SlSGT3* expression increased (Ramirez-Estrada *et al.*, 2017). The *SlSGTs* genes were also differentially regulated in response to biotic and abiotic stress. While the

expression of *SSGT4* and *SSGT2* increased in response to several abiotic stresses (osmotic, cold and salt) and after treatment with abscisic acid and methyl jasmonate, *SSGT1* and *SSGT3* seem to be non-stress responsive genes, since their expression remained almost unaltered under the assayed stress conditions (Ramírez-Estrada et al., 2017).

1.6. Steryl esters

It is well-established that membrane sterol levels must be tightly controlled to avoid the negative effects of perturbed sterol homeostasis on cell viability and overall plant performance (Ferrer et al., 2017). Regulation of FS levels in the membrane can be achieved by modulating the carbon flux of the sterol biosynthesis pathway and/or by converting excess FS into SE, which are a non-toxic form of storage sterols in the cytoplasm present in all plant tissues, although their levels may be affected by the organ or tissue type, the developmental stages and/or the environmental conditions. HIGH STEROL ESTER 1 (HISE1) has been identified as a key regulatory factor in Arabidopsis sterol homeostasis (Shimada et al., 2019). It has been proposed that HISE1 suppresses excess sterol formation by downregulating the protein levels of HMG-CoA reductase, the major rate-limiting enzyme of the sterol pathway whose activity is tightly controlled at different levels from transcriptional to post translational (Wentzinger et al., 2002; Nieto et al., 2009; Leivar et al., 2011; Doblas et al., 2013; Robertlee et al., 2017). When an excess of sterols is still present, they can be acylated to form SE, which are subsequently segregated and stored in cytoplasmic lipid droplets (LD). The buffering effect of SE formation is especially evident when sterol biosynthesis is enhanced, since in these conditions FS levels remain essentially unchanged while excess sterols accumulate as SE in LD (Maillot-Vernier et al., 1991; Gondet et al., 1994; Wilkinson et al., 1994; Schaller et al., 1995; Bouvier-Navé et al., 2010; Shimada et al. 2019). These intracellular structures are present in the seed and leaf cells of many plants, and their function and content may differ depending on the plant tissue and species. Thus, seed LD function as storage compartments for lipids, while in leaves they seem to act as subcellular factories with a role in senescence and fungal infection (McKegney et al., 1995; Bouvier-Navé et al., 2010; Shimada et al. 2014, 2015). Regarding the neutral lipid composition of these vesicular-structures, although TAGs are the major component on most seed LD (Tzen et al., 1993), some of them, like those from canola, lotus or maize, are enriched in SE (Hernández-Pinzón et al., 1999; Harker et al., 2003; Kemp and Mercer., 1968), while leaf LD accumulate mainly SE or wax esters (Parker and Murphy., 1981). LD are dynamic organelle which size and number can be modulated by genetic or environmental factors (Tatenaka et al., 2019). The proposed model for maintaining membrane sterol homeostasis (Shimada et al., 2019) highlights a central role of SE in this process. As mentioned before, these conjugated sterols have a long-chain fatty acid group esterified at the C3 position of the FS, whose length range from C12 to C22, being palmitic, stearic, oleic, linoleic, and linolenic acids the most common species (Dyas and Goad, 1993). The sterol moiety of SE includes the bulk sterol species

present in the FS fraction and many other less abundant sterols and biosynthetic intermediates, the latter being in some cases the predominant sterols in the SE fraction, due probably to regulatory mechanisms affecting the post-squalene segment of the sterol pathway (Ferrer et al., 2017; Lara et al., 2018). The structural diversity of plants SE reflects the importance of the esterification process and their specialized functions in different tissues and organs. This sterol fraction is particularly abundant in anther tapetum cells, pollen grains, seeds and in the phloem (primarily cholesterol) of several plant species. High levels of SE are also accumulated in senescent leaves (Bouvier-Nave et al. 2010), in mutant plants overproducing sterols (Gondet et al., 1994; Schaller et al., 1995; Shimada et al., 2020), and when the flux through the sterol pathway is increased by supplying cell cultures with pathway intermediates (Wilkinson et al., 1994). Thus, the existing data indicate that SE serve as a reversible storage pool of sterols that helps to maintain the proper levels of FSs in cell membranes during normal plant growth and development, preventing the potential destabilizing effect that changes of FS levels above or below a certain threshold may have on membrane structure and function. This is especially important under some circumstances, such as stress conditions (Kumar et al., 2018), senescence and aging (Bouvier-Navé et al., 2010) and also when free sterols are required immediately in important quantities, for instance during seed germination and early seedling development, and pollen tube growth (Dyas and Goad., 1993). To meet these demands, it is necessary to achieve the correct balance between SE formation and mobilization, two biochemical processes that are still poorly understood in plants (Behmer et al., 2013).

1.7. Sterol acyltransferases

The esterification of a long-chain fatty acid group to the free hydroxyl at C3 position of the FS four-ring backbone to form ES is catalysed by a family of enzymes known as sterol acyltransferases. These enzymes are classified based on the acyl donor group into acyl-CoA:sterol acyltransferases (ASAT; EC 2.3.1.26), if the donor is a long-chain fatty acyl-CoA, and phospholipid:sterol acyltransferases (PSAT; EC 2.3.1.43), if the donor is a phospholipid (Korber et al., 2017) (Figure 5). Plant sterol acyltransferase activity has been reported to be primarily associated with membrane fractions in different species (Garcia and Mudd., 1978; Zimowski and Wojciechowski., 1981 ; Kalinowska et al., 1989; Bouvier-Navé and Benveniste., 1995; Banas et al., 2005; Chen et al., 2007), but so far only ASAT and PSAT enzymes from Arabidopsis (ASAT1 and PSAT1) and tomato (SIASAT1 and SIPSAT1) have been cloned and functionally characterized (Banas et al., 2005; Chen et al., 2007; Lara et al., 2018).

The Arabidopsis ASAT1 is structurally related to acyl-CoA sterol acyltransferases from yeast and animal systems and therefore has been included in the family of membrane-bound O-acyltransferases (MBOATs; Chang et al., 2011). Biochemical characterization of ASAT1 expressed in a mutant yeast strain lacking the two endogenous ASATs Are1p and Are2p revealed that the sterol precursor cycloartenol is the preferred acceptor of acyl groups. In line with this observation, overexpression of ASAT1 in Arabidopsis seeds resulted in the accumulation of cycloartenyl esters and to a lesser extent of 24-methylene cycloartenyl esters at the expense of campesteryl and β -sitosteryl esters and FSs, whose levels were substantially reduced (Chen et al., 2007). Arabidopsis PSAT1 was biochemically characterized using microsomal fractions obtained from leaves and roots of transgenic Arabidopsis overexpressing the enzyme. Phosphatidylethanolamine was the preferred acyl donor for sterol esterification and the enzyme was able to esterify several sterols and sterol intermediates (Banas et al., 2005). The tomato enzymes also exhibit different substrate preferences; while SIASAT preferentially esterifies the biosynthetic intermediates cycloartenol and 24-methylene cycloartanol, SIPSAT preferred the final sterols (campesterol, β -sitosterol, stigmasterol, and cholesterol) as a substrate (Lara et al., 2018). In Arabidopsis, the characterization T-DNA insertion mutants defective in the expression of *PSAT1* and *ASAT1* genes revealed a differential contribution of the corresponding enzymes to SE biosynthesis depending on the tissue. Thus, a strong reduction of SE levels was observed in seeds of the *psat* mutants but not in those of the *asat* mutant, suggesting a major role of PSAT1 in the synthesis of SE in seeds. On the contrary, SE levels were found to decrease in

the leaves of both mutants. Despite this, a phenotype of premature senescence associated to decreased SE levels was observed only in leaves of the *psat* mutant, which supports the idea that PSAT1 plays an important role in the maintenance of leaf viability during aging (Bouvier-Navé et al., 2010). More recently, it has been reported that the *Arabidopsis hise1* mutant shows normal growth phenotype and similar sterol content than WT leaves, because excess sterols are esterified by PSAT1 and stored in LD (Shimada et al. 2019). However, the *hise1-3 psat1-2* double mutant exhibited a severe growth phenotype due to high sterol content in the leaves, in which the presence of LD was not detected, while these structures were present in WT and *hise1* mutant leaves (Shimada et al. 2019). Thus, PSAT1 plays a critical role in the suppression of sterol overaccumulation through their esterification and subsequent storage in LD.

1.8. Role of sterols in plant growth and development

Several studies have associated alterations in sterol composition with abnormalities in plant growth and development (Jang et al., 2000; Schrick et al., 2000; Schaeffer et al., 2001; Clouse., 2002; Boutté and Grebe., 2009; Song et al., 2019). Mutant plants deficient in early sterol biosynthetic pathway steps often exhibit phenotypic alterations such as dwarfism and reduced fertility, which have been attributed to their role as brassinosteroid precursors, since this hormone is essential for the correct plant development (Valitova et al., 2016). However, in some of these mutants, like *smt2* that encodes 24-sterol C-methyltransferase (Figure 4) or *hyd2/fackel* that encodes a sterol C-14 reductase, the growth defects cannot be recovered by exogenous addition of brassinosteroids, indicating that alterations in sterol composition are the direct cause for the observed phenotype (Carland et al., 2002; Schaller., 2004; Vriet et al., 2013), since these compounds can reduce the cell growth as a result of the changes induced in the PM physical properties (Valitova et al., 2016) (Section 1.2). It has also been reported that some sterol species, such as β -sitosterol and stigmasterol, play an essential role in cell differentiation and proliferation (Piironen et al., 2000).

On the other hand, alterations in PM integrity induced by changes in sterol levels can impact the localization of proteins residing in lipid rafts involved in cell polarization (Carland et al., 2002; Willemsen et al., 2003). For instance, PIN proteins, which are involved in auxin transport and cell polarity, require SMT1 function for correct positioning in Arabidopsis (Willemsen et al., 2003). Moreover, sterols are also important for maintaining cellulose levels and cell wall (CW) integrity. In Arabidopsis, treatment with sterol biosynthesis inhibitors, such as 15-azasterol and fenpropimorph, lead to CW gaps in dividing root cells and a reduction in the bulk cellulose content (Schrick et al., 2004).

Despite the abundance of studies relating phytosterols with plant development, the information about the role of glycosylated sterols in this process is limited. At present, a series of forward- and reverse-genetics studies support the view that a proper ratio of glycosylated versus free sterol forms in cell membranes is crucial for normal plant cell function and overall plant performance. Reduced levels of glycosylated sterols in the Arabidopsis null mutant *ugt80A2;B1*, lacking the two SGT present in this species, lead to slow growth phenotype, elongation defects in embryogenesis, defects in seed cell morphology (DeBolt et al., 2009) and the male gametophyte (Choi et al., 2014), and abnormal root epidermal cell patterning (Pook et al., 2017). Downregulation of *SGTs* in *W. somnifera* leads to reduced leaf area and plant height compared to control plants (Singh et al., 2016), while overexpression of *WsSGTL1* improves seed germination in Arabidopsis (Mishra et al., 2013) and enhances

growth of *W. somnifera* plants (Saema et al., 2016), in contrast to the stunted growth phenotype observed when this enzyme was expressed in *Nicotiana tabacum* (Pandey et al., 2014). In tomato, *SLSGT1* silencing also resulted in plant dwarfism (Chávez et al., 2023; Cisneros et al., 2023).

The knowledge about the function of sterols in fruit development is much more limited, although it has been suggested that an active synthesis of sterols is needed during the early stages of tomato fruit development to meet the increasing demand of membranes in actively dividing and expanding cells during the fruit growth phase (Narita and Grissem., 1989). In fact, enhanced sterol levels during the early development of melon fruits were correlated with larger fruit size (Kobayashi et al., 2002), and expression of the catalytic domain of melon HMGR in tomato fruit pericarp cells induced cell division and elongation leading to bigger fruits (Kobayashi et al., 2003). Recently, has been reported that maintenance of appropriate levels of glycosylated sterols during the early stages of fruit development is essential for normal tomato fruit growth, since reduced levels of these conjugated sterols, induced by *SLSGT1* silencing, trigger a transcriptional downregulatory response that affects genes involved in processes that are critical for proper fruit development, such as seed filling, cell wall extension and auxin signalling (Chávez et al., 2023).

1.9. Sterols and plant response to stress

The PM acts as a physical barrier that protects the cell and, consequently, plays an essential role during stress responses. The lipids integrated in this membrane, and specifically sterols, have dynamic responses to cell external perturbations, therefore variations in their composition may alter the plant response to environmental stimuli (Valitova et al., 2016). There are several studies supporting the role of sterols in the plant response to different abiotic stresses, including heat shock (Beck et al., 2007), salt stress (Kerkeb et al., 2001; Mishra et al., 2013; Pandey et al., 2014), drought (Posé et al., 2009; Kumar et al., 2015), cold (Takahashi et al., 2016; Rogowska and Szakiel, 2020), metal ions (Hossain Khan et al., 2009) and oxidative stress (Wang et al., 2012). In relation to conjugated sterols, little is known about the cellular and molecular bases that would explain the function of these sterols, especially sterol esters, in the stress responses (Kopischke et al., 2013; Kumar et al., 2015; Li et al., 2014).

Regarding glycosylated sterols, forward and reverse-genetic approaches have shown that changes in *SGTs* expression levels are associated to altered responses of different plant species to abiotic stress conditions. An increased sensitivity to heat and cold stress has been reported in *Arabidopsis* and *W. somnifera* plants with reduced levels of SGT (Mishra et al., 2015; Singh et al., 2017), whereas enhanced tolerance to heat, cold and salt stress has been associated to overexpression of SGT in *Arabidopsis*, tobacco and *W. somnifera* (Mishra et al., 2013; Pandey et al., 2014; Saema et al., 2016). These observations are consistent with the induction of *SGT* genes in response to abiotic stress reported in tomato (Ramírez-Estrada et al., 2017), *W. somnifera* (Chaturvedi et al., 2012) and cotton (Li et al., 2014), and also with changes observed in the relative proportions of glycosylated sterols in the PM of oat, rye and potato in association with cold acclimation and freezing tolerance (Palta et al., 1993; Takahashi et al., 2016), during tomato and apple fruit chilling and after tomato fruit re-warming (Whitaker, 1991, 1994; Rudell et al., 2011), in wheat leaves under high day and night temperature (Narayanan et al., 2016), and in *Arabidopsis* under drought stress conditions (Tarazona et al., 2015). The role of SG in abiotic stress responses is further supported by the observation that the *Arabidopsis ugt80b1* T-DNA insertion mutant shows increased sensitivity to cold compared to WT plants (Mishra et al., 2015).

In the case of SE, the double *Arabidopsis* mutant *bise1-3 psat1-2*, which as mentioned in Section 1.6 has higher sterol content than the WT, shows a general up-regulation of abiotic and biotic stress-responsive genes, including *RESPONSIVE TO DESICCATION 29B/LOW-TEMPERATURE-INDUCED 65 (RD29B/LTI65)* and *COLD-REGULATED*

15A (*COR15A*) in leaves, as well as senescence-related genes, suggesting that an excess of sterols induces senescence on leaves (Shimada et al., 2020), a phenotype that has been related with autophagy (Barros et al., 2020).

A number of studies have also highlighted the role of sterols in improving the biotic stress resistance in plants (Moreau et al., 2018; Aboobucker and Suza, 2019). Pathogens colonize a host and take up nutrients from the apoplast, where they grow. The apoplast usually contains minimal nutrients that came from the exchange with the cytosol via PM permeability (Sattelmacher, 2001). Some enzymes such as SQS, and C22 desaturase are overexpressed after pathogen infections, and regulate nutrient efflux into the apoplast through modification of membrane permeability (Wang et al., 2012). There are several studies showing the relevance of β -sitosterol and stigmasterol in plant-pathogen interactions, since changes in their ratio can influence the biophysical properties of membrane microdomains and thereby modulate plant defense signaling (Griebel and Zeier, 2010; Wang et al., 2012; Wang et al., 2012). Moreover, the antifungal properties of some phytosterols including β -sitosterol, campesterol and stigmasterol have been proven (Choi et al., 2017).

Experimental evidence supporting a role of conjugated sterols in mediating plant responses against biotic stress is more limited. The enhanced response to *Phytophthora infestans* showed by the Arabidopsis mutant *psat1*, deficient in the synthesis of SE (Kopischke et al., 2013), suggests the participation of this sterol fraction in the pathogen-inducible response against this oomycete. However, the biochemical analysis showed that not only the SE levels were altered on this mutant, but also those of SG and ASG, making it difficult to attribute the resistance phenotype to the reduced levels of SE or to changes in the glycosylated fraction. It has also been reported that downregulation of *SGTs* in *W. somnifera* results in increased susceptibility to *Alternaria alternata*, but alteration in the pathogen tolerance could be due not only to changes in the SG and ASG levels but rather to changes in the levels of whitanolides, a type of glycosylated sterol-related specialized metabolites (Singh et al., 2016). Furthermore, the overexpression of *WsSGT1* in Arabidopsis enhanced the plant resistance against the necrotrophic fungi *Alternaria brassicicola*. The resistance phenotype of these transgenic plants was attributed to the accumulation of phenolic compounds (ferulic acid, caffeic acid, chlorogenic acid, protocatechuic acid and rutin) and the over-expression of defense marker genes (*VSP2*, *PDF1.2*, *LoX2*, *PAD3* and *PAL*) after pathogen inoculation (Mishra et al., 2017). It has also been reported that the Arabidopsis double mutant *ugt80A2;B1*, which as mentioned before is severely affected in the biosynthesis of glycosylated sterols, displayed an increased resistance to *Botrytis cinerea* infection, which correlates with increased levels of JA,

the up-regulation of defense gene markers (*PDF1.2* and *PR4*) and the accumulation of camalexin, the major *Arabidopsis* phytoalexin (Castillo et al., 2019). These data support a role of glycosylated sterols in the plant response to biotic stress. However, the molecular mechanisms beyond this effect remain unclear. It has been also reported that plant positive-strand RNA virus replication is highly dependent on host cell sterol levels, but very little is known about the specific role of glycosylated sterols in virus replication (Altabella et al., 2021). Recently, has been demonstrated that tomato plants with reduced levels of glycosylated sterols induced by *SSGT1* silencing are hypersusceptible to potato spindle tuber viroid (PSTVd), most likely because the imbalance of sterol glycosylation facilitates the viroid movement and, consequently, favours viroid infection (Cisneros et al., 2023).

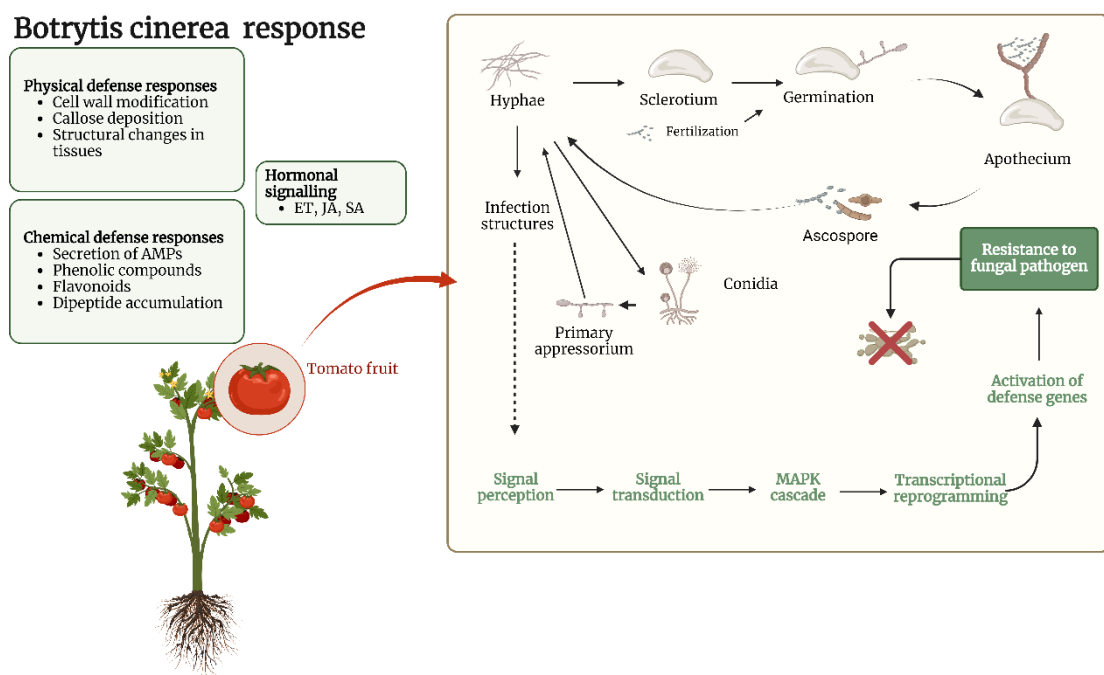


Figure 6. *Botrytis cinerea* infection diagram. Physical/Chemical and hormonal responses of tomato plant response against fungi. Lifecycle of *B. cinerea*, with different stages of sexual and asexual development. Arrows show the direction of reproductions and plant response against *B.cinerea*.

1.10. Tomato, agronomic crop and research plant model

Solanum lycopersicum, belong to the Solanaceae family, which encompasses around 1500 species, including other significant crops like potatoes (*Solanum tuberosum*) and eggplant (*Solanum melongena*). The origin and domestication of tomato have been proposed to occur in America, with two main hypotheses suggesting Peru or Mexico as potential domestication sites (Ranc et al., 2008). By the 15th century, tomato reached a fairly advanced stage of domestication before being introduced to Europe. Over time, extensive morphological diversity, cultivars, and forms have been developed from a single species, *S. lycopersicum*, through plant breeding (Trivedi et al., 2016).

The domestication of tomato has been focused mainly on various growth characteristics (plant height, self-pruning) and fruit traits (size, shape, colour, taste), but also to enhance production under different stress conditions. Tomatoes face challenges from over 200 species of pests and pathogens, leading to significant economic losses annually (Kimura & Sinha, 2008). Traditional control methods using chemical compounds may not always be fully effective and require compliance with chemical-use regulations, which increase the total cost production. Additionally, the subtropical origin of tomatoes limits their optimal production to relatively small crop growing areas, due to various unfavourable conditions like extreme temperatures, water availability and soil characteristic. Recent studies utilizing transcriptomics, proteomics, and metabolomics have contributed to a better understanding of the biochemical and metabolic processes involved in the development and stress responses of tomato plants and fruits (Gan et al., 2024).

Tomato hold a prominent position as one of the most consumed fruit crops globally, being a fundamental component in the diets of various cultures due to their rich content of vitamins, minerals, fiber, and antioxidants. In 2021, the worldwide production of tomatoes exceeded 189 million tons, with China leading the production with 67.5 million tons, followed by India, Turkey, and the United States. Spain also stands among the top 10 tomato producers, contributing 4.7 million tons to the global production (Ricupero et al., 2021).

Apart from its agricultural and economic significance, tomato serve as a model system for studying fruit development and ripening, due to their fleshy fruit nature, unlike other plant models such as rice (*Oryza sativa*) or *Arabidopsis thaliana*. The diploid genome, short life cycle, and fully sequenced genome of tomato make this plant species highly manageable for fruit studies. Moreover, the easy identification of ripening phenotype, along with the availability of germplasm collections and mutants related with ripening processes, further enhance their suitability for research purposes (Kimura & Sinha, 2008; Klee & Giovannoni, 2011)

Tomato plants produce globular or ovoid fruits that exhibit typical berry characteristics, with fleshy fruits derived from the ovary containing seeds enclosed in the pulp. The most external tissue, known as pericarp, is covered by a cuticle, while inside is the placenta containing the seeds, which include the embryo surrounded by the endosperm and a protective outer layer called testa (Barry & Giovannoni, 2007; OECD, 2017). The development and ripening of tomato fruits span approximately seven to nine weeks from anthesis to the end of ripening, with ethylene playing a crucial role in regulating the ripening process, which can be divided into two phases. The early phase (I) involves cell divisions and expansion to increase fruit size, and requires an active sterol biosynthesis (Gutensohn & Dudareva, 2016). During the phase II, various physiological changes such as colour, sugar metabolism, fruit softening, and volatile synthesis, take place (Figure 7) (Legge et al., 1986). An increase in conjugated sterols has been observed during tomato (cv. Rutgers) fruit development and ripening. It has been proposed that these changes can modulate the activities of membrane-bound enzymes involved in ripening and senescence processes (Whitaker., 1988). More recently, has been reported that glycosylated sterols play a major role in fruit development, since reduced levels of this sterol fraction negatively affect the early steps of fruit development (Chávez et al., 2023).

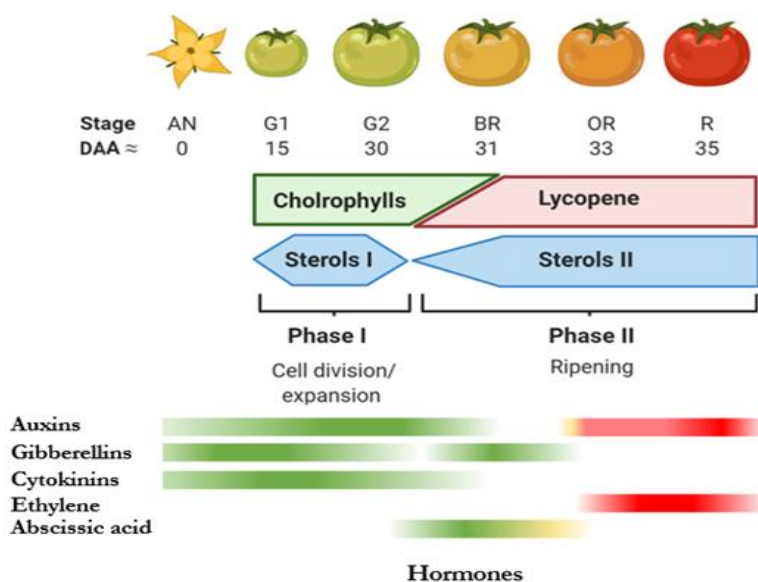


Figure 7. Tomato fruit development. The phase I of fruit development involves cell division and expansion events till reach the final fruit size (approximately 30 days post-anthesis (DAA)). The phase II involves the ripening of the fruit, and it is characterized by important changes in organoleptic properties. At the beginning of the second phase, chlorophyll is degraded and lycopene begins to accumulate. The action of hormones is differential depending on the tomato growth or maturation stage. G1, Green; G2, mature green; BR, breaker, OR, orange; R, red. Adapted from Quinet et al., 2019.

2. OBJECTIVES

2.1. General Objective

This thesis is based in *S.lycopersicum* conjugate sterols following the research performed by our research group. FS are the common precursors of SG and SE, which are synthesized by the UDP-glucose:sterol glycosyltransferases (SGT) and the acyl-CoA/phospholipid:sterol acyltransferases (ASAT/PSAT), respectively that were cloned and initially characterized by our group (Ramírez-Estrada et al., 2017; Lara et al., 2018; Burciaga-Monge et al., 2022). The main objective of the thesis project is to establish the role SLASAT1, SIPSAT1 and SLSGT3 isoenzyme in the metabolism of conjugated sterols during growth and development of the tomato plant and fruit, and in the response of plants and fruit to conditions of biotic stress. To achieve this objective, the following specific objectives are proposed.

2.2. Detailed objectives

Objective 1. Generation of loss of function SLASAT1 and SIPSAT1 double knock-out mutant to explore the resulting physiological, and metabolic changes derived from different sterol composition during plant and tomato growth and development.

Objective 2. Generation of tomato transgenic lines carrying SLSGT3 gene promoter fused to the GUS reporter and plants carrying SLSGT3 gene under constitutive or fruit specific promoters to analyse the expression pattern of the SLSGT3 gene in tomato transgenic lines and characterize at a phenotypic, biochemical, and molecular level plants with increased levels of the activity of this enzyme.

Objective 3. Analysis of tomato membrane sterol composition and special distribution setting up a protocol to isolate sterol-rich detergent-resistant (DRM) and sterol-depleted detergent-soluble (DSF) fractions from the root and leaf tissue and a proof-of-concept method to perform the analysis of the spatial distribution of sterols by MALDI-MSI and confocal analysis.

3. RESULTS

3.1. CHAPTER I

Role of steryl ester biosynthesis on plant growth and developmental processes

3.1.1. Generation of tomato *slpsat31* x *slsat34* double knock-out mutants

Tomato (cv Micro-Tom) CRISPR-Cas9-edited loss-of-function single mutants lacking either SIPSAT1 (*slpsat28* and *slsat31*) or SIASAT1 (*slsat34* and *slsat35*), generated and characterized previously in our research group (Burciaga., 2020), were used for obtaining the corresponding double mutant to study the role of SE in different developmental processes. For this, multiple crosses between *slsat34* (♀) and *slpsat31* (♂) homozygous lines were performed and analysed for the presence of mutated alleles for both SIASAT1 and SIPSAT1 genes. From 14 obtained lines, line 9 was selected and propagated to the next generation to obtain homozygous lines for both mutations as it was the line which gave more seeds and had both mutations. The mutant *slpsat31* presents a 4-nucleotide deletion that results in the appearance of a single *Xho*I restriction site in the 293-bp fragment amplified for genotyping. Thus, digestion with this enzyme generates two fragments of 174 and 118 bp when the mutated sequence is in homozygosity (Burciaga., 2020). Using this approach 2 lines (9.2 and 9.9) were selected as homozygous for the *slpsat31* mutation.

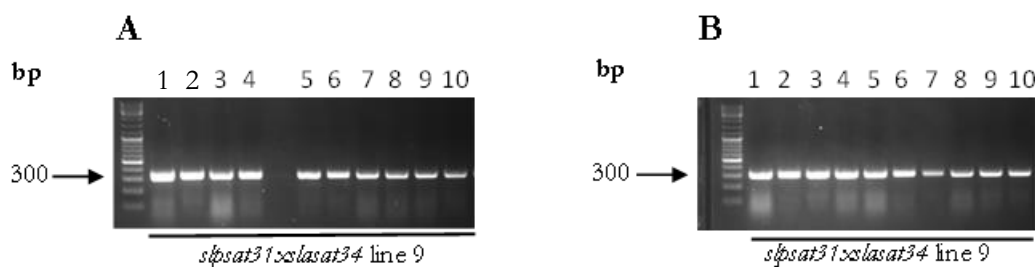


Figure 8. Electrophoresis gel. PCR amplification of *SIASAT1* (303 bp) (A) and *SIPSAT1* (293 bp) (B) genomic fragments from 10 individual colonies harbouring the corresponding recombinant pGEM-Teasy clones. The cloned fragments in the positive colonies were subsequently sequenced to confirm the zygosity of each line.

To check the *slsat34* zygosity degree, a genomic fragment of 303 bp encompassing the corresponding sgRNA target site was amplified by PCR (Figure 8) using the primers ASAT1 crispr Genotip Fw/Rv and Crispr PSAT Genot FW /Rv (Table 18), cloned into the pGEM®-T Easy vector, and sequenced. The comparison of the obtained sequences with those of the equivalent genomic region of WT plants, using the DNA Dragon Software

(Colmán et al., 2018), confirmed that the selected lines 9.2 and 9.9 were also homozygous for the slsat34 mutation. This sequencing-based strategy was also used to confirm the homozygosity of slpsat31 mutation in both lines. From that point, line 9.2 was used to continue with the experimental procedure as line 9.

3.1.2. Effect of SLPSAT1 and SLASAT1 inactivation on the sterol profile of tomato leaves

The levels of free and esterified sterols were quantified in extracts obtained from leaves of mature plants (fourth and fifth leaves of 8-week-old plants). The inactivation of the SLPSAT1 gene led to a severe depletion of SE levels in both slpsat1 transgenic lines, as SE levels were reduced below 30% (26.7% in slpsat28 and 29% in slsat31) compared to WT (Figure 9A and Table 1). Unexpectedly, the levels of SE in the two slsat1 mutant lines increased instead of decreasing. Indeed, the total SE content increased 3.8-fold in line slsat34 and 4-fold in line slsat35 compared to WT (Figure 9A and Table 1). The impaired sterol esterification resulted in a moderate but significant enhancement of total FS levels in the leaves of slpsat28, slpsat31 and slsat34 and slsat35 mutants, ranging from 1.3- to 1.7-fold the WT levels (Figure 9B and Table 1).

A detailed analysis of SE and FS profiling showed that inactivation of both tomato sterol acyltransferases affected to a greater or lesser extent the contents of all measured free and esterified sterol species (Table 1), which resulted in a strong reduction of the SE levels of all the analysed species in leaves of slpsat1 mutants compared to WT (Table 1). In fact, only esterified sitosterol and cholesterol could be detected in leaves of slpsat28 and slpsat31 mutant lines, with reductions from approximately 3- to 4.5-fold, respectively. In slsat34 and slsat35 mutants a general increase of the four major sterol species was detected in the SE fraction.

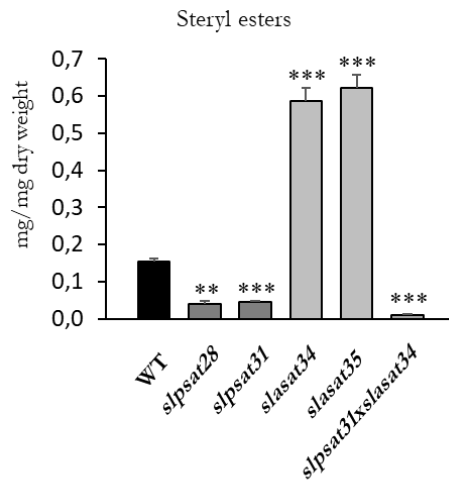
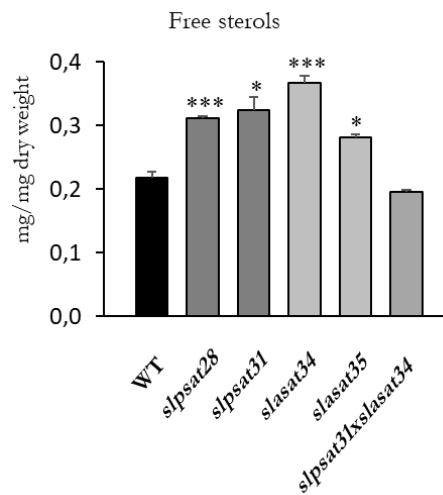
A**B**

Figure 9. Total levels of SE and FS in leaves of *slpsat1*, *slasat1*, and *slpsat31* $\times$ *slasat34* mutants. Quantification of esterified (A) and free sterols (B) was carried out in two-month-old plants. Data are presented as mean $\pm$ SEM from three biological replicates per genotype. Asterisks indicate values that are significantly different compared to those in WT plants determined by t-test (* $P < 0.05$; ** $P < 0.01$; *** $P < 0.005$).

The sterol profile analysis in the leaves of the double *slpsat31* $\times$ *slasat34* mutant revealed a metabolic phenotype very similar to the *slpsat28* and *slpsat31* mutants, though there was a 4-fold additional reduction of total SE levels compared to the single *slpsat* mutants, which resulted in a further depletion to 7% the content in WT leaves (Figure 9A and Table 1), while FS levels were restored to those of WT (Figure 9B and Table 1). Overall, these results showed a predominant role of SI Ψ SAT1 over SI Δ SAT1 in tomato SE biosynthesis in leaves.

Table 1. FS and SE quantification in leaves of WT, *slasat34*, *slasat35*, *slpsat28*, *slpsat31*, and *slpsat31 x slasat34* mutants. Data are shown as average values from three biological replicates with SEM in parentheses. n.d. stands for not detected. Significant changes compared to WT seeds are indicated by asterisks (*P<0.05; **P<0.01; ***P<0.005).

	WT	<i>slasat34</i>	<i>slasat35</i>	<i>slpsat28</i>	<i>slpsat31</i>	<i>slpsat31 x slasat 34</i>
	(µg/mg dry weight)					
Total FS	0.2184 (0.0094)	0.3676*** (0.0109)	0.2808* (0.0050)	0.3115*** (0.0036)	0.3245* (0.0202)	0.1949 (0.0035)
Cholesteryl	0.0248 (0.0015)	0.0504* (0.0046)	0.0408* (0.0037)	0.0187*** (0.0008)	0.0256 (0.0009)	0.0336* (0.0003)
Campesteryl	0.0090 (0.0006)	0.0331* (0.0046)	0.0291* (0.0050)	0.0086 (0.0006)	0.0105 (0.0008)	0.0024*** (0.0002)
Stigmasteryl	0.1012 (0.0047)	0.1060 (0.0072)	0.0846* (0.0036)	0.1169 (0.0045)	0.1480* (0.0044)	0.1082 (0.0015)
Sitosteryl	0.0834 (0.0034)	0.1780** (0.0151)	0.1263* (0.0094)	0.1674*** (0.0027)	0.1404* (0.0150)	0.0507* (0.0028)
	WT	<i>slasat34</i>	<i>slasat35</i>	<i>slpsat28</i>	<i>slpsat31</i>	<i>slpsat31 x slasat 34</i>
	(µg/mg dry weight)					
Total SE	0.1529 (0.0099)	0.5874*** (0.0348)	0.6233*** (0.0352)	0.0408** (0.0067)	0.0443*** (0.0037)	0.0106*** (0.0013)
Cholesteryl	0.0163 (0.0020)	0.097*** (0.0062)	0.0750*** (0.0022)	0.0037** (0.0003)	0.0035** (0.0006)	n.d.
Campesteryl	0.0095 (0.0007)	0.0360** (0.0049)	0.0313*** (0.0021)	n.d.	n.d.	n.d.
Stigmasteryl	0.0081 (0.0011)	0.0387* (0.0052)	0.0254* (0.0022)	n.d.	n.d.	n.d.
Sitosteryl	0.0459 (0.0027)	0.2651*** (0.0257)	0.2330*** (0.0134)	0.0142*** (0.0030)	0.0157*** (0.0014)	0.0106*** (0.0013)

3.1.3. Effect of SIPSAT1 and SLASAT1 inactivation on lipid droplet abundance in tomato leaves

To explore the potential relationship between SE levels and cytosolic LD abundance, discs from the fourth leaf of WT and mutant plants were stained with TopFluor® cholesterol (Gocze and Freeman, 1994) and observed with confocal microscopy. As shown in figure 10, leaves from *slpsat28*, *slpsat31* and *slpsat31* × *slasat34* mutants contain less LD than WT and both *slasat1* single mutant leaves. Quantitative analysis of stained LD corroborated this result, since reductions of approximately 63, 51, and 74% in the number of LD were detected in leaves of *slpsat28*, *slpsat31*, and *slpsat31* × *slasat34* mutants, respectively, compared to WT (Figure 10). Surprisingly, both *slasat1* mutants also had less LD than WT plants, showing reductions of 18% (*slasat34*) and 35% (*slasat35*) (Figure 10), despite the levels of SE in the leaves of these mutants were higher than in WT (Figure 9A). Thus, the direct correlation between SE levels (Figure 9A) and LD abundance (Figure 10) observed in *slpsat1* and *slpsat31* × *slasat34* mutant leaves does not seem to exist in *slasat34* and *slasat35* leaves.

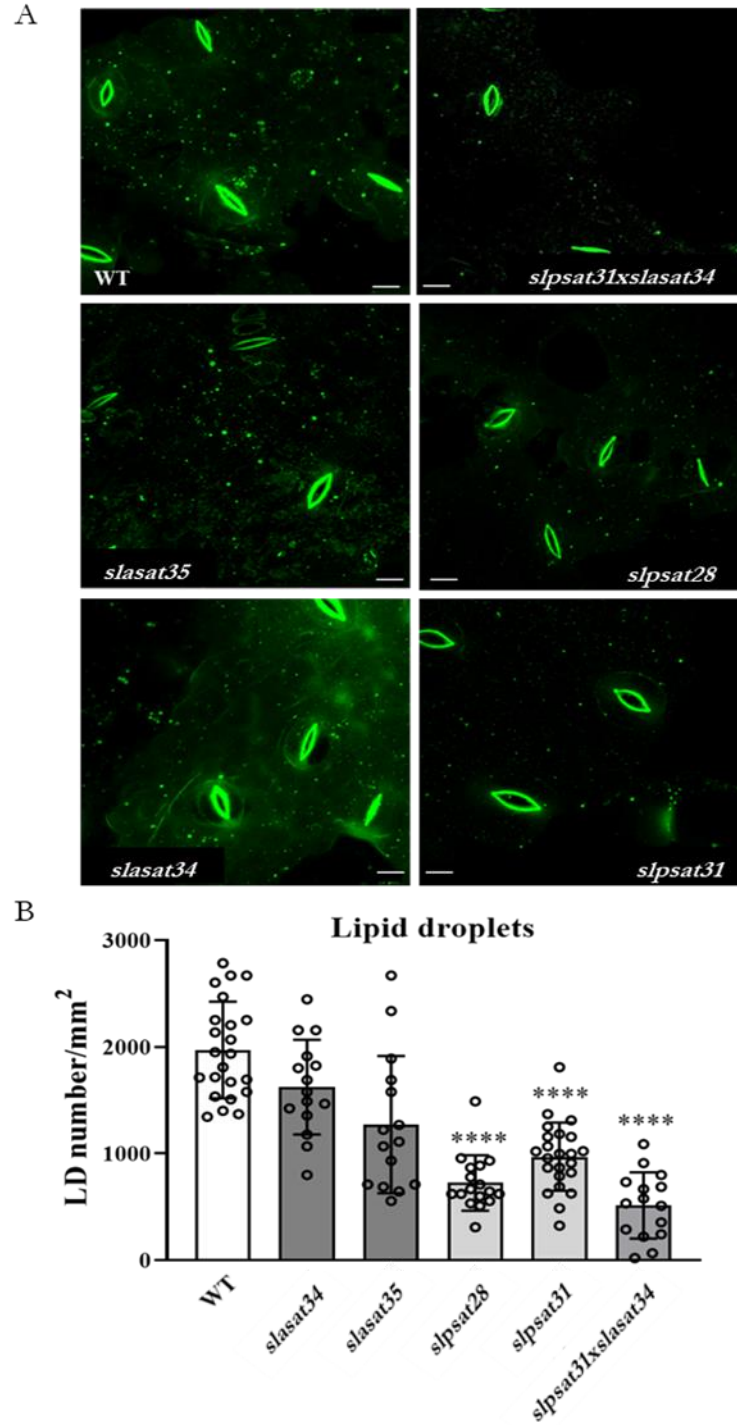


Figure 10. Intracellular presence of lipid droplets in leaf epidermal cells of WT, *slpsat28*, *slpsat31*, *slasat34*, *slasat35* and *slpsat31 x slasat34* knock-out mutants. (A) Lipid droplets were visualized by staining leaf disks with TopFluor® Cholesterol and detection by confocal scanning fluorescence microscopy. Excitation: 488 nm; fluorescence detection: 490-520 nm. (B) The abundance of lipid droplets was counted using ImageJ 1.48v software. Data are presented as mean $\pm$ SEM from three biological replicates per genotype with n=15-23 images per genotype analysed. Asterisks indicate values that are significantly different compared to those in the WT plants determined by t-test (* $P \leq 0.05$; *** $P \leq 0.005$; **** $P \leq 0.001$).

3.1.4. Knock-out mutants *slpsat1* and *slpsat31* $\times$ *slasat34* exhibit reduced size and early leaf senescence

Tomato mutant lines were examined for morphological phenotype alterations on the vegetative organs associated with the loss of function of SIPSAT1, SIASAT1 or both. The size (height) of seven- and ten-week-old *slasat34* and *slasat35* mutant plants was almost identical than that of WT plants (Figure 11A and C). However, *slpsat28* and *slpsat31* mutants were approximately 50% shorter than WT plants (Figure 11C), while a 25% reduction in height was observed in the double mutant *slpsat31* $\times$ *slasat34* compared to WT (Figure 11C). These results demonstrated that a functional SIPSAT1 is essential for normal tomato plant growth while, at least under normal growth conditions, the lack of functional SIASAT1 has no evident effects on plant growth. Interestingly, the loss of function of SIASAT1 partially reverses the dwarf phenotype caused by SIPSAT1 inactivation, since a compensatory size effect was observed in the *slpsat31* $\times$ *slasat34* double mutant compared with the single *slpsat1* mutants (Figure 11A and C). On the other hand, when mutant plants were about 10 week-old, the oldest (basal) leaves of both *slpsat1* mutant plants exhibited chlorosis, whereas those of the *slpsat31* $\times$ *slasat34* double mutant turned brown and dried out as typical senescent leaves. In contrast, all leaves in both *slasat1* mutants, like those of WT plants, remained green (Figure 11B). These observations indicate that a reduced SE content in tomato leaves was associated to an early senescence phenotype, which was more pronounced the lower the SE content was (compare Figure 9A and B). The positive correlation between diminished SE levels and premature leaf senescence was confirmed by quantifying the expression of the senescence marker gene *SAG12* (Noh and Amasino., 1999). For this, total RNA was extracted from leaves of two different ages (second and third leaves) obtained from seven-week-old WT and mutant plants. At this developmental stage, the third leaves of the different mutants and the WT plants were still green, while the second leaves of *slpsat1* mutants displayed senescence symptoms, which were more pronounced in the *slpsat31* $\times$ *slasat34* double mutant (Figure 11B). As expected, similar basal levels of *SAG12* mRNA were detected in the third leaves of WT and mutant plants (Figure 11D).

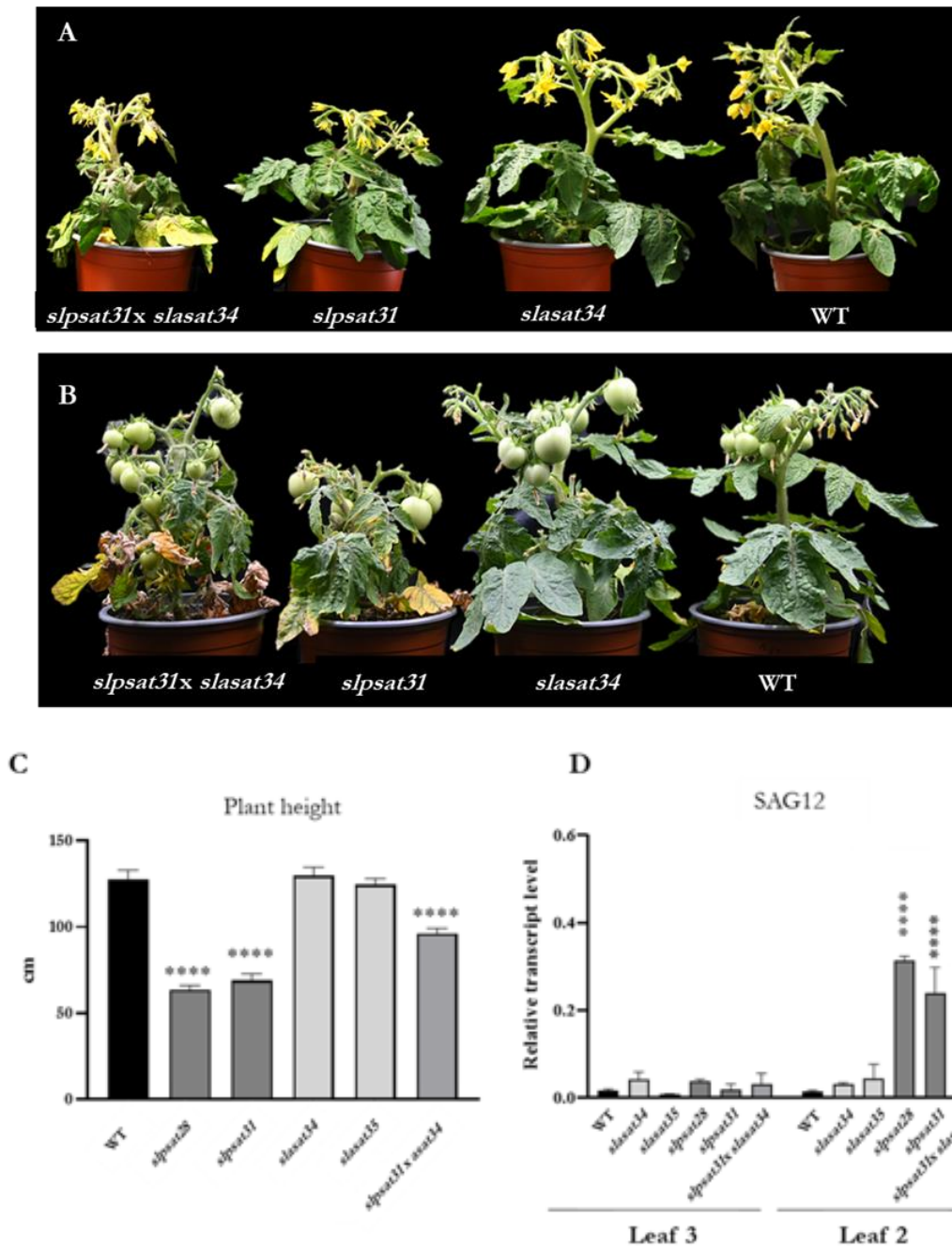


Figure 11. Phenotypic characterization of *slpsat28*, *slpsat31*, *slsat34*, *slsat35* and *slpsat31* x *slsat34* mutant plants. Representative images of 7-week-old (A) and 10-week-old (B) *slpsat1*, *slsat1*, and *slsat1* x *slpsat1* knock-out mutants grown under greenhouse conditions. (C) Quantitative analysis of plant height to first inflorescence of 10-week-old plants. (D) SISAG12 mRNA levels measured by RT-qPCR in RNA samples from the 2nd and 3rd leaves of 7-week-old plants. The mRNA levels of the actin gene were used to normalize SISAG12 transcript levels. Data are presented as mean $\pm$ SEM from three biological replicates per genotype with three technical replicates each (n=9). Asterisks indicate values that are significantly different compared to those in the WT plants determined by t-test (****P $\leq$ 0.001).

However, the expression of *SISAG12* was drastically induced in the second leaves of both *slpsat1* mutants compared to the equivalent leaves of WT plants (approximately 28- and 16-fold higher in *slpsat28* and *slpsat31*, respectively). Interestingly, the induction of *SISAG12* expression was more pronounced in the *slpsat31* $\times$ *slsat34* double mutant compared to single *slpsat1* mutants (approximately 34-fold higher than WT). Conversely, no significant differences in *SISAG12* transcript levels were observed in the second leaves of both *slsat1* mutants compared to WT leaves (Figure11D). To explore whether the early senescence phenotype was a consequence of developmental alterations affecting leaf natural senescence

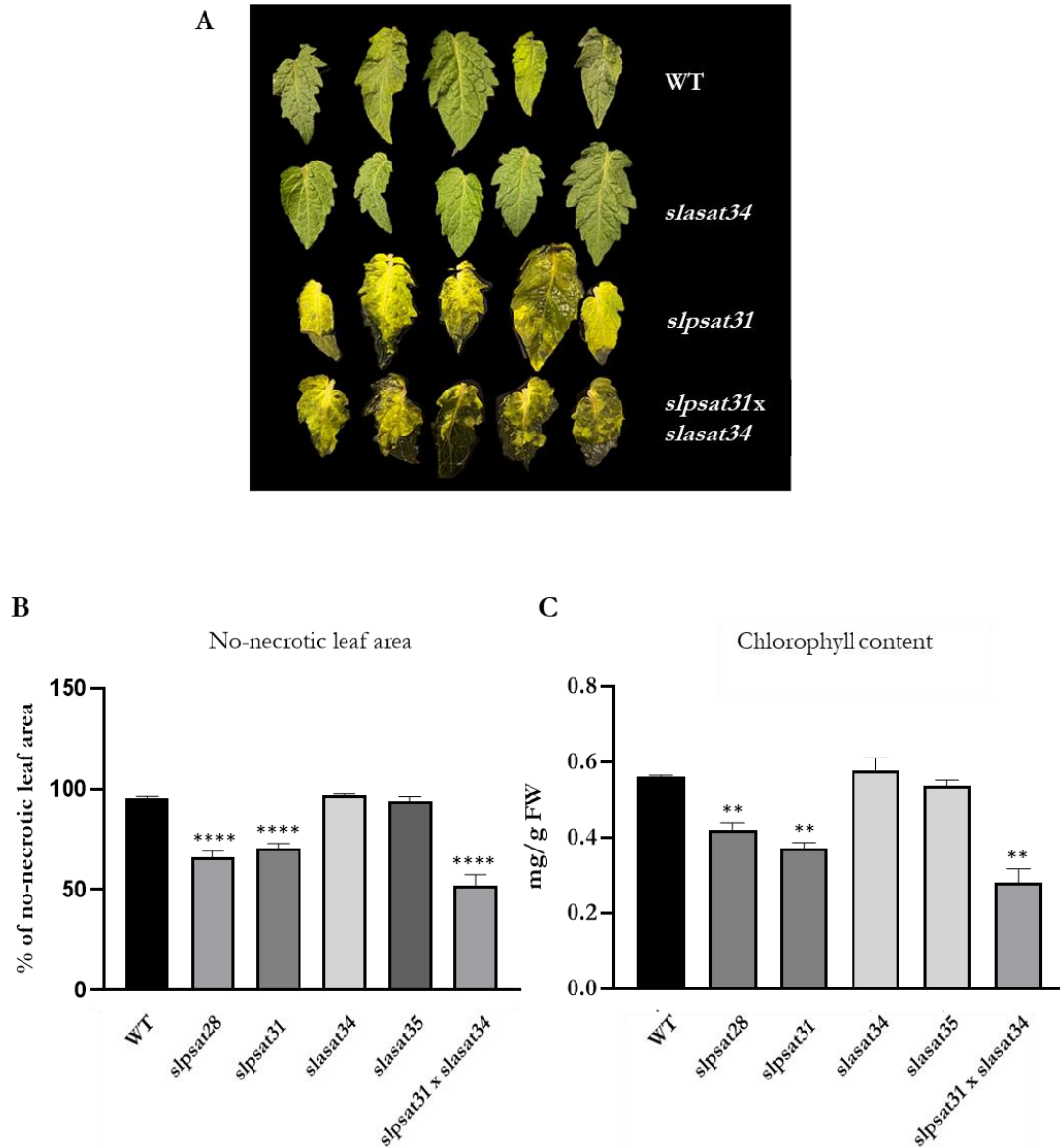


Figure 12. Induced senescence assay using detached leaves maintained in darkness. Representative image depicting detached leaves from WT, *slpsat31*, *slsat34*, and *slpsat31* $\times$ *slsat34* mutant plants following a 10-day water incubation in Petri dishes at 24°C under permanent darkness is presented (A). (B) The quantification of the percentage of non-necrotic leaf area was performed through leaf imaging using the ImageJ2 software. (C) Chlorophyll content was measured (Zang et al., 2009) in both wt and mutant plant leaves after 10-day incubation under the conditions. Statistical significance was assessed by the t-test, with asterisks denoting values significantly differing from those in the WT plants (** $P < 0.01$; **** $P < 0.001$).

or it could involve other regulatory processes, an induced leaf senescence assay was conducted. Leaflets from equivalent fully green leaves of WT and mutant plants (fourth leaf of 7-week-old plants) were detached and incubated in water in permanent darkness. After ten days of incubation, the leaflets from WT and *slasat34* and *slasat35* mutant leaves remained completely green, while those from *slpsat1* and *slpsat31* $\times$ *slasat34* mutant leaves exhibited clear senescence symptoms (yellow and necrotic areas) (Figure 12A). In fact, both *slasat1* mutant leaflets showed approximately the same percentage of non-necrotic area (97% in *slasat34* and 94% in *slasat35*) than WT (96%), whereas this percentage decreased significantly in *slpsat1* mutants (~66% in *slpsat28* and ~70% in *slpsat31*) and was even lower in the double mutant *slpsat31* $\times$ *slasat34* (~52%) (Figure 12B). The leaves of mutants *slpsat28* and *slasat35*, not shown in this figure, exhibited analogous phenotypes to *slpsat31* and *slasat35* leaves, respectively. These results were supported by the chlorophyll levels measured in the corresponding leaflet samples. Thus, no differences in chlorophyll content were observed between both *slasat1* mutants and WT plants (0.59 and 0.57 mg/g FW in *slasat34* and *slasat35*, respectively, compared to 0.58 mg/g FW in WT), while the pigment content was significantly lower in the *slpsat1* mutants (0.40 and 0.37 mg/g FW in *slpsat28* and *slpsat31*, respectively) compared to WT. In the double mutant the content was only about 0.30 mg/g FW (Figure 12C). The overall results demonstrated that normal levels of SIPSAT1, in contrast to SLASAT1, are required for proper leaf senescence progression, although in the absence of a functional SIPSAT1, the loss of SLASAT1 function has a synergistic effect in the premature induction of this physiological process.

3.1.5. Effect of SIPSAT1 and SLASAT1 inactivation on the sterol profile of tomato seeds

The loss of function of *SIPSAT1* and *SLASAT1* has the same qualitative effects on the SE levels in seeds than in leaves, but there are largely quantitative differences. Thus, inactivation of *SIPSAT1* resulted in a more severe SE reduction in seeds than in leaves, as SE levels were reduced to less than 10% (8.9% in *slpsat28* and 8.2% in *slpsat31*) of WT content (Figure 13B). However, as observed in leaves, the levels of SE increased significantly in both *slsat1* mutant seeds compared to WT, although at lower extent (48% in line *slsat34* and 61% *slsat35*) (Figure 13B). In contrast, the effects of impaired sterol esterification on FS levels were clearly different in leaves and seeds. While, as mentioned above, the levels of FS in leaves of both *slpsat* and *slsat1* mutants showed a moderate but significant enhancement compared to WT (Figure 9B), SIPSAT1 inactivation had no significant impact on seeds FS content and SLASAT1 knock-out caused a reduction in FS levels of about 60% (58% in *slsat34* and 63% in *slsat35*) those in WT (Figure 13A and Table 2). A detailed analysis of SE profiling showed that, as in leaves, the inactivation of both tomato sterol acyltransferases affected to a greater or lesser extent the contents of all measured esterified sterol species in seeds (Table 2).

In the *slpsat31* $\times$ *slsat34* double mutant, an additional reduction of SE levels was observed compared to the single *slpsat1* mutants (5% the content in WT seeds), while the levels of FS were similar to those of WT seeds (Figure 13A and B, Table 2). These results support the predominant role of SIPSAT1 in SE biosynthesis, while SLASAT1 would mainly have a regulatory role of the sterol biosynthesis pathway. Taken together, the results of the FS and SE profiling in leaves and seeds of the single and double mutants support the view that different regulatory mechanisms operate in both tomato organs.

Inactivation of SIPSAT1 and SLASAT affects also the content of glycosylated sterols in seeds. The loss of SIPSAT1 function resulted in a significant increase in SG (~ 3 -fold in *slpsat28* and ~ 2 -fold in *slpsat31*) and ASG (~ 2.4 - and 1.8 -fold in *slpsat28* and *slpsat31*, respectively) levels compared to WT (Figure 13C and D, Table 2). However, in both *slsat1* mutants the levels of SG and ASG were, in general, similar to those of WT (Figure 13C, D and Table 2). In the double mutant *slpsat31* $\times$ *slsat34* the fraction of glycosylated sterols almost doubled that in the WT (~ 1.5 -fold *vs* 1.3 -fold). This was due to the high levels of both for SG and ASG, which increased 3.3 - and 2.6 -fold, respectively, compared to WT seeds (Figure 13 C and D and Table 2)

The drastic reduction in SE levels in seeds of the *slpsat31* $\times$ *slsat34* mutant does not lead to a decrease in sterol synthesis, but rather to a moderate over-accumulation (1.7 fold) (Table 2),

which is accompanied by an internal reallocation of the total sterol pool. Thus, the levels of membrane sterols increased to about 1.2-fold in the double mutant compared to WT (Table 2). The fact that changes in the flux of one of the branches of the conjugated sterols pathway alters also the flux through the other and vice versa cannot be considered unexpected since FS are the common precursors of both glycosylated and esterified sterols.

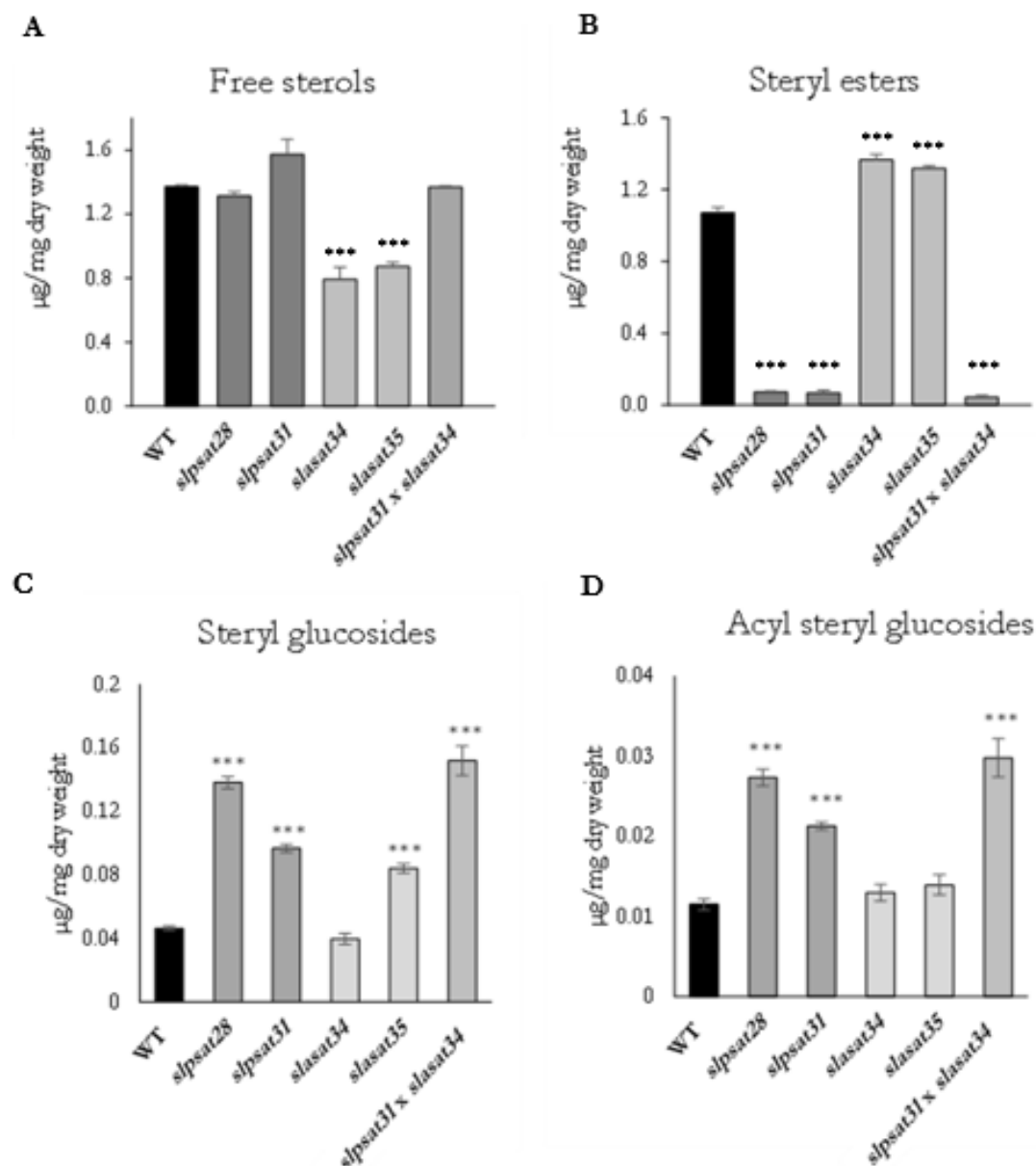


Figure 13. Total levels of free and conjugated sterols in seeds of *slpsat1*, *slsat1*, and *slpsat31 x slsat34* mutants. Quantification of free sterols (A) esterified sterols (B), steryl glucosides (C) and acyl steryl glucosides (D) was carried out in 1-week seeds. Data are presented as mean $\pm$ SEM from three biological replicates per genotype. Asterisks indicate values that are significantly different compared to those in the control plants determined by t-test (* $P < 0.005$)

Table 2. FS, SE, SG and ASG quantification in seeds of WT, *slasat34*, *slasat35*, *slpsat28*, *slpsat31* and *slpsat31* x *slasat34* mutants. Data shown as average values from three biological replicates with SEM in parentheses. n.d. stands for not detected. Significant changes compared to wild-type (WT) seeds are indicated by asterisks (*P<0.05; **P<0.01; ***P<0.005).

Seeds	WT	<i>slasat34</i>	<i>slasat35</i>	<i>slpsat28</i>	<i>slpsat31</i>	<i>slpsat31</i> x <i>slasat34</i>
(µg/mg dry weight)						
Total SE	0.8193 (0.0776)	1.2154** (0.0178)	1.3188*** (0.0161)	0.0733** (0.0054)	0.0673** (0.0155)	0.0429** (0.0101)
Cholesteryl	0.2617 (0.0182)	0.3663* (0.0047)	0.3171 (0.0104)	0.0044*** (0.0004)	n.d.	0.0035** (0.0003)
Campesterol	0.0439 (0.0019)	0.0459 (0.0021)	0.0368* (0.0007)	n.d.	n.d.	n.d.
Stigmasteryl	0.0323 (0.0037)	0.0597 (0.0033)	0.0303 (0.0020)	0.0005* (0.0003)	n.d.	0.0054* (0.0034)
Sitosterol	0.3675 (0.0432)	0.4947 (0.0133)	0.7561*** (0.0343)	0.0472* (0.0067)	0.0673** (0.0155)	0.0236* (0.0058)
Total FS	1.3710 (0.0090)	0.7923* (0.0761)	0.8711** (0.0277)	1.3121 (0.0270)	1.5726 (0.0927)	1.3689 (0.0079)
Total SG	0.0464 (0.0013)	0.0399 (0.0034)	0.0842 (0.0030)	0.1382 (0.0038)	0.0967 (0.0026)	0.1519 (0.0093)
Total ASG	0.0114 (0.0006)	0.0129 (0.0010)	0.0139 (0.0012)	0.0273 (0.0010)	0.0212 (0.0004)	0.0298 (0.0024)
Total sterols	2.2481 (0.0885)	2.0605 (0.0983)	2.2880 (0.0480)	1.5509*** (0.0372)	1.7578*** (0.1112)	1.5940*** (0.0297)

3.1.6. Tomato SIPSAT1 and SIASAT1 gene mutations increase the germination speed

It is generally accepted that mature seeds accumulate SE to meet the rapidly increasing demand for sterols when they germinate and during the early stages of seedling growth (Ferrer et al. 2017). Since loss of function of SIPSAT1 and SIASAT1 leads to altered levels of SE in seeds, being particularly remarkable the strong depletion in both single *slpsat1* and *slpsat31* $\times$ *slasat34* mutants (Figure 13B and Table 2), we analysed the effects of SIPSAT1 and SIASAT1 loss of function on the rate and speed of germination. As shown in Figure 14, the double mutant *slpsat31* $\times$ *slasat34* seeds germinated significantly faster compared to WT and both *slpsat1* and *slasat1* single mutants, whose seeds germinated also faster than WT (Figure 14A). Thus, the germination percentage of the double mutant was approximately 10-fold higher than WT 2 days after seed imbibition, but these differences decreased to 4-fold at day 3, when a significant increase of about 3-fold was observed in the germination percentage of both single *slpsat1* mutant seeds and, to a lesser extent (about 2-fold), on that of both *slasat1* mutant seeds (Figure 14B). These differences were also reflected in the calculated t50 values, which were only 1.92 days for *slpsat31* $\times$ *slasat34* mutant seeds compared to 3.56 days for WT seeds. A slight decrease in this value was also observed in the single mutants compared to WT (Figure 14B). Notably, at the end of the experimental process (7 days), no significant differences were detected between the germination percentage values of WT seeds and those from the different mutant genotypes (Figure 14B). All these data demonstrated that changes in SE content have no effect on tomato seeds final germination rate but cause an early germination phenotype, observed not only when the SE levels are decreased, but also, although more slightly, when they are increased. This unexpected result was confirmed by the stronger early germination phenotype shown by *slpsat31* $\times$ *slasat34* seeds, which demonstrated a synergistic effect of the two mutations in the regulation of this physiological process (Figure 14).

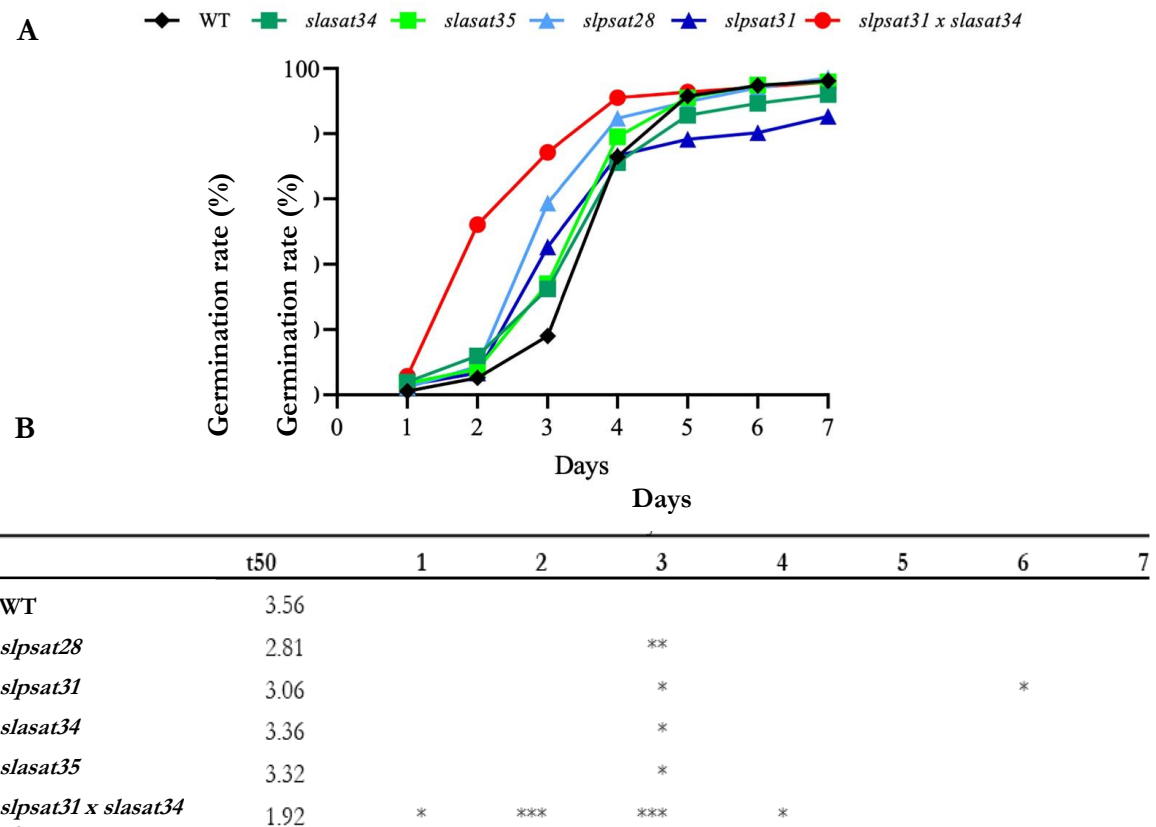


Figure 14. Germination rate of seeds from *slpsat1*, *slsat1*, and *slpsat31 x slsat34* knock-out mutants. Sterilized seeds (n=60 per genotype) were sown on MS plates and allowed to germinate under long day conditions (16h light/8h dark) at 24°C. The percentage of germinated seeds at the indicated time-points (A) was calculated by dividing the number of seeds showing radicle emergence by the total number of seeds. Data are presented as mean $\pm$ SEM from n=4-5 replicates per genotype. The t50 values (B) were calculated using the formula of Coolbear et al. (1984). Asterisks indicate values that are significantly different compared to those in the control plants determined by t-test (*P < 0.05; **P < 0.01; ***P < 0.005).

3.1.7. Effect of SIPSAT1 and SIASAT1 inactivation on the sterol profile of tomato mature fruit

The sterol profile was analysed on red tomato fruit pericarp. As observed previously in leaves and seeds, the SE content was markedly depleted in the *slpsat1* mutants, although this reduction was less severe than in seeds (5 and 4.6-fold in *slpsat28* and *slpsat31* mutants, respectively) (Figure 15B, Table 3). A detailed analysis of SE profiling showed that, as in leaves and seeds, the inactivation of SIPSAT1 affected to a greater or lesser extent the contents of all measured esterified sterol species, being the esterified cholesterol fraction the less affected one (Table 3). However, in contrast to that observed in leaves and seeds, the levels of SE did not increase significantly as a result of SIASAT1 inactivation, since similar amounts of SE were detected in red fruits of WT and both *slsat1* mutant lines (Figure 15B, Table 3). Neither significant changes were observed in the levels of FS in *slpsat1* and *slsat1* mutant fruits compared to WT (Figure 15A and Table 3). Like in seeds, an additional reduction of SE levels was observed in the *slpsat31* × *slsat34* double mutant fruits, compared to the single *slpsat1* mutants (12-fold lower than WT) (Figure 15B, Table 3), while the levels of FS were 1.6-fold higher in the double mutant than in WT fruits (Figure 15A, Table 3). These results agree with the predominant role of SIPSAT1 in SE biosynthesis mentioned previously in leaves and seeds, but also suggest a synergistic effect of both sterol acyl transferases in the regulation of SE and FS accumulation in fruits.

The analysis of glycosylated sterol profile showed that SIPSAT1 and SIASAT1 inactivation had different effects on the overall composition of this sterol fraction in fruits than in seeds. As observed in seeds, the levels of SG increased significantly in fruits of both *slpsat28* and *slpsat31* mutant lines (1.7- and 1.1-fold respectively), but this increase was less than that of seeds (between ~2-3-fold), and no significant changes on SG levels were detected on the *slsat1* mutant lines compared to WT (Figure 15C, Table 3). However, in contrast to the clear increase of ASG levels described in *slpsat1* mutant seeds (around 2-fold, Figure 15D), the levels of this sterol fraction were strongly depleted in *slpsat1* mutant fruits (~8.5-fold in *slpsat28* and ~11-fold in *slpsat31*), and a similar pattern was observed in fruits of *slsat1* mutant lines (7.6-fold decrease in *slsat34* and 5.4-fold in *slsat35* compared to WT). The inactivation of both sterol acyltransferases resulted in an increase of SG levels similar to that detected in the single *slpsat1* mutant fruits (1.8-fold compared to WT) (Figure 15C, Table 3), and a significant reduction of ASG levels (1.8-fold compared to WT), although clearly less marked than that observed in the single *slpsat1* and *slsat1* mutants (Figure 15D, Table 3). This lower

reduction made the double mutant maintain membrane sterols content (FS+SG+ASG) which in fact increased about 1.2-fold comparing to WT levels.

The profile of sterols in fruits show that, as previously reported by our group (Chavez et al., 2023) glycosylated sterols is the predominant sterol fraction in WT red tomato fruit (67%), being ASG the more abundant (39%) followed by SG (28%), while FS and SE are minor forms, representing only 19 % and 14% of the total sterols, respectively. The impairment of sterol esterification by inactivation of SIPSAT1 and SLASAT1 strongly altered the WT fruit sterol pattern. Thus, in contrast to that observed in WT mature fruits, SG was the more abundant fraction in the single (*slpsat1* and *slasat1*) and double *slpsat31* $\times$ *slasat34* mutants (about 50% of total content), followed by FS (about 28%), while ASG (about 21%) and SE (about 1%) were minor fractions. These results confirmed, that as observed in seeds, changes in the flux of one of the branches of the conjugated sterols pathway may alters also the flux through the other.

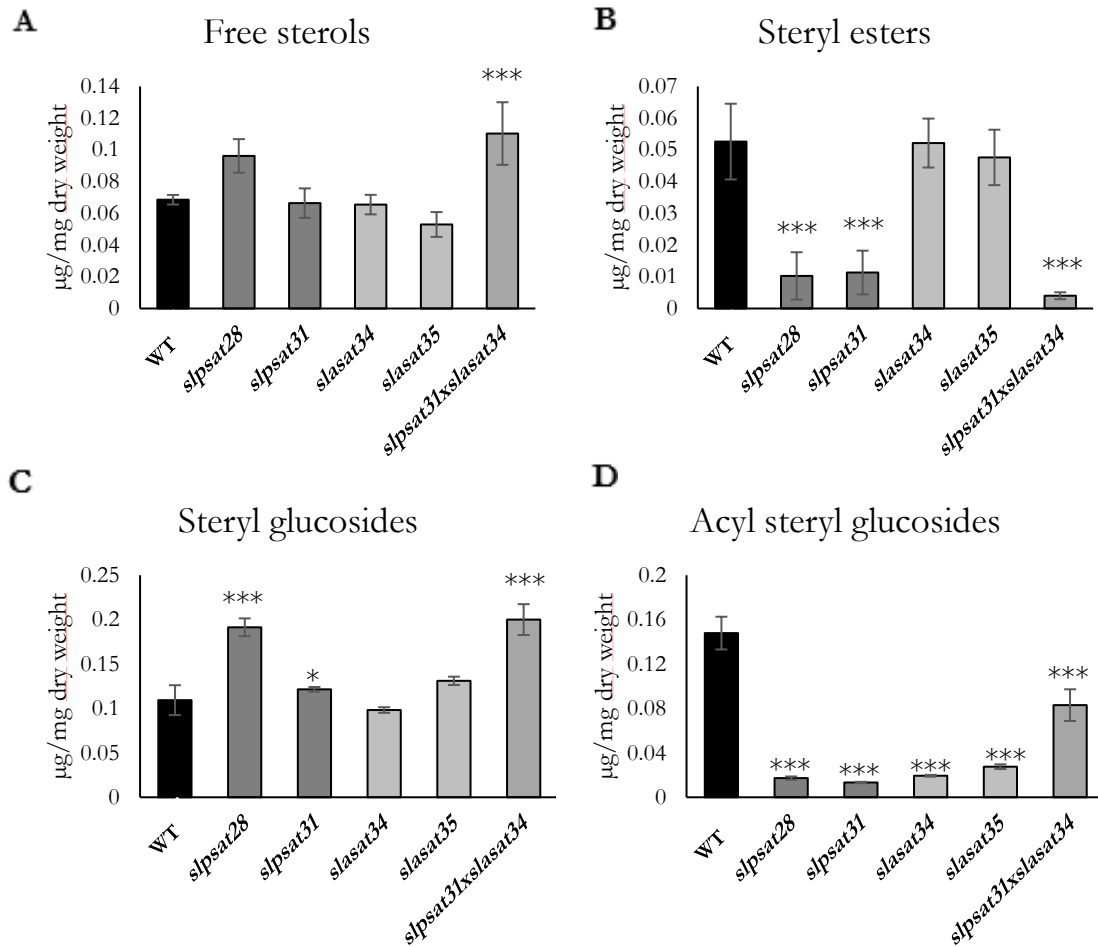


Figure 15. Total levels of free and conjugated sterols in fruits of *slpsat1*, *slasat1*, and *slpsat31 x slasat34* mutants. Quantification of free sterols (A) esterified sterols (B), sterol glucosides (C) and acyl sterol glucosides (D) was carried out in red ripe fruits. Data are presented as mean $\pm$ SEM from three (seeds) biological replicates per genotype. Asterisks indicate values that are significantly different compared to those in the control plants determined by t-test (* $P < 0.005$)

Table 3. FS, SE, SG and ASG quantification in fruits of WT, *slasat1*, *slpsat1* and *slpsat31 x slasat34* mutants. Data shown as average values from three biological replicates with SEM in parentheses. n.d. stands for not detected. Significant changes compared to WT seeds are indicated by asterisks (*P<0.05; **P<0.01; ***P<0.005).

	WT	<i>slasat34</i>	<i>slasat35</i>	<i>slpsat28</i>	<i>slpsat31</i>	<i>slpsat31 x slasat 34</i>
	(µg/ mg dry weight)					
Total SE	0.0526 (0.0119)	0.0522 (0.0077)	0.0476 (0.0087)	0.0102*** (0.0075)	0.0113*** (0.0069)	0.0040*** (0.0011)
Cholesteryl	0.0051 (0.0018)	0.0057 (0.0014)	0.0043 (0.0001)	0.0015** (0.0005)	0.0014** (0.0009)	0.0015** (0.0001)
Campsteryl	0.0057 (0.0003)	0.0065 (0.0007)	0.0056 (0.0008)	0.0004*** (0.0003)	0.0002*** (0.0001)	0.0004*** (0.0001)
Stigmasteryl	0.0084 (0.0020)	0.0084 (0.0005)	0.0066 (0.0002)	0.0005*** (0.0003)	0.0003*** (0.0001)	0.0004*** (0.0001)
Sitosteryl	0.0189 (0.0003)	0.0233* (0.0028)	0.0230* (0.0027)	0.0010*** (0.0005)	0.0007*** (0.0002)	0.0011*** (0.0005)
Total FS	0.0686 (0.0030)	0.0655 (0.0062)	0.0530 (0.0078)	0.0962* (0.0106)	0.0664 (0.0093)	0.1103*** (0.0197)
Total SG	0.1093 (0.0168)	0.0982 (0.0031)	0.1311 (0.0047)	0.1914*** (0.0101)	0.1215* (0.0027)	0.2000*** (0.0174)
Total ASG	0.1479 (0.0147)	0.0194*** (0.0008)	0.0275*** (0.0021)	0.0173*** (0.0015)	0.0133*** (0.0006)	0.0830*** (0.0143)
Total sterols	0.3784 (0.0464)	0.2383* (0.0178)	0.2345* (0.0233)	0.3151 (0.0297)	0.2125* (0.0195)	0.3973 (0.05250)

3.1.8. Effect of impaired steryl ester biosynthesis on tomato fruit quality

Given the contrasting sterol profile between WT and inactivated sterol acyltransferases mutant fruits, we decided to study if these changes could affect some fruit characteristics of agronomic/commercial interest. Different parameters, such as size, hardness, seed production and resistance to *Botrytis cinerea* infection were analysed in red WT and mutant fruits. Inactivation of SLPSAT1 and SLASAT1 did not affect fruit growth, since the area and weight of the single (*slpsat1* and *slasat1*) and double *slpsat31* $\times$ *slasat34* mutants were similar to that of WT (Figure 16A). The fruit hardness was neither affected in the single nor in the

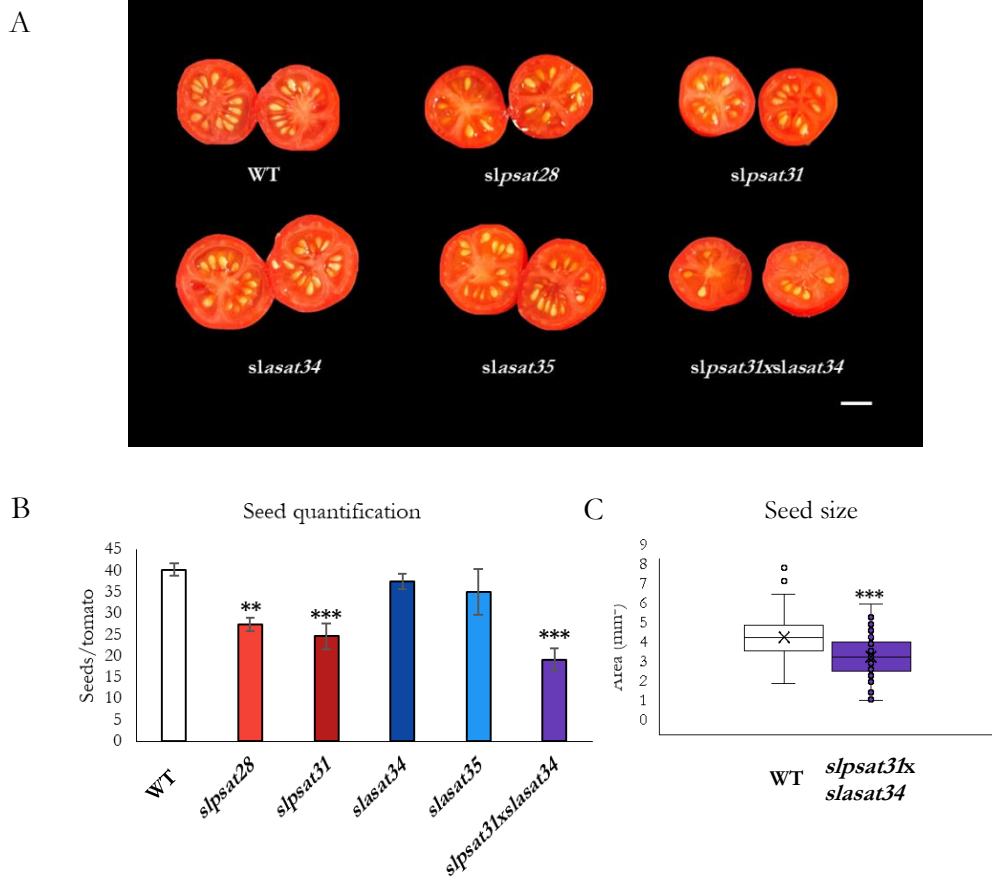


Figure 16. Physiological characteristics of red tomato fruit and seeds. (A) Seed quantification for WT, *slpsat28*, *slpsat31*, *slasat34*, *slasat35* and *slpsat31* $\times$ *slasat34* (n=30 fruits). (B) seed area represented for WT and *slpsat31* $\times$ *slasat34* respectively (n=50). (C) The appearance of tomato fruits at 36 DAA of WT, *slpsat28*, *slpsat31*, *slasat34*, *slasat35* and *slpsat31* $\times$ *slasat34*. Data presented as mean $\pm$ Asterisks indicate values that are significantly different compared to those in the WT plants determined by t-test (**P<0.01; ***P $\leq$ 0.005).

double mutants compared to WT. However, the seed production was lower in the *slpsat1* mutants than in WT fruits, with reductions about 32% and 39% in *slpsat28* and *slpsat31*, respectively, which reached a 52% decrease in the double *slpsat31* $\times$ *slasat34*. In contrast, no differences on seed production were detected between the *slasat1* mutants and WT fruits (Figure 16B). These results agree with those observed in plant senescence (Section 3.1.4) and

reinforce the idea that adequate levels of SLPSAT1, in contrast to SLASAT1, are required for the normal progression of different physiological processes, including the seed production. It is worth to mention that the double mutant seeds were significantly smaller than the WT, as demonstrated a 20% reduction in the area of the *slpsat31* $\times$ *slasat34* seeds compared to WT (Figure 16C).

Previous work by our group demonstrated that alterations in conjugated sterol levels, induced by changes in the expression of genes encoding sterol acyltransferases or SGTs, affected the Arabidopsis resistance to *Pseudomonas syringe* (Burciaga, 2020) and *B. cinerea* (Castillo et al. 2019). This fungus, causative of the gray mold, is one of the main causes of postharvest rot of fresh market tomatoes and can be a problem in greenhouse-grown

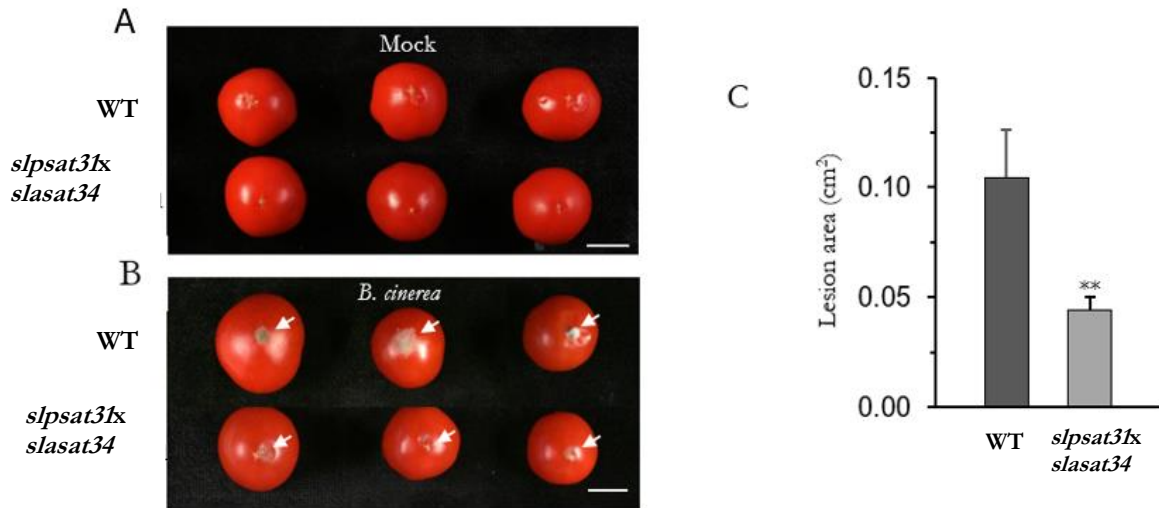


Figure 17. The *slpsat31* $\times$ *slasat34* fruits show enhanced resistance to *B. cinerea* infection. Representative images of fruits from WT and *slpsat31* $\times$ *slasat34* plants that were mock-treated (A) or inoculated with *B. cinerea* (B). The images were taken 7 days after treatment. Scale bar = 1 cm. (C) Data represent the mean $\pm$ SEM of lesion area (white arrows) in 20 fruits. The experiment was carried out twice with similar results. Asterisks indicate values that are significantly different compared to those in the control plants determined by t-test (**P<0.01).

tomatoes, being considered the second most important plant pathogen (Dean et al., 2012). This prompted us to investigate if the changed sterol profile observed in the double *slpsat31* $\times$ *slasat34* mutant fruits compared to WT resulted in different response against the infection with *B. cinerea*. To this end, red tomatoes (36 DAA) obtained from WT and double mutant plants were inoculated with a *B. cinerea* spore suspension, and the size of the resulting lesions was measured 7 days after inoculation. The results of three independent experiments showed a significant reduction (around 70%) on the average lesion diameter in *slpsat31* $\times$ *slasat34* fruits when compared with the lesion size in WT fruits (Figure 17). These results suggest that the alteration in sterol profile induced by inactivation of both sterol acyltransferases in tomato fruits results in increased resistance against *B. cinerea*. These data were further confirmed by the lower amount of genomic fungal DNA, measured as the amount of fungal

β -tubulin, detected in infected tomato fruits of the double *slpsat31* $\times$ *slasat34* mutant compared to the WT (58% reduction), which indicated that *Botrytis* growth in the mutant red fruit is clearly impaired compared to WT.

3.1.9. Altered sterol levels cause organ specific metabolic perturbations in fruits and seeds

The chemical composition of tomato fruits determines its quality and thus its commercial value, but also influences its stability under different environmental conditions, including pathogen attack. It is therefore important to establish the metabolic shifts occurring after introduction of genetic perturbations in order to understand both the resulting phenotypic alterations and the impact on fruit quality (Tohge & Fernie, 2015; Zhu et al., 2018). As a first step filling this gap, we have established the metabolic fingerprints in WT and

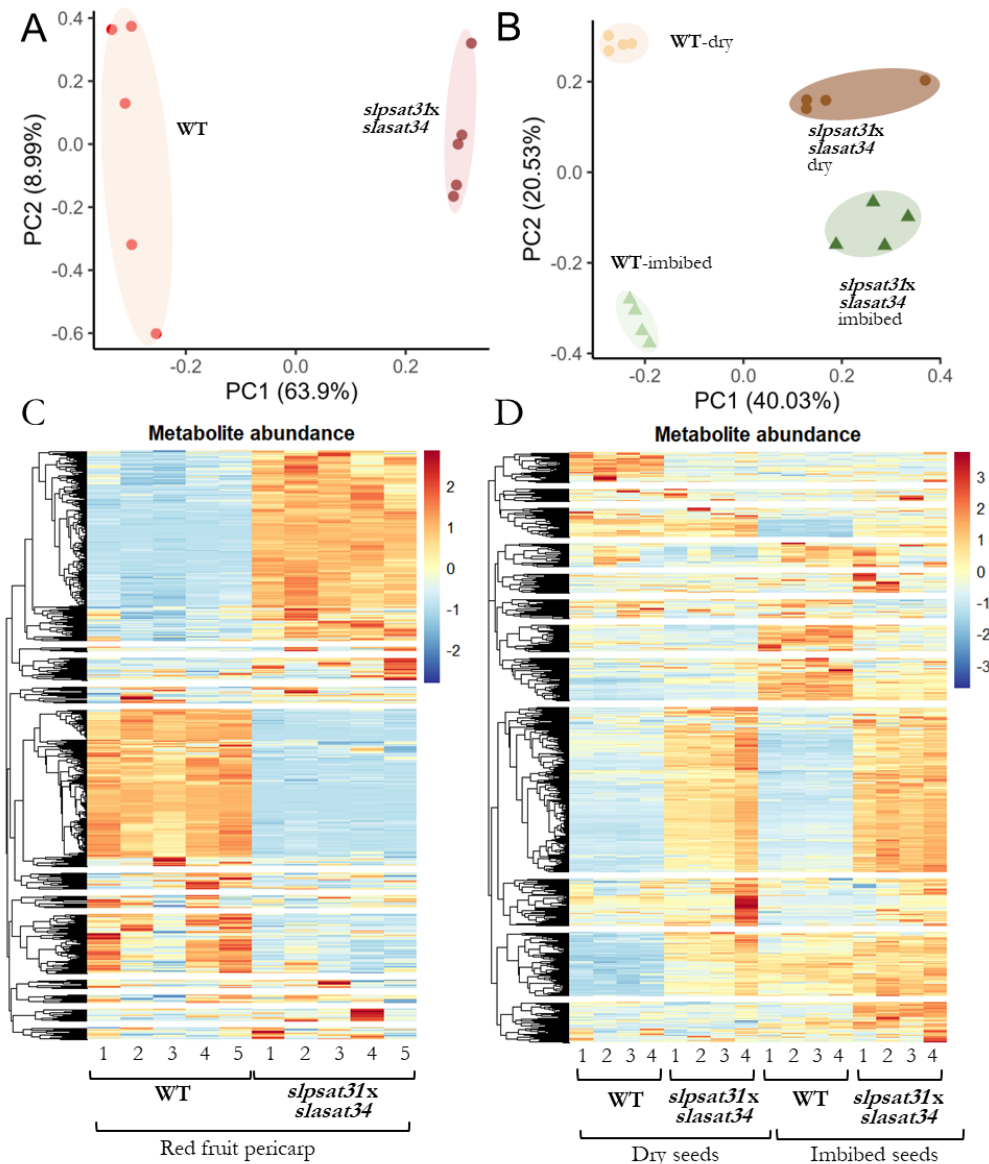


Figure 18. Metabolic profile distribution in WT and *slpsat31 x slasat34* tissues. (A-B) Principal component analysis (PCA) of the complete annotated metabolite dataset including primary, secondary and lipid metabolic profiles of red fruit (A) and dry and imbibed seed (B) tissue. The values represent the metabolite abundance previously normalized to the internal standard (ribitol, isovitexin and phosphatidylcholine, respectively) and tissue weight. (C-D) Clustered heatmap displaying the overall metabolite abundance of red fruit (C) and seed tissue (D). The scale is row-based.

slpsat31slaast34 tomato fruits (n=5) and dry and imbibed seeds (n=4). This analysis may also give some light about the molecular mechanism behind the phenotypes induced by the simultaneous inactivation of both sterol acyltransferases in tomato fruits and seeds. In total, 730 (350 positive and 380 negatively regulated compared to WT), 656 (467 positive and 184 negative) and 676 (488 positive and 188 negative) metabolites were identified in fruit pericarp, dry seeds and imbibed seeds, respectively. The PCA showed a clear segregation between WT and mutant fruit samples (Figure 18A). In seeds, WT and mutant samples segregate in clearly different groups according to both the imbibition treatment and the genotype (Figure 18B). Notably, the difference between mutant seeds upon imbibition is not as pronounced as in the WT. A hierarchical clustering heatmap confirmed the results of the

PCA as it shows several clearly contrasting patterns of primary and specialized metabolites between WT and mutant fruits (Figure 18C) and seeds (Figure 18D).

A more detailed analysis revealed important changes in the lipid composition of *slpsat31* $\times$ *slpsat34* red fruits compared to WT, which affected both storage lipids TAG and major lipid components of the PM (phospholipids, lysophospholipids, and sphingolipids) and photosynthetic membranes (galactolipids) (Figure 19). Among the four main classes of

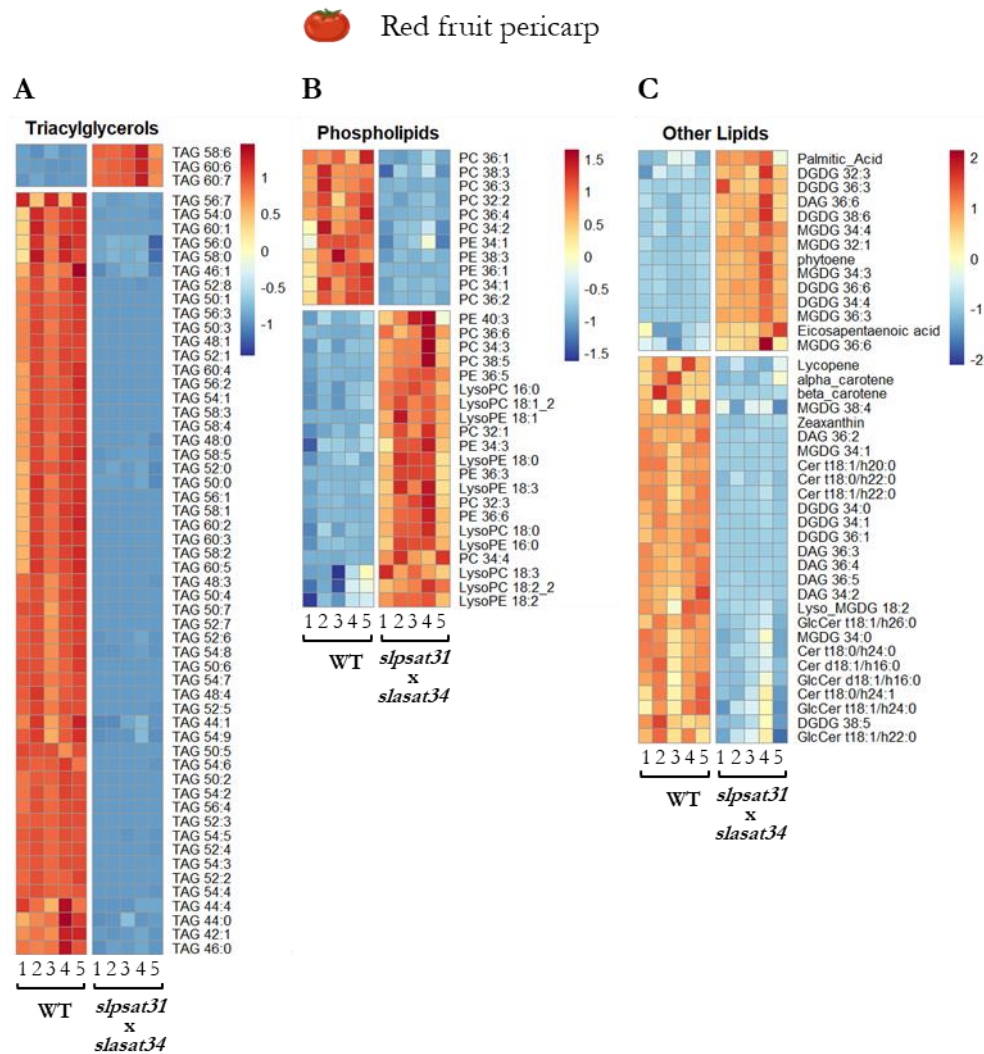


Figure 19. Highlighted lipid abundance and distribution in *slpsat31* $\times$ *slpsat34* and WT tissues. Significantly different accumulated metabolites (adjusted $p < 0.05$, Holm–Bonferroni method) with different patterns in *slpsat31* $\times$ *slpsat34* and wildtype were observed in red fruit pericarp (A–C) for triacylglycerols (A), phospholipids (B), other lipids (C). The scale is row-based

sphingolipids (Michaelson et al., 2016), the levels of glycosylinositolphosphoceramides and free long chain bases remained unchanged, while those of certain ceramides and glycosylceramides were notably reduced (Figure 19C). Conversely, mutant fruits had higher levels of lysophosphatidylcholine and lysophosphatidylethanolamine species than WT fruits (Figure 19B). The impact on major plant glycerophospholipids (phosphatidylcholine and

phosphatidylethanolamine), was uneven since the number of compounds with increased levels was the same as those with decreased levels, although the compounds with more unsaturated fatty acids tend to increase at the expense of those with a lower degree of unsaturation (Figure 19B). A similar mixed response, with the same trend towards species with more unsaturated fatty acids, was observed in major galactolipids, mono- and digalactosyldiacylglycerols (MGDG and DGDG) (Figure 19C). A tendency towards lower levels of diacylglycerols (DAGs), the common precursor of glycerophospholipids and galactolipids, was also noted (Figure 19C).

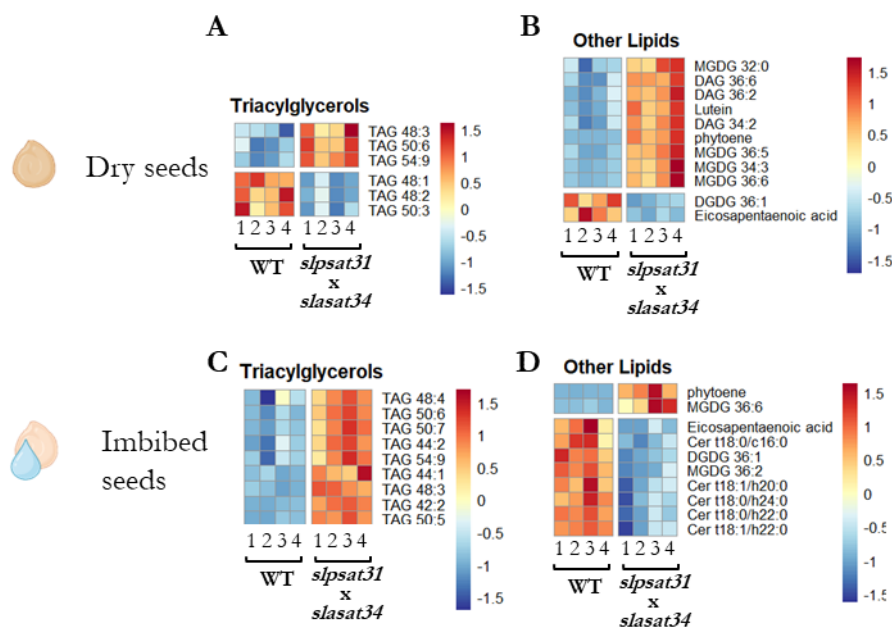


Figure 20. Highlighted lipid abundance and distribution in *slpsat31* x *slsat34* and wildtype tissues. Significantly different accumulated metabolites (adjusted $p < 0.05$, Holm–Bonferroni method) with different patterns in *slpsat31* x *slsat34* and WT. In dry seeds (A, B), differential patterns are shown for triacylglycerols (A), other lipids (B) and in imbibed seeds (C, D) for triacylglycerols (C), other lipids (D). The scale is row-based.

Interestingly, the effects of the *slpsat31* x *slsat34* mutation on the lipidome of dry and imbibed seeds was much less pronounced than in fruits (Figure 15B). Only the concentration of a few TAG, DAG, and galactolipid species were affected in dry seeds, (Figures 20A and B), and some TAG, ceramide, and galactolipid species in imbibed seeds (Figures 20C and D). Thus, it seems that the progression of *slpsat31* x *slsat34* mutant seeds from the dry to the imbibed stage was associated to higher levels of TAGs, and lower levels of DAGs, ceramides, MGDGs and DGDGs, compared to WT seeds. It is also worth to note that reduced SE levels led only to slight changes in seed TAG contents, while strong alterations were caused in fruits (compare Figure 20 and 21).

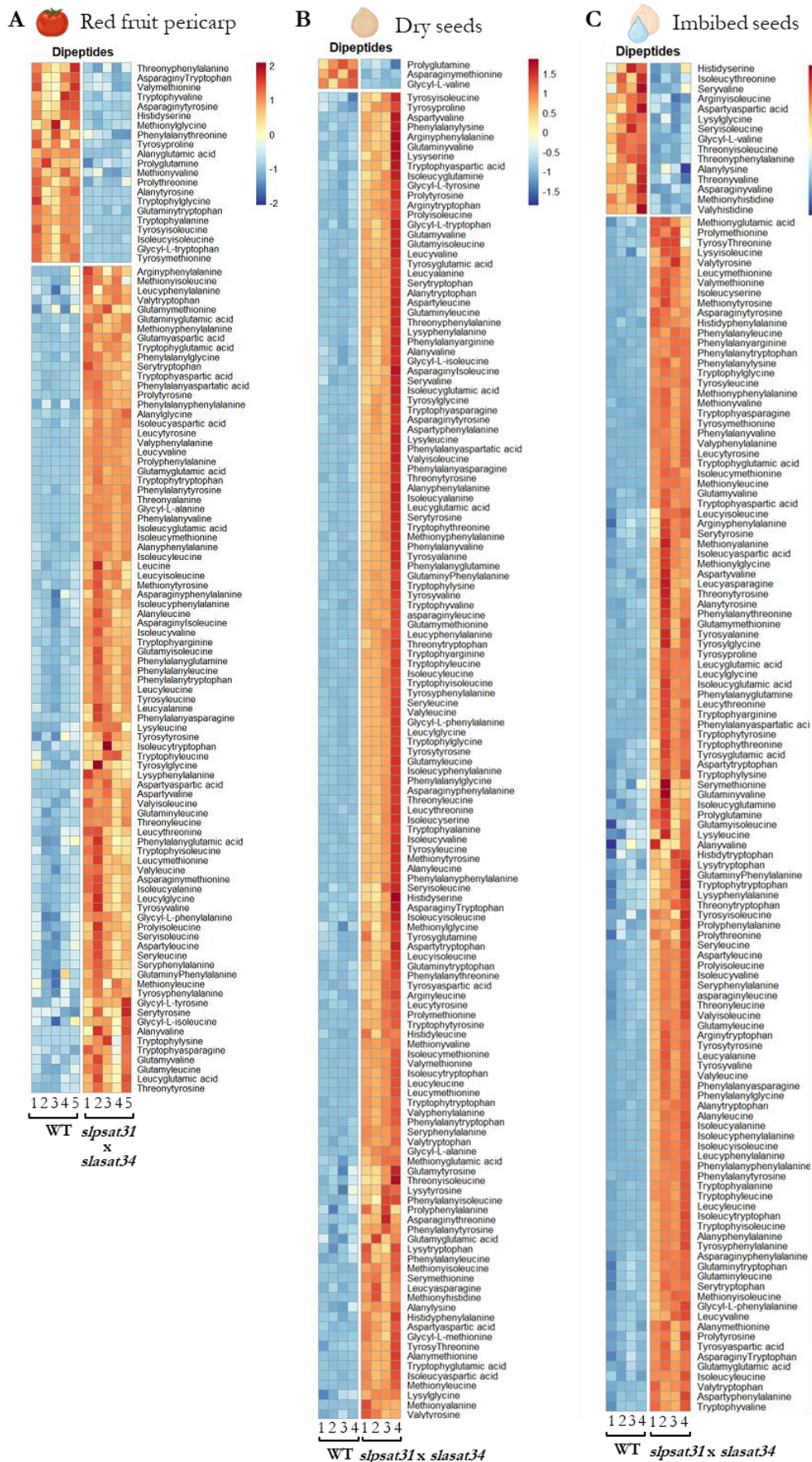


Figure 21. Highlighted dipeptide abundance and distribution in *slpsat31* x *slsat34* and WT tissues. Significantly different accumulated metabolites (adjusted $p < 0.05$, Holm-Bonferroni method) with different patterns in *slpsat31* x *slsat34* and wildtype were observed in red fruit pericarp (A), dry seeds (B) and in imbibed seeds (C). The scale is row-based.

Regarding specialized metabolites, phenylpropanoids were widely affected. In the fruit pericarp most of the significantly altered flavonoids were decreased in *slpsat31xslpsat34* mutants compared to WT. The majority of significantly altered phenylpropanoids in the *slpsat31 x slpsat34* fruit pericarp decrease their levels compared to the WT (Figure 22A). These include hydroxycinnamic acids, particularly mono-, di- and tri-caffeoylquinic acid species, anthocyanins like oenin, and flavonoids such as luteolin, neohesperidin, catechin and several quercetin and kaempferol derivatives. Chalcone naringenin and naringenin, the common precursors of anthocyanins and flavonoids, are also slightly reduced. Conversely, p-coumaric acid, an intermediate in the central phenylpropanoid pathway and its precursor phenylalanine are both increased, like the isoflavone genistein, which is a valuable estrogen mimicking compound in the pharmaceutical industry as well as an agent against pathogen infection

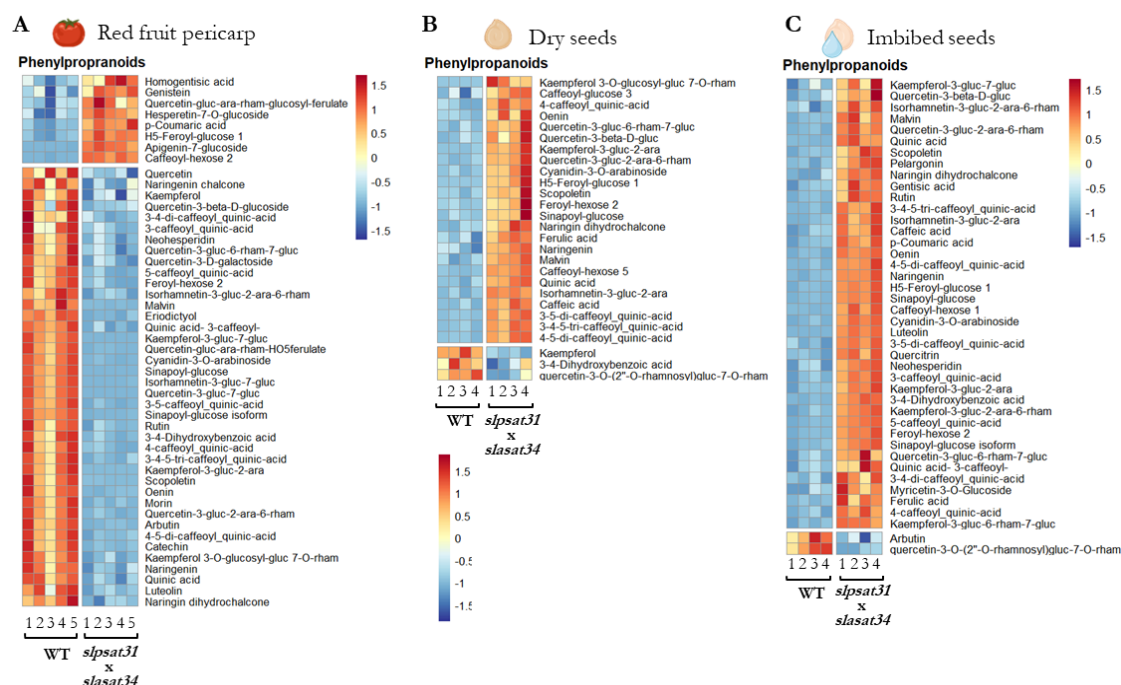


Figure 22. Highlighted phenylpropanoid abundance and distribution in *slpsat31 x slpsat34* and WT tissues. Significantly different accumulated metabolites (adjusted $p < 0.05$, Holm–Bonferroni method) with different patterns in *slpsat31 x slpsat34* and wildtype were observed in red fruit pericarp (A), dry seeds (B) and in imbibed seeds (C) The scale is row-based.

(Liggins et al. 2000; Liu et al. 2007; Jiang et al. 2012). Thus, it appears that the anthocyanin and flavonoid branches of the phenylpropanoid pathway (Ramaroson et al., 2022) are preferentially downregulated in the *slpsat31 x slpsat34* mutant. The impact of these changes on tomato fruit quality is difficult to assess, since despite a general decrease in phenylpropanoid contents, some of them significantly increase their levels in response to altered sterol levels (Figure 22A). This is the case of genistein, apigenin-7-glucoside and hesperitin-7-glucoside, all known for their antioxidant properties and therapeutic applications (Hojati et al., 2011; Falcone Ferreyra et al., 2012; Nazari-Khanamiri and

Ghasemnejad-Berenji, 2021), and quercetin-glucoside-arabinoside-rhamnosyl-glucosyl-ferulate (QGRAG). This is the only measured quercetin derivative accumulating to higher levels in the mutant, suggesting that this form is more stable in the mutant fruits and/or is synthesized in greater quantity.

Contrasting the fruit pericarp, dry and imbibed *slpsat31* x *slsat34* seeds exhibit higher levels of hydroxycinnamic acids, namely caffeic, ferulic, quinic, cafeoylquinic, their precursor p-coumaric acid, and a number of sugar conjugated forms. The levels of anthocyanins like malvin, oenin and pelargonin, and flavonoids such as luteolin, neohesperidin, kaempferol, rutin, and quercetin derivatives, were also significantly enhanced compared to WT seeds (Figure 22B and C). These changes suggest a general activation of the phenylpropanoid pathway (Rasmaroson et al., 2022), being this effect quantitatively and qualitatively more pronounced in imbibed seeds, which tend to accumulate higher levels of phenylpropanoids that are significantly altered in both dry and imbibed seeds and show a higher number of compounds that increase in abundance compared to dry seeds (Figure 22B and C).

In contrast to the differential response of the fruit and seed lipid and phenylpropanoid metabolism to the impairment of SE biosynthesis, both *slpsat31* x *slsat34* organs showed an important accumulation of dipeptides compared to the WT (Figure 21), and to a lesser extend of single amino acids (Supplemental Figure 2), with only a few dipeptides displaying lower levels in the mutant organs compared to the wt. This effect was more pronounced in seeds (Figure 22B and C) than in fruits (Figure 22A). Dipeptides, with a few exceptions, are proteolytic products that accumulate in response to the induction of autophagy (Thirumalaikumar et al., 2020), a catabolic process responsible for degrading unwanted or damaged cytoplasmic components, including proteins, to recycle their basic building.

Taking all together, in fruit pericarp, a variety of up- and downregulated metabolites was observed (Figure 23C). Notably, the volcano plots (Figure 23A and B) revealed that in seeds

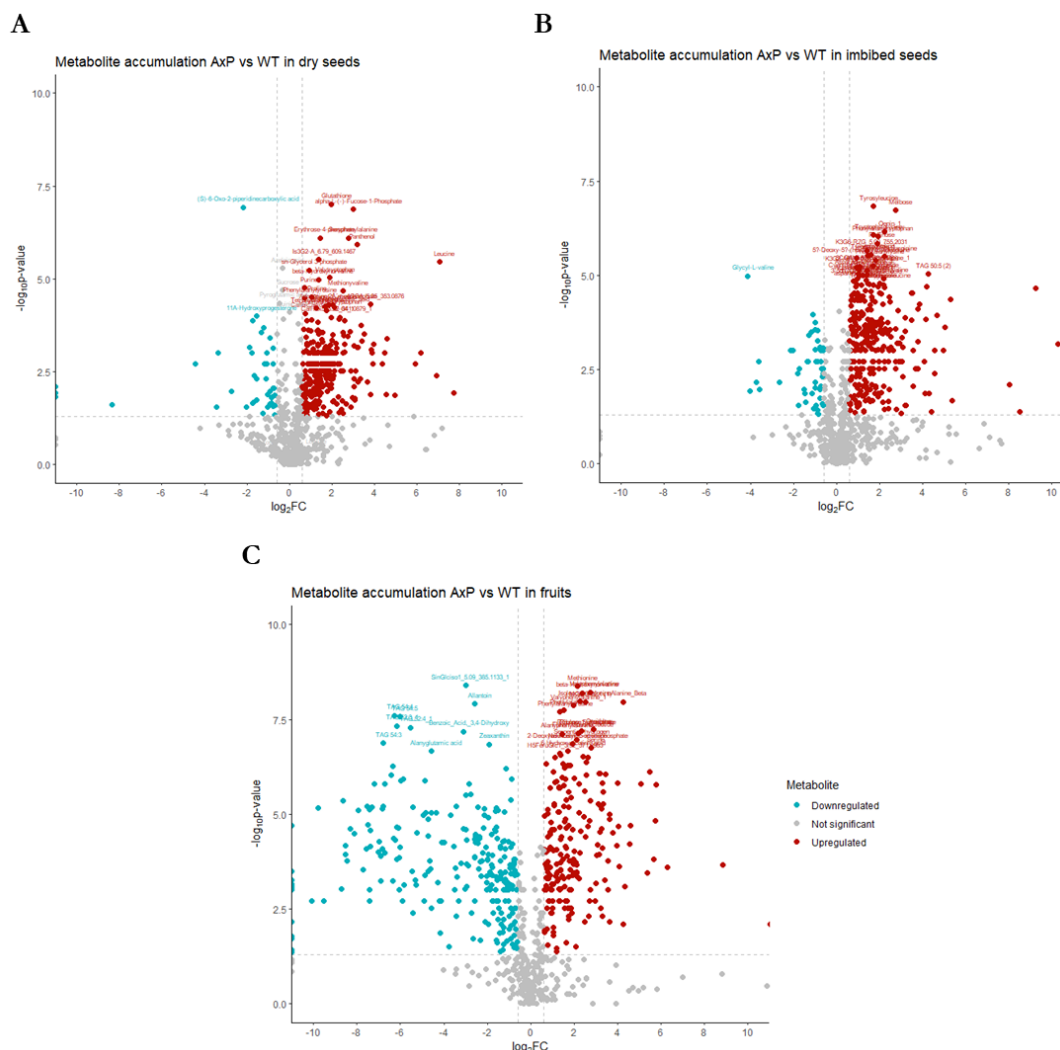


Figure 23. Differential metabolite abundance in *slpsat31* x *slasat34* versus WT in different tissues. A-C Volcano plot analysis of metabolites accumulated in *slpsat31* x *slasat34* normalized against the WT ($\log_2\text{Foldchange} > 0.6$ and $p\text{-value} < 0.05$) in dry seed (A), imbibed seed (B) and red fruit (C) tissues.

of *slpsat31* $\times$ *slasat34* mutants compared to WT, more compounds were upregulated than downregulated pointing towards a more active metabolism and an activation of biosynthetic processes. Moreover, the PCA results suggested that mutant seeds appear to be in a more activated state already prior inhibition (Figure 18B). The analysis of significant altered pathways (false discovery rate (FDR) below 0.05), using MetaboAnalyst 5.0 (<https://www.metaboanalyst.ca/>) (Le et al. 2023), also revealed alterations in the starch and sucrose metabolism, supporting a higher activity (Figure 24B). The changes in various amino acid pathways reflect those in dipeptides (Figure 21) and amino acids (Supplemental Table 4). In red fruit tissue, these included valine, leucine, and isoleucine biosynthesis, as well as

glycine, serine, and threonine metabolism. Both seeds and fruits, also showed significant changes in flavone and flavonol biosynthesis and glycerolipid metabolism.

Taken together, these findings underscore significant metabolic rewiring in *slpsat31* $\times$ *slsat34* mutants, suggesting intricate metabolite alterations that might explain the observed phenotypic differences compared to WT counterparts (Figure 24A).

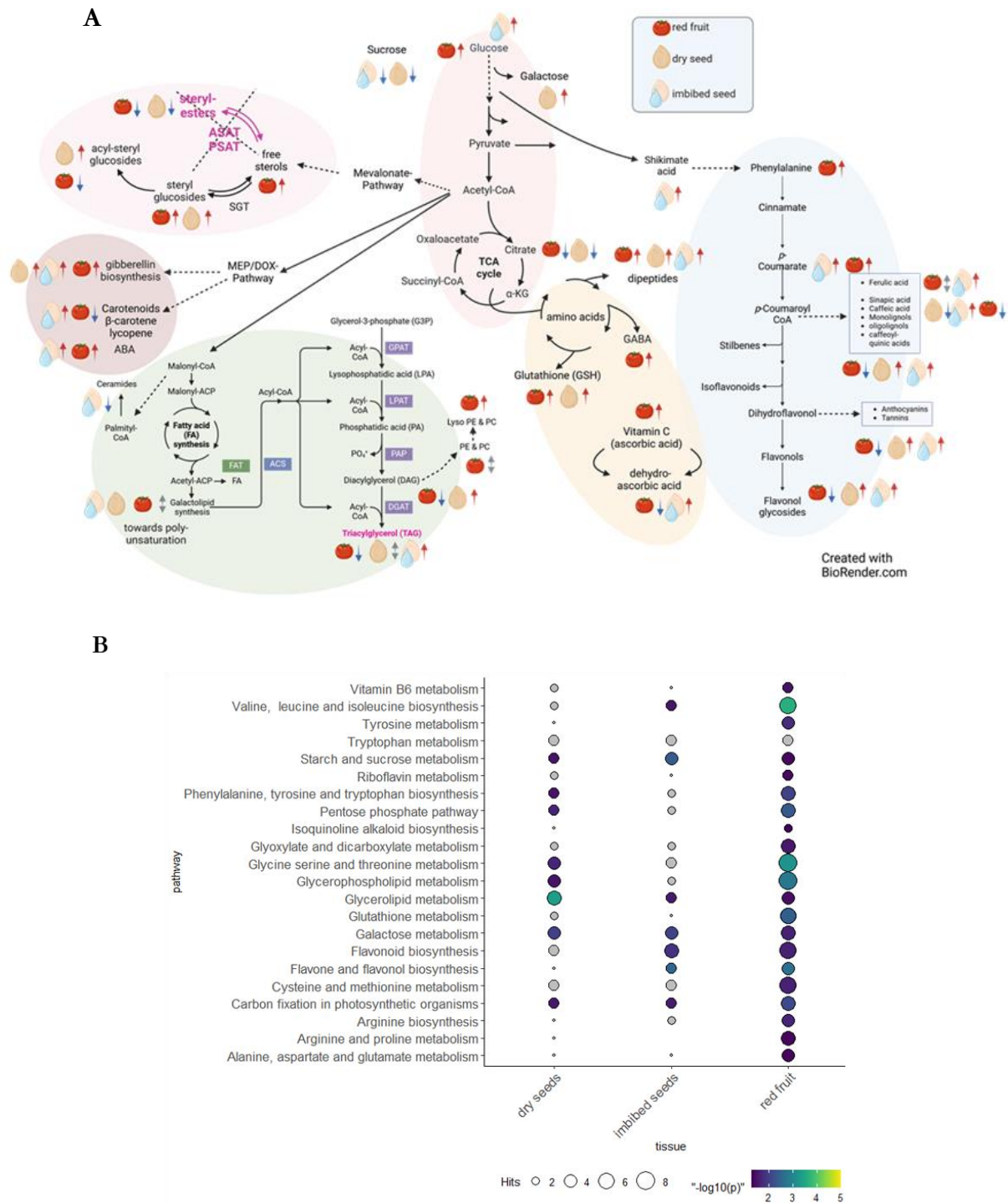


Figure 24. Differential metabolite pathways in *slpsat31* x *slasat34* versus WT in different tissues. (A) schematic representation of pathways changed in fruit or seed tissue in *slpsat31* x *slasat34* compared to the wildtype. Pathways are based on KEGG. (B) Metabolic pathway analysis computed with the help of MetaboAnalyst 5.0 (<https://www.metaboanalyst.ca/>) (Le et al. 2023) based on differentially accumulated metabolites (adjusted $p < 0.05$) respective to the WT median in dry seed, imbibed seed and red fruit tissues. Non-significant pathways in a tissue are depicted in grey.

3.2. CHAPTER II

From germination to fruit: Unraveling the role of *SlSGT3* on tomato (*Solanum lycopersicum* cv MicroTom) plant growth and development

This chapter focuses on investigating the impact of *SlSGT3* sterol glycosylation on tomato plant and fruit development. For this, we generated transgenic lines in which the *SlSGT3* gene was overexpressed under the control of a constitutive and a fruit specific promoter. Moreover, to understand the endogenous regulation of *SlSGT3*, we have obtained transgenic lines expressing the *GUS* reporter gene under the control of the *SlSGT3* promoter.

3.2.1. Generation of tomato plants expressing the *GUS* reporter gene under native *SlSGT3* promoter

To establish the spatial and temporal expression pattern of the *SlSGT3* gene in tomato plants, we obtained transgenic tomato lines containing the β -glucuronidase (*GUS*) reporter gene under the control of the *SlSGT3* promoter. Since this promoter region has not been defined, a fragment comprising 2358 bp of the 5'-flanking region of the *SlSGT3* gene from the first translated codon was amplified (Figure 25B) and cloned into the binary vector pGWB443, which contains the coding region for the *GUS* gene and the gene conferring resistance to kanamycin (*NPTII*) as a selection marker (Figure 25A). The resulting *proSlSGT3::GUS* transgene (Figure 25C) was introduced into tomato plants by *Agrobacterium tumefaciens* mediated transformation of cotyledons (Section 6.6) and transgenic plants were selected by their resistance to kanamycin. The presence of the transgene in the 5 kanamycin-resistant plants obtained was confirmed by PCR (Figure 25C) using genomic DNA as a template and *nptII* primers (Table 11). Subsequently, the number of copies of the transgene was determined by qPCR using the tomato *LAT52* (Soly10g007270) as endogenous single copy gene (Section 6.3.6). The results of this analysis showed that 3 (plants 42.1, 50.1, 50.2) out of the 5 T₀ transgenic plants contained a single transgene copy per genome. Among them, only plants 42.1 and 50.1 yielded seeds so it was decided to continue working with these 2 plants. Segregation analysis by qPCR of the *proSlSGT3::GUS* transgene in successive generations allowed us to select 2 independent homozygous lines, further referred to as #42 and #50, with a single transgene copy that were used for further characterization.

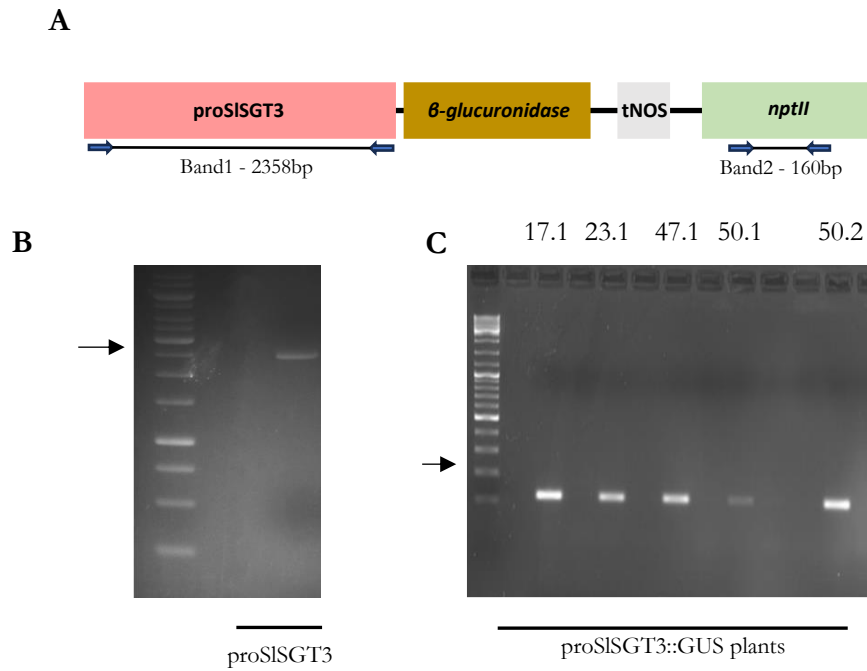


Figure 25. *SISGT3* promoter amplification and *proSISGT3::GUS* transgene analysis. (A) Schematic representation of the T-DNA in the binary vector used for tomato transformation to express GUS gene using a the *SISGT3* gene promoter. The nopaline synthase terminator (tNOS), and the marker gene for resistance to kanamycin (*nptII*) are shown. Arrows show the position of the primers used to amplify the *SISGT3* promoter (B) and for transgene detection (C). (B) Agarose gel electrophoresis showing the 2385 bp band corresponding to the amplified promoter fragment from tomato genomic DNA and primers containing the att recombination sites for gateway cloning into pGWB443. The position of the 2500 bp marker is shown by an arrow (C) Agarose gel electrophoresis showing the 160 bp amplicon obtained with *nptII* gene primers and genomic DNA from plants 17.1, 23.1, 47.1, 50.1 and 50.2. The position of the 250 bp marker is shown by an arrow.

3.2.2. Histochemical assay of GUS enzyme activity in *proSISGT3::GUS* transgenic tomato lines

To investigate the GUS expression pattern, histochemical analysis of GUS activity was carried out in fruits from transgenic lines 42 and 50 at different developmental stages (9, 15, 30, 32, 36 DAA) corresponding to small green (SG), green (G), mature green (MG), breaker (B) and red (R), respectively. Fruit slices were incubated in GUS staining solution as described (Dedow et al., 2022) for different time intervals (Figure 26). As expected, the staining kinetics assay revealed a progressive increase in staining intensity over time. It must be mentioned that both transgenic lines showed the same qualitative pattern of GUS activity. Notably, blue staining was observed in the seeds at all fruit developmental stages, except for

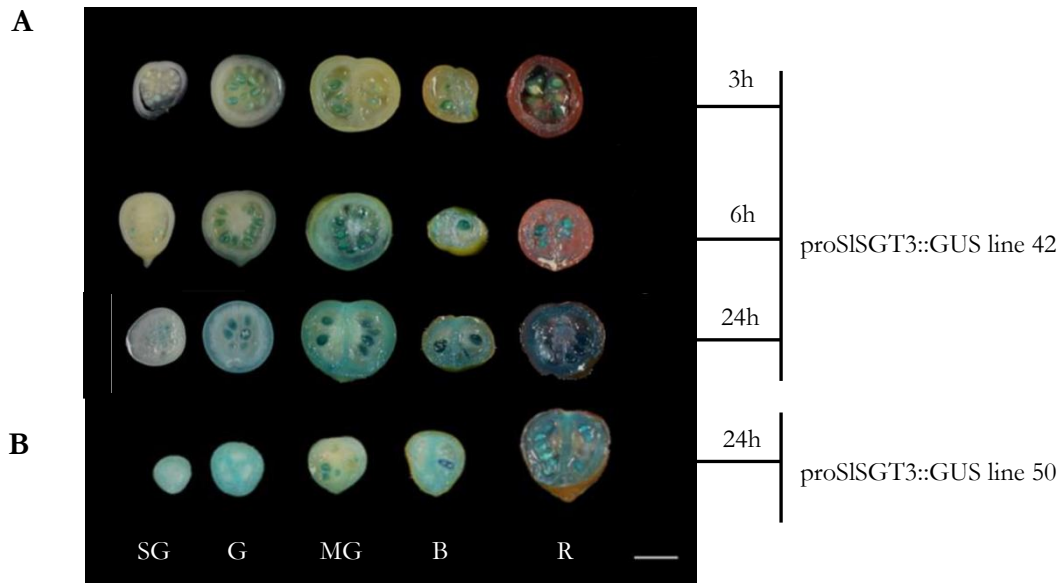


Figure 26. Representative images showing histochemical detection of GUS enzyme activity in *proSISGT3::GUS* tomato fruits at the indicated developmental stages. (A) Staining kinetics in fruits (line 42) after incubation with the GUS substrate for 3, 6 and 24 hours. (B) Staining (line 50) fruits incubated for 24 hours.

the small green (SG) stage where seeds were not yet present. Additionally, a less intense but clearly detectable blue staining was observed in the pericarp tissue, which was visible from the very early stages of fruit development until the R stage. Furthermore, especially after overnight incubation with the GUS substrate, the placenta also exhibited GUS activity. 24-hour period. Next, we investigated the expression of GUS activity in flowers. After overnight staining with the GUS substrate, significant staining in the male reproductive part of the flower, particularly in the filaments of stamens, was detected (Figure 27A and B), while no clear staining was observed in the anthers (Figure 27B). The female parts of the flower exhibited minimal GUS enzyme activity in the ovary and the style (Figure 27C and D), while

an intense blue staining was detected in the stigma (Figure 27D). The other parts of the flower such as petals and sepals did not exhibit any histochemical detectable signal.

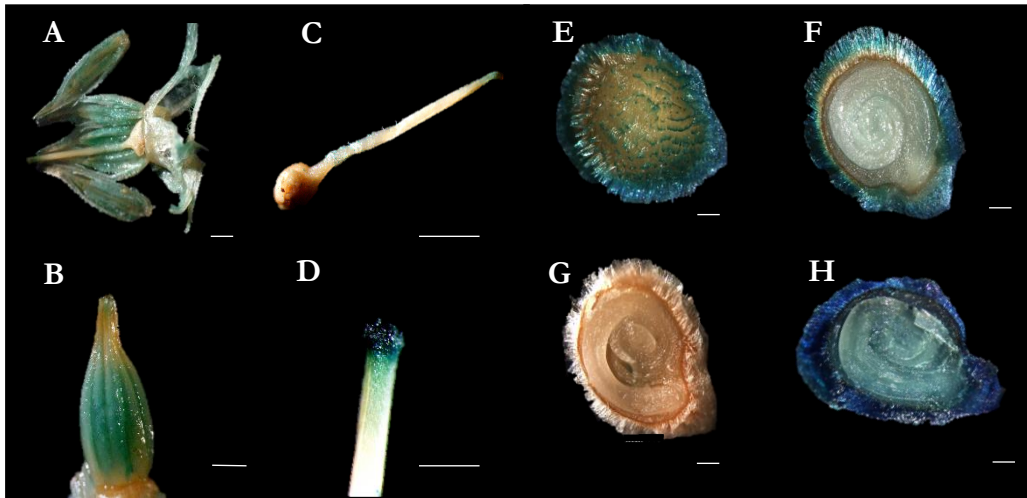


Figure 27. Representative images showing histochemical detection of GUS enzyme activity of the *proSISGT3::GUS* (line 42) tomato flowers and seeds. (A) Fully opened flower. (C) . Stamens. (C) Stigma. (D) Top of the stigma. (E) Whole pre-washed seed. (F) Longitudinal cut of a pre-washed fresh seed. (G) Longitudinal cut of dry seed. (H) Longitudinal cut of fresh seed collected from a previously stained tomato fruit. GUS activity in the different samples was assayed overnight. Scale bar = 300μm.

Given the pronounced staining observed in fruit seeds (Figure 26), a detailed examination of GUS staining in the seeds was also conducted. Dry seeds, fresh seeds rinsed with distilled water (pre-washed), and fresh seeds obtained from fully stained tomatoes were treated with the GUS staining solution (Figure 27E, F, G and H). Notably, dry seeds exhibited no staining (Figure 27G). Pre-washed seeds displayed a unique staining pattern, with neither the embryo nor the seed coat exhibiting staining (Figure 27E and F) concentrating the staining in the trichomes on the seed coat. However, most fresh seed tissues, were stained giving specifically more intensity in trichomes and the seed coat and in a lesser extend to the embryo (Figure 27H). Although the general staining observed in fresh seeds (Figure 27H), the blue staining was considerably less intense when seeds were fresh but had been washed before incubation with the GUS substrate, suggesting that trichome staining is likely attributable to GUS activity in the locular gel tissue adhered to the seed coat, rather than GUS activity in the trichomes (Figure 27E). As locular tissue has gel texture it was assumed that in fresh seeds, part of this locular tissue surrounding the seed kept contact with the rest of seed part making this unspecific staining observed in fresh seeds (Figure 27H).

3.2.3. Generation of tomato (*Solanum lycopersicum* cv MicroTom) plants overexpressing sterol glucosyltransferase 3 (SGT3)

To investigate the role of SSGT3 gene, we generated transgenic tomato lines constitutively overexpressing the cDNA encoding SSGT3 (SSGT3-ox). To this end, the chimeric gene *35SCaMV:SSGT3:Tnos* (Figure 28A) was introduced into tomato plants by *Agrobacterium tumefaciens* mediated transformation. Transgenic plants were selected by their resistance to kanamycin and 5 plants were obtained. The presence of the transgene in these plants was confirmed by PCR (Figure 28B) using genomic DNA as a template and nptII primers (Table

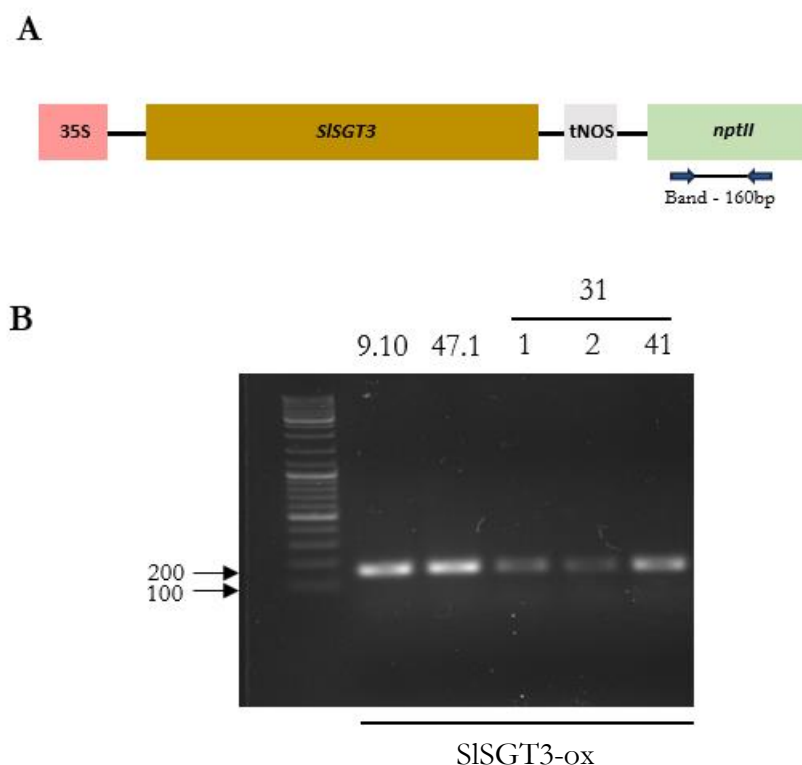


Figure 28. Identification of *35SCaMV:SSGT3:Tnos* transgene insertion in transformed tomato plants. (A) Schematic representation of the transgene to overexpress SSGT3 using the constitutive promoter CaMV35S (35S), Nos terminator (NOS-T), and the marker gene for resistance to kanamycin (NPTII). Arrows show the position of the primers used for transgenic lines genotyping, (B) Agarose gel electrophoresis showing the 160-bp PCR amplification product (nptII coding sequence) from genomic DNA of the T0 transgenic plants indicated on top of the image.

16). Next, we determined the number of copies of the transgene present in the T-DNA by qPCR using the tomato *LAT52* (Solyc10g007270) as endogenous single copy gene (Section 6.3.6). The results of this analysis showed that 3 (9.10, 47.1, 31.1) out of the 5 T0 transgenic plants contained a single transgene copy per genome. From this 3 plants, unfortunately, only plant #9 yielded seeds, so it was decided to continue working with this plant. As we had 2 remaining plants, we also decided to work with T0 plant #31.2, which had 2 copies of the transgene and seeds. Segregation analysis by qPCR of the *35SCaMV:SSGT3:Tnos* transgene

in successive generations allowed us to select 2 independent homozygous lines, further referred to as #9 and #31, with a single transgene copy that were used for further characterization.

3.2.4. Characterization of SISGT3-ox plants

3.2.4.1. Expression analysis of *SISGT3* in leaves of *SISGT3*-ox plants

The expression of *SISGT3* was quantified by RT-qPCR in the two selected *SISGT3*-ox homozygous lines using total RNA extracted from fourth leaf of 1-month-old plants. As expected, the expression of *SISGT3* was significantly higher and similar in both transgenic lines (4.3- and 4-fold in lines #9 and #31, respectively) compared with WT plants (Figure 29). It is worth to mention that, as reported previously by our research group (Ramírez-Estrada et al. 2017), the expression of *SISGT3* in WT plant leaves was very low.

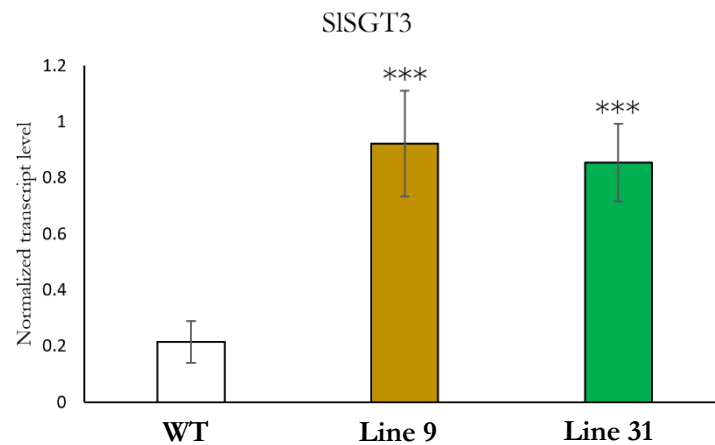


Figure 29. Expression levels of *SISGT3* in homozygous single transgene copy lines. Expression levels of *SISGT3* in the transgenic and WT plants were determined by RT-qPCR using RNA extracted from leaves of one-month-old plants. Data given for WT and mutant lines are expressed as normalized mRNA quantity using the actin gene (Solyc03g078400) as a housekeeping gene. Values are mean $\pm$ SEM from three biological replicates per genotype with three technical replicates each (n=9). Asterisks represented significant differences compared to WT determined by t-test (***P $\leq$ 0.005)

3.2.4.2. Sterol profile in leaves of *SISGT3-ox* plants

In order to investigate if the overexpression of *SISGT3* resulted in changes of the sterol profile in the leaves, the levels of the different sterol fractions were quantified in extracts obtained from the fourth leaves of WT and lines 9 and 31 from 1-month-old *SISGT3-ox* plants. As expected, the overexpression of *SISGT3* results in a general increase of total

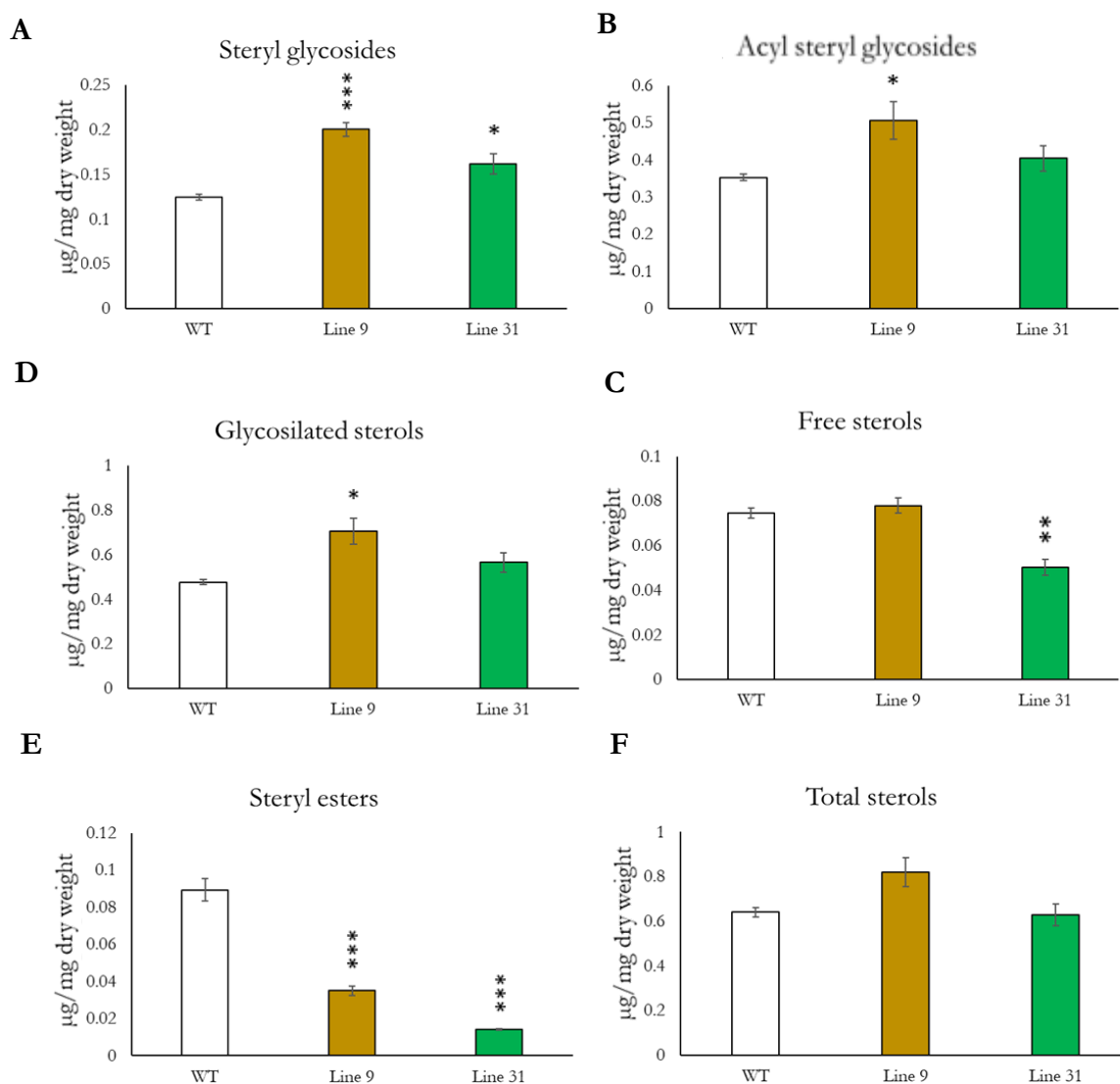


Figure 30. Content of free and conjugated sterol in leaves of WT and *SISGT3-ox* lines. (A) steryl glycosides, (B) acylated steryl glycosides, (C) glycosylated sterols (SG+ASG), (D) free sterols, (E) steryl esters, and (F) total sterols (four fractions) in WT and overexpressing lines 9 and 31. Total content in the different fractions includes cholesterol, campesterol, stigmasterol, and β -sitosterol species. Data are expressed as mean µg sterol per mg of dry weight and $\pm$ SEM from three biological replicates with three technical replicates each (n=9). Asterisks represented significant differences compared to WT determined by t-test (* $P \leq 0.05$; ** $P \leq 0.01$; *** $P \leq 0.005$)

glycosylated sterols (SG + ASG). This effect was mainly due to an increase in the SG content, which was around 66% and 30% in lines 9 and 31, respectively, compared to the WT plants. The content of ASG also increased but to a lesser extent, 43% in line 9 and 15% in line 31. (Figure 30A and B). As shown in Figure 30A, the four major glycosylated sterols were

increased in both transgenic lines compared to the WT albeit to a different extent. The levels of glycosylated cholesterol increased by about 66% and 59% in lines 9 and 31 (Figure 31A), respectively, while those of stigmasterol and β -sitosterol increased by about 100% and 35% only in line 9, while in line 31 the levels of these two glycosylated sterols were only slightly enhanced (Figure 31A). The content of glycosylated campesterol, were also higher than WT in both SLSGT3-ox lines (Figure 31A). As for the ASG, the levels of the four major species tends to increase being stigmasterol the only specie significantly increased compared to WT plants (Figure 31B). Although to a lesser extent, ASG showed a similar trend to the SG species. Interestingly, overexpression of SLSGT3 also induced a great decrease of the total SE levels in the transgenic lines (57% and 84% in lines 9 and 31, respectively) compared to WT (Figure 30E). These reductions were the result of a marked decrease in the content of

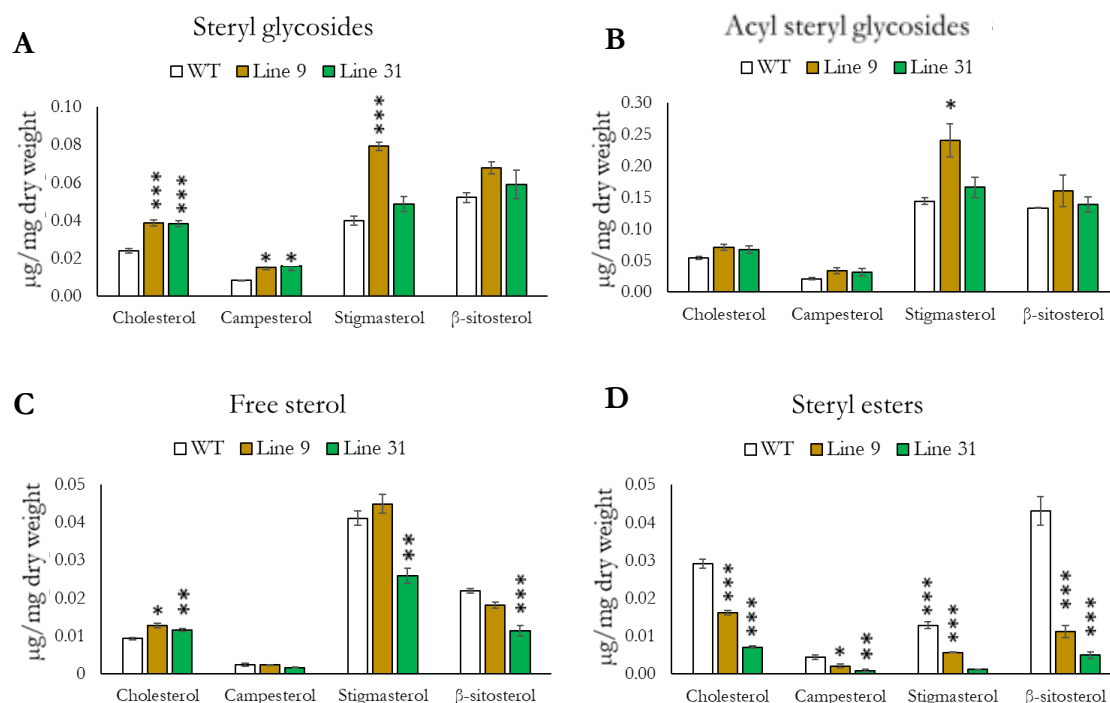


Figure 31. Content of the main sterol species in leaves of tomato WT and SLSGT3 overexpressing lines. The total sterol content in the different fractions: (A) steryl glycosides, (B) acylated steryl glycosides, (C) free sterols and (D) steryl esters. Includes the main sterols: cholesterol, campesterol stigmasterol and β -sitosterol. Data are expressed as mean μg sterol per mg of dry weight $\pm$ SEM from three biological replicates with three technical replicates ($n=9$). Asterisks represented significant differences compared to the WT determined by t-test (* $P \leq 0.05$; ** $P \leq 0.01$; *** $P \leq 0.005$).

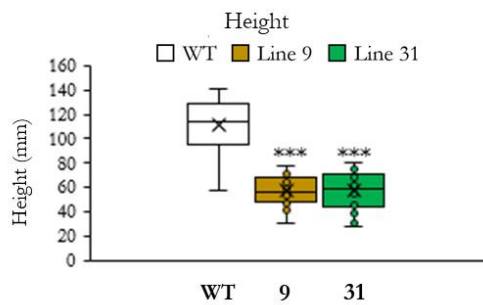
the four major esterified sterols having a higher decrease stigmasterol (56% line 9 and 91% line 31) and β -sitosterol (about 80%)(Figure 31D). However, the content of FS in the overexpressing line 9 and 31 was similar to WT plants in which there's a slight decrease observed in both lines mainly for lower levels of stigmasterol and β -sitosterol (Figure 31C). Overall, the increase in glycosylated sterols detected in the SLSGT3 overexpressing lines

resulted in a sterol level compensation which also diminished the content of steryl esters having almost the same total sterol amount in these lines compared to the WT (Figure 30F). The increase of glycosylated sterol levels observed in the transgenic lines could be attributed to the upregulation of SISGT3 (Figure 29) induced by the overexpression of SISGT3.

A



B



C

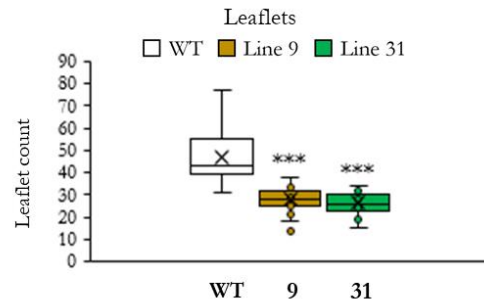


Figure 32. Phenotype of plants overexpressing SISGT3. (A) Representative images of one-month old WT and transgenic plants overexpressing SISGT3. (B)(C) Quantitative analysis of plant height and plants leaflets. Scale bar = 25cm. Data are the mean $\pm$ SD from 30 plants per genotype (n=30). Asterisks represent significant differences between transgenic lines and WT determined by t-test (* $P \leq 0.05$; ** $P \leq 0.01$; * $P \leq 0.005$).**

3.2.4.3. *Effect of SISGT3 overexpression on tomato vegetative development*

At the early stages of vegetative development (one-month-old) the height of transgenic plants was reduced approximately 50% compared to the WT. (Figure 32A and B). The reduction of plant height was due to internode shortening, being this effect was more pronounced in the apical part (Table 44). A leaflet reduction was also observed, which were reduced by 30% and 40%, respectively, in both transgenic lines compared to WT (Figure 32A and C) mainly due to a reduced number of leaves.

Table 4. Internode length. Values are the mean $\pm$ SD from 30 plants per genotype. Asterisks represent significant differences between transgenic lines and WT determined by t-test (* $P \leq 0.05$; ** $P \leq 0.01$; *** $P \leq 0.005$).

Genotype	Internode length (cm)					
	1	2	3	4	5	6
WT	9.57 $\pm$ 2.9	11.67 $\pm$ 5.7	14.45 $\pm$ 3.5	18.45 $\pm$ 4.0	21.27 $\pm$ 5.5	19.29 $\pm$ 7.9
		7	2	4	8	0
Line 9	6.18 $\pm$ 1.86	10.73 $\pm$ 3.2	12.97 $\pm$ 3.4	11.74 $\pm$ 4.2	9.71 $\pm$ 4.80	11.64 $\pm$ 7.8
	(***)	4	8	8	(***)	6
			(**)	(***)		(*)
Line 31	5.53 $\pm$ 2.35	10.07 $\pm$ 3.6	11.30 $\pm$ 5.0	11.61 $\pm$ 3.9	10.59 $\pm$ 4.1	9.78 $\pm$ 2.27
	(***)	4	0	1	2	(***)
				(***)	(***)	

The general reduction of plant size could be caused by alterations in cell division and/or expansion. As a first approach to investigate this issue, stem histological sections were prepared and analysed (Figure 33A). The internodes of transgenic lines 9 and 31 had an increase on cell size which was measured in the 2nd internode resulting bigger (~73% and ~117%) in lines 9 and 31, respectively, compared to the WT (Figure 33D) and bigger diameter (Figure 33C). To go further in this analysis, stem histological sections were observed under scanning electronic microscopy (SEM) (Figure 33B). The internode anatomy of the tomato mutants presented differences regarding the vessel elements and the tracheids, which were wider and abnormally distributed compared to the WT (Figure 33B). The collenchyma

and parenchyma were 73% larger in line 9 compared to the WT (Figure 33E) and the vascular tissue was 174% larger in mutant 9 line compared to the WT (Figure 33F). Altogether these results suggest that the dwarf phenotype displayed by SLSGT3-ox plants is the result of anomalies in both cell division and expansion caused by the enhanced levels of glycosylated sterols due to overexpression of SLSGT3.

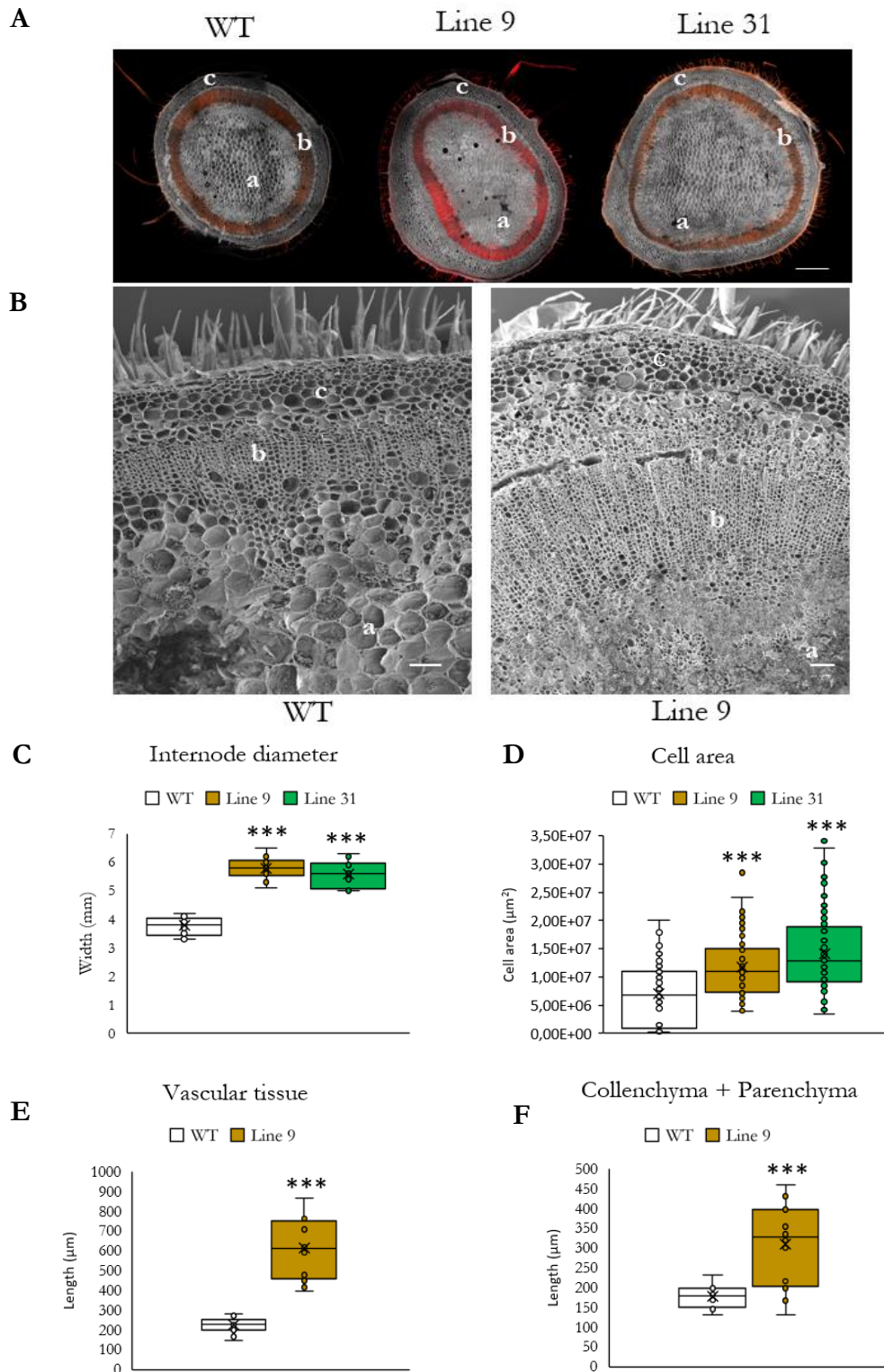


Figure 33. Morphometric analysis of SISGT3-ox plants. (A) Histological analysis of stem sections of one-month-old WT and SISGT3-ox plants. The pith tissue (a) vascular tissue (b) and collenchyma + parenchyma (c) are shown. Histological cuts were stained with CalcoFluor White (0.1%) and Basic Fuchsin (0.2%). Scale bar equals to 200 μm . **(B)** Scanning electronic microscopy images of one-month-old stems (2nd internode) from WT and line 9 plants. **(C)** 2nd Internode diameter was measured with vernier calliper. Cell size in the 2nd internode was quantified using histological cut from 2nd internode. Images were analysed using ImageJ. of WT and SISGT3-ox plants. Scale bar equals to 100 μm . **(E and F)** Size measurement of vascular tissue (b) and collenchyma + parenchyma (c). Values are mean $\pm$ SD from 3 samples per genotype ($n=3$). Asterisks represent significant differences between transgenic lines and WT determined by t-test (* $P \leq 0.05$; *** $P \leq 0.005$).

3.2.4.4. Expression analysis of *SISGT3* in red fruits of *SISGT3-ox* plants

The expression of *SISGT3* was quantified by RT-qPCR in the two selected *SISGT3-ox* homozygous lines using total RNA extracted from red tomato fruits pericarp (36DAA). As expected, the expression of *SISGT3* was significantly higher and similar in both transgenic lines (~120- and ~80-fold in lines #9 and #31, respectively) compared with WT plants (Figure 34). Compared with leaves, the overexpression of *SISGT3* in red fruit resulted in a higher increase (~9- and ~6- fold, respectively) It is worth to mention that, as reported previously by our research group (Ramírez-Estrada et al. 2017), the expression of *SISGT3* in WT plant leaves was very low.

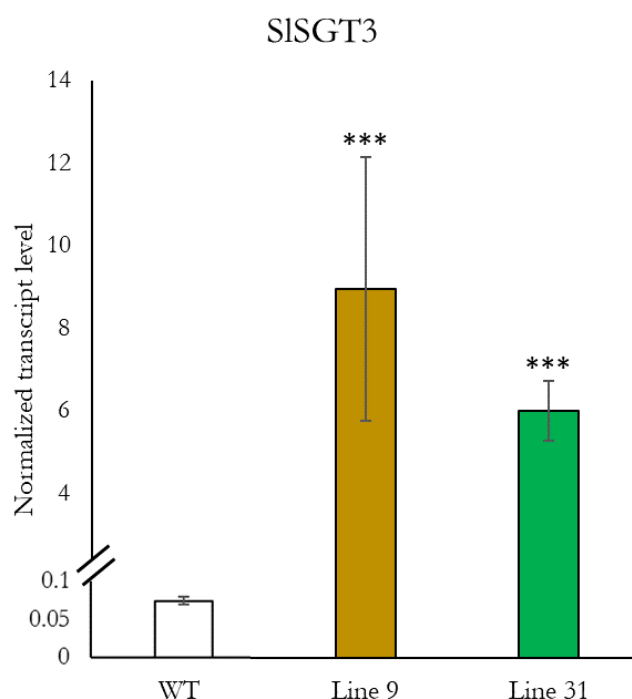


Figure 34. Expression levels of *SISGT3* in red fruits of WT and *SISGT3-ox* lines. Expression levels of *SISGT3* in the transgenic and WT plants were determined by RT-qPCR using RNA extracted from red fruit pericarp (36DAA). Data given for WT and mutant lines are expressed as normalized mRNA quantity using the Clathrin coat associated protein AP-50 (Soly08g006960) as a housekeeping gene. Values are mean $\pm$ SEM from three biological replicates per genotype with three technical replicates each (n=9). Asterisks represented significant differences compared to WT determined by t-test (***P $\leq$ 0.005).

3.2.4.5. Sterol profile in red fruits of *SISGT3-ox* plants

In order to investigate if the overexpression of *SISGT3* resulted in changes of the sterol profile in the red fruits, the levels of the different sterol fractions were quantified in extracts obtained from red ripe fruits of WT and lines 9 and 31. In that case, the overexpression of *SISGT3* resulted in an increase of SG content which do not modify the total glycosylated

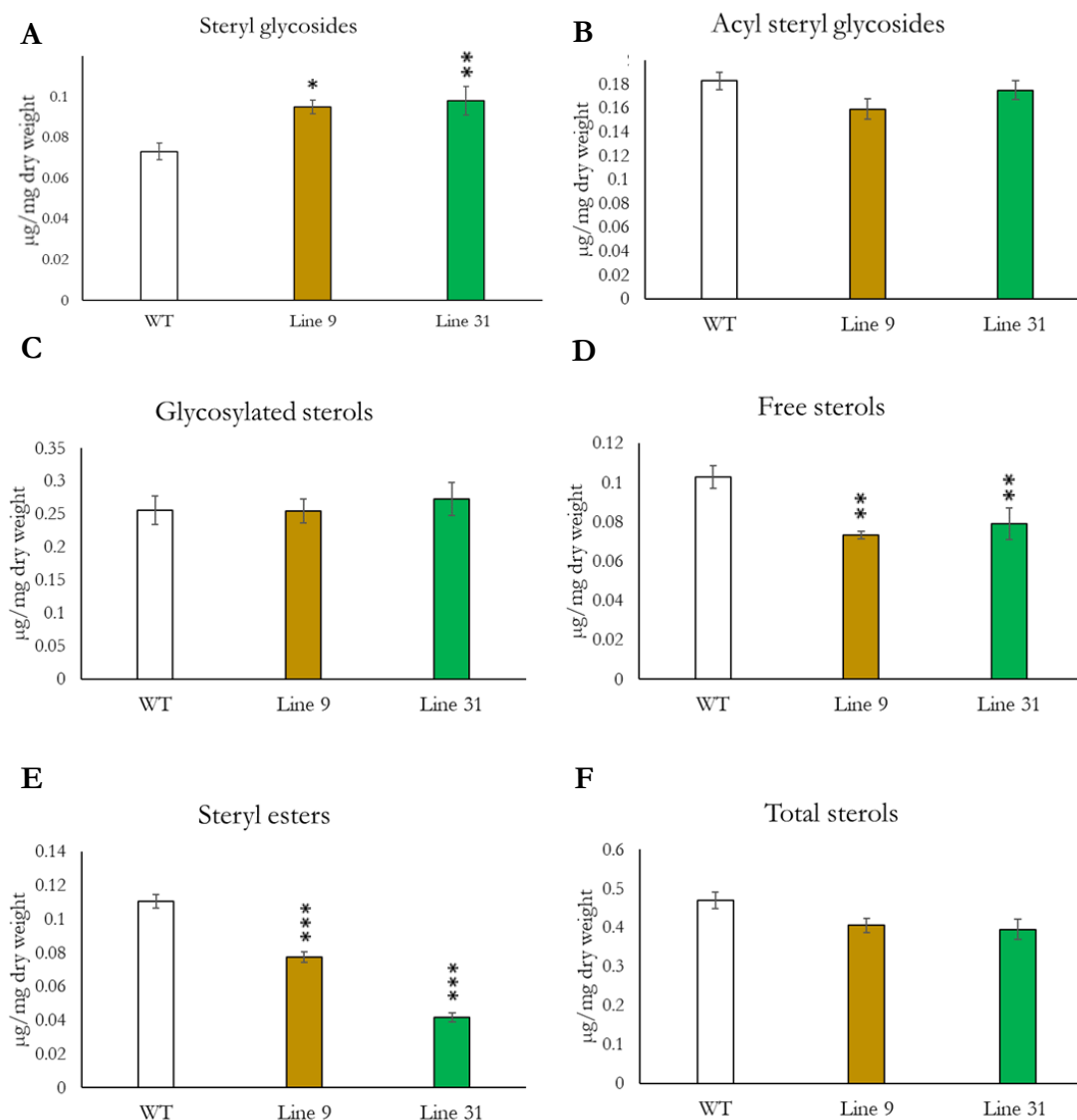


Figure 35. Content of free and conjugated sterol in red fruits of WT and *SISGT3-ox* lines. (A) steryl glycosides, (B) acyl steryl glycosides, (C) glycosylated sterols (SG+ASG), (D) free sterols, (E) steryl esters, and (F) total sterols (four fractions) in WT and overexpressing lines 9 and 31. Total content in the different fractions includes cholesterol, campesterol, stigmasterol, and β -sitosterol species. Data are expressed as mean μg sterol per mg of dry weight and $\pm\text{SEM}$ from three biological replicates with three technical replicates each ($n=9$). Asterisks represented significant differences compared to WT determined by t-test (* $P \leq 0.05$; ** $P \leq 0.01$; *** $P \leq 0.005$).

sterols (SG + ASG) (Figure 35A, B and C). The SG content increased around $\sim 30\%$ and $\sim 33\%$ in lines 9 and 31, respectively, compared to the WT plants while the content of ASG experienced a slight decrease, which compensated the SG increase on the total amount of

glycosylated sterols which remained unaltered but modifying the internal proportions (Figure 35A, B and C).

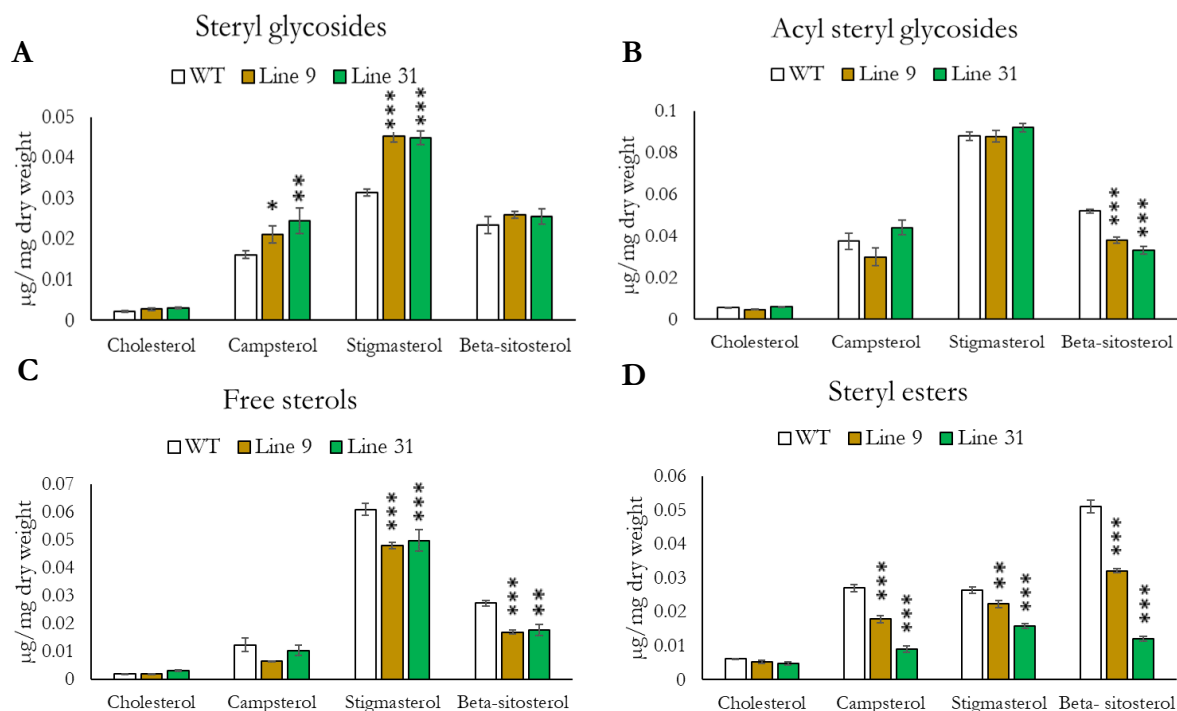


Figure 36. Content of the main sterol species in free and conjugated fractions in red fruits of from WT and SISGT3-ox lines. (A) steryl glycosides, (B) acylated steryl glycosides, (C) free sterols and (D) steryl esters. Data are expressed as mean μg sterol per mg of dry weight $\pm$ SEM from three biological replicates with three technical replicates ($n=9$). Asterisks represented significant differences compared to the WT determined by t-test (* $P \leq 0.05$; ** $P \leq 0.01$; *** $P \leq 0.005$).

As shown in Figure 36A, from the four major SG, only two were increased in both transgenic lines compared to the WT. The levels of glycosylated campesterol increased about ~30% and ~50% in lines 9 and 31, respectively, while those of stigmasterol increased around ~43% in both SISGT3-ox lines (Figure 36A). Levels of cholesterol and β -sitosterol were only slightly enhanced (Figure 36A). As for the ASG, the levels of the four major species tend to be maintained being β -sitosterol the only specie which significantly decrease compared to WT plants (Figure 36B) reinforcing the unaltered content of glycosylated sterols due to a shift on sterol species proportions. Interestingly, overexpression of SISGT3 also induces a great decrease of the total SE levels in the transgenic lines (~30% and ~60% in lines 9 and 31, respectively) compared to WT (Figure 35E). These reductions were the result of a marked decrease in the content of three out of the four major esterified sterols being cholesterol the only sterol which resulted only slightly decreased (Figure 36D). However, in contrast of what was observed in leaves (Section 3.2.4.2) the content of FS in the overexpressing line 9 and 31 was lower compared to WT plants in which there's a clear decrease observed in both lines mainly for lower levels of stigmasterol and β -sitosterol (Figure 36C). Overall, the increase in SG detected in the SISGT3 overexpressing lines resulted in a sterol level compensation which

also diminished the content of FS and SE having almost the same total sterol amount in these lines compared to the WT (Figure 35F).

The increase of SG levels observed in the transgenic lines could be attributed to the upregulation of SISGT3 (Figure 34) induced by the overexpression of SISGT3.

3.2.4.6. Effect of *SISGT3* overexpression on tomato fruit size

Fruit development was clearly affected in *SISGT3* overexpressing lines 9 and 31, as they were smaller (Figure 38) and weighed significantly less (25-30%) than WT fruits (Figure 37B). The reduced fruit size was concomitant to a sharp decrease in seed yield per fruit (Figure 37A). Moreover, transgenic fruits were also significantly harder than their WT counterparts (Figure 37C), but no obvious differences were detected in fruit setting or shape. Interestingly, fruits from both transgenic lines showed a clear delay in fruit ripening, since WT fruits needed

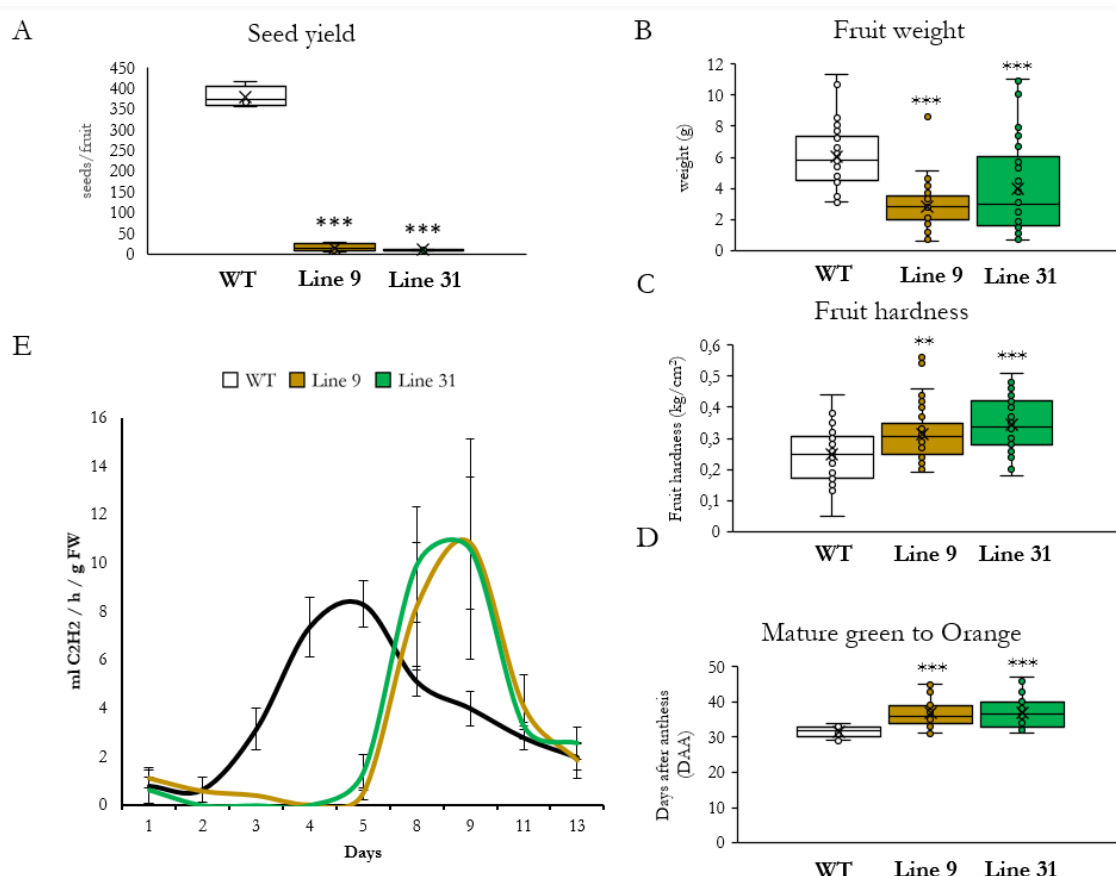


Figure 37. Phenotypic characterization of WT and *SISGT3*-ox fruits. (A) Seed yield (n=45) (B) Fruit weight (C) fruit hardness (D) fruit transition from mature green stage to orange of WT and *SISGT3*-ox plants. Data shown are the mean $\pm$ SD (n=30). (E) Fruit ethylene production measure from MG-Orange transition. Data shown are the mean $\pm$ SEM (n=5). Asterisks represent significant differences in overexpressing lines compared to WT fruits determined by t-test (*P $\leq$ 0.05; **P $\leq$ 0.01; ***P $\leq$ 0.005).

around 32 days to reach the OR stage while those from both *SISGT3*-ox lines needed 37 days (Figure 37D). It is worth to mention that no notable differences were observed in flowering between the transgenic lines and WT. This setback in the ripening process was confirmed by measuring ethylene levels in fruits at different time-point between MG stage to OR. Ethylene quantification was carried out at the *Instituto de Biología Molecular y Celular de Plantas* (IBMCP), Valencia, using the metabolomics platform. As shown in Figure 37E, the peak of ethylene in WT tomato fruits was observed in MG+5 days while in fruits of both

mutant lines was observed 4 days later, which corresponds to MG+9 days. To confirm that the late ripening phenotype observed in mutant fruits was actually due to the delay in ethylene production, green tomatoes from both WT and SISGT3-ox were treated with 5 ppm ethylene for 9 days. In all cases, tomatoes exposed to ethylene were able to ripen as WT fruits did, albeit it is worth to mention that in some cases mutant tomato fruits showed a slightly lighter red colour than WT tomatoes, thus suggesting that ethylene sensing might be somehow altered in the SISGT3-ox fruits (Figure 38).

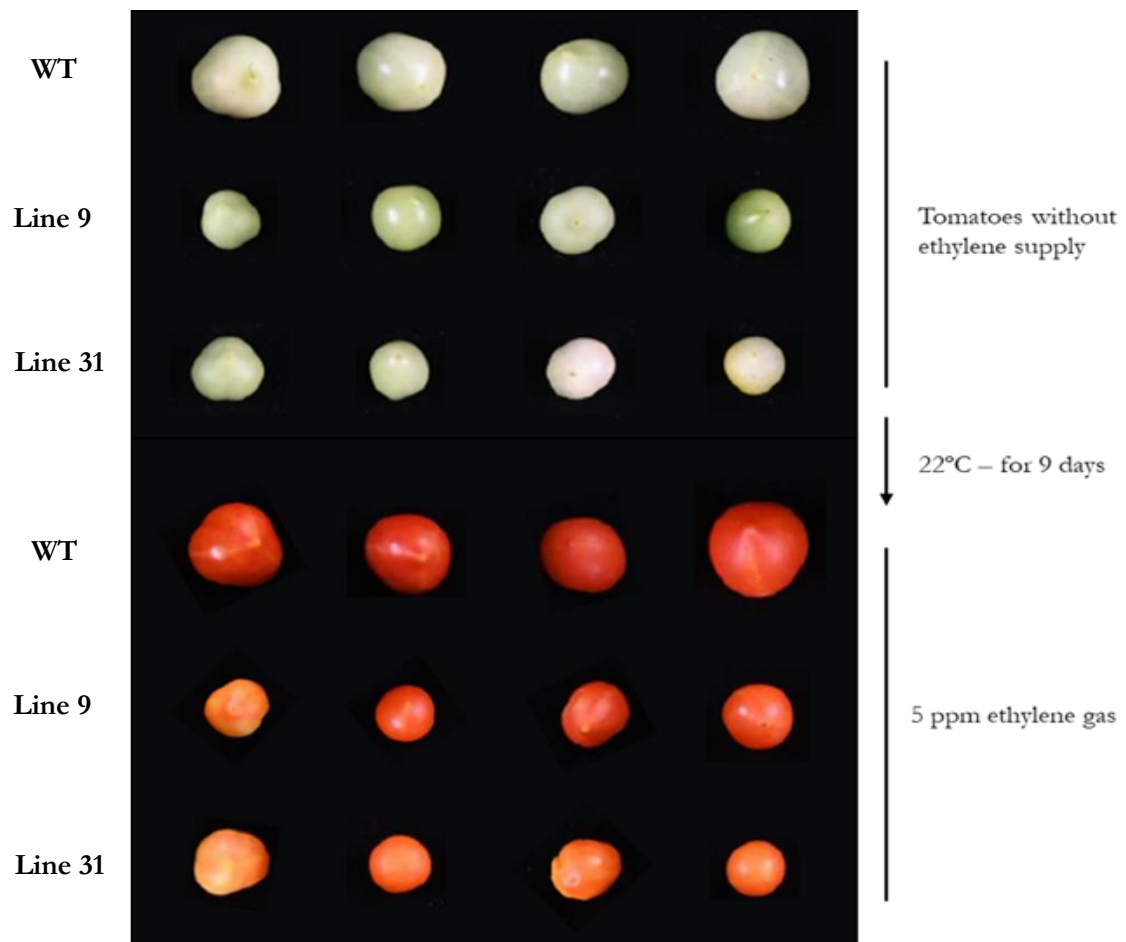


Figure 38. Representative images of red matured fruits. Green fruits transition to red fruit treated and untreated with 5 ppm of ethylene gas using fruits from WT, and SISGT3-ox lines 9 and 31.

3.2.4.7. Overexpression of *SISGT3* affects seed germination and viability

As indicated above, seed formation was drastically reduced in both *SISGT3*-ox lines (Figure 37A). The number of seeds per fruit was drastically reduced by about ~95% (Figure 37A).

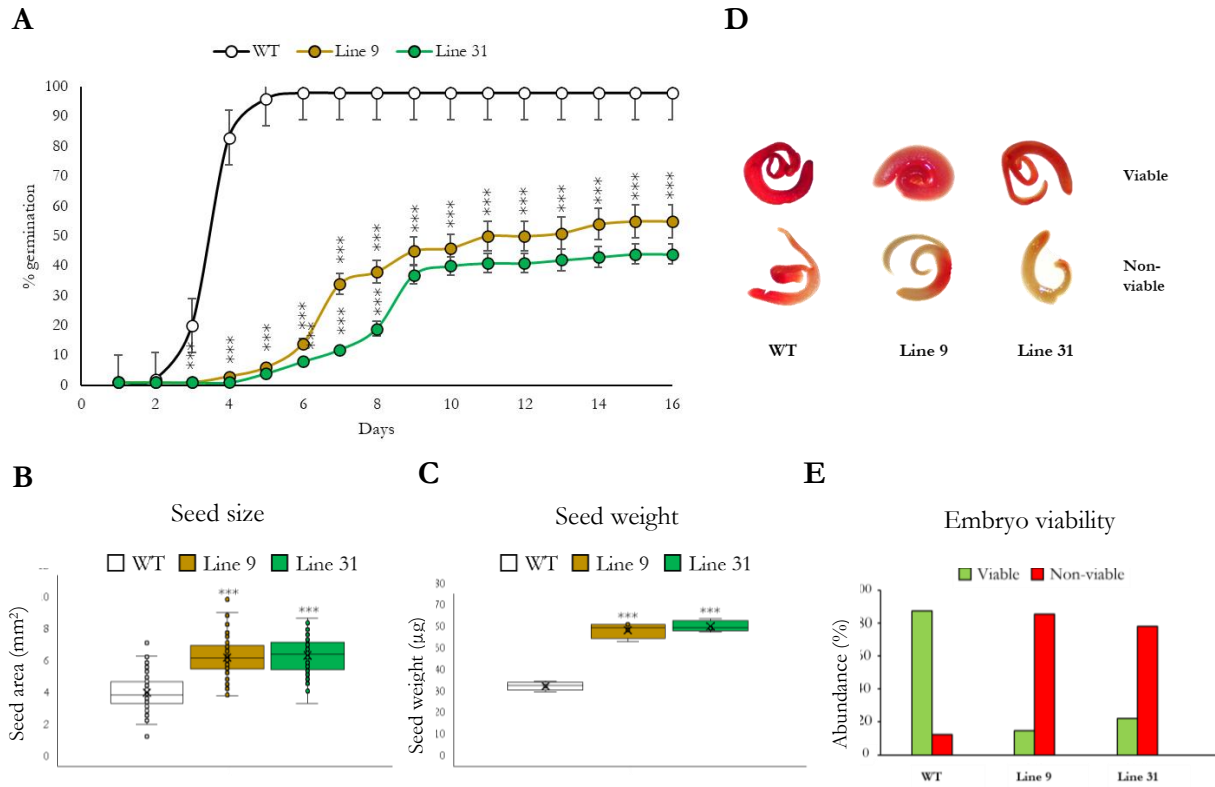


Figure 39. Phenotype and germination rate of seeds from *SISGT3*-ox plants. (A). Seed germination rate. Values are mean $\pm$ SD from 3 independent experiments (n=100) per genotype. (B) Seed area is expressed in mm² and values are mean $\pm$ SD of 100 seeds. (C) Seed weight values are mean $\pm$ SD of 3 independent experiments (15 seeds each) (n=3). (D) Representative images of viable (top) and non-viable (bottom) seed embryos. (E) Abundance of viable and non-viable embryos in WT and *SISGT3*-ox seeds (n=50). Asterisks represented significant differences between transgenic lines compared to WT determined by two-way ANOVA followed by Dunnett test (**P $\leq$ 0.01; ***P $\leq$ 0.001).

Moreover, overexpressing mutant seeds were ~50% bigger and 69% and 74% heavier in lines 9 and 31, respectively (Figure 39B and C). To investigate if these differences might affect the germination process, we next determined the rate of seed germination. To this end, seeds were sown in Petri dishes and seed germination, determined as the radicle emergence, was daily monitored for 16 days. As can be observed in Figure 39A, seed germination was drastically inhibited by about ~50% and delayed in both transgenic lines.

To further investigate the anomalous germination phenotype, seed embryos were isolated and stained with a tetrazolium salt solution (Figure 39D). Embryos were classified as viable if they were completely stained, and as non-viable if essential parts (radicle, cotyledons, or both) were not stained. *SISGT3*-ox lines exhibit around 20% of viable embryos, which is in sharp contrast to the 90% viable embryos observed in WT seeds, indicating that the *SISGT3*-

ox mutants have a much higher tendency to generate anomalous embryos (Figure 39D and E). This is consistent with the low rate of seed germination and seedling establishment observed in the SLSGT3-ox plants (Figure 39A). Altogether these results indicate that seeds from plants overexpressing SLSGT3 present different morphometric characteristics and clearly reduced germination rate compared to WT seeds.

3.2.4.8. *Ethylene triple response in transgenic tomato seedlings*

The phytohormone ethylene plays an important role in the regulation of a large variety of developmental processes, including fruit ripening and softening, and cell elongation and division. The phenotype of the SLSGT3-ox fruits described above might suggest a lower content of the hormone compared to WT, but it was demonstrated that the observed phenotype resulted from a delay in the ethylene production (Figure 40A). In contrast, the SLSGT3-ox plants display characteristics of WT plants treated with ethylene, such as thicker stems and petioles than WT (Barry et al., 2001) (Figure 40A and B). Most of what is known about the ethylene signalling pathway has arisen from a simple molecular genetic approach based on the triple response phenotype (Guzman and Ecker 1990; Stepanova & Alonso., 2005; Li et al. 2007). Thus, to determine if SLSGT3 overexpression may affect tomato ethylene response, we examined the phenotype of SLSGT3-ox seedlings (lines 9 and 31) growing during 6 days on 0,5x MS medium at 26°C in the dark. As can be observed in Figure 40A, SLSGT3-ox seedlings showed characteristics of the triple response phenotype, as inhibition of root growth, hypocotyl shortening and swelling and an exaggerated curvature of apical hook, which are typical characteristics of WT seedlings treated with ethylene (Fujino et al., 1989; Barry et al., 2001). These results suggest that SLSGT3 overexpression might result in a constitutive ethylene response.

The histological analysis of transversal hypocotyl sections from WT and SLSGT3-ox (Line 9) seedlings showed that, as observed previously in the stem of adult plants (Figure 33A, Section 3.2.4.3) the cell area and diameter increased about 108% and 54% respectively, in line 9 compared to WT (Figure 40B, Table 5).

A

B

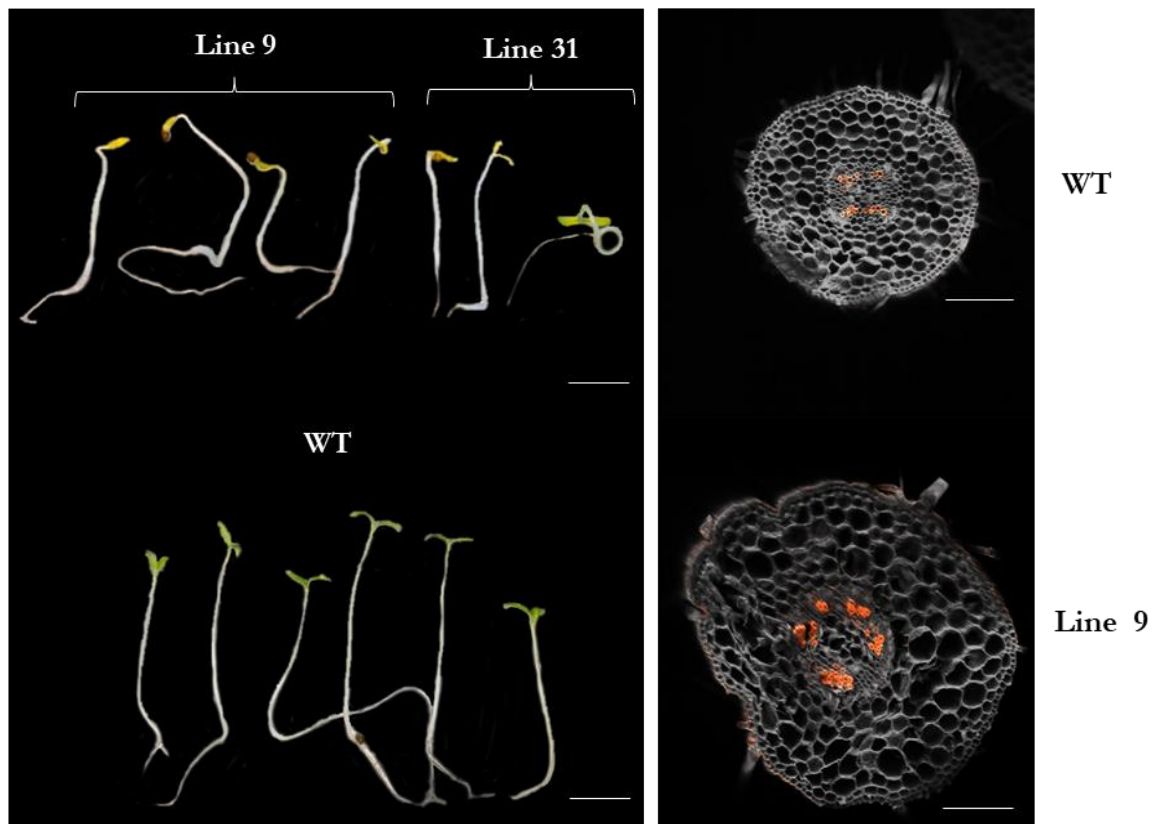


Figure 40. Seedling growth in darkness. (A) Ethylene triple response. 1-week old seedlings from WT and line 9 and 31, germinated on 0.5X MS media in the dark. Final 6h light exposition was performed. Scale bar = 2cm. (B) Histological analysis of seedlings grown in darkness from WT and line 9. Scale bar = 200 μm ..

Table 5. Quantification of diameter and cell area in WT and line 9.

	WT	Line 9
Diameter (μm)	930.5 ± 33.3	1436.7 ± 113.7
Cell area (μm^2)	1640.8 ± 161.3	3413.0 ± 337.8

3.2.4.9. *Transcriptional profiling of SISGT3-ox seedlings*

To further investigate the molecular mechanisms underlying the effect of *SISGT3* overexpression on dark-grown seedlings, global changes of gene expression were analysed

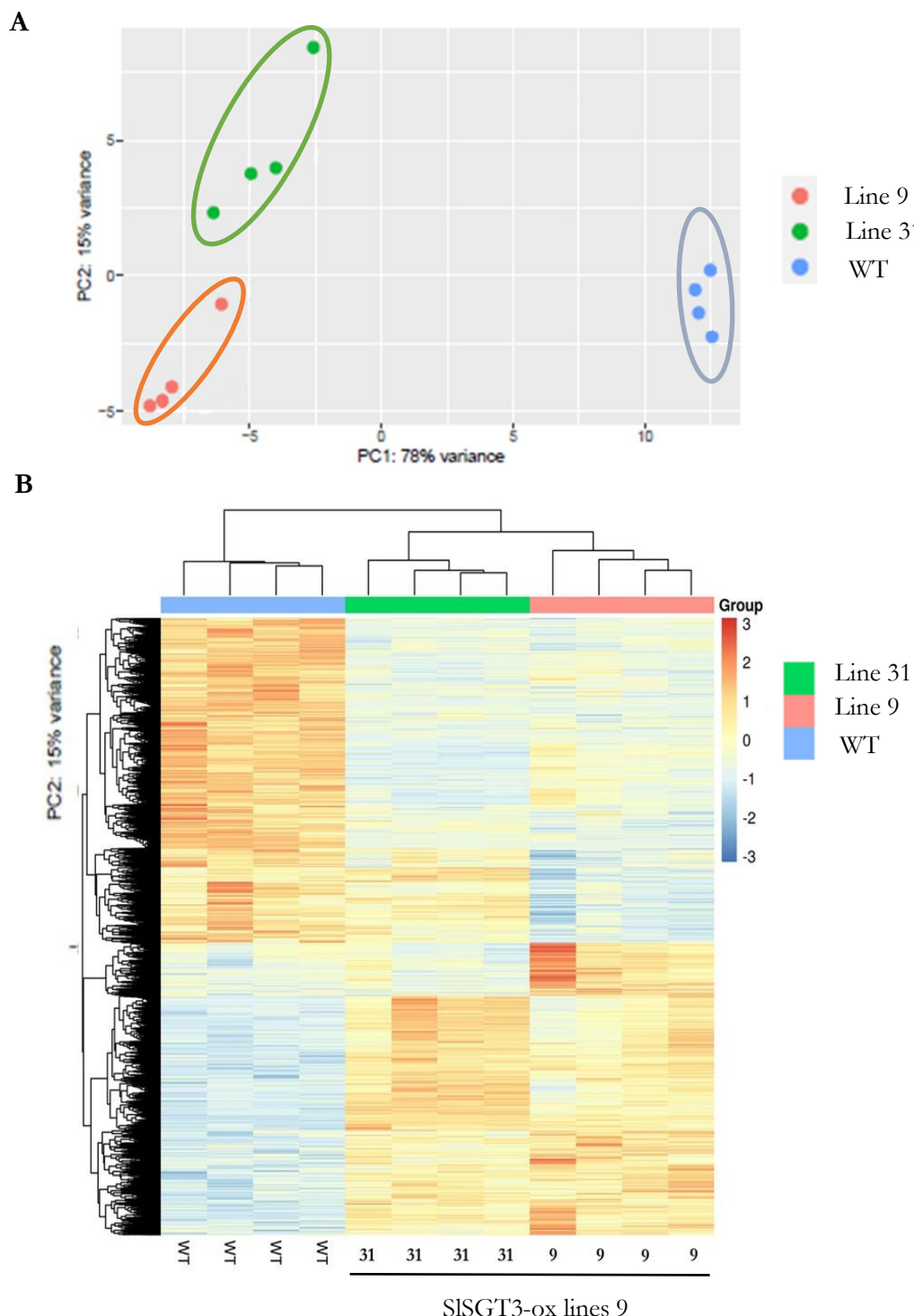


Figure 41. RNAseq results for tomato seedlings. (A) Principal component analysis (PCA) shows that the overall transcriptional profile of WT seedlings with *SISGT3* overexpressing seedlings for lines 9 and 31. (B) General heatmap depicting the normalized expression all differentially expressed genes. Normalized data is presented in a logarithmic scale. Blue color indicate blocks of genes that were downregulated and red color indicate upregulated genes.

using an RNA-seq approach and RNA samples from four independent biological replicates (1-4) of *SISGT3*-ox and WT tomato seedling collected after 6 days growing on the dark. Twelve cDNA libraries were constructed and sequenced with an Illumina HiSeq 2500 platform. Normalized read counts were obtained from each sample and employed for differential gene expression analysis. Principal component analysis (PCA) based on the normalized read counts of the whole set of replicates clearly separated the *SISGT3*-ox seedlings from the WT in the first component, with 78% of the variance at the transcript level (Figure 41A). These data were supported by the results presented in the heatmap, where it can be observed a clear similarity between the overall transcription profile of the two *SISGT3*-ox lines (9 and 31), which differ from that of WT seedlings (Figure 41B). These results shown that the samples were grouped as expected, and that most of the transcriptomic changes observed in tomato seedlings are likely due to *SISGT3* overexpression.

Differentially expressed genes (DEGs) between *SISGT3*-ox and WT seedling were identified, and significance was recognized only for those showing a false discovery rate (FDR) equal or below 0.05. A total of 2852 downregulated genes and 2477 upregulated genes were common between the two *SISGT3*-ox lines (Supplementary Table 6). Based on GO assignments, we found 157 categories significantly overrepresented ($FDR \leq 0.05$) among the upregulated genes based on biological process (89), molecular function (36) and cellular component (32), and 43 categories among the downregulated genes based on biological process (29), molecular function (6) and cellular component (8). The top 15 GO terms in these categories are shown in Supplementary Figure. 1. Considering a fold change (fc) ≥ 2 or ≤ -2 , only 369 common genes were downregulated and 171 upregulated in both *SISGT3*-ox lines.

Using the function assigned on Solgenomics (<https://solgenomics.net/>), the 369 downregulated genes were classified into 16 categories. The most represented ones included genes encoding transcription factors (TF), hormones and signalling transduction processes (Figure 43 and Supplementary Table 6 and 7).

In the context of the *SISGT3*-ox seedling, the prominent changes in could be partially attributed to a constitutive ethylene response. In that transcriptomic analysis, several ethylene biosynthetic genes involved in the Yang cycle were misregulated. Notably, ARD dioxygenases genes were mainly downregulated, indicating a potential decrease in its role in the ethylene biosynthesis pathway (Supplemental Table 7). In contrast, S-adenosylmethionine (SAM) synthase genes also exhibited misregulation but with an increased number of upregulated genes (Supplemental Table 6 and 7). The expression levels of ACC

oxidase genes ACO1 and ACO5 were significantly upregulated, suggesting an enhanced capacity for ethylene production (Supplemental Table 6), while ACO2 and ACC synthase (ACS) were downregulated, indicating a complex regulatory mechanism that may limit ethylene synthesis under certain conditions (Supplemental Table 7) (Mou et al., 2016; , Liang et al., 2019). Additionally, MTR kinase and MTR-P isomerase were both upregulated, indicating a complex regulatory network governing ethylene biosynthesis in response to environmental stimuli.

Regarding other ethylene related genes, multiple responsive genes and TF were found both up- and downregulated (Supplemental Table 6 and 7). Between them we could find upregulated the ETHYLENE INSENSITIVE 3 (EIN3) (Solyc07g008250.3) gene and multiple CONSTITUTIVE PHOTOMORPHOGENIC 1 (COP1) ethylene signalling genes activated in the dark. Consequently, the ELONGATED HYPOCOTYL5 (HY5) TF (Solyc08g061130.3) which suppress hypocotyl elongation due to ethylene signalling was found downregulated.

Surprisingly, the bHLH transcription factor 031 (Solyc04g007430.2) (PIF3) involved in light signalling which works closely with phytochromes to regulate photomorphogenesis was found upregulated. Ethylene signalling is known to promote hypocotyl elongation by stimulating the expression of PIF3, which is a key transcription factor involved in this process interacting with microtubules to reorganize them, facilitating cell elongation (Kim et al., 2021). Similarly occurred with Serine/threonine-protein kinase CTR that although a constitutive triple response was observed in SISGT3-ox seedlings grown in the dark, 2 different CTR genes were found, but one upregulated (Solyc04g076480.3) and the other downregulated (Solyc02g091180.1) confirming the gene misregulation observed in SISGT3-ox seedlings.

Moreover, the ethylene-responsive transcription factor CRF2-LIKE PROTEIN (Solyc05g024230.3) that regulates gene expression in response to ethylene and cytokinin signals was found upregulated (Supplemental Table 6). CRF2-like proteins are activated by ethylene and are responsible for modulating downstream genes that mediate ethylene responses, such as growth inhibition or acceleration depending on the tissue influencing cell growth, division, and differentiation. As seen, not only ethylene could participate in the phenotype observed. Some other hormonal downregulated genes changes could be related, such as the downregulation of CYTOKININ HYDROXYLASE (Solyc02g094860.3) related with the biosynthesis of trans-zeatin, auxin-related genes such as AUXIN EFFLUX FACILITATOR 10 (Solyc04g056620.2) that participate in auxin transport or the

downregulation of GIBBERELLIN 2-OXIDASE 3 (Solyc01g079200.4), involved in the transformation of inactive forms of gibberellins to active forms (gibberellin 1 and 4) (Supplemental Table 7).

These results suggested a multifaced cause for the phenotype observed. In relation to plant development and structure different genes were found which were not only specific from leaves. Starting with the seed, LATE EMBRYOGENIC ABUNDANT PROTEIN genes were found misregulated (11 upregulated and 18 downregulated). These genes should be highly expressed during the late stages of seed development and involved in protecting cells from desiccation and other stressors (Jia et al., 2022). Also, EMBRYO DEFECTIVE 1703/2006/2410 genes (Solyc01g096010.4/ Solyc03g020020.3/ Solyc08g067870.2) which were found upregulated in SISGT3-ox plants and are related to wide broad number of functions and related to embryo defects (Meinke., 2020). Then, regarding the seedling, the protein LIGHT-DEPENDENT SHORT HYPOCOTYLS 6 (Solyc07g062470.4) and SHORT HYPOCOTYL IN WHITE LIGHT 1 (Solyc01g106810.4) that modulate plant response to light, affecting the elongation of the hypocotyl particularly under low light conditions (Takeda et al., 2011) were found downregulated. Hypocotyl elongation and plant growth is highly tight with nutrient availability. The transcriptomic analysis of SISGT3-ox seedlings revealed that multiple transporter proteins were downregulated including those for inorganic molecules (boron, zinc, cooper, calcium, nitrate or sulphate), organic molecules (sugar, nicotineamine and aminoacid/peptide) and water (Supplementary Table 7). This general molecule transporting slowdown could be supported by the downregulation of various genes such as tetraspanin 8 (Solyc12g010570.1) which is an extracellular vesicular marker that contribute to the biogenesis of extracellular vesicles, influence the selection of cargo, and mediate the targeting and uptake by recipient cells (Jankovičová et al., 2020), tonoplast intrinsic protein (Solyc10g083880.2) that is a marker for vacuolar compartments (Gattolin et al., 2010), DC1 domain protein (Solyc01g073820.4) which the downregulation of this protein in Arabidopsis is linked to disruptions in vacuole formation, essential for gametophyte development and various plant growth processes (Supplemental Table 7) (D'Ippólito et al., 2017), or casparian strip membrane protein 3 (Solyc02g067190.4) which acts as a selective barrier in the root endodermis, ensuring that water and nutrients are transported symplastically, bypassing the apoplastic route facilitating controlled transport to the vascular tissues (Zhuang & Li, 2020). Related to stem reinforcement, 22 downregulated genes related to cell wall were found including various Xyloglucan endotransglucosylase that cuts and re-joins hemicellulose chains in the plant cell wall, contributing to wall assembly and

growth regulation (Sharples et al., 2017). In that group is has also been observed a misregulation of pectin metyl and acetylerase, compounds that controls cell wall porosity and has been shown to exhibit structural variation during plant growth and in response to stimuli (Wu et al., 2018) in coordination with different glycoproteins that make up a relatively small component of the extracellular matrix of plants influencing wall mechanics and

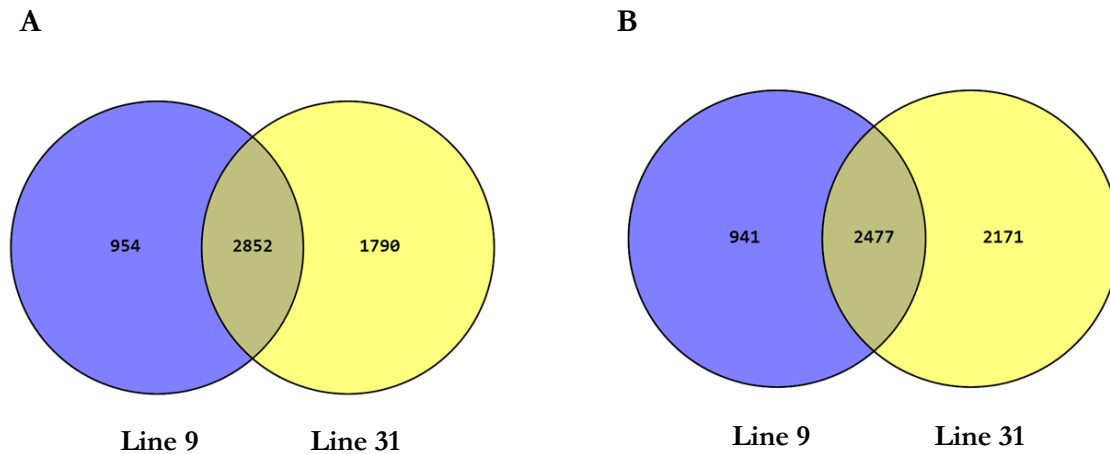


Figure 42. Venn diagrams from log2 fold change (fc) ≥ 2 and ≤ 2 genes down and upregulated in seedlings of the SISGT3-ox lines. Venn diagram showing the number of downregulated (A) and upregulated (B) genes in seedlings of the SISGT3-ox lines 9 and 31.

signalling related to cell expansion and division, embryogenesis, responses to stress, plant growth and development (Ma & Johnson., 2023). Also, ethylene could participate in these processes, for instance, xylanase receptor 2 (Soly07g008630.1) was found upregulated, that gene triggers ethylene production as part of the plant's immune response and can affect overall lant development slowing growth to prioritize defence (Bar et al., 2010). Interestingly, this gene also had some relationship with microtubules dynamics and cell division such as Kinesin-like protein also misregulated in SISGT3-ox lines (Supplemental Table 6 and 7). Those transcriptional changes (Supplementary Table 6 and 7) affect from seed to fruit, confirming the strong impact of SISGT3 overexpression on a broad net of genes related to cell wall, transport, signalling, trafficking and having multiple TF affected, which may contribute to the ethylene constitutive response observed at different levels in seedling and may hamper the aberrant development observed in SISGT3-ox plants.

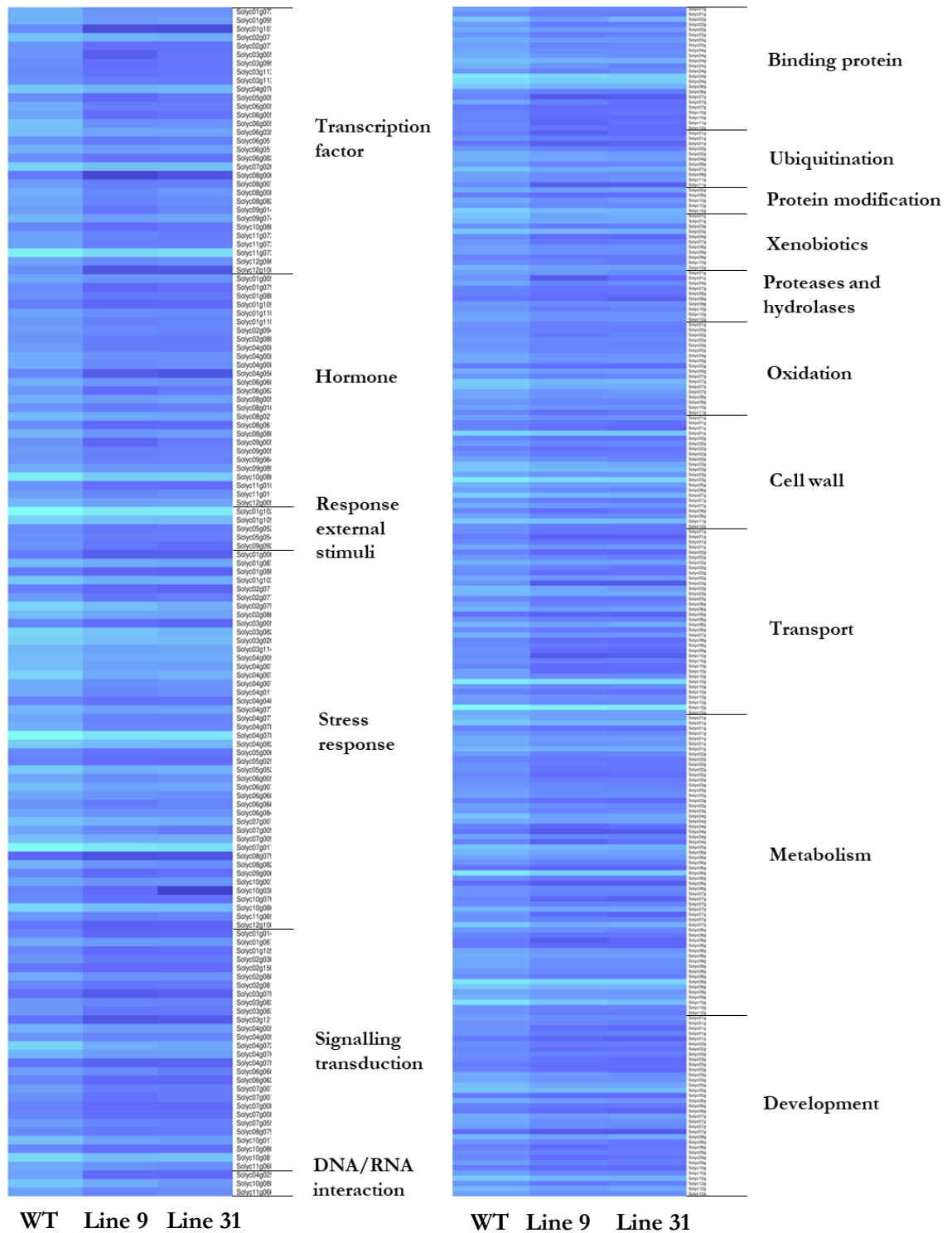


Figure 43. Genes downregulated in seedlings of SISGT3-ox considering a log2 fold change (fc) ≤ 2. Heatmaps showing expression changes of the 369 commonly downregulated genes with an assigned function. The colour scale shows the levels of gene expression as log2-scaled values of fragments per kilobase million (FPKM) (log2 FPKM), with values ranging from - 5 (lower expression, dark blue) to + 5 (higher expression, cyan), as indicate at the top.

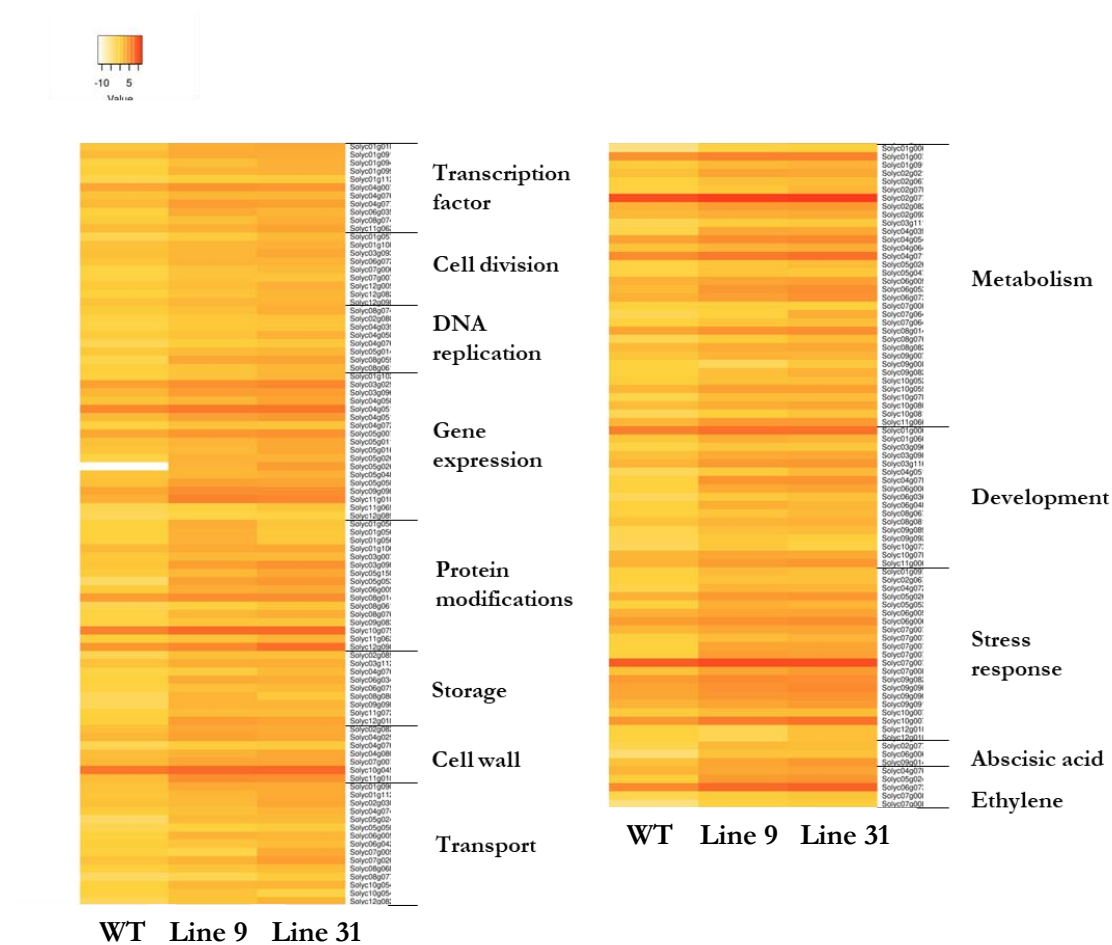


Figure 44. Genes upregulated in seedling of the SISGT3-ox considering a $\log_2$ fold change (fc) ≥ 2 . Heatmap showing expression changes of the 171 commonly upregulated genes in seedlings of the two SISGT3-ox. The colour scale shows the levels of gene expression as $\log_2$ -scaled values of fragments per kilobase million (FPKM) ($\log_2$ FPKM), with values ranging from -10 (lower expression, white) to $+5$ (higher expression, dark orange), as indicate at the top.

3.2.4.10. *Altered sterol levels cause metabolic perturbations in fruits*

As a first step to investigate the impact of SLSGT3 overexpression on the fruit metabolome, we have established the metabolic fingerprints in the pericarp of WT and SLSGT3-ox red fruits. In total, 703 (286 positive and 417 negatively regulated compared to WT) and 704 (306

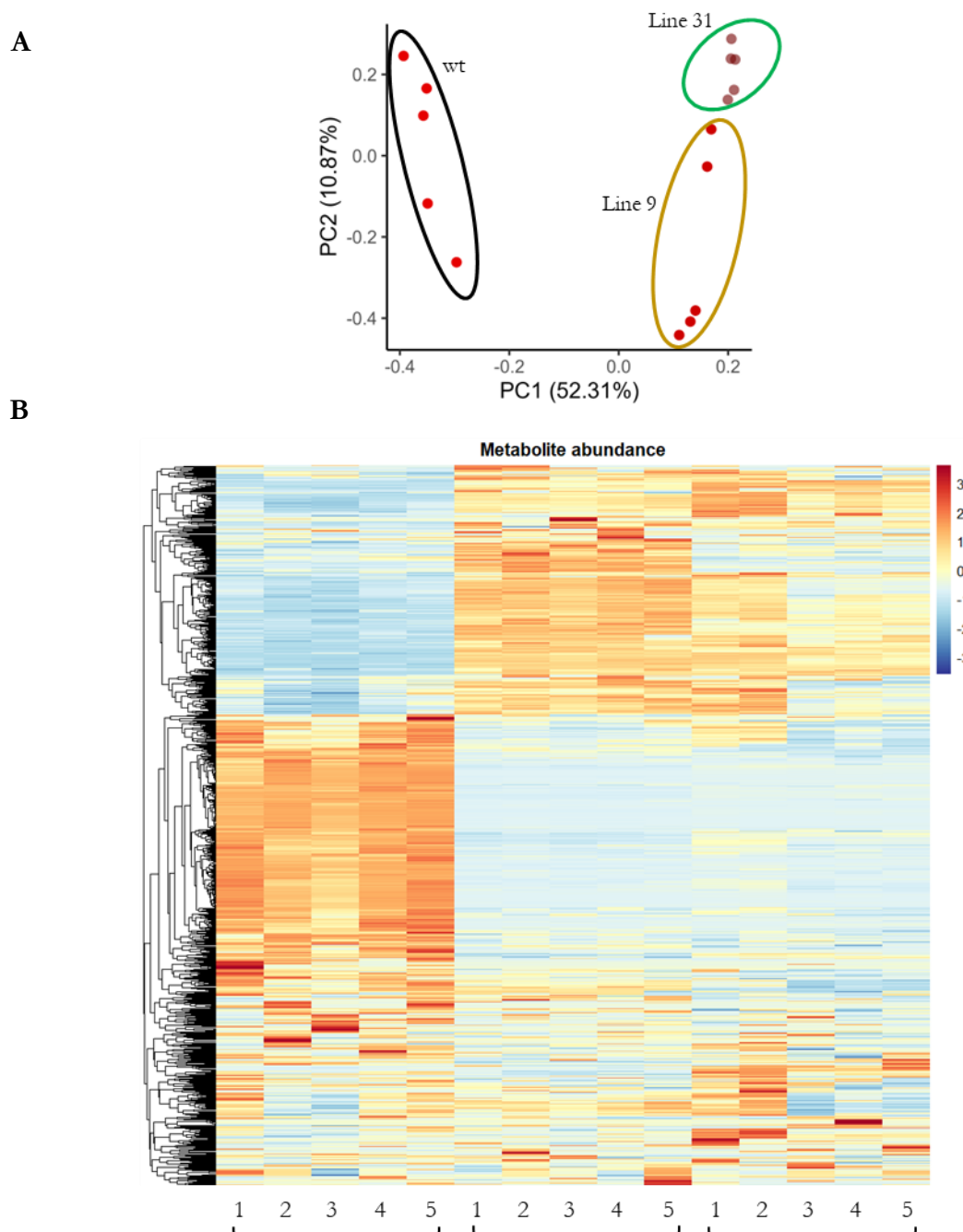


Figure 45. Metabolic profile distribution in WT and SLSGT3-ox red tomato fruit pericarp. (A) Principal component analysis (PCA) of the complete annotated metabolite dataset including primary, secondary and lipid metabolite profiles of red fruit. The values represent the metabolite abundance previously normalized to the internal standard (ribitol, isovitexin and phosphatidylcholine, respectively) and tissue weight. (B) Clustered heatmap displaying the overall metabolite abundance of red fruit. The scale is row-based.

positive and 398 negative) metabolites were identified in fruit pericarp from lines 9 and 31, respectively. A hierarchical clustering heatmap confirmed the results of the PCA as it showed

several clearly contrasting patterns of primary and specialized metabolites between WT and *SISGT3*-ox fruits (Figure 45). Overall, there are less metabolite accumulation, pointing towards a less active biosynthetic metabolism in fruits of plants overexpressing *SISGT3*. A more detailed analysis showed a strong perturbation of the lipidome in red fruits from transgenic lines 9 and 31 compared to the WT, affecting storage lipids (TAGs) and major lipid constituents of PM (phospholipids, lysophospholipids and sphingolipids) and photosynthetic membranes (galactolipids). There is a marked downregulation of a large number of TAG species (Figure 46A), which is also observed in the case of other essential lipid components of the PM such as sphingolipids and phospholipids (Figure 46B). Among

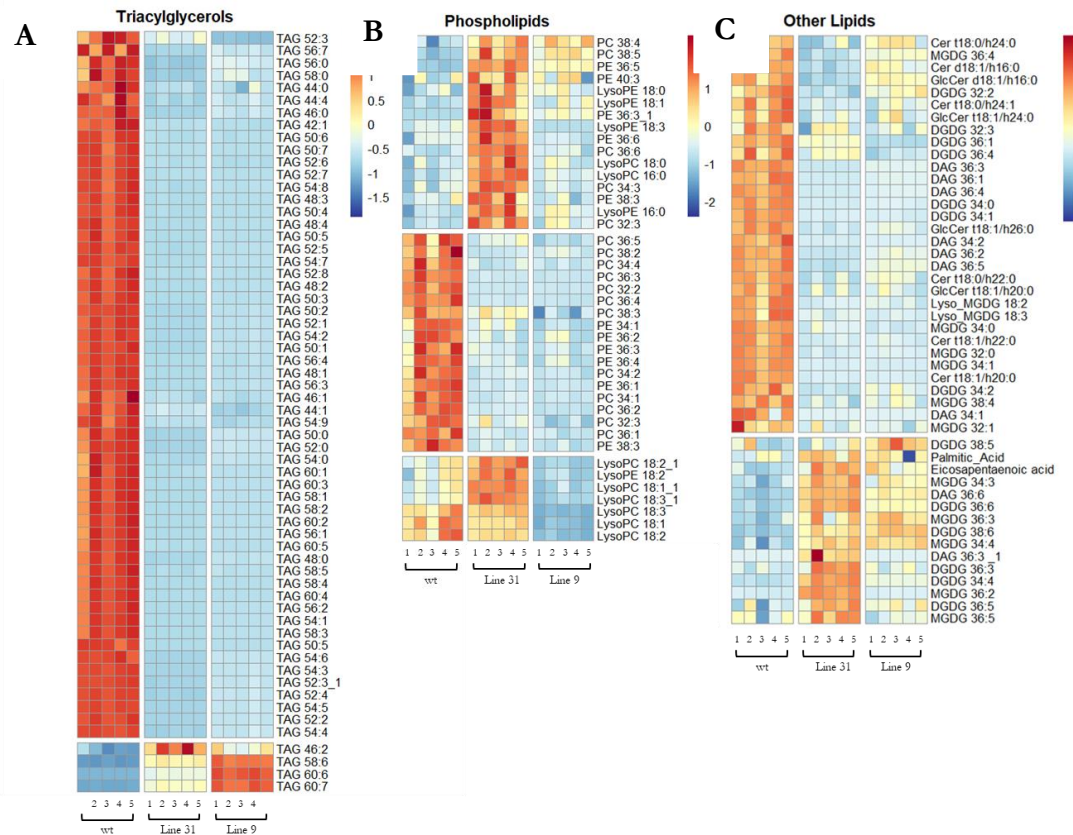


Figure 46. Highlighted lipid abundance in *SISGT3*-ox lines and WT tissues. Significantly different accumulated metabolites (adjusted $p < 0.05$, Holm–Bonferroni method) with different patterns in *SISGT3*-ox and wildtype were observed in red fruit pericarp for triacylglycerols (A), phospholipids (B), other lipids (C). The scale is row-based

the four major classes of sphingolipids (Michaelson et al., 2016), significant changes were observed in the levels of ceramides and glycosylceramides, while those of glycosylinositolphosphoceramides and free long chain bases were not altered (Figure 46C). In the case of phospholipids, the levels of phosphatidylcholine and phosphatidylethanolamine, the major plant glycerophospholipids, were clearly reduced in both transgenic lines, some are clearly similar (Figure 46B). However, the effects on

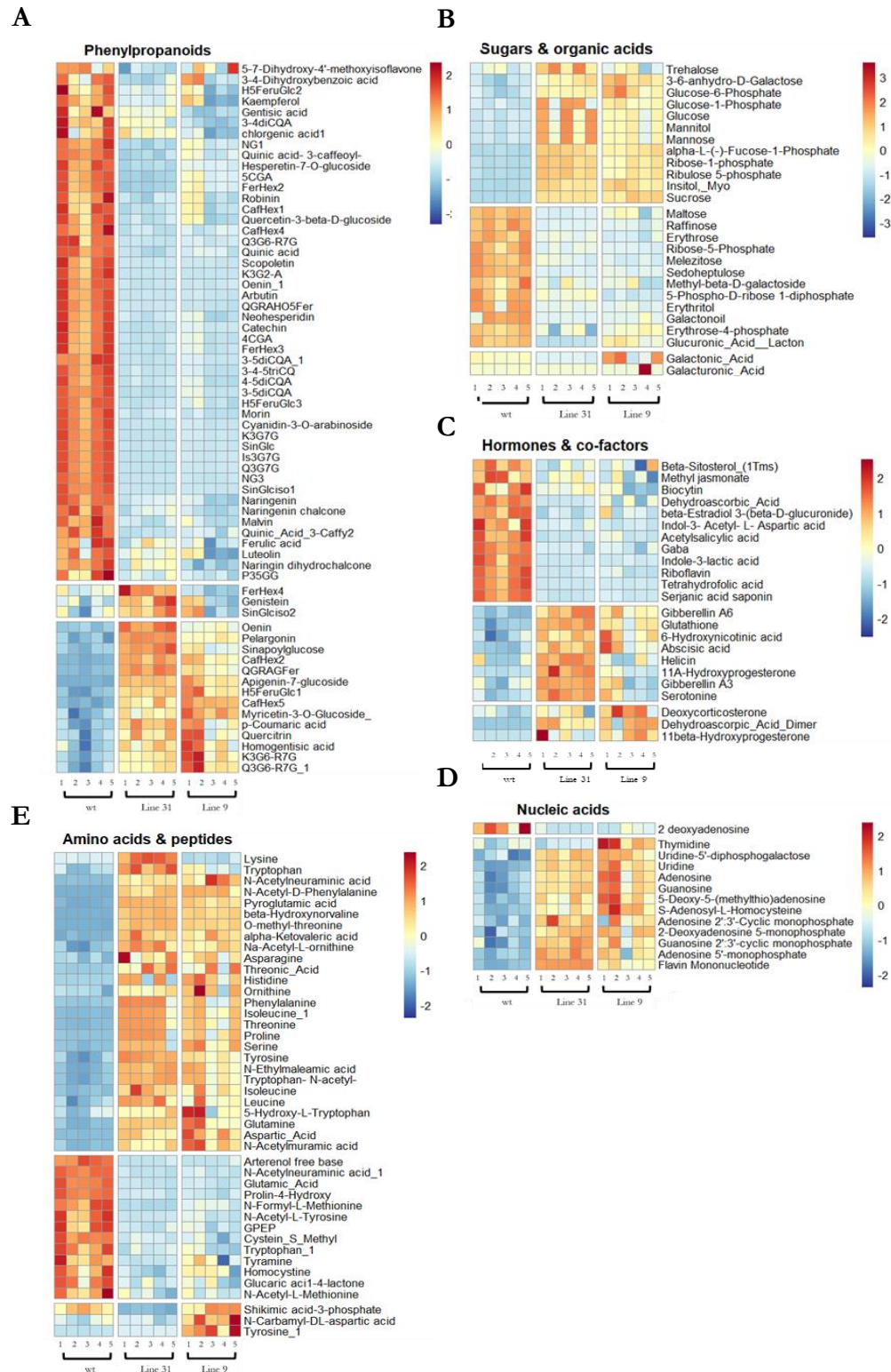


Figure 47. Highlighted metabolites abundance in pSISGT3-ox lines and WT tissues. Significantly different accumulated metabolites (adjusted $p < 0.05$, Holm-Bonferroni method) with different patterns in pSISGT3-ox and wildtype were observed in red fruit pericarp for phenylpropanoids (A), sugars and organic acids (B), hormones and co-factors (C), nucleic acids (D) and amino acids and peptides (E). The scale is row-based

lysophosphatidylcholine (lysoPC) and lysophosphatidylethanolamine (lysoPE) species were not consistent between the two transgenic lines (Figure 46B). A mixed response was

observed in major galactolipids, mono- and digalactosyldiacylglycerols (MGDG and DGDG), showing a trend towards species with higher unsaturation (Figure 46C). Additionally, a tendency towards lower levels of diacylglycerols (DAG), the precursor of glycerophospholipids and galactolipids, was also noted.

In the fruit pericarp of overexpressing lines 9 and 31, most significantly altered flavonoids were decreased compared to the WT (Figure 47A).

The phenylpropanoid pathway is central to the biosynthesis of flavonoids, essential for plant defence and UV protection show distinct variations between WT and the transgenic lines. Generally, phenylpropanoids seemed to be less accumulated in lines 9 and 31 compared to WT although exceptions exist. Flavonoid precursors had a differential pattern of accumulation, for example, naringenin chalcone, was more abundant in WT while p-coumaric acid was more abundant in lines 9 and 31 (Figure 47A). Moreover, other intermediates such as caffeic acid and ferulic acid, which contribute to lignin biosynthesis, were more abundant in WT. Final products like kaempferol were more abundant in WT fruits, conversely, quercetin showed the opposite pattern, being more abundant in lines 9 and 31 (Figure 47A). It was observed also an accumulative trend between lines 9 and 31 of glycosylated phenylpropanoids with some exceptions (Figure 47A). This could indicate that phenylpropanoid downstream pathway could be redirected towards enhanced glycosylated phenylpropanoids such as quercetin that contains an additional hydroxyl group at the R1 position (Dabeek & Marra., 2019)(Middleton & Teramura., 1993).

Sugars and organic acids, essential for energy metabolism and biosynthetic pathways, also show moderate variations. As there is not a clear differential pattern between WT and SISGT3-ox lines, glucose and glucose-6-phosphate, critical sugars for glycolysis and energy storage, were more abundant in lines 9 and 31, indicating enhanced glycolytic flux or sugar storage in the transgenic lines (Figure 47B) (Li et al., 2021). Also, trehalose, known for its role in stress protection, was more abundant in WT, suggesting a greater reliance on trehalose-mediated stress responses in SISGT3-ox lines compared to WT (Oszvald et al., 2018). In contrast, organic acids such as galactonic acid lactone, a precursor in the ascorbate (vitamin C) pathway, was more abundant in WT, implying that ascorbate synthesis and antioxidant defence might be more active in WT plants (Torres., 2021). Additionally, malic acid, a TCA cycle intermediate, was more abundant in lines 9 and 31, suggesting higher TCA cycle activity to meet increased energy demands in the transgenic lines (Figure 47B).

Hormonal regulation plays an important role in plant development and stress responses. In fruit, some differences in hormone accumulation were apparent between WT and transgenic

lines. Generally, hormones seemed to be reduced as methyl jasmonate and jasmonic acid, crucial for defense signaling (Fenn & Giovannoni., 2021), were more abundant in WT. Similarly, salicylic acid (SA), a hormone involved in systemic acquired resistance, was also more abundant in WT. Furthermore, indole-3-acetyl-L-aspartic acid, a conjugated auxin, was also more abundant in WT (Figure 47C). Conversely, gibberellins, that stimulate aspects of plant development, such as root and shoot elongation, seed germination, flower transition, and fruit set and expansion (Fenn & Giovannoni., 2021) were found more abundant in lines 9 and 31 compared to WT fruits and additionally, abscisic acid (ABA), a hormone involved in abiotic stress tolerance, seemed to be increased in line 31 and less pronounced in line 9 (Figure 47C). The hormonal decompensation with reduced levels of these hormones in the transgenic lines suggest a shift altering growth, decreasing biotic stress defence while promoting abiotic stress defence mechanisms in tomato fruits.

Amino acid metabolism shows considerable divergence between WT and transgenic lines. Generally, there was an accumulation of aminoacids and peptides. For example, tyrosine and phenylalanine, precursors for phenylpropanoid biosynthesis, were more abundant in SLSGT3-ox lines, which could confirm the changes in the metabolic efflux of this pathway (Figure 47A and 47D) (Deng & Lu, 2017). Interestingly, proline, an osmoprotectant aminoacid (Shafi et al., 2019), was more abundant in SLSGT3-ox lines, suggesting better performance against abiotic stress as observed previously with hormone abundancy. Overall, these results suggest that SLSGT3-ox plants maintain higher levels of amino acids, possibly reflecting their decreased metabolic demands due to high stress (Batista-Silva et al., 2019).

Nucleotide metabolism, essential for DNA/RNA synthesis and energy regulation, was also impacted by SLSGT3 overexpression. In general, there's an overaccumulation of nucleic acids in SLSGT3-ox lines (Figure 47E). 2-deoxyadenosine, which is linked to DNA repair, was more abundant in SLSGT3-ox plants. Similarly, uridine and thymine, both pyrimidine nucleotides, were more abundant in lines 9 and 31 possibly indicating higher DNA turnover and repair activity (Biswas et al., 2013).

Taken together, these findings underscore significant metabolic rewiring in overexpressing SLSGT3-ox plants, suggesting intricate metabolite alterations underlying observed phenotypic differences compared to WT counterparts.

3.2.5. Generation of E8::SlSGT3 tomato plants

To overcome the negative effects of SlSGT3 overexpression on plant and fruit development, we generated the E8::SlSGT3 construct in which the SlSGT3 coding sequence was cloned under the control of the E8 inducible promoter (proE8) (Zhao et al., 2009) (Figure 48A). The construction was introduced into tomato plants by *Agrobacterium*-mediated

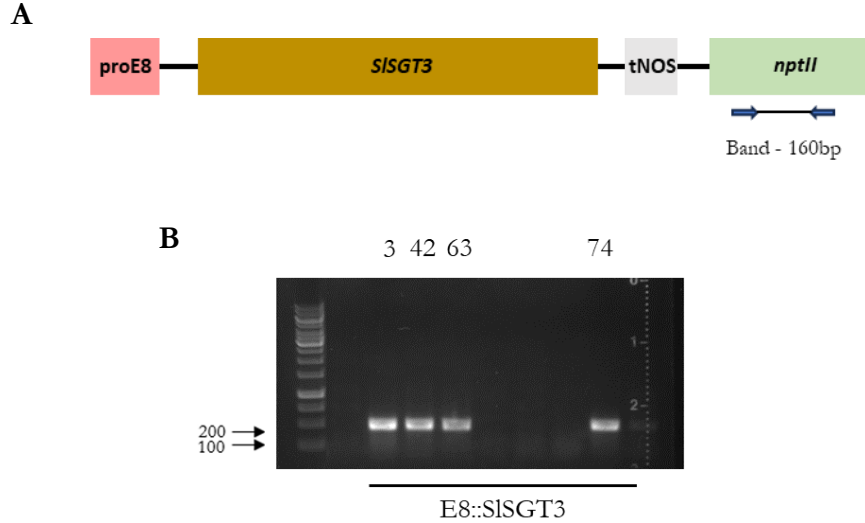


Figure 48. Identification of *E8::SlSGT3::Tnos* transgene insertion in transformed tomato plants. (A) Schematic representation of the transgene to overexpress SlSGT3 using the fruit specific promoter E8, Nos terminator (NOS-T), and the marker gene for resistance to kanamycin (NPTII). Arrows show the position of the primers used for transgenic lines genotyping, (B) Agarose gel electrophoresis showing the 160-bp PCR amplification product (nptII coding sequence) from genomic DNA of the T0 transgenic plants indicated on top of the image.

transformation.

The presence of the transgene in these plants was confirmed by PCR (Figure 48B) using genomic DNA as a template and nptII primers (Table 16). Next, we determined the number of copies of the transgene present in the T-DNA by qPCR using the tomato *LAT52* (Soly10g007270) as endogenous single copy gene (Section 6.3.6). The results of this analysis showed that 2 (13 and 24) out of the 10 T0 transgenic plants contained a single transgene copy per genome. These 2 plants did not produce seeds, so it was decided to continue working with lines 3, 42, 63 and 74, that produced the highest number of seeds. These lines were selected for propagation to obtain plants containing a single copy of the transgene. Using the same qPCR approach, 2 homozygous lines with a single transgene insertion (lines 3.1 and 63.9) were selected for further characterization.

3.2.6. Expression analysis of *SISGT3* mRNA in fruits of *E8::SISGT3* plants

The expression of *SISGT3* mRNA in lines 3.1 and 63.9 was quantified by RT-qPCR using total RNA extracted from green (15 DAA) and red fruits (39 DAA). *SISGT3* mRNA levels

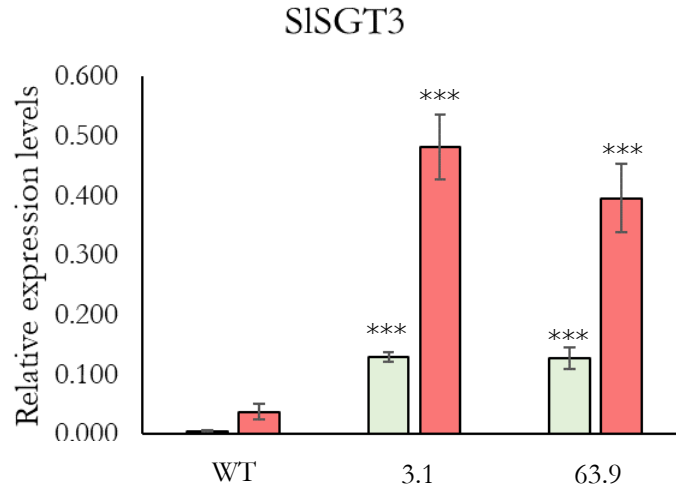


Figure 49. *Expression levels of *SISGT3* mRNA in *E8::SISGT3* homozygous transgenic lines.* The levels of *SISGT3* mRNA were determined by RT-qPCR using RNA extracted from green (15 DAA) and red (39 DAA) tomato fruits. Data were normalized using the CAC (Soly08g006960) as a housekeeping gene. Values are mean $\pm$ SD from two biological replicates per genotype with three technical replicates each (n=6). Asterisks represented significant differences compared to wt determined by t-test (***) $P \leq 0.005$.

in WT fruits were found to be higher (7.6-fold) in red fruits than in green ones (Figure 49). A similar response was observed in fruits of both transgenic lines (Figure 49), which showed much higher levels of *SISGT3* mRNA in red fruits compared to the green ones (3.7-fold and 3.1-fold increase in lines 3.1 and 63.9, respectively), although it is worth mentioning that this relative increase was much less pronounced than in wt fruits. This difference is due to the fact that basal levels of *SISGT3* mRNA in the transgenic green fruits are already much higher than in the wt counterpart. Anyway, the levels of *SISGT3* transcripts detected in red fruits of both transgenic lines were much higher than in the equivalent wt fruits (13-fold and 10.7-fold increase in lines 3.1 and 63.9, respectively).

3.2.7. Characterization of the phenotype of E8::SISGT3 plants

In order to analyze the effects of *SISGT3* expression under control of the *E8* inducible promoter, plants from lines 3.1 and 63.9 were grown in parallel with wt plants. During the vegetative growth phase no significant differences were observed between wt and transgenic lines, including plant height, number of leaves and leaflets per leaf, and flowering time (Figure 50A). However, both transgenic lines exhibited a delay of 2-3 days in reaching the breaker

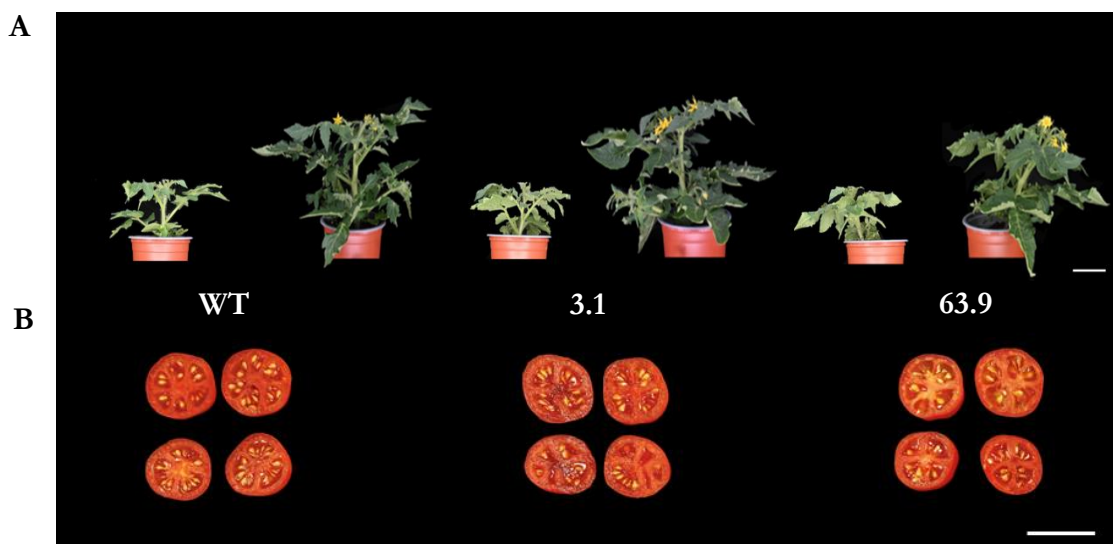


Figure 50. Phenotype of Micro-Tom plants expressing *SISGT3* under control of the *E8* promoter. (A) Representative images of one month old (images on the left side) and two and a half month old (images on the right side) from WT and transgenic *E8::SISGT3* plants. Scale bar = 10 cm. (B) Representative images of red ripe tomato fruits from WT and transgenic *E8::SISGT3* plants. Scale bar = 5 cm

stage compared to wt fruits, while transition from orange to red stage was slightly faster than in WT fruits, although in no case did it counteract the delay affecting the first stages of fruit development (Figure 50B). Furthermore, the characterization of red fruits revealed no significant differences in weight, size and hardness, but fruits from lines 3.1 and 63.9 produced less seeds per fruit than wt fruits (about 37% and 31% in lines 3.1 and 63.9, respectively) (Figure 50B and Table 6). Green and red fruits from these transgenic plants have been collected and will be used to determine the composition of free and conjugated sterols. This will allow us to investigate the effects of specific *SISGT3* expression during fruit ripening on the profile of sterols and confirm that the increased *SISGT3* mRNA expression in red fruits (Figure 49) leads to higher levels of glycosylated sterols.

Table 6. Number of days to reach the indicated fruit developmental stages, and the average number of seeds per fruit. Data are the mean $\pm$ SD from 25 fruits per genotype.

Breaker – Orange (Days)			Orange – Red (Days)			Seed number per fruit		
WT	3.1	63.9	WT	3.1	63.9	WT	3.1	63.9
1,51 $\pm$	1,48 $\pm$	1,46 $\pm$	1,86 $\pm$	1,35 $\pm$	1,44 $\pm$	27,2 $\pm$	17,0 $\pm$	18,7 $\pm$
0,63	0,51	0,55	0,70	0,49	0,60	3,4	2,4	7,6

3.3. CHAPTER III

Characterization of sterol spatial distribution in tomato plants: a focus on detergent-resistant membranes and histological 27-Alkine Cholesterol Detection

3.3.1. Characterization of lipid rafts (LR) in tomato leaves and roots

Sterols play a central role in determining the architecture and, consequently, in modulating the biological functions of LR, which have emerged as central players in a number of PM-dependent plant biological processes. An objective of our research group is to use a systems biology approach involving transcriptomics, lipidomics and proteomics to establish a working model of specifically altered biological mechanisms and processes mediated by LR underlying the phenotypes displayed by our conjugated sterols biosynthetic mutants, including those described in this work. As mentioned in the Introduction, LR can be isolated as the so-called detergent-resistant membrane (DRM) fraction because of their insolubility in non-ionic detergents at cold temperatures. Thus, as a first step to achieve the mentioned general objective, in this PhD work the methodology to isolate DRM and DSF (detergent-sensitive fractions) from purified PM samples from leaves and roots of the tomato WT plant has been set up and their sterol profile established, since DRM have been isolated from different plants and source materials, (Lefebvre et al., 2007; Yepes-Molina et al., 2020; Ozolina et al., 2021) but not yet from tomato.

3.3.2. Isolation of PM, DRM and DSF Fractions

The PM of tomato roots and leaves was obtained using a polyethylene glycol (PEG)–dextran aqueous two-phase partition system (Yepes-Molina, 2020) from the corresponding microsomal fractions, obtained as described in Materials and Methods (Section 6.11). This system allows the separation of PM (upper phase, polyethylene glycol) and endomembrane (EM, lower phase, dextran). Immunoblot analysis using specific PM H⁺ATPase antibody was performed to check possible cross-contamination between both membrane fractions. A single band of about 105 kD, which correspond to the size expected for the PM H⁺-ATPase was detected only in the PM fraction of leaves and roots, indicating that cross-contamination between both membranous fractions (PM and EM), if any, was negligible (Figure 51). H⁺-ATPase activity measurements showed that the enzyme activity detected in roots (0.694 μmol

Pi/mg prot/h) was about double than in leaves (0.3499 $\mu\text{mol Pi/mg prot/h}$). These results paralleled those of total H^+ -ATPase protein detected by western blot (Figure 51) and suggest

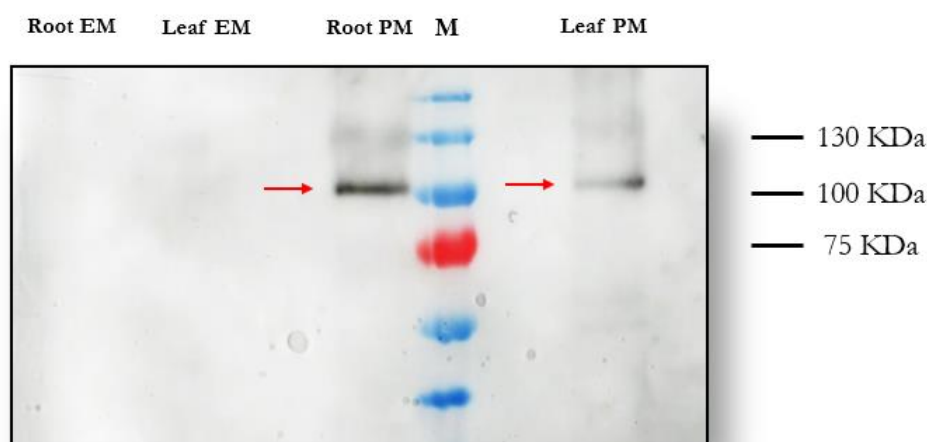


Figure 51. H^+ ATPase western blot analysis. H^+ ATPase protein (bands indicated with red arrows) in extracts of endomembrane (EM) and plasma membrane (PM) fractions from leaves and roots of tomato plants grown in hydroponic culture under LD conditions at 24°C. Each well was loaded with 15 μg of protein. Marker (M) size range is specified at the right.

that the enrichment in PM in the PEG fraction is higher in root samples than in those from leaves. These PM enriched fractions were used to obtain the DRM and DSF fractions as described in Materials and Methods (Section 6.11).

The recovery of PM fractions after the two-phase partition was higher in leaves (24,3%) than in roots (16,2%), while recovery of DRM fractions from the purified PM was somewhat greater in roots (19,1% proteins of the PM fraction) than in leaves (8,3 %) based on protein content measured using the Bradford assay (Table 7)

Table 7. Protein concentration ($\mu\text{g/g FW}$) in MF, PM, DRM and DSF from tomato leaves and roots. Plants were grown in hydroponic culture during 4 weeks . Data are means $\pm$ SE (n =3).

Fraction		$\mu\text{g /g FW}$	% (from MF)			$\mu\text{g /g FW}$	% (from MF)
Leaf	MF	1.060 $\pm$ 0.02	100	Root	MF	1.402 $\pm$ 0,03	100
	PM	0.258 $\pm$ 0.02	24.3		PM	0.226 $\pm$ 0.01	16.2
	DRM	0.021 $\pm$ 0.01	2.0		DRM	0.043 $\pm$ 0.01	3.1
	DSF	0.042 $\pm$ 0.02	3.9		DSF	0.087 $\pm$ 0,02	6.2

3.3.3. Determination of sterol profiles in leaves and roots of tomato plants

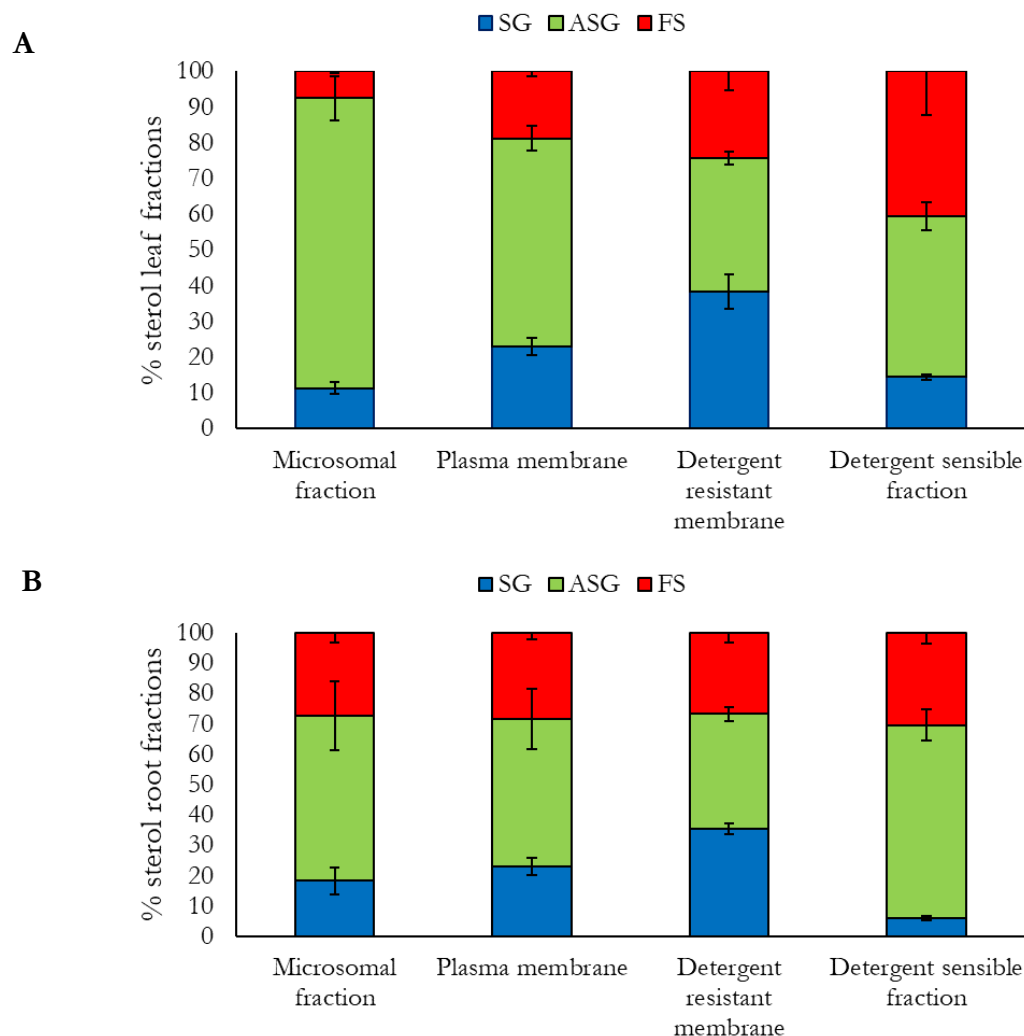


Figure 52. Sterol composition from four isolated fractions. Percentage species compositions of SG, ASG and FS in MF, PM, DRM and DSF fractions in leaves (A) and roots (B). The composition analysis was performed by GC-MS and each specie (SG, ASG and FS) was separated by TLC chromatography and then quantified by GC-MS analysis. Y-axis of the graph represents the proportional content derived from each sterol species based on each final total content. Error bars indicate standard deviations (n=3).

The profile of membrane sterols (FS, SG and ASG) was determined in the different membrane fractions (MF, PM, DRM, DSF) and the corresponding amounts expressed as μg of sterol/ μg of protein. The obtained results shown that the sterol profile was quite different depending on the membrane fraction, but a similar pattern was observed in the two analysed plant organs (leaves and roots). In leaves, ASG was the major sterol fraction (81%) in the MF, while SG and FS were minor fractions (11% and 7.6% respectively). These values were similar to those detected in whole leaves (Figure 30, Section 3.2.4.2). In the PM, ASG was still the major form, but decreased to 58.3% of total sterols, while SG and FS increased to

23,9% and 18,8%, respectively. In contrast, the SG and ASG proportions in DRM were almost the same (38,2% SG and 37,5% ASG) and FS reached 24,3%. In the DSF the SG proportion (14,4%) decreased compared to DRM, while a marked increase was observed in FS (40,7%), and the ASG increased slightly (44,8%) (Figure 52A). These results indicate that, in all the membrane fractions analysed in tomato leaves, glycosylated sterols (SG+ASG) were the major form, due mainly to the high amount of ASG, that was especially abundant in the MF, followed by PM, DSF and DRM. It is worth to mention the enrichment in SG and FS observed in DRM and DSF, respectively, compared with the PM. As in leaves, ASG was also the major sterol form in the MF (54,4% of total sterols) and PM (48%) of tomato roots, although the proportions were lower than in leaves (Figure 52A and B). FS represented 27,3% and 28,5% of the total sterols in MF and PM, respectively, while the minor proportion was that of SG (18,2% in MF and 23% in PM). In DRM, like in leaves, the proportions of ASG and SG were similar (37,9% and 35,3%, respectively), being FS the minor form (26,8%) (Figure 52B). ASG represent also the major proportion of sterols in DSF from tomato roots (63%), but this n was lower than that detected in the same leaf membrane fraction (Figure 49A and B). The proportion of FS was slightly higher than in DRM (30,5%), while that of SG decreased markedly (5,8%) (Figure 52B).

To obtain detailed compositional data, the four major sterol species, cholesterol, campesterol, β -sitosterol and stigmasterol were measured in the three sterol fractions (SG, ASG and FS) of PM and DRM. In leaf PM and DRM, campesterol (31% in PM and 40% in DRM), stigmasterol (~32% in PM and DRM) and cholesterol (~20%) were the predominant SG species, while β -sitosterol represented only 15% and 7,6% of the total SG fraction in PM and DRM, respectively (Figure 53A). The sterol pattern in root DRM was very similar to that described in the same membrane fraction of leaves (Figure 53A). However, the proportion of glycosylated β -sitosterol (24%) in the root PM increased compared with leaves, while that of glycosylated campesterol (~25%) decreased (Figure 53A). In contrast to that observed in SG, the ASG fraction of DRM was enriched in β -sitosterol (42% in leaves and 41% in roots), and this sterol specie was also higher (31% in leaves) or similar (23% in roots) than the corresponding SG in the PM. In contrast, the levels of stigmasterol in the ASG

fraction were lower than that of SG in all the analysed samples, and the same was observed

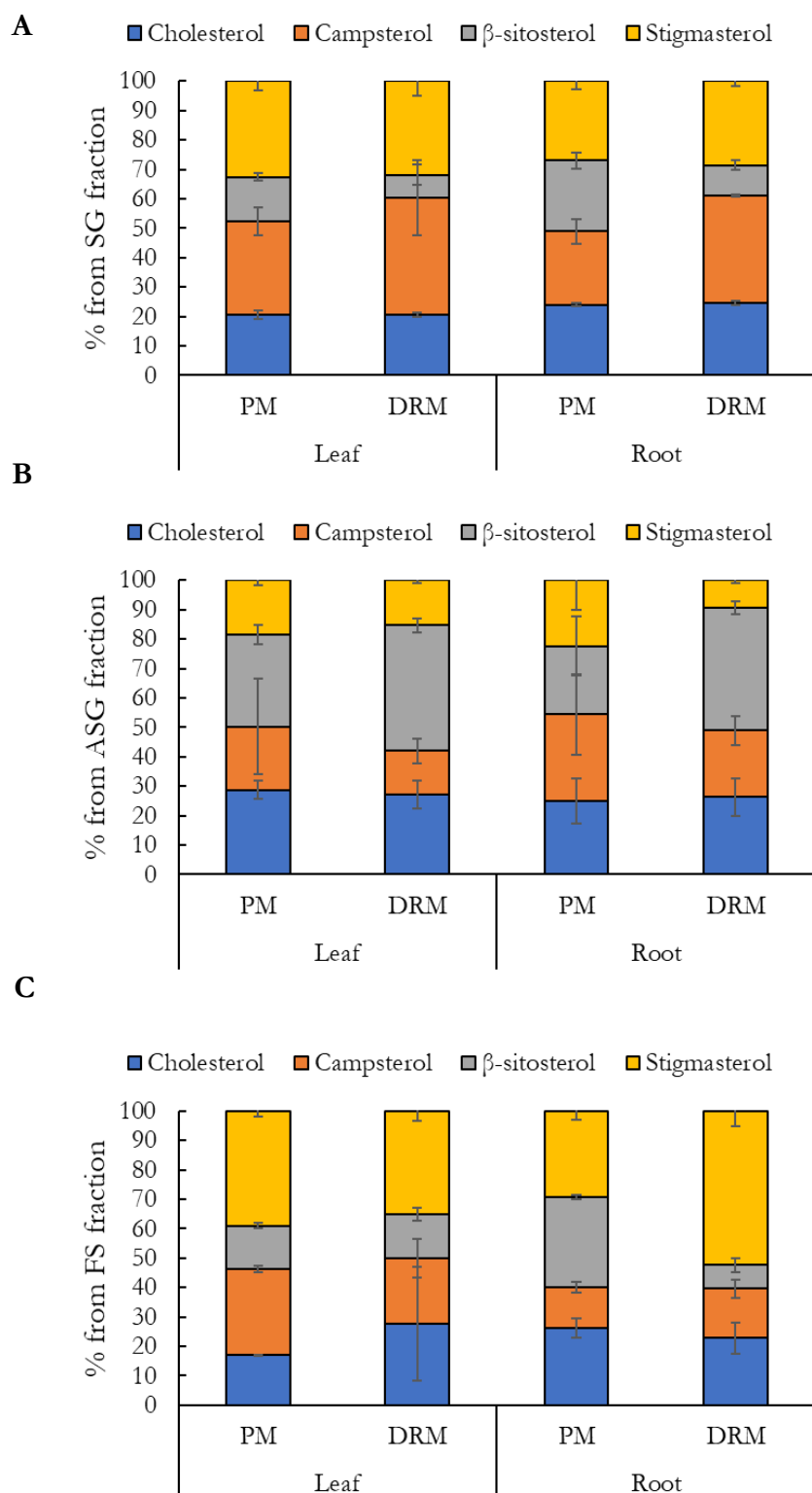


Figure 53. Sterol composition from PM and DRM from leaves and roots. Percentage species compositions of SG (A), ASG (B) and FS (C) in PM and DRM and DSF fractions in leaves and roots. The composition analysis was performed by GC-MS and each specie (SG, ASG and FS) was separated by TLC chromatography and then quantified by GC-MS analysis. Y-axis of the graph represents the proportional content derived from each sterol species based on each final total content. Error bars indicate standard deviations (n=3).

in the campesterol with the exception of root PM. The proportions of ASG cholesterol were similar to those of SG in PM and DRM from roots and leaves (~25-27% of total ASG sterols).

Finally, the proportion of FS showed a differential pattern between leaves and roots. In leaves, the cholesterol proportion was higher in DRM (~28 %) than in PM (17%), while the opposite was observed in campesterol (~22 % in DRM and ~29% in PM). However, in roots the proportions of both sterol species were similar in both membrane fractions (~24% cholesterol, ~14-16% campesterol). The proportions of β -sitosterol were ~14% in leaf PM and DRM, while in roots the levels in DRM (~30%) were markedly higher than in the PM (8%). A similar behaviour was observed in stigmasterol, whose proportions in leaves PM and DRM were similar (38%-35%), while clear differences were observed in roots (29% in PM and 52% in DRM) (Figure 53).

3.3.4. Ultrastructural analysis of tomato leaves and roots PM and DRM

Membrane fractions (PM and DRM) were processed by chemical fixation. Electron microscopy images showed that leaf and root PM and DRM fractions contained mostly membrane vesicles (Figure 54A). It must be noted that some size structural differences were observed between PM and DRM obtained from tomato roots and leaves. The determinations of vesicle area (Figure 54B) revealed a significant difference between leaf and root PM vesicles, since the root vesicles had a larger area (all populations were distributed in the range of 10 to 40 nm²) than those from leaves (ranging between 7 and 25 nm²) (Figure 54A). The DRM vesicles were clearly smaller than those of PM, but no significant differences were observed between roots and leaves (range between 2 to 5 nm²) (Figure 54B)(Table 8). These results suggest that although LR are dynamic assemblies of proteins and lipids, the morphological characteristics, such as the vesicle area, are stable and repetitive between different organs, which do not occur in the PM vesicles.

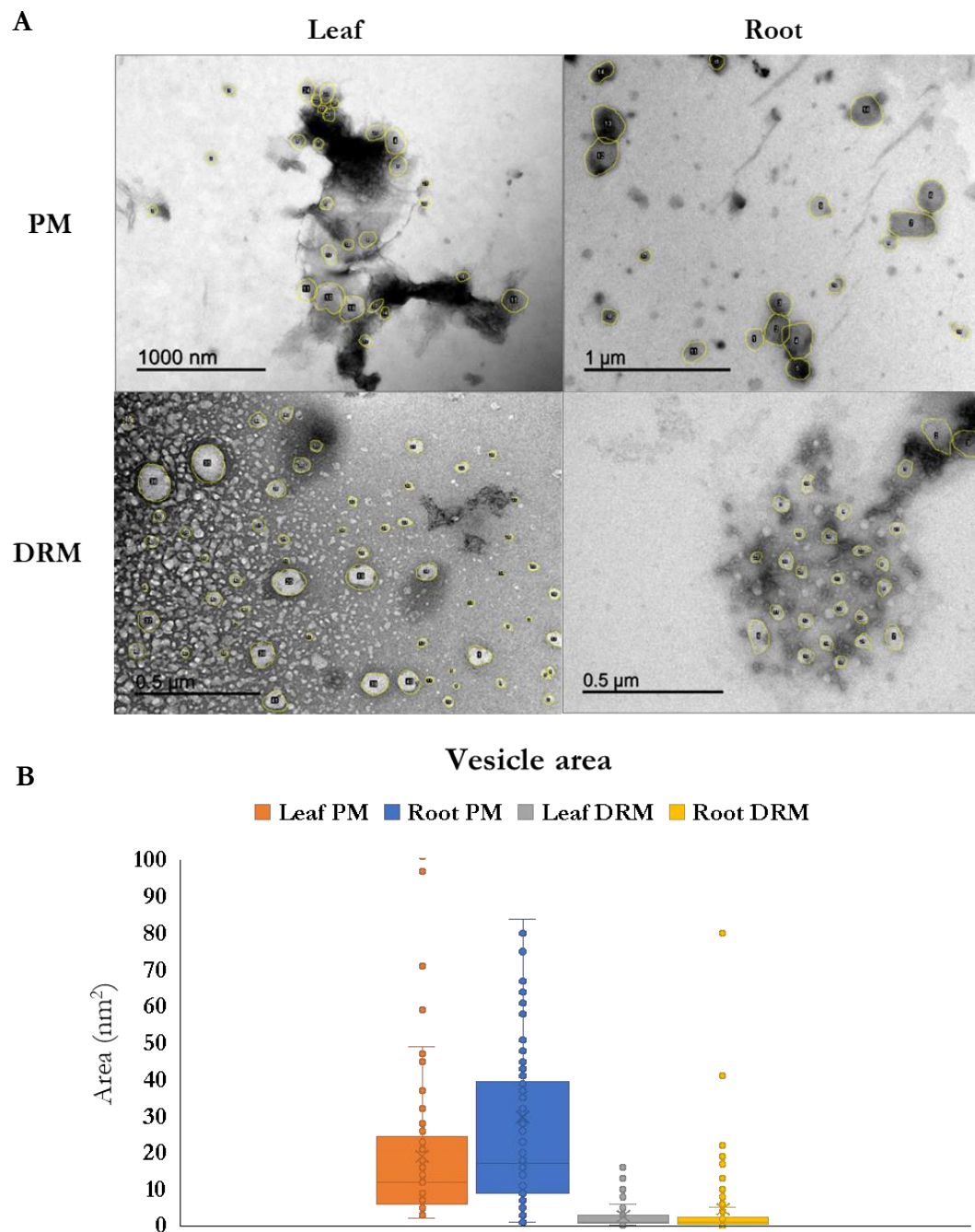


Figure 54. Ultrastructural analysis of tomato leaves and roots PM and DRM (A) Transmission electronic microscopy images (TEM) of tomato leaves and roots PM and DRM. Scale bars appear at the left bottom of each image. (B) Vesicle area size of leaf and root PM and DRM.

Table 8. PM and DRM vesicles size from tomato leaves and roots. Differences were calculated using Tukey's multiple comparison test and are represented on the table (**P<0.01; ***P<0.005; *P<0.0001).

Fraction		PM		DRM	
	Tissue	Leaf	Root	Leaf	Root
PM		19.0 ± 21.2	29.8 ± 33.4	2.6 ± 3.2	4.5 ± 10.54
	Leaf		**	****	***
	Root	***		****	****
DRM	Leaf				ns

3.3.5. Cellular imaging of phytosterols

3.3.5.1. *In situ* location of sterols and derivative compounds on tomato plants

Following the previous idea, the establishment of a working model to study biological mechanisms and processes mediated by LR could help to underlying the phenotypes displayed by our conjugated sterols biosynthetic mutants. At that moment, the specific localization of sterols throw-out plant cells is still unknown, so to start to shed light about the localization of these compounds and taking advantage of IBMP-CNRS of Strasbourg facilities, two different approaches were tested.

To determine the localization of sterols in plants, two strategies were tested: MALDI and click reaction. The aim of MALDI in this thesis was to detect 27-ALK cholesterol fed previously in tomato plants (Section 6.14.1) to check If the compound was internalized in

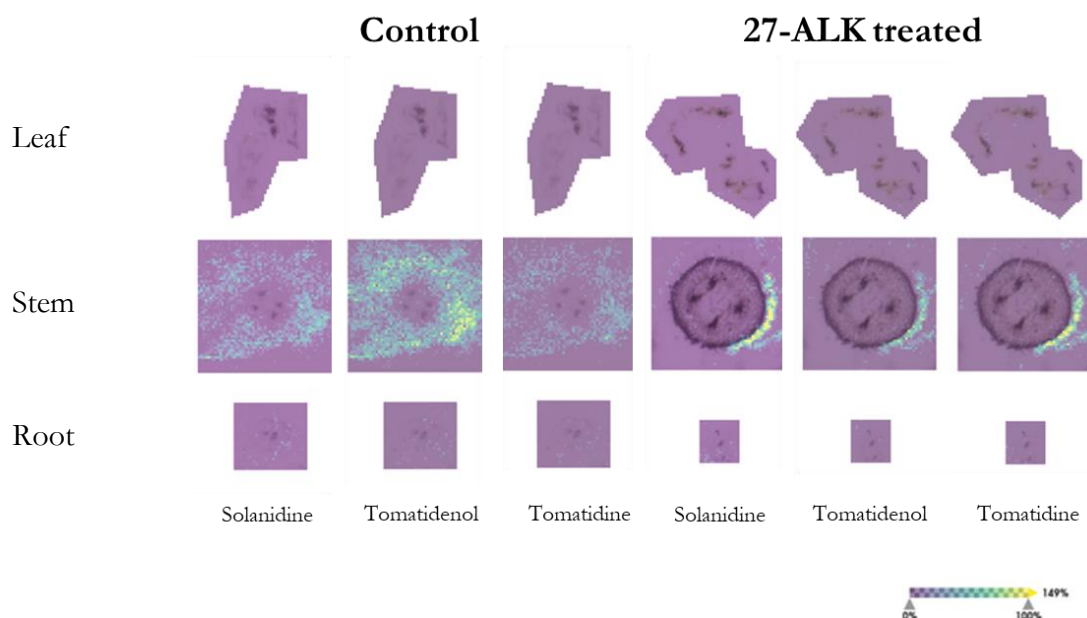


Figure 55. Distribution of plant metabolites annotated in *Solanum lycopersicum* cv MicroTom grown in hydroponic culture (control) and supplemented with 27-alkinecholesterol (27-ALK treated). The images show a representative figure of 1 out of 3 leaves, stems and roots analysed. The optical microscope image is merged with the signal intensity measured by MALDI-MSI. The value are registered as $[M+H]^+ m/z$ 398,34247 $\pm$ 3ppm for Solanidine, 414,33754 $\pm$ 3ppm for Tomatidenol and 416,35337 $\pm$ 3ppm for Tomatidine. The intensity is given by a scale bar in which the blue colour corresponds to lower levels of intensity and yellow to high levels calculated as %.

the plant tissues. MALDI could be a useful tool to detect whether feeding with 27-ALK cholesterol causes any disruption in the localization of other sterols. To perform the analysis, 3 different tomato tissues were selected considering different plant parts (leaves, roots and stems). First, both (control and 27-ALK treated) plants were selected to perform the cryofixation and the different cuts for MALDI-MSI analysis (Section 6.14.2). The leaves, stems and roots were prepared on the ITO plates as described in (Section 6.14.3). As this

was the first time trying to analyse this kind of compounds in tomato samples, and limited bibliography was available, some additional matrix selection had to be performed (Section 6.14.3).

These two different matrices (DHB I HCCA) were used to analyse the different standards we were interested to detect (Table 9). The results revealed that although some compounds were not detected using 2,5-dihydroxybenzoic acid (DHB) as a matrix, the intensity of the signal was equal or better with DHB so it was chosen for the sample analysis. Unfortunately, sitosterol glucoside was never detected, regardless of the matrix or method parameters used (Table 9). Signals obtained with the standards, except for solanidine, were generally found to be very low (Figure 55), close to background noise, despite the standards concentration used (10 µg/mL).

In cryosected tissues, 3 compounds were detected. These were solanidine which was also detected as standard and tomatidine and tomatidenol which the correspondent standards were tested by the metabolomic service previously. Notably, these compound were mostly found in stems, these compounds appeared to be excreted in specific localized areas in the treated samples, while in the control samples these compounds seemed to stay spread basically to the pith of the stem, indicating a slight distinct spatial pattern of distribution depending on the presence of 27-ALK and also within the plant tissues, as the roots and leaves showed distinct and lower levels of accumulation of these compounds. In any case, more studies are necessary to understand the nature of this result and to select a matrix which could perform correctly sterol and sterol derived compounds.

Table 9. Standard detection (10µg/mL) performed by MALDI-MSI using different matrix composition. DHB: 2,5-Dihydroxybenzoic acid, HCCA: α -cyano-4-hydroxycinnamic acid. n.d: non-detected n.a: not analysed. The column for leaves, stems and roots detection distinguish If the compound was detected or not in each tissue.

Compound	Formula	DHB detection (Intensity)	HCCA detection (Intensity)	Leaves detection	Stems detection	Roots detection
27-alkyne cholesterol (27ALC)	C28H44O	3x10 ⁵	4x10 ⁵	n.d	n.d	n.d
Cholesterol	C27H46O	1.2x10 ⁵	n.d	n.d	n.d	n.d
Cholesterol glucoside	C33H56O6	n.a	n.a	n.d	n.d	n.d
Stigmasterol glucoside	C35H58O6	n.a	n.a	n.d	n.d	n.d
Sitosterol glucoside acylated	C51H90O7	1.2x10 ⁵	n.d	n.d	n.d	n.d
Sitosterol glucoside palmitate	C51H90O7	n.a	n.a	n.d	n.d	n.d
Sitosterol glucoside	C35H60O6	n.a	n.a	n.d	n.d	n.d
Solanidine	C27H43NO	2x10 ⁸	1,2x10 ⁹	YES	YES	YES
Tomatidine	C27H45NO2	n.a	n.a	YES	YES	YES
Tomatidenol	C27H43NO2	n.a	n.a	YES	YES	n.d
α -tomatine	C50H83NO2	n.a	n.a	n.d	n.d	n.d
Sitosterol	C29H50O	1.5x10 ⁵	1x10 ⁵	n.d	n.d	n.d
Stigmasterol	C29H48O	1.5x10 ⁵	n.d	n.d	n.d	n.d

3.3.5.2. Subcellular localization of 27-Alkynecholesterol-Azide adduct on tomato stems

The investigation of sterol metabolism and localization in tomato plants using the copper-catalyzed azide-alkyne cycloaddition (CuAAC) click reaction and confocal visualization involved a series of experimental procedures to assess the incorporation and localization of 27-alkynecholesterol in the cell membranes. Three treated and untreated tomato plants were used to generate paraffin blocks (Section 6.15) for the click reaction, which was performed using the CuAAC method. The incorporation of 27-alkynecholesterol was facilitated through tomato root uptake (Section 6.14.1) and generate the adduct for visualization using confocal microscopy adding an azide to the system. In the laboratory we had three different azides with varying R chain sizes, each possessing distinct molecular weights (BD416 – 468.00 mol/g; BD223 – 512.05 mol/g; BD439 – 556.10 mol/g). These differences in molecular weight could influence the localization of the 27-ALK-Azide adduct in the membranes. To initiate the experiment, the azide with the largest R chain size (BD439), was selected due to its potential to facilitate transmembrane incorporation. This compound has an excitation wavelength of 598nm and an emission of 637nm.

To assess the generation of the adduct, in vitro reactions were conducted under three different conditions. The 27-ALK was solubilized in a buffer consisting of 0.5X MS medium with 15% dimethyl sulfoxide. The reaction buffer was prepared using sodium ascorbate, copper (II) sulphate at varying concentrations adding, the same azide concentration BD439 (Table 10) using the protocol Simon et al., 2018 as an example for the reaction buffers (Table 10). To visualize the adduct formation high-performance thin-layer chromatography was employed for separation, using dichloromethane: methanol (92:8) as solvent and making it visible using a 0.01% berberine sulphate solution.

Table 10. Mixture composition for in vitro alkyne-azide adduct formation. The final volume is reached by using the same buffer used for the delivery of the 27-ALK in tomato plants.

Compound	Condition A	Condition B	Condition C	Final Volume
Ascorbic acid	0.5 mM	5 μ M	0.5 μ M	Up to 1 mL of 0.5XMS
Cooper (II) sulfate	2.5 mM	5 μ M	0.5 μ M	
BD473 Azide		5 μ M		
27-ALK		5 μ M		

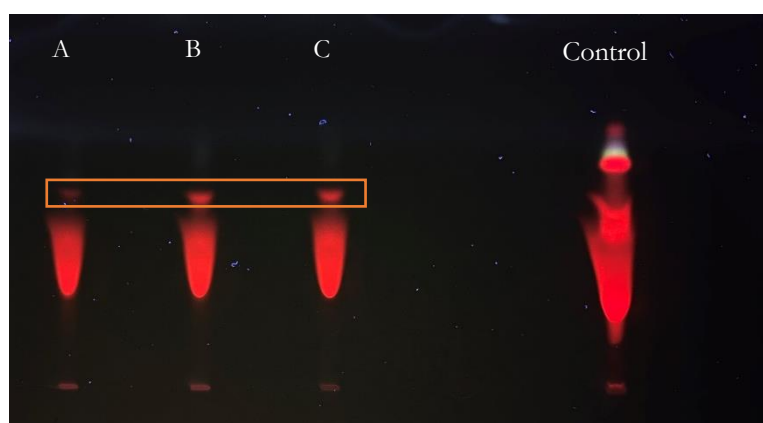


Figure 56. High-performance thin-layer chromatography. Visualized click reaction using 0,01% berbene sulphate. (A)(B) and (C) lanes represented the ALK-AZ adduct formation for every different condition described on Table 10. The control lane represents the BD439 azide.

The presence of the adduct in vitro was confirmed under all three conditions (Figure 56). Subsequently, plants fed with 27-ALK were fixed and paraffin blocks were made to cut 10 μ m sections as described in Section 6.15. Once deparaffined, slides containing the different tomato samples were subjected to treatment with solution A using the protocol as described (Simon et al., 2018). Upon observation at 598nm at the confocal microscope, it was evident that the 27-ALK-fed plants exhibited a distinct signal specifically localized in the xylem tubes (Figure 57). This observation not only demonstrated the successful formation of the adduct, also indicated a specific spatial distribution of 27-alkynecholesterol within the tomato cells in stems.

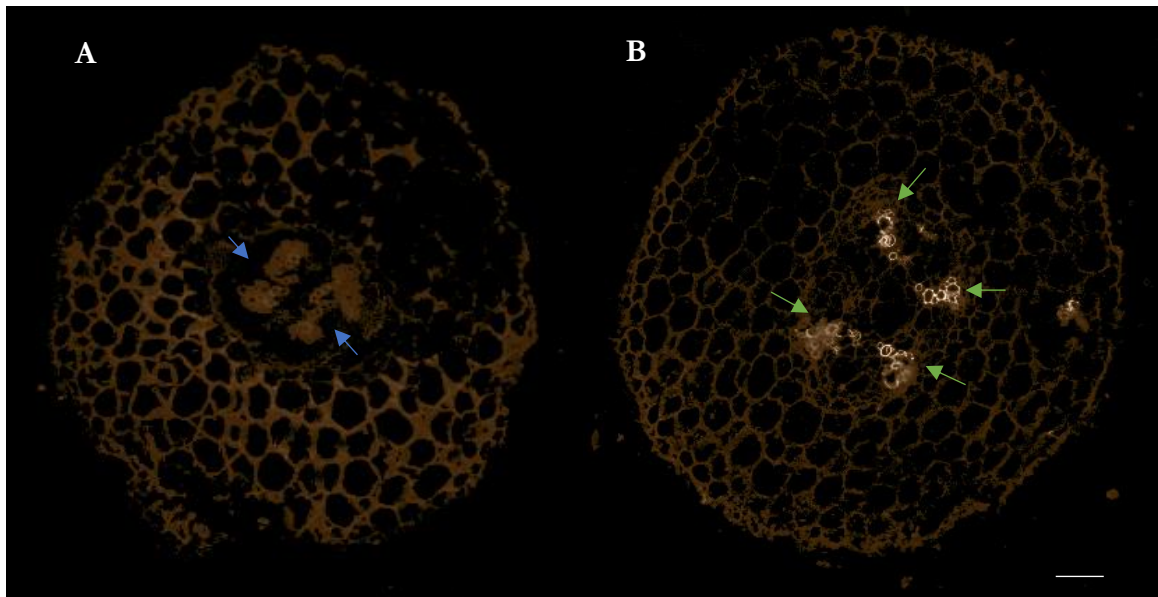


Figure 57. Tomato stem confocal microscopy. (A) Control tomato stem, blue arrows show the xylem vessels without the incorporation of 27-ALK. (B). 27-ALK tomato stem, green arrows show the visible adduct brightening concentrated in xylem vessels.

4. DISCUSSION

4.1. Chapter I

4.1.1. Generation and sterol profiling of tomato *slpsat31* x *slsat34* double knock-out mutant

The information currently available on plant SE biosynthesis and the sterol acyltransferases responsible for their formation is still limited. Hence, to further expand the knowledge about this metabolic process and its biological significance, we used (cv Micro-Tom) CRISPR/Cas9-induced single *slpsat1* and *slsat1* loss-of-function mutants previously generated in our laboratory (Burciaga., 2020) and generated and characterized tomato corresponding *slpsat31* x *slsat34* double mutant, which was obtained by crossing selected single mutants. Analysis of the total SE contents in *slpsat28*, *slpsat31*, *slsat34* and *slsat35* mutants demonstrated that SE formation in fruits, seeds and leaves depends almost solely on SIPSAT1 activity, since depletion of SE levels was observed only in the *slpsat1* mutants while SE levels in the *slsat1* mutants were increased instead of being depleted (Figure 9B, 13B and 15B). These results, along with the observation that the total amount of SE in the *slpsat31* x *slsat34* double mutant was even lower than in the *slpsat1* single mutants (Table 2 and 3), strongly suggests that SIASAT1-dependent sterol esterification plays a regulatory role in tomato FS biosynthesis, as previously suggested in Arabidopsis (Chen et al., 2007). It has been proposed that ASAT1 regulates the flux through the post-squalene segment of the sterol pathway, and therefore the amount of major sterol end products, by modulating the quantity of cycloartenol (Chen et al., 2007; Zhou et al., 2019), which is the first cyclic intermediate in the plant sterol pathway (Ohyama et al., 2009). A detailed analysis of the SE profiling data in fruits, seeds and leaves of the mutant plants revealed that the contents of all measured sterol species were enhanced in the *slsat1* mutants and depleted in both the *slpsat1* and the *slpsat31* x *slsat34* mutants (Table 1, 2 and 3), thus indicating that tomato PSAT1, like its Arabidopsis counterpart (Banas et al., 2005), has a broad sterol substrate specificity.

The qualitative impact of SIPSAT1 and SIASAT1 inactivation on the profile of total SE in fruits, seeds and leaves was almost identical, although important quantitative differences were detected. The relative effect of SIPSAT1 inactivation on SE levels was more pronounced in fruits and seeds than in leaves (about ~90% in fruits and seeds *vs* ~70% reduction in leaves, respectively, compared to WT), while that of ASAT1 inactivation in fruits and seeds was far smaller than in leaves (~95% in fruits and ~70 in seeds *vs* ~300% in leaves increase, respectively, compared to WT) (Figure 9B, 13B and 15B). It is also worth noting that the

increased amounts of SE found in seeds and leaves of the *slasat1* mutants compared to their WT counterparts cannot be attributed to *SIPSAT1* transcriptional upregulation, since its mRNA levels remained either unaltered in seeds or even slightly diminished in leaves (Burciaga., 2020). Thus, it remains to be established whether the observed accumulation of SE levels in the *slasat1* mutant seeds and leaves is due to post-transcriptional upregulation of the SIPSAT1 enzyme activity, simply to a greater availability of the FS substrates of PSAT1, or both. In fact, it has been proposed that PSAT1 is not rate-limiting for SE formation in Arabidopsis (Noiriel et al., 2004; Bouvier-Navé et al., 2010) and the tea tree (Zhou et al., 2019).

Interestingly, the inactivation of SIPSAT1 and SIASAT1 also led to changes in the levels of FS, albeit less pronounced than those of SE, which also differ depending on the organ and the mutant genotype. While in the leaves there was a moderate but significant increase of FS contents in both mutants, the content of FS in seeds remained unchanged in the *slpsat1* mutants and was significantly reduced in the *slasat1* mutants (Figure 9A and 13A). Similarly to seeds, in fruits FS also remained unchanged in *slpsat1* and *slasat1* mutant which significantly increased in *slpsat31* x *slasat34* mutant (Figure 15A). These organ-dependent and highly contrasting metabolic responses to SIPSAT1 and SIASAT1 inactivation likely reflect the differences in the physiological role and the regulatory mechanisms controlling SE levels in these organs. Seeds contain about 5 times more SE than leaves (Figure 9B and 13B, Tables 2 and 3), and their suggested primary role is to serve as a storage pool of sterols that can be easily mobilized to meet the increasing demand of plasma membrane components during the early stages of seedling growth. In the leaves, SE are also suggested to play a role in providing FS to support rapid expansion (Zhou et al., 2019), in addition to their involvement in maintaining sterol homeostasis in the cell membranes during growth and development, including the recycling of membrane sterols as senescence progresses or during stress (Bouvier-Navé et al., 2010; Kumar et al., 2018). Despite a number of metabolic responses in tomato plants lacking functional SIPSAT1 or SIASAT1 are similar to those previously reported in Arabidopsis, there are also some relevant differences. The dramatic increase of SE in leaves of the *slasat1* tomato mutants (Figure 9B) was not observed in the rosette leaves of the Arabidopsis *asat1-1* mutant, whose SE levels are even lower than those in the control leaves (Bouvier-Navé et al., 2010; Lara et al., 2019). Similarly, the increase of SE levels observed in tomato *slasat1* seeds (Figure 13B) is also in contrast to the unchanged content of SE in Arabidopsis seeds (Bouvier-Navé et al., 2010).

Regarding glycosylated sterols, in fruit and seeds, SG increase in *slpsat1* mutants and *slpsat31* x *slasat34* while in the *slasat1* mutants these levels vary, tending to experience a slight increase which could not be clearly described due to differences between lines (Figure 13C and 15C). In both tissues, the SG sterol levels of *slpsat31* x *slasat34* were higher than *slpsat1*. This behaviour followed the same trend in seeds regarding ASG levels (Figure 13D). Conversely, in fruits, ASG levels were dramatically reduced in *slpsat1* and in a lesser extend in *slasat1* and *slpsat31* x *slasat34* mutants (Figure 15D). These changes in sterol profiles result in different impacts on the total amount of sterols (free and conjugated forms) and PM-localized sterols (free and glycosylated forms) between seeds and fruits.

Specifically, in *slpsat31* x *slasat34* double mutant which had the lowest levels of SE in all tissues, and in that mutant, the differences in SE content led to a moderate reduction in the GS (SG+ASG) in fruits (72.6% compared to 79.0% in the WT) (Supplemental Table 1). This contrasts sharply with the strong increase observed in seeds, where the glycosylated sterols fraction almost doubles compared to the WT (57.9% vs 30.6%) (Supplemental Table 2). All four major GS species are similarly affected, with reductions ranging from 0.85- to 0.94-fold in mutant fruits (Supplemental Table 1) and increases ranging from 1.8- to 2.0-fold the WT levels in mutant seeds (Supplemental Table 2). These findings indicate that different regulatory mechanisms operate in the *slpsat31* x *slasat34* seeds and fruits to counterbalance the disruption of sterol homeostasis caused by impaired sterol esterification. The results also reveal that the inability to esterify sterols in the mutant organs leads to a moderate enhancement of sterol biosynthesis along with a substantial organ-specific reallocation of the total sterol pool. Changes in the metabolic flux of one branch of the conjugated sterols pathway influence the flux through the other, which is not unexpected since FS are common biosynthetic precursors of both glycosylated and esterified sterols. Lastly, it is also worth to mention that residual levels of SE were still detected in the *slpsat31* x *slasat34* double knock mutant, suggesting that other acyltransferases may contribute to SE formation in both seeds and leaves. In fact, the tomato genome contains up to seven additional genes coding for ASAT-like proteins (Lara et al., 2018).

Remarkable differences were also observed in the effects on plant growth and important developmental processes such as leaf senescence and seed germination. A functional SIPSAT1, but not SIASAT1, is necessary for proper tomato plant growth (Figure 11A and C), which is consistent with the suggested role of SE as a source of sterols to sustain rapid expansion of vegetative organs (Zhou et al., 2019). The reason why a similar phenotype was not observed in the *Arabidopsis* mutants lacking a functional PSAT1 (Bouvier-Navé et al.,

2010) is unclear, although it might be speculated that it could be due, at least in part, to the relative lower levels of SE in the vegetative organs of tomato *slpsat1* and *slpsat31* $\times$ *slasat34* mutants (Figure 9B, 13B and 15B) compared to those in the equivalent Arabidopsis mutants (Bouvier-Navé et al., 2010), so that the necessity of a minimum SE threshold level for proper plant growth cannot be excluded. The altered sterol profiles contribute early germination phenotype of *slpsat31* $\times$ *slasat34* seeds (Figure 14A) and lead to a reduction of about 50% in seed yield per fruit (Figure 16B). However, there are no significant effects on other fruit parameters such as hardness, weight (Figure 16A, B and C), fruit setting, shape, or ripening.

4.1.2. *Slpsat1* and *slpsat31* x *slasat34* knock-out mutants exhibit reduced size an early leaf senescence phenotype

The involvement of SE in tomato senescence regulation, as previously reported in *Arabidopsis* (Bouvier-Navé et al., 2010), would be mainly mediated by SIPSAT1, since an early senescence phenotype was observed in both *slpsat1* mutant lines, but not in the *slasat1* ones (Figure 11A and B). Interestingly, in contrast to that observed in *Arabidopsis*, where the *asatpsat* mutants showed the same early leaf senescence phenotype than the single *psat1* mutants (Bouvier-Navé et al., 2010), a synergistic effect of *slpsat1* and *slasat1* mutations was observed in tomato, since the senescence phenotype of the tomato double mutant *slpsat31* x *slasat34* was clearly stronger than that of *slpsat1* (Figure 11B and 12A). This observation is fully consistent with the expression profile of the senescence-marker gene *SISAG12* detected in leaves of different ages from WT and mutant plants (Figure 11D). Moreover, the senescence-promoting effect of the *slpsat1* mutation and the synergistic effect of both mutations were also observed in an induced senescence assay using detached leaves (Section 3.1.4). In aging tissues, sterols and fatty acids released from disorganized membranes would be converted to SE (Holmer et al., 1973; Chen et al., 2007). This explains the increase of SE content observed during senescence in several plant species and organs, including leaves (Dyas and Goad, 1993; Mckegney et al. 1995; Bouvier-Navé et al., 2010; Li et al., 2016). Thus, the impaired capacity of *slpsat1* and *slpsat31* x *slasat34* mutants to esterify FS in leaves (Figure 9A) is likely to be one of the reasons underlying the early senescence phenotype observed in the leaves of these mutants which, on the other hand, is not detected in the *slasat1* mutants (Figure 11B and 12A) that are able to produce and accumulate high levels of SE (Figure 9B). As mentioned previously, SE accumulate in cytosolic LD, whose primary role in leaves seems to be the removal of potentially toxic FS and other lipid catabolites scavenged from damaged membranes during stress or senescence (Huang, 2018). The reduced amounts of LD detected in leaves of tomato *slpsat1*, and *slpsat31* x *slasat34* mutant plants compared to WT (Figure 10) are in close correlation with the temporal senescence differences observed between these genotypes and the WT. Thus, it is reasonable to assume that the reduced abundance of LD in these mutants reflects the impaired capacity to esterify sterols which, in turn, prevents proper maintenance of FS membrane homeostasis and accelerates the onset of senescence.

4.1.3. SE levels lead to divergent patterns of LD formation in tomato leaves

A number of studies support the notion that LD formation is strongly associated with increasing levels of SE (Maillot-Vernier et al., 1991; Gondet et al., 1994; Bouvier-Navé et al., 2010; Shimada et al., 2019). However, such positive correlation between SE overaccumulation and enhanced LD abundance was not observed in the case of the *slsat1* leaves, in which the number of LD was lower than in WT leaves (Figure 10) despite their much higher levels of SE (Figure 9B). In this respect, it is interesting to note that a certain lack of correlation between LD abundance and SE contents has also been described during the diurnal cycle in tea leaves (Zhou et al., 2019). Either way, the enhanced capacity of *slsat1* leaves to form SE might explain why these mutants do not show any symptom of premature senescence, but at the same time raises the question about the reason underlying the unexpected, reduced accumulation of LD. It has been recently suggested that altered membrane sterol composition may compromise endoplasmic reticulum (ER)-based LD biogenesis in *Arabidopsis* seeds and leaves due to the capacity of sterols to modulate cell membranes physicochemical properties and the organization of putative PSAT1-localized ER microdomains where SE would be formed and segregated into LD (Yu et al., 2021). Thus, it might be speculated that the altered profile of FS in leaves of the *slsat1* mutants (Figure 9B, Table 1) may hamper proper formation of LD in their leaves through a similar mechanism.

4.1.4. Tomato *slpsat1* and *slasat1* mutations increase the germination speed

The rate of seed germination has been correlated with a proper seed reserve content (Sun et al., 2015; Shrestha et al., 2016; Zhao et al., 2018). This physiological process involves the breakdown of storage reserves accumulated in the endosperm, like carbohydrates, lipids and proteins, into soluble molecules that are mobilized through the embryo to allow seedling development (Bewley and Black, 1994; Pritchard et al., 2002). Previous studies indicate that changes in seed sterol levels affect seed germination (Du et al., 2022) and it is generally believed that SE are important to supply the necessary FS to sustain seed germination and seedling growth during the early development stages (Dyas and Goad, 1993; Harker et al., 2003). In this work we demonstrate that changes in tomato seeds SE contents, either a moderate increase or a strong reduction (Figure 13B), do not affect significantly the germination rate, as evidenced by the similar percentage of WT and the different mutant seeds germinated after 7 days (Figure 14A). On the contrary, the *slpsat31* $\times$ *slasat34* mutant seeds, which are almost completely devoid of SE, germinated significantly faster than the single *slpsat31* and *slasat34* mutant seeds, whose germination speed was slightly higher than that of WT seeds (Figure 14A). The difference in germination speed between *slpsat31* $\times$ *slasat34* and the *slpsat1* seeds is intriguing given the small differences in their SE content (Figure 13B and Table 2), although the possibility that SE levels in the *slpsat31* $\times$ *slasat34* seeds are below a given threshold necessary for germination to be unaltered cannot be excluded. In any case, this different germination behaviour cannot be attributed to differences in FS levels (Figure 13A) and, moreover, reinforces the synergistic effect of both mutations previously observed in the early senescence phenotype (Figure 11B and 12A).

Sterol mobilization during seed germination has been reported in several plant species, including tomato (Duperon et al., 1984; Garg and Nes, 1985; Huang and Grunwald, 1988; Guo et al., 1995; Zhang et al., 2007). The early germination phenotype of *slpsat31* $\times$ *slasat34* seeds could result from a better reserve mobilization rather than from changes in its content, which, as mentioned above, is primarily related with the germination rate. Moreover, germination is inversely proportional to a weaker endosperm and seed coat (Steinbrecher and Leubner-Metzger, 2017). It is thus tempting to hypothesize that early seed germination in tomato SE biosynthetic mutants could be due to the potential effect of the altered FS and ES profiles in the seed coat formation. Sterols might also affect directly the germination signalling pathway, since during plant growth and development phytosterols can interact with different hormone pathways (Vriese et al., 2019), including gibberellins (He et al., 2003),

which have been reported as essential factors for tomato seed germination (Groot and Karssen, 1987; Bassel et al., 2004).

The pre-germinative metabolism of *slpsat31* x *slsat34* seeds appears to be upregulated, as evidenced by the altered metabolite profiles (Figure 23A and B). Notably, there were more up-regulated metabolites in mutant fruits than in mutant seeds, and in both organs, there are more up-regulated compounds than down-regulated (Figure 23A, B and C). indicating a slight trend towards upregulation in mutant fruits (Figure 23C), and a much more pronounced upregulation in both dry and imbibed seeds (Figure 23A and B).

These findings suggest that impaired SE formation favours a general state of metabolic activation, particularly in seeds. The metabolic fluxes that are normally arrested in dry seeds are reactivated upon imbibition (Kazmi et al., 2017), as germinating seeds require a broad range of metabolites for cellular growth and differentiation, including those generated from the extensive protein breakdown associated with basal autophagy (Iglesias-Fernández et al., 2022). This proposed state of metabolic activation in *slpsat31* x *slsat34* seeds prior to imbibition could be linked to their early germination phenotype (Section 3.1.6), highlighting the impact of sterol metabolism on seed vigour and developmental timing.

4.1.5. Altered sterol levels cause organ specific metabolic perturbations in fruits and seeds

The chemical composition of tomato fruits is crucial for determining their quality, commercial value, and stability under different environmental conditions. Therefore, understanding the metabolic shifts resulting from genetic perturbations is essential for linking phenotypic changes with impacts on fruit quality (Tohge & Fernie, 2015; Zhu et al., 2018). Numerous studies have explored these shifts in recent years (Zhu et al., 2018; Otify et al., 2023; Alseekh et al., 2015). Similarly, the metabolome of tomato seeds has been analyzed to understand changes during imbibition (Kazmi et al., 2017) and across different varieties, highlighting important metabolic changes for development and adaptation (Alseekh et al., 2020). Despite these advances, the effects of sterol biosynthesis perturbations on the overall plant metabolome remain largely unexplored. To bridge this gap, we established the metabolic fingerprints of WT and *slpsat31* x *slasat34* mutant tomato fruits, as well as dry and imbibed seeds. In total, 703 (286 positive and 417 negatively regulated compared to WT) and 704 (306 positive and 398 negative) metabolites were identified in fruit pericarp from lines 9 and 31, respectively.

The metabolite composition of *slpsat31* x *slasat34* red fruits revealed a significant perturbation of the lipidome compared to WT fruits, affecting storage lipids like triacylglycerols (TAGs), as well as major lipid constituents of the PM, such as phospholipids, lysophospholipids, and sphingolipids, along with photosynthetic membrane lipids like galactolipids (Figure 19). The observed reduction in TAG levels (Figure 19A) aligned with the significantly reduced SE levels in the mutant (Figure 15B), since sterols are crucial for the assembly of LD and are a major component of their hydrophobic core alongside TAGs (Yu et al., 2021).

Among the four main classes of sphingolipids (Michaelson et al., 2016), levels of free long chain bases and glycosylinositolphosphoceramides remain unchanged, whereas certain ceramides and glycosylceramides were significantly reduced in the mutant (Figure 19C). Interestingly, *slpsat31* x *slasat34* fruits showed higher levels of lysoPC and lysoPE species compared to WT fruits (Figure 18B). In contrast, changes in phosphatidylcholine and phosphatidylethanolamine, the primary plant glycerophospholipids, displayed an uneven pattern with some compounds increasing and others decreasing. Notably, species with more unsaturated fatty acids tend to increase at the expense of those with lower unsaturation (Figure 18A). A similar pattern was observed in the galactolipids monogalactosyldiacylglycerols MGDG and DGDG, with a shift towards more unsaturated species (Figure 18C). There is also a trend towards reduced levels of (DAG), the common

precursors of glycerophospholipids and galactolipids. These alterations in PM lipid components are likely an adaptive response to the altered free and glycosylated sterol profile due to impaired SE biosynthesis, rather than a direct consequence of SE depletion.

In contrast to the substantial effects on the fruit lipidome, the impact of the *slpsat31* × *slsat34* mutation on the lipidome of dry and imbibed seeds was much less pronounced, affecting only a few TAG, DAG, and galactolipid species in dry seeds (Figure 20A and B) and some TAG, ceramide, and galactolipid species in imbibed seeds (Figure 20C and D). During the transition from dry to imbibed seeds, mutant seeds exhibit higher TAG levels but lower DAG, ceramide, MGDG, and DGDG levels compared to WT seeds. These results indicate that the altered sterol profile had a minimal impact on the seed lipidome, regardless of the rapid metabolic changes associated with seed imbibition (Kazmi et al., 2017), highlighting the distinct metabolic profiles between fruits and seeds. Additionally, the mild changes in seed TAG levels contrast with the drastic alterations observed in fruits, reflecting the differential roles of SE in lipid droplets of seeds and fruits. This is consistent with the tissue-specific composition of LD, where TAGs are the predominant component in seed LD (Guzha et al., 2023).

Regarding the phenylpropanoid profile, these compounds are crucial for fruit quality (Zhu et al., 2022) and play protective roles against environmental stresses (Brunetti et al., 2015; Dong & Lin, 2021). In *slpsat31* × *slsat34* fruits, most significantly altered phenylpropanoids, including hydroxycinnamic acids, anthocyanins like oenin, and flavonoids such as luteolin, neohesperidin, and several derivatives of quercetin and kaempferol, were decreased compared to WT (Figure 22A). Notably, key precursors like chalcone naringenin and naringenin were also slightly reduced. Conversely, intermediates such as p-coumaric acid and its precursor phenylalanine, along with genistein that increased suggesting a downregulation of the anthocyanin and flavonoid branches of the phenylpropanoid pathway in the mutant. Although these changes imply a reduction in phenylpropanoid content, some metabolites, including genistein, apigenin-7-glucoside, and hesperitin-7-glucoside, increase significantly. These compounds are known for their antioxidant properties and therapeutic potential (Hojati et al., 2011; Falcone Ferreyra et al., 2012; Nazari-Khanamiri & Ghasemnejad-Berenji, 2021). In contrast to the fruits, dry and imbibed *slpsat31* × *slsat34* seeds exhibited elevated levels of hydroxycinnamic acids, anthocyanins, and flavonoids compared to WT seeds (Figure 22B and C). These changes indicate a general activation of the phenylpropanoid pathway, particularly in imbibed seeds, which show higher levels of significantly altered phenylpropanoids and a greater number of metabolites that increase in abundance. The

distinct responses in fruits and seeds further emphasize the complexity and tissue-specific nature of metabolic regulation in response to altered sterol biosynthesis.

The impairment of SE biosynthesis induced autophagy in both fruits and seeds, as indicated by the significant accumulation of dipeptides in *slpsat31* $\times$ *slsat34* organs compared to the WT (Figure 21). The accumulation was more pronounced in seeds (Figure 21B and C) than in fruits (Figure 21A). Dipeptides are predominantly proteolytic products that tend to accumulate in response to the induction of autophagy, a catabolic process responsible for degrading unwanted or damaged cytoplasmic components, including proteins, to recycle their basic building blocks (Thirumalaikumar et al., 2020). Autophagy plays a crucial role in maintaining cellular homeostasis in various organs under both normal conditions and in response to developmental and environmental cues (Hofius et al., 2017; Thirumalaikumar et al., 2020; Alseekh et al., 2022; Wang et al., 2022; Ince et al., 2022). The observed accumulation of dipeptides suggests that the disruption of the balance between free and conjugated sterols in fruits and seeds is perceived as a stress signal, triggering autophagy as a compensatory mechanism (Manzano et al., 2016). This is further supported by the early leaf senescence phenotype displayed by the *slpsat31* $\times$ *slsat34* mutant (Burciaga-Monge et al., 2022), which aligns with the established link between autophagy and both normal and stress-induced leaf senescence (Avila-Ospina et al., 2014).

4.1.6. Fruits of the *slsat31* × *slpsat34* mutant show enhanced resistance to *B. cinerea* infection

Fruits of the *slpsat31* × *slsat34* mutant exhibit enhanced resistance to *Botrytis cinerea* infection, as the average lesion diameter in *slpsat31* × *slsat34* fruits was slightly less than half of that in WT fruits (Figure 17A and B), which is particularly notable given the increased susceptibility of ripe fleshy fruits to opportunistic pathogens like *B. cinerea* (Cantu et al., 2009). The complex metabolic rewiring in *slpsat31* × *slsat34* fruits complicates the identification of specific metabolite changes responsible for this enhanced resistance. However, it is likely that certain flavonoids and isoflavonoids, which are among the few metabolites that increase in the mutant, contribute to this phenotype. Notably, apigenin-7-glucoside, which has been identified as a biomarker for pathogen infection in tomato (Singh et al., 2023), and genistein, known for its antifungal properties (Aboody and Mickymaray, 2020), may play key roles.

Additionally, while the glycoalkaloid α -tomatine—a broad-spectrum toxic compound effective against herbivores and pathogens (You and van Kan, 2020)—was observed at lower levels, indole alkaloids such as loganin, secologanin, and tetrahydroalstonine were found at higher levels in mutant fruits (Supplemental Figure 4). Changes in antioxidant capacities, suggested by the accumulation of higher levels of glutathione and ascorbic acid alongside lower levels of dehydroascorbic acid, may further contribute by affecting reactive oxygen species homeostasis and thereby enhancing resistance to pathogens. The potential role of autophagy cannot be ignored either, given evidence linking autophagy to improved resistance against necrotrophic pathogens like *B. cinerea* (Hofius et al., 2017; Wang et al., 2022). Perturbations in plasma membrane lipids may also contribute by altering membrane geometry and physicochemical properties, which can influence the function of membrane proteins and the signalling roles of various lipid types (Levental and Lyman, 2023; He et al., 2003; Dong et al., 2012; Janda et al., 2013; Michaelson et al., 2016).

Thus, the enhanced resistance to *B. cinerea* in *slpsat31* × *slsat34* fruits likely arises from a combination of these factors, acting synergistically to modulate the plant's defence mechanisms.

4.2. Chapter II

4.2.1. Overexpression of *SlSGT3* affects tomato plant growth and development

The information currently available on plant SG biosynthesis and the sterol glycosyltransferases responsible for their formation is still limited. Of the four tomato genes encoding *SGTs*, *SlSGT3* is mainly expressed in roots and fruit, in that specific case, during maturation stages (Ramírez-Estrada et al., 2017). Hence, to further expand the knowledge about this metabolic process and its biological significance, we generated and characterized tomato (cv Micro-Tom) transgenic plants carrying the *SlSGT3* promoter fused to the *GUS* reporter gene (*SlSGT3::GUS*) (Figure 25) which could be a useful tool to unveil specific tissues in which *SlSGT3* enzyme was present. Also, plants overexpressing *SlSGT3* (*SlSGT3-ox*), constitutively using *2xCaMV* promoter (Figure 28) and fruit specific *E8* ripening dependent promoter.

To this end, we obtained 2 homozygous transgenic lines in which expression levels of *SlSGT3* were different depending on the tissue, having higher values in fruits than in leaves. In both case line 9 was leading the expression in leaves and in fruits compared to line 31, which in both cases was much higher than *SlSGT3* expression in WT leaves and fruits (Figure 29 and 34). Regarding sterol levels, GS levels increased significantly in the leaves of both transgenic lines compared to WT plants (Figure 30C), this increase was observed mostly in the SG fraction and in a lesser extend ASG sterol fraction. (Figure 30A and B). This significant increase of glycosylated sterol levels could be attributed to the significant *SlSGT3* overexpression observed in lines 9 and 31. However, in contrast to the *SlSGT3-ox* fruits, the levels of GS remain unaltered due to proportion changes. Interestingly, SG significantly increased while ASG, that is majoritarian sterol fraction slightly decrease (Figure 30A and B). UGTs involved in the glycosylation of sterols are known to be differentially expressed in leaves compared to fruits, leading to distinct profiles of glycosylated sterols in these tissues (Nyström et al., 2012) emphasizing variability in sterol profiles across plant tissues reflecting genuine biological differences (Nyström et al., 2012; Ramírez-Estrada., 2017). This is corroborated by findings that showed the total sterol content, including SG and ASG, were significantly different in fruits and leaves, particularly during the ripening process (Chávez et al., 2023). Considering that membranes are composed not only of GS but also contain FS, it is important to consider that in the leaves of *SlSGT3-ox* plants, the increase in GS was compensated by lower levels of SE, while FS levels remain unchanged (Figure 30E and F). In contrast, in the fruits of these same plants, the change in ratios resulted in GS maintained levels due to an increase in SG and a slight decrease in ASG (Figure 35A, B and C), which

triggers a decrease in both FS and SE, ultimately leading to a reduction in total sterols, including partially ASG and mainly FS (Figure 35 D, E and F), that comprise the membrane. The overexpression of SLSGT3 resulted in a negative effect in the plant size in lines 9 and 31 (Figure 32A and B) which is partially comparable to the phenotype induced by the depletion of SE (Figure 9A) in which SIPSAT1 inactivation led to slight dwarf phenotype which was partially compensated in the *slpsat31* x *slasat34* double mutant.

In leaves, these plants had an altered SE reservoir which increase in case of *slasat1* mutants and decrease in *slpsat1* mutants and *slpsat31* x *slasat34* (Figure 9A). In *slasat1* and *slpsat1* mutants FS increase but exceptionally remained unaltered in *slpsat31* x *slasat34* double mutant (Figure 9B). This sterol profile is similar to the one observed in SLSGT3-ox leaves, making conjugate sterol levels and proportions crucial, as *slpsat31* x *slasat34* developmental phenotype showed mainly differences in LD and premature senescence, while SLSGT3-ox plants showed a strong developmental phenotype which shortened internodes (Table 4) and made them wider making GS relevant to differentiate the observed phenotypes. Changes in the proportions of membrane sterols trigger sterol homeostatic unbalance with all the implications entailed in signalling, permeability and cell polarization (Shimada et al., 2019) (Schaller, 2004).

Dwarf tomato plants often exhibit reduced leaf number and overall stunted growth, which can be attributed to a significant decrease in total sterol content (Schaller, 2004). Sterols play critical roles in plant growth and development, influencing membrane integrity, hormone signalling, and stress responses. The manipulation of sterol biosynthesis pathways has been shown to directly affect plant morphology, including leaf size and plant height. The dwarf phenotype in tomato plants is often linked to mutations in genes involved in sterol biosynthesis. For instance, the *SIDWF1* gene, which encodes a sterol C-14 reductase, is crucial for the conversion of sterol precursors into active forms. Mutations in this gene can lead to a reduction in the levels of free sterols, which are vital for maintaining membrane integrity and fluidity. This reduction can hinder normal cell expansion and elongation, resulting in shorter internodes and smaller leaves (Montoya et al., 2005). The balance of different sterol types is also critical; for example, the ratio of FS to glycosylated forms can influence growth responses to environmental stimuli. A decrease in FS may lead to impaired signalling pathways that regulate growth and development, further exacerbating the dwarf phenotype (Kim et al., 2005).

From a vegetative point of view, the internodes of SLSGT3-ox plants were significantly shorter but wider (Figure 33C, Table 4). The histological analysis of lines 9 and 31 revealed

that the cell size area was significantly larger for both lines compared to the WT plants (Figure 33D). Further investigation using scanning electron microscopy (SEM) revealed that the internode anatomy of the SLSGT3-ox mutants exhibited notable differences in the structure of vessel elements and tracheid (Figure 33B and F). These vascular components were found to be wider and abnormally disposed compared to those in WT plants. Moreover, the collenchyma and parenchyma tissues were also found to be larger in line 9 compared to the WT (Figure 33F). This increase in cell size suggests that while the overall internode length is reduced, the individual cells within the internodes are larger, which can be indicative of altered growth regulation mechanisms. Ethylene is known to influence cell expansion and division, and its role in modulating these processes is well-documented (Guzman and Ecker 1990; Stepanova & Alonso., 2005; Li et al. 2007). For instance, highlighted that ethylene can modify cell wall properties, thereby affecting growth patterns in response to environmental stimuli (Vandenbussche & Straeten, 2018).

Ethylene has been shown to play a significant role in internodes shortening, vascular differentiation and the formation of xylem elements, which are crucial for water transport and structural support in plants (Ma, 2024; Firon et al., 2012). The increase in size of these tissues in the SLSGT3-ox lines may reflect an adaptive response to the altered ethylene signalling pathways, which can affect tissue differentiation and growth (López-Gresa et al., 2016). These observations were found in adult plants, but seedlings also followed the same pattern which experienced also an increased diameter and cell area (Figure 40B, Table 5). For that reason, SLSGT3-ox seeds were germinated under deprivation of light and were characterized by a thickened stem, reduced elongation of the hypocotyl, and exaggerated apical hook (Figure 40A).

In the context of the SLSGT3-ox lines, the prominent changes in seedling morphology could be attributed to the overproduction of ethylene, which mimics the effects typically seen in ethylene-treated WT plants. Is demonstrated that ethylene overproduction in tomato mutants leads to an ethylene triple response, resulting in leaf epinasty, stem thickening, and inhibited hypocotyl elongation (Mignolli et al., 2016). In seedlings grown in the dark, ethylene signalling activates ETHYLENE INSENSITIVE 3 (EIN3), which triggers the production of ETHYLENE RESPONSE FACTOR (ERF1) and WAVE-DAMPENED 5 (WDL5). These factors, along with CONSTITUTIVE PHOTOMORPHOGENIC 1 (COP1), inhibit hypocotyl elongation by suppressing ELONGATED HYPOCOTYL5 (HY5) activity and stabilizing cortical microtubules (Yu & Huang, 2017) (Ma et al., 2016). In the transcriptomic analysis performed in SLSGT3-ox plants it was found that some of these genes were modified

having the upregulated *EIN3* and *COP1* genes which consequently downregulates *HY5* gene (Figure 44 and 45, Supplemental Table 6 and 7), confirming the ethylene response to shorten tomato hypocotyls. In dark conditions, the regulation of *ACS* and *ACO*, contributes to the plant's ability to manage growth under unfavourable conditions. As found in *SlSGT3-ox* seedlings, the high upregulation of *ACO*, despite the downregulation of *ACS*, may allow for a fine-tuning of ethylene levels that can still promote the triple response without excessive elongation of the hypocotyl (Sun et al., 2015; Yu et al., 2013).

The hypocotyl elongation induced by ethylene under light conditions can be suppressed due to hindrance in auxin efflux. In normal conditions, the expression of the auxin transport genes is up-regulated due to the presence of ethylene (Liang et al., 2012; Smet et al., 2014; Hu et al., 2017) but in *SlSGT3-ox* plants there was a downregulation of auxin-related genes such as *AUXIN EFFLUX FACILITATOR 10* (Supplemental Table 7) that participate in auxin transport and in some manner could virtually simulate light condition interrupting hypocotyl elongation. The hypocotyl elongation could be stimulated by gibberellins through the degradation of DELLA proteins that impart a negative influence on growth (Hauvermale et al., 2012). Although not a lot of gibberellin-related genes were found in the transcriptomic analysis, a key gene, *GIBBERELLIN 2-OXIDASE 3*, involved in the transformation of inactive forms of gibberellins to active forms (gibberellin 1 and 4) was found downregulated (Supplementary Table 7). As described in Vandenbussche et al., 2007, when gibberellin biosynthesis is inhibited, it abolishes the ethylene-induced hypocotyl elongation completely, hence advising a GA-dependent regulation. Summarizing, ethylene can significantly impact stem structure and growth dynamics (Jenkins et al., 2022) which examining the cellular architecture of the hypocotyls, one can assess how ethylene influences cell size, number and arrangement (Figure 32,33 and 40) contributing to the observed phenotypic characteristics.

4.2.2. Overexpression of *SISGT3* results in an increase of SG levels shifting specie composition in red tomato fruits negatively affecting fruit size and seed set

Plants overexpressing *SISGT3* experienced a pleiotropic phenotype that was not only present during the vegetative stage. *SISGT3*-ox fruits were smaller and lighter following the same trend observed in internodes during vegetative stage (Figure 37B and 38, Table 4). *SISGT3* gene expression was highly increased due to overexpression resulting in an increase of SG levels but maintaining the GS due to a slight decrease of ASG (Figure 30A, B and C). Previously described in *Withania somnifera*, silencing of the *WsSGTL1* gene, accompanied by a significant reduction in glycosylated sterols (campesterol, β -sitosterol, and stigmasterol), negatively impacted overall plant development (Saema et al., 2015). Specifically, plants with reduced *WsSGTL1* expression exhibited stunted growth and smaller leaves. Further research revealed that downregulation of other related genes, including *WsSGTL2* and *WsSGTL4*, resulted in similar phenotypes. These changes in GS biosynthesis consistently produced reductions in plant size, evidenced by shorter plants and diminished leaf area (Singh et al., 2016). In *Arabidopsis thaliana*, the *ugt80A2:B1* double knock-out mutant, showed significantly lower levels of GS in leaves, stems, and inflorescences, presented with multiple morphological defects. In that case, these included abnormal embryonic development and a marked decrease in growth rates, further illustrating the essential role of glycosylated sterols in maintaining normal plant morphology and development (DeBolt et al., 2009).

Interestingly, our results do not show glycosylation decrease. In fact, there's a clear shift in GS proportions, reducing ASG levels which is the most abundant sterol and increasing SG (Figure 30A, B and C). Also, sterols species in SG fraction shifted their proportions (Figure 31A). In WT red fruits, stigmasterol is the most abundant specie, representing about ~43% of the total SG content followed ~32% β -sitosterol, ~22% campesterol and ~3% cholesterol. Although all species seemed to increase in absolute numbers, when values were referred to total sterol content and compared to WT, in *SISGT3*-ox plants stigmasterol increased representing ~47%, β -sitosterol decreased to ~26%, campesterol increased to ~23% and cholesterol remain almost unchanged (Supplemental Table 3). The ratio β -sitosterol/stigmasterol was clearly reduced due to *SISGT3* overexpression.

The reduction in the β -sitosterol/stigmasterol ratio in plants has been documented, particularly in the context of plant-pathogen interactions. Research indicates that infection by the plant parasitic nematode *Meloidogyne incognita* leads to a significant alteration in the sterol composition of host plants, specifically resulting in a decreased ratio of stigmasterol to

β -sitosterol (Cabianca et al., 2021). In cotton (*Gossypium hirsutum*), the response to different pathogens further illustrates this phenomenon. Infection with the fungal pathogen *Verticillium dahliae* resulted in an increase in the stigmasterol to β -sitosterol ratio, that improved the stability of the membrane and restricted the release of nutrients to the apoplast inhibiting the colonization of *Verticillium dahliae*, observing the opposite effect described during *M. incognita* infection, where the ratio was reduced (Huang et al., 2022). This indicates that the type of pathogen and the specific plant response can significantly influence the sterol composition, highlighting the dynamic nature of plant sterol metabolism and the specific β -sitosterol/stigmasterol ratio favouring different biotic response. Moreover, the sterol composition varies depending on plant tissues, with β -sitosterol often being more abundant in leaves, while stigmasterol predominates in roots (Gutiérrez-García et al., 2020) and in fruits (Chavez et al., 2023). This differential distribution is essential for understanding the physiological roles of these sterols in plant development and stress responses. The manipulation of these ratios may play a role in membrane stability and fluidity, changing lipid raft nanodomains region of membrane, which could not only affect the integrity, fluidity and permeability of the membrane, but can also sense and transmit signals to make cells divide or start the immune response of plant cells (Schaller., 2004; Bhat & Panstruga., 2005; Simons & Sampaio., 2011; Rogowska & Szakiel., 2020). That affirmation aligns with the fact that total sterol content can directly affect cell growth and cell proliferation as a result of possible changes in the physical properties of PM and lipid rafts (Piironen et al., 2000; Carland et al., 2002; Schaller, 2004; Laloï et al., 2007; Vriet et al., 2013).

It is also known that the accumulation of amino acids may influence the availability of precursors necessary for sterol biosynthesis. For example, the overexpression of certain genes involved in amino acid metabolism can lead to changes in the levels of sterol glycosides, as these compounds share biosynthetic pathways with amino acids (Jan et al., 2020).

As observed in Chapter I, the impairment of SE biosynthesis induced autophagy in fruits and seeds, indicated by the significant accumulation of dipeptides in slpsat31 x slsat34 organs compared to the WT. In the SLSGT3-ox fruits the situation was different as the number of accumulated dipeptides compared to WT was derisory. In fruits, high levels of tryptophan, tyrosine or proline, were found among others (Figure 47E). These could indicate less degradation of these amino acids (Wang et al., 2019). Also, leucine or glucose, which favour TOR pathway activation were found more accumulated in SLSGT3-ox lines (Figure 47B and E). Their elevated levels in SLSGT3-ox fruits may reflect impaired degradation

mechanisms, supporting the hypothesis of reduced autophagy via activation of TOR pathway which promotes the downstream processes of translation, transcription, ribosome biogenesis, and cell cycle while also blocking autophagy (Ince et al., 2022; Gou et al., 2019). The TOR pathway, may also play a role in regulating sterol glycosylation as the inhibition of autophagy through TOR activation could lead to an accumulation of metabolic intermediates that favour sterol biosynthesis, potentially altering the conjugation patterns of these compounds in transgenic tomato fruits (Deng et al., 2021). The observed accumulation of dipeptides in both *slpsat31* x *slsat34* double mutant and its accumulative differences in *SLSGT3-ox* fruits suggests that the disruption of the balance between free and conjugated sterols in fruits could be perceived as a stress signal, triggering or not autophagy as a compensatory mechanism depending on the total sterol composition (Manzano et al., 2016). Altogether, the results presented in this thesis demonstrate for the first time that specific shifts in SG composition can lead to similar alterations as those observed when the overall sterol content is disrupted leading to a wide-broad number of phenotypes and metabolic changes. This highlights the crucial role of glycosylated sterols in regulating tomato plant growth through membrane signalling and trafficking.

The formation of seeds marks the completion of the reproductive cycle in plants. In tomatoes, it has been observed that an increase in fruit weight, is often linked to an increase in seed production (Imanishi and Hiura, 1975; Prudent et al., 2009). In line with this observation, smaller *SLSGT3-ox* fruits gave significantly less seeds compared to those in WT plants (Figure 37A). Since seeds serve as a storage organ, their development competes for assimilates stored in the fruit. Consequently, larger fruits tend to have more assimilates available for seed production (Nitsch, 1970; Bertin et al., 1998; Prudent et al., 2009). In *SLSGT3-ox* plants, the increase in seed size and weight (Figure 39B and C), despite the reduced number of seeds (Figure 37A), indicates a shift in resource allocation. Our findings indicate that alterations in sterol ratios, particularly SG, significantly influence tomato fruit development and ripening leading to the formation of larger seeds in *SLSGT3-ox* lines that might accumulate more storage reserves, but the increased seed size does not compensate for the reduced viability, possibly due to impaired development or stress responses.

Seed reserve content is crucial for germination success (Min et al., 2022). During germination, stored reserves in the endosperm, such as carbohydrates, lipids, and proteins, are broken down into soluble molecules that are transported to the embryo, facilitating seedling development (Bewley and Black, 1994; Pritchard et al., 2002; Hills, 2004; Miernyk and Hajduch, 2011). Despite lines 9 and 31 had bigger seeds which higher weight compared to

WT, embryo viability experienced a great breakdown making only 20% of total seeds viable. These transgenic lines exhibited significantly reduced germination rates (Figure 39D and E), suggesting that low embryonic viability and seed reserve content or the mobilization of these reserves during germination was impaired.

The role of sterols in germination remains under debate. Several studies have reported the mobilization of sterols during seed germination in various plant species, including tomatoes (Bush and Grunwald, 1972; Huang and Grunwald, 1988; Heupel et al., 1986; Guo et al., 1995; Garg and Nes, 1985; Zhang et al., 2007; Shewry and Stobart, 1974; Duperon et al., 1984). In tomato seeds, SE and FS are the most abundant sterol fractions, while GS are present at relatively low levels. However, during germination, GS become the dominant fraction (Duperon et al., 1984). As described in Figure 13C and D, the double knock-out mutant *slpsat31* x *slasat34* exhibited altered levels sterols in seeds, with higher SG and ASG levels, lower SE levels and unchanged FS, resulting in an early germination phenotype. These findings suggest that changes in sterol content or the balance between different conjugated fractions, particularly GS, may influence tomato seed germination. As observed in histochemical analysis, SLSGT3 was mainly accumulated throughout all fruit tissues but specifically during the ripening stages (Figure 26). In proSLSGT3::GUS plants, GUS accumulation was distributed throughout all fruit but mainly in locular tissue (Figure 26) that plays a significant role in the synthesis of storage proteins in seeds, which is crucial for seed development. Also, the tissue's osmotic properties help to maintain these proteins synthesis and prevent early germination preventing premature seed germination by maintaining an osmotic environment and abscisic acid with levels that inhibit germination (Berry & Bewley, 1993) (T & Jd, 1992). As shown in Figure 47C and E, fruits overexpressing *SLSGT3* accumulated high levels of peptides and ABA, which could be influenced by the *SLSGT3* overexpression and tissue specificity.

Nevertheless, the possibility that altered sterol levels, including GS, directly impact the germination signalling pathway cannot be ruled out. Phytosterols are known to act as signalling molecules interacting with various hormone pathways during plant growth and development (Vriese et al., 2019), including gibberellins, which play an essential role in tomato seed germination (He et al., 2003; Groot and Karssen, 1987; Bassel et al., 2004).

Jasmonic acid is known to be involved in various physiological processes, including seed development, fruit ripening, and responses to biotic and abiotic stresses. In the context of SLSGT3-ox lines, the observed decrease in jasmonic acid levels in fruits (Figure 47C) may lead to impaired seed maturation processes, resulting in reduced seed yield per fruit. Studies

have shown that JA positively influences seed size and number, and its deficiency can lead to lower seed viability (Salem & Giavalisco, 2019). Salicylic acid, on the other hand, is primarily associated with plant defence mechanisms and stress responses. It plays a significant role in regulating plant responses to pathogens and environmental stresses, and it has been shown to influence seed germination and seedling vigour. The lower levels of salicylic acid in SLSGT3-ox fruits (Figure 47C) could compromise the plant's ability to respond effectively to stress, further impacting seed development and viability due to reduced seed quality and germination rates (Salem & Giavalisco, 2019). The plant material generated in this thesis offers a valuable resource for future research exploring the specific role of glycosylated sterols in tomato seed germination.

4.2.3. Overexpression of SLSGT3 results in delayed fruit ripening and differential ethylene-sensing

Observations of delayed fruit ripening in SLSGT3-ox lines could be linked to changes in ethylene production and sensing. While WT fruits reach the orange stage in about 32 days, transgenic lines with SLSGT3 overexpression take approximately 37 days to reach the same stage (Figure 37D). It is also important to notice that in the E8::SLSGT3 plants, fruits were fairly similar to those from WT plants indicating that the ethylene disruption is cause before the fruit maturation starting.. In the SLSGT3-ox fruits, the delay is linked to a postponement in ethylene production, which was confirmed by measuring ethylene levels (Figure 37E). Although the intensity of ethylene peak in SLSGT3-ox plants was highly similar to the measured in WT plants, in transgenic lines happened about ~5 days after than WT plants (Figure 37E). The postponement in lines 9 and 31 also include a higher deviation as fruits weren't maturing at the same time indicating some alterations in ethylene production initiation process.

When green fruits were treated with ethylene, both WT and mutant fruits ripen, although the mutant fruits sometimes exhibit a lighter red colour, suggesting potential alterations in ethylene sensing in SLSGT3-ox fruits (Figure 38). All these results reflect that delayed ripening and ethylene sensing differences in SLSGT3-ox tomatoes are the result of a multifaceted disruption. In the transcriptomic analysis of SLSGT3-ox seedlings, multiple ethylene related genes were found. Specifically, ACS was found downregulated while ACO upregulated (Supplemental Table 6). Ethylene biosynthesis is regulated by ACS that is traditionally considered the rate-limiting enzyme, but under certain conditions, ACO can also become rate-limiting (Khan et al., 2024).

In tomatoes, increased ACS enzyme dosage has been linked to the initiation of climacteric ethylene production, which is crucial for the ripening process. This suggests that ACS plays a significant role in ethylene production during the climacteric phase of fruit ripening (Chen et al., 2022). In SLSGT3-ox fruits, there is a clear delay on ethylene initiation process that, once initiated, proceeds like in WT fruits. This observation perfectly correlates with the process described by Chen et al., 2022 and it could be due to the limited ACS expression that ethylene initiation is delayed and although there's limited substrate, ACO upregulation might somehow overcome this limitation but needing more time. It also correlates with a biosynthetic approach as general maturation was experienced when green tomatoes were exposed to exogenous ethylene to ripe which along different sensing, all tomatoes could mature (Figure 38). Both ACS and ACO genes are expressed during fruit ripening, with

specific genes being inducible by ethylene treatments, indicating their role in ethylene-mediated ripening processes (Yuan et al., 2020). Regarding sensing genes, in the seedling transcriptomic analysis multiple sensing and response factors were misregulated, which can also impact in ethylene normal sensing condition. These affirmations are hypothetical as transcriptomic analysis was not performed in fruit and as observed with sterols previously, every tissue could react and interact differently as hormones and metabolism is most of the times tissue specific.

Regarding the metabolic analysis of WT and SLSGT3-ox fruits revealed low levels of the vast majority of triacylglycerols and the reduction of phospholipids and lysophospholipids which limit membrane fluidity and vesicle trafficking, both essential for correct fruit development, signal transduction and molecule transport in lines 9 and 31. These changes plus the hormonal misregulation and reduced antioxidant components could contribute to the ethylene sensing and the delayed ripening phenotype observed. Lipidic compounds were mainly less accumulated in SLSGT3-ox fruits. Compounds like TAG, were markedly more abundant in WT fruits. TAG are vital components of membrane lipids and serve as significant energy reserves in plant tissues. They are crucial for maintaining cell structure and function, particularly in the context of fruit development (Sah et al., 2024). TAG play a significant role in fruit development by providing energy and structural components necessary for growth. In tomatoes, TAG lipases such as SITGLa10 have been found to negatively regulate growth and development, affecting seed weight, germination, and fruit size (Zhan et al., 2023). Also, the manipulation of TAG metabolism, such as through the knockdown of TAG lipases, can enhance fruit development and improve cold tolerance (Zhan et al., 2023) (Wang et al., 2022). In SLSGT3-ox fruits, the markedly lower levels of TAG in SLSGT3-ox fruits may compromise fruit development and membrane integrity, which is essential for maintaining turgor pressure and overall fruit texture and development. This is particularly relevant as the hardness of fruit is often associated with cell wall composition and turgor pressure, both of which are influenced by lipid composition. Also, phospholipids are fundamental components of cell membranes serving as signalling molecules, coordinating processes like development and stress adaptation (Zhang et al., 2024). The balance between phosphatidylcholine and phosphatidylethanolamine is crucial for maintaining membrane fluidity, which affects vesicle formation and trafficking. Alterations in this balance can influence cellular processes such as nutrient release and hormone signalling (Zhang et al., 2023). The interaction between phospholipids and proteins at membrane contact sites is crucial for efficient vesicle trafficking. For instance, the

transport of diacylglycerol and its conversion to phosphatidic acid at ER-PM contact sites is vital for maintaining membrane stability and function during stress (García-Hernández et al., 2024).

Comparing the metabolic result of red fruits in both SISGT3-ox fruits (lines 9 and 31) and *slpsat31* x *slasat34*, there is a general decrease in TAG, but with distinct differences. The *slpsat31* x *slasat34* accumulates some long-chain TAG, while SISGT3-ox follows a similar trend but accumulates different TAG with shorter chains. Regarding phospholipid levels, both *slpsat31* x *slasat34* and SISGT3-ox lines show a mix of under- and over-accumulation of phospholipids compared to the WT. However, the extent of changes in phospholipid abundance patterns is greater in SISGT3-ox fruits, with some differences observed between lines 9 and 31. That similarly was observed with the other lipid classes in which both lines exhibit a mixed response in the accumulation of mono- and digalactosyldiacylglycerols. While both *slpsat31* x *slasat34* and SISGT3-ox show distinct abundance patterns, SISGT3-ox shows a clear trend of decreasing content for these compounds.

Overall, the overexpression of SISGT3 in tomatoes and the changes caused due to membrane sterol proportions and ratio shifting in SG fraction causes significant alterations in fruit and seed development. The reduction in fruit size and weight, coupled with the delayed ripening and changes in seed characteristics, are likely due to the altered metabolic and hormonal profiles associated with SISGT3 overexpression. These findings highlight the complex interplay between metabolic pathways and developmental processes that could be influenced by SISGT3, offering insights into how this gene modulates fruit and seed characteristics in tomato plants.

4.3. Chapter III

4.3.1. Characterization of LR in tomato leaves and roots

Plant sterols within LR are crucial for maintaining cellular integrity and facilitating various physiological processes in plants. LR are specialized membrane microdomains enriched in sterols and sphingolipids, which play a significant role in organizing membrane proteins and signalling molecules. This organization is essential for processes such as signal transduction, cell communication, and response to environmental stimuli (Kumar et al., 2018; Grosjean et al., 2018; Iswanto & Kim, 2017). The presence of sterols within these rafts influences membrane fluidity and permeability, thereby affecting the functionality of membrane-associated proteins and the overall cellular response to stressors (Tugizimana et al., 2014; Demir et al., 2013). Research indicates that LR serve as platforms for the compartmentalization of signalling pathways in plant cells, similar to their role in animal cells. Additionally, LR are implicated in the regulation of plasmodesmata, which are channels that facilitate intercellular communication in plants. The accumulation of callose at these sites is modulated by the lipid composition of rafts, highlighting the importance of sterols in maintaining symplasmic connectivity (Iswanto & Kim, 2017; Ozolina et al., 2021). Moreover, the dynamic nature of LR allows for the rapid reorganization of membrane components in growth and response to environmental changes. This adaptability is crucial for plants, which must constantly adjust to varying conditions. Overall, understanding the localization and function of plant sterols in LR is essential for elucidating the mechanisms underlying plant physiology and their responses to environmental challenges.

The isolation of tomato LR was set up to shed light about plant physiological mechanism of the phenotypes displayed by our conjugated sterols biosynthetic mutants. This protocol included different measurements like H^+ -ATPase activity and western blot to assure that the isolation process was correctly performed. In our isolation, H^+ -ATPase activity and western blot protein detection was in both cases higher in roots than in leaves (Figure 51) suggesting that the enrichment in PM in the PEG fraction was higher in root samples than in those from leaves. Additionally, the dynamic nature of LR allows for the rapid reorganization of membrane components in response to environmental stimuli. This adaptability is particularly important for roots, which must respond to varying soil conditions and nutrient availability (Zeng et al., 2018). The ability of LR to modulate protein interactions and signalling pathways in response to external cues may explain the observed differences in H^+ -ATPase activity and western blot protein abundance between roots and leaves (Iswanto & Kim, 2017).

The determination of vesicle area in the context of DRM and PM vesicles provided information about differences between plant tissues, particularly between roots and leaves. The observed difference in vesicle area, with root PM vesicles exhibiting a larger area (ranging from 10 to 40 nm²) compared to leaf PM vesicles (ranging from 7 to 25 nm²) (Figure 54), suggested that the composition and organization of LR may vary between these organs. Larger vesicle area in root PM vesicles may be indicative of a higher concentration of specific proteins that are essential for root functions, such as nutrient uptake. This observation aligns with the understanding that roots require a more extensive membrane surface area to facilitate the absorption of water and nutrients from the soil (Hamada et al., 2005). In contrast, the DRM vesicles, which were found to be smaller (ranging from 2 to 5 nm²) than PM vesicles and exhibited no significant differences between roots and leaves. This suggested that the structural characteristics of DRM vesicles are more stable and consistent across different plant organs, indicating that while LR are dynamic assemblies, their morphological features may be conserved (Kazakova et al., 2020). Vesicle size of tomato LR was in line to vesicle size determination performed in other plants species such as broccoli suggesting the importance of a conserved size throughout species to perform its functions (Yepes-Molina., 2020). The stability of DRM vesicle size across tissues may reflect a fundamental role in maintaining membrane integrity and facilitating essential cellular processes, regardless of the specific functions of the root or leaf (Gong et al., 2003).

The analysis of membrane sterols in different membrane fractions of WT tomato leaves and roots revealed significant information about sterol composition and its variations across plant organs. The results indicated that the profile of sterols, specifically FS, SG, and ASG, varied markedly depending on the membrane fraction analysed. In both leaves and roots, ASG were identified as the predominant sterol type, constituting 81% of total sterols in the PM of leaves, and 54.4% in roots (Figure 52). This dominance of ASG is consistent with previous findings that highlight the role of GS in plant membranes, which are known to stabilize membrane structures and contribute to various physiological functions (Beyzi et al., 2019). In the PM, the proportion of ASG decreased to 58.3% in leaves, while the proportions of SG and FS increased to 23.9% and 18.8%, respectively (Figure 52). These shifts suggest a selective enrichment of different sterol types specifically in PM. The observed increase in SG and FS in the PM compared to the MF aligns with the understanding that the PM plays a critical role in cellular signalling and transport processes, where different sterol types may influence membrane fluidity and protein interactions (Zauber et al., 2013).

The distribution of sterols in DRM and DSF further illustrates the complexity of sterol partitioning within plant membranes. Surprisingly, in DRM, SG and ASG proportions were nearly equal, indicating that DRM fraction is enriched basically in SG comparing it to PM composition, making GS the major sterol specie and suggesting a balanced role of these sterols in maintaining membrane functionality (Figure 52). Notably, the DSF fraction was highly enriched with FS (~41% total fraction), compared to DRM indicating differential sterol patterns between DRM and the rest of PM (DSF) and highlight the adaptive mechanisms plants employ to modulate membrane composition in response to physiological demands suggesting different membrane dynamics and cellular signalling pathways (Singh et al., 2015).

Additionally, detailed compositional analysis of the four major sterol species—cholesterol, campesterol, β -sitosterol, and stigmasterol— in PM and DRM revealed that in SG fraction campesterol and stigmasterol were predominant in both leaf and root PM and DRM, with β -sitosterol being less abundant (Figure 53A and B). Contrarily, the ASG fraction was enriched in β -sitosterol with low levels of stigmasterol (Figure 53B). It is clear that different phytosterols play different functions. Although cholesterol is primarily associated with animal cells, it is present in tomato plants contributing to the structural integrity of membranes. It is particularly important in forming LR, which are microdomains that facilitate protein-protein interactions and signaling pathways (Valitova et al., 2014). Campesterol is one of the most prevalent phytosterols in plants and plays a vital role in maintaining membrane integrity and fluidity. It is a precursor for the biosynthesis of brassinosteroids, a class of plant hormones that regulate growth and development (Valitova et al., 2016). Campesterol's structural properties allow it to modulate membrane characteristics, which is essential for cellular processes such as endocytosis and vesicle trafficking (Cao et al., 2020). Additionally, campesterol has been shown to enhance plant resistance to abiotic stresses by stabilizing membranes under unfavourable conditions (Rogowska & Szakiel, 2020). Stigmasterol is another significant phytosterol found in various plant tissues. It is involved in membrane stabilization and fluidity, similar to campesterol (Du et al., 2022). Stigmasterol also plays a role in plant defence mechanisms, as it is implicated in the response to pathogens and environmental stresses (Griebel & Zeier, 2010). The conversion of β -sitosterol to stigmasterol is an important metabolic pathway that influences plant-pathogen interactions, suggesting that stigmasterol may enhance resistance to certain diseases (Griebel & Zeier, 2010). Furthermore, stigmasterol has been associated with the regulation of plant growth and development, acting as a precursor for various signalling molecules (Valitova et al., 2016). β -

Sitosterol is one of the most abundant phytosterols in plants and is crucial for maintaining membrane integrity. It functions similarly to other sterols by modulating membrane fluidity and permeability (Du et al., 2022). β -Sitosterol is also involved in plant defence mechanisms and has been shown to enhance resistance to pathogens and pests (Behmer et al., 2010). Its role in the phloem is particularly noteworthy, as it influences the suitability of host plants for phloem-feeding insects, thereby affecting plant-insect interactions (Behmer et al., 2010). Additionally, β -sitosterol is a precursor for various bioactive compounds, including steroid hormones, which are essential for regulating growth and development (Valitova et al., 2016). All these affirmations of common and differential functions of sterol species in plants reinforce the results observed in Chapter I and Chapter II. As observed in *slpsat31* $\times$ *slasat34*, the lack of SE lead to substantial changes in membrane sterols and generate multiple metabolic alterations and a great diversity of phenotypes (ex: early senescence, early seed germination, increased *B.cinerea* resistance in tomato fruits, etc). Moreover, in SLSGT3-ox plants, the increase of SG levels and the specie ratio changes lead to some common metabolic alterations but differential phenotypes (internodes shortening and widening, delayed seed germination or delayed fruit maturation). Some of these changes could be attributed to the differential capacity of these mutant plant membranes to perform its functions. In fact, SLSGT3-ox plants had higher levels of stigmasterol and campesterol which was translated to transcriptomic alterations in genes related to cell wall, plasmodesma and vesiculation (Section 3.2.4.9) validating that sterols species homeostasis in every fraction is crucial for the correct LR formation and functioning.

Also, FS fraction showed a differential pattern between leaves and roots in which cholesterol was enriched in DRM from leaves, compared to PM, and stigmasterol was enriched in DRM from roots, compared to PM. The variations in the proportions of these sterols between leaves and roots may reflect their distinct functional roles in different plant tissues, as well as their involvement in different developmental processes (Isaac et al., 2019). The distribution and function of these sterols can vary significantly between different plant tissues. For instance, in leaves, the higher concentrations of stigmasterol and campesterol may reflect the need for enhanced membrane stability and fluidity due to exposure to environmental stressors such as light and temperature fluctuations (Rogowska & Szakiel, 2020; Valitova et al., 2024). In contrast, roots may exhibit a different sterol profile that supports nutrient uptake and interaction with soil microorganisms. The balance of sterols in roots, particularly the higher levels of β -sitosterol, may reflect adaptations to their specific physiological roles (Du et al., 2022). These changes can be observed in *slpsat31* $\times$ *slasat34* mutant, that due to

impaired capacity of SE led to increase GS fraction and maintain FS levels in tomato which gave the capacity to resist better the infections of *B.cinerea*.

4.3.2. Sterol localization in tomato plants tissues

The investigation into the localization of sterols and their derivatives in tomato plants using MALDI-MSI and click chemistry highlighted the complexities of sterol localized detection. Multiple tomato plants were fed with chemical modified cholesterol which incorporated an alkyne group as a lateral chain and allowed the visualization via adduct formation with an external azide to produce fluorescence employing two primary strategies: MALDI-MSI and the CuAAC click reaction.

MALDI-MSI was utilized to detect the presence of 27-ALK cholesterol in various tomato tissues (leaves, stems, and roots) and other sterols or sterol-derivative compounds. The choice of matrices (DHB and HCCA) was a crucial point for optimizing the detection of sterols (Thomas et al., 2012; Bowman et al., 2019), with DHB ultimately selected due to its superior signal intensity for most compounds tested. However, the failure to detect sitosterol glucoside across all conditions indicated potential limitations in the sensitivity or specificity of the matrix used, confirmed in the failure detecting other sterols in the analysed tissues (Table 9) suggesting that their concentrations may be below the detection limits of the methods employed necessitating further optimization of the experimental protocols. In any case, solanidine, tomatidine, and tomatidenol were detected in the cryosected tissues, these compounds were more concentrated in specific regions of the stem in fed plants compared to the more diffuse distribution in control samples (Figure 55) which could indicate that the introduction of 27-ALK cholesterol could disrupt sterol localization due to incorporation of an external cholesterol source (Behmer et al., 2013).

Another approach, the click reaction, particularly the use of the CuAAC method was tested. This method facilitated the visualization of the 27-ALK cholesterol adducts in tomato stems. The incorporation of long chain azide allowed the visualization and localization of 27-ALK cholesterol in vitro and incorporated within the plant cell membranes. The successful visualization of the adducts in xylem tubes suggests a potential role in vascular tissue function or signalling (Brycki et al., 2014).

Future studies should focus on optimizing detection methods for sterol derivatives and exploring the functional implications of altered sterol profiles in response to exogenous feeding. Additionally, investigating the interactions between sterols and other cellular components, such as proteins and lipids, could provide deeper insights into their roles in plant physiology (Mishra et al., 2015).

5. CONCLUSIONS

1. The changes in SE levels induced in different tomato organs by inactivation of one or both sterol acyltransferases involved in the synthesis of these compounds (SIPSAT and SIASAT) demonstrate that SIPSAT1 has a predominant role in SE biosynthesis, while SIASAT1 would mainly have a regulatory role of the sterol biosynthesis pathway.
2. The regulatory mechanisms controlling the perturbation of sterol homeostasis induced by impaired sterol esterification are different depending of the tomato organ, since the changes in free and glycosylated sterol levels produced as a result of sterol acyltransferases inactivation are different in the analysed organs (leaves, fruits and seeds).
3. A decrease of SE content in tomato leaves is associated to an early senescence phenotype, which is more pronounced the lower the SE content is. This effect is mainly induced by SIPSAT1 inactivation, but in these conditions the loss of function of SIASAT1 has a synergistic effect, since the phenotype is more pronounced in the double *slpsat1* × *slasat1* mutant than in the single *slpsat1* mutant, and is not observed in *slasat1*.
4. The changes in SE content induced by the loss of function of SIPSAT1 and/or SIASAT1 have no effect on tomato seeds final germination rate but cause an early germination phenotype not only when the SE levels are decreased, but also, although more slightly, when they are increased. The stronger early germination phenotype shown by *slpsat31* × *slasat34* seeds confirms this result and demonstrates a synergistic effect of both mutations.
5. The altered sterols profiles induced by impaired sterol ester biosynthesis in the double mutant *slpsat1* × *slasat1* fruits has no effects on fruit setting, development (size and ripening) and hardness, but results in increased tolerance to *Botrytis cinerea* infection.
6. The changes in SE biosynthesis modifies the profile of FS and GS in fruits and seeds, and triggers a number of significant organ-specific qualitative and quantitative shifts in their primary and specialized metabolomes. The consequence of the combined action of multiple metabolic perturbations acting together results in phenotypes of early seed germination and increased resistance of ripe fruits to *B. cinerea* infection.

7. Histochemical detection of GUS activity in fruits expressing a chimeric *SLSGT3::GUS* reveals that GUS staining increase along fruit ripening and seems to be more intense in seeds. However, a detailed analysis shows that staining is concentrated in the locular gel tissue adhered to the seed coat.
8. We have obtained and partially characterized tomato transgenic lines constitutively overexpressing the *SLSGT3* gene that present increased levels of SG in leaves and fruits compared to *wild-type*. This increase on SG is paralleled by a decrease of SE in leaves and fruits resulting in a virtually unaltered total sterols content.
9. *SLSGT3* plays an important role during tomato plant growth and development since the changes in sterol profile induced by *SLSGT3* overexpression give rise to smaller plants with very thickened stems compared to the *wild-type*. This highlights the importance of sterols homeostasis for a right tomato plant growth and development.
10. *SLSGT3* plays also a prominent role on fruit development and ripening, since *SLSGT3-ox* fruits show reduced size and seed production, increased hardness and delayed ripening. This last characteristic is due to a delay in ethylene biosynthesis, while the hormone levels are similar in the *SLSGT3-ox* fruit than in *wild-type*.
11. *SLSGT3-ox* seedlings present a constitutive ethylene triple response. The misregulation observed in these seedlings includes genes encoding proteins involved in the ethylene biosynthetic pathway which helps to understand this phenotype and that observed in adult plants, which resembles the one described in *wild-type* plants treated with ethylene.
12. The use of E8 promoter allows to express the *SLSGT3* specifically in tomato ripening fruits, avoiding the developmental phenotype observed in *SLSGT3-ox* plants. *E8::SLSGT3* fruits experiences ~2 days delay in reaching the breaker stage while transition from orange to red stage was slightly faster than in *wild-type*. Furthermore, the characterization of red fruits revealed no significant differences in weight, size and hardness.

13. A method for lipid raft isolation from tomato leaves and roots has been successfully set up, and has allowed to determine that GS (SG+ASG) are the predominant form in all PM fractions but are not homogeneously distributed, while PM is enriched in ASG, SG are the predominant form in DRM. In contrast, SG ratio decrease in the DSF fraction to expenses of an increase in ASG and FS.

14. The absorption and localization under confocal microscopy of 27-alkynecholesterol adduct in tomato plants was successfully performed using CuAAC click reaction indicating a specific spatial distribution of 27-alkynecholesterol being accumulated in stem vessels. Although this procedure worked in silico and invitro under microscope visualization, must be refined to use MALDI-MSI approach as the ionization of sterols in physiological concentrations was not possible and only solanidine, tomatidine and tomatidienol could be detected.

6. MATERIALS AND METHODS

6.1. Microbiological material

6.1.1. Bacterial strains.

Escherichia coli TOP10 [F[−] mcrA Δ (mrr-hsdRMS-mcrBC) φ80lacZΔM15 ΔlacX74 recA1 araD139 Δ (ara-leu) 7697 galU galK λ[−] rpsL (StrR) endA1 nupG] was employed for the transformation of recombinant plasmids carrying polymerase chain reaction (PCR) amplification products and plasmid recombination products of the Gateway system.

Agrobacterium tumefaciens GV3101::pMP90, a rifampicin and gentamicin-resistant strain carrying the Ti pMP90 plasmid (pTiC58DT-DNA) containing essential vir genes for T-DNA insertion into the plant genome, was used to generate transgenic tomato plants.

6.1.2. Culture media

LB (Luria-Bertani) medium consisted of 10 g/L NaCl, 5 g/L yeast extract and 10 g/L tryptone (pH 7.4). The solid medium was prepared by adding 15 g/L bacteriological agar.

YEB (Yeast Extract Broth) medium consisted of 1 g/L yeast extract, 5 g/L meat extract, 5 g/L peptone, 5 g/L sucrose, and 0.5 g/L MgSO₄·7H₂O (pH 7.2). The solid medium was prepared by adding 15 g/L bacteriological agar. Antibiotics, if used, were added at the concentrations noted in Table 11.

Table 11. Antibiotics and supplements used in the preparation of media for bacterial cultures.

Antibiotic	Stock concentration	Working concentration
Kanamycin	25 mg/mL	25 µg/mL
Rifampicin	50 mg/mL	100 µg/mL
Gentamycin	100 mg/mL	25 µg/mL
Spectinomycin	50 mg/mL	100 µg/mL

6.1.3. Bacterial strains transformation

Aliquots of 100 μ L of *Escherichia coli* competent cells were transformed by the addition of 10 ng of plasmid DNA in a maximum volume of 10 μ L. The cells were maintained on ice for 15 min, following a brief incubation at 42°C for 30 s, and then returned to ice for 2 min. Subsequently, 300 μ L of LB medium was added, and the mixture was incubated at 37°C for one hour to allow for cell recovery. Aliquots of 100 μ L were plated onto solid LB medium supplemented with the appropriate antibiotics and incubated overnight at 37°C. Transformed colonies were subsequently identified using colony PCR.

Aliquots of 250 μ L of *A. tumefaciens* competent cells were mixed with 500 ng of plasmid DNA. The mixture was kept in ice for 5 min, placed into liquid nitrogen for 5 min, and incubated at 37°C in a water bath for 5 min. After heat shock treatment, the mixture was placed again on ice for 2 min, and 300 μ L of YEB liquid media was added. Cells were then incubated in agitation for 2 hours at 28°C. Aliquots of 100 μ L were plated on petri dishes containing solid YEB medium supplemented with the appropriate antibiotics and incubated for 48 hours at 28°C. Transformed *Agrobacterium* colonies were identified by PCR as described in chapter II. .

6.2. Tomato (*Solanum lycopersicum*) cv. Micro-Tom cultivation

6.2.1. Soil

Seeds were sown at a depth of 5 mm in peat (Klasmann TS2), perlite and vermiculite (3:1:1) that had been pre-moistened in small pots (5 x 5 x 6.5 cm) and placed in plastic trays filled with water up to a height of 1,5 cm. The trays were covered with plastic film to create a relative humidity of 100%, and transferred to a greenhouse under long-day conditions (16 h light/8 h dark) and a temperature ranging from 25-28°C during the day and 22-24°C during the night. After approximately one week, when the cotyledons emerge, the plastic cover was perforated to allow ventilation and initiate seedling acclimatization to the greenhouse environment. After 2 days, the cover was removed, resulting in a relative humidity of 60-70%. At this stage, the seedlings had fully expanded cotyledons and developed two pairs of true leaves. The seedlings were then transferred to larger pots (13 cm diameter x 10 cm height) using the same substrate mixture described above. The plants were kept under the same greenhouse conditions until they completed their life cycle. The seeds were collected from ripe red fruits, washed with distilled water in a strainer, placed on filter paper sheets and left to dry for 3 to 4 days. Finally, the dry seeds were collected and stored in paper envelopes at room temperature.

6.2.2. Hydroponic conditions

To acclimate the seeds to hydroponic growing conditions, they were first submerged in distilled water in an Erlenmeyer flask for 24 h in constant air pumping to oxygenate the solution. Afterwards, the seeds were distributed on a plastic tray filled with distilled water and vermiculite, and allowed to germinate in darkness at 24°C. After 5 days, when the tomato seedlings had developed the two cotyledons, they were transplanted into a 20L hydroponic cultivation tank filled with 16L of Hoagland nutrient solution (Table 12) and allowed to grow under long-day conditions (16h light/8h dark) at 22°C.

Table 12. Composition, stock concentration, and added volume of macronutrients and micronutrients in the Hoagland nutrient solution for hydroponic cultivation.

Composition	Stock concentration (g/L)	Added volume (mL) for 16L
KNO₃ 1M	101.11	96
Ca(NO₃)₂·4H₂O 1M	235.15	64

KH₂PO₄ 1M	136.09	16
MgSO₄ 7H₂O 1M	246.48	16
Fe-EDTA	18.60	16
H₃BO₃	1.546	3.2
MnSO₄·H₂O	0.338	3.2
ZnSO₄·7H₂O	0.575	3.2
CuSO₄·5H₂O	0.125	3.2
(NH₄)₆Mo₇O₂₄·4H₂O	0.088	3.2

6.2.3. Axenic culture

To sterilize seeds, they were rinsed in sterile water for 30 min, followed by a treatment with 40% (v/v) sodium hypochlorite (NaClO) solution for 15 min (8% commercial bleach) containing 0.01% Tween 20. Then, seeds were rinsed three additional times with sterile water for 5 min each washing step. Next, they were transferred to petri dishes containing solid 0.5X MS medium (2.5 g/L Murashige-Skoog basal salts (MS) supplemented with Gamborg B5 vitamins (100 mg/L inositol, 1 mg/L nicotinic acid, 1 mg/L pyridoxine, and 1 mg/L thiamine), and 8g/L agar, pH of 5.7-5.9). The plates were incubated at 24°C under long-day conditions (16h light/8h dark) at an irradiance of 150 $\mu\text{E m}^{-2} \text{s}^{-1}$.

6.3. Molecular methods and analysis

6.3.1. Genomic DNA extraction.

Young tomato leaf tissue (200mg) was collected, frozen in liquid nitrogen and grinded. Then 600 μ L of cetyl trimethyl ammonium bromide (CTAB) buffer + 80 μ L of SDS 10% (Table 13) was added, mixed for 4 min, incubated at room temperature for 15 min and centrifuged at 1000rpm for 10 minutes.. Next, 180 μ L of NaAc 3M was added to the supernatant and incubated in ice during 30 min, centrifuged at 1000 rpm for 15 min and once the supernatant was completely clear, it was collected and transferred to a new Eppendorf tube which contained equal volume of isopropanol. The mixture was incubated in ice for 30 min and centrifuged at 10000 rpm for 10 min. Then the supernatant was discarded and the pellet dried at 65°C in a thermoblock. The pellet was resuspended in 375 μ L of Tris-HCL buffer, and 375 μ L of CTAB solution was added. After incubation for 15 min at 65°C, the sample was cooled at room temperature, and 375 μ L of chloroform was added. The sample was centrifuged at 14000 rpm for 5 min, and the upper aqueous layer was recovered. The same volume of isopropanol was added and the mixture was stored at -20°C overnight. The DNA was recovered by centrifugation at 1000 rpm at 4°C for 10 min. The supernatant was discarded and the DNA pellet was dried for 1h at room temperature, and finally resuspended with 100 μ L of sterile miliQ water. The concentration of the DNA was measured using NanoDrop spectrophotometer, and the sample stored at -20°C until further use. Alternatively, genomic DNA was extracted using Wizard® Genomic DNA Purification Kit (Promega). while for agarose gel electrophoresis DNA fragments, DNA purification was carried out using the Gel and PCR clean-up kit (Macherey-Nagel) following the manufacturer's instructions. Samples were resuspended in nuclease-free water and stored at -20°C until further use.

Table 13. CTAB Composition and final concentration of CTAB buffer for DNA extraction

CTAB buffer	Concentration
Cetyltrimethylammonium bromide (CTAB)	2% p/v
Sodium chloride (NaCl)	2 M
ethylenediaminetetraacetic acid (EDTA)	0.05 M
Tris-HCl (pH 8.0)	0.2 M

6.3.2. Miniprep extraction for plasmid DNA

A single colony containing the recombinant plasmid of interest was inoculated into 3 mL of LB medium supplemented with appropriate selection antibiotics, and incubated at 37°C with agitation at 180 rpm overnight. The cells were harvested by centrifugation at 14,000 rpm for 30 s, and plasmid DNA was purified using the Wizard® Plus SV Minipreps DNA Purification Systems (Promega) according to the manufacturer's instructions. The purified plasmid DNA was stored at 4°C in TE buffer until further use. For long-term storage, the purified plasmid DNA was stored at -20°C.

6.3.3. Amplification of DNA fragments by polymerase chain reaction (PCR)

The reaction mixtures for plant genotyping was prepared in ice as described in Table 14. The reaction conditions consisted of an initial denaturation step at 94°C for 2 min, followed by 30 cycles consisting each of 15 s of denaturation at 94°C, 30 s of primer annealing at 4°C below the lower T_m value of the primers, 30 s per kilobase of extension at 72°C, and a final extension of 5 min at 72°C. The resulting amplification products were analysed by agarose gel electrophoresis.

Table 14. Composition of the PCR mixture for plant genotyping

NZYTaq II 2x Green Master Mix (NZYtech)		
Composition	Volume	Concentration
NZYTaq II 2x Green Master Mix	10 μ L	1X
Fw/Rv Primers	0.25 μ L	0.25 μ M
Template genomic DNA	1 μ L	100 ng/ μ L
Nuclease-free water	Up to 10 μ L	

The amplification of DNA fragments for cloning was performed using AccuPrime™ Taq DNA Polymerase High Fidelity (Thermo Fisher Scientific). The reaction mixtures were prepared in ice as described in Table 15.

Table 15. Composition of the PCR mixture for DNA fragment amplification

AccuPrime™ High-Fidelity Mix		
Composition	Volume	Concentration
AccuPrime™ 10X Buffer II	5 μ L	1X
Fw/Rv Primers	1 μ L	0.5 μ M
AccuPrime High Fidelity DNA polymerase	0.2 μ L	0.02 U/ μ L
Template DNA	1 μ L	100ng/ μ L
Autoclaved H₂O	Up to 20 μ L	

The reaction conditions consisted of an initial denaturation step at 94°C for 5 min, followed by 25 cycles consisting each of 30 s of denaturation at 94°C, 30 s of primer annealing at a

3°C below the lower T_m value of the primers, 1 minute per kilobase of extension at 68°C, and a final extension of 5 min at 68°C. The resulting amplification products were analysed by agarose gel electrophoresis.

6.3.4. Analysis of recombinant clones by colony PCR

Ten randomly selected bacterial colonies grown on a petri dish were transferred using a sterile pipette tip to a new plate containing LB medium. Then the bottom of a PCR tube was gently touched with the pipette tip to transfer the remaining portion of the colony, which would serve as the DNA template in the PCR reaction. The PCR reaction mixture was then added and the PCR was run as described (Section 6.3.3). The resulting amplification products were analysed by agarose gel electrophoresis.

6.3.5. Gene expression analysis by RT-qPCR

Total RNA was isolated using Maxwell® 16 LEV Plant RNA Kit (Promega) following the manufacturer's instructions, using 100 mg of ground frozen tissue (seeds, leaves, or fruits). RNA was quantified by NanoDrop and its quality was assessed by electrophoresis on 0.8% agarose gels. RNA samples were stored frozen at -80 °C until use. The cDNA synthesis reaction by reverse transcription (RT) was performed, according to the manufacturer's instructions. The integrity of the cDNA was verified by the amplification of a 81 bp fragment of the β -actin gene (Soly04g011500.2) using primers shown in Table 17.

Table 16. Composition of the PCR mixture for RT-qPCR DNA fragment amplification

SYBR Green I Mix		
Composition	Volume	Concentration
SYBR Green I Master Mix	5 μ L	2X
Fw/Rv Primers	1.5 μ L	0.25 μ M
Template cDNA	2 μ L	1:10 dilution
Nuclease-free water	Up to 10 μ L	

The PCR reaction mixture was prepared as described in Table 16. The analysis was performed using the LightCycler 480 Real-Time PCR System (Roche), and the qPCR programme consisted of an initial denaturation step at 95°C for 5 min, followed by 54 cycles consisting each of 10 s of denaturation at 95°C, 30 s of primer annealing at a temperature 4°C below the lower T_m value of the primers, 30 s per kilobase of extension at 72°C, and a final cooling step at 4°C for 1 minute.

The raw qPCR data from the LightCycler software 1.5.0 was used for analysis. Normalized transcript abundances were calculated by subtracting the cycle threshold (C_t) value of the target gene from the C_t value of the reference gene. The fold-change was determined using the $2^{-\Delta C_t}$ equation, with the tomato actin gene (Soly03g078400) serving as the endogenous reference gene (Livak and Schmittgen, 2001) for tomato leaves and seeds and Clathrin coat associated protein AP-50 (CAC) (Soly08g006960) for tomato fruits.

6.3.6. Gene copy number analysis by qPCR

In the different generations of transgenic plants, transgene copy number was determined by qPCR as described by Yang et al., (2005), using the tomato LAT52 gene (Soly01g007270) as an endogenous single copy gene and NPTII as target gene. In this case, the $2^{(\Delta\Delta C_t)}$ value of an heterozygous plant that contains a single copy of the transgene must be equal or close to 0.5, while $2^{(\Delta\Delta C_t)}$ values equal or close to 1.0 are expected from homozygous plants with a single transgene copy. The PCR reaction mixture was prepared as described in Table 16 and the qPCR programme used is describes in Section 3.9.5.

Table 17. Primers used for genotyping and transgene copy number quantification in transgenic tomato plants and RT-qPCR

Name	Sequence (5'-3')	Gene
SGT1qpcr for	TAGGCCCTCAACCCAT AGAA	<i>SSGT1</i> (Soly06g007980)
SGT1qpcr rev	TCAAATGGACCGCTCT TATC	
SGT2qpcr for	CCTCGATCTTGATCT GGTTAT	<i>SSGT2</i> (Soly09g061860)

SGT2qpcr rv	GGCTCTTGAACAGGA AGACTAC	
SGT3qpcr for	CATGTTGTGCCAAAGC CTAAA	<i>SSGT3</i> (Solyc04g071540)
SGT3qpcr rev	CTTCAGGAGGT'TGGT AGT'TTCTC	
SGT4qpcr for	GGGAT'TCGGGATGTG GTAAA	<i>SSGT4</i> (Solyc04g051150)
SGT4qpcr rev	AAAGGCACATCTGAAT GGAAAC	
qPCR Gus fw	CCGGGTGAAGGT'TAT CTCTATG	β -glucuronidase
qPCR Gus rv	CATGACGACCCAAAGC CAGTA	
qPCR.Actin fw	CCTTCCACATGCCATTC TCC	<i>SLACT</i> (Solyc03g078400)
qPCR.Actin rv	CCACGCTCGGTCAGGA TCT	
qPCR CAC.fw	CCTCCGTTGTGATGTA ACTGG	
qPCR CAC.rv	ATTGGTGGAAAGTAA CATCATCG	SlCAC (Solyc08g006960)
Lat1	AGACCACGAGAACGA TATT'TGC	
Lat2.1	GCCTTTTCATATCCAG ACACAC	LAT52 (Solyc10g007270)
Ntp 1-5	GACAGGTTCGGTCTTG ACAAAAAG	NPTII
Ntp 1-3	GAACAAGATGGAT'TG CACGC	Neomycin phosphotransferase II

6.4. Generation of transgenic tomato lines

6.4.1. Generation of transgenic plants carrying the pSISGT3::GUS transgene.

A 2358 bp fragment containing the promoter region of *SISGT3* (SL2.50ch04:58.606.081 - 58.608.439) was amplified by PCR using genomic DNA from tomato leaves, primers proSGT3_Fw_pGWB and proSGT3_Rv_pGWB, including the attB1 and attB2 sequences, respectively (Table 18), and Accuprime™ Taq DNA polymerase (Invitrogen™). The amplified fragment was cloned “in frame” into pDONOR207™ using BP Clonase™ enzyme mix (BP reaction), yielding the corresponding pENTRY clone (1:1 molar ratio of insert to vector). The promoter fragment was then transferred to the binary plasmid pGWB433 using LR Clonase™ enzyme mix (LR reaction), yielding plasmid pSISGT3::GUS, where the *SISGT3* promoter fragment was fused in frame with the coding sequence of the bacterial GUS (β -glucuronidase) reporter enzyme. The cloned insert was sequenced to confirm the absence of any amplification-induced mutations. The pSISGT3::GUS gene was introduced into tomato plants as described in chapter II using *A. tumefaciens* GV3101.

6.4.2. Generation of transgenic plants carrying the CaMV35S::SGT3 transgene.

The open reading frame of SISGT3 (1932 bp) was amplified by PCR using Accuprime™ Taq DNA polymerase (Invitrogen™), a TOPO™ entry vector containing the cDNA of SISGT3 obtained previously in our laboratory as template, and primers Fw_attB1_SGT3 and Rv attB2 SGT3 containing the corresponding attB1 and attB2 recombination sites, respectively (Table 18). The resulting amplification product was cloned “in frame” into the pDONOR207 vector using BP Clonase™ enzyme mix, yielding pENTR-SISGT3 plasmid (1:1 molar ratio of insert to vector). The insert was sequenced to rule out the presence of any amplification-induced mutation, and subcloned into the binary vector pGWB414 using LR Clonase™ enzyme mix, yielding plasmid p35S::SISGT3. The coding sequence was flanked by the 35SCMV promoter and the Nos terminator sequence. The cloned insert was sequenced and the resulting p35S::SISGT3 gene was introduced into tomato plants as described in chapter II using *A. tumefaciens* GV3101.

6.4.3. Generation of transgenic plants carrying the pE8::SGT3 transgene.

An "in frame" fusion between the ethylene-inducible promoter E8 ((Deikman et al., 1992, the coding sequence of the SLSGT3 gene and the tNOS terminator sequence was obtained using three-fragment Gateway®-MultiSite cloning technique (Katzen., 2007). The coding sequence for SLSGT3 was amplified as previously mentioned (section 3.2.3) using primers Fw_attB4r_SGT3 and Rv attB3r SGT3 (Table 18) containing the *attB4r* and *attB3r* recombination sites, respectively, required for triple recombination events. The amplification product was cloned into the Gateway®-compatible pENTR221 vector using BP Clonase™ enzyme mix, yielding the pENTR221:SLSGT3 pEntry clone (3:1 molar ratio of insert to vector).. Next, entry clones pENTR221:SLSGT3, pEF-1-E8-4 (RRID:Addgene_20090) and pEF-3-tNOS-2 (RRID:Addgene_20103) were recombined with pKGW destination vector using LR Clonase™ enzyme mix, according to the MultiSite Gateway® Three-Fragment Vector Construction protocol provided by Invitrogen. The resulting pKGW:E8:SLSGT3:tNOS gene was introduced into tomato plants as described in chapter II using *A. tumefaciens* GV3101.

Table 18. Primers used to generate the different constructs into Gateway plasmids.

Name	Sequence (5' - 3')	Gene
proSGT3_Fw_pGWB	GGGGACAAGTTTGTACAAAAAAGCA GGCTTC GAATTAACTAACAAGGATGCTAGG	Solyc04g071540. 2
proSGT3_Rv_pGWB	GGGGACCACTTTGTACAAGAAAGCT GGGTC TTCAAATGATGAACTCCAAAACC	
Fw_attB1_SGT3	GGGGACAAGTTTGTACAAAAAAGCA GGCTTC ATGGATAGTAGTGGGCTTAATGG	Solyc04g071540. 2
Rv_attB2_SGT3	GGGGACCACTTTGTACAAGAAAGCT GGGTC TCAGAGCCAAGAACCACAAG	
Fw_attB4r_SGT3	GGGGACAAC TTTTCTATACAAAGTTG GC ATGGATAGTAGTGGGCTTAATGG	Solyc04g071540. 2
Rv_attB3r_SGT3	GGGGACAAC TTTATTTATACAAAGTTG TC TCAGAGCCAAGAACCACAAG	Solyc04g071540. 2
attb1 E8 5 UTR Fw	GGGGACAAGTTTGTACAAAAAAGCA GGCTTCGTTCACGTAATTAAGTTTTG TGGAAG	Ethylene responsive promoter
attb4 E8 5 UTR Rv	GGGGACAAC TTTGTATAGAAAAGTT GGGTGGTCTTTTGCACGTGAATGAT TAG	
att3-Tnos-2.for	GGGGACAAC TTTGTATAATAAAGTTG CTCGTTCAAACATTTGGCAATAAAGT TTCT	Nopaline synthase terminator
att2-Tnos-3.rev	GGGGACCACTTTGTACAAGAAAGCT GGGTACCCGATCTAGTAACATAG	

6.5. Generation of tomato *slpsat1xslasat1* double knock-out mutant

The double mutant *slpsat31 x slasat34* was generated by crossing the two single CRISPR/Cas9 knock-out mutants, *slpsat1* (*slpsat31-19*) and *slasat1* (*slasat34-2*), obtained previously in our lab (Burciaga-Monge et al., 2022). The *slasat34-2* mutant was selected as the pollen receptor plant (female), while *slpsat31-19* mutant was selected as a pollen donor (male). First, we carefully removed all closed flowers, and all the fruit set formed, leaving only fully receptive flowers. Anthers were removed to avoid auto fecundation and facilitate *slpsat31-19* pollen contact with the *slasat34-2* stigma. To collect the pollen, 3 flowers from *slpsat31-19* that were fully receptive were cut and placed in a 2mL Eppendorf tube. The tube was vortexed to release pollen that was used to pollinate the *slasat34-2* emasculated flowers, which were then labelled. The tomato plants were covered with transparent plastic bags for two days to prevent excessive humidity loss. The plants were kept in the greenhouse under long-day conditions (16h light/8h dark) and seeds were collected and sown to obtain the corresponding plants for subsequent genotyping

6.5.1. Detection of CRISPR/Cas9-induced mutations in cross-pollinated *slpsat31 x slasat34* mutant plants

Genomic DNA was extracted from the obtained transgenic plants after cross-pollination following the protocol described above. From genomic DNA (Section 6.3.1) samples of plants where the transgene was detected. A region of approximately 300 bp encompassing the sgRNA target site was amplified by PCR using genomic DNA samples of candidate plants, AccuPrime™ Taq DNA Polymerase High Fidelity (Section 6.3.3), and the primers shown in (Table 19), which adds a single deoxyadenosine to the 3' end of the PCR products, facilitating ligation through base complementarity with the pGEM®-T Easy vector (Promega). The resulting amplification products were analysed by agarose gel electrophoresis, purified and cloned into the pGEM®-T Easy vector (3:1 molar ratio of insert to vector). Colonies harbouring recombinant plasmids were selected on LB plates containing 0.5 mM IPTG, 0.08 mg/mL X-Gal, and 0.1 mg/mL carbenicillin. The ligation reactions were incubated overnight at 4°C, and 1 µL of the ligation mixture was used to transform competent Top10 cells. From a minimum of 10 positive colonies from each transgenic line, a liquid culture was prepared, and plasmid DNA was extracted (Section 6.3.2). The cloned inserts were sequenced using the M13 FW and M13 RV primers (Table 19), and

the results were analysed using DNAdragon from Sequentix (<https://www.dna-dragon.com/download.php>).

Table 19. Primers used to check the CRISPR/Cas9 mutations in the *slpsat1xslsat1* double knock-out mutants.

Name	Sequence 5' -3'	Gene
ASAT crispr Genotip FW	GCAAAGTCCAACAAAGGTC AAAAAG	Solyc11g012260
ASAT crispr Genotip RV	TATTTCGCGGAGAGGCTTAG A	
Crispr PSAT Genot FW	CCAATTCCCAGCGGCAAAA AGTC	Solyc09g072710
Crispr PSAT Genot RV	AGTGTCGAGCCAGACTAAA TCG	
M13 Fw	GTAAAACGACGGCCAGT	pGEM-Teasy sequence
M13 Rv	AACAGCTATGACCATG	

6.6. Tomato transformation

Transgenic tomato lines were generated using the cotyledon transformation method (Wittmann et al. 2015) with some modifications. First, the seeds were sterilized with 10% bleach solution and sown in sterile glass jars. Cotyledons were obtained from 14-day-old seedlings growing *in vitro* at 24°C. The cotyledons were longitudinally cut into two pieces, keeping only the central part and discarding the apexe and base. Approximately 60 explants were placed adaxial surface down in Petri dishes (20 cotyledons per petri dish) containing a conditioning medium (4.3g/L MS, 30g/L sucrose, 100 mg/L inositol, 10 mg/L thiamine, 1 mg/L nicotinic acid, 1 mg/L pyridoxine, and 8g/L agar). After autoclaving, BAP (0.1 mg/L) and NAA (1 mg/L) were added. The Petri dishes were incubated in darkness for 48 hours at 22°C.

Overnight cultures of *A. tumefaciens* GV3101 strain harbouring the different binary vectors, were grown at 28°C in LB medium supplemented with rifampicin, gentamycin and kanamycin (Table 11) for 24h to an O.D. higher than 1. Agrobacterium cells were collected by centrifugation at 5000 rpm for 15 min. The resulting pellet was suspended with the

resuspension buffer (10 mM MgSO₄ and 200 µM acetosyringone) to a final OD₅₉₅ of 0.9. Two droplets of the *Agrobacterium* suspension were applied per cotyledon, and co-cultivation took place for 48 hours in the dark at 22°C. Subsequently, the cotyledons were placed abaxial surface down on petri dishes containing selective media (SM1) consisting of 4.3 g/L MS, 30 g/L sucrose, 100 mg/L inositol, 10 mg/L thiamine, 1 mg/L nicotinic acid, 1 mg/L pyridoxine, and 8g/L agar (pH 5.8). After autoclaving, zeatin (1 mg/L), timentin (250 mg/L), and kanamycin (35 mg/L) were added. The selective media was replaced every week and kanamycin concentration was increased every two weeks: 35 mg/L in SM1; 50 mg/L in SM2 and 100 mg/L in SM3. Developing calli must have a healthy appearance, with some white colour and green areas, as well as initial signs of tissue differentiation. If necessary, necrotic tissue areas were carefully removed using a sterile scalpel before transferring the callus to the new medium. Once stem and leaf tissue formation was achieved, the explants were cleaned to eliminate any residual callus tissue, and were transferred to glass jars, a maximum of 5 explants per jar, containing rooting medium consisting of 4.3 g/L MS, 30 g/L sucrose, 100 mg/L inositol, 10 mg/L thiamine, 1 mg/L nicotinic acid, 1 mg/L (pH 5.8). Seedlings with developing roots were carefully removed from the medium, washed with water to eliminate any remnants of medium and callus, and transferred to small pots. Subsequently, the plants were moved to the greenhouse and subjected to the same acclimatization process outlined before (Section 6.2.1).

6.7. Whole genome expression analysis by RNA-Seq

For RNA-seq expression analysis, four independent pools of seedlings germinated in darkness for 10 days were prepared for RNA extraction. Total RNA was isolated from 100 mg of each sample replicate using the Maxwell RSC Plant RNA Kit with the Maxwell RSC Instruments (Promega) according to manufacturer's instructions. Total RNA concentration was measured using Qubit® 2.0 Fluorometer (Life Technologies), and integrity was assessed using the RNA Nano 6000 Assay Kit with a Bioanalyzer 2100 system (Agilent Technologies). Sequencing was performed by Sequentia Biotech SL (Barcelona, Spain) using 3 µg of RNA per sample as the input material. Libraries were prepared according to Illumina protocols and sequenced using an Illumina HiSeq 2500 machine to perform 2 x 75 bp paired-end sequencing. The quality of the reads obtained by HiSeq 2500 sequencing was checked with FastQC software (<http://www.bioinformatics.bbsrc.ac.uk/projects/fastqc/>). The reads were aligned against the *S. lycopersicum* (SL3.0) reference genome with STAR aligner (version

2.5.2b). FeatureCounts (version 1.5.1) was used to calculate gene expression values as raw fragments counts (annotation version ITAG 3.2). Normalization was applied to the raw fragment counts by using the Trimmed Mean of M-values (TMM) and Fragments per Kilobase Million (FPKM) normalization. All the statistical analyses were performed with R with the packages HTSFilter, edgeR and NOISeq. No expressed genes and the ones showing high variability were removed. The HTSFilter package was chosen for this scope, which implements a filtering procedure for replicated transcriptome sequencing data based on a Jaccard similarity index.

6.8. Embryo analysis

Dry seeds collected in parallel were pre-conditioned to achieve proper solution penetration and prevent embryo damage. The seeds were hydrated with distilled water for 18 hours at 37°C, and the seed coat was punctured with a needle to approximately one-third of the seed length, between the micropyle and the embryo. The seeds were placed in plastic pots containing 10 mL of triphenyl tetrazolium chloride (Sigma) (0.1% w/v), and incubated overnight in darkness at 37°C. Finally, the tetrazolium salt solution was removed, and the seeds were rinsed with cold water. For embryo observation, the seeds were longitudinally cut with a scalpel, the embryo was extracted using fine forceps and observed under a microscope with a 40X objective. The embryos were classified as viable or non-viable based on the staining.

6.9. Lipid body staining

Leaf lipid bodies were stained with TopFluor® Cholesterol for *in situ* visualization (Zhou et al., 2019). Leaf disks (0.5 cm diameter) were excised from fresh leaves and transferred to a 10 mL syringe containing 2 mL of 10 μ M TopFluor® Cholesterol solution (Avanti Polar Lipids, diluted in DMSO) containing 30 μ M methyl- β -cyclodextrin (diluted in 95% ethanol) and infiltrated under negative pressure by pulling the plunger for 30 s. After restoring atmospheric pressure, the leaf disks were kept in darkness for 4 hours before observation using a confocal laser microscopy (Olympus FV1000 microscope). The stained disks were placed on a microscope slide and covered with a water droplet and a coverslip. Lipid bodies were observed using a water-immersion objective with a numerical aperture of 1.20 at 60X magnification. A 488 nm argon laser was used for excitation of the TopFluor® probe signal. The emission window for fluorescence visualization was set between 490-520 nm. Image capture was performed using FV10-ASW software (Olympus) in Z-stack mode. Lipid bodies

were counted in each image using ImageJ 1.48v software and averaged per leaf area (Rasband, 2012) and expressed as the number of LD per mm².

6.10. Sterol Analysis

Fresh tissue was collected, immediately frozen in liquid nitrogen and ground into a fine powder using a mortar, and lyophilized for 48h. Approximately 20 mg of lyophilized seed tissue or 30 mg in the case of leaves, root and fruit were placed in Pyrex glass tubes (10 x 15 mm) and 3 mL of chloroform:methanol (2:1) were added to the samples, which were vigorously shaken for 5 min and subsequently sonicated in an ultrasonic bath (Selecta Ultrasons-H) for 15 min at room temperature. Next, 1.5 mL of 0.9% (w/v) NaCl solution was added to facilitate phase separation. The samples were centrifuged for 5 min at 5,000 rpm and room temperature to recover the organic phase (lower phase) containing the sterols. The organic phase was collected using a glass Pasteur pipette and transferred to a Pyrex glass tube, passing it through another Pasteur pipette with a cotton filter previously washed with methanol. The filtrate was evaporated to dryness using a Speed-Vac. The extraction process was repeated by adding another 3 mL of chloroform-methanol (2:1 v/v) to the remaining aqueous phase. The combined dry extracts were resuspended in 100 µl of chloroform-methanol (2:1 v/v) and separated by thin layer chromatography (TLC) using silica gel 60 F254 plates (20 x 20 cm, Merk, Darmstadt) that were previously activated by heating in an oven at 80°C for 30 min. The samples were carefully deposited 1 cm from the bottom edge of the plate. In a separate lane, 40 µL of a mixture of internal standards dissolved in chloroform-methanol (2:1 v/v) was also deposited. The standard mix contained cholestanol, cholestanol palmitate, cholestanol- β -D-glucoside and palmitoyl-glucosylcholestanol at a concentration of 0.25 mg/mL each. The last three compounds were synthesized in the laboratory of Dr. Lavilla (Faculty of Pharmacy and Food Sciences, University of Barcelona). The TLC was developed using a mixture of dichloromethane-methanol (92:8 v/v) as a mobile phase till the solvent front reached 2 cm from the top edge of the plate. The chromatographic cuvette was filled at least 1 hour before separation using a mixture of dichloromethane-methanol (92:8 v/v). For visualization of the fractions, plates were sprayed with a 0.01% primulin (Sigma-Aldrich) solution and detected using a UV lamp. All fractions were individually scraped from the silica plates and transferred to glass tubes. To perform acidic hydrolysis of SG and ASG, 1.5 mL of a 0.5 N HCl methanolic solution was added to the silica powder, while for the basic hydrolysis of SE, 1.5 mL of a 7.5% (w/v) KOH

methanolic solution was used. After incubation at 85°C for 2 hours, the reaction was stopped with 1.5 mL of a 0.9% (w/v) NaCl solution, and the released FS moieties were extracted twice with 3 mL of n-hexane. The mixture was vigorously vortexed for 5 min and centrifuged at 5,000 rpm for 5 min. The hexanic phases were collected in a pyrex glass tube and evaporated to dryness. One hundred μ l of cholestanol (0.025 mg/mL) dissolved in chloroform:methanol (2:1) was added as a standard. Sterol extracts were resuspended in 50 μ l of tetrahydrofuran (THF) (CHROMASOLV Plus, Honeywell) and derivatized by adding 50 μ l of N,O-Bis(trimethylsilyl)trifluoroacetamide (BSTFA) (Regis Technologies). The mixture was incubated for 30 min at 70°C and evaporated to dryness. Samples were dissolved in 50 μ l of isooctane and transferred to 1.5 mL amber glass vials (VWR) with a 0.1 mL glass insert (VWR). GC-MS analysis was performed using an Agilent 7890A gas chromatograph equipped with a Sapiens-X5MS capillary column (30 m x 0.25 mm x 0.25 μ m) (Teknokroma), coupled with a 5975C mass spectrometer (Agilent). Constant helium flow mode was used with an initial flow of 1mL/min at a nominal pressure of 8,68 psi. The oven temperature was programmed at 70°C with a gradual increase from 70°C to 255°C at a rate of 20°C/minute for 40 min, followed by an increase from 255°C to 300°C at a rate of 3°C per minute for 5 min. The total program duration was 69.75 min. Using a 10 μ L syringe, 1 μ L of each sample was injected in splitless mode at 270°C. The mass spectrometer operated in scan mode with an electron impact source operating at 69.92 eV. The ion source temperature was set at 230°C, and the interface temperature was set at 280°C. Peaks identification was performed by comparing the mass spectra and retention times of known standards and comparing with the database incorporated in the program software. The content of each sterol was calculated by integrating the area of the peaks of interest using the MSD Productivity ChemStation (Agilent) program, which was normalized to the peak area of the internal standard 5 α -cholestanol. The concentration of the different sterols was expressed in μ g of sterols per mg of tissue dry weight.

6.11. Lipid raft isolation

6.11.1. MF, PM, DRM and DSF fractions obtention

Plants were grown hydroponically (Section 6.2.2) for 1 month. Afterwards, leaves and roots were collected, washed with chilled distilled water, dried on filter paper, and weighed (600g for leaves and 300g for roots). The plant material was then mixed with extraction buffer (Table 20) at a ratio of 2 ml per gram of plant tissue, and 100 mg insoluble PVP (Sigma P-6755) were added. Vacuum was applied for 10 min to facilitate the extraction process. All procedures were carried out in a cold chamber (4°C). The plant material was triturated with a blender until a homogeneous mixture was obtained. Subsequently, the mixture was filtered through a funnel with a 100-micron pore size. The filtrate was transferred to centrifuge tubes which were centrifuged at 10,000 g and 4°C for 30 min. The resulting supernatant was carefully transferred to ultracentrifuge tubes. Ultracentrifugation was carried out using a Type 50.2 Ti rotor at 131,251 g (33,000 rpm) and 4°C for 35 min. The supernatant was carefully discarded, ensuring thorough removal. The dry pellet was resuspended in microsomal resuspension buffer (Table 20) to a final volume of 2 mL. Aliquots of the obtained microsomal fraction were stored at -80°C for further analysis and the remaining part was used to isolate the corresponding plasma membrane (PM) fraction. To this end, a 6 g PEG-dextran phase system was prepared (Table 20) by adding 2 g of microsomal fraction. After centrifugation at 5000 g for 5 min, the upper phase enriched in PM was collected and diluted in 10 ml of TBS buffer (Table 20) for raft isolation. PM fractions were stored at -80°C for subsequent analysis. Ultracentrifugation was then carried out using a Type 50.2 Ti rotor at 108,569 g (30,000 rpm) and 4°C for 35 min. The resulting pellet was resuspended in 500 µl of TBS buffer containing 0.5µl of a cocktail of protease inhibitors (Sigma-Aldrich[®]: P9599) and 5 µl 1 M DTT /mL of buffer. At this point protein concentration was determined using the Bradford method with BSA as the standard. Then 50 µl of 10% (w/v) TX100 was added to the PM fraction and incubated for 30 min on ice with intermittent shaking. The solubilized membranes were then mixed with 400 µl 60% (w/w) sucrose to achieve a final concentration of 48% (w/w) sucrose. A sucrose gradient was generated by carefully layering 3 mL of 40%, 35%, 30%, and 20% (w/w) sucrose solutions using a 1 ml pipette in a perpendicular manner. Ultracentrifugation was performed at 100,000 g (23,500 rpm) and 4°C for 20 hours using a Type SW 28 rotor. The opaque band containing the membrane fraction insoluble in Triton X-100 (detergent-resistant membrane (DRM) fraction) was collected from the 30-35%

interface, and the pellet containing the soluble in Triton X-100 (detergent soluble fraction (DSF)) was transferred to a clean ultracentrifuge tube containing 3 ml of TBS buffer and ultracentrifuged again at 150,000 g (35,300 rpm) using Type 50.2 Ti rotor. The washed pellet was resuspended in 250 μ l of TBS buffer containing 0.5 μ l protease inhibitors and 5 μ l 1M DTT /mL of buffer. The protein concentration was determined using the Bradford method. Samples were stored at -80°C until further use.

Table 20. Lipid raft buffers and enrichment separation phases composition.

Extraction buffer		
Compound	Final concentration	Final volume 1L
Sucrose	500 mM	171.15 g
Glycerol	10% (w/v)	100 g
Na₂EDTA 200 mM	20 mM	100 ml
EGTA 200 mM	20 mM	100 ml
NaF500 mM	50 mM	100 ml
β-glycerophosphate	5 mM	1.09 g
1,10-phenanthroline	1 mM	0.2 g
Ascorbic acid	5 mM	0.88 g
Tris-MES (pH 8.0)	50 mM	6.06 g
Adjust pH with MES		
Resuspension buffer		
Compound	Final concentration	Final volume 200 mL
Sucrose	250 mM	17.11 g
	5 mM	5 ml of KPB buffer
Phosphate buffer (KPB)	KPB buffer	
0.2 M (pH 6.5)	- K ₂ HPO ₄	11,412g / 250ml [basic salt]
	- KH ₂ PO ₄ *3H ₂ O	6.805g / 250ml [acid salt]
PBS buffer		
Compound	Final concentration	Final volume 1L
NaCl	140 mM	8.18g
KCl	3 mM	0.224g
Tris-HCL (pH 7.5)	25 mM	3.03g
PEG-Dextran phase		

Compound	Final concentration	Up to 6.2 g
Dextran 20%	8% (w/v)	2.48 g
PEG 40%	8% (w/v)	1.24 g
Distilled H ₂ O		1.55g
KPB 0.2M	5 mM	150 µl
KCl 2M	6.45 mM	20 µl
Sucrose	12.3% (w/v)	0.76 g
6.2 g + 2 g microsomal fraction		

6.12. ATPase activity

To quantify the amount of inorganic phosphate released in the enzyme activity assay, a series of solutions of varying concentrations of inorganic phosphate (KH₂PO₄) ranging from 5 to 100 mM were prepared from 500 mM KH₂PO₄ stock solution. The assay method outlined by Ames., (1966) involves the formation of phosphomolybdic acid from the reaction of 300µL KH₂PO₄ (at the described concentrations) with 700 µL of Reactive A (Table 21) which contains ammonium molybdate and ascorbic acid, that generates a blue-coloured complex. The optical density (O.D.) is measured at 820 nm after a 30-minute incubation at 37°C, and a regression line was calculated, and the slope value obtained.

Table 21. Composition and concentration of the compounds used to generate the Pi slope

Regression line preparation	
Composition	Concentration
KH ₂ PO ₄	5/10/20/50/100 mM
Reactive A	300 mM
Autoclaved water	Up to 1 mL
Reactive A composition:	
- Ascorbic Acid (10%)	1 Volume
- Ammonium molybdate (0.42%)	6 Volumes
Dilute 4.2 g ammonium molybdate in 28.6 mL H ₂ SO ₄ up to 1L of water)	

To determine the H⁺-ATPase activity, samples containing 2 µg of protein were mixed with ATPase buffer described (Table 22) in 1ml final volume . Two independent sets of tubes were prepared for each sample: one with 40 µL of the specific P-type ATPase inhibitor sodium orthovanadate and the other without the inhibitor (40 µL of autoclaved H₂O). After a 30-minute incubation period, 300 µL were transferred to a new Eppendorf tube and the inorganic phosphate released from the hydrolysis of ATP to ADP by the H⁺-ATPase was measured by adding 700 µL of Reactive A, the solution containing ammonium molybdate and ascorbic acid, and after 10 min at 37°C, the O.D. at 820 nm was measured. The amount of inorganic phosphate released by the enzyme is calculated from the difference in O.D. values (with and without vanadate) using the slope value obtained previously using the different KH₂PO₄ series. Alternatively H⁺-ATPase activity can be determined using the kit Elabscience®ATPase Activity Assay Kit. In all cases, buffers were prepared fresh and stored at 4°C for 1 week.

Table 22. Composition and concentration of the ATPase assay buffer.

ATPase assay buffer		
Composition	Volume	Concentration
HEPES	500 µL	100 mM
MgSO ₄	10 µL	300mM
ATP	20 µL	100 µM
KCl	100 µL	500 mM
Sample		2 µg
Na ₃ VO ₄	40 µL	10 mM
Autoclaved H ₂ O	Up to 1 mL	

6.13. Western blot analysis

To detect the H⁺ATPase in PM enriched samples, polyacrylamide gel electrophoresis under denaturing conditions (SDS-PAGE) was performed using the BioRad Mini Protean II system. Stacking gels (4% polyacrylamide) and separating gels (10% polyacrylamide) were prepared as described in (Moore., 1981). Each sample was mixed with loading buffer (Table 23) at a concentration of 1 µg of protein/µL. Samples were heated at 65°C for 10 minutes for denaturation just before loading them into the gel.

Table 23. Composition and concentration of the loading buffer.

Composition	Concentration
Tris-HCl pH 6.8	0.5M
Glycerol	20%
SDS	4%
β-mercaptoethanol	0.2%
bromophenol blue	1%
Water	Up to 10 mL

Up to 15 µL of the sample was loaded per well in gels of 1.5 mm thickness, along with an aliquot of the PageRuler™ Prestained Protein Ladder marker ranging from 15 to 180 kDa (ThermoScientific).

Once SDS-PAGE separation was completed, the proteins were transferred to a cellulose membrane (Amersham Biosciences) in a semi dry system at 15V for 10 min. After the transfer, the membrane was blocked by gently shaking for 1 hour with non-fat dry milk (Blotto, Chem-Cruz). Then, it was washed three times for 10 minutes each with PBS-Tween buffer and incubated with the primary anti-H⁺ATPase antibody (Agrisera) at a 1:10000 dilution at 4°C overnight. Three consecutive washes of 10 minutes each with PBS-Tween buffer were performed, and the membrane was incubated with the secondary antirabbit antibody (Agrisera) at a 1:20000 dilution for one hour. Finally, a last 10-minute wash with

PBS was performed, and immunodetection was carried out by chemiluminescence using the ECL reagent from the Western Blotting Detection kit (Amersham). The images were captured with the Chemi Doc Touch DE equipment (Bio Rad).

6.14. Matrix-Assisted Laser Desorption/Ionization Mass Spectrometry Imaging (MALDI-MSI imaging)

6.14.1. Tomato cv MicroTom feeding for sterol MSI imaging

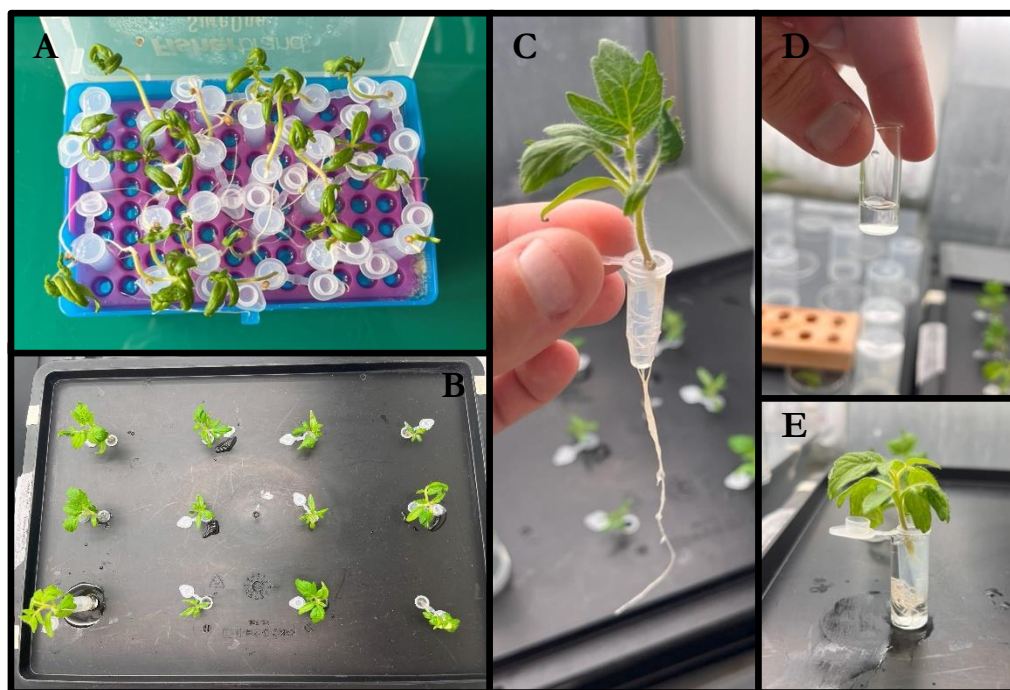


Figure 58. Tomato seed and plant manipulation for 27-alkinecholesterol feeding. (A) Seedlingd growing on 0,5XMS media for 7 days. (B) Seedlings growing hydroponically. (C) Representative seedling ready to be transferred to new 0,5XMS medium with/without 27-ALK supplementation. (D) Glass vial containing 500 μL of 0,5XMS medium. (E) Tomato seedling feed with 27-ALK for 4 days.

In order to perform the sterol analogue localization in tomato, plant were sterilized as described in (Section 6.6). The seeds were placed on top of 0,5 mL eppendorf tubes filled with semisolid 0.5X MS medium. The bottom of the tubes was cut previously to allow the roots grow vertically. The eppendorf tubes were placed in a container filled with 0.5X MS liquid media and incubated at 22°C under long-day conditions (16 h light/8 h dark) at an irradiance of $150 \mu\text{E m}^{-2} \text{s}^{-1}$. Once the seedlings had 2 pairs of true leaves they were split in 2 groups of 6 plants each. The first group was the control and was grown under the same conditions as before. The second group was treated with the sterol analogue 27-alkil-cholesterol (27-ALK), as cholesterol is one of the major sterol species in tomato plants. The feeding was performed providing 10 μg of sterol analogue/plant in a final volume of 500 μL of 0.5X MS solution. After 4 days of uptake, the roots were rinsed with fresh media and the glass vial was refilled with 500 μL of 0.5X MS solution (without analogue) to remove any 27-alkil-cholesterol adsorbed on the root surface.

6.14.2. Cryosectioning for MALDI-MSI imaging

Tissues from control/treated plants were cut and placed in the cryosectioning mold. Once the sample was properly oriented, the embedding solution M-1 Embedding matrix (ThermoScientific) was poured inside the mold and the sample was rapidly frozen into liquid nitrogen. This is a critical step to correctly preserve the sample. The cryostat chamber temperature was set at -20°C and 10 µm cutting sections thickness was selected. Once the matrix was completely frozen, the mold was cut, and the block was placed on the tissue holder. The fixation between the sample and the tissue holder was performed by adding 5 drops of OCT cryo embedding matrix between them till it was completely frozen. The tissue holder was placed on the specimen head in a 45° angle orientation to start with the cuts. The tissue slices were placed carefully using a brush on a microscope slide coated with indium-tin oxide (ITO) (50x75mm slide, Brunker). ITO coated glass has high electrical conductivity, which allows efficient ionization and ion transfer during the MALDI process, which is important for proper generation and detection of ions, thus enhancing the sensitivity and signal quality in MSI.

6.14.3. MSI acquisition

Preliminary standards and matrix check was conducted for the acquisition of mass spectrometry imaging (MSI) data. As explained in the previous section, the slices are deposited on a microscope slide coated with indium-tin oxide (ITO) and MALDI matrix could be applied. This matrix will be used to extract the analytes of interest without impacting on their spatial distribution by absorbing the laser wavelength and inducing electronic transitions. In our case, Two different matrixes were tested, α -Cyano-4-hydroxycinnamic acid (HCCA) and 2,5-dihydroxybenzoic acid (DHB). Both are appropriate for positive mode analysis, but while HCCA is used for the detection of middle-weight molecules, DHB is recommended for high molecular weight compounds. The different standards used (Table 24) were diluted in ethanol. To offer a reliable result sildenafil-d3 (0.1 µg/mL) and tryptophan were used as quality controls to obtain the order of magnitude for the different detected compounds. The test revealed that some compounds were not detected using 2,5-dihydroxybenzoic acid (HCCA) as the matrix, while the intensity of the signal was equal or better with DHB when both matrices allowed the detection of the compounds. Notably, sitosterol glucoside was never detected, regardless of the matrix or method parameters used (Table 24). Consequently, DHB matrix was chosen for the sample analysis

Slides were immediately sprayed with 40 mg/mL 2,5-dihydroxybenzoic acid (DHB) in 70 % methanol, using the MS sprayer (HTX Technologies), allowed to air-dry, and scanned in order to select the regions of MSI interest. The samples deposited on ITO slides were loaded into the dual source of a 7 T Fourier transform ion cyclotron mass spectrometer (FT-ICR-MS) Solarix XR (Bruker). The instrument was equipped with a Paracell and had a resolving power of $R = 120,000$ at $m/z = 400$ that provided a visual representation of the FT-ICR-MS used for the analysis. Subsequently, MSI acquisition was carried out following (Villette et al., 2015). The laser optics of the Smartbeam-II system was employed with a small laser focus (20–30 μm) and a laser power of 30%. A 50 μm x-y raster width was set for scanning. The region of interest was taught using flexImaging 5.0. Each pixel on the slide provided a spectrum accumulated from 50 laser shots. The laser operated at a frequency of 1000 Hz, and the ions were externally accumulated (hexapole) before being transferred into the ICR cell for a single scan. To internally calibrate the spectra, a matrix cluster of DHB was used with a maximum deviation of 0.200 ppm. The mass range selected for data acquisition was $100 < m/z < 2000$, and all samples were analysed using the positive ion mode with a transient size of 2 M.

Table 24. Standards tested for MSI

Compound	Molecular weight (g/mol)	Raw formula
27-alkyne	396.339	$\text{C}_{28}\text{H}_{44}\text{O}$
cholesterol		
(27ALK)		
Cholesterol	386.354	$\text{C}_{27}\text{H}_{46}\text{O}$
Cholesterol	548.407	$\text{C}_{33}\text{H}_{56}\text{O}_6$
glucoside		
Sitosterol	814.668	$\text{C}_{51}\text{H}_{90}\text{O}_7$
glucoside		
palmitate		
Solanidine	397.334	$\text{C}_{27}\text{H}_{43}\text{NO}$
Sitosterol	414.386	$\text{C}_{29}\text{H}_{50}\text{O}$
Stigmasterol	412.370	$\text{C}_{29}\text{H}_{48}\text{O}$

6.15. Tissue Fixation and Embedding

Stem cuts were obtained from untreated and 27-ALK cholesterol treated tomato seedlings (Section 6.14.1). Samples were placed in fixation buffer (Table 25).

Table 25. Composition, volume and concentration of the fixation buffer.

Composition	Volume	Concentration
Paraformaldehyde (PFA)	10 ml	3,2%
Acetic acid	5 ml	5%
Ethanol	50 ml	50%
Water	Up to 100ml	

The samples were vacuumed 2 x 30 min and then incubated overnight at 4°C. Subsequently, the samples were washed twice with 50% ethanol, followed by two washes with 70% ethanol and a final wash with ethanol 96% until complete bleaching. The samples were then washed with absolute ethanol (3 washes x 40 min), and then placed in ethanol/Histoclear solutions with a growing percentage of Histoclear, including ethanol 75%/Histoclear 25%, ethanol 50%/Histoclear 50%, and ethanol 25%/Histoclear 75% for 15 min each step. This was followed by 3 washes of 30 min each with Histoclear 100%. Subsequently, the samples were placed in a solution of 50% Histoclear/50% Paraplast for 2 hours and then transferred to Paraplast 100% and incubated overnight at 60°C. The Paraplast solution was replaced by fresh Paraplast and incubated for additional 24 hours. Next, samples were placed inside the molds with clean Paraplast and allowed to cool at RT slowly before storage at 4°C until further use.

To prepare the sections, the fixed and embedded plant tissue samples were cut using a microtome set at a cutting section thickness of 15 µm. Next samples were deparaffinized in eight washing steps. The samples were first washed with Histoclear 100% for 10 min, followed by a wash with a solution of Histoclear 50%/Ethanol 50% for 10 min. Subsequently, the samples were washed with ethanol 100%min, followed by successive 3-minute washes with ethanol 95%min, 70%min, 50%min, and 30%min, and a final wash with 0.5xMS medium. It is important to note that the ethanol dilutions were performed with

0.5xMS media to ensure uniformity with the media used during the 27-ALK tomato feeding. Finally, samples were visualised under confocal microscope.

6.16. Metabolite Extraction and Quantification.

6.16.1. Procedure

The whole metabolite extraction and quantification pipeline from seeds, both dry and imbibed, and fruit pericarp followed the guidelines as described in Giavalisco et al. (2011), Salem et al. (2020) and Bulut et al. (2023). Briefly, fruit, dry and imbibed seed tissue was harvested, immediately frozen in liquid nitrogen, ground to a fine powder, and lyophilized. Next, 10-30 mg of lyophilized tissue were extracted in 1 ml of pre-cooled (20°C) methyl tert-butyl ether:methanol (3:1 v/v) by vortexing, shaking and sonicating. Subsequently, 500 µl of water:methanol (3:1 v/v) solution was added and samples were centrifuged for 10 min at 14000 rpm (4°C). The lower semi-polar phase was used for analysis of semi-polar secondary and primary metabolites, and the upper hydrophobic phase for lipid analysis. Each phase was transferred to a new tube and dried. For secondary semi-polar metabolites analysis, dried extracts were resuspended in water:methanol (1:1 v/v) and metabolites were analyzed using a Thermo Q Exactive Focus (Thermo Fisher Scientific, Waltham, MA, USA) coupled to a reverse-phase C18 column. The column was maintained at 40°C with a flow rate of 400 µl/min, and the eluent system consisted of water (eluent A) and acetonitrile (eluent B), both containing 0.1% formic acid. Mass spectra were acquired in full scan mode over a range of 100-1500 m/z in negative mode. For primary semi-polar metabolites analysis, dried extracts were derivatized as described in Lisec et al. (2006). Derivatization was carried out at 37°C for 120 min using 40 µl of 20 mg/ml methoxyamine hydrochloride in pyridine, followed by a 30-min treatment at 37°C with 70 µl of trimethylsilyl-N-methyl trifluoroacetamide (MSTFA). The derivatized samples (1 µl) were injected in splitless mode into a gas chromatograph coupled to a time-of-flight mass spectrometer (Leco Pegasus HT TOF-MS; LECO Corporation, St. Joseph, MI, USA). Gas chromatography was performed on a 30-m DB-35 column using helium as the carrier gas. The initial temperature of the oven was 85°C, and it was ramped up at a rate of 15°C/min to a final temperature of 360°C. Mass spectra were recorded in the range of 70-600 m/z at a rate of 20 scans/s. For the analysis of lipids, dried extracts were resuspended in a solvent mixture of acetonitrile and isopropanol (7:3 v/v), and lipids were separated and identified using an Orbitrap LC-MS system (Exactive, ThermoScientific) coupled to a reverse-phase C18 column. The mobile phase consisted of water and acetonitrile:2-propanol (7:3 v/v), with both solvents containing 0.1% acetic acid. The column temperature was maintained at 60°C, and the flow rate of the mobile phase was 400 µl/min. Mass spectra were acquired in full scan mode over a range of 150 to 1500 m/z in positive mode.

6.16.2. Data Processing and Compound Annotation and Analysis.

LC-MS full scan data were processed using MS-Refiner (Expressionist 14.0). Processing of chromatograms, peak detection, and integration were performed using RefinerMS (version 5.3; GeneData). Metabolite identification and annotation were performed using in-house reference compound library, tandem MS (MS/MS) fragmentation, and metabolomics databases (Alseekh et al., 2021). For the annotation of metabolites measured by GC-MS the Golm Metabolome Database was used (Kopka et al., 2005). Raw intensities of annotated spectra were normalized to the metabolite abundance previously normalized to the internal standard (ribitol, isovitexin and phosphatidylcholine for primary metabolites, semi-polar secondary metabolites and lipids, respectively) and tissue weight before statistical analysis. Data analysis including statistics and volcano plotting was performed using the tidyverse (Wickham et al. 2019) and rstatix (Kassambara 2023) R packages. Heatmaps based on the intensity values were generated with pheatmap (Kolde, 2019) and principal component analysis was visualized with the help of the plotly package (Sievert, 2020). Metabolic pathway analysis was computed with the help of MetaboAnalyst 5.0 (<https://www.metaboanalyst.ca/>) (Le et al. 2023) based on differentially accumulated metabolites (adjusted $p < 0.05$) respective to the WT median in dry seed, imbibed seed and red fruit tissues.

7. Bibliography

1. Aboobucker, S. I. and W. P. Suza (2019). "Why Do Plants Convert Sitosterol to Stigmasterol?" *Frontiers in Plant Science* 10: 354-354. <https://doi.org/10.3389/fpls.2019.00354>
2. Alseekh, S., Tohge, T., Wendenberg, R., Scossa, F., Omranian, N., Li, J., Kleessen, S., Giavalisco, G., Pleban, T., Mueller-Roeber, B., Zamir, D., Nikoloski, Z., & Fernie, A.R. (2015) Identification and mode of inheritance of quantitative trait loci for secondary metabolite abundance in tomato. *Plant Cell*, 27, 485-512, doi:org/10.1105/tpc.114.132266.
3. Alseekh, S., Ofner, I., Liu, Z., Osorio, S., Vallarino, J., Last, R.L., Zamir, D., Tohge, T. & Fernie, A.R. (2020) Quantitative trait loci analysis of seed-specialized metabolites reveals seed-specific flavonols and differential regulation of glycoalkaloid content in tomato. *Plant Journal*, 103, 2007-2024. doi:org/10.1111/tpj.14879
4. Alseekh, S., Perez de Souza, L., Benina, M., & Fernie, A.R. (2020) The style and substance of plant flavonoid decoration; towards defining both structure and function. *Phytochemistry* 174: 112347. doi: 10.1016/j.phytochem.2020.112347.
5. Alseekh, S., Aharoni, A., Brotman, Y., Contrepolis, K., D'Auria, J., Ewald, J., Fraser, P.D., Giavalisco, P., Hall, R.D., Heinemann, M., Link, H., Luo, J., Neumann, S., Nielsen, J., Perez de Souza, L., Saito, K., Sauer, U., Schroeder, F.C., Schuster, S., Siuzdak, G., Skirycz, A., Sumner, L.W., Snyder, M.P., Tang, H., Tohge, T., Wang, Y., Wen, W., Wu, S., Xu, G., Zamboni, N. & Fernie, A. R. (2021). Mass spectrometry-based metabolomics: a guide for annotation, quantification and best reporting practices. *Nature Methods*, 18, 747-756. doi: 10.1038/s41592-021-01197-1.
6. Alseekh, S., Zhu, F., Vallarino, J.G., Sokolowska, E.M., Yoshida, T., Bergmann, S., Wendenburg, R., Bolze, A., Skirycz, A., Avin-Wittenberg, T., & Fernie, A.R. (2022) Autophagy modulates the metabolism and growth of tomato fruit during development. *Horticulture Research*. 13, 9:uhac129. doi: 10.1093/hr/uhac129.
7. Altabella Artigas, T., Ramírez Estrada, K., & Ferrer i Prats, A. (2021). Phytosterol metabolism in plant positive-strand RNA virus replication. *Plant Cell Reports*, 2021, vol. 41, num. 2, p. 281-291.
8. Ames, B. N. (1966). [10] Assay of inorganic phosphate, total phosphate and

phosphatases. In *Methods in enzymology* (Vol. 8, pp. 115-118). Academic Press.

9. Andersson, S. A., Skinner, J., Ellegård, L., Welch, A., Bingham, S., Mulligan, A. A., ... & Khaw, K. (2004). "Intake of dietary plant sterols is inversely related to serum cholesterol concentration in men and women in the epic norfolk population: a cross-sectional study." *European Journal of Clinical Nutrition*, 58(10), 1378-1385. <https://doi.org/10.1038/sj.ejcn.1601980>
10. Avila-Ospina, L., Moison, M., Yoshimoto, K., & Masclaux-Daubresse, C. (2014) Autophagy, plant senescence, and nutrient recycling. *Journal of Experimental Botany*. 65, 3799-3811. doi:10.1093/jxb/eru039.
11. Bach, T. J. and P. Benveniste (1997). "Cloning of cDNAs or genes encoding enzymes of sterol biosynthesis from plants and other eukaryotes: Heterologous expression and complementation analysis of mutations for functional characterization." *Progress in Lipid Research* 36(2): 197-226. [https://doi.org/10.1016/S0163-7827\(97\)00009-X](https://doi.org/10.1016/S0163-7827(97)00009-X).
12. Banaś, A., Carlsson, A. S., Huang, B., Lenman, M., Banaś, W., Lee, M., ... Stymne, S. (2005). "Cellular sterol ester synthesis in plants is performed by an enzyme (phospholipid:Sterol acyltransferase) different from the yeast and mammalian acyl-CoA:Sterol acyltransferases." *Journal of Biological Chemistry*, 280(41), 34626-34634. <https://doi.org/10.1074/jbc.M504459200>
13. Barkai-Golan, R. (2001). *Postharvest diseases of fruits and vegetables: development and control*. Elsevier.
14. Barry, C. S., & Giovannoni, J. J. (2007). "Ethylene and Fruit Ripening." *Journal of Plant Growth Regulation*, 26(2), 143-159. <https://doi.org/10.1007/s00344-007-9002-y>
15. Barry, T. N., McNeill, D. A., & McNabb, W. C. (2001). *Plant secondary compounds; their impact on forage nutritive value and upon animal production*.
16. Bassel, G. W., Zielinska, E., Mullen, R. T., Bewley, J. D. (2004). Down-regulation of DELLA genes is not essential for germination of tomato, soybean, and arabidopsis seeds. *Plant Physiol*. 136, 2782-2789. doi: 10.1104/pp.103.034876
17. Beck, J. G., D. Mathieu, C. Loudet, S. Buchoux and E. J. Dufourc (2007). "Plant sterols in "rafts": a better way to regulate membrane thermal shocks." *The FASEB Journal* 21(8): 1714-1723. <https://doi.org/10.1096/fj.06-7809com>

18. Behmer, S. T., Olszewski, N., Sebastiani, J., Palka, S., Sparacino, G., Sciarrno, E., & Grebenok, R. J. (2013). "Plant phloem sterol content: Forms, putative functions, and implications for phloem-feeding insects." *Frontiers in Plant Science*, 4, 370.
19. Behr, M., Neutelings, G., Jaziri, M. E., & Baucher, M. (2020). "You want it sweeter: how glycosylation affects plant response to oxidative stress." *Frontiers in Plant Science*, 11. <https://doi.org/10.3389/fpls.2020.571399>
20. Belin, B. J., Busset, N., Giraud, É., Molinaro, A., Silipo, A., & Newman, D. K. (2018). "Hopanoid lipids: from membranes to plant-bacteria interactions." *Nature Reviews Microbiology*, 16(5), 304-315. <https://doi.org/10.1038/nrmicro.2017.173>
21. Benveniste, P. (2002). "Sterol metabolism." *The arabidopsis book* 1: e0004-e0004. <https://doi.org/10.1199/tab.0004>
22. Berry, T., Bewley, Jd. (1992). "A Role for the Surrounding Fruit Tissues in Preventing the Germination of Tomato (*Lycopersicon esculentum*) Seeds : A Consideration of the Osmotic Environment and Absciscic Acid." *Plant Physiology*.
23. Bertin, N., Gautier, H., & Roche, C. (2002). "Number of cells in tomato fruit depending on fruit position and source-sink balance during plant development." *Plant Growth Regulation*, 36, 105-112.
24. Bewley, J. D., Black, M. (1994). *Seeds: Physiology of development and germination*. (New York: Plenum Press) doi: 10.1007/978-1-4899-1002-8
25. Beyzi, E., Beyzi, S., & Karaman, K. (2019). "Sterol profile of some medicinal and aromatic plants: effect of silyl derivatization step." *European Journal of Science and Technology*, 360-365.
26. Bhat, R.A.; Panstruga, (2005) "Lipid rafts in plants." *Planta*.
27. Boronat, A. (2010). "Chapter 8 The Methylerythritol 4-Phosphate Pathway: Regulatory Role in Plastid Isoprenoid Biosynthesis. *The Chloroplast: Basics and Applications*." C. A. Rebeiz, C. Benning, H. J. Bohnert et al. Dordrecht, Springer Netherlands: 119-126. https://doi.org/10.1007/978-90-481-8531-3_8
28. Boutté, Y. and M. Grebe (2009). "Cellular processes relying on sterol function in plants." *Current Opinion in Plant Biology* 12(6): 705-713. <https://doi.org/10.1016/j.pbi.2009.09.013>

29. Bouvier-Navé, P. and P. Benveniste (1995). "Sterol acyl transferase and steryl ester hydrolase activities in a tobacco mutant which overproduces sterols." *Plant Science* 110(1): 11-19. [https://doi.org/10.1016/0168-9452\(95\)04181-S](https://doi.org/10.1016/0168-9452(95)04181-S)
30. Bouvier-Navé, P., Berna, A., Noiriél, A., Compagnon, V., Carlsson, A. S., Banas, A., ... Schaller, H. (2010). "Involvement of the Phospholipid Sterol Acyltransferase1 in Plant Sterol Homeostasis and Leaf Senescence." *Plant Physiology*, 152(1), 107-119. <https://doi.org/10.1104/pp.109.145672>
31. Bowman, A., Bogie, J., Hendriks, J., Haidar, M., Belov, M., Heeren, R., ... & Ellis, S. (2019). "Evaluation of lipid coverage and high spatial resolution maldi-imaging capabilities of oversampling combined with laser post-ionisation." *Analytical and Bioanalytical Chemistry*, 412(10), 2277-2289.
32. Brunetti C, Guidi L, Sebastiani F, Tattini M (2015) Isoprenoids and phenylpropanoids are key components of the antioxidant defense system of plants facing severe excess light stress. *Env. Exp Bot.* 119, 54-62. doi.org/10.1016/j.envexpbot.2015.04.007.
33. Brycki, B., Koenig, H., Kowalczyk, I., & Pospieszny, T. (2014). "Synthesis, spectroscopic and theoretical studies of new quaternary n,n-dimethyl-3-phthalimidopropylammonium conjugates of sterols and bile acids." *Molecules*, 19(4), 4212-4233.
34. Bulut, M., Wendenburg, R., Bitocchi, E., Bellucci, E., Kroc, M., Gioia, T., Susek, K., Papa, R., Fernie, A.R. and Alseekh, S. (2023), A comprehensive metabolomics and lipidomics atlas for the legumes common bean, chickpea, lentil and lupin. *Plant J*, 116: 1152-1171. [doi: org/10.1111/tpj.16329](https://doi.org/10.1111/tpj.16329).
35. Burciaga, Alma (2020). *Metabolismo de esteroides esterificados en plantas: implicación en el desarrollo y la respuesta a estrés*. Universitat de Barcelona
36. Burciaga-Monge, A., López-Tubau, J. M., Laibach, N., Deng, C., Ferrer, A., & Altabella, T. (2022). "Effects of impaired steryl ester biosynthesis on tomato growth and developmental processes." *Frontiers in Plant Science*, 13. <https://doi.org/10.3389/fpls.2022.984100>
37. Bush, P. B., & Grunwald, C. (1974). "Steryl Glycoside Formation in Seedlings of *Nicotiana tabacum* L." *Plant Physiology*, 53(2), 131-135. <https://doi.org/10.1104/pp.53.2.131>
38. Cabianca, A., Müller, L., Pawlowski, K., & Dahlin, P. (2021). "Changes in the plant β -

- sitosterol/stigmasterol ratio caused by the plant parasitic nematode *meloidogyne incognita*. *Plants*, 10(2), 292.
39. Cao, Y., He, Q., Qi, Z., Zhang, Y., Liang, L., Xue, J., ... & Li, R. (2020). "Dynamics and endocytosis of flot1 in arabidopsis require cpi1 function." *International Journal of Molecular Sciences*, 21(5), 1552.
 40. Carland, F.M., Fujioka, S., Takatsuto, S., Yoshida, S., and Nelson, T. (2002). "The identification of CVP1 reveals a role for sterols in vascular patterning." *Plant Cell* 14, 2045.–2058.
 41. Carland, F., Fujioka, S., & Nelson, T. (2010). "The Sterol Methyltransferases SMT1, SMT2, and SMT3 Influence Arabidopsis Development through Nonbrassinosteroid Products." *Plant Physiology*, 153(2), 741-756. <https://doi.org/10.1104/pp.109.152587>
 42. Carretero-Paulet, L., Cairó, A., Botella-Pavía, P., Besumbes, O., Campos, N., Boronat, A., & Rodríguez-Concepción, M. (2006). "Enhanced flux through the methylerythritol 4-phosphate pathway in Arabidopsis plants overexpressing deoxyxylulose 5-phosphate reductoisomerase." *Plant Molecular Biology*, 62(4-5), 683-695. <https://doi.org/10.1007/s11103-006-9051-9>
 43. Castillo, N., V. Pastor, Á. Chávez, M. Arró, A. Boronat, V. Flors, A. Ferrer and T. Altabella (2019). "Inactivation of UDP-Glucose Sterol Glucosyltransferases Enhances Arabidopsis Resistance to Botrytis cinerea." *Frontiers in Plant Science* 10(1162). <https://doi.org/10.3389/fpls.2019.01162>
 44. Chang, C. C. Y., Sun, C., and Chang, T.-Y. (2011). "Membrane-bound O-acyltransferases (MBOATs)." *Front. Biol.* 6:177. <https://doi.org/10.1007/s11515-011-1149-z>
 45. Chaturvedi, P., P. Misra and R. Tuli (2011). "Sterol Glycosyltransferases-The Enzymes That Modify Sterols." *Applied Biochemistry and Biotechnology* 165(1): 47-68. <https://doi.org/10.1007/s12010-011-9232-0>
 46. Chaturvedi, P., M. Mishra, N. Akhtar, P. Gupta, P. Mishra and R. Tuli (2012). "Sterol glycosyltransferases-identification of members of gene family and their role in stress in *Withania somnifera*." *Molecular Biology Reports* 39(10): 9755-9764. <https://doi.org/10.1007/s11033-012-1841-3>
 47. Chávez, A., Castillo, N., López-Tubau, J.M., Atanasov, K.E., Fernández-Crespo, E.,

- Camañes, G., Altabella, T., Ferrer, A. (2023) Tomato STEROL GLYCOSYLTRANSFERASE 1 silencing unveils a major role of steryl glycosides in plant and fruit development. *Env. Exp. Bot.* 206:105181. doi.org/10.1016/j.envexpbot.2022.105181
48. Chen, H., Bai, S., Kusano, M., Ezura, H., & Wang, N. (2022). Increased ACS Enzyme Dosage Causes Initiation of Climacteric Ethylene Production in Tomato. *International Journal of Molecular Sciences*, 23(18), 10788.
 49. Chen, Q., Steinhauer, L., Hammerlindl, J., Keller, W., & Zou, J. (2007). "Biosynthesis of Phytosterol Esters: Identification of a Sterol O -Acyltransferase in Arabidopsis." *Plant Physiology*, 145(3), 974-984. <https://doi.org/10.1104/pp.107.106278>
 50. Choi, H., K. Ohyama, Y.-Y. Kim, J.-Y. Jin, S. B. Lee, Y. Yamaoka, T. Muranaka, M. C. Suh, S. Fujioka and Y. Lee (2014). "The role of Arabidopsis ABCG9 and ABCG31 ATP binding cassette transporters in pollen fitness and the deposition of steryl glycosides on the pollen coat." *The Plant cell* 26(1): 310-324. <https://doi.org/10.1105/tpc.113.118935>
 51. Cisneros, A. E., Lisón, P., Campos, L., López-Tubau, J. M., Altabella, T., Ferrer, A., ... & Carbonell, A. (2023). Down-regulation of tomato STEROL GLYCOSYLTRANSFERASE 1 perturbs plant development and facilitates viroid infection. *Journal of experimental botany*, 74(5), 1564-1578.
 52. Clouse, S. D. (2002). "Arabidopsis mutants reveal multiple roles for sterols in plant development." *The Plant cell* 14(9): 1995-2000. <https://doi.org/10.1105/tpc.140930>
 53. Coolbear, P., Francis, A., Grierson, D (1984). The effect of low temperature pre-sowing treatment on the germination performance and membrane integrity of artificially aged tomato seeds. *J. Exp. Bot* 35, 1609-1617. doi: 10.1093/jxb/35.11.1609
- A. Colmán, Janaina L. Alves, Meiriele da Silva, Robert W. Barreto (2018): Phoma destructiva causing blight of tomato plants: a new fungal threat for tomato plantations in Brazil *Trop. plant pathol.* 43: 257. DOI: 10.1007/s40858-017-0200-2
54. Dabeek, W. M., & Marra, M. V. (2019). Dietary quercetin and kaempferol: Bioavailability and potential cardiovascular-related bioactivity in humans. *Nutrients*, 11(10), 2288.
 55. Darnet, S., Blary, A., Chevalier, Q., & Schaller, H. (2021). "Phytosterol profiles, genomes and enzymes - an overview." *Frontiers in Plant Science*, 12.

<https://doi.org/10.3389/fpls.2021.665206>

56. Dean, R., Van Kan, J. A., Pretorius, Z. A., Hammond-Kosack, K. E., Di Pietro, A., Spanu, P. D., ... & Foster, G. D. (2012). The Top 10 fungal pathogens in molecular plant pathology. *Molecular plant pathology*, 13(4), 414-430.
57. DeBolt, S., W. Scheible, K. Schrick, M. Auer, F. Beisson, V. Bischoff, P. Bouvier-Nave, A. Carroll, K. Hématy, Y. Li-Beisson, J. Milne, M. Nair, H. Schaller, M. Zemla and C. Somerville (2009). "F." *Plant Physiology*, v.151, 78-87 (2009) 151. <https://doi.org/10.1104/pp.109.140582>
58. Dedo, J. E. d., Fernández-Golbano, I. M., Pastor, L., Meler, P., Ferrer-Orta, C., Rebollo, E., ... & Geli, M. (2021). "Coupled sterol synthesis and transport machineries at er-endocytic contact sites." *Journal of Cell Biology*, 220(10). <https://doi.org/10.1083/jcb.202010016>
59. Dedow, L. K., Oren, E., & Braybrook, S. A. (2022). Fake news blues: A GUS staining protocol to reduce false-negative data. *Plant direct*, 6(2), e367.
60. Demir, F., Horntrich, C., Blachutzik, J., Scherzer, S., Reinders, Y., Kierszniowska, S., ... & Kreuzer, I. (2013). "Arabidopsis nanodomain-delimited aba signaling pathway regulates the anion channel slah3." *Proceedings of the National Academy of Sciences*, 110(20), 8296-8301.
61. Deng, Y., & Lu, S. (2017). Biosynthesis and regulation of phenylpropanoids in plants. *Critical reviews in plant sciences*, 36(4), 257-290.
62. Deng, K., Yin, H., Xiong, F., Feng, L., Dong, P., & Ren, M. (2021). Genome-wide miRNA expression profiling in potato (*Solanum tuberosum* L.) reveals TOR-dependent post-transcriptional gene regulatory networks in diverse metabolic pathway. *PeerJ*, 9, e10704. <https://doi.org/10.7717/peerj.10704>
63. Desmond, E. and Gribaldo, S. (2009). "Phylogenomics of sterol synthesis: insights into the origin, evolution, and diversity of a key eukaryotic feature." *Genome Biology and Evolution*, 1, 364-381. <https://doi.org/10.1093/gbe/evp036>
64. D'ippólito, S., Rey-Burusco, M. F., Feingold, S. E., & Guevara, M. G. (2021). Role of proteases in the response of plants to drought. *Plant Physiology and Biochemistry*, 168, 1-9.
65. Doblas, V. G., Amorim-Silva, V., Posé, D., Rosado, A., Esteban, A., Arró, M., et al. (2013).

The SUD1 gene encodes a putative E3 ubiquitin ligase and is a positive regulator of 3-hydroxy-3-methylglutaryl coenzyme a reductase activity in arabidopsis. *Plant Cell* 25, 728-743. doi: 10.1105/tpc.112.108696

66. Dong, N-Q., Lin, H-X. (2021) Contribution of phenylpropanoid metabolism to plant development and plant-environment interactions. *J Integr Plant Biol.* 63, 180-209. doi: 10.1111/jipb.13054.
67. Dong, W., Lv, H., Xia, G., Wang, M. (2012) Does diacylglycerol serve as a signaling molecule in plants? *Plant Signal. Behav.* 7, 472-475. doi: 10.4161/psb.19644.
68. Du, Y., Fu, X., Chu, Y., Wu, P., Liu, Y., Ma, L., ... & Zhu, B. (2022). "Biosynthesis and the roles of plant sterols in development and stress responses." *International Journal of Molecular Sciences*, 23(4), 2332. <https://doi.org/10.3390/ijms23042332>
69. Dufourc, É. J. (2008). "Sterols and membrane dynamics." *Journal of Chemical Biology*, 1(1-4), 63-77. <https://doi.org/10.1007/s12154-008-0010-6>
70. Duperon, R., Thiersault, M., Duperon, P. (1984). High level of glycosylated sterols in species of solanum and sterol changes during the development of the tomato. *Phytochemistry* 23, 743-746. doi: 10.1016/S0031-9422(00)85016-5
71. Dupont, S., Beney, L., Ferreira, T., & Gervais, P. (2011). "Nature of sterols affects plasma membrane behavior and yeast survival during dehydration." *Biochimica Et Biophysica Acta (BBA) - Biomembranes*, 1808(6), 1520-1528. <https://doi.org/10.1016/j.bbamem.2010.11.012>
72. Dyas, L., & Goad, L. J. (1993). "Steryl fatty acyl esters in plants." *Phytochemistry*, 34(1), 17-29. [https://doi.org/10.1016/S0031-9422\(00\)90777-5](https://doi.org/10.1016/S0031-9422(00)90777-5)
73. Ediriweera, M. K., Moon, J. Y., Nguyen, Y. T., & Cho, S. K. (2020). "10-gingerol targets lipid rafts associated pi3k/akt signaling in radio-resistant triple negative breast cancer cells." *Molecules*, 25(14), 3164. <https://doi.org/10.3390/molecules25143164>
74. Escamilla-Treviño, L. L., Chen, W., Card, M. L., Shih, M. C., Cheng, C. L., & Poulton, J. E. (2006). Arabidopsis thaliana β -glucosidases BGLU45 and BGLU46 hydrolyse monolignol glucosides. *Phytochemistry*, 67(15), 1651-1660.
75. Falcone Ferreyra ML, Rius SP, Casati P (2012) Flavonoids: Biosynthesis, biological functions, and biotechnological applications. *Frontiers in Plant Science* 3: 1-15.

<https://doi.org/10.3389/fpls.2012.00222>

76. Fenn, M. A., & Giovannoni, J. J. (2021). Phytohormones in fruit development and maturation. *The Plant Journal*, 105(2), 446-458.
77. Ferrer, A., T. Altabella, M. Arró and A. Boronat (2017). "Emerging roles for conjugated sterols in plants." *Progress in Lipid Research* 67: 27-37. <https://doi.org/10.1016/j.plipres.2017.06.002>
78. Field, F. J., Born, E., & Mathur, S. N. (2004). "Stanol esters decrease plasma cholesterol independently of intestinal abc sterol transporters and niemann-pick c1-like 1 protein gene expression." *Journal of Lipid Research*, 45(12), 2252-2259. <https://doi.org/10.1194/jlr.M400208-JLR200>
79. Friedman, M. (2002). Tomato glycoalkaloids: role in the plant and in the diet. *Journal of agricultural and food chemistry*, 50(21), 5751-5780.
80. Gan, J., Qiu, Y., Tao, Y., Zhang, L., Okita, T. W., Yan, Y., ... & Tian, L. (2024). "Rna-seq analysis reveals transcriptome reprogramming and alternative splicing during early response to salt stress in tomato root." *Frontiers in Plant Science*, 15. <https://doi.org/10.3389/fpls.2024.1394223>
81. Garcia, R. E. and J. B. Mudd (1978). "Identification of an Acyl Donor in Steryl Ester Biosynthesis by Enzyme Preparations from Spinach Leaves." *Plant Physiology* 62(3): 348-353. <https://doi.org/10.1104/pp.62.3.348>
82. García-Hernández, S., Rubio, L., Rivera-Moreno, M., Pérez-Sancho, J., Morello-López, J., Esteban del Valle, A., ... & Botella, M. A. (2024). Functional and Structural Analysis Reveals Distinct Biological Roles of Plant Synaptotagmins in Response to Environmental Stress. *Plant, Cell & Environment*.
83. Garcia-Parajo, M. F., Cambi, A., Torreno-Pina, J. A., Thompson, N. & Jacobson, K. "Nanoclustering as a dominant feature of plasma membrane organization. *J. Cell Sci.*127, 4995-5005 (2014)." <https://doi.org/10.1242/jcs.146340>
84. Garg, V. K., Nes, W. R. (1985). Changes in Δ^5 - and Δ^7 -sterols during germination and seedling development of *Cucurbita maxima*. *Lipids* 20, 876-883. doi: 10.1007/BF02534771
85. Ghosh, S. (2017). "Triterpene structural diversification by plant cytochrome p450

- enzymes." *Frontiers in Plant Science*, 8. <https://doi.org/10.3389/fpls.2017.01886>
86. Giavalisco, P., Li, Y., Matthes, A., Eckhardt, A., Hubberten, H. M., Hesse, H., Segu, S., Hummel, J., Köhl, K. & Willmitzer, L. (2011). Elemental formula annotation of polar and lipophilic metabolites using ¹³C, ¹⁵N and ³⁴S isotope labelling, in combination with high-resolution mass spectrometry. *The Plant Journal*, 68(2), 364-376. <https://doi.org/10.1111/j.1365-313X.2011.04682.x>
 87. Gimenez, E., Castañeda, L., Pineda, B., Pan, I. L., Moreno, V., Angosto, T., & Lozano, R. (2016). TOMATO AGAMOUS1 and ARLEQUIN/TOMATO AGAMOUS-LIKE1 MADS-box genes have redundant and divergent functions required for tomato reproductive development. *Plant molecular biology*, 91, 513-531.
 88. Gocze, P. M., Freeman, D. A. (1994). Factors underlying the variability of lipid droplet fluorescence in MA-10 leydig tumor cells. *Cytometry J. Int. Soc. Anal. Cytol.* 17, 151-158. doi: 10.1002/cyto.990170207
 89. Gondet, L., R. Bronner and P. Benveniste (1994). "Regulation of Sterol Content in Membranes by Subcellular Compartmentation of Steryl-Esters Accumulating in a Sterol-Overproducing Tobacco Mutant." *Plant Physiology* 105(2): 509-518. <https://doi.org/10.1104/pp.105.2.509>
 90. Gong, L., Hafez, I., Toledo, G., & Lindau, M. (2003). "Secretory vesicles membrane area is regulated in tandem with quantal size in chromaffin cells." *Journal of Neuroscience*, 23(21), 7917-7921.
 91. Gou, W., Li, X., Guo, S., Liu, Y., Li, F., & Xie, Q. (2019). Autophagy in Plant: A New Orchestrator in the Regulation of the Phytohormones Homeostasis. *International journal of molecular sciences*, 20(12), 2900. <https://doi.org/10.3390/ijms20122900>
 92. Griebel, T., & Zeier, J. (2010). A role for β -sitosterol to stigmasterol conversion in plant-pathogen interactions. *The Plant Journal*, 63(2), 254-268.
 93. Groot, S. P. C., Karssen, C. M. (1987). Gibberellins regulate seed germination in tomato by endosperm weakening: a study with gibberellin-deficient mutants. *Planta* 171, 525-531. doi: 10.1007/BF00392302
 94. Grosjean, K., Der, C., Robert, F., Thomas, D., Mongrand, S., Simon-Plas, F., ... & Gerbeau-Pissot, P. (2018). "Interactions between lipids and proteins are critical for organization of

- plasma membrane-ordered domains in tobacco by-2 cells." *Journal of Experimental Botany*, 69(15), 3545-3557.
95. Guo, D. A., Venkatramesh, M., Nes, W. D. (1995). Developmental regulation of sterol biosynthesis in *Zea mays*. *Lipids* 30, 203-219. doi: 10.1007/BF02537823
 96. Guo, W., Teng, X., Zhao, A., Li, R., Li, P., Lei, K., ... & Ji, L. (2023). "First identification of auxin glycosyltransferase MdUGT74BP1 from apple." PREPRINT (Version 1) available at Research Square.Lim, E. and Bowles, D. J. (2004). "A class of plant glycosyltransferases involved in cellular homeostasis." *The EMBO Journal*, 23(15), 2915-2922. <https://doi.org/10.21203/rs.3.rs-2389638/v1>
 97. Gutensohn, M., & Dudareva, N. (2016). "Tomato Fruits-A Platform for Metabolic Engineering of Terpenes." In *Methods in Enzymology* (Vol. 576, pp. 333-359). <https://doi.org/10.1016/bs.mie.2016.03.012>
 98. Gutiérrez-García, L., Arró, M., Altabella, T., Ferrer, A., & Boronat, A. (2020). "Structural and functional analysis of tomato sterol c22 desaturase."
 99. Guzha, A., Whitehead, P., Ischebeck, T., Chapman, K.D. (2023) Lipid Droplets: Packing hydrophobic molecules within the aqueous cytoplasm. *Annu. Rev. Plant Biol.* 2023. 74:195-223. doi:org/10.1146/annurev-arplant-070122-021752.
 100. Guzman, P., & Ecker, J. R. (1990). Exploiting the triple response of *Arabidopsis* to identify ethylene-related mutants. *The Plant Cell*, 2(6), 513-523.
 101. Hamada, T., Sato, Y., Yoshikawa, K., & Nagasaki, T. (2005). "Reversible photoswitching in a cell-sized vesicle." *Langmuir*, 21(17), 7626-7628.
 102. Harker, M., Hellyer, A., Clayton, J. C., Duvoix, A., Lanot, A., & Safford, R. (2003). "Co-ordinate regulation of sterol biosynthesis enzyme activity during accumulation of sterols in developing rape and tobacco seed." *Planta*, 216(4), 707-715. <https://doi.org/10.1007/s00425-002-0913-3>
 103. Harker, M., Holmberg, N., Clayton, J. C., Gibbard, C. L., Wallace, A. D., Rawlins, S., et al. (2003). Enhancement of seed phytosterol levels by expression of an n-terminal truncated *Hevea brasiliensis* (rubber tree) 3-hydroxy-3-methylglutaryl-CoA reductase. *Plant Biotechnol. J.* 1, 113-121. doi: 10.1046/j.1467-7652.2003.00011.x
 104. Hartmann, M. (1998). "Plant sterols and the membrane environment." *Trends in Plant*

Science, 3(5), 170-175. [https://doi.org/10.1016/S1360-1385\(98\)01233-3](https://doi.org/10.1016/S1360-1385(98)01233-3)

105. Haslekas, C., Viken, M. K., Grini, P. E., Nygaard, V., Nordgard, S. H., Meza, T. J., & Aalen, R. B. (2003). Seed 1-cysteine peroxiredoxin antioxidants are not involved in dormancy, but contribute to inhibition of germination during stress. *Plant physiology*, 133(3), 1148-1157.
106. Hauvermale, A. L., Ariizumi, T., & Steber, C. M. (2012). "Gibberellin signaling: a theme and variations on DELLA repression." *Plant physiology*, 160(1), 83-92.
107. He, J-X., Fujioka, S., Li, T-C., Kang, S.G., Seto, H., Takatsuto, S., Yoshida, S., Jang, J-C. (2003) Sterols regulate development and gene expression in Arabidopsis. *Plant Physiol.* 27, 1258-1269. <https://doi.org/10.1104/pp.014605>
108. Hernández-Pinzón, I., Ross, J. H. E., Barnes, K. A., Damant, A. P., & Murphy, D. J. (1999). "Composition and role of tapetal lipid bodies in the biogenesis of the pollen coat of *Brassica napus*." *Planta*, 208(4), 588-598. <https://doi.org/10.1007/s004250050597>
109. Heupel, R. C., Y. Sauvaire, P. H. Le, E. J. Parish and W. D. Nes (1986). "Sterol composition and biosynthesis in sorghum: Importance to developmental regulation." *Lipids* 21(1): 69-75.
110. Hills, M. J. (2004). "Control of storage-product synthesis in seeds." *Current Opinion in Plant Biology* 7(3): 302-308.
111. Hodzic, A., M. Rappolt, H. Amenitsch, P. Laggner and G. Pabst (2008). "Differential Modulation of Membrane Structure and Fluctuations by Plant Sterols and Cholesterol." *Biophysical Journal* 94(10): 3935-3944. <https://doi.org/10.1529/biophysj.107.123224>
112. Hofius, D., Li, L., Hafrén, A., Coll, N.S. (2017) Autophagy as an emerging arena for plant-pathogen interactions. *Curr Opin Plant Biol.*, 38,117-123. doi: 10.1016/j.pbi.2017.04.017.
113. Hojati M, Modarres-Sanavy SAM, Ghanati F, Panahi M (2011) Hexaconazole induces antioxidant protection and apigenin-7-glucoside accumulation in *Matricaria chamomilla* plants subjected to drought stress. *Journal of Plant Physiology* 168: 782-791 <https://doi.org/10.1016/j.jplph.2010.11.009>
114. Holmer, G., Ory, R. L., Høy, C. E. (1973). Changes in lipid composition of germinating barley embryo. *Lipids* 8, 277-283. doi: 10.1007/BF02531905

115. Hossain Khan, M. S., K. Tawaraya, H. Sekimoto, H. Koyama, Y. Kobayashi, T. Murayama, M. Chuba, M. Kambayashi, Y. Shiono, M. Uemura, S. Ishikawa and T. Wagatsuma (2009). "Relative abundance of $\Delta 5$ -sterols in plasma membrane lipids of root-tip cells correlates with aluminum tolerance of rice." *Physiologia Plantarum* 135(1): 73-83. <https://doi.org/10.1111/j.1399-3054.2008.01175.x>
116. Houben, M., Vaughan-Hirsch, J., Pattyn, J., Mou, W., Roden, S., Martinez, A. R., ... & Van de Poel, B. (2024). 1-Aminocyclopropane-1-carboxylic acid oxidase determines the fate of ethylene biosynthesis in a tissue-specific way to fine-tune development and stress resilience. *bioRxiv*, 2024-02.
117. Hu, Y., Vandenbussche, F., & Van Der Straeten, D. (2017). "Regulation of seedling growth by ethylene and the ethylene–auxin crosstalk." *Planta*, 245, 467-489
118. Hu, S., Hu, Y., & Yan, W. (2023). Extracellular vesicle-mediated interorgan communication in metabolic diseases. *Trends in Endocrinology & Metabolism*.
119. Huang J, Gu M, Lai Z, Fan B, Shi K, Zhou Y-H, Yu J-Q, Chen Z (2010) Functional Analysis of the Arabidopsis PAL Gene Family in Plant Growth, Development, and Response to Environmental Stress. *Plant Physiology* 153: 1526-1538 <https://doi.org/10.1104/pp.110.157370>
120. Huang, A. H. C. (2018). Plant lipid droplets and their associated proteins: potential for rapid advances. *Plant Physiol.* 176, 1894-1918. doi: 10.1104/pp.17.01677
121. Huang, H., Zhao, W., Qiao, H., Li, C., Sun, L., Yang, R., ... & Wang, S. (2022). *SlWRKY45* interacts with jasmonate-ZIM domain proteins to negatively regulate defense against the root-knot nematode *Meloidogyne incognita* in tomato. *Horticulture Research*, 9, uhac197.
122. Huang, L. H., Nishi, K., Li, S., Ho, T., Dong, R., Chang, C. C. Y., et al. (2014). Acyl-coenzyme a: cholesterol acyltransferase 1 - significance of single nucleotide polymorphism at residue 526 and the role of Pro347 near the fifth transmembrane domain. *FEBS J.* 281, 1773-1783. doi: 10.1111/febs.12739
123. Huang, L. S., Grunwald, C. (1988). Sterol and phospholipid changes during alfalfa seed germination. *Phytochemistry* 27, 2049-2053. doi: 10.1016/0031-9422(88)80095-5
124. Iglesias-Fernández, R., Vicente-Carbajosa, J. A (2022) View into seed autophagy: From

- development to environmental responses. *Plants*, 11, 3247. doi:org/10.3390/plants11233247. <https://doi.org/10.3390/plants11233247>
125. Iijima, Y., B. Watanabe, R. Sasaki, M. Takenaka, H. Ono, N. Sakurai, N. Umemoto, H. Suzuki, D. Shibata and K. Aoki (2013). "Steroidal glycoalkaloid profiling and structures of glycoalkaloids in wild tomato fruit." *Phytochemistry* 95: 145-157.
 126. Imanishi, S., & Hiura, I. (1975). "Relationship between fruit weight and seed content in the tomato." *Journal of the Japanese Society for Horticultural Science*, 44(1), 33-40.
 127. Ince, Y.Ç., Krahmer, J., Fiorucci, A.S., Fiorucci, A.-S., Trevisan, M., Galvão, V.C., Wigger, L., Pradervand, S., Fouillen, L., Van Delft, P., Genva, M., Mongrand, S., Gallart-Ayala, H., Ivanisevic, J., Fankhauser, C., (2022) A combination of plasma membrane sterol biosynthesis and autophagy is required for shade-induced hypocotyl elongation. *Nat. Commun.* 13, 5659. doi:org/10.1038/s41467-022-33384-9.
 128. Isaac, D. M., Alzaben, A. S., Mazurak, V. C., Yap, J., Wizzard, P., Nation, P. N., ... & Turner, J. (2019). "Mixed lipid, fish oil, and soybean oil parenteral lipids impact cholestasis, hepatic phytosterol, and lipid composition." *Journal of Pediatric Gastroenterology and Nutrition*, 68(6), 861-867.
 129. Iswanto, A. and Kim, J. (2017). "Lipid raft, regulator of plasmodesmal callose homeostasis." *Plants*, 6(2), 15.
 130. Itkin, M., Rogachev, I., Alkan, N., Rosenberg, T., Malitsky, S., Masini, L., Meir, S., Iijima, Y., Aoki, K., De Vos, R., Prusky, D., Burdman, S., Beekwilder, J., & Aharoni, A. (2011). "GLYCOALKALOID METABOLISM1 is required for steroidal alkaloid glycosylation and prevention of phytotoxicity in tomato." *The Plant Cell*, 23(12), 4507-4525. <https://doi.org/10.1105/tpc.111.088732>
 131. Jaceldo-Siegl, K., Lütjohann, D., Sirirat, R., Mashchak, A., Fraser, G. E., & Haddad, E. (2017). "Variations in dietary intake and plasma concentrations of plant sterols across plant-based diets among north american adults." *Molecular Nutrition & Food Research*, 61(8). <https://doi.org/10.1002/mnfr.201600828>
 132. Jaillais, Y. & Ott, T. "The nanoscale organization of the plasma membrane and its importance in signaling-a proteolipid perspective." *Plant Physiol.* (2019). <https://doi.org/10.1104/pp.19.01349>

133. Jan, R., Khan, M. A., Asaf, S., Lee, I., Bae, J., & Kim, K. M. (2020). Overexpression of *oscm* alleviates blb stress via phytohormonal accumulation and transcriptional modulation of defense-related genes in *oryza sativa*. *Scientific Reports*, 10(1). <https://doi.org/10.1038/s41598-020-76675-1>
134. Janda, M., Planchais, S., Djafi, N., Martinec, J., Burketova, L., Valentova, O., Zachowski, A., Ruelland, E. (2013) Phosphoglycerolipids are master players in plant hormone signal transduction. *Plant Cell Rep.* 32:839-851. doi: 10.1007/s00299-013-1399-0.
135. Jang, J. C., S. Fujioka, M. Tasaka, H. Seto, S. Takatsuto, A. Ishii, M. Aida, S. Yoshida and J. Sheen (2000). "A critical role of sterols in embryonic patterning and meristem programming revealed by the *fackel* mutants of *Arabidopsis thaliana*." *Genes & development* 14(12): 1485-1497. <https://doi.org/10.1101/gad.14.12.1485>
136. Jankovičová, J., Sečová, P., Michalková, K., & Antalíková, J. (2020). Tetraspanins, more than markers of extracellular vesicles in reproduction. *International Journal of Molecular Sciences*, 21(20), 7568.
137. Jenkins, T., Kubota, C., Rivard, C. L., & Pliakoni, E. D. (2022). "Evaluating ethylene sensitivity and exogenous ethylene impact on early growth of grafted and nongrafted tomato seedlings." *HortTechnology*, 32(2), 129-133
138. Jessica, A, S, Barros., Jessica, A, S, Barros., Sahar, Magen., Taly, Lapidot-Cohen., Leah, Rosental., Yariv, Brotman., Wagner, L., Araújo., Tamar, Avin-Wittenberg. (2020). "Autophagy is required for lipid homeostasis during dark-induced senescence in *Arabidopsis*." *bioRxiv*,
139. Jia, Q., Bai, Y., Xu, H., Liu, Q., Li, W., Li, T., ... & Zhang, Q. (2022). Mitochondrial GPAT-derived LPA controls auxin-dependent embryonic and postembryonic development. *Proceedings of the National Academy of Sciences*, 119(49), e2212881119.
140. Jiang YN, Haudenschild JS, Hartman GL (2012) Response of soybean fungal and oomycete pathogens to apigenin and genistein. *Mycology* 3: 153-157 <https://doi.org/10.1080/21501203.2012.684360>
141. Kalinowska, M., Zimowski, J., Bucholc, M., and Wojciechowski, Z. A. (1989). "Reversible enzymatic transesterification between wax esters and sterols in *Sinapis alba* roots." *Phytochemistry* 28, 2931-2935. [https://doi.org/10.1016/0031-9422\(89\)80256-0](https://doi.org/10.1016/0031-9422(89)80256-0)

142. Kassambara A (2023). rstatix: Pipe-Friendly Framework for Basic Statistical Tests. R package version 0.7.2, <https://rpkgs.datanovia.com/rstatix/>.
143. Kazakova, T., Suchalko, O., Ivanov, A., Alova, A., & Maksimov, G. (2020). "Acetylcholine as a trigger of the somatic exocytosis in retzius neurons." *bioRxiv*, 2020-12.
144. Kazmi, R.H., Willems, L.A.J., Joosen, R.V.L. et al. Metabolomic analysis of tomato seed germination. *Metabolomics* 13, 145 (2017). <https://doi.org/10.1007/s11306-017-1284-x>
145. Kemp, R. J., Mercer, E. I. (1968). The sterol esters of maize seedlings. *Biochem. J.* 110, 111-118. doi: 10.1042/bj1100111
146. Kerkeb, L., J. P. Donaire, K. Venema and M. P. Rodríguez-Rosales (2001). "Tolerance to NaCl induces changes in plasma membrane lipid composition, fluidity and H⁺-ATPase activity of tomato calli." *Physiologia Plantarum* 113(2): 217-224. <https://doi.org/10.1034/j.1399-3054.2001.1130209.x>
147. Kim, H. B., Schaller, H., Goh, C. H., Kwon, M., Choe, S. S., An, C. S., ... & Feyereisen, R. (2005). "Arabidopsis cyp51 mutant shows postembryonic seedling lethality associated with lack of membrane integrity." *Plant Physiology*, 138(4), 2033-2047. <https://doi.org/10.1104/pp.105.061598>
148. Kim, J. S., Jeon, B. W., & Kim, J. (2021). Signaling peptides regulating abiotic stress responses in plants. *Frontiers in Plant Science*, 12, 704490.
149. Kimura, S., & Sinha, N. (2008). Tomato (*Solanum lycopersicum*): A model fruit-bearing crop. *Cold Spring Harbor Protocols*, 3(11). <https://doi.org/10.1101/pdb.emo105>
150. Klausner, R. D., Donaldson, J. G., & Lippincott-Schwartz, J. (1992). Brefeldin A: insights into the control of membrane traffic and organelle structure. *The Journal of cell biology*, 116(5), 1071-1080.
151. Klee, H. J., & Giovannoni, J. J. (2011). "Genetics and Control of Tomato Fruit Ripening and Quality Attributes." *Annual Review of Genetics*, 45(1), 41-59. <https://doi.org/10.1146/annurev-genet-110410-132507>
152. Kolde, R. (2019). Pheatmap: pretty heatmaps. R package version, 1(2), 726.
153. Kopischke, M., L. Westphal, K. Schneeberger, R. Clark, S. Ossowski, V. Wewer, R. Fuchs, J. Landtag, G. Hause, P. Dörmann, V. Lipka, D. Weigel, P. Schulze-Lefert, D. Scheel and S.

- Rosahl (2013). "Impaired sterol ester synthesis alters the response of *Arabidopsis thaliana* to *Phytophthora infestans*." *The Plant Journal* 73(3): 456-468. <https://doi.org/10.1111/tpj.12046>
154. Kopka, J., Schauer, N., Krueger, S., Birkemeyer, C., Usadel, B., Bergmüller, E., Dörmann, P., Weckwerth, W., Gibon, Y., Stitt, M., Willmitzer, L., Fernie, A.R. & Steinhauser, D. (2005). GMD@CSB. DB: the Golm metabolome database. *Bioinformatics*, 21(8), 1635-1638. <https://doi.org/10.1093/bioinformatics/bti236>
 155. Korber, M., Klein, I., & Daum, G. (2017). "Steryl ester synthesis, storage and hydrolysis: A contribution to sterol homeostasis." *Biochimica et Biophysica Acta - Molecular and Cell Biology of Lipids*, 1862(12), 1534-1545. <https://doi.org/10.1016/j.bbalip.2017.09.002>
 156. Kortner, T. M., Björkhem, I., Krasnov, A., Timmerhaus, G., & Krogdahl, Å. (2014). "Dietary cholesterol supplementation to a plant-based diet suppresses the complete pathway of cholesterol synthesis and induces bile acid production in atlantic salmon (*salmo salar*l.)." *British Journal of Nutrition*, 111(12), 2089-2103. <https://doi.org/10.1017/S0007114514000373>
 157. Kumar, K., Gibbs, H., Yeh, A., & Griffing, L. (2021). "The sterol trafficking pathway in *arabidopsis thaliana*." *Frontiers in Plant Science*, 12.
 158. Kumar, M. S. S., K. Ali, A. Dahuja and A. Tyagi (2015). "Role of phytosterols in drought stress tolerance in rice." *Plant Physiology and Biochemistry* 96: 83-89. <https://doi.org/10.1016/j.plaphy.2015.07.014>
 159. Kumar, M. S. S., Mawlong, I., Ali, K., Tyagi, A. (2018). Regulation of phytosterol biosynthetic pathway during drought stress in rice. *Plant Physiol. Biochem.* 129, 11-20. doi: 10.1016/j.plaphy.2018.05.019
 160. Kuzuyama, T. (2017). "Biosynthetic studies on terpenoids produced by *Streptomyces*." *Journal of Antibiotics*, 70(7), 811-818. <https://doi.org/10.1038/ja.2017.12>
 161. Laloi, M., Perret, A. M., Chatre, L., Melser, S., Cantrel, C., Vaultier, M. N., ... & Moreau, P. (2007). "Insights into the role of specific lipids in the formation and delivery of lipid microdomains to the plasma membrane of plant cells." *Plant physiology*, 143(1), 461-472.
 162. Lange, B. M., Poirier, B. C., Lange, I., Schumaker, R., & Ríos-Esteva, R. (2020). "Organ-

- specificity of sterol and triterpene accumulation in *arabidopsis thaliana*." <https://doi.org/10.1101/2020.03.23.004358>
163. Lara, J. A., Burciaga-Monge, A., Chávez, A., Revés, M., Lavilla, R., Arró, M., ... Ferrer, A. (2018). "Identification and Characterization of Sterol Acyltransferases Responsible for Steryl Ester Biosynthesis in Tomato." *Frontiers in Plant Science*, 9, 588. <https://doi.org/10.3389/fpls.2018.00588>
 164. Lefebvre, B., Furt, F., Hartmann, M. A., Michaelson, L. V., Carde, J. P., Sargueil-Boiron, F., ... & Mongrand, S. (2007). Characterization of lipid rafts from *Medicago truncatula* root plasma membranes: a proteomic study reveals the presence of a raft-associated redox system. *Plant Physiology*, 144(1), 402-418.
 165. Legge, R. L., Cheng, K., Lepock, J. R., & Thompson, J. E. (1986). "Differential effects of senescence on the molecular organization of membranes in ripening tomato fruit." *Plant Physiology*, 81(4), 954-959.
 166. Leivar, P., Antolín-Llovera, M., Ferrero, S., Closa, M., Arro, M., Ferrer, A., et al. (2011). Multilevel control of *arabidopsis* 3-hydroxy-3-methylglutaryl coenzyme a reductase by protein phosphatase 2A. *Plant Cell* 23, 1494-1511. doi: 10.1105/tpc.107.052142
 167. Levental, I., Lyman, E., (2023) Regulation of membrane protein structure and function by their paralipidomes. *Nat. Rev. Mol. Cell. Biol.* 24, 107-122. doi:10.1038/s41580-022-00524-4.
 168. Li, L., Zhao, J., Zhao, Y., Lu, X., Zhou, Z., Zhao, C., Xu, G. (2016). Comprehensive investigation of tobacco leaves during natural early senescence via multiplatform metabolomics analyses. *Sci. Rep* 6, 37976. doi: 10.1038/srep37976
 169. Li, S., Nakayama, H., & Sinha, N. R. (2023). How to utilize comparative transcriptomics to dissect morphological diversity in plants. *Current Opinion in Plant Biology*, 76, 102474.
 170. Li, X., T. Xia, J. Huang, K. Guo, X. Liu, T. Chen, W. Xu, X. Wang, S. Feng and L. Peng (2014). "Distinct biochemical activities and heat shock responses of two UDP-glucose sterol glucosyltransferases in cotton." *Plant Science* 219-220: 1-8. <https://doi.org/10.1016/j.plantsci.2013.12.013>
 171. Li, X., Wang, Y., Li, G., Liu, Q., Pereira, R., Chen, Y., & Nielsen, J. (2021). Metabolic network remodelling enhances yeast's fitness on xylose using aerobic glycolysis. *Nature*

Catalysis, 4(9), 783-796.

172. Li, Y., Zhu, B., Xu, W., Zhu, H., Chen, A., Xie, Y., ... & Luo, Y. (2007). LeERF1 positively modulated ethylene triple response on etiolated seedling, plant development and fruit ripening and softening in tomato. *Plant cell reports*, 26, 1999-2008.
173. Liang, X., Wang, H., Mao, L., Hu, Y., Dong, T., Zhang, Y., ... & Bi, Y. (2012). "Involvement of COP1 in ethylene-and light-regulated hypocotyl elongation." *Planta*, 236, 1791-1802.
174. Liang, S., Xiong, W., Yin, C., Xie, X., Jin, Y., Zhang, S., ... & Luan, W. (2019). Overexpression of *osard1* improves submergence, drought, and salt tolerances of seedling through the enhancement of ethylene synthesis in rice. *Frontiers in Plant Science*, 10. <https://doi.org/10.3389/fpls.2019.01088>
175. Liggins J, Bluck LJC, Runswick S, Atkinson C, Coward WA, Bingham SA (2000) Daidzein and genistein contents of vegetables. *British Journal of Nutrition* 84: 717-725. <https://doi.org/10.1017/S0007114500002075>
176. Lim, E. and Bowles, D. J. (2004). "A class of plant glycosyltransferases involved in cellular homeostasis." *The EMBO Journal*, 23(15), 2915-2922.
177. Lisec, J., Schauer, N., Kopka, J., Willmitzer, L., & Fernie, A. R. (2006). Gas chromatography mass spectrometry-based metabolite profiling in plants. *Nature protocols*, 1(1), 387-396.
178. Liu R, Hu Y, Li J, Lin Z (2007) Production of soybean isoflavone genistein in non-legume plants via genetically modified secondary metabolism pathway. *Metabolic Engineering* 9: 1-7. <https://doi.org/10.1016/j.ymben.2006.08.003>
179. Livak, K. J., & Schmittgen, T. D. (2001). Analysis of relative gene expression data using real-time quantitative PCR and the 2- $\Delta\Delta CT$ method. *methods*, 25(4), 402-408.
180. López-Gresa, M. P., Lisón, P., Yenush, L., Conejero, V., Rodrigo, I., & Bellés, J. M. (2016). "Salicylic acid is involved in the basal resistance of tomato plants to citrus exocortis viroid and tomato spotted wilt virus." *PLoS One*, 11(11)
181. Ma, L., Hu, Z., Shen, W., Zhang, Y., Wang, G., Chang, B., ... & Lin, J. (2024). Three-dimensional reconstruction and multiomics analysis reveal a unique pattern of embryogenesis in *Ginkgo biloba*. *Plant Physiology*, 196(1), 95-111.

182. Ma, Y., & Johnson, K. (2023). Arabinogalactan proteins—multifunctional glycoproteins of the plant cell wall. *The Cell Surface*, 9, 100102.
183. Madina, B. R., L. K. Sharma, P. Chaturvedi, R. S. Sangwan and R. Tuli (2007). "Purification and physico-kinetic characterization of 3 β -hydroxy specific sterol glucosyltransferase from *Withania somnifera*. <https://doi.org/10.1016/j.bbapap.2006.12.009>
184. Maillot-Vernier, P., Gondet, L., Schaller, H., Belliard, G. (1991). Genetic study and further biochemical characterization of a tobacco mutant that overproduces sterols. *Molec. Gen. Genet.* 231, 33-40. doi: 10.1007/BF00293818
185. Malinsky, J., M. Opekarová, G. Grossmann and W. Tanner (2013). "Membrane Microdomains, Rafts, and Detergent-Resistant Membranes in Plants and Fungi." *Annual Review of Plant Biology* 64(1): 501-529. <https://doi.org/10.1146/annurev-arplant-050312-120103>
186. Manzano, D., Andrade, P., Caudepón, D., Altabella, T., Arró, M., Ferrer, A. (2016). Suppressing farnesyl diphosphate synthase alters chloroplast development and triggers sterol-dependent induction of jasmonate-and Fe-related responses. *Plant Physiol.* 172, 93-117. doi:10.1104/pp.16.00431
187. McClements, D. J., & Öztürk, B. (2021). "Utilization of nanotechnology to improve the handling, storage and biocompatibility of bioactive lipids in food applications." *Foods*, 10(2), 365. <https://doi.org/10.3390/foods10020365>
188. McKegney, G., Yao, K., Ghosh, S., Huff, A., Mayak, S., & Thompson, J. E. (1995). "The lipid composition of cytosolic particles isolated from senescing bean cotyledons." *Phytochemistry*, 39(6), 1335-1345. [https://doi.org/10.1016/0031-9422\(95\)00111-J](https://doi.org/10.1016/0031-9422(95)00111-J)
189. Meinke, D. W. (2020). Genome-wide identification of EMBRYO-DEFECTIVE (EMB) genes required for growth and development in *Arabidopsis*. *New Phytologist*, 226(2), 306-325.
190. Michaelson, L.V., Napier, J.A., Molino, D., Faure, J-D., (2016) Plant sphingolipids: Their importance in cellular organization and adaption. *Biochim. Biophys. Acta* 1861, 1329-1335. doi:org/10.1016/j.bbalip.2016.04.003
191. Middleton, E. M., & Teramura, A. H. (1993). The role of flavonol glycosides and carotenoids in protecting soybean from ultraviolet-B damage. *Plant physiology*, 103(3), 741-752.

192. Miernyk, J. A. and M. Hajduch (2011). "Seed proteomics." *Journal of Proteomics* 74(4): 389-400.
193. Mignolli, F., Rojas, G. B., & Vidoz, M. L. (2016). "Supraoptimal ethylene acts antagonistically with exogenous gibberellins during *Solanum lycopersicum* (Solanaceae) hypocotyl growth." *Boletín de la Sociedad Argentina de Botánica*, 51, 235-242.
194. Milner, S. E., N. P. Brunton, P. W. Jones, N. M. O' Brien, S. G. Collins and A. R. Maguire (2011). "Bioactivities of Glycoalkaloids and Their Aglycones from *Solanum* Species." *Journal of Agricultural and Food Chemistry* 59(8): 3454-3484. <https://doi.org/10.1021/jf200439q>
195. Min, L., Wen, D. X., Sun, Q. Q., Wu, C. L., Yan, L. I., & Zhang, C. Q. (2022). "Factors influencing seed reserve utilization during seedling establishment in maize inbred lines." *Journal of Integrative Agriculture*, 21(3), 677-684.
196. Mishra, J., Singh, R., & Arora, N. K. (2017). Alleviation of heavy metal stress in plants and remediation of soil by rhizosphere microorganisms. *Frontiers in microbiology*, 8, 1706.
197. Mishra, M. K., P. Chaturvedi, R. Singh, G. Singh, L. K. Sharma, V. Pandey, N. Kumari and P. Misra (2013). "Overexpression of WsSGTL1 gene of *Withania somnifera* enhances salt tolerance, heat tolerance and cold acclimation ability in transgenic *Arabidopsis* plants." *PloS one* 8(4): e63064-e63064.
198. Mishra, M. K., G. Singh, S. Tiwari, R. Singh, N. Kumari and P. Misra (2015). "Characterization of *Arabidopsis* sterol glycosyltransferase TTG15/UGT80B1 role during freeze and heat stress." *Plant signaling & behavior* 10(12): e1075682-e1075682. <https://doi.org/10.1080/15592324.2015.1075682>
199. Mongrand, S., Morel, J., Laroche, J., Claverol, S., Carde, J., Hartmann, M., ... & Bessoule, J. (2004). "Lipid rafts in higher plant cells." *Journal of Biological Chemistry*, 279(35), 36277-36286. <https://doi.org/10.1074/jbc.M403440200>
200. Montoya, T., Nomura, T., Yokota, T., Farrar, K., Harrison, K., Jones, J. G., ... & Bishop, G. J. (2005). "Patterns of Dwarf expression and brassinosteroid accumulation in tomato reveal the importance of brassinosteroid synthesis during fruit development." *The Plant Journal*.
201. Moore, C. (2009). Introduction to western blotting. *AbD serotec*, 4-20.

202. Moreau, R. A., & Hicks, K. B. (2004). "The in vitro hydrolysis of phytosterol conjugates in food matrices by mammalian digestive enzymes." *Lipids*, 39(8), 769-776. <https://doi.org/10.1007/s11745-004-1294-3>
203. Moreau, R. A., B. D. Whitaker and K. B. Hicks (2002). "Phytosterols, phytostanols, and their conjugates in foods: structural diversity, quantitative analysis, and health-promoting uses." *Progress in Lipid Research* 41(6): 457-500. [https://doi.org/10.1016/S0163-7827\(02\)00006-1](https://doi.org/10.1016/S0163-7827(02)00006-1)
204. Mou, W., Li, D., Bu, J., Jiang, Y., Khan, Z. U., Luo, Z., ... & Ying, T. (2016). Comprehensive analysis of aba effects on ethylene biosynthesis and signaling during tomato fruit ripening. *Plos One*, 11(4), e0154072. <https://doi.org/10.1371/journal.pone.0154072>
205. Müller, M., & Munné-Bosch, S. (2015). Ethylene response factors: a key regulatory hub in hormone and stress signaling. *Plant physiology*, 169(1), 32-41.
206. Narayanan, S., Tamura, P. J., Roth, M. R., Prasad, P. V., & Welti, R. (2016). Wheat leaf lipids during heat stress: I. High day and night temperatures result in major lipid alterations. *Plant, cell & environment*, 39(4), 787-803.
207. Narita, J. O., & Gruissem, W. (1989). "Tomato hydroxymethylglutaryl-CoA reductase is required early in fruit development but not during ripening." *The Plant Cell*, 1(2), 181-190.
208. Nazari-Khanamiri, F., & Ghasemnejad-Berenji, M. (2021) Cellular and molecular mechanisms of genistein in prevention and treatment of diseases: An overview. *Journal of Food Biochemistry*, 45, e13972. doi: 10.1111/jfbc.13972.
209. Nes, W. D. (2011). "Biosynthesis of cholesterol and other sterols." *Chemical reviews* 111(10): 6423-6451. <https://doi.org/10.1021/cr200021m>
210. Ngo, Q. A., Baroux, C., Guthörl, D., Mozerov, P., Collinge, M. A., Sundaresan, V., & Grossniklaus, U. (2012). The Armadillo repeat gene ZAK IXIK promotes Arabidopsis early embryo and endosperm development through a distinctive gametophytic maternal effect. *The Plant Cell*, 24(10), 4026-4043.
211. Nieto, B., Forés, O., Arró, M., Ferrer, A. (2009). Arabidopsis 3-hydroxy-3-methylglutaryl-CoA reductase is regulated at the post-translational level in response to alterations of the sphingolipid and the sterol biosynthetic pathways. *Phytochemistry* 70, 53-59. doi:

10.1016/j.phytochem.2008.10.010

212. Nitsch, J. P. (2012). "Perennation through seeds and other structures: fruit development." *Plant physiology, a treatise*, vol. VIA, 413-501.
213. Noh, Y. S., Amasino, R. M. (1999). Identification of a promoter region responsible for the senescence-specific expression of SAG12.. *Plant Mol Biol* 41, 181-194. doi: 10.1023/A:1006342412688
214. Noiriél, A., Benveniste, P., Banas, A., Stymne, S., Bouvier-Navé, P. (2004). Expression in yeast of a novel phospholipase A1 cDNA from *Arabidopsis thaliana*. *FEBS J.* 271, 3752-3764. doi: 10.1111/j.1432-1033.2004.04317.x
215. Nyström, L., Lampi, A., Rita, H., Aura, A., Oksman-Caldentey, K., & Piironen, V. (2007). "Effects of Processing on Availability of Total Plant Sterols, Steryl Ferulates and Steryl Glycosides from Wheat and Rye Bran." *Journal of Agricultural and Food Chemistry*, 55(22), 9059-9065. <https://doi.org/10.1021/jf071579o>
216. Nyström, L., A. Schär and A.-M. Lampi (2012). "Steryl glycosides and acylated steryl glycosides in plant foods reflect unique sterol patterns." *European Journal of Lipid Science and Technology* 114(6): 656-669. <https://doi.org/10.1002/ejlt.201200033>
217. Ochoa-Jiménez, V. A., Berumen-Varela, G., & Fernandez-Valle, R. (2018). Rhamnogalacturonan lyase: a pectin modification enzyme of higher plants. *Emirates Journal of Food and Agriculture*, 30(11), 910-917.
218. OECD. (2017). "Tomato (*Solanum lycopersicum*).". In *Safety Assessment of Transgenic Organisms in the Environment* (Vol. 7). <https://doi.org/10.1787/9789264279728-6-en>
219. Ohyama, K., Suzuki, M., Kikuchi, J., Saito, K., Muranaka, T. (2009). Dual biosynthetic pathways to phytosterol via cycloartenol and lanosterol in *Arabidopsis*. *Proc. Natl. Acad. Sci. U. S. A.* 106, 725-730. doi: 10.1073/pnas.0807675106
220. Oiestad, A. J., Martin, J. M., Cook, J., Varella, A. C., & Giroux, M. J. (2017). Identification of candidate genes responsible for stem pith production using expression analysis in solid-stemmed wheat. *The plant genome*, 10(2), plantgenome2017-02.
221. Oszvald, M., Primavesi, L. F., Griffiths, C. A., Cohn, J., Basu, S. S., Nuccio, M. L., & Paul, M. J. (2018). Trehalose 6-phosphate regulates photosynthesis and assimilate partitioning in reproductive tissue. *Plant Physiology*, 176(4), 2623-2638.

222. Otify, A. M., Ibrahim, R. M., Abib, B., Laub, A., Wessjohann, L. A., Jiang, Y., & Farag, M. A. (2023). Unveiling metabolome heterogeneity and new chemicals in 7 tomato varieties via multiplex approach of UHPLC-MS/MS, GC-MS, and UV-Vis in relation to antioxidant effects as analyzed using molecular networking and chemometrics. *Food chemistry*, 417, 135866. <https://doi.org/10.1016/j.foodchem.2023.135866>
223. Ovečka, M., Berson, T., Beck, M., Derksen, J., Šamaj, J., Baluška, F., ... & Lichtscheidl, I. (2010). "Structural sterols are involved in both the initiation and tip growth of root hairs in *arabidopsis thaliana*." *The Plant Cell*, 22(9), 2999-3019. <https://doi.org/10.1105/tpc.109.069880>
224. Ozolina, N. V., Kapustina, I. S., Gurina, V. V., Bobkova, V. A., & Nurminsky, V. N. (2021). Role of plasmalemma microdomains (rafts) in protection of the plant cell under osmotic stress. *The Journal of Membrane Biology*, 254, 429-439.
225. Palta, J.P., Whitaker, B.D., Weiss, L.S. (1993) Plasma membrane lipids associated with genetic variability in freezing tolerance and cold acclimation of *Solanum* species. *Plant Physio.* 103:793-803. <https://doi.org/10.1104/pp.103.3.793>
226. Pandey, V., A. Niranjana, N. Atri, K. Chandrashekhar, M. K. Mishra, P. K. Trivedi and P. Misra (2014). "WsSGTL1 gene from *Withania somnifera*, modulates glycosylation profile, antioxidant system and confers biotic and salt stress tolerance in transgenic tobacco." *Planta* 239(6): 1217-1231. <https://doi.org/10.1007/s00425-014-2046-x>
227. Parker, M. L., Murphy, G. J. P. (1981). Oleosomes in flag leaves of wheat: their distribution, composition and fate during senescence and rust-infection. *Planta* 152, 36-43. doi: 10.1007/BF00384982
228. Pierrette, Bouvier-Navé., Anne, Berna., Alexandre, Noiriél., Vincent, Compagnon., Anders, S., Carlsson., Antoni, Banas., Sten, Stymne., Hubert, Schaller. (2009). "Involvement of the Phospholipid Sterol Acyltransferase1 in Plant Sterol Homeostasis and Leaf Senescence." *Plant Physiology*. <https://doi.org/10.1104/pp.109.145672>
229. Piironen, V., D. G. Lindsay, T. A. Miettinen, J. Toivo and A.-M. Lampi (2000). "Plant sterols: biosynthesis, biological function and their importance to human nutrition." *Journal of the Science of Food and Agriculture* 80(7): 939-966. [https://doi.org/10.1002/\(SICI\)1097-0010\(20000515\)80:7<939::AID-JSFA644>3.0.CO;2-C](https://doi.org/10.1002/(SICI)1097-0010(20000515)80:7<939::AID-JSFA644>3.0.CO;2-C)
230. Plat, J. and Mensink, R. P. (2002). "Increased intestinal abca1 expression contributes to

- the decrease in cholesterol absorption after plant stanol consumption." *The FASEB Journal*, 16(10), 1248-1253. <https://doi.org/10.1096/fj.01-0718hyp>
231. Platre, M. P. et al. "Developmental control of plant Rho GTPase nano-organization by the lipid phosphatidylserine." *Science* 364, 57-62 (2019). <https://doi.org/10.1126/science.aav9959>
 232. Pook, V. G., Nair, M., Ryu, K., Arpin, J. C., Schiefelbein, J., Schrick, K., & DeBolt, S. (2017). "Positioning of the SCRAMBLED receptor requires UDP-Glc: sterol glucosyltransferase 80B1 in Arabidopsis roots." *Scientific Reports*, 7(1), 5714.
 233. Posé, D., I. Castanedo, O. Borsani, B. Nieto, A. Rosado, L. Taconnat, A. Ferrer, L. Dolan, V. Valpuesta and M. A. Botella (2009). "Identification of the Arabidopsis dry2/sqe1-5 mutant reveals a central role for sterols in drought tolerance and regulation of reactive oxygen species." *The Plant Journal* 59(1): 63-76. <https://doi.org/10.1111/j.1365-313X.2009.03849.x>
 234. Potocka, A., & Zimowski, J. (2008). "Metabolism of conjugated sterols in eggplant." Part 2. Phospholipid: steryl glucoside acyltransferase. *Acta Biochimica Polonica*, 55(1), 135-140. https://doi.org/10.18388/abp.2008_3167
 235. Pritchard, S. L., Charlton, W. L., Baker, A., Graham, I. A. (2002). Germination and storage reserve mobilization are regulated independently in arabidopsis. *Plant J.* 31, 639-647. doi: 10.1046/j.1365-313x.2002.01376.x
 236. Prudent, M., Causse, M., Génard, M., Tripodi, P., Grandillo, S., & Bertin, N. (2009). "Genetic and physiological analysis of tomato fruit weight and composition: influence of carbon availability on QTL detection." *Journal of experimental botany*, 60(3), 923-937.
 237. Pulido, P., C. Perello and M. Rodriguez-Concepcion (2012). "New Insights into Plant Isoprenoid Metabolism." *Molecular Plant* 5(5): 964-967. <https://doi.org/10.1093/mp/sss088>
 238. Quinet, M., Angosto, T., Yuste-Lisbona, F. J., Blanchard-Gros, R., Bigot, S., Martinez, J. P., & Lutts, S. (2019). "Tomato fruit development and metabolism." *Frontiers in plant science*, 10, 1554. <https://doi.org/10.3389/fpls.2019.01554>
 239. Ramarosan, M.-L., Koutouan, C., Helesbeux, J.-J., LeClerc, V., Hamama, L., Geoffriau, E.; & Briard, M. (2022) Role of phenylpropanoids and flavonoids in plant resistance to pests

- and diseases. *Molecules*, 27, 8371.
240. Ramirez-Estrada, K., Castillo, N., Lara, J. A., Arró, M., Boronat, A., Ferrer, A. et al. (2017). Tomato UDP-glucose sterol glycosyltransferases: A family of developmental and stress regulated genes that encode cytosolic and membrane-associated forms of the enzyme. *Front. Plant Sci.* 8: 984. doi: 10.3389/fpls.2017.00984.
 241. Ranc, N., Muños, S., Santoni, S., & Causse, M. (2008). "A clarified position for *solanum lycopersicum* var. *cerasiforme* in the evolutionary history of tomatoes (solanaceae)." *BMC Plant Biology*, 8(1). <https://doi.org/10.1186/1471-2229-8-130>
 242. Ricupero, M., Biondi, A., Russo, A., Zappalà, L., & Mazzeo, G. (2021). The cotton mealybug is spreading along the mediterranean: first pest detection in italian tomatoes. *Insects*, 12(8), 675. <https://doi.org/10.3390/insects12080675>
 243. Robertlee, J., Kobayashi, K., Suzuki, M., Muranaka, T. (2017). AKIN 10, a representative arabidopsis SNF 1-related protein kinase 1 (Sn RK 1), phosphorylates and downregulates plant HMG-CoA reductase. *FEBS Lett.* 59, 1159-1166. doi: 10.1002/1873-3468.12618.
 244. Roche, Y., Gerbeau-Pissot, P., Buhot, B., Thomas, D., Bonneau, L., Gresti, J., ... & Simon-Plas, F. (2008). "Depletion of phytosterols from the plant plasma membrane provides evidence for disruption of lipid rafts." *The FASEB Journal*, 22(11), 3980-3991. <https://doi.org/10.1096/fj.08-111070>
 245. Rodríguez-Concepción, M. and A. Boronat (2002). "Elucidation of the Methylerythritol Phosphate Pathway for Isoprenoid Biosynthesis in Bacteria and Plastids. A Metabolic Milestone Achieved through Genomics." *Plant Physiology* 130(3): 1079-1089. <https://doi.org/10.1104/pp.007138>
 246. Rogowska, A. and A. Szakiel (2020). "The role of sterols in plant response to abiotic stress." *Phytochemistry Reviews*. <https://doi.org/10.1007/s11101-020-09708-2>
 247. Rudell, D. R., Buchanan, D. A., Leisso, R. S., Whitaker, B. D., Mattheis, J. P., Zhu, Y., & Varanasi, V. (2011). Ripening, storage temperature, ethylene action, and oxidative stress alter apple peel phytosterol metabolism. *Phytochemistry*, 72(11-12), 1328-1340.
 248. Saema, S., Rahman, L. u., Niranjan, A., Ahmad, I. Z., & Misra, P. (2015). "Rnai-mediated gene silencing of *wssgt1* in *w.somnifera* affects growth and glycosylation pattern." *Plant Signaling & Behavior*, 10(12), e1078064.

<https://doi.org/10.1080/15592324.2015.1078064>

249. Saema, S., Rahman, L. U., Singh, R., Niranjana, A., Ahmad, I. Z., & Misra, P. (2016). "Ectopic overexpression of WsSGLT1, a sterol glucosyltransferase gene in *Withania somnifera*, promotes growth, enhances glycowithanolide and provides tolerance to abiotic and biotic stresses." *Plant cell reports*, 35, 195-211.
250. Sah, S. K., Fan, J., Blanford, J., Shanklin, J., & Xu, C. (2024). "Physiological functions of phospholipid: diacylglycerol acyltransferases." *Plant and Cell Physiology*, 65(6), 863-871.
251. Salem, M. A., & Giavalisco, P. (2019). Regulatory-associated protein of TOR 1B (RAPTOR1B) regulates hormonal switches during seed germination in *Arabidopsis thaliana*. *Plant signaling & behavior*, 14(7), 1613130.
252. Salem, M. A., Perez de Souza, L., Serag, A., Fernie, A. R., Farag, M. A., Ezzat, S. M., & Alseekh, S. (2020). Metabolomics in the context of plant natural products research: From sample preparation to metabolite analysis. *Metabolites*, 10(1), 37.
253. Sartorel, E. et al. "Phosphatidylserine and GTPase activation control Cdc42 nanoclustering to counter dissipative diffusion." *Mol. Biol. Cell* 29, 1299-1310 (2018).
<https://doi.org/10.1091/mbc.E18-01-0051>
254. Sattelmacher, B. (2001). The apoplast and its significance for plant mineral nutrition. *New Phytologist*, 149(2), 167-192.
255. Schaeffer, A., R. Bronner, P. Benveniste and H. Schaller (2001). "The ratio of campesterol to sitosterol that modulates growth in *Arabidopsis* is controlled by STEROL METHYLTRANSFERASE 2;i." *The Plant journal : for cell and molecular biology* 25: 605-615.
<https://doi.org/10.1046/j.1365-313x.2001.00994.x>
256. Schaller, H., Crausem, B., Benveniste, P., Chye, M., Tan, C., Song, Y. et al. (1995). Expression of the *Hevea brasiliensis* (H. B. K.) Müll. Arg. tobacco results in sterol overproduction. *Plant Physiol.* 109, 761-770. doi: 10.1104/pp.109.3.761
257. Schaller, H. (2003). "The role of sterols in plant growth and development." *Progress in Lipid Research* 42(3): 163-175. [https://doi.org/10.1016/S0163-7827\(02\)00047-4](https://doi.org/10.1016/S0163-7827(02)00047-4)
258. Schaller, H. (2004). "New aspects of sterol biosynthesis in growth and development of higher plants." *Plant Physiology and Biochemistry*, 42(6), 465-476.
<https://doi.org/10.1016/j.plaphy.2004.05.012>

259. Schrick, K., U. Mayer, A. Horrichs, C. Kuhnt, C. Bellini, J. Dangl, J. Schmidt and G. Jürgens (2000). "FACKEL is a sterol C-14 reductase required for organized cell division and expansion in Arabidopsis embryogenesis." *Genes & development* 14(12): 1471-1484. <https://doi.org/10.1101/gad.14.12.1471>
260. Schrick, K., Fujioka, S., Takatsuto, S., Stierhof, Y., Stransky, H., Yoshida, S., ... & Jürgens, G. (2004). A link between sterol biosynthesis, the cell wall, and cellulose in arabidopsis. *The Plant Journal*, 38(2), 227-243. <https://doi.org/10.1111/j.1365-313X.2004.02039.x>
261. Schuler, I., A. Milon, Y. Nakatani, G. Ourisson, A. M. Albrecht, P. Benveniste and M. A. Hartman (1991). "Differential effects of plant sterols on water permeability and on acyl chain ordering of soybean phosphatidylcholine bilayers." *Proceedings of the National Academy of Sciences* 88(16): 6926-6930. <https://doi.org/10.1073/pnas.88.16.6926>
262. Sehayek, E. (2003). "Genetic regulation of cholesterol absorption and plasma plant sterol levels." *Journal of Lipid Research*, 44(11), 2030-2038. <https://doi.org/10.1194/jlr.R300008-JLR200>
263. Sezgin, E., Levental, I., Mayor, S. & Eggeling, C. "The mystery of membrane organization: composition, regulation and roles of lipid rafts." *Nat. Rev. Mol. Cell Biol.*18, 361-374 (2017). <https://doi.org/10.1038/nrm.2017.16>
264. Sharples, S. C., Nguyen-Phan, T. C., & Fry, S. C. (2017). Xyloglucan endotransglucosylase/hydrolases (XTHs) are inactivated by binding to glass and cellulosic surfaces, and released in active form by a heat-stable polymer from cauliflower florets. *Journal of plant physiology*, 218, 135-143.
265. Sheen, Khan., Ameena, Fatima, Alvi., Sadaf, Saify., Noushina, Iqbal., Nafees, A., Khan. (2024). "The Ethylene Biosynthetic Enzymes, 1-Aminocyclopropane-1-Carboxylate (ACC) Synthase (ACS) and ACC Oxidase (ACO): The Less Explored Players in Abiotic Stress Tolerance."Preprint.
266. Shewry, P. R. and A. K. Stobart (1974). "Effect of gibberellic acid on sterol production in *Corylus avellana* seeds." *Phytochemistry* 13(2): 347-355.
267. Shimada, T. L., Takano, Y., Shimada, T., Fujiwara, M., Fukao, Y., Mori, M., et al. (2014). Leaf oil body functions as a subcellular factory for the production of a phytoalexin in arabidopsis. *Plant Physiol.* 164, 105-118. doi: 10.1104/pp.113.230185

268. Shimada, T. L., Takano, Y., Hara-Nishimura, I. (2015). Oil body-mediated defense against fungi: From tissues to ecology. *Plant Signal. Behav.* 10, e989036. doi: 10.4161/15592324.2014.989036 <https://doi.org/10.4161/15592324.2014.989036>
269. Shimada, T. L., Shimada, T., Okazaki, Y., Higashi, Y., Saito, K., Kuwata, K., et al. (2019). "HIGH STEROL ESTER 1 is a key factor in plant sterol homeostasis." *Nat. Plants* 5, 1154-1166. <https://doi.org/10.1038/s41477-019-0537-2>
270. Shimada, T. L., Yamaguchi, K., Shigenobu, S., Takahashi, H., Murase, M., Fukuyoshi, S., & Hara-Nishimura, I. (2020). "Excess sterols disrupt plant cellular activity by inducing stress-responsive gene expression." *Journal of plant research*, 133(3), 383-392. <https://doi.org/10.1007/s10265-020-01181-4>
271. Shiva, S., Samarakoon, T., Lowe, K. A., Roach, C., Vu, H. S., Colter, M., Porras, H., Hwang, C., Roth, M. R., Tamura, P., Li, M., Schrick, K., Shah, J., Wang, X., Wang, H., & Welti, R. (2020). "Leaf Lipid Alterations in Response to Heat Stress of *Arabidopsis thaliana*." *Plants*, 9(7), 845. <https://doi.org/10.3390/plants9070845>
272. Shrestha, P., Callahan, D. L., Singh, S. P., Petrie, J. R., Zhou, X. R. (2016). Reduced triacylglycerol mobilization during seed germination and early seedling growth in *arabidopsis* containing nutritionally important polyunsaturated fatty acids. *Front. Plant Sci.* 7. doi: 10.3389/fpls.2016.01402
273. Sievert C (2020). Interactive Web-Based Data Visualization with R, plotly, and shiny. Chapman and Hall/CRC. ISBN 9781138331457, <https://plotly-r.com>. <https://doi.org/10.1201/9780429447273>
274. Silvestro, D., Andersen, T. G., Schaller, H., & Jensen, P. E. (2013). "Plant sterol metabolism. δ^7 -sterol-c5-desaturase (*ste1/dwarf7*), $\delta^5,7$ -sterol- δ^7 -reductase (*dwarf5*) and δ^{24} -sterol- δ^{24} -reductase (*diminuto/dwarf1*) show multiple subcellular localizations in *arabidopsis thaliana* (heynh) l." *PLoS ONE*, 8(2), e56429. <https://doi.org/10.1371/journal.pone.0056429>
275. Simons, K.; Sampaio, J.L. Membrane Organization and Lipid Rafts. (2011). Cold Spring Harb. Perspect. Biol.
276. Singh, D.P., Maurya, S., Yerasu, S.R. et al. (2023) Metabolomics of early blight (*Alternaria solani*) susceptible tomato (*Solanum lycopersicum*) unfolds key biomarker metabolites and involved metabolic pathways. *Sci. Rep.* 13, 21023. <https://doi.org/10.1038/s41598->

277. Singh, G., M. Tiwari, S. P. Singh, S. Singh, P. K. Trivedi and P. Misra (2016). "Silencing of sterol glycosyltransferases modulates the withanolide biosynthesis and leads to compromised basal immunity of *Withania somnifera*." *Scientific Reports* 6(1): 25562. <https://doi.org/10.1038/srep25562>
278. Singh, G., Tiwari, M., Singh, S., Singh, R., Shirke, P. A., Trivedi, P. K., ... & Misra, P. (2017). "Sterol glycosyltransferases required for adaptation of *withania somnifera* at high temperature." *Physiologia Plantarum*, 160(3), 297-311. <https://doi.org/10.1111/ppl.12563>
279. Slik, F., Pinho, B. X., Griffith, D. M., Webb, E., Raghubanshi, A. S., Quaresma, A. C., ... & Hemati, Z. (2024). Wind dispersed tree species have greater maximum height. *Global Ecology and Biogeography*, e13878.
280. Smet, D., Depaepe, T., Vandenbussche, F., Callebert, P., Nijs, I., Ceulemans, R., & Van Der Straeten, D. (2020). "The involvement of the phytohormone ethylene in the adaptation of *Arabidopsis* rosettes to enhanced atmospheric carbon dioxide concentrations." *Environmental and Experimental Botany*, 177, 104128.
281. Sonawane, P. D., J. Pollier, S. Panda, J. Szymanski, H. Massalha, M. Yona, T. Unger, S. Malitsky, P. Arendt, L. Pauwels, E. Almekias-Siegl, I. Rogachev, S. Meir, P. D. Cárdenas, A. Masri, M. Petrikov, H. Schaller, A. A. Schaffer, A. Kamble, A. P. Giri, A. Goossens and A. Aharoni (2016). "Plant cholesterol biosynthetic pathway overlaps with phytosterol metabolism." *Nature Plants* 3(1): 16205. <https://doi.org/10.1038/nplants.2016.205>
282. Song, J., S. Sun, H. Ren, M. Grison, Y. Boutté, W. Bai and S. Men (2019). "The SMO1 Family of Sterol 4 α -Methyl Oxidases Is Essential for Auxin- and Cytokinin-Regulated Embryogenesis." *Plant Physiology* 181(2): 578-594. <https://doi.org/10.1104/pp.19.00144>
283. Steel, C. C., & Drysdale, R. B. (1988). Electrolyte leakage from plant and fungal tissues and disruption of liposome membranes by α -tomatine. *Phytochemistry*, 27(4), 1025-1030.
284. Stefano Gattolin, Mathias Sorieul, Lorenzo Frigerio. (2020). Tonoplast intrinsic proteins and vacuolar identity. *Biochem Soc Trans* 1 J; 38 (3): 769–773. doi: <https://doi.org/10.1042/BST0380769>
285. Steinbrecher, T., Leubner-Metzger, G. (2017). The biomechanics of seed germination, J.

Exp. Bot. 68, 765-783. doi: 10.1093/jxb/erw428

286. Stepanova, A. N., & Alonso, J. M. (2009). Ethylene signaling and response: where different regulatory modules meet. *Current opinion in plant biology*, 12(5), 548-555.
287. Sun, J., Wu, D., Xu, J., Rasmussen, S. K., Shu, X. (2015). Characterization of starch during germination and seedling development of a rice mutant with a high content of resistant starch. *J. Cereal Sci.* 62, 94-101. doi: 10.1016/j.jcs.2015.01.002
288. Takahashi, D., Uemura, M., & Kawamura, Y. (2018). Freezing tolerance of plant cells: from the aspect of plasma membrane and microdomain. *Survival strategies in extreme cold and desiccation: Adaptation mechanisms and their applications*, 61-79.
289. Takeda, S., Hanano, K., Kariya, A., Shimizu, S., Zhao, L., Matsui, M., ... & Aida, M. (2011). CUP-SHAPED COTYLEDON1 transcription factor activates the expression of LSH4 and LSH3, two members of the ALOG gene family, in shoot organ boundary cells. *The Plant Journal*, 66(6), 1066-1077.
290. Tannis, Berry., J., Derek, Bewley. (1993). " Comparisons between the roles of the fruit tissues, osmoticum and abscisic acid in maintaining tomato seed development and storage protein synthesis." *Seed Science Research*
291. Tapken, W. and A. S. Murphy (2015). "Membrane nanodomains in plants: capturing form, function, and movement." *Journal of Experimental Botany* 66(6): 1573-1586. <https://doi.org/10.1093/jxb/erv054>
292. Tarazona, P., Feussner, K., & Feussner, I. (2015). An enhanced plant lipidomics method based on multiplexed liquid chromatography–mass spectrometry reveals additional insights into cold-and drought-induced membrane remodeling. *The Plant Journal*, 84(3), 621-633.
293. Tatenaka, Y., Kato, H., Ishiyama, M., Sasamoto, K., Shiga, M., Nishitoh, H., et al. (2019). Monitoring lipid droplet dynamics in living cells by using fluorescent probes. *Biochem.* 56, 499-503 doi: 10.1021/acs.biochem.8b01071
294. Thirumalaikumar V. P., Wagner, M., Balazadeh, S., Skirycz, A. (2021) Autophagy is responsible for the accumulation of proteogenic dipeptides in response to heat stress in *Arabidopsis thaliana*. *FEBS J.* 288, 281-292 doi:10.1111/febs.153
295. Thirumalaikumar, V. P., Gorka, M., Schulz, K., Masclaux-Daubresse, C., Sampathkumar,

- A., Skirycz, A., ... & Balazadeh, S. (2021). Selective autophagy regulates heat stress memory in Arabidopsis by NBR1-mediated targeting of HSP90. 1 and ROF1. *Autophagy*, 17(9), 2184-2199.
296. Tholl, D. (2015). Biosynthesis and Biological Functions of Terpenoids in Plants. *Biotechnology of Isoprenoids*. J. Schrader and J. Bohlmann. Cham, Springer International Publishing: 63-106. https://doi.org/10.1007/10_2014_295
297. Thomas, A., Charbonneau, J., Fournaise, E., & Chaurand, P. (2012). "Sublimation of new matrix candidates for high spatial resolution imaging mass spectrometry of lipids: enhanced information in both positive and negative polarities after 1,5-diaminonaphthalene deposition." *Analytical Chemistry*, 84(4), 2048-2054.
298. Tiwari, P., R. S. Sangwan, Asha, B. N. Mishra, F. Sabir and N. S. Sangwan (2014). "Molecular cloning and biochemical characterization of a recombinant sterol 3-O-glucosyltransferase from *Gymnema sylvestre* R.Br. catalyzing biosynthesis of steryl glucosides." *BioMed research international* 2014: 934351-934351. <https://doi.org/10.1155/2014/934351>
299. Tjellström, H., Hellgren, L., Wieslander, Å., & Sandelius, A. S. (2009). "Lipid asymmetry in plant plasma membranes: phosphate deficiency-induced phospholipid replacement is restricted to the cytosolic leaflet." *The FASEB Journal*, 24(4), 1128-1138. <https://doi.org/10.1096/fj.09-139410>
300. Tohge, T., Fernie, A. R., (2015) Metabolomics-Inspired Insight into Developmental, Environmental and Genetic Aspects of Tomato Fruit Chemical Composition and Quality. *Plant Cell Physiol.* 56, 9, 1681-1696, doi: [org/10.1093/pcp/pcv093](https://doi.org/10.1093/pcp/pcv093)
301. Torres, I., Castrejón-Téllez, V., Soto, M. E., Rubio-Ruiz, M. E., Manzano-Pech, L., & Guarner-Lans, V. (2021). Oxidative stress, plant natural antioxidants, and obesity. *International journal of molecular sciences*, 22(4), 1786.
302. Trivedi, M., Singh, R., Shukla, M., & Tiwari, R. K. (2016). "GMO and Food Security." In *Ecofriendly Pest Management for Food Security* (pp. 703-726). <https://doi.org/10.1016/B978-0-12-803265-7.00023-3>
303. Tugizimana, F., Steenkamp, P., Piater, L., & Dubery, I. (2014). "Multi-platform metabolomic analyses of ergosterol-induced dynamic changes in nicotiana tabacum cells." *Plos One*, 9(1), e87846.

304. Tzen, J. T. C., Cao, Y. Z., Laurent, P., Ratnayake, C., Huang, A. H. C. (1993). Lipids, proteins, and structure of seed oil bodies from diverse species. *Plant Physiol.* 101, 267-276. doi: 10.1104/pp.101.1.267
305. Valitova, J., Sulkarnayeva, A., Kotlova, E., Ponomareva, A., Mukhitova, F. K., Murtazina, L., ... & Minibayeva, F. (2014). Sterol binding by methyl- β -cyclodextrin and nystatin—comparative analysis of biochemical and physiological consequences for plants. *The FEBS journal*, 281(8), 2051-2060.
306. Valitova, J. N., Sulkarnayeva, A. G., & Minibayeva, F. (2016). "Plant sterols: diversity, biosynthesis, and physiological functions." *Biochemistry (Moscow)*, 81(8), 819-834. <https://doi.org/10.1134/s0006297916080046>
307. Valitova, J., Renkova, A., Beckett, R., & Minibayeva, F. (2024). Stigmasterol: An Enigmatic Plant Stress Sterol with Versatile Functions. *International journal of molecular sciences*, 25(15), 8122.
308. Vandenbussche, F., Habricot, Y., Condiff, A. S., Maldiney, R., Straeten, D. V. D., & Ahmad, M. (2007). "HY5 is a point of convergence between cryptochrome and cytokinin signalling pathways in *Arabidopsis thaliana*." *The Plant Journal*, 49(3), 428-441.
309. Venkatesh, P., Thirumalaikumar., Mateusz, Wagner., Mateusz, Wagner., Salma, Balazadeh., Salma, Balazadeh., Aleksandra, Skirycz. (2021). "Autophagy is responsible for the accumulation of proteogenic dipeptides in response to heat stress in *Arabidopsis thaliana*." *FEBS Journal*, 288(1):281-292. doi: 10.1111/FEBS.15336
310. Villette, C., Berna, A., Compagnon, V., & Schaller, H. (2015). "Plant Sterol Diversity in Pollen from Angiosperms." *Lipids*, 50(8), 749-760. <https://doi.org/10.1007/s11745-015-4008-x>
311. Vranová, E., D. Coman and W. Gruissem (2013). "Network Analysis of the MVA and MEP Pathways for Isoprenoid Synthesis." *Annual Review of Plant Biology* 64(1): 665-700. <https://doi.org/10.1146/annurev-arplant-050312-120116>
312. Vriese, K. D., J. Pollier, A. Goossens, T. Beeckman and S. Vanneste (2019). "The use of mutants and inhibitors to study sterol biosynthesis in plants." *bioRxiv*: 784272.
313. Vriet, C., E. Russinova and C. Reuzeau (2013). "From Squalene to Brassinolide: The Steroid Metabolic and Signaling Pathways across the Plant Kingdom." *Molecular Plant* 6(6): 1738-

1757. <https://doi.org/10.1093/mp/sst096>
314. Wachtler, V., Rajagopalan, S., & Balasubramanian, M. K. (2003). "Sterol-rich plasma membrane domains in the fission yeast *Schizosaccharomyces pombe*." *Journal of Cell Science*, 116(5), 867-874. <https://doi.org/10.1242/jcs.00299>
 315. Wang, H., D. A. Nagegowda, R. Rawat, P. Bouvier-Navé, D. Guo, T. J. Bach and M.-L. Chye (2012). "Overexpression of *Brassica juncea* wild-type and mutant HMG-CoA synthase 1 in *Arabidopsis* up-regulates genes in sterol biosynthesis and enhances sterol production and stress tolerance." *Plant Biotechnology Journal* 10(1): 31-42. <https://doi.org/10.1111/j.1467-7652.2011.00631.x>
 316. Wang, K., M. Senthil-Kumar, C.-M. Ryu, L. Kang and K. S. Mysore (2012). "Phytosterols Play a Key Role in Plant Innate Immunity against Bacterial Pathogens by Regulating Nutrient Efflux into the Apoplast." *Plant Physiology* 158(4): 1789-1802. <https://doi.org/10.1104/pp.111.189217>
 317. Wang, C., Li, C., Duan, G., Wang, Y., Zhang, Y., & Yang, J. (2019). Overexpression of *magnaporthe oryzae* systemic defense trigger 1 (*mosdt1*) confers improved rice blast resistance in rice. *International Journal of Molecular Sciences*, 20(19), 4762. <https://doi.org/10.3390/ijms20194762>
 318. Wang, S., Hu, W., Liu, F., (2022) Autophagy in the lifetime of plants: from seed to seed. *Int. J. Mol. Sci.* 23, 11410. doi: [org/10.3390/ijms231911410](https://doi.org/10.3390/ijms231911410)
 319. Warnecke, D. C., M. Baltrusch, F. Buck, F. P. Wolter and E. Heinz (1997). "UDP-glucose:sterol glucosyltransferase: cloning and functional expression in *Escherichia coli*." *Plant Molecular Biology* 35(5): 597-603. <https://doi.org/10.1023/A:1005806119807>
 320. Warnecke, D., Erdmann, R., Fahl, A., Hube, B., Müller, F., Zank, T., ... & Heinz, E. (1999). "Cloning and functional expression of *ugt* genes encoding sterol glucosyltransferases from *Saccharomyces cerevisiae*, *Candida albicans*, *Pichia pastoris*, and *Dictyostelium discoideum*." *Journal of Biological Chemistry*, 274(19), 13048-13059. <https://doi.org/10.1074/jbc.274.19.13048>
 321. Wentzinger, L. F., Bach, T. J., Hartmann, M. A. (2002). Inhibition of squalene synthase and squalene epoxidase in tobacco cells triggers an up-regulation of 3-hydroxy-3-methylglutaryl coenzyme A reductase. *Plant Physiol.* 130, 334-346. doi: [10.1104/pp.004655](https://doi.org/10.1104/pp.004655) <https://doi.org/10.1104/pp.004655>

322. Wewer, V., Brands, M., & Dörmann, P. (2014). "Fatty acid synthesis and lipid metabolism in the obligate biotrophic fungus *Rhizophagus irregularis* during mycorrhization of *Lotus japonicus*." *Plant Journal*, 79(3), 398-412. <https://doi.org/10.1111/tpj.12566>
323. Whitaker, B.D. (1988) Changes in the steryl lipid content and composition of tomato fruit during ripening. *Phytochemistry*. 27:3411-3416. [https://doi.org/10.1016/0031-9422\(88\)80740-4](https://doi.org/10.1016/0031-9422(88)80740-4)
324. Whitaker, B. D. (1991). Changes in lipids of tomato fruit stored at chilling and non-chilling temperatures. *Phytochemistry*, 30(3), 757-761.
325. Whitaker, B. D. (1994). "Lipid Changes in Mature-green Tomatoes during Ripening, during Chilling, and after Rewarming subsequent to Chilling." *Journal of the American Society for Horticultural Science*, 119(5), 994-999. <https://doi.org/10.21273/JASHS.119.5.994>
326. Wickham H, Averick M, Bryan J, Chang W, McGowan LD, François R, Golemund G, Hayes A, Henry L, Hester J, Kuhn M, Pedersen TL, Miller E, Bache SM, Müller K, Ooms J, Robinson D, Seidel DP, Spinu V, Takahashi K, Vaughan D, Wilke C, Woo K, Yutani H (2019). "Welcome to the tidyverse." *Journal of Open Source Software*, 4(43), 1686. doi:10.21105/joss.01686. <https://doi.org/10.21105/joss.01686>
327. Wilkinson, S.C., Powls, R., Goad, L.J. (1994). The effects of excess exogenous mevalonic acid on sterol and steryl ester biosynthesis in celery (*Apium graveolens*) cell suspension cultures. *Phytochemistry* 37, 1031-1035. doi:10.1016/S0031-9422(00)89523-0
328. Willemsen, V., J. Friml, M. Grebe, A. van den Toorn, K. Palme and B. Scheres (2003). "Cell polarity and PIN protein positioning in *Arabidopsis* require STEROL METHYLTRANSFERASE1 function." *The Plant cell* 15(3): 612-625. <https://doi.org/10.1105/tpc.008433>
329. Wittmann, J., Brancato, C., Berendzen, K. W., & Dreiseikelmann, B. (2016). Development of a tomato plant resistant to *Clavibacter michiganensis* using the endolysin gene of bacteriophage CMP1 as a transgene. *Plant Pathology*, 65(3), 496-502.
330. Wojciechowski, Z. A. and J. Zimowski (1975). "Acyl composition and biosynthesis of acylated steryl glucosides in *Calendula officinalis*." *Biochimica et Biophysica Acta (BBA) - Lipids and Lipid Metabolism* 398(1): 111-117. [https://doi.org/10.1016/0005-2760\(75\)90174-5](https://doi.org/10.1016/0005-2760(75)90174-5)

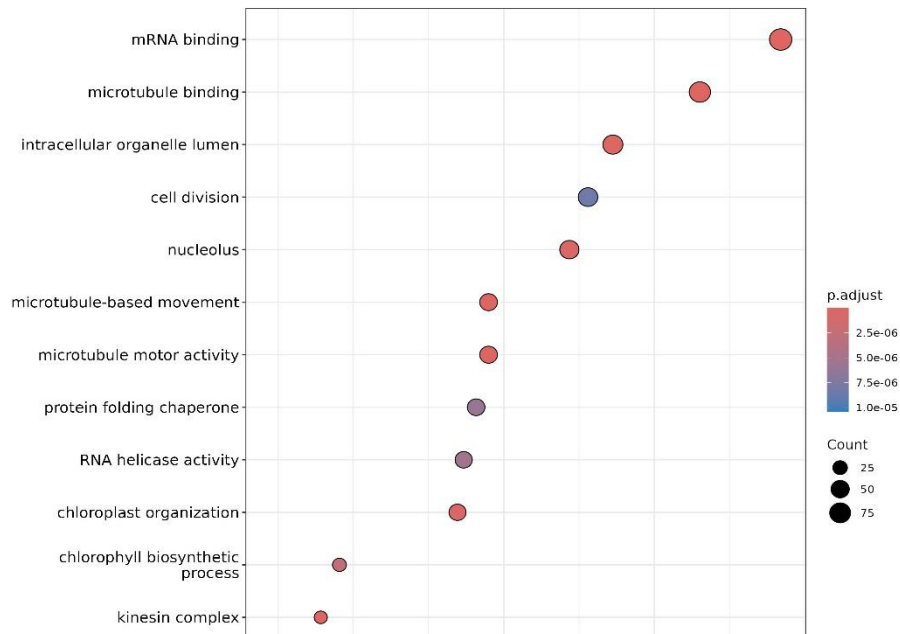
331. Wu, H. C., Bulgakov, V. P., & Jinn, T. L. (2018). Pectin methylesterases: cell wall remodeling proteins are required for plant response to heat stress. *Frontiers in plant science*, 9, 1612.
332. Yamauchi, Y., Reid, P. C., Sperry, J. B., Furukawa, K., Takeya, M., Chang, C. C., & Chang, T. (2007). "Plasma membrane rafts complete cholesterol synthesis by participating in retrograde movement of precursor sterols." *Journal of Biological Chemistry*, 282(48), 34994-35004. <https://doi.org/10.1074/jbc.M703653200>
333. Yang, L., Pan, A., Jia, J., Ding, J., Chen, J., Cheng, H., ... & Zhang, D. (2005). Validation of a tomato-specific gene, LAT52, used as an endogenous reference gene in qualitative and real-time quantitative PCR detection of transgenic tomatoes. *Journal of Agricultural and Food Chemistry*, 53(2), 183-190.
334. Yepes-Molina, L., Carvajal, M., & Martínez-Ballesta, M. C. (2020). Detergent resistant membrane domains in broccoli plasma membrane associated to the response to salinity stress. *International Journal of Molecular Sciences*, 21(20), 7694.
335. You, Y., & van Kan, J.A.L. (2021) Bitter and sweet make tomato hard to (b)eat. *New Phytologist*. 230,90-100. doi: 10.1111/nph.17104.
336. Yu, Y., Wang, J., Zhang, Z., Quan, R., Zhang, H., Deng, X. W., ... & Huang, R. (2013). "Ethylene promotes hypocotyl growth and hy5 degradation by enhancing the movement of cop1 to the nucleus in the light." *PLoS Genetics*, 9(12), e1004025.
337. Yu, Y., & Huang, R. (2017). Integration of ethylene and light signaling affects hypocotyl growth in Arabidopsis. *Frontiers in plant science*, 8, 57.
338. Yuan, J., Yu, Z., Lin, T., Wang, L., Chen, X., Liu, T., ... & Li, Y. (2020). BcERF070, a novel ERF (ethylene-response factor) transcription factor from non-heading Chinese cabbage, affects the accumulation of ascorbic acid by regulating ascorbic acid-related genes. *Molecular Breeding*, 40, 1-18.
339. Zauber, H., A. Burgos, P. Garapati and W. X. Schulze (2014). "Plasma membrane lipid-protein interactions affect signaling processes in sterol-biosynthesis mutants in Arabidopsis thaliana." *Frontiers in Plant Science* 5: 78-78. <https://doi.org/10.3389/fpls.2014.00078>
340. Zauber, H., Szymanski, W., & Schulze, W. (2013). "Unraveling sterol-dependent membrane phenotypes by analysis of protein abundance-ratio distributions in different

- membrane fractions under biochemical and endogenous sterol depletion." *Molecular & Cellular Proteomics*, 12(12), 3732-3743.
341. Zeng, J., Zhang, H., Tan, Y., Sun, C., Liang, Y., Yu, J., ... & Zou, H. (2018). "Aggregation of LR activates c-met and c-src in non-small cell lung cancer cells." *BMC Cancer*, 18(1).
 342. Zhang, H., Vasanthan, T., Wettasinghe, M. (2007). Enrichment of tocopherols and phytosterols in canola oil during seed germination. *J. Agric. Food Chem.* 55, 355-359. doi: 10.1021/jf060940o
 343. Zhang, W., Jiang, X., Liu, L., Zhao, Y., Bai, F., Wang, J., ... & Xu, X. (2024). "The influence mechanism of phospholipids structure and composition changes caused by oxidation on the formation of flavor substances in sturgeon caviar." *Food Chemistry*, 460, 140585.
 344. Zhang, X., Sun, S., Nie, X., Boutté, Y., Grison, M., Li, P., ... & Men, S. (2016). "Sterol methyl oxidases affect embryo development via auxin-associated mechanisms." *Plant Physiology*, 171(1), 468-482. <https://doi.org/10.1104/pp.15.01814>
 345. Zhang, X., K. Lin and Y. Li (2020). "Highlights to phytosterols accumulation and equilibrium in plants: Biosynthetic pathway and feedback regulation." *Plant Physiology and Biochemistry* 155: 637-649. <https://doi.org/10.1016/j.plaphy.2020.08.021>
 346. Zhang, X. P., Lu, Y. Q., Zhang, Y. Q., & Li, X. J. (2023). "Advances in plant extracellular vesicles and analysis techniques." *Biotechnology Bulletin*, 39(5), 32.
 347. Zhao, L., Lu, L., Zhang, L., Wang, A., Wang, N., Liang, Z., ... & Tang, K. (2009). Molecular evolution of the E8 promoter in tomato and some of its relative wild species. *Journal of biosciences*, 34, 71-83.
 348. Zhao, M., Zhang, H., Yan, H., Qiu, L., Baskin, C. C. (2018). Mobilization and role of starch, protein, and fat reserves during seed germination of six wild grassland species. *Front. Plant Sci.* 9. doi: 10.3389/fpls.2018.00234
 349. Zhou, X., Chen, X., Du, Z., Zhang, Y., Zhang, W., Kong, X. et al. (2019). Terpenoid esters are the major constituents from leaf lipid droplets of camellia sinensis. *Front. Plant Sci.* 10; 179. doi: 10.3389/fpls.2019.00179
 350. Zhou, Y. et al. "Lipid-sorting specificity encoded in K-Ras membrane anchor regulates signal output." *Cell* 168, 239-251 e216 (2017). <https://doi.org/10.1016/j.cell.2016.11.059>

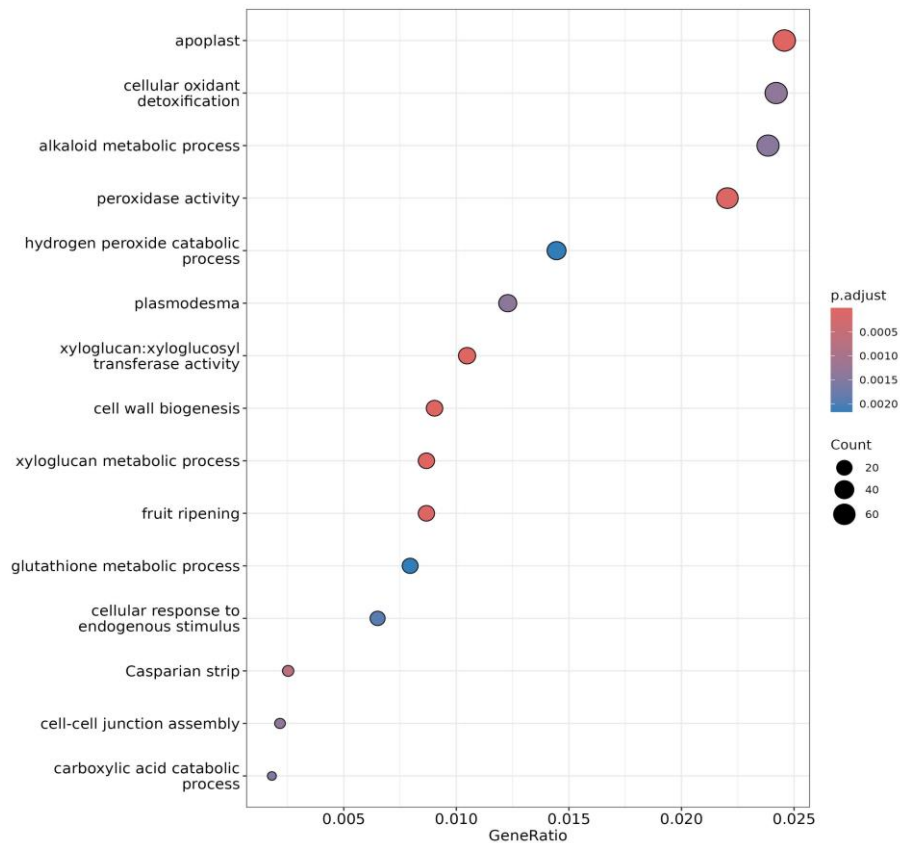
351. Zhu F, Wen W, Cheng Y, Fernie AR (2022) The metabolic changes that effect fruit quality during tomato fruit ripening. *Molecular Horticulture* 2: 2 doi: 10.1186/s43897-022-00024-1.
352. Zhu, Z., Zhang, Y., Liu, J., Chen, Y., & Zhang, X. (2018). Exploring the effects of selenium treatment on the nutritional quality of tomato fruit. *Food chemistry*, 252, 9-15.
353. Zhuang, Y., & Li, L. (2020). Are cuproproteins part of the multi-protein framework for making the Casparian strip?. *Plant Signaling & Behavior*, 15(10), 1798605.
354. Zimowski, J. and Z. A. Wojciechowski (1981). "Partial purification and specificity of triacylglycerol: Sterol acyltransferase from *Sinapis alba*." *Phytochemistry* 20(8): 1799-1803. [https://doi.org/10.1016/0031-9422\(81\)84007-1](https://doi.org/10.1016/0031-9422(81)84007-1)

8. Supplemental material

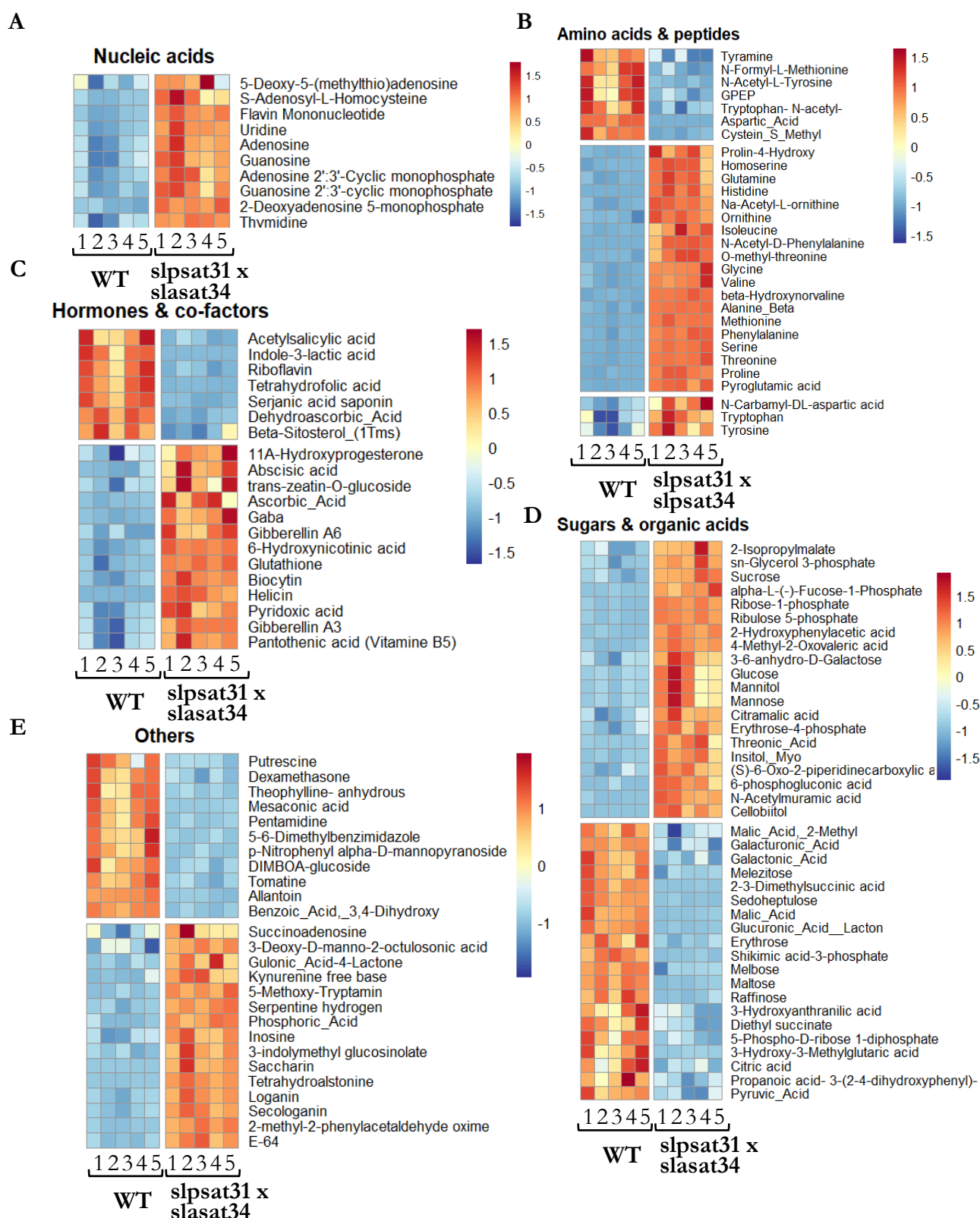
A



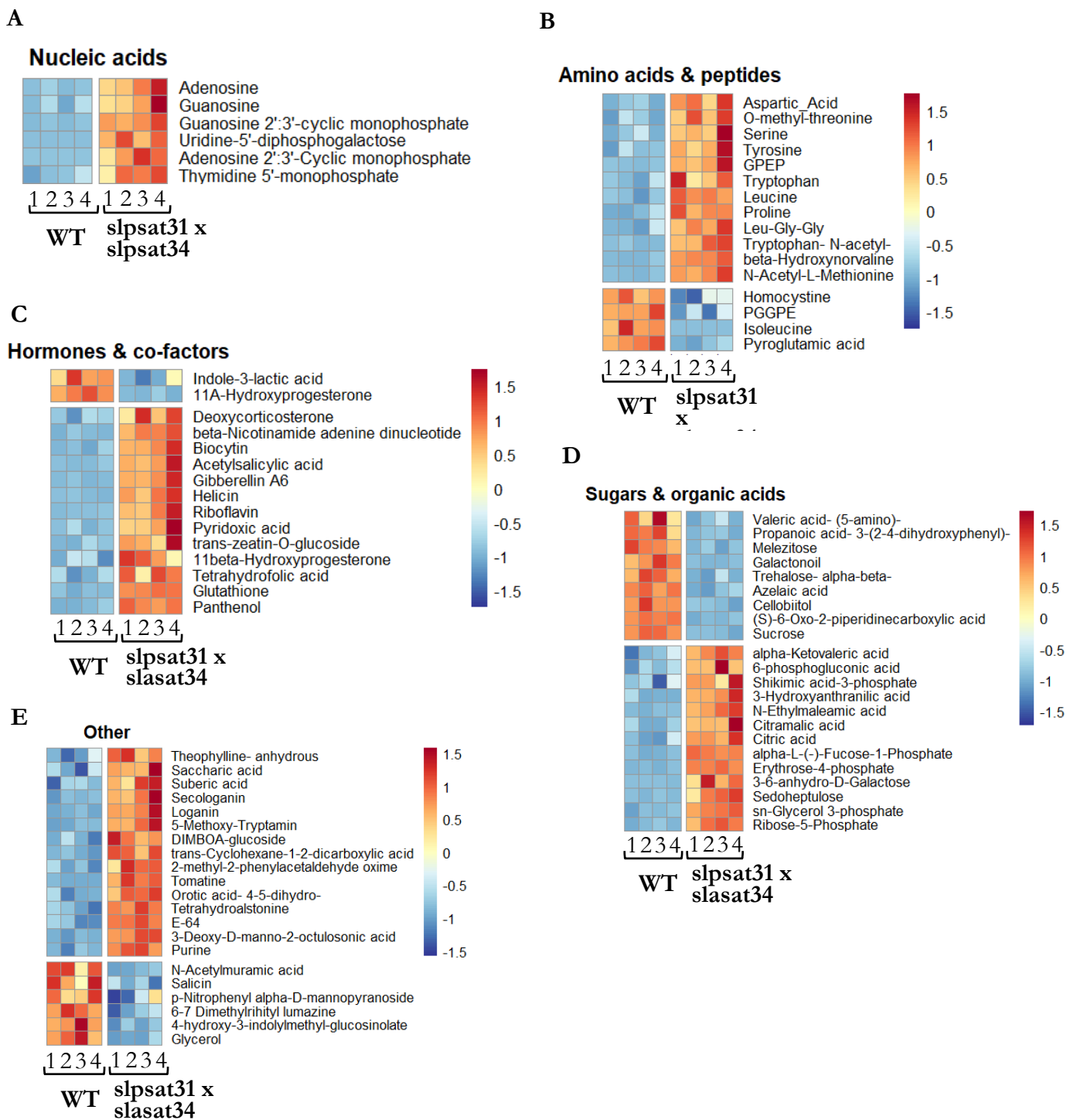
B



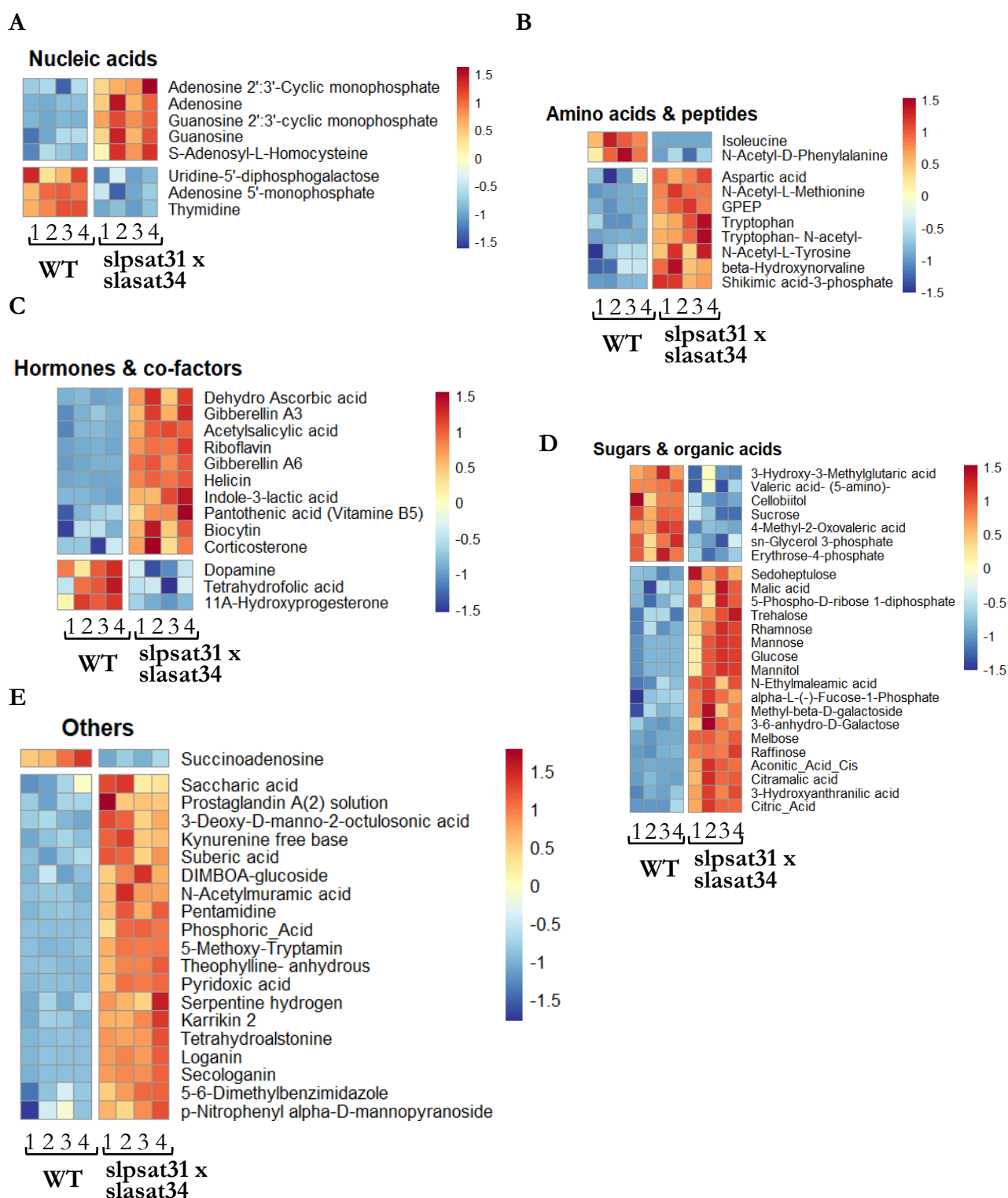
Supplemental Figure 1. Bubble plots showing significantly enriched GO terms for the DEGs (A) upregulated and (B) downregulated in SISGT3-ox lines 9 and 31 vs WT in seedlings. Size of the bubbles is proportional to the number of DEGs assigned to the GO term. The y-axis represents the negative logarithm of the adjusted p value [false discovery rate (FDR)] for the GO terms, and the x-axis displays gene ratio using the GOplot R-Package.



Supplemental Figure 2: Heatmap analysis displaying changes of metabolite abundance in *slpsat31* x *slasat34* and WT fruits. Heatmaps show significantly differentially accumulated (adjusted $p < 0.05$, Holm–Bonferroni method) (A) nucleic acids, (B) amino acids and peptides, (C) hormones and co-factors, (D) sugars and organic acids, and (E) other not further classified metabolites. Blue and red colours indicate low and high intensity, respectively. The scale is row-based.



Supplemental Figure 3: Heatmap analysis displaying changes of metabolite abundance in *slpsat31xslsat34* and WT dry seeds. Heatmaps show significantly differentially accumulated (adjusted $p < 0.05$, Holm–Bonferroni method) (A) nucleic acids, (B) amino acids and peptides, (C) hormones and co-factors, (D) sugars and organic acids, and (E) other not further classified metabolites. Blue and red colours indicate low and high intensity, respectively. The scale is row-based.



Supplemental Figure 4: Heatmap analysis displaying changes of metabolite abundance in *slpsat31* x *slasat34* and WT imbibed seeds. Heatmaps show significantly differentially accumulated (adjusted $p < 0.05$, Holm–Bonferroni method) (A) nucleic acids, (B) amino acids and peptides, (C) hormones and co-factors, (D) sugars and organic acids, and (E) other not further classified metabolites. Blue and red colours indicate low and high intensity, respectively. The scale is row-based.

Supplemental Table 1. Quantification of FS, SE, SG and ASG in fruit pericarp of WT and *slpsat31 x slasat34* mutant plants. Data are expressed as (µg/mg dry weight) and shown as average values from three biological replicates with SEM in parentheses. Esterified and glycosylated sterol fractions were calculated according to the formulas $SE \times 100 / (SE + FS)$ and $(SG + ASG) \times 100 / (SG + ASG + FS)$, respectively. Significance levels of changes in the mutant compared to WT are indicated by asterisks (* $P < 0.05$; ** $P < 0.01$; *** $P < 0.005$; **** $P < 0.001$).

FS	WT	<i>slpsat31 x slasat34</i>	SE	WT	<i>slpsat31 x slasat34</i>	Esterified fraction	
						WT	<i>slpsat31 x slasat34</i>
Cholesterol	0.0031 (0.0001)	0.0034 (0.0006)	Cholesteryl	0.0051 (0.0011)	0.0015 (0.0001)	62.3	30.4
Campesterol	0.0055 (0.0001)	0.0131* (0.0017)	Campesteryl	0.0057 (0.0002)	0.0004**** (0.0001)	50.6	2.7
Stigmasterol	0.0441 (0.0013)	0.0561 (0.0033)	Stigmasteryl	0.0084 (0.0012)	0.0004* (0.0001)	15.9	0.6
Sitosterol	0.0153 (0.0002)	0.0333 (0.0049)	Sitosteryl	0.0189 (0.0002)	0.0011*** (0.0003)	55.2	3.1
Total	0.0681 (0.0012)	0.1059* (0.0099)	Total	0.03802 (0.0012)	0.0032**** (0.0002)	35.8	3.0

SG	WT	<i>slpsat31 x slasat34</i>	ASG	WT	<i>slpsat31 x slasat34</i>	Glycosylated fraction	
						WT	<i>slpsat31 x slasat34</i>
Cholesteryl	0.0049 (0.0001)	0.0045 (0.0003)	Cholesteryl	0.0073 (0.0001)	0.0024*** (0.0002)	79.7	67.5
Campesteryl	0.0138 (0.0004)	0.0278* (0.0037)	Campesteryl	0.0198 (0.0003)	0.0131** (0.0010)	85.8	77.0
Stigmasteryl	0.0378 (0.0003)	0.0620** (0.0052)	Stigmasteryl	0.0459 (0.0008)	0.0271** (0.0022)	65.5	61.4
Sitosteryl	0.0552 (0.0062)	0.0929 (0.0058)	Sitosteryl	0.0715 (0.0058)	0.0403* (0.0050)	89.2	80.0
Total	0.1085 (0.0034)	0.1977** (0.0086)	Total	0.1479 (0.0037)	0.0830*** (0.0063)	79.0	72.6

Supplemental Table 2. Quantification of SG and ASG quantification in seeds of WT and *slpsat31 x slasat34* mutant plants. Data are expressed as (μg/mg dry weight) and shown as average values from three biological replicates with SEM in parentheses. Glycosylated sterol fraction was calculated according to the formula (SG+ASG)*100/(SG+ASG+FS). Significance levels of changes in the mutant compared to WT are indicated by asterisks (*P<0.05; **P<0.01; ***P<0.005).

SG	WT	<i>slpsat31x asat34</i>	ASG	WT	<i>slpsat31x slasat34</i>	Glycosylated fraction	
						Wt	<i>slpsat31xslasat34</i>
Cholesteryl	0.0595 (0.0017)	0.1347*** (0.0030)	Cholesteryl	0.0242 (0.0003)	0.0330* (0.0013)	50.8	90.6
Campesterol	0.0431 (0.0022)	0.1363*** (0.0035)	Campesterol	0.0139 (0.0010)	0.0289* (0.0031)	46.7	81.2
Stigmasteryl	0.0894 (0.0026)	0.2780*** (0.0123)	Stigmasteryl	0.0211 (0.0004)	0.0541* (0.0031)	35.5	63.1
Sitosteryl	0.2628 (0.0042)	0.9467*** (0.0337)	Sitosteryl	0.0557 (0.0043)	0.1820* (0.0090)	25.2	51.6
Total	0.4548 (0.0063)	1.4957** * (0.0512)	Total	0.1150 (0.0040)	0.2980** (0.0138)	30.6	57.9

Supplemental Table 3. Percentage of SG and ASG species for each fraction in leaves and red fruits of WT and S1SGT3-ox lines. SG and ASG were calculated according to the formula (SG specie *100/SG total fraction and ASG specie *100/ASG total fraction).

<i>Leaves</i>							
SG	WT	Line 9	Line 31	ASG	WT	Line 9	Line 31
Cholesteryl	19.3	19.2	23.7	Cholesteryl	15.3	14.1	16.7
Campesteryl	6.5	7.6	9.8	Campesteryl	6.0	6.6	7.8
Stigmasteryl	32.2	39.5	30.1	Stigmasteryl	40.8	47.6	41.2
Sitosteryl	42.1	33.7	36.4	Sitosteryl	37.8	31.7	34.4
Total (Fraction)	100	100	100	Total (Fraction)	100	100	100
<i>Fruits</i>							
SG	WT	Line 9	Line 31	ASG	WT	Line 9	Line 31
Cholesteryl	3.0	2.9	3.1	Cholesteryl	3.0	3.0	3.4
Campesteryl	22.1	22.2	24.9	Campesteryl	20.5	18.7	25.1
Stigmasteryl	43.0	47.6	45.9	Stigmasteryl	48.1	54.7	52.5
Sitosteryl	31.9	27.3	26.1	Sitosteryl	28.4	23.6	19.0
Total (Fraction)	100	100	100	Total (Fraction)	100	100	100

Supplemental Table 4. Metabolites detected in dry/wet seed and red tomato fruit from *slpsat31 x slsat34* vs WT filtered by p-value 0.05. Values correspond to *slsat31 x slsat34* Log10 fc vs WT median.

Compound	Dry seed	Compound	Wet seed	Compound	Red fruit
Methionyalanine	4.043717159	Phosphoric_Acid	3.575941052	PE 36:3_2	3.68681349
Uridine-5'-diphosphoglucose	3.279757357	Luteolin	3.27558663	Threonic_Acid	3.52844207
Adenosine 2':3'-Cyclic monophosphate_1	2.998301686	Helicin	3.030705834	Histidine	3.41312441
Methionylhistidine	2.945779658	Citric_Acids	2.786417033	Cellobiitol	3.13016163
Sermethionine	2.22350274	Naringin dihydrochalcone_1	1.588732315	Threonytyrosine	2.65607499
Leucine	2.1225	Adenosine 3' monophosphate	1.519088096	Helicin	2.46811359
Polymethionine	2.044512346	Valyphenylalanine	1.398230357	N-Acetyl-D-Phenylalanine	2.32580815
Tomatine	1.871603715	Polymethionine	1.3728106	Tryptophylglutamic acid	2.22924009
Kaempferol 3-O-glucosyl-glucoside 7-O-rhamnoside	1.632225232	TAG 50:5 (2)	1.281036355	Phenylalanyaspargine	2.19712853
Isoleucylmethionine_1	1.3794575	NG2_8.09_433.2084_1	1.263868815	Lysylphenylalanine	2.16586241
phytoene_carotenoids related	1.346572518	Methionylphenylalanine	1.25146881	Alanyvaline	2.13214994
Helicin	1.316416087	Valytyrosine_1	1.223499194	Seryltryptophan	1.94543419
Leucylmethionine_1	1.193559841	4CGA_5.25_353.0876	1.153489719	LysoPE 18:1	1.88794285
Tryptophyllysine_1	1.178776253	Isoleucylmethionine_1	1.141668915	Tryptophyllysine_1	1.86320451
Alanylmethionine_1	1.165281229	Aconitic_Acid_Cis	1.136048751	5-Methoxy-Tryptamin	1.73420392
Glutamylmethionine	1.163222566	phytoene_carotenoids related	1.134208181	Apigenin-7-glucoside_1	1.72561547
4CGA_5.25_353.0876	1.149543324	Serpentine hydrogen	1.101272784	Saccharin_1	1.65943251
trans-zeatin-O-glucoside	1.106707117	Myricetin-3-O-Glucoside_Saleh_standards_47	1.068854712	Proline	1.64632267
Methionyleucine	1.062050077	TAG 42:2 (2)	1.06416965	Isoleucine_1	1.61902997
Valymethionine	1.020944148	Methionyleucine	1.046550343	6-phosphogluconic acid	1.6076478
Leucyltyrosine	1.013094546	Leucylmethionine_1	1.046434846	Leucylvaline	1.5226565
Naringin dihydrochalcone_1	1.002473512	Phenylalanytyrosine_1	0.954492028	Leucylisoleucine	1.38498464
N-Acetylneuraminic acid_1 (Sialic acid)	0.98868851	Valymethionine	0.953579653	TAG 60:7	1.3844741
Valyphenylalanine	0.966669873	Is3G2-A_6.79_609.1467	0.928154257	Glutamine	1.37259623

Panthenol	0.958414486	Methionytyrosine	0.911124305	Pyridoxamine-5'-phosphate (PMP) Vit B6	1.30591408
Cytidine 5Â'-monophosphate	0.934980746	Q3G6-R7G_4.67_771.1984	0.910096776	Alanine_Beta	1.27927238
MGDG 36:6 (1)	0.918906791	Malvin	0.882867291	PC 34:4 (1)	1.22324613
N-Acetyl-L-Methionine	0.9131	Adenosine 2Â' monophosphate	0.873232228	TAG 58:6	1.21113947
GPEP	0.910775416	5-Methoxy-Tryptamin_1	0.860015414	Prolyphenylalanine	1.19865552
alpha-L(-)-Fucose-1-Phosphate	0.904471369	Trehalose	0.847584905	Glutaminyglutamic acid	1.19293698
Tryptophythrone_1	0.87268698	Phenylalanyphenylalanine	0.826569516	Methionytyrosine	1.17043266
Methionytyrosine	0.8646468	Melbose	0.826222754	N-Acetylmuramic acid_1	1.13179056
Leu-Gly-Gly	0.855523505	Methionyalanine	0.825558061	Tetrahydroalstonine	1.09541362
Seryphenylalanine	0.832820615	Cytidine 5Â'-monophosphate	0.78889649	TAG 60:6 (1)	1.09171385
Methionisoleucine_1	0.823085073	Leucylglycine_1	0.761719875	alpha-L(-)-Fucose-1-Phosphate	1.07534226
Valytyrosine_1	0.782620164	Tryptophyarginine	0.760435736	LysoPE 18:3	1.07264479
Tryptophyarginine	0.776601223	Lysisileucine	0.746299646	Gibberellin A6	1.061067294
trans-Cyclohexane-1-2-dicarboxylic acid_1	0.767662785	GPEP	0.744148305	Phenylalanyvaline	1.04120758
Methionylphenylalanine	0.763818467	Phenylalanyleucine_1	0.735568772	DGDG 36:3 (1)	1.02464658
Adenosine 3Â' monophosphate	0.762722905	Pelargonin	0.733444794	Glutamylglutamic acid_1	1.00562833
Glutamylglutamic acid_1	0.762417293	Leucyasparagine	0.720653249	CafHex2_4.09_341.0879_1	1.0010968
Methionylvaline	0.760224474	Leucythreonine	0.71999006	3-indolymethylglucosinolate	0.99600649
FerHex2_4.65_355.1031_1	0.748683195	Phenylalanyasparagine	0.70917739	N-Acetylneuraminic acid_1 (Sialic acid)	0.98868851
Tryptophyasparagine_1	0.727130235	Leucytyrosine_1	0.708648566	PE 40:3	0.98772424
E-64_1	0.710000099	Leucylvaline	0.698249715	Valytryptophan	0.97999942
Asparaginytyrosine_1	0.708395007	Tetrahydroalstonine	0.683370942	MGDG 36:3 (2)	0.97701512
Tryptophytryptophan	0.701427392	Dehydro Ascorbic acid	0.674142774	2-Hydroxyphenylacetic acid	0.96337738
Leucythreonine	0.683150878	Phenylalanyarginine	0.669694447	Prolytyrosine	0.95887578
Theophylline-anhydrous_1	0.665131711	trans-Cyclohexane-1-2-dicarboxylic acid_1	0.667918254	DGDG 34:4 (2)	0.95567945
Tryptophyglutamic acid_1	0.661870647	N-Acetyl-L-Methionine	0.667199233	alpha-ketovaleic acid	0.948118
Tryptophyleucine	0.661786824	Oenin_1	0.667042762	Leucytyrosine	0.94360697

Arginytryptophan	0.659055882	Gibberellin A6	0.659238167	Pyroglutamic acid	0.93831808
Methionylglutamic acid	0.640877235	Citramalic acid	0.658366002	O-methyl-threonine	0.92491055
5-Methoxy-Tryptamin_1	0.640213533	Methionylvaline	0.653474431	Homoserine	0.9137763
Lysytyrosine	0.637166808	Isoleucyphenylalanine_1	0.651317588	PC 32:3 (4)	0.90017141
Tetrahydrofolic acid	0.635054455	Isoleucyalanine	0.648534724	Lysyleucine	0.89071856
Phenylalanyasparagine	0.63280527	Glutamymethionine_1	0.640375748	Ornithine	0.8706579
Q3G6-R7G_4.67_771.1984	0.632091789	TAG 48:3 (2)	0.630093537	Tryptophyleucine	0.86875506
Glutamylvaline	0.627717982	5-Phospho-D-ribose 1-diphosphate	0.625497388	Glycyl-L-tyrosine	0.84618092
K3G2-A_6.67_579.1348	0.626297078	Loganin_1	0.621389709	Phenylalanyphenylalanine	0.84204478
Tryptophyalanine	0.622763574	Rhamnose	0.620242413	Serine	0.83157467
Leucyphenylalanine	0.616063582	Isoleucyaspargic acid_1	0.613978176	Methionylphenylalanine	0.8291218
Isoleucylglutamic acid	0.615251741	Leucyalanine	0.611240274	Valylphenylalanine	0.82217094
Leucyasparagine	0.611833804	Tyrosylvaline_1	0.610375821	Tyrosine	0.8210866
Adenosine 2Â' monophosphate	0.610958339	Methionylisoleucine	0.607262514	MGDG 34:4	0.81447707
Phenylalanylglutamine	0.609121131	Leucylglutamic acid	0.604039014	Dehydroascorbic Acid Dimer	0.81060637
Tryptophylglycine	0.601139927	Riboflavin	0.598317308	4-Methyl-2-Oxovaleric acid	0.79405435
Tryptophytyrosine	0.600980676	Leucyphenylalanine	0.597336563	Tryptophyaspargic acid	0.78876501
Sedoheptulose	0.599108201	Phenylalanylglutamine	0.594579595	Threonyalanine_1	0.77247919
GlutaminyPhenylalanine	0.597398922	Isoleucylglutamic acid	0.589757725	Threonine	0.76898257
DAG 36:2	0.596108233	Ferulic acid	0.588587019	Glutamylaspargic acid	0.76110935
Glutathione	0.594542116	Alanylmethionine_1	0.584729987	MGDG 32:1 (1)	0.75722642
Aspartylvaline	0.58949417	Tryptophytyrosine	0.58186184	Aspartylvaline	0.74478198
CaffHex5_5.22_341.0879_1	0.589368771	Phenylalanytryptophan	0.576474624	AsparaginyIsolucine	0.74128294
Isoleucyalanine	0.582480113	Raffinose	0.564450721	Tryptophyarginine_1	0.72838652
Phenylalanyaspartic acid	0.582287469	Leucyleucine_1	0.547145725	beta-Hydroxynorvaline	0.71174308
Threonytyrosine	0.581840174	SinGlc_5.24_385.1133	0.544992146	Ribose-1-phosphate	0.70197926
Isoleucytryptophan_1	0.577994532	Theophylline-anhydrous	0.542875155	Ribulose 5-phosphate	0.70197926
Gibberellin A6	0.573380158	Aspartylvaline	0.54283306	Alanylglutamine	0.69111848
Phenylalanyphenylalanine	0.572924933	Phenylalanylysinine	0.541542639	Isoleucymethionine	0.68399711
Scopoletin	0.571915658	Tyrosymethionine	0.533553239	Kynurenine free base	0.68080465
Valyltryptophan	0.570561548	Pyridoxic acid	0.533144817	Tryptophyltryptophan_1	0.67345139
Phenylalanyarginine	0.565794025	Tryptophylglycine	0.51897795	Tryptophyisoleucine	0.67149882

Phenylalanylysine	0.564741993	Valytryptophan	0.518977397	PE 36:5	0.66935605
Leucyvaline	0.563030353	Tyrosyalanine	0.51877537	Flavin Mononucleotide	0.65488248
Tyrosyvaline_1	0.561914924	Phenylalanyaspartic acid	0.518424874	Methionine	0.65108574
Leucylglycine_1	0.560717953	Tyrosyleucine	0.518381575	PC 38:5	0.63666643
Leucyleucine_1	0.559062606	Histidylphenylalanine_1	0.516861023	PC 36:6	0.63576059
Glutamyleucine	0.556841487	TAG 44:1	0.514189114	Serpentine hydrogen 2-	0.63464699
Glycyl-L-alanine	0.556113735	Tyrosytyrosine	0.512835845	Isopropylmalate	0.63402302
asparaginyne	0.5556786	Indole-3-lactic acid	0.511681626	Tyrosyphenylalanine	0.63231548
Threonyphenylalanine	0.555623266	Scopoletin	0.508905471	PE 36:6	0.62835412
Isoleucyphenylalanine_1	0.555546303	Adenosine 2':3'-Cyclic monophosphate_1	0.506689686	LysoPE 18:0	0.60198134
Asparaginyphenylalanine_1	0.553891685	Tryptophyllysine_1	0.502280992	Glycyl-L-alanine	0.60006858
Valyleucine	0.552480358	MGDG 36:6 (1)	0.498636876	Prolin-4-Hydroxy 3-ureido-propanoic acid	0.59261791
Isoleucyaspatic acid_1	0.549348133	Rutin_1	0.497239463	Aspartaspartic acid	0.59209759
Threonytryptophan	0.543432805	Is3G2-A6-R_6.44_755.2034	0.496176057	Phenylalanyglutamine	0.58890994
Isoleucyserine	0.542143426	Phenylalanyvaline	0.493286708	Isoleucyvaline	0.58300083
Leucylglutamic acid	0.535207895	Tyrosyphenylalanine	0.488388494	Na-Acetyl-L-ornithine	0.58254366
Leucyvaline	0.53514573	Methionylglutamic acid	0.487446118	2-Deoxyadenosine 5-monophosphate	0.58070136
Threonyleucine	0.531359922	CafHex1_3.87_341.0879_1	0.481900708	Isoleucytryptophan	0.57971576
Glutaminyleucine	0.530577882	Tyrosylglycine	0.477838555	Tyrosytyrosine	0.56646449
Phenylalanyglutamine	0.529114213	Glutamyvaline	0.477177844	Glutamymethionine	0.56035502
Phenylalanytryptophan	0.528122326	Tryptophylglutamic acid_1	0.476453795	S-Adenosyl-L-Homocysteine	0.55881339
Tyrosyalanine	0.527191075	Isoleucytryptophan_1	0.471688866	phytoene_carotenoids related	0.55452395
Tyrosylglycine	0.524360815	Isoleucyisoleucine	0.470920347	Homogentisic acid	0.54908796
AsparaginyIsoleucine	0.524229736	Q3G2-A6-R_5.93_741.1879_1	0.470897379	Glutamyisoleucine	0.54535304
Isoleucyleucine_1	0.52077493	Alanyphenylalanine	0.469033906	Isoleucylglutamic acid	0.54505154
Lysytryptophan	0.516192846	Arginytryptophan	0.468179208	MGDG 34:3	0.54205324
Alanyphenylalanine	0.512879511	K3G2-A_6.67_579.1348	0.464405617	Phenylalanyglycine	0.53131866
Prolyisoleucine	0.511936626	Secologanin	0.459350578	Phenylalanyaspartic acid	0.52949803
Tyrosyphenylalanine	0.511269387	Mannose	0.455818016		0.52911441

Glutaminyltryptophan_1	0.510629996	Glucose	0.455199458	Ascorbic_Acid	0.52839233
Isoleucine	0.5106	Mannitol	0.455192699	Mannose	0.52675131
Tryptophyisoleucine	0.509354041	Valyleucine	0.451521806	Mannitol	0.52665494
Acetylsalicylic acid_1	0.501313174	Phenylalanythreonine	0.441970662	Leucythreonine	0.5263612
Tyrosylaspartic acid	0.50084097	DIMBOA-glucoside	0.437685644	Glucose	0.52347035
Malvin	0.498647836	Tyrosylaspartic acid	0.436996083	6-Hydroxynicotinic acid	0.5150068
Aspartylphenylalanine	0.498602352	Tryptophyleucine	0.436046126	(S)-6-Oxo-2-piperidinecarboxylic acid	0.51446067
Aspartyleucine_1	0.497701685	Sedoheptulose	0.433348929	Isoleucyleucine_1	0.51155359
NG2_8.09_433.2084_1	0.497392183	Tryptophyalanine	0.429700053	Leucymethionine_1	0.50712615
Prolytyrosine_1	0.491845965	Alanytryptophan	0.426118158	Leucine	0.49403003
Alanytryptophan	0.479314087	Methyl-beta-D-galactoside	0.425447929	Valine	0.49278494
Aspartic_Acid	0.4779	Phenylalanyglutamine	0.42418011	E-64	0.4837703
Biocytin	0.477607281	Isoleucyserine	0.422341057	Leucylglutamic acid	0.48258757
Aspartyltryptophan	0.475109007	K3G6-R7G_5.09_755.2031	0.42004922	Adenosine 2':3'-Cyclic monophosphate_1	0.47963847
Serylucine_1	0.473010366	Glucaric acid 1-4-lactone	0.417315963	Tyrosyleucine	0.47479818
DIMBOA-glucoside	0.467850549	TyrosylThreonine	0.415625742	Isoleucylaspartic acid	0.47413064
Alanyleucine	0.466899869	Tryptophylaspartic acid	0.413140661	Methionylisoleucine	0.47217646
Lutein_5.48_568.43	0.463721384	Tryptophylasparagine_1	0.407830216	Leucylglycine_1	0.46997519
Histidylphenylalanine_1	0.462741019	Karrikin 2	0.406942495	Glycine	0.4653524
Prolyphenylalanine	0.461705592	Tryptophyisoleucine	0.402190204	Secologanin	0.46050916
Loganin_1	0.461216243	Pentamidine	0.40020544	Gaba	0.46036552
Histidyleucine	0.460152319	Prolyphenylalanine_1	0.399999234	PC 32:1 (2)_1	0.45853036
Tryptophylvaline	0.456211363	Alanyleucine	0.39935165	Phenylalanine	0.45673509
Seryltryptophan	0.454891227	Quinic acid_1	0.399211361	Biocytin	0.44935421
Isoleucylglutamine	0.454515829	Reichstein's Substance S	0.396518899	Insitol_Myo	0.44576774
Lysylphenylalanine	0.453052209	4-5diCQA_7.11_515.12	0.396094131	Alanyphenylalanine	0.43937092
Glycyl-L-phenylalanine_1	0.449966044	SinGlciso1_5.09_385.1133	0.393392235	Phenylalanyltryptophan_1	0.43452674
Tyrosylglutamic acid	0.448604417	Quinic acid- 3-caffeoyl-N-Acetylmuramic acid	0.392062471	Asparaginemethionine	0.43372285
Arginyleucine	0.446513888	Neohesperidin	0.375450989	Arginylphenylalanine	0.43330726
Glutaminylvaline	0.446312948	H5FeruGlc1_3.92_371.0983	0.374243058	Isoleucylvaline	0.42406592
Tyrosyltyrosine	0.446051866		0.373414895	LysoPC 18:1_2	0.41778193

Phenylalanyisol eucine	0.443361775	Isoleucyleucine	0.372229553	LysoPE 16:0	0.41728937
Tyrosyleucine	0.434994518	Threonytyrosin e	0.3689288	DGDG 36:6 (2)	0.41700393
Valyisoleucine_ 1	0.432945692	TAG 50:7 (2)	0.363736765	Prolyisoleucine	0.41313643
Erythrose-4- phosphate	0.431980679	Prolyisoleucine	0.36360702	Seryisoleucine	0.410489
MGDG 34:3	0.425715222	Gibberellin A3	0.363464987	Asparaginyphe nylalanine_1	0.40985688
Asparaginythre onine	0.421637417	Prolytyrosine_1	0.362898605	Tryptophyaspa ragine_1	0.40742288
Serytyrosine_1	0.417596645	Glutamyleucin e	0.351953607	Phenylalanytyr osine	0.40574516
Is3G2- A_6.79_609.146 7	0.41267142	Tyrosyproline_ 1	0.349313366	Uridine	0.40297066
beta- Nicotinamide	0.412235154	3-Deoxy-D- manno-2- octulosonic acid	0.348906633	H5FeruGlc1_3. 92_371.0983	0.40091313
adenine dinucleotide	0.409869819	Aspartyleucine _1	0.348011514	Eicosapentaen oic acid- 5-8-11- 14-17-(Z-Z-Z- Z-Z)-	0.40045257
alpha- Ketovaleric acid	0.4082	3-4- Dihydroxybenz oic acid	0.345740385	p-Coumaric acid	0.39841303
beta- Hydroxynorvali ne	0.4073	3CGA_3.82_353 .0876	0.342312388	Gulonic_Acid_ 1-4-Lactone	0.39334448
O-methyl- threonine	0.405872403	Histidyltryptop han	0.340259269	Glutamyvaline	0.39313706
Tyrosylglutami ne	0.404218535	FerHex2_4.65_ 355.1031	0.332705283	Leucyleucine_1	0.38926268
Ribose-5- Phosphate	0.402575922	5CGA_4.58_353 .0876	0.328641725	Glutathione	0.38824863
DAG 34:2	0.401973321	Pyridoxine Vit B6	0.319891068	2-methyl-2- phenylacetalde hyde oxime	0.38723688
Phenylalanythr eonine	0.401025017	Acetylsalicylic acid_1	0.317149349	Threonyleucine	0.38110425
Aspartyaspartic acid	0.399852914	Asparaginytyro sine_1	0.316213482	Tyrosyvaline	0.3758242
TAG 54:9	0.393175035	TAG 50:6 (3)	0.316132829	Genistein	0.369324
Isoleucyvaline	0.392266292	Kynurenine free base_1	0.313547855	PC 34:3_1	0.36126558
TyrosyThreoni ne	0.392074804	Glutaminytrypt ophan	0.31238937	Cytidine 5Å'- monophosphat e_1	0.35801996
Leucyisoleucin e	0.391832718	Aspartylphenyla lanine	0.311632566	LysoPC 16:0	0.35686825
Arginyphenylal anine	0.391340153	Threonyleucine	0.309882219	Valyisoleucine_ 1	0.35284956
Lysyleucine	0.3906	Serymethionine	0.308350833	Leucyalanine	0.3430931
Serine	0.38877951	Cyanidin-3-O- arabinoside	0.302061775	Loganin_1	0.33184317
MGDG 36:5 (1)	0.378949346	TAG 44:2	0.293651656	Phenylalanyleu cine_1	0.32787753
11beta- Hydroxyproges terone_1	0.377033748	Seryphenylalan ine_1	0.292775399	Glutaminyleuci ne	0.32755207
Lysyserine	0.374755308	Adenosine	0.289147401	LysoPC 18:0	0.32484288
Tetrahydroalst onine_1	0.3744	3- Hydroxyanthra nilic acid	0.287772069	Alanyleucine	0.31426605
Tryptophan- N-acetyl-					

N-Ethylmaleamic acid	0.367721381	3-5diCQA_7.48_515.12	0.287641058	Pyridoxine Vit B6	0.31205097
Glutamylisoleucine_1	0.366105339	Prostaglandin A(2) solution_1	0.287029176	Tyrosylglycine	0.310114
MGDG 32:0	0.361487211	Lysytryptophan	0.285898485	Glycyl-L-isoleucine_1	0.2933634
Lysylglycine	0.3546372	K3G2-A6-R_6.36_725.1929	0.284002051	Palmitic_Acid	0.29210537
Citramalic acid	0.354410794	Alanytyrosine	0.283585022	Adenosine	0.28841823
Pyridoxic acid	0.353755257	Corticosterone	0.28222348	Serytyrosine_1	0.28690075
Glycyl-L-tryptophan	0.351139434	Glycyl-L-phenylalanine_1	0.279489956	Isoleucyphenylalanine_1	0.28401558
TAG 50:6 (2)	0.33971938	Aspartytryptophan	0.278429085	Leucyphenylalanine	0.28107866
DAG 36:6	0.333731386	Glutamylglutamic acid	0.277180556	Valyleucine	0.27556296
Glycyl-L-tyrosine	0.332149531	5'-Deoxy-5'-(methylthio)adenosine	0.276338729	DAG 36:6	0.27422759
Phenylalanyvaline	0.328470351	3-6-anhydro-D-Galactose	0.272747632	Citramalic acid	0.27402545
Quinic acid_1	0.325910529	Methionylglycine	0.270221633	Pyridoxic acid	0.27380421
Q3G2-A6-R_5.93_741.1879_1	0.311641287	Seryleucine_1	0.268010744	LysoPE 18:2	0.2707223
Proline	0.3116	Isoleucyglutamine	0.267933938	Abciscic acid	0.26997272
3-Deoxy-D-manno-2-octulosonic acid	0.309793041	Shikimic acid-3-phosphate	0.266107243	Sucrose_1	0.26486093
Alanylysine	0.305030651	Aspartic acid	0.265728399	N-Ethylmaleamic acid	0.26366571
4-5diCQA_7.11_515.12_1	0.29945341	Tryptophyvaline	0.264345202	Tryptophan	0.26321802
CafGluc3_3.51_371.0618	0.291348104	Caffeic acid_1	0.262895354	DGDG 38:6 (1)	0.24494386
H5FeruGlc1_3.92_371.0983	0.2886684	Isoleucyvaline	0.257415551	LysoPC 18:3_1	0.24334248
Seryvaline	0.288422818	3-4-5triCQA_8.99_677.1522	0.253830367	3-6-anhydro-D-Galactose	0.24055117
2-methyl-2-phenylacetaldehyde oxime	0.287343068	Asparaginyphenylalanine_1	0.244484023	sn-Glycerol 3-phosphate	0.23797469
Riboflavin	0.283755535	Valyisoleucine_1	0.242263887	Inosine	0.23306887
sn-Glycerol 3-phosphate	0.282301089	asparaginyneucine	0.237536543	Seryleucine_1	0.23283001
Pyridoxamine-5'-phosphate (PMP)	0.277950692	p-Coumaric acid	0.234685294	PE 34:3	0.23033303
Adenosine	0.277702058	Prolythreonine	0.23048546	DGDG 32:3 (1)	0.22908518
Methionylglycine	0.276808016	Quercitrin	0.224729293	Tryptophan-N-acetyl-	0.22746489
Tryptophyaspartic acid_1	0.274224337	Prolyglutamine	0.220877769	Aspartyleucine_1	0.22564514
Isoleucylisoleucine	0.271764949	Threonytryptophan	0.220065042	Methionyleucine	0.22418314
Phenylalanyleucine	0.267575318	Gentisic acid	0.219741519	QGRAGFer_6.06_1079.288	0.2179524

Alanyvaline	0.266587879	N-Acetylneuraminic acid_1	0.217905808	Phosphoric_Acid	0.21069852
Glycyl-L-isoleucine_1	0.2623297	S-Adenosyl-L-Homocysteine	0.214394894	Guanosine	0.20946339
Guanosine 2':3'-cyclic monophosphate	0.25239153	Tyrosylglutamic acid	0.20836765	Glutamyleucine	0.20901076
3-4-5triCQA_8.99_677.1522	0.244487085	Glutaminyleucine	0.206425266	Glycyl-L-phenylalanine_1	0.20892854
3-Hydroxyanthranilic acid	0.243442848	Serytryptophan	0.20503382	Hesperetin-7-O-glucoside	0.2086675
5'-Deoxy-5'-(methylthio)adenosine	0.242074442	Leucyisoleucine	0.197804783	Pantothenic acid (Vitamin B5)	0.20061401
Glucaric acid 1-4-lactone	0.240680635	AsparaginyTryptophan	0.19774615	LysoPC 18:2_2	0.20034653
Secologanin	0.240344062	Tryptophytryptophan	0.197195227	Glutaminylphenylalanine	0.19391208
Ferulic acid	0.23457591	Biocytin	0.193656838	Erythrose-4-phosphate	0.19077811
TAG 48:3 (2)	0.229764371	N-Ethylmaleamic acid	0.186024941	Seryphenylalanine_1	0.18882529
Tyrosyisoleucine	0.225304025	Glutaminylphenylalanine	0.182936263	5?-Deoxy-5?-(methylthio)adenosine	0.17827563
Caffeic acid_1	0.220206704	Lysylphenylalanine	0.182377316	Gibberellin A3	0.17342653
Threonyisoleucine	0.22010908	Tryptophan	0.177823335	Phenylalanyglutamic acid	0.17163841
Phenylalanytyrosine	0.213676947	Tryptophythyreonine	0.175470094	trans-zeatin-O-glucoside	0.14721426
Seryisoleucine	0.210882984	Tryptophan-N-acetyl-Glutaminylvaline	0.169674702	Succinoadenosine	0.13574732
Purine	0.208689712	alpha-L-(-)-Fucose-1-Phosphate	0.169389723	MGDG 36:6 (1)	0.12863018
SinGlc_5.24_385.1133	0.201610742	3-4diCQA_6.96_515.12	0.162799367	N-Carbamyl-DL-aspartic acid	0.11472554
Cyanidin-3-O-arabinoside	0.199312494	Isoleucine	0.161019203	Guanosine 2':3'-cyclic monophosphate	0.09094263
Citric acid	0.198315916		0.160395992	3-Deoxy-D-manno-2-octulosonic acid	0.06371147
3-5diCQA_7.48_515.12	0.197614126	TAG 54:9	0.159042397	11A-Hydroxyprogesterone_1	0.06286461
Saccharic acid	0.186893113	Tyrosyisoleucine	0.158737533	Thymidine_1	0.04137846
Oenin_1	0.183240514	Arginylphenylalanine	0.157855213	GlcCer t18:1/h24:0	-0.08716536
Glutamytyrosine	0.178140453	Serytyrosine_1	0.155223495	GlcCer t18:1/h22:0	-0.09775864
AsparaginyTryptophan	0.167390973	Suberic acid	0.154012313	5-Phospho-D-ribose 1-diphosphate	-0.10008572
6-phosphogluconic acid	0.156928929	5-6-Dimethylbenzimidazole	0.143710262	Citric acid	-0.1148123
Tyrosyproline	0.154200747	TAG 48:4	0.128124936	MGDG 38:4	-0.1151392

Reichstein's Substance S	0.147759013	Pantothenic acid (Vitamin B5)	0.12367876	Threonylphenyl alanine	-0.13247578
Guanosine	0.147506003	N-Acetyl-L-Tyrosine	0.114590335	Cer t18:0/h24:1	-0.14603854
Histidylserine	0.142310721	Lysylleucine	0.111265226	Pyruvic_Acid	-0.14621712
3-6-anhydro-D-Galactose	0.138725721	Guanosine	0.109196125	Quercetin-3-D-galactoside_Saleh_standards_463.098_6.98	-0.15031334
Deoxycorticosterone_1	0.134839945	Saccharic acid	0.108420465	Quercetin-3-beta-D-glucoside	-0.15125461
Orotic acid- 4-5-dihydro-	0.128855013	Quercetin-3-beta-D-glucoside	0.102372734	Rutin_1	-0.16288034
Suberic acid	0.087622294	Guanosine 2':3'-cyclic monophosphate	0.089793603	Diethyl succinate_1	-0.16457331
Quercetin-3-beta-D-glucoside	0.077811591	beta-Hydroxynorvaline	0.085466271	DGDG 38:5 (2)	-0.16517467
Thymidine 5'-monophosphate	0.075951876	Glutamylisoleucine_1	0.08357756	Kaempferol	-0.16920643
Tyrosine	-0.0438	Malic acid	0.075729537	3-Hydroxyanthranilic acid	-0.17371089
Homocystine	-0.0539	Alanylvaline	0.066428937	MGDG 34:0	-0.19127151
3-4-Dihydroxybenzoic acid	-0.058005817	K3G7G_6.14_609.1462	0.064592287	Q3G6-R7G_4.67_771.1984_1	-0.19548219
TAG 50:3 (1)	-0.061913306	p-Nitrophenyl alpha-D-mannopyranoside	0.053445628	Asparagyltryptophan	-0.20554196
Prolylglutamine	-0.075654234	Thymidine_1	0.031452482	Kaempferol 3-O-glucosyl-glucoside 7-O-rhamnoside	-0.21563946
Melezitose	-0.084775865	Alanylysine	-0.049199431	GlcCer d18:1/h16:0	-0.21986238
p-Nitrophenyl alpha-D-mannopyranoside	-0.092472422	Histidylserine	-0.070190425	3-4diCQA_6.96_515.12	-0.22161135
Sucrose	-0.095643998	Aspartylaspartic acid	-0.084564859	Valylmethionine	-0.22346191
Azelaic acid	-0.096489732	Sucrose	-0.0864879	Prolylthreonine	-0.23179185
Salicin	-0.112709129	Tetrahydrofolic acid	-0.09894491	Lycopene_1	-0.2352886
TAG 48:2_1	-0.113923308	Nalpa-Acetyl-L-ornithine	-0.104305245	Neohesperidin	-0.25008052
Pyroglutamic acid	-0.1459	Arbutin	-0.118535117	Propanoic acid- 3-(2-4-dihydroxyphenyl)-	-0.25610326
Indole-3-lactic acid	-0.153698208	Serylvaline	-0.121358242	Naringenin chalcone_Saleh_standards_271.061_10.44	-0.25671506
quercetin-3-O-(2''-O-rhamnosyl)glucoside-7-O-rhamnoside	-0.169617544	sn-Glycerol 3-phosphate	-0.126789695	Galactonic_Acid	-0.25701637

TAG 48:1_1	-0.180163884	Cellobiitol	-0.153445382	Quinic acid- 3-caffeoyl-GlcCer t18:1/h26:0 Cer t18:0/h24:0	-0.26171575
Valeric acid-(5-amino)-4-hydroxy-3-indolylmethyl-glucosinolate 6-7	-0.222243749	Valeric acid-(5-amino)-3-Hydroxy-3-Methylglutaric acid	-0.163898256		-0.27429896
Dimethylrihityl lumazine	-0.234120468	Erythrose-4-phosphate	-0.16437902		-0.27471314
Asparaginymenthionine	-0.271433164		-0.165040057	Malic_Acid_2-Methyl	-0.27515975
PGGPE	-0.319137404	Valyhistidine	-0.172050031	FerHex2_4.65_355.1031	-0.27589731
Tryptophan	-0.322503378	Succinoadenosine	-0.182791192	Theophylline-anhydrous	-0.27878177
	-0.3335	Cer t18:0/h24:0	-0.183207707	5CGA_4.58_353.0876	-0.2836086
Propanoic acid- 3-(2-4-dihydroxyphenyl)-	-0.358242773	quercetin-3-O-(2"-O-rhamnosyl)glucoside-7-O-rhamnoside	-0.188732913	Methionylvaline	-0.29002398
Cellobiitol	-0.368838483	11A-Hydroxyprogesterone_1	-0.192145065	3CGA_3.82_353.0876	-0.30343257
Kaempferol	-0.394514247	Cer t18:1/h22:0	-0.198614339	Acetylsalicylic acid_1	-0.3094181
Eicosapentaenoic acid- 5-8-11-14-17-(Z-Z-Z-Z-Z)-11A-Hydroxyprogesterone	-0.459923193	Isoleucythreonine	-0.204665474	Tomatine	-0.31131956
N-Acetylmuramic acid_1	-0.463290454	Threonyphenyl alanine	-0.221254262	PC 34:2	-0.3176405
Trehalose-alpha-beta-DGDG 36:1 (2)	-0.496599185	Cer t18:1/h20:0	-0.221904633	Pentamidine	-0.32991601
Glycerol	-0.521548895	Cer t18:0/h22:0	-0.230385581	Cer t18:0/h22:0	-0.34160468
(S)-6-Oxo-2-piperidinecarboxylic acid	-0.52927013	Adenosine 5'-monophosphate	-0.259994215	Tyrosyproline_1	-0.34758091
Shikimic acid-3-phosphate	-0.564363565	Dopamine	-0.260000125	Riboflavin	-0.35114823
Galactonoil	-0.650896564	Threonyisoleucine	-0.263074938	TAG 44:0	-0.3574835
Glycyl-L-valine	-0.73086594	Uridine-5'-diphosphogalactose	-0.275742221	4-5diCQA_7.11_515.12_1	-0.35769339
	-1.015257349	Lysylglycine	-0.27919555	Quinic acid_1	-0.36234228
	-1.330149033	Seryisoleucine	-0.29457427	Maltose	-0.36334444
		4-Methyl-2-Oxovaleric acid	-0.298346104	Prolyglutamine	-0.36354709
		Eicosapentaenoic acid- 5-8-11-14-17-(Z-Z-Z-Z-Z)-Methionylhistidine	-0.303412157	Beta-Sitosterol_(1Tms)	-0.36647159
		MGDG 36:2	-0.333678827	3-4-Dihydroxybenzoic acid	-0.36887125
		DGDG 36:1 (2)	-0.349661205	PE 34:1	-0.36893917
		Asparaginyvaline_1	-0.389524547	Putrescine	-0.37659704
		N-Acetyl-D-Phenylalanine	-0.413088225	Quercetin	-0.37885193
			-0.517604955	N-Formyl-L-Methionine	-0.39165658

Cer t18:0/c16:0	-0.541341942	Erythrose	-0.40432204
Threonyvaline	-0.610802508	GPEP	-0.41396484
Arginysoleucine	-0.645757722	TAG 56:0	-0.41703578
Glycyl-L-valine	-1.240222731	Q3G2-A6-R_5.93_741.187_9_1	-0.41877079
		Naringin dihydrochalcone	-0.4202972
		3-5diCQA_7.48_515.12	-0.42324487
		Cer d18:1/h16:0	-0.4248726
		Luteolin_1	-0.44716834
		TAG 54:9	-0.4510569
		Tryptophyvaline	-0.45456701
		Asparaginytyrosine	-0.4582771
		Cystein_S_Met hyl	-0.46471285
		3-4-5triCQA_8.99_677.1522	-0.46777992
		Cer t18:1/h22:0	-0.47430332
		Morin	-0.47530256
		Dehydroascorbic_Acid	-0.47913723
		TAG 46:0	-0.48275467
		4CGA_5.25_353.0876_1	-0.4901105
		TAG 44:1	-0.49079087
		PC 38:3 (1)	-0.50149289
		N-Acetyl-L-Tyrosine	-0.51532408
		Lyso_MGDG 18:2 (1)	-0.52786495
		Malic_Acid	-0.52989869
		TAG 58:0	-0.53071292
		DIMBOA-glucoside	-0.53560866
		PC 36:1	-0.54108735
		Raffinose	-0.54360061
		PC 34:1	-0.54450541
		Tyramine	-0.56591184
		Oenin_1	-0.56647125
		Phenylalanythreonine_1	-0.56919673
		alpha_carotene_11.92_536.445	-0.56996842
		Zeaxanthin	-0.57270497
		PC 36:3 (1)	-0.58239406
		Sedoheptulose	-0.59047842
		TAG 46:1	-0.5937096
		Serjanic acid saponin # 1	-0.59961654

Galacturonic_Acid	-0.60967934
Tyrosymethionine	-0.61103993
Eriodictyol	-0.64316715
Melbose	-0.64666087
DAG 36:5	-0.65637447
PC 36:4 (2)	-0.66973823
Histidylserine	-0.67412333
PE 38:3 (2)	-0.69062283
PC 36:2	-0.696431
TAG 50:0	-0.70449907
Melezitose	-0.71388539
Glucuronic_Acid_Lactone	-0.72830025
Shikimic acid-3-phosphate	-0.73086594
MGDG 34:1	-0.76618887
TAG 52:0	-0.76750232
PC 32:2 (1)	-0.77155007
Allantoin	-0.77298477
DGDG 34:0 (2)	-0.77681428
5-6-Dimethylbenzimidazole	-0.78155617
Dexamethasone	-0.78164459
Methionylglycine	-0.82226415
DGDG 34:1	-0.83231748
TAG 54:0	-0.8647639
Cyanidin-3-O-arabinoside	-0.89141846
TAG 48:0	-0.90329179
TAG 52:6 (1)	-0.90360239
Catechin	-0.90866038
Benzoic_Acid_3,4-Dihydroxy	-0.92730532
TAG 58:5	-0.93056859
Is3G2-A6-R_6.44_755.2034_1	-0.96247318
Arbutin	-1.02442645
TAG 54:8	-1.02828241
QGRAHO5Fer_6.77_933.2288	-1.04904897
Alanytyrosine	-1.0582851
TAG 42:1	-1.06519218
Glutaminyltryptophan	-1.1111497
Naringenin	-1.2032454
DAG 36:2	-1.22816334
DAG 34:2	-1.29069677

TAG 52:7 (1)	-1.30977492
TAG 48:3 (2)_1	-1.37473256
3-Hydroxy-3-Methylglutaric acid	-1.3788115
Alanyglutamic acid	-1.38178107
Isoleucyisoleucine	-1.39304728
Is3G7G_6.22_639.1567	-1.39665676
Tyrosyisoleucine	-1.4165695
TAG 50:3 (1)	-1.4605647
Tetrahydrofolic acid	-1.46872924
TAG 52:5	-1.47153417
Tryptophyalanine_1	-1.48490704
TAG 52:8 (1)	-1.57847737
p-Nitrophenyl alpha-D-mannopyranoside	-1.58578756
TAG 56:7	-1.59617595
TAG 48:1_1	-1.63001725
TAG 52:4_1	-1.66383487
Mesaconic acid	-1.75461591
TAG 54:6	-1.7648138
Scopoletin	-1.77941773
TAG 54:7	-1.79786129
TAG 60:5 (2)	-1.80725409
TAG 54:5	-1.8164505
TAG 44:4	-1.81852656
beta_Carotene_12.15_536.4455	-1.82411375
TAG 58:4	-1.82883111
TAG 52:3_1	-1.85663878
SinGlc_5.24_385.1133	-1.85897535
TAG 58:3	-1.85967194
DAG 36:4	-1.87572997
TAG 54:4	-1.88949489
SinGlciso1_5.09_385.1133	-1.90147872
PE 36:1	-1.91223731
TAG 52:2_1	-1.91489176
TAG 50:2 (2)	-1.938917
TAG 56:4	-2.0209908
TAG 58:1	-2.02212275
TAG 54:3	-2.04320102
TAG 50:1_1	-2.04499042
TAG 58:2	-2.05494517

TAG 50:4 (1)	-2.06016598
Malvin	-2.07503104
K3G7G_6.14_60 9.1462	-2.07920467
DGDG 36:1 (2)	-2.10606847
TAG 60:2	-2.10747541
TAG 54:2	-2.17251195
TAG 52:1	-2.19650045
TAG 60:3	-2.21788254
TAG 56:2 (1)	-2.21805385
K3G2- A_6.67_579.134 8	-2.23221871
Tryptophylglyc ine_1	-2.23733111
DAG 36:3 (1)	-2.26111852
TAG 56:3	-2.27086094
2-3- Dimethylsucc inic acid	-2.28266067
TAG 60:1	-2.31994207
Indole-3-lactic acid	-2.39141138
TAG 48:4	-2.39275995
TAG 60:4	-2.44789671
TAG 54:1	-2.49923216
Q3G7G_5.68_6 25.1412	-2.54891674
Cer t18:1/h20:0	-2.56786513
TAG 56:1 (1)	-2.57227419
Aspartic_Acid	-2.59733062
Glycyl-L- tryptophan_1	-2.80559818
TAG 50:5 (3)	-2.95055109
TAG 50:7 (2)	-3.22360559
TAG 50:6 (3)	-3.45751418

Supplemental Table 5. Metabolites detected in red tomato fruit from S1SGT3-ox lines 9 and 31 vs WT filtered by p-value 0.05. Values correspond to lines 9 and 31 Log10 fc vs WT median.

Compound	Line 9	Compound	Line 31
N-Acetylneuraminic acid	3.98702564	Leucine	4.003738269
Leucine	3.96433445	Glucose-1-Phosphate	3.942705424
Sucrose	3.932108264	N-Acetylneuraminic acid	3.892690154
Glucose-1-Phosphate	3.642271795	Threonic_Acid	3.507752893
Ethanolamine	3.283547997	Histidine	3.269775359
Threonic_Acid	3.257889927	Glycerol-2-Phosphate	2.773068919
Histidine	3.20714165	Threonytyrosine	2.527128343
Glycerol-2-Phosphate	3.14052353	Benzoic_Acid	1.967934354
Threonytyrosine	2.475576036	O-methyl-threonine	1.527690635
Glycerol	2.006336921	Glutamine	1.436437395
Benzoic_Acid	1.980088428	Apigenin-7-glucoside	1.407317041
TAG 60:6 (1)	1.707818344	5-Methoxy-Tryptamin	1.387209817
Ascorbic_Acid	1.694960304	TAG 58:6	1.360105043
TAG 60:7	1.616677289	TAG 60:7	1.298142463
TAG 58:6	1.585173785	TAG 60:6 (1)	1.271567584
O-methyl-threonine	1.471733147	Sucrose	1.269268758
5-Methoxy-Tryptamin	1.408848638	beta-Hydroxynorvaline	1.26003365
Apigenin-7-glucoside	1.341008352	Proline	1.254123651
Sucrose	1.316744024	Isoleucine	1.23105496
O-methyl-threonine (2)	1.222145911	Leucyvaline	1.206982196
beta-Hydroxynorvaline	1.217033614	alpha-Ketovaleric acid	1.177090844
Proline	1.205055761	Glutaric_Acid_2Oxo	1.174813467
alpha-Ketovaleric acid	1.12117866	O-methyl-threonine (2)	1.146890608
Isoleucine	1.113318794	Proline	1.127332297
Aspartic_Acid	1.065062275	3-indolymethyl glucosinolate	1.126140041
Leucyvaline	1.030287838	LysoPE 18:1	1.120334462
Proline	1.024191574	Valytryptophan	1.109481801
Glutaric_Acid_2Oxo	0.999752403	Sucrose	1.026455797
Isoleucytryptophan	0.974362641	Q3G2-A6-R_5.93_741.1879	0.982387928
Valytryptophan	0.972123782	Saccharin	0.965270864
Trehalose_Alph_Alph	0.947160277	Lactic_Acid_219	0.918455771
Lactic_Acid_219	0.942526217	Isoleucytryptophan	0.899933519
Q3G2-A6-R_5.93_741.1879	0.892275309	Aspartic_Acid	0.894577917
N-Acetylmuramic acid	0.85583825	AsparaginyIsoleucine	0.88993807
Sucrose	0.809483704	Calystegine_A	0.861879144
2-Hydroxyphenylacetic acid	0.807147586	Calystegine_B2	0.861879144
Phenylalanyvaline	0.804452268	Phenylalanyvaline	0.847089122
2_Glucuronic_Acid_Lactone	0.802234257	Tryptophyarginine	0.847010712
Dehydroascorpic_Acid_Dimer	0.800584321	Isoleucine	0.842420146
Cysteine	0.790803961	Trehalose_Alph_Alph	0.830950029
Glutamine	0.790387937	alpha-L-(-)-Fucose-1-Phosphate	0.82681082

Saccharin	0.790184906	CafHex2_4.09_341.0879	0.822258916
3-indolymethyl glucosinolate	0.788720105	Methionylphenylalanine	0.791471312
Isoleucine	0.78572151	Leucytyrosine	0.785192714
Pyridoxamine-5'-phosphate	0.774939483	2-Hydroxyphenylacetic acid	0.777688778
Tyrosine	0.764306766	beta-hydroxycapric acid	0.756451086
alpha-L-(-)-Fucose-1-Phosphate	0.757211202	Tryptophyisoleucine	0.750264256
CafHex2_4.09_341.0879	0.675167586	Glutaminyglutamic acid	0.749066056
Valylphenylalanine	0.669797126	QGRAGFer_6.06_1079.288	0.742768445
Leucytyrosine	0.665868418	LysoPE 18:3	0.741579458
Prolyphenylalanine	0.651810392	Valylphenylalanine	0.726801563
Glutaminyglutamic acid	0.634843624	FerHex2_4.65_355.1031	0.717310062
Tryptophyarginine	0.633245879	Serpentine hydrogen	0.71623044
Insitol_Myo	0.631010341	Tyrosytyrosine	0.697316128
CafHex5_5.22_341.0879	0.630296708	N-Acetylmuramic acid	0.678862475
Pyroglutamic acid	0.603897902	Alanylphenylalanine	0.676472089
Asparagine	0.601354848	Glutamyaspartic acid	0.675186642
Calystegine_A	0.600123859	MGDG 36:2	0.672331298
Calystegine_B2	0.600123859	Dehydroascorpic_Acid_Dimer	0.662020198
Threonine	0.589609427	Threonine	0.66189973
Tyrosytyrosine	0.589370096	Pyroglutamic acid	0.659245845
AsparaginyIsoleucine	0.589028121	Flavin Mononucleotide	0.656193456
Ornithine	0.587907027	Tyrosyleucine	0.649079222
Tryptophyisoleucine	0.58157087	Prolytyrosine	0.646580366
Aspartyvaline	0.577341857	Leucythreonine	0.641301598
TAG 52:6 (2)	0.573311721	Asparagine	0.62338446
Tetrahydroalstonine	0.570662219	Phenylalanine	0.621170893
Glutamyaspartic acid	0.563369583	Lysine	0.615622225
Prolytyrosine	0.547669964	Tetrahydroalstonine	0.610703679
Fucose	0.540662646	4-Methyl-2-Oxovaleric acid	0.601288723
Adipic acid	0.536323264	Leucylglutamic acid	0.596960132
Phenylalanine	0.532101048	Eicosapentaenoic acid-5-8-11-14-17-(Z-Z-Z-Z-Z)-	0.594099905
Alanylphenylalanine	0.524291125	Insitol_Myo	0.592923633
Isoleucyalanine	0.517910667	Tyrosyphenylalanine	0.591121949
Methionylphenylalanine	0.510218502	DGDG 34:4 (2)	0.580021369
QGRAGFer_6.06_1079.288	0.506267408	Isoleucyalanine	0.571073013
Tyrosyleucine	0.495032747	Aspartyvaline	0.567441544
LysoPE 18:1	0.48471709	TAG 52:6 (2)	0.555710698
Adenosine 2':3'-Cyclic monophosphate	0.484709212	Glutamine	0.549867671
FerHex2_4.65_355.1031	0.48340494	Valylphenylalanine	0.548796483
4-Methyl-2-Oxovaleric acid	0.481480769	Ribose-1-phosphate	0.547136946
Flavin Mononucleotide	0.472810957	Ribulose 5-phosphate	0.547136946
Tyrosyphenylalanine	0.467580142	Adenosine 2':3'-Cyclic monophosphate	0.546511318
Pyridoxine	0.460401144	Phenylalanyglutamine	0.531274722

Lycopene	0.455074304	Isocitric_Acid	0.529617649
Serpentine hydrogen	0.450946292	2_Insitol,_Myo	0.529444571
Ribose-1-phosphate	0.446631359	Phenylalanyaspartatic acid	0.528340306
Ribulose 5-phosphate	0.446631359	Fucose	0.522276109
H5FeruGlc1_3.92_371.09 83	0.437682538	cis-Aconitic acid	0.522145863
Glutamine	0.432740197	Isoleucyleucine	0.519931964
Serine	0.431730167	Leucytyrosine	0.514686152
Homogentisic acid	0.431554225	Phenylalanylglycine	0.513764494
2-Isopropylmalate	0.429254754	CafHex5_5.22_341.0879	0.510054265
Phenylalanyaspartatic acid	0.419764141	Pelargonin	0.501298826
Loganin	0.412793025	Ascorbic_Acid	0.498244083
Leucylglutamic acid	0.409938185	Glutamymethionine	0.497800197
S-Adenosyl-L-Homocysteine	0.408762164	Leucymethionine	0.488596898
Phenylalanylglycine	0.405006157	N-Ethylmaleamic acid	0.477926249
Isoleucyaspatic acid	0.402046967	Prolyphenylalanine	0.477245634
N-Ethylmaleamic acid	0.395696642	Mannose	0.473589473
Uridine	0.391448513	Glucose	0.473488418
Adenosine 5'-monophosphate	0.385321724	Mannitol	0.473488418
Eicosapentaenoic acid-5-8-11-14-17-(Z-Z-Z-Z-Z)-	0.380250323	PE 38:3 (3)	0.468390853
MGDG 34:4	0.379145886	Leucylglycine	0.457733852
PE 40:3	0.377846586	Lycopene	0.456370292
Gulonic_Acid_1-4-Lactone	0.373130242	Adenosine 5'-monophosphate	0.456019528
6-methylthiohexylglucosinolate	0.372748245	DGDG 36:3 (1)	0.454752667
Isoleucyvaline	0.362651126	Isoleucyaspatic acid	0.45280785
Leucythreonine	0.353440436	Leucyleucine	0.449565193
Kynurenine free base	0.353403634	PE 40:3	0.445043725
Tryptophan	0.34623423	Kynurenine free base	0.444788813
Apigenin-7-glucoside	0.343316591	Ornithine	0.444001001
Valyphenylalanine	0.337840989	Tyrosyvaline	0.442499534
2-Deoxyadenosine 5-monophosphate	0.337293568	11A-Hydroxyprogesterone	0.44092198
Tyrosylglycine	0.332548228	E-64	0.439685532
Pelargonin	0.328648388	H5FeruGlc1_3.92_371.09 83	0.434302213
6-7 Dimethylrihityl lumazine	0.328108047	2-Methylcitric acid	0.433354206
Urea	0.327377691	Apigenin-7-glucoside	0.431358942
Isoleucylglutamic acid	0.322607765	Glyceric_Acid	0.429353189
Orotic acid	0.321162546	PC 32:3 (4)	0.42895659
Galactonic_Acid	0.312434409	Tryptophan	0.426010116
Phenylalanyglutamic acid	0.311828599	Glutamyvaline	0.42576001
5?-Deoxy-5?-(methylthio)adenosine	0.311767184	2-Isopropylmalate	0.423577256
2_Insitol,_Myo	0.310918882	Phenylalanyleucine	0.418436516
Methionine	0.30319533	Pyridoxine	0.415884314

Lysytryptophan	0.299457855	Isoleucylglutamic acid	0.409006998
hesperidine_Saleh_standards_609.18_7.93	0.298393844	Cyanidin-3-O-arabinoside	0.406933817
Isoleucyleucine	0.294691572	Serine	0.404473255
Phenylalanylgutamine	0.287496375	PE 36:5	0.403918647
Glutamylisoleucine	0.285490999	(S)-6-Oxo-2-piperidinecarboxylic acid	0.403139089
Myricetin-3-O-Glucoside_Saleh_standards_479.08_6.36	0.283023608	Trehalose	0.400779737
Glutathione	0.277549588	Glutamylisoleucine	0.399710829
Indole-3-acetamide	0.270308741	Oenin	0.394827338
Mannose	0.26815728	Homogentisic acid	0.390426238
Glucose	0.268136859	Uridine	0.387783559
Mannitol	0.268136859	Asparaginyphenylalanine	0.386611148
DGDG 38:6 (1)	0.265993027	Leucine	0.379760445
Asparaginyphenylalanine	0.264367684	Prolyisoleucine	0.377314056
Glutamylvaline	0.262322976	6-methylthiohexylglucosinolate	0.376875464
H5Ferulic1_3.92_371.0983	0.259678628	Loganin	0.372812681
Phenylalanytyrosine	0.259595291	MGDG 34:4	0.371199118
(S)-6-Oxo-2-piperidinecarboxylic acid	0.259070863	TAG 46:2 (2)	0.370122732
Glutamic acid- N-acetyl-	0.257056317	Tryptophan	0.366361963
Naringin	0.256437746	Sinapoylgucose	0.356580194
dihydrochalcone		Glutathione	0.355985885
Prolyisoleucine	0.251786252	Isoleucylvaline	0.353786208
Caffeic acid	0.250882843	Serylisoleucine	0.353191884
DGDG 34:4 (2)	0.24593129	Tyrosylglycine	0.351990589
PE 36:5	0.243972231	Glycyl-L-phenylalanine	0.350410786
DAG 36:6	0.237153456	Naringin	0.348130824
Tyrosine	0.231775387	dihydrochalcone	
Cyanidin-3-O-arabinoside	0.231031612	Homoserine	0.347915506
4-Hydroxyphenylpyruvic acid	0.230593807	Phenylalanytyrosine	0.34725838
3-6-anhydro-D-Galactose	0.227526701	Isoleucylphenylalanine	0.345453432
Serylisoleucine	0.225831628	Genistein	0.344311928
2-Methylcitric acid	0.224013453	Threonylvaline	0.343173645
Tryptophan	0.223070774	LysoPC 18:3_2	0.342115058
Glucose-6-Phosphate	0.221893538	2-Deoxyadenosine 5-monophosphate	0.334630448
Leucine	0.22165106	2_Citric_Acids	0.333588758
Adenosine	0.221388125	DAG 36:6	0.332053537
TAG 46:2 (2)	0.216338989	Valylisoleucine	0.3318944
Guanosine	0.214799107	LysoPE 18:0	0.33030267
Rhamnose	0.212716781	Leucylalanine	0.330224502
Leucyltyrosine	0.20954017	Orotic acid	0.330081793
Na-Acetyl-L-ornithine	0.208078082	Glutaminylvaline	0.329202074

Leucylglycine	0.204840329	Leucyphenylalanine	0.327086285
Uridine-5'-diphosphogalactose	0.203486223	Valyleucine	0.325525119
Fructose	0.201918161	Tryptophan	0.316656191
K3G6-R7G_5.09_755.2031	0.200041127	FerHex3_5.17_355.1031	0.312069115
Guanosine 2':3'-cyclic monophosphate	0.197877377	Tyrosine	0.294622983
PC 38:5	0.197079684	hesperidine_Saleh_standards_609.18_7.93	0.294036598
Threonylucine	0.19376986	H5FeruGlc1_3.92_371.0983	0.290347447
beta-Hydroxypalmitic acid	0.192330519	Na-Acetyl-L-ornithine	0.279533965
Glycyl-L-tryptophan	0.19184623	S-Adenosyl-L-Homocysteine	0.279417337
Isoleucylaspartic acid	0.189414916	Aspartylphenylalanine	0.271605686
Phosphoric_Acid	0.184199332	PC 36:6	0.266582803
3-4-dimethoxycinnamic acid	0.182814604	DGDG 36:6 (2)	0.266247777
Leucylucine	0.1822503	PC 38:5	0.255636126
Phenylalanylucine	0.179490748	Dehydro Ascorbic acid	0.244823674
Oenin	0.175676962	3-Methylglutaric acid	0.242025189
5-Hydroxy-L-Tryptophan	0.174516266	Palmitic_Acid	0.239673688
PC 34:4 (1)	0.172642116	5?-Deoxy-5?-(methylthio)adenosine	0.237315637
p-Coumaric acid	0.172339624	Serotonin	0.236034504
Thymidine	0.171556041	LysoPC 16:0	0.235587024
Propanoic acid- 3-ureido-	0.171250049	Lysyltryptophan	0.233500741
Inosine	0.167362221	Fructose	0.232051519
6-Hydroxynicotinic acid	0.164581671	Sucrose	0.23203947
Dehydro Ascorbic acid	0.162110648	Guanosine 2':3'-cyclic monophosphate	0.231570936
Palmitic_Acid	0.159990022	Adenosine-5-Monophosphate	0.23089071
Purine	0.15961622	Glutamylucine	0.228761262
DGDG 36:6 (2)	0.159353543	Glycyl-L-phenylalanine	0.226355219
gamma-Glutamylseleno-Methylseleno-Cysteine	0.157774891	Purine	0.22460338
3-Deoxy-D-manno-2-octulosonic acid	0.157483847	p-Coumaric acid	0.218063555
Isocitric_Acid	0.157268225	Serylphenylalanine	0.214916286
Serylphenylalanine	0.152863688	Phenylalanylgutamic acid	0.212758694
Q3G6-R7G_4.67_771.1984	0.152044749	Myricetin-3-O-Glucoside_Saleh_standards_479.08_6.36	0.207737464
Glycine	0.151740917	Tyrosine	0.205238454
PC 38:4 (1)	0.151490698	DGDG 38:6 (1)	0.203797808
Sinapoylglucose	0.149151853	LysoPE 16:0	0.203524963
Gaba1	0.145794114	Serylucine	0.200894677
FerHex3_5.17_355.1031	0.143289331	Aspartylucine	0.200122305
Spermidine_(5Tms)	0.142447988	Methionylucine	0.199137542
Phenylalanysoleucine	0.138750508	Tryptophythyreonine	0.197731271
Aspartylphenylalanine	0.136454997	Leucylglycine	0.197726824
Guanosine	0.134727051	Abciscic acid	0.19708515

Glycyl-L-isoleucine	0.132614392	Urea	0.196391235
Valyisoleucine	0.131025529	Adenosine	0.195409785
LysoPE 18:0	0.129459146	Rhamnose	0.195099119
Abscisic acid	0.129189614	Glutamylisoleucine	0.19439644
PC 32:3 (4)	0.123553868	Guanosine	0.194375396
alpha_carotene_11.92_53 6.445	0.122811203	6-7 Dimethylrihityl lumazine	0.192879302
Leucyalanine	0.122501305	Maleic_Acid	0.187961578
Serytyrosine	0.121885147	Uridine-5'- diphosphogalactose	0.187940421
beta-hydroxycapric acid	0.119277292	Corticosterone	0.185829573
Isoleucyphenylalanine	0.118852492	LysoPC 18:1_2	0.184807293
Loganin	0.118046084	5-Hydroxy-L- Tryptophan	0.182845173
Tryptophyaspartic acid	0.116968802	LysoPC 18:0	0.182595107
Glutaminyleucine	0.115242603	alpha_carotene_11.92_53 6.445	0.18174526
DGDG 36:3 (1)	0.114802805	Propanoic acid- 3- ureido- PC 38:4 (1)	0.180802271
Glycyl-L-alanine	0.112097305	3-6-anhydro-D- Galactose	0.175157962
Glycyl-L-phenylalanine	0.108835017	LysoPC 18:2_2	0.174477518
Leucymethionine	0.108152759	Threonyalanine	0.174464071
2-Deoxyadenosine 5- monophosphate	0.106354013	Glucose-6-Phosphate	0.169762815
4- Dimethylaminopyridine	0.104251233	2-Deoxyadenosine 5- monophosphate	0.167882926
Tyrosyvaline	0.103070481	6-Hydroxynicotinic acid	0.162412248
Quercitrin	0.10282805	FerHex4_5.37_355.1031	0.158517287
Tryptophan	0.100799233	Histidyltryptophan	0.157239471
Glutamymethionine	0.100035387	LysoPE 18:2	0.156973058
Glutamylisoleucine	0.099553777	Tryptophytyrosine	0.156766598
MGDG 36:3 (2)	0.096499661	beta-hydroxycapric acid	0.15669505
Isoleucytryptophan	0.091160672	K3G6- R7G_5.09_755.2031	0.156389008
Serylucine	0.081745438	PC 34:3	0.155764639
Valyleucine	0.079791639	PE 36:6	0.154435282
Adenosine 2':3'-Cyclic monophosphate	0.079279007	progesterone	0.15129794
Citramalic acid	0.078668863	Glycyl-L-alanine	0.148410464
DGDG 38:5 (2)	0.077893799	Citramalic acid	0.147289758
MGDG 34:3	0.073367176	phytoene_carotenoids related	0.144512572
Aspartyleucine	0.067826471	PC 34:4 (1)	0.143484086
Saccharic acid	0.067284857	Glycolic_Acid	0.139195111
Deoxycorticosterone	0.067189419	Inosine	0.138340214
Q3G2-A_6.19_595.1315	0.064982164	Adenosine 2':3'-Cyclic monophosphate	0.136175296
phytoene_carotenoids related	0.063415378	Glycyl-L-tryptophan	0.134690982
Aspartyaspartic acid	0.062159146	Phosphoric_Acid	0.133465389
Deoxycorticosterone	0.059513717	Tyrosyvaline	0.132537098
N-Carbamyl-DL- aspartic acid	0.059320572	Gulonic_Acid_1-4- Lactone	0.132290367
MGDG 36:2	0.05923053	Spermidine_(5Tms)	0.127439986
Caffeic acid	0.056910994		

11A-Hydroxyprogesterone	0.056876747	GlutaminyPhenylalanine	0.125926302
Leucyphenylalanine	0.056196397	MGDG 34:3	0.125098551
Prolythreonine	0.05489133	Q3G2-A_6.19_595.1315	0.121904757
progesterone	0.054769693	Quercitrin	0.120583089
Shikimic acid-3-phosphate	0.053500341	Tyrosytryptophan	0.119920001
Glutamyleucine	0.05283681	Caffeic acid	0.11821364
Thymidine 5'-monophosphate	0.052459419	Glycyl-L-isoleucine	0.117978152
Aconitic_Acid_Cis	0.048360067	Serytyrosine	0.114933609
Astaxanthin	0.04635394	Q3G6-R7G_4.67_771.1984	0.114717413
PC 36:6	0.045912868	Gibberellin A3	0.108027765
LysoPE 16:0	0.04544281	Serytyrosine	0.106878258
Prolyphenylalanine	0.044852291	Alanyleucine	0.105952025
Secologanin	0.042169759	Guanosine	0.105199912
3-(2-Hydroxyethyl)Indole	0.040075462	Tyrosyleucine	0.105048187
Arginine	0.039733937	Quercetin-3-D-galactoside_Saleh_standards_463.098_6.98	0.10389889
Azelaic acid	0.037521951	Saccharic acid	0.09817941
Threonyalanine	0.037194184	PC 32:0 (2)	0.096007626
LysoPC 16:0	0.031959792	Thymidine 5'-monophosphate	0.094231033
Tyrosyleucine	0.031390633	3-4-dimethoxycinnamic acid	0.089661664
Leucylglycine	0.02981662	Isoleucyaspatic acid	0.089435866
gamma-GlutamySe-Methylseleno-Cysteine	0.029317538	SinGlciso2_5.47_385.1133	0.08894245
Quinic_Acid_Trans	0.029035978	DGDG 36:5 (1)	0.084846543
DGDG 36:5 (1)	0.027320188	3-Deoxy-D-manno-2-octulosonic acid	0.084706352
11A-Hydroxyprogesterone	0.024560706	MGDG 36:3 (2)	0.080818533
Valine	0.023555178	Is3G2-A6-R_6.44_755.2034	0.076575337
Glycerol-3-Phosphate	0.020084461	asparaginyleucine	0.072440088
Glycyl-L-phenylalanine	0.019222563	Phenylalanythreonine	0.070310746
Trehalose	0.018159327	Glycine	0.069704977
Serotonin	0.017613331	Secologanin	0.064610628
Tyrosyvaline	0.015017513	Threonyphenylalanine	0.061794548
Alanylmethionine	0.012738412	LysoPC 18:3_1	0.060643291
E-64	0.010693989	quercetin-3-O-(2"-O-rhamnosyl)glucoside-7-O-rhamnoside	0.055953674
N-Dodecanoyl-DL-homoserine lactone	0.010481078	Glutamic acid- N-acetyl-	0.054531985
GlutaminyPhenylalanine	0.009481707	Shikimic_Acid	0.053722603
Succinic_Acid	0.009134638	MGDG 36:5 (1)	0.052584917
Aspartic acid	0.006382962	Succinoadenosine	0.049836792
N-Acetylmuramic acid	0.005393781	Valine	0.04756367
trans-zeatin-O-glucoside	0.0037925	PC 34:4 (2)	0.045873474
PC 32:0 (2)	0.001339036	Loganin	0.040279181
Pantothenic_Acid	0.000825941	Tryptophyaspatic acid	0.038636233
LysoPC 18:0	-0.000270789	Deoxycorticosterone	0.033928764

Theophylline-anhydrous	-0.000431027	Deoxycorticosterone	0.031804196
Alanyisoleucine	-0.001363946	Prolythreonine	0.029689996
Mevalonic acid lactone	-0.002857211	Phenylalanytryptophan	0.027525418
Adenosine-5-Monophosphate	-0.004024093	DGDG 38:5 (2)	0.026075482
2_Maltose	-0.004535341	Theophylline-anhydrous	0.023656124
Pelargonin	-0.005102924	Astaxanthin	0.022400457
4-Aminobenzoic acid	-0.005495867	3-Hydroxyanthranilic acid	0.018923755
Tryptophytryptophan	-0.006239176	Phenylalanyisoleucine	0.018532059
GlcCer t18:1/h22:0	-0.006503051	N-Dodecanoyl-DL-homoserine lactone	0.015457441
2_Fructose	-0.007427848	Q3G2-A6-R_5.93_741.1879	0.014485282
MGDG 34:2 (2)	-0.009050352	Guanosine-5Â'-Monophosphate	0.013765705
2_Glucose	-0.013992209	Adenine	0.013339791
2_Glucose-6-Phosphate	-0.013992209	Caffeic acid	0.00730676
2_Mannitol	-0.013992209	Tyrosyaspatic acid	0.005327242
2_Mannitol	-0.014059133	Azelaic acid	0.005299637
Pyroglutamic_Acid	-0.015588171	K3G2-A6-R_6.36_725.1929	0.004246663
MGDG 36:5 (1)	-0.016838018	Glycerol-3-Phosphate	0.003523032
Caffeine	-0.017739566	2_Inositol-1-Phosphate	0.00347006
Alanyleucine	-0.018204903	5-beta-pregnane-3-20-dione	0.001556028
2_Citric_Acids	-0.019931165	N-Acetylmuramic acid	-0.000283351
PC 34:3	-0.020002641	Aspartic acid	-0.00096133
Salicin	-0.021108672	5-beta-pregnane-3-20-dione	-0.002929956
FerHex1_3.89_355.1031	-0.024373634	trans-zeatin-O-glucoside	-0.006775607
SinGlciso2_5.47_385.1133	-0.025332413	Mevalonic acid lactone	-0.007094264
Panthenol	-0.025550245	N-Carbamyl-DL-aspartic acid	-0.007322129
Suberic acid	-0.025931945	Arginine	-0.007775179
PE 36:6	-0.025956035	MGDG 36:6 (1)	-0.007983579
Melbose	-0.027361631	GlcCer t18:1/h22:0	-0.008235104
Is3G2-A6-R_6.44_755.2034	-0.028345397	Tryptophyasparagine	-0.010433136
Testosterone	-0.030749065	Testosterone	-0.015740232
beta-Nicotinamide adenine dinucleotide	-0.033572696	Pyruvic_Acid	-0.016671916
11beta-Hydroxyprogesterone	-0.035358724	Adenosine 2Â'monphosphate	-0.016760587
Gibberellin A3	-0.038572763	Indole-3-acetyl-L-aspartic acid	-0.017823313
MGDG 36:6 (1)	-0.041123807	2_Maltose	-0.01814559
Rutin	-0.041283035	2_Fructose	-0.018208536
Methionisoleucine	-0.041793633	PE 34:3	-0.020074016
PC 32:1 (2)	-0.043117162	4-Aminobenzoic acid	-0.020148092
CafGluc3_3.51_371.0618	-0.04333512	MGDG 34:2 (2)	-0.020192773
Homocystine	-0.044367966	LysoPC 18:2_1	-0.021501493
Cer t18:0/h24:0	-0.044927924	11A-Hydroxyprogesterone	-0.02310287
Adenosine 2Â'monphosphate	-0.045003662	2_Mannitol	-0.023285482

quercetin-3-O-(2"-O-rhamnosyl)glucoside-7-O-rhamnoside	-0.047077683	Rutin	-0.023570471
Threonyalanine	-0.048488066	2_Glucose	-0.024027568
Fumaric_Acid	-0.048759161	2_Glucose-6-Phosphate	-0.024027568
Gibberellin A1	-0.049442037	2_Mannitol	-0.024027568
Rutin	-0.051508643	11beta-Hydroxyprogesterone	-0.025741283
asparaginyneucine	-0.05237666	Aconitic_Acid_Cis	-0.027611617
Succinoadenosine	-0.055636527	Tryptophyasparagine	-0.027810988
Indole-3-acetyl-L-aspartic acid	-0.056080437	2_Malic_Acid, 2-Methyl	-0.028327493
K3G2-A6-R_6.36_725.1929	-0.061260227	Suberic acid	-0.033800861
Pipecolinic acid	-0.064232778	Melbose	-0.034833696
GlcCer t18:1/h24:0	-0.064830042	Thymidine	-0.036463515
NG3_8.16_433.1136	-0.070913977	Pyroglutamic_Acid	-0.038771447
Tryptophyasparagine	-0.071401639	gamma-GlutamySe-Methylseleno-Cysteine	-0.039094475
Q3G2-A6-R_5.93_741.1879	-0.074336097	Is3G2-A6-R_6.44_755.2034	-0.0418957
alpha-Tocopherol acetate	-0.077063989	5-Methoxy-Tryptamin	-0.042499494
Quercetin	-0.077411558	DGDG 36:4 (1)	-0.043098429
DGDG 36:4 (1)	-0.078212049	Karrikin 2	-0.044251613
Lutein_5.48_568.43	-0.079215759	beta-Nicotinamide adenine dinucleotide	-0.044703503
Citric acid	-0.079321795	Orotic acid- 4-5-dihydro-	-0.046019825
Glyceric_Acid	-0.07980537	CafGluc3_3.51_371.0618	-0.047526487
Pantothenic acid (Vitamine B5)	-0.079872395	Methyl jasmonate	-0.04787354
Methyl jasmonate	-0.081915457	Asparaginyphenylalanine	-0.049923601
3-Hydroxyanthranilic acid	-0.086732886	PC 32:1 (2)	-0.050643162
Serytyrosine	-0.089963738	Pantothenic acid (Vitamine B5)	-0.054688849
cyclo-Gly-Pro	-0.091937484	Isoleucyleucine	-0.055173796
Phenylalanytryptophan	-0.097413319	CafHex3_4.48_341.0879	-0.056575557
Leucymethionine	-0.098890624	Glutamytyrosine	-0.058142612
PE 38:3 (3)	-0.100829558	Alanyisoleucine	-0.058695444
Guanosine-5Â'-Monophosphate	-0.101966188	GlcCer t18:1/h24:0	-0.066251629
6-Phospho-Gluconate	-0.102744507	Gibberellin A1	-0.068656286
2_Malic_Acid, 2-Methyl	-0.102780769	2_Glucuronic_Acid__Lactone	-0.068866919
Phenylalanythreonine	-0.104746722	beta_Carotene_12.15_536.4455	-0.071009731
Glucuronic_Acid__Lactone	-0.10978757	Panthenol	-0.071905644
Methyl-beta-D-galactoside	-0.112184195	Pyruvic_Acid, 3-Hydroxy	-0.072152171
FerHex4_5.37_355.1031	-0.113299535	DGDG 32:3 (1)	-0.072239424
MGDG 36:4 (2)	-0.11527939	gamma-GlutamySe-Methylseleno-Cysteine	-0.073356864
Cer t18:0/h24:1	-0.11633549	Rutin	-0.07436323
GlcCer d18:1/h16:0	-0.117088055	3-Hydroxy-3-Methylglutaric acid	-0.077853703
Homoserine	-0.11776149	Asparaginyvaline	-0.079082625

PE 34:3	-0.118265641	5-Phospho-D-ribose 1-diphosphate	-0.079374065
Quercetin-3-D-galactoside_Saleh_standards_463.098_6.98	-0.118463359	Leucymethionine	-0.081843891
5-Phospho-D-ribose 1-diphosphate	-0.119414179	TAG 44:2	-0.082996069
CafHex3_4.48_341.0879	-0.119866699	Cer t18:0/c16:0	-0.083990242
Tyramine	-0.120623714	alpha tocopherol	-0.084261281
Tryptophytyrosine	-0.120942473	Androstendione	-0.085225071
PC 34:4 (2)	-0.122156544	trans-Cyclohexane-1-2-dicarboxylic acid	-0.085470206
Fructose6Phosphate	-0.122453277	Sugar_Xylose_Or_Smilir	-0.091709665
Is3G2-A6-R_6.44_755.2034	-0.1229081	Pipecolic_Acid	-0.092395865
Methionyleucine	-0.123997185	Lutein_5.48_568.43	-0.095400332
Threonyphenylalanine	-0.125918615	Glycerol	-0.09549441
5-Methoxy-Tryptamin	-0.126266353	LysoPC 18:1_1	-0.098243678
Tyrosytryptophan	-0.129314717	Gaba1	-0.103632022
Diethyl succinate	-0.130105953	Citric acid	-0.103890662
Caffeic Acid	-0.135308734	chlorgenic acid_Saleh_standards_353.088_4.91	-0.106193832
DGDG 32:3 (1)	-0.135879764	Homocystine	-0.106414086
Glutamtyrosine	-0.139275765	Pantothenic_Acid	-0.106791955
Pyruvic_Acid_3-Hydroxy	-0.143901845	4-Hydroxyphenylpyruvic acid	-0.107521892
Glucaric aci1-4-lactone	-0.144247332	PE 34:2	-0.110750968
Asparaginyvaline	-0.148715324	Methyl-beta-D-galactoside	-0.111090254
Adenosine 3Â' monophosphate	-0.154124886	Putrescine	-0.11424857
H5FeruGlc2_4.76_371.0983	-0.155467374	K3G6-R_6.89_593.1501	-0.118499045
trans-Cyclohexane-1-2-dicarboxylic acid	-0.155645495	H5FeruGlc2_4.76_371.0983	-0.119217036
Malic acid	-0.156191319	Benzylalcohol	-0.121505643
DAG 34:3	-0.156959834	3CGA_3.82_353.0876	-0.123559094
Kaempferol 3-O-glucosyl-glucoside 7-O-rhamnoside	-0.157622312	PC 38:3 (1)	-0.123617893
Karrikin 2	-0.158361939	Diethyl succinate	-0.124364155
PE 34:2	-0.158432473	Adipic acid	-0.126091176
K3G6-R_6.89_593.1501	-0.159854606	alpha-Tocopherol acetate	-0.126187255
Prolyglutamine	-0.161363295	Pantethaine	-0.126286902
Cer t18:0/c16:0	-0.162302723	Alanine	-0.128490582
Diethyl succinate	-0.162677202	Diethyl succinate	-0.129520421
LysoPC 18:1_2	-0.168510974	Threonyalanine	-0.130296903
3-4-Dihydroxybenzoic acid	-0.169927192	Tyrosylglutamic acid	-0.130397184
Cer t18:0/h22:0	-0.17055691	3-4diCQA_6.96_515.12	-0.131911102
Genistein	-0.171406142	Phenylalanytryptophan	-0.134164567
LysoPC 18:2_2	-0.172086698	Glucaric aci1-4-lactone	-0.134930879
Sugar_Xylose_Or_Smilir	-0.174418733	Cysteine	-0.140873825
Putrescine	-0.180273963	Hydroxylamine	-0.141868788

LysoPE 18:2	-0.180698291	Reichstein's Substance S	-0.141916067
Cer d18:1/h16:0	-0.180718641	PC 32:3 (1)	-0.141997052
Myricetin-3-O-Glucoside_Saleh_standards_479.08_6.36	-0.181218095	Adenylosuccinic acid	-0.142798797
CafHex1_3.87_341.0879	-0.18215361	Cer t18:0/h24:1	-0.143409996
Benzylalcohol	-0.182343917	Salicin	-0.145801425
Tryptophyglutamic acid	-0.183478005	Ferulic acid	-0.147453471
GlcCer t18:1/h20:0	-0.188778522	Valymethionine	-0.148781224
Asparaginyphenylalanine	-0.189310836	Seryleucine	-0.152187106
DIMBOA-glucoside	-0.190581133	Alanylglycine	-0.153422783
Ferulic acid	-0.192958804	Biocytin	-0.154333736
Maleic_Acid	-0.197024718	PC 32:2 (3)	-0.154364708
PC 32:3 (1)	-0.197363217	4-Dimethylaminopyridine	-0.156773949
TAG 44:2	-0.198454957	Malic acid	-0.160121613
Thymidine	-0.200750299	Kaempferol 3-O-glucosyl-glucoside 7-O-rhamnoside	-0.161051612
Theophylline-anhydrous	-0.20098683	Quinic_Acid_Trans	-0.161299361
beta_Carotene_12.15_536.4455	-0.202451374	Prolyglutamine	-0.164201831
Cytidine 5'-monophosphate	-0.202772307	2-Isopropylmalic acid	-0.165877061
Tyrosyglutamic acid	-0.204679079	6-Phospho-Gluconate	-0.168778137
CafHex1_3.87_341.0879	-0.20530361	3-(2-Hydroxyethyl)Indole	-0.169449265
DGDG 32:2 (1)	-0.206197297	NG3_8.16_433.1136	-0.170808844
Tyrosyproline	-0.206465334	DIMBOA-glucoside	-0.171616509
PC 32:2 (3)	-0.20660064	Tryptophyglutamic acid	-0.174273363
MGDG 38:4	-0.211370924	Thymidine	-0.174661824
Lycopene	-0.211969139	CafHex2_4.09_341.0879	-0.175112755
2_Inositol-1-Phosphate	-0.21603865	FerHex1_3.89_355.1031	-0.17538186
MGDG 32:1 (1)	-0.216283879	Alanymethionine	-0.178065379
Robinin_Saleh_standard_s_739.21_6.43	-0.221882246	Lycopene	-0.180414584
Orotic acid- 4-5-dihydro-	-0.222439225	4CGA_5.25_353.0876	-0.183340834
Erythrose-4-phosphate	-0.225064722	Theophylline-anhydrous	-0.186938344
Uracil	-0.230322967	MGDG 36:4 (2)	-0.190912359
Androstendione	-0.234164775	Myricetin-3-O-Glucoside_Saleh_standards_479.08_6.36	-0.192071459
Tryptophan- N-acetyl-	-0.235133388	Quercetin	-0.192364432
5-beta-pregnane-3-20-dione	-0.235269658	Valyisoleucine	-0.192631859
3CGA_3.82_353.0876	-0.235324936	Uracil	-0.192879386
5-7-Dihydroxy-4'-methoxyisoflavone	-0.244406529	Tryptophan- N-acetyl-	-0.193500723
Methionylglycine	-0.249046791	Gentisic acid	-0.193974365
Tryptophyasparagine	-0.249530064	DAG 34:3	-0.201485735
GlcCer t18:1/h26:0	-0.255440577	3-4-Dihydroxybenzoic acid	-0.202844992
Adenylosuccinic acid	-0.259099326	Tryptophytryptophan	-0.203451908
AsparaginyTryptophan	-0.259905974	CafHex1_3.87_341.0879	-0.208680882

3-Methylglutaric acid	-0.263309859	CafHex1_3.87_341.0879	-0.212036992
progesterone	-0.267894936	Adenosine	-0.217068933
SinGlciso1_5.09_385.1133	-0.268009423	3Å' monophosphate	-0.217613136
N-Formyl-L-Methionine	-0.273887928	Arginyleucine	-0.217613136
Maltose	-0.275862694	Cer t18:0/h24:0	-0.217975107
FerHex2_4.65_355.1031	-0.276564079	Robinin_Saleh_standard	-0.218078778
3-Hydroxy-3-Methylglutaric acid	-0.27891627	s_739.21_6.43	-0.22114738
DAG 36:5	-0.279974803	Fumaric_Acid	-0.22114738
5CGA_4.58_353.0876	-0.283498719	GlcCer t18:1/h20:0	-0.222049297
Biocytin	-0.283750743	Prolyphenylalanine	-0.223967548
Gaba	-0.284562811	4-5diCQA_7.11_515.12	-0.225588212
Beta-Sitosterol_(1Tms)	-0.284980327	Kaempferol	-0.230373561
TAG 44:0	-0.288097923	PE 36:2	-0.233207872
Isoleucyleucine	-0.294011438	Luteolin	-0.234068198
Lysine	-0.29413656	Galactonic_Acid	-0.234904129
2-Isopropylmalic acid	-0.295129368	Galacturonic_Acid	-0.235090685
Dehydroascorbic_Acid	-0.300833258	Cytidine 5Å'-monophosphate	-0.237090526
PC 38:3 (1)	-0.30335799	Tyrosproline	-0.237701279
NG1_7.39_433.1136	-0.305046872	Tyramine	-0.24288223
MGDG 32:0	-0.305334258	PC 36:5	-0.247806806
PC 34:2	-0.310564123	Erythrose-4-phosphate	-0.250240065
PE 36:2	-0.310649927	Arginytryptophan	-0.250730068
3-4diCQA_6.96_515.12	-0.314999936	Methionylvaline	-0.25280968
Methionylvaline	-0.316842448	DGDG 36:1 (2)	-0.254173437
Zeaxanthin	-0.317117133	Gibberellin A1	-0.260306425
PC 36:5	-0.319456445	Naringin	-0.261243202
Histidylserine	-0.322910035	dihydrochalcone	-0.26160596
beta-Estradiol 3-(beta-D-glucuronide)	-0.323609834	MGDG 32:1 (1)	-0.26160596
Alanylglycine	-0.324173035	Propanoic acid- 3-(2-4-dihydroxyphenyl)-	-0.265274848
PE 36:3_1	-0.324427578	GlcCer d18:1/h16:0	-0.268240012
Glutaminytryptophan	-0.327816262	PE 36:4	-0.271979585
Quercetin-3-beta-D-glucoside	-0.329193072	Salicylic_Acid	-0.272894421
chlorgenic acid_Saleh_standards_35	-0.329222026	Pyridoxic acid	-0.279566343
3.088_4.91	-0.329784513	PC 34:2	-0.283847415
TAG 56:0	-0.329784513	Cer t18:0/h22:0	-0.2879566
Glyoxylic_Acid	-0.330870647	progesterone	-0.293984395
Quinic acid- 3-caffeoyl-	-0.331039453	Shikimic acid-3-phosphate	-0.295984194
N-Acetylneuraminic acid	-0.333176583	TAG 44:0	-0.296558243
PE 36:4	-0.334014973	Gaba	-0.301712141
Glycolic_Acid	-0.33980547	Xylose	-0.303404713
Arginyleucine	-0.341064768	AsparaginyTryptophan	-0.303446864
Arginytryptophan	-0.341200587	MGDG 38:4	-0.3044732
Gibberellin A1	-0.343366836	Inositol-1-Phosphate	-0.305534015
		MGDG 34:0	-0.305590073
		Quercetin-3-beta-D-glucoside	-0.309661387

Quinic acid	-0.343985421	PE 36:3_1	-0.309676905
Methionylphenylalanine	-0.344792194	Pelargonin	-0.314436796
H5FeruGlc3_5.28_371.09 83	-0.347064841	Beta-Sitosterol_(1Tms)	-0.320569008
LysoPC 18:2_1	-0.354373113	Quinic_Acid,_3- Caffeoyl-Cis	-0.320834622
MGDG 34:0	-0.356214287	MGDG 32:0	-0.321581689
Alanine_Beta	-0.360532356	Citric_Acids	-0.32244506
Cer t18:1/h22:0	-0.362861522	PE 34:1	-0.323234882
Adenine	-0.363046438	Tryptophan- N-acetyl-	-0.330423509
4CGA_5.25_353.0876	-0.363655411	DAG 34:4 (2)	-0.333879053
P35GG_6.64_597.18	-0.36459289	GlcCer t18:1/h26:0	-0.341872954
Methionymethionine	-0.370409293	Indole-3-acetamide	-0.343262166
Salicylic_Acid	-0.371588573	Methionylisoleucine	-0.349314836
4-5diCQA_7.11_515.12	-0.379747993	N-Acetylneuraminic acid	-0.350321566
Pyridoxic acid	-0.380846992	H5FeruGlc3_5.28_371.09 83	-0.351006797
Valymethionine	-0.383157455	Methionylglycine	-0.360202252
alpha tocopherol	-0.387948988	Zeaxanthin	-0.364787946
Tyrosylaspartic acid	-0.39598731	CafHex5_5.22_341.0879	-0.365940556
TAG 58:0	-0.396487857	Eriodictyol	-0.370208036
Kaempferol	-0.398125476	Histidylserine	-0.375266415
NG1_7.39_433.1136	-0.398904541	beta-Estradiol 3-(beta- D-glucuronide)	-0.377183536
CafHex5_5.22_341.0879	-0.410380159	Naringenin	-0.377873559
Valylisoleucine	-0.417059543	chalcone_Saleh_standar ds_271.061_10.44	-0.380066663
TAG 46:0	-0.41905817	P35GG_6.64_597.18	-0.3806605616
GPEP	-0.419357846	Naringenin	-0.387164761
Acetylsalicylic acid	-0.424079508	Naringenin	-0.395500063
CafHex2_4.09_341.0879	-0.431138075	Cer t18:1/h22:0	-0.401629614
DAG 34:4 (2)	-0.435202667	Maltose	-0.407427798
Gentisic acid	-0.437932485	FerHex2_4.65_355.1031	-0.408070894
Citric_Acids	-0.438635146	Neohesperidin	-0.415506694
Asparaginytyrosine	-0.439181607	5CGA_4.58_353.0876	-0.425100869
Propanoic acid- 3-(2-4- dihydroxyphenyl)-	-0.441768613	N-Formyl-L-Methionine	-0.42591215
Glutamylglutamic acid	-0.44332574	Riboflavin	-0.429118439
LysoPC 18:3_2	-0.452767739	Quinic acid	-0.430565811
PE 34:1	-0.454200118	Acetylsalicylic acid	-0.434236486
2-3-Dimethylsuccinic acid	-0.454536681	NG1_7.39_433.1136	-0.443796353
Riboflavin	-0.455844786	Cer d18:1/h16:0	-0.446298754
Hydroxylamine	-0.45614676	GPEP	-0.449301857
Neohesperidin	-0.461893911	Stigmasterol_(1Tms)	-0.449966139
Tyrosylproline	-0.463577206	Glutamylglutamic acid	-0.451165257
Sedoheptulose	-0.46599717	Isoleucylphenylalanine	-0.454902298
Tryptophan- N-acetyl-	-0.470266793	Benzoic_Acid,_3,4- Dihydroxy	-0.458092623
Eriodictyol	-0.476504662	Methionylphenylalanine	-0.460893711
Luteolin	-0.490140698	Dehydroascorbic_Acid	-0.467013377
		Glucuronic_Acid__Lacto n	

PC 34:1	-0.490470514	DAG 36:5	-0.470638439
LysoPC 18:1_1	-0.50733426	TAG 56:0	-0.477086277
Glutamic_Acid	-0.508908185	Erythrose	-0.477756346
Asparaginemethionine	-0.510329476	Caffeine	-0.484694499
Aspartyleucine	-0.511590165	Tryptophythyreonine	-0.485142327
DGDG 34:1	-0.524420645	Cystein_S_Methyl	-0.491651595
Acetylsalicylic acid	-0.529928406	Asparaginemethionine	-0.492934356
PC 36:1	-0.538836536	4-5diCQA_7.11_515.12	-0.493360332
Benzoic_Acid_3,4-Dihydroxy	-0.54234575	PC 34:1	-0.495803843
Naringenin chalcone_Saleh_standards_271.061_10.44	-0.543048404	Lyso_MGDG 18:3 (2)	-0.49696684
Quinic_Acid	-0.544012251	DGDG 34:1	-0.502495764
Malic_Acid	-0.544188793	Glyoxylic_Acid	-0.504115805
TAG 46:1	-0.55077429	PC 36:1	-0.510669001
Tomatine	-0.553362468	Ribose-5-Phosphate	-0.514336111
Xylose	-0.555082294	Quinic acid- 3-caffeoyl-	-0.516142065
N-Acetyl-L-Methionine	-0.555288091	TAG 54:9	-0.524433723
Alanylgutamic acid	-0.555599326	Glutamic_Acid	-0.52869898
Glycyl-L-isoleucine	-0.556018995	NG1_7.39_433.1136	-0.52999532
N-Acetyl-L-Tyrosine	-0.557819538	TAG 46:0	-0.535044965
4-5diCQA_7.11_515.12	-0.558243961	TAG 44:1	-0.535652362
threo-3-isopropylmalic acid	-0.560751919	N-Acetyl-L-Methionine	-0.536433087
Cytidine 5Â'-monophosphate	-0.565970946	SinGlciso1_5.09_385.1133	-0.537644039
Naringenin	-0.57442788	Glycyl-L-isoleucine	-0.538117805
TAG 54:9	-0.575462222	threo-3-isopropylmalic acid	-0.541108327
cis-Aconitic acid	-0.578648692	Mevalonic acid lactone	-0.542180543
Isoleucyphenylalanine	-0.579068126	Sedoheptulose	-0.545190223
Pipecolic_Acid	-0.581305981	Glutaminytryptophan	-0.548045848
Lyso_MGDG 18:3 (2)	-0.581588026	TAG 58:0	-0.552852075
Hesperetin-7-O-glucoside	-0.5832978	TAG 46:1	-0.561734938
Cystein_S_Methyl	-0.58554413	5-7-Dihydroxy-4'-methoxyisoflavone	-0.562004349
ReichsteinÂ's Substance S	-0.587374357	PC 36:2	-0.568844586
DGDG 36:1 (2)	-0.591772297	N-Acetyl-L-Tyrosine	-0.572804229
DAG 36:2	-0.597595422	DGDG 32:2 (1)	-0.575396639
Naringenin	-0.607945288	Asparaginytyrosine	-0.583073185
Ribose-5-Phosphate	-0.621762242	Pentamidine	-0.585730454
Prolin-4-Hydroxy	-0.624846192	TAG 52:3	-0.588865355
4CGA_5.25_353.0876	-0.628078494	Prolin-4-Hydroxy	-0.596591895
Pentamidine	-0.631308905	P35GG_6.64_597.18	-0.597281458
P35GG_6.64_597.18	-0.638830374	PC 36:4 (2)	-0.614674833
TAG 58:5	-0.648822689	Acetylsalicylic acid	-0.615080453
Isoleucymethionine	-0.651332742	Malic_Acid	-0.618033833
TAG 50:0	-0.65559638	4CGA_5.25_353.0876	-0.618628093
Quinic_Acid_3-Caffy2	-0.662971561	Morin	-0.622487406
TAG 52:0	-0.668825863	Methionisoleucine	-0.62250643

3-5diCQA_7.48_515.12	-0.669034702	Tyrosyproline	-0.622724272
PC 36:4 (2)	-0.683240615	Secologanin	-0.627391708
Phenylalanytryptophan	-0.686362775	3-Methylglutaric acid	-0.628450171
Methionyisoleucine	-0.688414235	Isoleucymethionine	-0.628850688
FerHex3_5.17_355.1031	-0.691227086	2-3-Dimethylsuccinic acid	-0.646603267
FerHex3_5.17_355.1031	-0.692556021	Cytidine 5Â'-monophosphate	-0.658016974
DGDG 34:2	-0.692961459	Quercetin-3-beta-D-glucoside	-0.672092194
PC 36:2	-0.693783323	Caffein_Saleh_standards_190.93_5.19	-0.688642521
MGDG 34:1	-0.699460482	TAG 58:5	-0.690084691
Allantoin	-0.69982333	PC 36:3 (1)	-0.701412459
Naringin dihydrochalcone	-0.700941828	MGDG 34:1	-0.705173474
Lyso_MGDG 18:2 (1)	-0.708827326	Caffeic Acid	-0.712350437
TAG 44:1	-0.709195637	FerHex3_5.17_355.1031	-0.717134672
Lyso_DGDG 16:0 (2)	-0.718987952	PE 38:3 (2)	-0.722539429
Raffinose	-0.721276789	FerHex3_5.17_355.1031	-0.724754833
Quercetin-3-beta-D-glucoside	-0.732697554	Ethanolamine	-0.737871013
Serjanic acid saponin # 1	-0.733157103	3-5diCQA_7.48_515.12	-0.74039061
Tryptophytreonine	-0.740731655	Melezitose	-0.766772139
Pyruvic_Acid	-0.744959165	Phenylalanythreonine	-0.77680357
Secologanin	-0.746717066	Serjanic acid saponin # 1	-0.790108829
PC 36:3 (1)	-0.752519923	Succinic_Acid	-0.792193805
TAG 54:8	-0.759387529	TAG 50:6 (2)	-0.803990383
Catechin	-0.763198721	TAG 54:8	-0.837993931
TAG 54:0	-0.780366732	5-6-Dimethylbenzimidazole	-0.838100051
Erythrose	-0.782870324	Raffinose	-0.843557879
2 deoxyadenosine	-0.786680965	3-4-5triCQA_8.99_677.1522	-0.844290297
TAG 50:6 (2)	-0.789890457	TAG 52:6 (1)	-0.852364368
Quinic_Acid_3-Caffeoyl-Cis	-0.792240899	Lyso_MGDG 18:2 (1)	-0.85500735
TAG 48:0	-0.794351543	Alanyglutamic acid	-0.85729205
Morin	-0.801996563	Quinic_Acid_3-Caffÿ2	-0.864571238
LysoPC 18:3_1	-0.851591121	2-methyl-2-phenylacetaldehyde oxime	-0.86570568
CafHex4_4.7_341.0879	-0.856076305	Luteolin	-0.87164376
TAG 52:4	-0.856877792	PC 32:1 (2)	-0.876762448
Cyanidin-3-O-arabinoside	-0.862437032	Catechin	-0.884565049
TAG 52:6 (1)	-0.866375084	Indol-3- Acetyl- L-Aspartic acid	-0.885197688
TAG 56:7	-0.870380912	Allantoin	-0.889323549
DAG 36:3 (1)	-0.87038522	Kynurenine free base	-0.894681244
DGDG 34:0 (2)	-0.872325596	Tomatine	-0.898757321
Tyrosyisoleucine	-0.887039169	Malvin	-0.907801001
Alanytyrosine	-0.89121066	Cyanidin-3-O-arabinoside	-0.90785277
3-5diCQA_7.48_515.12	-0.893744197	TAG 50:0	-0.910721848
TAG 54:4	-0.902181688	QGRAHO5Fer_6.77_933.2288	-0.913649689

Lyso_MGDG 18:2 (2)	-0.903193514	Quinic_Acid	-0.923255627
PE 38:3 (2)	-0.903667548	TAG 52:0	-0.930490598
TAG 52:3	-0.910162683	Erythritol	-0.93595603
PC 34:4 (1)	-0.919679781	Alanytyrosine	-0.943863371
3-4- 5triCQA_8.99_677.1522	-0.9238123	Nicotinic_Acid	-0.95234872
TAG 54:5	-0.942391807	TAG 54:0	-0.965169357
Kynurenine free base	-0.946524699	3-5diCQA_7.48_515.12	-0.967308541
TAG 44:4	-0.951272499	Cholesterol	-0.974701849
PC 38:2 (1)	-0.956721095	TAG 48:0	-0.986831446
TAG 52:2	-0.960288529	DGDG 34:0 (2)	-1.013200145
Inositol-1-Phosphate	-0.989176484	Hesperetin-7-O- glucoside	-1.01718369
TAG 52:5	-0.991171454	NG3_8.16_433.1136	-1.059777573
DAG 36:1	-0.998174468	PC 34:4 (1)	-1.070849577
TAG 54:6	-1.003102118	Malic_Acid,_2-Methyl	-1.078147002
2-methyl-2- phenylacetaldehyde oxime	-1.010635828	Alanine_Beta	-1.089239137
Oenin	-1.012462206	Lyso_DGDG 16:0 (2)	-1.090535525
TAG 54:3	-1.013407908	Arbutin	-1.094690586
DAG 36:4	-1.017053087	PC 32:2 (1)	-1.107561066
NG3_8.16_433.1136	-1.019430142	Tyrosymethionine	-1.120815983
DAG 34:2	-1.049592317	Oenin	-1.12632251
Cholesterol	-1.059009055	TAG 42:1	-1.133304356
TAG 50:5 (2)	-1.07511989	Tryptophyvaline	-1.136572532
Erythritol	-1.075142152	TAG 50:5 (2)	-1.210764202
QGRAHO5Fer_6.77_933 .2288	-1.078068948	TAG 52:5	-1.214946122
Q3G6- R7G_4.67_771.1984	-1.079825324	TAG 52:4	-1.249895702
Arbutin	-1.088237477	TAG 56:7	-1.257327938
PC 32:2 (1)	-1.118980921	Isoleucyisoleucine	-1.263677532
TAG 50:1	-1.139275763	TAG 48:3 (2)	-1.267300661
TAG 48:3 (2)	-1.147636824	TAG 52:2	-1.294501805
TAG 50:3 (1)	-1.155467376	DAG 36:2	-1.297197379
TAG 54:2	-1.170928498	DAG 34:2	-1.331868882
Indol-3- Acetyl- L- Aspartic acid	-1.177051642	TAG 50:3 (1)	-1.340799293
Stigmasterol_(1Tms)	-1.179179017	Guanidine	-1.379350829
TAG 52:1	-1.182807285	beta-Hydroxypalmitic acid	-1.381247837
Guanidine	-1.18412803	TAG 52:7 (1)	-1.388482887
TAG 42:1	-1.187096846	Fructose6Phosphate	-1.393208917
Tryptophyaspartic acid	-1.190400859	PC 38:2 (1)	-1.413829604
Nicotinic_Acid	-1.193030559	TAG 60:5 (2)	-1.456740931
TAG 50:2 (2)	-1.198002317	TAG 52:4	-1.463918685
Tyrosymethionine	-1.201305593	TAG 52:8 (1)	-1.466623408
TAG 54:7	-1.208740808	PE 36:1	-1.541194719
Luteolin	-1.210050374	TAG 48:1	-1.576327187
5-6- Dimethylbenzimidazole	-1.219416186	TAG 54:7	-1.579745748
Tryptophyvaline	-1.227906231	Q3G6- R7G_4.67_771.1984	-1.583725623

TAG 58:3	-1.233457583	TAG 58:4	-1.598981099
TAG 48:1	-1.264543195	SinGlc_5.24_385.1133	-1.607341853
K3G7G_6.14_609.1462	-1.273321215	K3G7G_6.14_609.1462	-1.650757929
TAG 56:3	-1.275417962	TAG 54:4	-1.681932406
TAG 58:1	-1.298327408	TAG 56:4	-1.700297781
TAG 56:2 (1)	-1.304189479	Pipecolic acid	-1.700761948
TAG 56:4	-1.305205604	TAG 58:3	-1.701760039
TAG 60:5 (2)	-1.327376428	TAG 52:3	-1.711420148
TAG 52:7 (1)	-1.335779758	TAG 52:2	-1.713574678
SinGlc_5.24_385.1133	-1.337179691	TAG 54:6	-1.72404786
Is3G7G_6.22_639.1567	-1.340295585	TAG 54:3	-1.739348977
TAG 52:8 (1)	-1.356019325	TAG 54:5	-1.742478879
Shikimic_Acid	-1.359874501	DAG 36:4	-1.748613086
TAG 58:2	-1.366980433	TAG 50:2 (2)	-1.758931556
TAG 58:4	-1.373202058	Cer t18:1/h20:0	-1.764982023
TAG 54:1	-1.383745807	Galactonoil	-1.791529825
TAG 56:1 (1)	-1.393078242	TAG 58:2	-1.847842239
PE 36:1	-1.456071151	TAG 56:3	-1.853789859
TAG 60:2	-1.471551922	Is3G7G_6.22_639.1567	-1.889616743
TAG 60:3	-1.499456471	Mesaconic acid	-1.892762437
Q3G7G_5.68_625.1412	-1.50225486	TAG 50:1	-1.893207323
Cer t18:1/h20:0	-1.516007422	TAG 56:1 (1)	-1.915593434
Galactonoil	-1.538025062	TAG 58:1	-1.939634465
TAG 48:2	-1.552409503	DAG 36:3 (1)	-1.965763748
TAG 52:3	-1.574764313	TAG 50:4 (1)	-1.967046542
SinGlciso1_5.09_385.1133	-1.575604217	TAG 60:2	-1.973768804
TAG 60:1	-1.582882513	TAG 48:2	-2.025861095
Tryptophyalanine	-1.587025505	Tetrahydrofolic acid	-2.04607628
Galacturonic_Acid	-1.639422253	TAG 56:2 (1)	-2.059306895
TAG 50:4 (1)	-1.649698745	TAG 54:2	-2.06711005
TAG 60:4	-1.672817435	SinGlciso1_5.09_385.1133	-2.077176335
Tetrahydrofolic acid	-1.688834095	Scopoletin	-2.104403859
TAG 48:4	-1.714049304	TAG 60:3	-2.13712922
Malic_Acid,_2-Methyl	-1.806627317	TAG 60:4	-2.1486959
Alanine	-1.819175104	TAG 52:1	-2.197950269
TAG 50:5 (3)	-1.858777593	TAG 48:4	-2.339406468
Phenylalanythreonine	-1.86211148	Q3G7G_5.68_625.1412	-2.430851839
Mesaconic acid	-1.966501434	Methionine	-2.45782787
Scopoletin	-2.123273358	TAG 60:1	-2.463039012
Pantethaine	-2.313084571	TAG 54:1	-2.507095382
TAG 52:4	-2.583115957	K3G2-A_6.67_579.1348	-2.639614102
K3G2-A_6.67_579.1348	-2.619174621	Tryptophyaspartic acid	-2.732125822
		Ergothioneine inner salt	-4.781119537

Supplemental Table 6. List of common upregulated genes defined as the genes in SISGT3-ox lines 9 and 31 with F-test FDR value less than 0.05.

ID	Line 9 logFC	FDR	Line 31 logFC	FDR	Annotation
Solyc06g005340.3	9.266931405	2.4836E-44	8.921478759	2.15055E-39	Ras-related protein
Solyc05g026260.1	8.791068626	7.24136E-44	10.36395822	7.71692E-89	High mobility group family
Solyc06g035940.3	8.462955855	2.0325E-184	7.416309111	6.1708E-132	Homeobox-leucine zipper protein ANTHOCYANINLESS 2
Solyc04g078075.1	7.711491493	1.8403E-199	7.538332964	9.0803E-190	Putative F-box/LRR-repeat protein-like
Solyc01g056450.3	7.185156618	1.8011E-99	4.247170066	6.56032E-25	Glutamate-ammonia ligase-like protein
Solyc06g006000.3	7.044842324	3.8291E-122	7.52499414	4.6123E-150	Maternal effect embryo arrest 59
Solyc12g010030.3	5.814477864	3.61284E-17	8.094623458	3.07711E-54	Cytosol aminopeptidase domain-containing protein
Solyc01g056440.1	5.768392735	1.81756E-47	3.636815061	5.87082E-15	Glutamate-ammonia ligase
Solyc12g082730.3	5.70927585	1.50105E-34	6.649359117	1.72068E-50	Kinesin-like calmodulin-binding protein
Solyc01g056430.2	5.626254582	1.6145E-54	3.610219211	3.43828E-21	GS catalytic domain-containing protein
Solyc07g007750.3	5.34268032	1.6492E-89	5.057309521	1.83486E-80	Putative gamma-thionin
Solyc05g053170.3	5.323071695	2.15945E-45	5.957795124	1.43138E-54	chalcone synthase
Solyc07g008570.3	5.076701417	6.84227E-42	4.73867144	4.17843E-36	Purple acid phosphatase
Solyc07g007710.4	4.704814004	4.93806E-39	4.531372627	1.51859E-36	Low-molecular-weight cysteine-rich protein LCR69, putative
Solyc12g010020.3	4.606733047	3.18909E-19	7.072589305	1.3495E-73	Cytosol aminopeptidase domain-containing protein
Solyc01g097240.3	4.404002283	1.38981E-41	3.697349668	1.78614E-29	Pathogenesis-related protein PR-4-like
Solyc08g080480.3	4.156146169	1.37428E-28	2.305627413	4.84737E-09	2S sulfur-rich seed storage protein 2-like
Solyc09g098120.3	4.114261459	1.12692E-65	3.875229247	1.66211E-58	Oil body-associated protein 1A
Solyc08g059700.2	4.094011856	9.70866E-60	4.357604293	4.05812E-68	Histone acetyltransferase
Solyc04g039670.3	4.05502697	8.4402E-132	3.911453005	6.3253E-124	ATP citrate synthase
Solyc06g006022.1	3.901479145	2.64838E-24	3.848735025	5.85901E-24	Probable LRR receptor-like serine/threonine-protein kinase At3g47570
Solyc05g024230.3	3.715802051	2.74354E-56	4.019756009	1.64653E-69	Cytokinin response factor 2
Solyc11g010530.2	3.64042672	2.3364E-128	3.082665061	3.74349E-94	Glycine-rich RNA-binding protein 2-like isoform X1
Solyc09g014750.1	3.638164218	8.32601E-72	3.322794739	2.83713E-60	Carrot ABA-induced in somatic embryos 3

Solyc05g024120.3	3.617939636	5.85544E-37	3.626207331	2.75772E-38	Vacuolar protein-sorting-associated protein 33 homolog
Solyc12g010920.2	3.609698338	6.86774E-33	3.170453047	4.09787E-26	Oleosin
Solyc01g006540.4	3.518430533	1.20064E-30	4.015767347	7.43524E-44	Lipoxygenase
Solyc11g010520.1	3.473018608	8.1586E-70	3.222460767	6.73686E-61	Glycine-rich protein 3 short isoform-like isoform X1
Solyc06g048840.3	3.381650102	8.54994E-28	2.574932789	2.70029E-16	Embryonic abundant protein 1
Solyc04g072470.4	3.335783202	5.32429E-26	2.57538986	1.07636E-15	Defensin-like protein 1 isoform X1
Solyc07g008630.1	3.165054254	2.79703E-25	3.624493798	4.31302E-35	EIX receptor 1
Solyc10g054800.2	3.10196015	4.7979E-15	1.510665985	0.000321145	Aquaporin, MIP family, PIP subfamily
Solyc03g098795.1	3.051793733	3.39384E-92	3.985576857	3.136E-161	Trypsin proteinase inhibitor
Solyc06g034040.1	3.045019966	2.78135E-21	2.789868448	2.73213E-18	Oleosin
Solyc07g007260.4	2.982358149	3.14426E-10	3.553090195	1.98539E-14	Metalloprotease inhibitor
Solyc02g077970.4	2.960150887	2.55886E-36	2.655294236	1.69986E-29	ABA-inducible protein PHV A1-like
Solyc12g082720.1	2.843586188	4.55419E-18	4.029742577	1.41353E-40	Folate-biopterin transporter 1, chloroplastic
Solyc05g053350.3	2.770689405	1.11876E-21	2.311338662	8.03861E-16	Desiccation-related protein PCC13-62
Solyc05g026250.3	2.757449936	1.07763E-16	2.444728553	1.4959E-13	High mobility group family
Solyc09g008670.3	2.717634224	1.02821E-08	4.77935993	6.26749E-32	Threonine dehydratase
Solyc02g085590.4	2.668149115	5.79061E-36	2.513289888	1.36234E-32	Vicilin-like seed storage protein At2g18540
Solyc06g053510.3	2.613607465	6.6244E-118	3.3260008	1.4781E-191	Putrescine N-methyltransferase
Solyc06g073580.4	2.561245508	2.8467E-183	3.295013791	7.52E-288	Hyoscyamine 6-dioxygenase
Solyc07g005670.3	2.430188609	2.88455E-07	6.207812544	2.64972E-84	Integral membrane HRF1 family protein
Solyc06g036470.3	2.356278009	3.89558E-16	2.966043834	8.13709E-26	Receptor-like serine/threonine-protein kinase
Solyc07g008710.3	2.354581588	4.12029E-41	3.092591042	1.08743E-71	Bet v I/Major latex protein domain-containing protein
Solyc10g078220.2	2.3534883	4.22098E-21	2.396494825	2.17581E-22	Coumarate 3-hydroxylase
Solyc04g051730.1	2.272842023	1.46835E-13	3.557306933	2.5646E-35	Alkane hydroxylase MAH1-like
Solyc09g089820.2	2.268990484	9.42923E-21	2.463236601	3.53581E-26	Desacetoxyvindoline 4-hydroxylase
Solyc10g054790.2	2.249132749	2.14566E-14	2.258775729	6.82855E-15	Aquaporin, MIP family, PIP subfamily
Solyc05g050130.4	2.236218992	2.04156E-41	2.107681641	1.64777E-37	chitinase
Solyc10g007960.1	2.235739117	2.52004E-86	3.162739254	1.5747E-162	9-divinyl ether synthase
Solyc11g066710.3	2.210998981	1.7421E-126	2.318545759	1.4398E-141	Phosphatidylcholine-sterol acyltransferase
Solyc06g005720.4	2.178247443	1.61027E-30	2.49988386	7.428E-41	Tropinone reductase
Solyc04g077450.3	2.156496843	3.99074E-46	1.866655088	3.42567E-35	Putative DNA-binding protein-like
Solyc02g021220.1	2.119564291	1.766E-62	1.764718699	3.98994E-44	Subtilisin-like protease

Solyc08g076620.1	2.090278972	3.92053E-20	2.856622435	2.46456E-38	Basic 7S globulin 2 small subunit
Solyc01g099920.4	2.065399427	3.19744E-14	2.367476227	8.03611E-19	PAR1 domain-containing protein
Solyc03g096040.3	2.048096927	2.07648E-31	1.844803793	4.76001E-26	Peroxiredoxin
Solyc01g090360.3	2.043606678	1.156E-11	1.827835474	9.5674E-10	Non-specific lipid-transfer protein
Solyc02g082920.4	2.028181854	1.94387E-22	1.829616403	9.55963E-19	Acidic endochitinase Q
Solyc01g091170.3	2.014233655	4.0987E-43	2.032297595	1.70979E-45	Arginase
Solyc10g073357.1	2.009293228	1.53448E-07	1.108267305	0.004608197	Exocyst complex component Sec3
					PIP2-binding N-terminal domain-containing protein
Solyc10g075050.2	1.998867537	4.51531E-69	1.847865543	8.19069E-60	Non-specific lipid-transfer protein
Solyc01g066680.3	1.958693943	3.00334E-15	1.600785186	1.15989E-10	Phylloplanin
Solyc01g057320.3	1.911167302	2.346E-06	3.001875796	3.22747E-14	Kinesin-like protein KIN-12C isoform X2
Solyc03g116390.4	1.900023076	1.06087E-30	2.043428898	6.22461E-36	Late embryogenesis abundant protein Dc3
Solyc01g094050.1	1.86785314	0.000341279	2.974350554	7.95879E-09	Beige-related and WD-40 repeat-containing protein isoform 1
Solyc03g096260.3	1.823565089	2.49175E-13	1.070942648	2.76863E-05	Yippee domain-containing protein
Solyc09g098400.3	1.812604789	7.39198E-26	1.941918713	5.53904E-30	Glycine-rich RNA-binding protein 2-like isoform X2
Solyc11g006740.3	1.796028949	9.19936E-54	2.174679562	2.91161E-82	F-box protein PP2-B12 isoform X2
Solyc03g112440.1	1.768114064	1.53501E-08	1.604016371	2.01928E-07	Oleosin
Solyc04g051295.1	1.767279135	6.49808E-12	2.203322981	4.33916E-19	RNase H type-1 domain-containing protein
Solyc04g025750.3	1.758290223	1.39034E-31	1.312149943	3.53437E-18	EamA domain-containing protein
Solyc05g026245.1	1.747501082	2.54291E-33	1.800584795	4.68753E-36	Retrovirus-related Pol polyprotein from transposon 'TNT' 1-94
Solyc03g098740.1	1.699068029	5.29477E-16	1.98234594	1.40192E-22	Nb cell death marker
Solyc02g067870.3	1.687154262	9.42947E-06	1.754861584	2.17198E-06	Fatty-acid-binding protein 1-like isoform X2
Solyc01g010600.4	1.68695065	7.48835E-14	1.882589249	1.40907E-17	Homeobox-leucine zipper protein
Solyc10g055620.2	1.661994862	1.3115E-38	1.516829484	7.4992E-33	Heparan-alpha-glucosaminide N-acetyltransferase-like isoform X1
Solyc04g076330.3	1.647685905	1.60462E-05	1.924834014	1.71722E-07	Pentatricopeptide repeat-containing protein
Solyc10g081550.2	1.638258046	3.72566E-10	2.543787677	1.73683E-27	Nicotine N-demethylase
Solyc05g150130.1	1.636153318	2.07946E-05	2.979480219	6.79719E-16	Alcohol dehydrogenase
Solyc02g082880.2	1.622087157	1.06348E-92	1.903854129	5.4694E-133	Acyl-activating enzyme 2
Solyc08g076970.3	1.617222927	1.25522E-09	2.619341137	8.90163E-27	Peptidase M20 dimerisation

Solyc09g090970.4	1.605522826	1.22712E-17	2.240560068	3.31208E-33	domain-containing protein
Solyc06g075280.3	1.592808951	6.74578E-14	1.947580393	1.15848E-21	Pathogenesis-related protein STH-21
Solyc07g007620.3	1.560943904	9.22104E-10	1.283627802	4.16829E-07	Vicilin-like seed storage protein At2g28490
Solyc04g076640.3	1.556846107	9.6123E-05	1.612129654	2.92141E-05	monogalactosyldiacylglycerol synthase
Solyc09g092600.3	1.549456316	0.001424489	1.264744327	0.007699562	rhamnogalacturonan endolyase
Solyc09g007150.3	1.529507978	9.71645E-17	1.467129315	4.26453E-16	Cytochrome P450, family 71, subfamily B, polypeptide 23
Solyc09g091000.4	1.524227252	9.52124E-10	2.137710319	2.13866E-18	GST N-terminal domain-containing protein
Solyc01g112230.4	1.516329396	4.19758E-12	0.581166268	0.012969166	Pathogenesis-related protein STH-21
Solyc11g072380.2	1.502775017	7.70807E-13	1.429565959	4.37394E-12	Plant EC metallothionein-like protein family 15
Solyc01g020528.1	1.492422275	1.09465E-07	0.629270744	0.034964113	Vicilin-like seed storage protein At2g28490
Solyc05g047530.3	1.464172912	8.65371E-07	1.143214356	0.000109903	Glyoxal oxidase N-terminal domain-containing protein
Solyc08g077490.2	1.450106739	0.03761144	2.906234283	8.33752E-06	Cinnamate 4-hydroxylase
Solyc04g071540.4	1.445534814	5.92592E-62	2.094814371	6.4058E-126	Pleckstrin (PH) domain-containing protein isoform 2
Solyc07g006620.4	1.442680845	3.66833E-08	1.999526369	2.42652E-15	Sterol 3-beta-glucosyltransferase UGT80B1
Solyc04g050520.3	1.437712866	0.004940434	2.661719556	8.99877E-08	Probable receptor-like serine/threonine-protein kinase At5g57670
Solyc04g072043.1	1.43091229	3.23212E-13	1.238104924	2.08464E-10	Translational activator GCN1
Solyc07g008590.1	1.424092001	1.09216E-10	1.883647394	2.72333E-19	Polyadenylate-binding protein
Solyc04g054740.3	1.392877247	1.07264E-62	1.805424952	1.0219E-105	EIX receptor 1
Solyc03g111130.1	1.38794687	0.000164765	1.580097078	7.43378E-06	inositol-3-phosphate synthase
Solyc07g026920.1	1.380924772	0.000270757	2.732187888	9.39989E-15	Malate synthase
Solyc03g025610.3	1.368303103	0.000434271	1.861327711	8.35929E-07	Hippocampus abundant transcript-like protein 1
Solyc03g025200.3	1.364578704	4.67631E-35	0.43158867	0.000252173	tripeptidyl-peptidase II
Solyc04g051280.4	1.355325607	4.22122E-91	1.530722739	2.909E-116	Protein DETOXIFICATION
Solyc01g105070.3	1.339820636	7.36285E-40	0.683217852	4.55734E-11	Eukaryotic translation initiation factor 5B-like isoform X1
Solyc09g082280.3	1.339183106	3.90881E-07	2.50745185	1.07299E-25	Peroxidase
					Non-specific lipid-transfer protein-like protein At5g64080 isoform X2

Solyc06g072290.3	1.323500599	1.96741E-09	1.371821009	2.00663E-10	Kinase-interacting family protein-like
Solyc06g073570.4	1.319381192	4.7513E-32	2.3823515	1.5727E-104	Nicotine N-demethylase
Solyc02g079980.3	1.319101266	5.38007E-13	0.682259717	0.0002942	Sulfite exporter TauE/SafE family protein
Solyc07g007190.3	1.314841964	9.04961E-15	1.613272787	3.16145E-22	Peptidyl-prolyl cis-trans isomerase cyp8
Solyc04g007430.2	1.312906925	1.34644E-22	1.215469488	5.29769E-20	Transcription factor PIF3
Solyc01g007940.4	1.310863751	2.43504E-66	1.274089272	2.44329E-63	alanine transaminase
Solyc10g078770.2	1.305387686	1.07931E-05	1.204325455	3.18299E-05	Seed maturation protein LEA 4
Solyc08g061890.4	1.292978041	0.000506194	2.205909353	2.10324E-10	E3 ubiquitin-protein ligase RBBP6
Solyc10g007800.3	1.288057508	2.97994E-11	1.245308122	4.86734E-11	Protodermal factor 1
Solyc09g083060.4	1.267676543	2.94202E-10	1.363627157	1.4961E-12	RING-type E3 ubiquitin transferase
Solyc06g005430.1	1.254662837	1.18531E-15	0.809369675	3.14393E-07	CENP-T/Histone H4 histone fold domain-containing protein
Solyc04g076550.3	1.253566202	0.038898817	2.573915775	6.66777E-06	FMP27/BLTP2/Hobbit GFWDK motif-containing RBG unit domain-containing protein
Solyc01g112340.3	1.252965972	0.007454718	2.005500541	7.1519E-06	Brefeldin A-inhibited guanine nucleotide-exchange protein 1
Solyc02g067150.4	1.251905374	9.74711E-06	1.38696213	3.10504E-07	Latex abundant protein 1
Solyc12g089010.3	1.244075515	0.009419429	1.445710569	0.00140794	RNA helicase
Solyc08g014490.1	1.243617785	5.3256E-36	1.842490047	3.44832E-80	Acylsugar acyltransferase 3
Solyc01g102550.4	1.242504011	0.004507627	2.178180513	1.48561E-07	Nuclear pore complex protein NUP160 domain-containing protein
Solyc08g074680.3	1.242471386	3.64154E-19	0.334497226	0.023466115	catechol oxidase
Solyc04g064470.2	1.242289462	8.27621E-07	1.486841927	5.90583E-10	Dehydroascorbate reductase
Solyc04g014750.1	1.233563275	7.10092E-12	0.96113098	8.47771E-08	TNFR/CD27/30/40/95 cysteine-rich region
Solyc07g064600.3	1.224995552	0.00083389	4.100932112	1.32346E-47	Inducible plastid-lipid associated protein
Solyc08g067870.2	1.202770948	0.016651131	2.122453233	8.34649E-06	FMP27 GFWDK domain-containing protein
Solyc05g016460.2	1.20126287	0.007242547	2.431209865	1.3821E-08	Mediator of RNA polymerase II transcription subunit 23
Solyc07g007755.1	1.196620867	2.01459E-36	1.162271895	1.32319E-34	Low-molecular-weight cysteine-rich protein LCR69, putative
Solyc04g015120.3	1.186899797	2.33264E-06	0.607939059	0.018357696	U-box domain-containing protein 35
Solyc09g082340.2	1.18534132	7.49742E-33	1.113083565	2.23387E-29	Vicilin-like antimicrobial peptides 2-2

Solyc03g034455.1	1.180865165	1.02739E-15	0.803635023	6.70191E-08	RING-type E3 ubiquitin transferase
Solyc10g085750.2	1.173336033	2.82994E-05	0.932603808	0.000700623	Polyadenylate-binding protein
Solyc02g077020.3	1.169980133	6.09966E-66	1.501212879	6.1311E-107	Phospholipase A1
Solyc07g055100.4	1.166627003	1.7384E-05	0.985129888	0.000211734	6b-interacting protein 1
Solyc04g071083.1	1.165784435	4.66567E-11	0.448329114	0.014544636	Extensin domain-containing protein
Solyc01g106860.4	1.164447421	6.56729E-06	0.965498123	0.000145077	Serine/threonine-protein kinase TOR
Solyc10g080870.3	1.163069269	8.9984E-19	1.669200817	1.10941E-39	Alkane hydroxylase MAH1
Solyc01g006660.3	1.16105779	2.06892E-19	0.982432977	2.18077E-14	CO(2)-response secreted protease
Solyc05g014750.2	1.158720138	0.002706097	1.503081783	4.0696E-05	DNA topoisomerase
Solyc05g050360.3	1.1582734	2.36723E-05	1.585310203	4.85139E-10	Cyclic nucleotide-binding domain-containing protein
Solyc10g045240.2	1.157784309	8.12565E-50	1.17075209	4.02525E-51	Beta-glucosidase 13
Solyc09g090990.2	1.157596556	4.89556E-10	1.288232121	1.75206E-12	Pathogenesis-related protein STH-21
Solyc08g074520.2	1.155057182	0.027708862	2.322492517	2.91751E-06	TATA-binding protein-associated factor BTAF1
Solyc08g014330.3	1.153485403	1.03481E-55	1.280316038	2.49334E-69	N-methylputrescine oxidase 1, peroxisomal
Solyc07g007180.4	1.151757828	1.75695E-10	1.461289008	5.12179E-17	RING-H2 finger protein ATL2K
Solyc05g048860.3	1.150723939	0.000638856	1.60569148	3.2091E-07	DEAD-box ATP-dependent RNA helicase 8
Solyc04g080620.3	1.149656762	9.81458E-14	1.711410306	5.53774E-31	mannan endo-1,4-beta-mannosidase
Solyc12g098607.1	1.148792003	0.001725652	2.936666021	2.92358E-16	Cysteine proteinase inhibitor B
Solyc05g007950.4	1.147822499	1.82801E-22	1.547888075	9.2615E-42	Ribonuclease T(2)
Solyc02g092490.3	1.143160902	8.59391E-20	1.336843535	5.02441E-28	Probable N-acetyltransferase HLS1
Solyc01g091540.3	1.142805945	6.73448E-13	1.041518982	3.44794E-11	Growth-regulating factor
Solyc02g030100.4	1.138926663	8.09448E-05	1.920440387	2.80413E-12	Vacuolar protein sorting-associated protein 54 C-terminal domain-containing protein
Solyc11g062320.2	1.13751428	0.013247223	2.221388651	2.02731E-07	Proteasome-associated protein ECM29 homolog
Solyc04g074880.2	1.128153919	6.44006E-07	1.849378079	6.9714E-19	Probable purine permease
Solyc04g150161.1	1.118539855	3.81017E-22	0.636697515	6.04781E-08	Extensin domain-containing protein
Solyc07g007050.1	1.118393466	4.13467E-17	0.422926007	0.002277101	Zinc finger, SWIM-type
Solyc04g076480.3	1.117062194	1.58004E-28	1.331880948	3.15067E-41	Serine/threonine-protein kinase CTR1
Solyc04g039940.3	1.109519231	0.00053301	1.448873256	1.882E-06	Pentatricopeptide repeat-containing protein
Solyc01g106840.2	1.106628764	0.000561185	1.413974111	2.58405E-06	Serine/threonine-protein kinase TOR
Solyc05g011890.1	1.106170885	3.96869E-07	1.908563199	1.63093E-20	Sulfotransferase
Solyc08g061520.3	1.100589846	0.005681774	1.98373131	1.16947E-07	Myosin-15

Solyc05g024160.3	1.095705729	5.94459E-08	0.963142105	1.24791E-06	Pyruvate dehydrogenase E1 component subunit beta
Solyc05g026070.1	1.091780068	0.00735803	1.84250904	1.17793E-06	Tyrosine-protein kinase ephrin type A/B receptor-like domain-containing protein
Solyc08g081710.3	1.086947942	1.38349E-08	1.200462874	1.189E-10	Membrane-associated kinase regulator 2
Solyc12g005260.1	1.081705582	0.003525055	2.029925174	1.76339E-09	Kinesin motor domain-containing protein
Solyc03g116700.4	1.080504357	1.87525E-09	0.631853511	0.000555487	Cucumber peeling cupredoxin-like
Solyc08g082480.3	1.079682136	8.01435E-19	1.273801515	1.30882E-26	1-phosphatidylinositol 4-kinase
Solyc01g006400.4	1.078085728	1.02551E-27	1.007852656	1.5074E-24	Cysteine-rich extensin-2
Solyc02g080950.3	1.072472846	4.09707E-05	1.47071479	2.5575E-09	Pentatricopeptide repeat-containing protein
Solyc07g064990.3	1.072444176	0.000416841	1.288145056	7.77877E-06	Indole-3-acetate O-methyltransferase 1
Solyc01g112190.3	1.06576936	7.85401E-07	1.19928287	5.27555E-09	Plant regulator RWP-RK family protein
Solyc11g065250.1	1.065723093	0.00023688	1.92889339	2.54854E-13	DYW domain-containing protein
Solyc04g076280.4	1.062760495	6.70869E-07	1.122736449	4.79235E-08	MADS transcriptional factor
Solyc03g093250.2	1.062531373	0.002170238	1.779032635	7.28658E-08	SMC hinge domain-containing protein
Solyc04g015610.3	1.062284829	2.68348E-42	0.894131371	9.54704E-31	DUF642 domain-containing protein
Solyc02g086310.2	1.06160128	1.02187E-19	0.60238787	4.15746E-07	Bifunctional inhibitor/plant lipid transfer protein/seed storage helical domain-containing protein
Solyc01g108670.4	1.051663658	3.58139E-10	1.296287445	3.36641E-15	Kinesin-like protein KIN-12D isoform X1
Solyc08g068040.3	1.046750819	0.019364382	1.873345933	7.56466E-06	Putative Coatomer subunit beta'-1
Solyc11g062220.2	1.046660648	0.019703974	2.010181346	2.22129E-06	RDR2-independent DNA methylation protein
Solyc10g052490.2	1.042281208	0.000439185	1.303399306	2.90824E-06	Phenylcoumaran benzylic ether reductase POP1
Solyc06g005520.4	1.04208854	5.08745E-18	1.068737631	1.94359E-19	Probable serine/threonine-protein kinase PBL19
Solyc12g098630.2	1.041378014	1.14997E-15	1.150901534	1.39607E-19	Phragmoplast-associated kinesin-related protein
Solyc06g006090.1	1.036123445	1.63006E-11	1.12478948	7.46742E-14	Josephin-like protein (Fragment)
Solyc11g066100.2	1.034021774	1.0564E-20	0.724347524	8.97054E-11	Putative mediator of RNA polymerase II transcription subunit 37c

Solyc06g005970.2	1.029796126	1.89097E-32	1.086926525	2.42535E-37	Beta-xylosidasealpha-l-arabinofuranosidase 2
Solyc01g109750.2	1.019889639	8.63746E-05	0.662258891	0.010658435	Syntaxin-related protein KNOLLE
Solyc06g042960.3	1.019215635	0.041308017	1.561849497	0.000809189	Vacuolar protein sorting/ targeting protein like
Solyc02g070970.1	1.016125823	0.001428038	2.393695846	8.40819E-19	Chlorophyll a-b binding protein, chloroplastic
Solyc03g007720.3	1.015081147	9.76431E-06	1.065609904	1.3048E-06	Membrane-associated kinase regulator 2
Solyc04g050160.4	1.01128488	0.015334139	2.212812496	8.5936E-09	Chromatin remodeling complex subunit isoform 3
Solyc02g071500.2	1.006743143	0.00110368	0.889373884	0.002872828	Codeine O-demethylase
Solyc10g081810.3	1.004031637	2.32926E-08	0.413207863	0.027577331	MD-2-related lipid-recognition domain-containing protein
Solyc01g060050.3	0.99287018	0.022240436	1.913078031	2.42993E-06	PH-interacting protein isoform X1
Solyc07g054720.2	0.988751749	4.47101E-17	0.363324346	0.003467774	Proteinase inhibitor type-2 CEVI57
Solyc05g007010.3	0.988552361	7.22821E-05	1.474075547	1.85656E-10	Galactose oxidase-like Early set domain-containing protein
Solyc08g074620.3	0.98535454	8.52969E-29	1.247629639	3.118E-46	catechol oxidase
Solyc10g076920.3	0.980700521	1.24099E-05	0.799833078	0.000294832	ABSCISIC ACID-INSENSITIVE 5-like protein 2
Solyc02g082740.1	0.978984679	6.567E-05	0.726922706	0.0026271	Dirigent protein (Fragment)
Solyc12g005420.2	0.976615814	3.9777E-06	1.201597895	3.63251E-09	B box-type domain-containing protein
Solyc05g053120.1	0.97655321	3.78638E-30	1.282361248	8.89672E-54	Zeatin O-xylosyltransferase
Solyc10g085740.2	0.97551171	0.000508658	1.033505244	0.000117197	GDSL esterase/lipase
Solyc06g072310.3	0.97039363	0.000194792	0.904760711	0.00033598	Homeodomain GLABROUS 11
Solyc07g007440.1	0.969698321	3.12996E-10	1.174908965	1.54118E-15	RING-H2 finger protein ATL43
Solyc12g049520.2	0.969095145	0.010113541	2.072238948	1.67643E-09	COP1-interacting protein 7
Solyc09g072610.3	0.968672254	5.0993E-11	1.099253752	1.07186E-14	Long-chain-alcohol oxidase
Solyc07g007970.3	0.967184136	2.20575E-19	0.773604555	5.15325E-13	Membrane protein YjcL
Solyc07g056060.4	0.958940752	2.65197E-12	0.83128865	9.65093E-10	MHD1 domain-containing protein
Solyc08g016060.1	0.953170556	0.040664488	1.853972216	1.74621E-05	Guanine nucleotide exchange factor SPIKE 1
Solyc11g062250.2	0.94686836	0.004200088	1.231957652	6.34695E-05	SLOW GROWTH1
Solyc08g067530.1	0.944945409	7.81887E-14	0.704833856	2.99515E-08	Non-specific lipid-transfer protein
Solyc01g091320.3	0.944695668	2.41439E-19	1.569128745	3.72783E-52	Methylsterol monooxygenase 1-1-like
Solyc12g099440.3	0.941515714	5.25097E-38	0.992391754	2.322E-42	Glyoxysomal fatty acid beta-oxidation multifunctional protein MFP-a

Solyc03g118790.3	0.940066099	0.016468303	1.60717041	9.04615E-06	Pentatricopeptide repeat-containing protein
Solyc07g005500.2	0.935678288	0.00188838	1.604209789	1.54912E-08	Tensin phosphatase
Solyc01g006360.4	0.934680395	0.037458375	2.115895732	5.07769E-07	1,3-beta-glucan synthase
Solyc06g067980.3	0.932266591	1.33604E-05	0.778190861	0.000220229	Anther-specific protein
Solyc03g119940.3	0.930218433	3.25737E-17	0.630123077	1.48725E-08	Trichohyalin
Solyc07g007560.3	0.929594485	3.25227E-13	1.199107356	1.00706E-22	Phosphate transporter 45
Solyc10g007120.4	0.928562742	5.4215E-38	0.937931281	1.37014E-39	DUF3082 domain-containing protein (Fragment)
Solyc02g085720.1	0.926723019	2.98999E-09	0.845005837	3.36097E-08	Geranylgeranyl pyrophosphate synthase
Solyc03g058390.2	0.92595774	0.004611517	1.8519275	2.3516E-09	Eukaryotic translation initiation factor 5B
Solyc02g069490.4	0.921739097	1.82532E-24	0.87693766	1.84972E-22	Sterol side chain reductase
Solyc07g052230.3	0.918252535	1.45167E-14	0.894439545	2.60554E-14	L-ascorbate oxidase
Solyc12g005670.2	0.91821178	3.02315E-07	0.939348968	7.44101E-08	Potassium transporter
Solyc03g098420.3	0.916163483	0.013128364	1.780806728	1.90745E-07	DYW domain-containing protein
Solyc04g076260.2	0.916157735	1.92395E-05	0.506026553	0.020007037	Putative WRKY transcription factor 51-like
Solyc04g074160.3	0.911742922	0.021715337	1.600751463	1.07475E-05	Pentatricopeptide repeat-containing protein
Solyc06g059850.2	0.907717272	5.50566E-07	1.192171225	7.00108E-12	2-oxoisovalerate dehydrogenase subunit alpha 1, mitochondrial
Solyc12g100200.2	0.904564665	1.44816E-30	0.964556858	2.4598E-35	Selenoprotein O
Solyc06g005910.4	0.903136481	1.06711E-11	0.706896989	9.83916E-08	Tubulin beta chain
Solyc08g042030.3	0.900946661	0.00096981	1.324421649	2.52299E-07	Armadillo repeat-containing kinesin-like protein 1 isoform X7
Solyc10g009080.4	0.899029048	1.78049E-05	0.829601441	5.02793E-05	Squamosa promoter-binding-like protein
Solyc12g010820.2	0.898649613	1.68355E-07	0.637855022	0.000191427	Seed biotin-containing protein SBP65
Solyc07g007800.3	0.897888578	1.86104E-10	1.533062864	5.52543E-30	Heptahelical transmembrane protein 1-like
Solyc12g099610.1	0.897389993	6.63252E-05	0.825387426	0.000166146	Flowering-promoting factor 1-like protein 3
Solyc11g066690.2	0.8967891	3.89436E-05	0.585690217	0.007041783	RecQ-mediated genome instability protein 2
Solyc12g006350.3	0.893408166	0.014724533	1.349921299	8.78783E-05	Auxin response factor
Solyc07g008060.1	0.889458825	8.58568E-13	0.786226854	2.14405E-10	Epsin N-terminal domain-containing protein / clathrin assembly protein-related
Solyc08g066010.2	0.88553661	0.017991638	1.675204026	1.79211E-06	Calcineurin-binding protein 1 isoform X2

Solyc03g080150.3	0.884773775	8.21125E-21	0.342642339	0.000551957	Peroxidase
Solyc08g066120.4	0.884302873	0.000523158	1.414091385	6.46135E-09	Polynucleotide phosphorylase 1
Solyc11g008260.2	0.883670834	7.14502E-11	0.856562477	1.18766E-10	Cysteine proteinase
Solyc09g010690.4	0.881564284	9.22421E-19	0.946618622	1.07952E-21	E3 ubiquitin-protein ligase XBAT31
Solyc11g066670.1	0.876627255	4.51249E-10	0.598977389	2.27733E-05	Glycosyltransferase
Solyc09g065180.3	0.876020623	6.46672E-24	0.909976867	2.90319E-26	Chloroplast stem-loop binding protein of 41 kDa a, chloroplastic
Solyc11g013820.2	0.875222984	0.030275971	2.006343263	1.62192E-08	1-phosphatidylinositol-3-phosphate 5-kinase
Solyc07g150103.1	0.872994519	5.42348E-23	0.825522634	5.44849E-21	Phytoeyanin domain-containing protein
Solyc07g055840.3	0.870993575	3.7903E-09	0.703653693	1.51269E-06	Citrate synthase
Solyc12g096070.2	0.869021254	3.69811E-16	0.697752511	6.11068E-11	Growth-regulating factor
Solyc06g063330.3	0.86886096	0.00020328	0.59813797	0.009976268	V-type proton ATPase catalytic subunit A
Solyc02g081120.4	0.867687683	2.69206E-07	1.231219935	4.10091E-15	Homeobox protein SHOOT MERISTEMLESS
Solyc12g056200.2	0.86679047	0.000149546	1.141827829	1.31012E-07	Transferring glycosyl group transferase
Solyc12g017380.3	0.865712488	5.33044E-12	1.464958095	6.67622E-36	Organic cation/carnitine transporter 3
Solyc07g007370.3	0.860652489	1.25243E-21	0.659529881	2.42557E-13	NEDD8 ultimate buster 1
Solyc05g005330.3	0.860276958	2.32211E-05	1.223416577	1.83038E-10	Late blight resistance protein R1-A
Solyc06g075440.3	0.859895099	0.003006671	1.413101062	7.99754E-08	Nitrate excretion transporter 1, putative
Solyc02g064690.3	0.859342844	7.01739E-20	1.029965667	5.40006E-29	Probable N-acetyltransferase HLS1
Solyc11g010620.3	0.858947787	0.002178274	0.967906634	0.00029863	Basic helix-loop-helix (BHLH) DNA-binding superfamily protein (Fragment)
Solyc01g080460.3	0.858873739	1.15368E-22	0.987092713	4.2471E-30	pyruvate, phosphate dikinase
Solyc03g006900.2	0.858809951	0.001133552	0.710506027	0.005298767	Protein kinase domain-containing protein
Solyc08g075950.3	0.855201759	4.49459E-14	0.70462206	4.29658E-10	Growth-regulating factor
Solyc12g040790.2	0.855041364	1.97378E-28	0.779444098	4.37449E-24	Phosphoethanolamine N-methyltransferase
Solyc02g065220.4	0.85222826	6.61419E-06	0.868842912	2.08556E-06	Geraniol 10-hydroxylase
Solyc08g083270.3	0.85088908	0.000148541	0.490164301	0.030106373	Hop-interacting protein THI143
Solyc07g063080.4	0.85063641	5.94388E-12	0.938343158	5.42375E-15	Dynamin-related protein 5A
Solyc03g117630.1	0.850254734	4.19496E-05	0.943686033	1.95904E-06	Heat shock protein 70
Solyc04g079480.2	0.850210176	4.20158E-05	0.500919991	0.016434507	Serpin domain-containing protein
Solyc08g008020.1	0.848236934	1.02198E-17	0.933821738	9.25508E-22	FT-interacting protein 1

Solyc07g007850.2	0.847914673	0.002257576	1.68045217	8.77304E-11	Spen paralogue and orthologue SPOC C-terminal domain-containing protein
Solyc07g065210.4	0.847059562	5.24592E-22	0.840052618	3.87667E-22	Kinesin-like protein KIN-12F isoform X1
Solyc02g067100.3	0.844839932	6.75324E-12	0.738423223	1.16981E-09	TPX2 C-terminal domain-containing protein
Solyc02g085430.4	0.844765782	0.000433796	0.971000882	2.0166E-05	non-specific serine/threonine protein kinase
Solyc06g082850.4	0.843490688	0.000169707	0.627349309	0.004442115	High mobility group B protein 6
Solyc11g011030.2	0.842572666	6.7124E-05	1.476113177	6.02835E-14	Jasmonate Zim-domain protein
Solyc06g054620.4	0.842226265	1.38944E-06	0.789587519	3.75422E-06	Zinc finger CCH domain-containing protein 58
Solyc09g008203.1	0.841575506	9.67781E-06	0.933704059	2.00838E-07	Mannan synthase
Solyc04g078390.3	0.841460587	2.80342E-16	0.577986032	2.70066E-08	F-box protein GID2
Solyc01g108630.3	0.837263072	1.33686E-31	0.999970104	1.70979E-45	Ferredoxin--nitrite reductase, chloroplastic
Solyc02g069250.4	0.836967764	0.000105099	1.29853092	4.65922E-11	Probable cinnamyl alcohol dehydrogenase 6
Solyc07g054780.1	0.836496852	3.91538E-06	0.505159768	0.005676456	Wound-responsive family protein
Solyc02g093760.4	0.833084634	9.81685E-07	0.61650336	0.00025951	LON peptidase N-terminal domain and RING finger protein 3-like
Solyc08g014000.3	0.832792076	5.86623E-41	0.994992347	2.77639E-58	Linoleate 9S-lipoxygenase A
Solyc08g076060.3	0.8316771	2.62526E-07	1.055008041	3.93889E-12	Receptor-like serine/threonine-protein kinase
Solyc07g017990.3	0.831673344	7.9459E-05	1.311153132	3.89424E-11	DNA ligase
Solyc04g074790.3	0.8299299	2.18279E-07	0.695501139	1.01885E-05	RING-type E3 ubiquitin transferase
Solyc09g056130.4	0.827783987	0.013172477	1.642218197	6.56384E-08	Ribosomal protein L15
Solyc05g050840.3	0.826978276	3.3928E-09	0.838955116	6.38313E-10	Hop-interacting protein
Solyc03g111140.3	0.826784578	8.30575E-37	0.984269643	5.10449E-52	Malate synthase
Solyc08g007800.3	0.824512226	0.001017575	1.174522973	5.1569E-07	SPX domain-containing protein
Solyc05g007510.4	0.822559489	3.11484E-06	1.19418426	4.76501E-13	RNA dependant RNA polymerase
Solyc06g064550.3	0.822355616	9.85241E-25	0.968461103	1.67249E-34	Bifunctional aspartokinasehomoserine dehydrogenase, chloroplastic
Solyc08g062940.4	0.822198126	5.36944E-09	0.637306851	5.63699E-06	Putative Grave disease carrier protein
Solyc06g036290.3	0.821108064	1.44035E-21	0.509302632	5.46537E-09	Heat shock protein 83
Solyc09g018340.2	0.819275323	0.031911593	1.852737345	1.33332E-07	Mon2/Sec7/BIG1-like HUS domain-containing protein
Solyc12g007020.2	0.813140544	2.6015E-07	0.797789664	2.29935E-07	DUF936 domain-containing protein
Solyc09g005330.3	0.813082653	0.033164934	1.543747997	1.48369E-05	Symplekin

Solyc04g009820.3	0.813000017	1.16657E-09	0.418554874	0.002233466	GRF1-interacting factor 1
Solyc09g075550.3	0.812716223	9.24623E-18	0.867843164	7.7067E-21	Cellulose synthase-like protein D5
Solyc12g019100.2	0.81204829	0.016270522	1.808877435	7.499E-09	valine--tRNA ligase
Solyc12g027800.1	0.811838721	0.001302132	1.088699302	4.42258E-06	Rhodanese-like domain-containing protein 8, chloroplastic
Solyc10g079410.2	0.811772977	7.32081E-28	0.887204406	6.35607E-34	Patatin-like phospholipase family protein isoform 1
Solyc07g008290.4	0.810000319	0.00021994	1.193809851	8.98056E-09	O-fucosyltransferase family protein
Solyc01g087080.4	0.808186998	3.10168E-11	0.451864536	0.000272338	TPX2 central domain-containing protein
Solyc06g075090.4	0.806136411	6.40213E-14	0.653803521	9.50761E-10	Cytokinin riboside 5'-monophosphate phosphoribohydrolase
Solyc05g050790.3	0.805235206	0.006177697	0.634386635	0.026469537	Ethylene-responsive transcription factor 13
Solyc06g007780.3	0.803084101	2.79463E-12	0.409451466	0.000517177	Putative ras GTPase-activating protein-binding protein 1-like
Solyc10g054910.1	0.802548664	0.000231032	0.48464197	0.026603946	Peptidyl-prolyl cis-trans isomerase
Solyc11g018720.1	0.801858834	0.00114023	1.225919735	9.70373E-08	ALBINO3-like protein 2, chloroplastic
Solyc01g087500.3	0.801778103	1.56223E-18	1.04333885	2.66324E-31	DNA topoisomerase 2
Solyc05g015250.2	0.801324554	0.018351018	1.388386061	6.44133E-06	Mannosyl-oligosaccharide glucosidase
Solyc02g083610.4	0.801112086	1.95237E-07	0.473541507	0.00231001	Nitrate regulatory gene2 protein-like
Solyc04g072200.3	0.800602307	0.002791728	1.088215449	1.8989E-05	Testis specific protein Y-linked
Solyc06g083720.2	0.799197694	0.021394608	1.604269645	1.22113E-07	Subtilisin-like protease SBT1,2
Solyc02g071800.3	0.798398472	3.99953E-17	0.584923335	8.653E-10	Putative LRR receptor-like serine/threonine-protein kinase
Solyc06g052010.2	0.798038301	1.45867E-06	0.679654632	2.48919E-05	Protein IQ-DOMAIN like
Solyc07g018290.4	0.797747051	3.41042E-14	1.210663598	3.76901E-32	AP2-like ethylene-responsive transcription factor AIL5
Solyc02g086456.1	0.79727682	0.01470156	1.769442742	4.95311E-09	Enolase-phosphatase E1-like
Solyc01g106340.3	0.796899923	7.24797E-07	1.015128444	5.15173E-11	Fatty acid amide hydrolase
Solyc04g076320.4	0.795364077	1.30645E-11	0.68482265	4.79634E-09	Fumarate lyase N-terminal domain-containing protein
Solyc07g007110.4	0.790853347	3.77166E-16	0.904712208	1.15848E-21	Peptidyl-prolyl cis-trans isomerase
Solyc02g063480.2	0.790698581	1.18002E-10	1.689635037	3.70402E-50	Xyloglucan-specific endoglucanase inhibitor 10
Solyc03g007130.4	0.79029278	1.66742E-18	0.796802678	1.6275E-19	65-kDa microtubule-associated protein 3

Solyc03g119220.3	0.789819999	2.67703E-13	0.719537944	1.69009E-11	Kinesin-like protein NACK2
Solyc03g122360.3	0.789028988	9.98254E-22	0.867359692	1.25493E-26	Flavonoid 3'-monooxygenase
Solyc11g056640.3	0.788336301	2.33897E-06	0.939030163	3.14232E-09	Putative Golgin subfamily A member 4
Solyc07g026650.3	0.784253939	4.35643E-05	0.846659953	4.49102E-06	1-aminocyclopropane-1-carboxylate oxidase 1
Solyc04g076660.3	0.783979966	6.35316E-05	0.647691747	0.000734952	rhamnogalacturonan endolyase
Solyc02g080150.3	0.780284627	8.58133E-07	0.564324642	0.000356185	DDE Tnp4 domain-containing protein
Solyc04g016080.2	0.778203298	3.89492E-08	0.693203458	6.04569E-07	Kinesin-like protein KIN-14L isoform X2
Solyc07g007980.3	0.777996713	4.67593E-15	0.615752187	5.34755E-10	Receptor-like serine/threonine-protein kinase At3g01300
Solyc11g069790.2	0.77741228	1.40325E-32	0.898947032	1.80927E-43	RuBisCO large subunit-binding protein subunit alpha
Solyc01g106540.4	0.777088998	8.00995E-09	0.586943446	1.22038E-05	TPX2 central domain-containing protein
Solyc05g008620.4	0.777060581	0.003846619	0.527470613	0.047057688	GINS subunit domain-containing protein
Solyc04g082840.4	0.776990807	2.51685E-20	0.650038678	9.47558E-15	B2-type cyclin dependent kinase
Solyc06g062460.3	0.774984682	2.54741E-10	1.283516512	3.32958E-29	Transcription factor bHLH87
Solyc10g076510.2	0.773803352	7.3974E-11	0.799325026	7.99029E-12	pyruvate decarboxylase
Solyc04g076100.4	0.773485486	3.04313E-12	1.077415807	1.87963E-23	Pesticidal crystal cry8Ba protein
Solyc02g078950.4	0.772212251	2.07166E-25	0.84139273	9.54007E-31	Beta-galactosidase 8
Solyc10g018300.3	0.771242259	4.90301E-19	1.155416499	1.0276E-41	transketolase
Solyc11g045215.1	0.770988219	0.030741601	1.297863175	8.27664E-05	DEAD-box ATP-dependent RNA helicase 50
Solyc07g045010.3	0.770431137	2.52232E-12	0.630316966	7.97707E-09	Aspartyl/glutamyl-tRNA(Asn/Gln) amidotransferase subunit
Solyc08g080220.3	0.768432381	0.003094668	1.345260696	2.97672E-08	DNA-directed RNA polymerase
Solyc04g077830.2	0.767475541	3.30494E-10	1.028543331	2.86226E-18	No pollen germination related 1
Solyc07g054920.2	0.767200912	1.67742E-08	0.755569167	1.39968E-08	Anthocyanin synthase (Fragment)
Solyc03g062700.4	0.765047696	4.26397E-07	0.906729477	2.69822E-10	Survival motor neuron interacting protein 1
Solyc02g069560.3	0.763732155	2.88447E-08	0.842857656	1.93227E-10	Peroxisome bioproteins protein 7
Solyc06g005710.3	0.760333241	5.95425E-26	0.889833581	2.30681E-36	Protein plastid transcriptionally active 16, chloroplastic
Solyc01g102470.2	0.759592618	0.000131889	0.53711454	0.006190918	Pentatricopeptide repeat-containing protein

Solyc11g071730.3	0.75913724	5.85662E-13	0.873606899	1.9165E-17	Kinesin-like protein KIN-12E
Solyc11g043200.1	0.758143264	0.007447228	1.155472777	1.41873E-05	Dynamin-related protein 3A
Solyc03g115040.4	0.757880706	7.00822E-07	0.412943929	0.007758966	Basic 7S globulin
Solyc05g009430.3	0.756292992	0.000623859	0.904637364	1.03155E-05	Aspergillus nuclease S1
Solyc02g088170.2	0.755798782	0.000151473	0.673509079	0.000499652	Pentatricopeptide repeat-containing protein
Solyc09g009350.2	0.755261982	0.034125344	1.706428317	9.37678E-08	Phosphatidylinositol-4, 5-bisphosphate phosphodiesterase gamma
Solyc04g077510.4	0.752441018	6.33366E-22	0.767959639	3.20574E-23	Growth-regulating factor
Solyc09g090320.2	0.752162239	4.16536E-06	0.777984702	8.28573E-07	Kinesin-like protein KIN-10A
Solyc03g025540.3	0.750766708	1.78109E-11	0.71413387	1.01854E-10	Cleavage and polyadenylation specificity factor subunit 2
Solyc12g088790.3	0.750454982	1.43501E-08	0.789298691	1.17291E-09	Transcription factor HEC2
Solyc05g014270.4	0.749753713	1.23721E-07	0.941526959	3.40391E-12	TPX2 C-terminal domain-containing protein
Solyc03g007890.3	0.748808733	2.01323E-09	0.565346113	5.74674E-06	Heat shock protein 83
Solyc04g075000.1	0.748406123	4.74532E-08	0.84842361	9.76597E-11	Serine/threonine-protein kinase-like protein At3g51990
Solyc04g016540.2	0.747921449	0.027299918	1.68860805	4.03467E-08	Pentatricopeptide repeat-containing protein
Solyc02g067360.3	0.747450024	2.56052E-08	0.75631991	8.02215E-09	Protease Do-like 8, chloroplastic
Solyc06g062800.4	0.74516175	7.36264E-06	0.865749174	4.17744E-08	Eukaryotic initiation factor
Solyc04g058130.3	0.744510173	0.005877427	1.044566873	3.2982E-05	Hexokinase-1 isoform X1
Solyc03g082430.1	0.743361198	0.000199708	0.921497963	1.05644E-06	Growth-regulating factor
Solyc11g071240.2	0.742296888	6.19089E-09	0.58813902	3.6782E-06	U-box domain-containing protein 26
Solyc11g006430.1	0.742022945	0.000283702	0.480521312	0.017904145	Glutaredoxin domain-containing protein
Solyc11g040170.3	0.737585288	0.000208969	1.164589178	4.91492E-10	mRNA-capping enzyme-like isoform X2
Solyc01g080910.2	0.73507807	7.53221E-08	1.04370782	9.31231E-16	Polyadenylate-binding protein 1-B-binding protein
Solyc12g005480.2	0.734463061	2.48946E-06	0.570936115	0.000217624	TPX2 C-terminal domain-containing protein
Solyc03g005620.4	0.734384595	5.65119E-06	0.702879145	7.86318E-06	Kinesin-like protein KIN-10A
Solyc04g077440.4	0.732372758	1.38252E-18	0.689426687	9.31942E-17	Squalene monooxygenase
Solyc09g075950.1	0.731776251	5.14111E-05	0.781116191	6.08377E-06	Heat shock 70 kDa protein 8
Solyc07g056460.3	0.731631644	0.001263959	0.708061278	0.001214078	Glutathione S-transferase
Solyc03g115230.3	0.729799174	7.71995E-15	0.737740153	1.66883E-15	Chaperone protein ClpB1

Solyc10g081880.3	0.729702862	0.043699289	1.653896265	6.05348E-07	Pentatricopeptide repeat-containing protein
Solyc06g084450.4	0.729573577	2.03292E-05	0.453447602	0.008303227	Rho GTPase-activating protein 2
Solyc01g097110.2	0.729443818	0.002185536	0.795570941	0.000419718	Fanconi anemia group D2 protein homolog
Solyc03g020050.3	0.727415698	0.023567617	1.316007781	4.85122E-06	Trypsin proteinase inhibitor
Solyc02g085390.4	0.727217368	2.18903E-18	0.902695014	1.0899E-28	DECREASED DNA METHYLATION 1 family protein
Solyc03g007230.4	0.72690366	2.2593E-19	0.891714017	3.19858E-29	protein-serine/threonine phosphatase
Solyc12g087980.3	0.726845888	0.002661843	1.17617866	1.11586E-07	Anthranilate N-benzoyltransferase protein
Solyc09g015170.4	0.726734637	6.53652E-25	0.717029401	8.71287E-25	Probably inactive leucine-rich repeat receptor-like protein kinase IMK2
Solyc05g055110.4	0.723109341	0.023518151	1.266156855	2.25661E-05	Nuclear pore complex protein NUP1
Solyc05g014540.3	0.723036266	1.54551E-07	0.821459757	6.81388E-10	DNA polymerase alpha subunit B
Solyc02g082820.3	0.722972044	1.73744E-08	0.576131462	5.76673E-06	G2/mitotic-specific cyclin-2 isoform X1
Solyc07g054690.1	0.72290555	2.33198E-07	0.786785274	6.58018E-09	TPX2 C-terminal domain-containing protein
Solyc08g013940.3	0.721978849	3.11571E-07	0.888779275	6.39154E-11	Serine/threonine-protein kinase RUNKEL
Solyc04g078670.3	0.721111671	0.039940696	1.437897017	4.69673E-06	NAC domain-containing protein
Solyc04g074220.4	0.720303718	8.1058E-09	0.849416724	1.54323E-12	Monoacylglycerol lipase ABHD6
Solyc07g065600.3	0.720171829	1.0893E-05	1.043884219	2.02466E-11	Inner centromere protein ARK-binding domain-containing protein
Solyc04g049380.4	0.720016196	0.013193072	1.31200711	1.39391E-06	Ubiquinone biosynthesis protein coq-8, putative
Solyc01g096840.3	0.719650216	3.29508E-06	0.405871479	0.009328597	Protein ENDOSPERM DEFECTIVE 1
Solyc02g065190.3	0.718470158	1.27388E-12	1.202242663	1.13966E-36	Geraniol 10-hydroxylase
Solyc08g061560.3	0.718008675	1.38969E-29	0.886037556	3.44128E-45	LRR receptor-like serine/threonine-protein kinase ERECTA
Solyc08g006950.4	0.717511568	0.000169816	0.455156626	0.016651819	AT-hook motif nuclear-localized protein
Solyc03g007970.2	0.71729149	0.003826254	0.679169974	0.003969317	UDP-N-acetylmuramate--L-alanine ligase
Solyc04g077270.4	0.717270093	0.002981849	1.390338835	1.50033E-10	Receptor-like serine/threonine-protein kinase

Solyc04g076400.3	0.716357506	4.58616E-14	0.774485639	5.13014E-17	Oberon PHD finger domain-containing protein
Solyc04g077930.4	0.716031435	6.32221E-15	0.819796712	5.09184E-20	CUE domain-containing protein
Solyc05g051510.4	0.714165122	0.000376648	0.55619506	0.004701104	Prohibitin
Solyc03g117190.1	0.714104239	0.000167933	0.737755969	5.53325E-05	Pollen-specific leucine-rich repeat extensin-like protein 3
Solyc07g055060.3	0.714026345	1.40597E-22	0.771255834	1.37239E-26	phosphoenolpyruvate carboxylase
Solyc02g081530.1	0.713073923	0.008778626	0.961943984	0.000143433	PORR domain-containing protein
Solyc11g010400.3	0.709885236	1.2869E-10	0.659606196	1.32794E-09	Hyoscyamine 6-dioxygenase
Solyc05g013200.1	0.708080746	0.024462568	1.372865286	1.30245E-06	DYW domain-containing protein
Solyc07g062530.3	0.707874826	1.33387E-08	0.588174375	1.85372E-06	phosphoenolpyruvate carboxylase
Solyc12g099280.2	0.706541732	6.68856E-10	0.839995563	3.26074E-14	Pre-mRNA polyadenylation factor Fip1 domain-containing protein
Solyc04g008410.3	0.706340701	0.032897747	1.380021587	5.06079E-06	Pentacotriptide-repeat region of PRORP domain-containing protein
Solyc07g064720.3	0.706305623	0.030336791	1.193579803	5.53325E-05	GDSL esterase/lipase
Solyc07g018190.4	0.705458455	0.03417061	1.398002095	2.97465E-06	Probable LRR receptor-like serine/threonine-protein kinase At3g47570
Solyc05g012300.1	0.705232678	0.003824123	0.493336838	0.039237179	Diphthine methyltransferase homolog
Solyc09g061260.2	0.705061576	3.20266E-05	0.929260128	5.40261E-09	Oberon PHD finger domain-containing protein
Solyc05g008300.3	0.704815214	1.10923E-16	0.709429769	1.43573E-17	HMA domain-containing protein
Solyc05g018630.1	0.703060682	0.001762045	0.725529889	0.000791324	Ultraviolet-B receptor UVR8
Solyc03g019880.3	0.700839102	2.14496E-06	0.393196581	0.008750964	UPF0426 protein, chloroplastic
Solyc01g110060.3	0.700622634	9.82324E-15	0.766992909	5.45516E-18	Purple acid phosphatase
Solyc05g054315.1	0.700432033	4.61578E-09	1.037148277	9.25484E-20	AB hydrolase-1 domain-containing protein
Solyc05g014730.1	0.699505314	0.000660061	0.452070923	0.02643758	DNA topoisomerase
Solyc09g075480.3	0.69523838	8.78626E-09	0.790751042	1.82638E-11	Kinesin-like protein KIN-14I isoform X2
Solyc04g025160.3	0.694631099	2.74133E-09	0.717579861	3.47652E-10	ATPase ARSA1 isoform C
Solyc02g071700.3	0.694580739	2.37258E-10	1.613079122	1.8762E-52	GDSL esterase/lipase
Solyc02g081440.4	0.694071618	6.31864E-08	0.616633132	1.07468E-06	Serine/arginine repetitive matrix protein 2-like
Solyc01g088520.3	0.693560232	0.01998096	1.46244723	9.60364E-08	Dynamin-related protein 1E
Solyc06g065900.4	0.693443297	1.74434E-16	0.475606664	2.17776E-08	Serine-rich protein-like protein

Solyc02g083640.4	0.693267934	1.60474E-14	0.618027223	3.96363E-12	N-terminal acetyltransferase A, auxiliary subunit
Solyc03g063720.4	0.692368422	0.000387578	0.544625655	0.004075163	Zinc finger PHD-type domain-containing protein
Solyc07g042580.3	0.691233752	1.0337E-08	0.862294358	1.08258E-13	Microtubule-associated protein TORTIFOLIA1
Solyc09g010710.4	0.691173041	0.000426644	0.80465312	1.39201E-05	Peptide transporter family protein
Solyc07g008660.3	0.691050581	3.44073E-10	0.36843665	0.001052397	Ribosomal protein S16
Solyc01g091090.4	0.689755957	0.022583965	1.394894757	5.8324E-07	Tubulin-folding cofactor D
Solyc11g008850.2	0.689473779	1.13815E-08	0.472713597	9.29381E-05	Protease Do-like PDZ domain-containing protein
Solyc03g113250.4	0.688758865	0.000293481	1.033259697	2.7363E-09	Proton-dependent oligopeptide transporter
Solyc12g099080.3	0.688014108	1.70744E-19	0.530587593	4.42064E-12	ADP-ribosylation factor
Solyc10g075110.2	0.687012519	5.55593E-18	0.952126348	5.88869E-34	Non-specific lipid-transfer protein
Solyc11g045370.1	0.685065223	0.000132689	0.634778865	0.000255962	FAD-linked oxidases family protein isoform 1
Solyc09g057910.3	0.684712677	0.014430493	1.255484435	1.17751E-06	Phagocyte signaling-impaired protein
Solyc05g009560.4	0.684352158	0.004431748	0.579820559	0.012686365	Homologous-pairing protein 2 homolog
Solyc09g090510.3	0.683833571	2.37826E-16	0.877567108	8.20309E-27	Amine oxidase domain-containing protein
Solyc09g061860.4	0.681059968	3.40511E-21	0.768766824	2.05483E-27	Sterol 3-beta-glucosyltransferase
Solyc03g005060.4	0.680601682	1.89513E-09	0.746399133	1.24332E-11	C2 NT-type domain-containing protein
Solyc12g099000.3	0.679893117	8.61699E-21	0.481636029	5.5256E-11	S-adenosylmethionine synthase
Solyc01g096370.4	0.678693501	0.000337769	0.479532001	0.010216905	Transcription factor
Solyc05g005580.3	0.677480524	4.09294E-06	0.507912196	0.000496514	Leucine-rich repeat-containing protein 50
Solyc05g051750.3	0.677116305	3.13492E-05	0.78426333	5.68925E-07	Prosystemin
Solyc11g066350.2	0.676479988	8.0271E-05	0.389281744	0.024159526	Shugoshin C-terminal domain-containing protein
Solyc04g049680.2	0.676405495	0.00315574	1.512800642	6.95742E-13	Pseudo response regulator isoform 3
Solyc07g008800.4	0.675767797	2.33244E-08	0.331862511	0.007481894	10 kDa chaperonin
Solyc11g007710.2	0.674287944	5.99248E-06	0.474783854	0.001321996	DUF455 domain-containing protein
Solyc04g077220.3	0.673395524	1.43665E-08	1.186045411	8.7327E-26	Homeobox-leucine zipper protein HAT22
Solyc12g099650.2	0.673308939	6.03639E-09	0.489079698	2.56378E-05	Photosystem II 5 kDa protein, chloroplastic
Solyc07g007140.3	0.672221909	4.98291E-08	0.75612948	3.88243E-10	Homeobox protein knotted-1-like LET12-like isoform X1

Solyc10g079730.3	0.670119525	1.98126E-06	0.879534227	5.70596E-11	Condensin-1 complex subunit CAP-D2
Solyc07g006700.1	0.669986025	0.033301948	1.495220932	1.28154E-07	Pathogenesis-related protein PR-1
Solyc06g075420.1	0.66977524	1.17871E-07	0.690553489	1.33218E-08	18S pre-ribosomal assembly protein gar2-related protein
Solyc04g074960.4	0.669314454	1.72275E-05	0.901261184	8.91445E-10	Folic acid and derivative biosynthetic process
Solyc04g076310.4	0.668744807	1.3279E-07	0.887859452	2.95634E-13	Kinesin-like protein KIN-4C isoform X1
Solyc01g098190.3	0.668701593	0.000180122	0.364910006	0.042516038	Sodium/hydrogen exchanger
Solyc03g096890.3	0.666199827	0.000311774	0.974523171	2.61125E-08	Serine/threonine-protein kinase TIO
Solyc11g006060.2	0.665650511	6.8565E-14	0.697699314	1.90145E-15	Rubisco accumulation factor 1 C-terminal domain-containing protein
Solyc06g034370.1	0.664991925	0.004032494	0.875876593	5.29486E-05	Pectinesterase inhibitor domain-containing protein
Solyc01g098770.1	0.66490185	1.10073E-05	1.011101565	7.17028E-13	Gamma conglutin 2
Solyc11g020160.2	0.664874709	0.018379141	1.098976053	2.89853E-05	Nuclear pore complex protein NUP88
Solyc11g013240.3	0.663570288	1.04336E-06	0.696180375	1.1914E-07	Serine/threonine-protein kinase MPS1 isoform X1
Solyc12g056280.3	0.663083904	0.044496334	1.272626323	1.29344E-05	E3 ubiquitin-protein ligase UHRF1
Solyc10g080950.2	0.662778905	2.03725E-11	0.559536939	1.1654E-08	Cyclin N-terminal domain-containing protein
Solyc01g096680.4	0.661641057	0.00031808	0.718920169	4.07916E-05	65-kDa microtubule-associated protein 5
Solyc06g043150.4	0.661145609	3.86123E-09	0.32006624	0.005465418	B-type cell cycle switch protein ccs52B
Solyc02g085650.4	0.660423678	1.6898E-06	0.533590353	8.57092E-05	Pentatricopeptide repeat-containing protein
Solyc11g030600.3	0.660388353	1.41651E-10	0.959953611	8.86026E-22	DNA (cytosine-5)-methyltransferase
Solyc03g083100.3	0.66033491	4.404E-13	0.584812204	9.6875E-11	Protein IQ-DOMAIN like
Solyc06g008180.3	0.659660194	0.011640605	0.784888666	0.001280902	Pentacotriptide-repeat region of PRORP domain-containing protein
Solyc03g111100.1	0.65964695	1.14809E-10	0.528960531	1.86876E-07	von willebrand factor A domain protein
Solyc07g043480.1	0.658374724	1.47535E-18	0.66368948	3.06327E-19	Glycosyltransferase
Solyc12g096770.1	0.658284863	0.029217201	1.38218478	1.90826E-07	Anthocyanin acyltransferase
Solyc08g005430.3	0.658065125	6.18914E-15	0.444211041	1.87143E-07	Growth-regulating factor
Solyc03g006360.3	0.658010693	3.89087E-23	0.612410251	2.41782E-20	Auxin-repressed 12,5 kDa protein-like
Solyc04g009860.4	0.657849008	8.75902E-05	1.18874739	5.11705E-14	1-aminocyclopropane-1-carboxylate oxidase-like protein

Solyc03g093490.3	0.657634939	0.001760156	0.861605535	1.43665E-05	WD repeat-containing protein WRAP73
Solyc04g054250.4	0.656626281	1.87937E-21	0.858831001	3.32874E-37	Flavonoid 3-hydroxylase
Solyc05g013470.4	0.65540581	1.86539E-06	0.798786805	1.32875E-09	Protein DETOXIFICATION
Solyc04g082430.3	0.65504778	2.17384E-10	0.633362214	3.97125E-10	G2/mitotic-specific cyclin-2-like isoform X1
Solyc08g008470.2	0.654992695	0.04232092	1.021922196	0.000659026	MalT-like TPR region domain-containing protein
Solyc02g068050.4	0.654893915	8.79073E-12	0.830853168	3.57989E-19	Rubisco LSMT' substrate-binding domain-containing protein
Solyc12g096030.1	0.654358979	7.30223E-14	0.739295685	3.66529E-18	Solute carrier family 25 member 44
Solyc08g081120.4	0.654232419	0.004583226	1.47472102	6.18555E-12	Kinesin-like protein KIN-14J isoform X1
Solyc06g072810.4	0.654229801	4.95778E-13	0.515976863	1.18533E-08	Putative beta-tubulin polyglutamylase
Solyc04g078590.3	0.654035425	1.81128E-12	0.600367529	5.91798E-11	Putative inactive receptor kinase
Solyc09g092700.3	0.65387588	8.18793E-16	0.82323702	8.70017E-25	Glycine-rich protein isoform X1
Solyc05g014710.4	0.653225832	1.16197E-15	0.782123813	1.61044E-22	Remorin C-terminal domain-containing protein
Solyc10g079620.2	0.651801227	5.76448E-15	0.790404966	3.8007E-22	Haloacid dehalogenase-like hydrolase domain-containing protein 3
Solyc08g023490.4	0.650732514	0.02569007	1.371670628	3.49932E-07	Pentacotriptide-repeat region of PRORP domain-containing protein
Solyc02g068510.2	0.650657174	4.78038E-05	0.871779349	1.08264E-08	B box-type domain-containing protein
Solyc05g007760.2	0.650619395	0.000463904	0.923247206	9.00172E-08	SET domain-containing protein
Solyc09g082500.4	0.6504112	3.25525E-14	0.767864003	3.7513E-20	Tesmin/TSO1-like CXC domain-containing protein putative isoform 1
Solyc01g102570.4	0.647455561	0.037939066	1.351066355	2.82903E-06	Eukaryotic translation initiation factor 3 subunit C
Solyc01g087200.3	0.645302619	5.04953E-05	0.894976127	2.41384E-09	Late blight resistance protein homolog R1A-10
Solyc06g051990.4	0.644953596	7.48375E-09	0.743070963	3.89526E-12	Protein DEFECTIVE IN MERISTEM SILENCING 3
Solyc01g110130.3	0.643314414	2.17957E-13	0.632981663	3.03349E-13	DNA replication licensing factor MCM4
Solyc01g079130.2	0.643065667	0.000118069	0.626449498	9.00613E-05	Polygalacturonase
Solyc04g050960.3	0.642996428	8.60886E-09	0.732953215	1.45807E-11	Protein CHROMATIN REMODELING 4
Solyc07g055120.4	0.641962775	5.41629E-06	0.343038792	0.016442641	F-box protein MAX2
Solyc11g008460.1	0.641828388	0.020898645	1.238589563	1.62002E-06	SART-1 family protein DOT2

Solyc11g010920.3	0.640337136	7.71316E-10	0.671200039	4.22788E-11	Kinesin-like protein KIN-14R
Solyc06g073760.3	0.640239856	0.000529251	0.538308853	0.002569384	Beta-xylosidasealpha-l-arabinofuranosidase 2
Solyc06g075640.2	0.639390578	0.014344509	0.561606942	0.024108054	Stress up-regulated Nod protein
Solyc03g119860.3	0.639075291	2.2978E-13	0.688091141	8.50959E-16	PPIase cyclophilin-type domain-containing protein
Solyc08g083320.4	0.638922081	4.2184E-17	0.768894201	1.07175E-24	Granule-bound starch synthase (Fragment)
Solyc07g007200.4	0.638891266	4.41314E-05	0.482858082	0.001682129	Receptor homology region, transmembrane domain-and RING domain-containing protein 4
Solyc11g069870.1	0.638348905	9.03457E-11	0.722258332	4.84853E-14	Kiwellin
Solyc12g011290.2	0.638317958	9.30607E-08	0.736139095	2.2596E-10	Kinesin motor domain-containing protein
Solyc03g094010.3	0.637923826	6.52715E-05	0.765138004	4.47577E-07	Glutamate dehydrogenase
Solyc12g098440.2	0.635443464	6.04699E-16	0.52117968	3.20484E-11	RPM1-interacting protein 4 isoform X2
Solyc04g010320.1	0.634999733	3.98427E-10	0.46857845	3.77083E-06	Cytochrome P450, family 87, subfamily A, polypeptide 6
Solyc01g060410.4	0.634371535	1.09361E-07	0.614755688	1.34966E-07	Protein LONGIFOLIA like
Solyc11g017130.2	0.633559178	0.00638662	0.763273051	0.000484023	Parallel spindle 1
Solyc09g098620.2	0.633155178	4.63009E-10	0.737766793	7.24617E-14	Iridoid oxidase
Solyc11g006940.3	0.630653006	0.012442314	0.704975479	0.002944015	Pentatricopeptide repeat-containing protein
Solyc10g007320.3	0.630236063	1.85938E-14	0.710249316	1.66576E-18	Uroporphyrinogen decarboxylase
Solyc02g005350.3	0.629812641	1.05036E-10	0.416778479	2.19882E-05	Succinate--CoA ligase [ADP-forming] subunit alpha, mitochondrial
Solyc10g006900.3	0.629796665	2.63393E-19	0.601381917	7.78946E-18	NADPH-protochlorophyllide oxidoreductase
Solyc03g013304.2	0.629330337	0.026117714	0.691707762	0.009248707	Replication factor A C-terminal domain-containing protein
Solyc04g074400.1	0.627785219	1.20879E-14	0.560650033	5.07479E-12	Phosphate-induced protein
Solyc04g082750.3	0.627115129	5.05887E-12	0.663489592	8.21097E-14	Short-chain dehydrogenase/reductase family 42E member 1
Solyc12g099840.1	0.626850097	0.001411848	0.4112195	0.034479557	Pentatricopeptide repeat-containing protein
Solyc05g041430.3	0.626604232	3.72702E-05	0.691586076	2.17198E-06	PTB domain-containing engulfment adapter protein 1
Solyc10g008210.3	0.626553581	2.25021E-08	0.467769151	2.71643E-05	Targeting protein for Xklp2
Solyc06g075010.4	0.626507169	1.05392E-16	0.486847002	1.3611E-10	RuBisCO large subunit-binding

Solyc10g086470.2	0.626227267	0.011973249	0.601140285	0.011298649	protein subunit alpha Mitochondrial import inner membrane translocase subunit
Solyc08g068320.3	0.625676467	9.50822E-09	0.775814863	1.62757E-13	Transcription factor MYB3R-1
Solyc06g068230.4	0.625425586	9.29227E-10	1.006007054	3.67418E-24	Clu domain- containing protein
Solyc01g014373.1	0.624913737	0.013601527	0.637789291	0.007628172	IRK-interacting protein isoform X1
Solyc01g005790.1	0.624811019	0.042290888	0.856262907	0.002690941	Pentatricopeptide repeat-containing protein
Solyc09g007270.3	0.62422777	4.42905E-08	0.538277005	1.76742E-06	L-ascorbate peroxidase
Solyc08g080400.2	0.624006514	6.27369E-08	0.461422682	5.48651E-05	Scarecrow-like protein 28
Solyc02g063150.3	0.62369181	7.43882E-14	0.453602752	7.01047E-08	Ribulose biphosphate carboxylase small subunit, chloroplastic
Solyc09g082180.3	0.622626923	0.002404339	0.590764631	0.002497178	C-8 sterol isomerase
Solyc08g065220.3	0.622232533	1.1995E-11	0.740264254	2.34947E-16	Glycine cleavage system P protein
Solyc05g053410.4	0.621789435	2.29055E-05	1.197327568	5.78173E-18	Phytochrome
Solyc10g080400.2	0.621681383	1.59286E-05	0.397503053	0.005660921	Uv-b-insensitive 4
Solyc07g054480.3	0.621361315	0.022410852	1.214628142	7.1329E-07	Pentacotriptide- repeat region of PRORP domain- containing protein
Solyc01g105450.4	0.620257507	1.6891E-08	1.156294092	7.90948E-29	White-brown complex homolog protein 11 (Fragment)
Solyc04g074710.3	0.619229009	0.001200576	0.887498591	5.1424E-07	Queuine tRNA- ribosyltransferase catalytic subunit 1
Solyc04g076570.4	0.61821697	0.000136443	0.433563925	0.006705461	CRT (Chloroquine- resistance transporter)- liketransporter 2
Solyc02g069110.4	0.617457403	0.000970937	0.653419402	0.000242075	Cathepsin B
Solyc06g076560.2	0.61725716	0.000199402	0.349924693	0.036193145	Class I small heat shock protein 20,1
Solyc11g065760.2	0.616630168	1.08156E-06	0.479117384	0.000122311	Thymidine kinase
Solyc03g119180.1	0.616543827	0.007731186	0.492475367	0.027438514	Transmembrane protein
Solyc08g068190.3	0.615455791	2.07882E-07	0.245316076	0.046946193	Benzaldehyde dehydrogenase, mitochondrial
Solyc08g066050.3	0.614697145	2.23343E-09	0.25505101	0.016852525	Aurora kinase
Solyc06g008980.3	0.614401884	7.93271E-06	0.453369211	0.00084001	Heat shock transcription factor family
Solyc03g121760.3	0.613915227	0.005208296	0.530569212	0.012397657	IQ-domain 6
Solyc07g063450.3	0.612428324	0.000171284	0.967017505	1.74413E-10	SWIRM domain- containing protein
Solyc05g046110.4	0.612116408	0.020021508	0.744925511	0.002215815	O-fucosylpeptide 3- beta-N- acetylglucosaminyltra nsferase
Solyc03g116920.3	0.612083401	0.000400205	0.495912647	0.003157156	Tudor domain- containing protein

Solyc07g008260.3	0.611676163	9.98739E-07	0.4412373	0.000399818	Germin-like protein subfamily 1 member 15
Solyc03g095600.1	0.611569458	1.44958E-11	0.516986571	8.45236E-09	NAB domain-containing protein
Solyc01g105520.3	0.611303067	0.006031345	0.758685587	0.000239688	DNA helicase
Solyc09g091470.3	0.610287791	1.58796E-16	0.267010528	0.000498358	3-ketoacyl-CoA thiolase 2, peroxisomal
Solyc03g082420.3	0.609476319	0.028754729	0.829501179	0.001280902	Small heat shock protein, chloroplastic
Solyc03g095680.2	0.609220945	0.029109572	1.21201715	2.35839E-06	E3 ubiquitin-protein ligase SHPRH
Solyc12g006470.2	0.609166618	1.12894E-09	1.047120683	2.36048E-27	Gamma aminobutyrate transaminase 3, chloroplastic-like
Solyc04g074760.3	0.608874935	0.000609862	0.376863265	0.033578617	Myocardial zonula adherens protein
Solyc01g100910.3	0.607918784	0.030661068	1.030869329	4.7885E-05	ADP-ribosylation factor 2
Solyc01g009040.4	0.607328885	3.30078E-12	0.535165478	5.25064E-10	Cyclin N-terminal domain-containing protein
Solyc02g065510.1	0.605978176	0.012085529	1.043033636	1.37989E-06	Pentatricopeptide repeat-containing protein
Solyc04g011640.3	0.605950062	0.018160052	0.950708527	6.2837E-05	Scarecrow-like protein 14
Solyc02g062780.4	0.605826498	1.60885E-10	0.756206609	1.4611E-16	DECREASED DNA METHYLATION 1 family protein
Solyc01g066610.4	0.605731052	7.62645E-05	0.653208652	7.19764E-06	Fanconi anemia group I protein
Solyc05g052640.3	0.605033072	5.2124E-10	0.4150259	2.337E-05	Peroxisomal nicotinamide adenine dinucleotide carrier
Solyc04g008880.4	0.604036188	0.000275757	0.859552176	2.31614E-08	UDP-MurNAc-pentapeptide synthetase
Solyc02g087880.3	0.603924066	8.21701E-14	0.441452573	5.94773E-08	Tubulin alpha chain
Solyc01g111350.3	0.603523656	0.000530659	0.553715428	0.000939651	Nodulin-like domain-containing protein
Solyc02g067440.3	0.602110973	6.35017E-15	0.84730917	9.04997E-30	cysteine dioxygenase
Solyc07g045140.4	0.60155627	0.004688985	0.650250091	0.001285602	Steroid nuclear receptor ligand-binding
Solyc03g025160.4	0.601501503	1.34764E-09	0.237209982	0.021704613	ATP synthase subunit beta like
Solyc04g077570.1	0.600379127	0.000140105	0.321070865	0.044022057	WRKY domain-containing protein (Fragment)
Solyc04g077860.4	0.599419582	1.1316E-11	0.547979973	3.1577E-10	Probable strigolactone esterase
Solyc06g072013.1	0.599377825	0.04656504	1.092300542	4.43489E-05	DAD2
Solyc01g100600.4	0.59896877	1.61312E-14	0.57573298	6.85135E-14	Prolamin-like domain-containing protein
Solyc06g053760.3	0.597738298	1.75408E-09	0.382023979	0.000134447	Acyl-CoA-binding domain-containing protein 4-like isoform X2
					Syntaxin-related protein KNOLLE

Solyc06g008760.1	0.597562335	0.012607006	0.821613694	0.000177528	Monothiol glutaredoxin-S11
Solyc02g076750.3	0.597206504	0.016698671	1.209292847	1.48443E-07	Low-temperature-induced cysteine proteinase-like
Solyc07g062480.2	0.597106617	4.72775E-06	0.70723863	1.31361E-08	Epidermis-specific secreted glycoprotein EP1
Solyc03g119530.3	0.596853273	2.79195E-14	0.232943541	0.004451812	LOB domain-containing protein
Solyc02g080390.2	0.594476153	0.003481233	1.053571423	2.05E-08	Abnormal spindle-like microcephaly-associated protein homolog
Solyc02g086140.2	0.593917636	0.006651346	0.488674108	0.020261031	Crossover junction endonuclease
Solyc09g089770.3	0.593345924	0.001996656	0.980234135	2.36468E-08	1-aminocyclopropane-1-carboxylate oxidase-like 1
Solyc02g069070.3	0.592700938	0.005049632	0.409324862	0.048432316	Ribonuclease H2 subunit C
Solyc10g076940.3	0.592600266	0.000360194	0.657377018	3.16641E-05	Protein ZINC INDUCED FACILITATOR-LIKE 1-like
Solyc06g060320.4	0.591649359	1.33032E-05	0.539496497	4.58782E-05	Filament-like plant protein isoform X1
Solyc02g075620.4	0.591644666	2.23578E-09	0.586466685	2.02973E-09	Pectinesterase
Solyc08g080170.3	0.591455576	4.63314E-16	0.424217839	7.35701E-09	Hydroxymethylglutaryl-CoA synthase
Solyc07g008330.3	0.591346662	6.87365E-18	0.629411468	1.08805E-20	Nucleolar and coiled-body phosphoprotein 1
Solyc01g068540.3	0.590732753	0.001415086	0.423470046	0.019274612	Orcinol O-methyltransferase
Solyc07g021710.3	0.590546242	0.006731007	0.912158279	3.58979E-06	Thiamine phosphate phosphatase-like protein
Solyc07g062680.3	0.590427245	2.60775E-06	0.686900069	1.17906E-08	Lanceolate
Solyc02g093170.4	0.58966744	2.60137E-09	0.466829763	1.98866E-06	Cyclin delta-3
Solyc05g008150.3	0.589095301	0.013747401	1.033278346	1.88777E-06	Fruit-specific protein
Solyc05g052100.3	0.587858128	1.83294E-06	0.486503071	5.50286E-05	Glutamate dehydrogenase
Solyc06g069000.3	0.587541429	0.003982298	0.492466467	0.011951682	SPARK domain-containing protein
Solyc11g065190.3	0.586380188	1.35272E-12	0.561902315	5.70437E-12	Ubiquitin-conjugating enzyme E2 20
Solyc06g073320.3	0.586134541	2.7528E-16	0.335123604	4.62649E-06	GDP-L-galactose phosphorylase 1
Solyc01g008800.3	0.585883101	2.73439E-05	0.925473296	2.75252E-12	Bacterial spot disease resistance protein 4
Solyc11g020720.1	0.585613486	9.05748E-07	0.322861337	0.007662885	DUF676 domain-containing protein
Solyc07g008610.3	0.585000361	5.36778E-14	0.618342179	7.70453E-16	ATP-binding cassette, subfamily F, member 1
Solyc01g095900.4	0.584833268	3.41193E-06	1.024588838	1.73303E-17	Clu domain-containing protein
Solyc09g007360.3	0.584475097	2.20231E-10	0.64510668	6.2569E-13	Interactor of constitutive active ROPs 2, chloroplastic
Solyc01g110010.3	0.583577966	0.020817809	0.691588777	0.003271618	Pentatricopeptide repeat-containing protein

Solyc12g008890.3	0.583349028	0.012575783	0.795262734	0.000226803	Zinc finger CCH domain-containing protein 64
Solyc10g018260.1	0.583031137	7.13879E-08	0.363074238	0.00086609	UDP-glucuronate 4-epimerase 3
Solyc07g053790.2	0.582765586	1.51853E-05	0.518985151	7.73003E-05	TPX2 C-terminal domain-containing protein
Solyc04g070980.4	0.582747224	9.48874E-12	0.742824143	5.39388E-19	Terpene cyclase/mutase family member
Solyc03g007550.4	0.582385236	0.00012177	0.525906962	0.000349571	Treslin N-terminal domain-containing protein
Solyc02g065470.1	0.582240987	4.34539E-05	0.502378132	0.000335889	SCP domain-containing protein
Solyc07g014590.4	0.581079629	3.32359E-16	0.759210964	3.7353E-28	Isoamylase 1, chloroplastic
Solyc04g014850.3	0.58093265	0.005782615	0.614333952	0.001896678	Epidermal growth factor receptor substrate 15 homolog
Solyc08g014050.2	0.579857445	6.84154E-06	0.573706676	4.42839E-06	Gallate 1-beta-glucosyltransferase
Solyc09g005660.4	0.579661009	0.000400401	0.795723339	2.32525E-07	DUF659 domain-containing protein
Solyc01g109610.4	0.578893618	5.12356E-10	0.723808914	8.50038E-16	Erythronate-4-phosphate dehydrogenase family protein
Solyc10g009420.3	0.578528878	0.002082912	0.673368824	0.000146785	RING-type E3 ubiquitin transferase
Solyc08g081170.4	0.578242871	2.7508E-06	0.746757682	2.74092E-10	UDP-N-acetylmuramoyl-L-alanyl-D-glutamate--2, 6-diaminopimelate ligase-like
Solyc03g031460.1	0.577636937	1.93293E-07	0.504097276	3.5903E-06	Pentatricopeptide repeat-containing protein
Solyc02g076950.2	0.577379963	0.009718809	0.950704727	3.08161E-06	Maternal effect embryo arrest 18
Solyc04g005070.3	0.576585889	0.002155394	0.69481017	8.68102E-05	LATD/NIP
Solyc12g056120.1	0.576553405	2.10608E-15	0.502117153	4.64042E-12	6-phosphogluconate dehydrogenase, decarboxylating
Solyc07g043490.1	0.576461987	8.56675E-13	0.485813533	1.4648E-09	Solanidine galactosyltransferase (Fragment)
Solyc03g118310.4	0.574376316	5.41748E-09	0.699356489	1.99998E-13	Transcription factor Inducer of CBF expression 1 (Fragment)
Solyc03g118970.3	0.574052532	5.21433E-16	0.666750312	1.0353E-21	Protein DETOXIFICATION
Solyc08g081740.3	0.573451054	3.32125E-09	0.849882747	8.3084E-20	Transitional endoplasmic reticulum ATPase homolog 2-like
Solyc09g042710.3	0.573186589	1.92699E-07	0.624571147	4.87444E-09	DUF827 domain-containing protein (Fragment)
Solyc05g023770.4	0.571412353	1.32013E-07	0.776516874	7.49084E-14	Coiled-coil domain-containing protein SCD2

Solyc01g098980.4	0.570963063	3.49795E-11	0.43140162	5.29096E-07	Mitogen-activated protein kinase kinase NPK1
Solyc02g089560.4	0.569300869	0.018905242	1.003205706	7.09143E-06	Pentatricopeptide repeat-containing protein, mitochondrial
Solyc04g082460.4	0.568224697	9.56878E-13	0.617033551	2.84238E-15	Catalase
Solyc01g099270.2	0.566325564	0.000415132	0.428438046	0.006338444	Microtubule-binding protein TANGLED
Solyc07g007030.1	0.566201944	1.28479E-08	0.5356783	5.17308E-08	Transmembrane 9 superfamily member
Solyc12g009160.2	0.565847564	0.01561767	0.467635673	0.038678776	Inter-alpha-trypsin inhibitor heavy chain
Solyc12g042760.1	0.565016764	7.14216E-06	0.863224817	2.89677E-13	Protein TOO MANY MOUTHS
Solyc11g008560.2	0.564566527	0.000126011	1.031320333	3.30753E-14	AP2-like ethylene-responsive transcription factor BBM2
Solyc06g062290.1	0.564290723	0.025059157	0.668923971	0.003895309	Glycosyltransferase
Solyc12g006690.2	0.563005527	5.51849E-05	0.780021833	3.54546E-09	Protein kinase PINOID 2
Solyc03g116590.3	0.561665581	1.55817E-07	0.344721885	0.001447198	Embryo-specific protein 3
Solyc08g068570.4	0.561627701	0.000221651	0.451952263	0.002368421	Tocopherol cyclase
Solyc11g042890.2	0.560690835	0.004403195	0.794304586	1.19644E-05	Late embryogenesis abundant protein LEA-2 subgroup domain-containing protein
Solyc08g067150.4	0.559385456	2.65919E-08	0.677869799	3.85103E-12	CRC domain-containing protein
Solyc04g009200.3	0.559162208	6.59318E-14	0.539675659	3.43369E-13	glutamate-1-semialdehyde 2,1-aminomutase
Solyc08g079430.3	0.557687602	2.04039E-08	0.490790145	6.13573E-07	Amine oxidase
Solyc02g080560.1	0.557635811	0.000156767	0.370206268	0.011004823	Leucine-rich repeat transmembrane neuronal protein 2
Solyc03g093850.2	0.557393858	0.011701782	1.002458753	7.18231E-07	DNA 3'-5' helicase
Solyc10g081250.3	0.556902667	7.61897E-08	0.6539016	5.37669E-11	DNA polymerase
Solyc01g010480.3	0.5563329	4.47812E-06	0.745134279	8.24937E-11	PAS/LOV protein A
Solyc06g065450.3	0.5562251	0.003689566	0.398128267	0.032075084	Parallel spindle 1
Solyc02g083110.1	0.555351317	5.19418E-12	0.464021411	7.03322E-09	DUF641 domain-containing protein
Solyc03g044090.4	0.555269807	2.245E-05	0.564387427	7.8879E-06	BTB/POZ domain-containing protein NPY4-like isoform X1
Solyc12g011010.2	0.554303683	4.36532E-07	0.327914129	0.003180475	Protodermal factor 1
Solyc01g111470.4	0.552440847	0.030876531	1.129897316	1.24791E-06	Pentatricopeptide repeat-containing protein
Solyc02g079210.3	0.552265665	1.03147E-11	0.28690412	0.000559784	Multiple organellar RNA editing factor 1, mitochondrial
Solyc11g005090.2	0.550840204	6.71351E-07	0.70152349	4.22003E-11	Cyclin-A1-1 like
Solyc01g067480.4	0.550634801	1.24409E-11	0.626010607	1.77764E-15	Acyl-CoA-binding domain-containing protein 4
Solyc04g008600.4	0.550513282	0.001446395	0.430806266	0.010325567	TIMELESS-interacting protein isoform X1

Solyc09g061840.4	0.550501665	1.36954E-09	0.292645781	0.001564741	3-ketoacyl-CoA thiolase 2, peroxisomal
Solyc03g078230.3	0.549455315	6.11537E-05	0.332190425	0.015541728	E3 ubiquitin-protein ligase CHFR
Solyc06g069280.4	0.549251787	2.00612E-07	0.480210574	3.78614E-06	DFDF domain-containing protein
Solyc03g114690.4	0.548834709	1.43069E-06	0.337495878	0.003202953	WD repeat and HMG-box DNA-binding protein 1
Solyc04g045660.4	0.548209986	0.000218617	0.62828834	8.96601E-06	DNA mismatch repair protein S5 domain-containing protein
Solyc10g018590.2	0.547913105	0.000400745	0.833921762	9.90726E-09	Putative plastid-lipid-associated protein 11
Solyc01g107560.3	0.547500391	0.000964542	0.467377044	0.003525716	Gallate 1-beta-glucosyltransferase
Solyc01g011430.4	0.547052569	0.024122661	1.171767909	9.29954E-08	Wax synthase
Solyc01g006100.4	0.546940049	5.99248E-06	0.57453986	8.57995E-07	Chromomethylase 3
Solyc10g049890.3	0.546921586	1.32612E-10	0.394957933	3.61829E-06	D-3-phosphoglycerate dehydrogenase
Solyc03g120890.3	0.546502807	1.50877E-10	0.32860724	0.000149792	GATA transcription factor
Solyc06g048460.2	0.546428825	0.001857034	0.710965355	2.04926E-05	Anaphase-promoting complex subunit 1
Solyc04g077660.3	0.54606862	2.14832E-10	0.679481656	3.96011E-16	peptidylprolyl isomerase
Solyc01g097770.4	0.545037648	8.91677E-12	0.808751959	1.56141E-25	Putative LOV domain-containing protein
Solyc01g103160.3	0.544624236	4.28471E-08	0.530431297	5.572E-08	Glutamine-rich protein 23
Solyc10g085120.3	0.544273779	0.006473251	0.513515797	0.006449673	LRR receptor-like serine/threonine-protein kinase
Solyc01g095720.3	0.544233031	6.83185E-06	0.853054028	4.38368E-14	Phospholipase A1 PLIP1, chloroplastic
Solyc07g054460.4	0.544193849	9.67148E-06	0.633261563	7.25064E-08	H/ACA ribonucleoprotein complex non-core subunit NAF1
Solyc02g070230.2	0.543438818	0.021174964	0.93889448	1.18181E-05	Twinkle homolog protein, chloroplastic/mitochondrial isoform X3
Solyc09g010060.3	0.543142437	2.30508E-08	0.507343446	1.04217E-07	Kinesin-like protein KIN-5C
Solyc10g006760.3	0.542174814	1.66886E-09	0.356149833	8.78783E-05	Adenine nucleotide alpha hydrolases-like superfamily protein
Solyc04g077170.3	0.541813698	5.6722E-05	1.240714574	2.20383E-23	Epidermal patterning factor-like protein
Solyc11g008940.1	0.5418029	0.00108411	0.407953423	0.011853406	Chlororespiratory reduction 2
Solyc06g008900.4	0.540820128	4.88844E-05	0.399783567	0.002156572	E3 ubiquitin-protein ligase RF298
Solyc02g081900.4	0.539706538	0.012201218	0.63354627	0.001682038	DYW domain-containing protein
Solyc04g072860.3	0.539493391	1.55393E-05	0.586564235	1.02975E-06	Probable beta-D-xylosidase 7
Solyc04g005650.3	0.539094012	1.89393E-14	0.227911505	0.001819128	Peroxisomal nicotinamide adenine dinucleotide carrier

Solyc03g097020.4	0.539011983	6.08287E-08	0.263478809	0.009600196	AAA+ ATPase domain-containing protein
Solyc03g025470.4	0.53896228	4.44241E-06	0.543642706	1.68672E-06	Kinesin-like protein KIN-10C isoform X2
Solyc01g087810.2	0.538366952	0.008826133	0.690140185	0.000316147	Subtilisin-like protease
Solyc03g083490.3	0.538261196	6.34092E-07	0.243959003	0.028476122	Chaperonin 60 subunit beta 3, chloroplastic-like protein
Solyc04g076040.3	0.537777396	9.80905E-07	0.97243366	9.8991E-21	Cyclin N-terminal domain-containing protein
Solyc07g021120.3	0.53767699	0.008335962	1.101064303	2.7196E-09	CST complex subunit CTC1
Solyc08g080150.1	0.536678883	4.77168E-07	0.663860659	7.47891E-11	Transcription factor TCP9
Solyc11g068540.2	0.535723676	3.35379E-13	0.415351468	1.94401E-08	Nitrilase-like protein 1
Solyc04g063210.3	0.535599313	0.000828359	0.428928567	0.005938995	Probable coffeoyl-CoA O-methyltransferase At4g26220
Solyc02g071770.3	0.535125982	0.008995479	0.723621268	0.000132056	Oil body-associated protein 2B
Solyc08g075120.3	0.53488466	1.08079E-06	0.544918485	3.05314E-07	Rop guanine nucleotide exchange factor 14
Solyc05g051520.3	0.534589948	3.82528E-07	0.73867458	2.44364E-13	tRNA (Cytosine(34)-C(5))-methyltransferase
Solyc12g005250.2	0.53384087	5.04058E-07	0.678436218	2.23952E-11	Kinesin motor domain-containing protein
Solyc02g083620.3	0.533225041	3.19077E-08	0.588668592	3.16303E-10	L-ascorbate peroxidase
Solyc03g113760.3	0.532899886	0.000186082	0.751937342	2.0045E-08	Transcription factor E2F/dimerization partner (TDP)
Solyc10g084670.3	0.530910935	2.6555E-12	0.606770729	2.44155E-16	Eukaryotic translation initiation factor 3 subunit A
Solyc09g007320.4	0.530858029	0.000193272	0.514056864	0.00017998	Pentatricopeptide repeat-containing protein
Solyc01g087780.2	0.530796468	3.12396E-08	0.810529689	1.29068E-18	Subtilisin-like protease
Solyc04g051350.3	0.530075149	1.21621E-05	0.477671334	5.50826E-05	Ribonucleoside-diphosphate reductase
Solyc07g008040.4	0.530010652	2.6556E-06	0.616450763	1.786E-08	Topless- protein 4
Solyc08g081040.3	0.529994642	0.00046417	0.537735746	0.000212769	Ribonuclease P
Solyc03g117800.4	0.529130743	0.007829355	0.707177679	0.000123379	ECERIFERUM 3
Solyc01g107260.4	0.528969153	0.000931868	0.636121859	2.43673E-05	DNA double-strand break repair Rad50
Solyc02g083890.4	0.528765976	8.23688E-12	0.378944785	9.57249E-07	ATPase
Solyc07g056140.3	0.528566296	6.49016E-17	0.562102335	2.49629E-19	Chalcone-flavanone isomerase family protein
Solyc11g071640.3	0.528490459	5.59432E-13	0.512937544	1.94929E-12	Glucose-1-phosphate adenylyltransferase
					Beta-xylosidasealpha-l-

					arabinofuranosidase 2
Solyc02g080520.4	0.528401004	4.79673E-08	0.853917289	1.47585E-20	Probable DNA double-strand break repair Rad50 ATPase isoform X2
Solyc07g053700.4	0.527961997	3.68459E-06	0.549181285	5.91817E-07	Reticulon-like protein (Fragment)
Solyc07g042970.4	0.527819059	0.042293223	0.79528569	0.000905614	RCC1 domain- containing protein RUG3, mitochondrial
Solyc07g026640.3	0.527341256	0.02015378	0.502072328	0.018765459	Fanconi Anaemia group E protein C- terminal domain- containing protein
Solyc09g014210.3	0.526958454	0.036541097	1.015515372	4.08095E-06	Pentacotriptide- repeat region of PRORP domain- containing protein
Solyc05g006810.4	0.526855761	0.009974657	0.436680908	0.025345504	2,4-dichlorophenol 6-monoxygenase isoform X1
Solyc03g114740.4	0.526717711	0.014134083	0.693422879	0.000428209	BSD domain- containing protein
Solyc03g118280.1	0.526564368	0.007187848	1.03189996	9.84999E-09	Pentacotriptide- repeat region of PRORP domain- containing protein
Solyc03g078570.3	0.526244072	0.002861012	2.634128617	2.66036E-68	Variant 2, Ras- protein RABH1e
Solyc01g007800.3	0.525871473	0.006251154	0.366209937	0.050015854	Transcription repressor
Solyc09g090550.3	0.525712632	0.036193471	0.712103443	0.001980648	Arp2/3 complex 34 kDa subunit
Solyc11g012610.2	0.525183154	0.000253607	0.618509545	6.19341E-06	Epidermal growth factor receptor substrate 15 homolog
Solyc04g015940.3	0.525161129	0.000121346	0.74627972	8.47291E-09	Ribosomal RNA- processing protein 12-like conserved domain-containing protein
Solyc01g091270.3	0.524665591	0.000135099	0.309012882	0.024858999	Myeloid leukemia factor
Solyc04g076390.3	0.524260903	4.39109E-08	0.692010704	7.23733E-14	cysteine--tRNA ligase
Solyc10g054860.2	0.523418656	0.002989158	0.835059012	4.23772E-07	Nucleolar 27S pre- rRNA processing Urb2/Npa2 C- terminal domain- containing protein
Solyc06g051320.3	0.523368231	0.01921044	0.571540772	0.006567214	Vinorine synthase
Solyc06g074680.4	0.523216599	0.023285619	1.049238784	3.78049E-07	Phosphatidylcholine- sterol acyltransferase
Solyc10g078360.3	0.523141019	0.039940696	1.440348675	1.88035E-10	3-oxoacyl-[acyl- carrier-protein] reductase
Solyc01g008600.4	0.522952039	1.32576E-08	0.441237797	1.13636E-06	Zinc finger CCH domain-containing protein 53-like
Solyc01g091230.3	0.52293557	4.71809E-11	0.482372955	7.74583E-10	Protein kinase domain-containing protein
Solyc11g062130.2	0.522312287	1.3557E-06	0.566481217	9.30383E-08	ADP/ATP translocase

Solyc12g006575.1	0.522188094	0.045701098	0.699700682	0.003340015	DYW domain-containing protein
Solyc10g079120.3	0.522073312	4.26211E-06	0.398060589	0.00041516	Zinc finger CCCH domain-containing protein 30
Solyc10g051140.3	0.521851325	0.000248797	0.929539665	1.19701E-12	Zinc finger, RING/FYVE/PHD-type, Methyltransferase, trithorax
Solyc12g009840.2	0.520285181	2.83304E-07	0.37310577	0.000209359	H(+)-exporting diphosphatase
Solyc01g007170.4	0.52007676	0.000162308	0.345096531	0.011891781	C2 domain-containing protein
Solyc12g098700.1	0.518772041	0.003111514	0.974342591	3.19614E-09	ATP-dependent RNA helicase
Solyc01g108600.3	0.518377416	0.000140054	0.887442187	7.17343E-12	Peptidase M16C associated domain-containing protein
Solyc04g005380.3	0.518193778	0.00101853	0.851579419	5.35088E-09	Ninja-family protein (Fragment)
Solyc03g098450.3	0.517942072	3.52873E-06	0.666466089	3.82341E-10	Kinase-interacting family protein-like
Solyc08g077120.2	0.517633965	0.013346491	1.129423824	4.05251E-09	Smr domain-containing protein
Solyc06g071290.3	0.517382624	1.80765E-07	0.276008452	0.006160297	Aminoaldehyde dehydrogenase 2
Solyc06g076520.1	0.517004235	3.24904E-06	0.244837202	0.031842734	Cytosolic class I small heat shock protein 3B
Solyc04g080490.4	0.516984276	1.48389E-08	0.910572351	3.30887E-26	Zinc-finger homeodomain protein 6
Solyc02g084720.3	0.516499782	4.46198E-12	0.689402872	3.59727E-21	SUEL-type lectin domain-containing protein
Solyc01g110190.4	0.515562205	0.002997276	0.667480657	4.7885E-05	Kinesin-like protein KIN-7D, mitochondrial
Solyc10g048190.1	0.515042859	0.000667224	0.380450881	0.010326284	Thymocyte nuclear protein 1
Solyc11g008380.3	0.51476213	7.39885E-07	0.636788644	2.14405E-10	Glycerol-3-phosphate dehydrogenase
Solyc01g111870.3	0.514353661	0.003636679	0.730281052	1.05166E-05	non-specific serine/threonine protein kinase
Solyc09g097860.4	0.514260279	1.57887E-06	0.659103504	1.189E-10	Kinesin-like protein KIN-12B
Solyc03g114540.2	0.513811006	4.70331E-06	0.459493399	3.0604E-05	Strictosidine synthase conserved region domain-containing protein
Solyc06g066430.3	0.51361181	1.65606E-08	0.42245622	2.83833E-06	Iq-domain 14 isoform 1
Solyc01g110960.4	0.513296087	1.09916E-10	0.734592652	1.10478E-21	Ubiquitin-protein ligase BRE1A
Solyc11g069270.2	0.513284685	1.84188E-14	0.619638946	2.9534E-21	SUEL-type lectin domain-containing protein
Solyc11g066740.2	0.513214931	0.006325467	0.363614026	0.048142522	Reticulata-related 1
Solyc06g074090.3	0.513159759	7.37162E-06	0.406156266	0.000321317	7-dehydrocholesterol reductase
Solyc01g091800.3	0.512323962	1.92395E-05	0.420062992	0.000366474	rRNA adenine N(6)-methyltransferase
Solyc04g081070.3	0.512238119	8.24795E-08	0.633478842	6.95149E-12	Protein ACCUMULATION AND

					REPLICATION OF CHLOROPLASTS
Solyc06g050560.3	0.511935169	0.000117607	0.366866034	0.004951454	6, chloroplastic Probably inactive leucine-rich repeat receptor-like protein kinase IMK2
Solyc09g091180.3	0.511661172	6.10745E-13	0.330952269	4.2624E-06	GroEL-like equatorial domain superfamily
Solyc01g091340.3	0.510891527	5.60399E-07	0.607920802	5.3182E-10	peptidylprolyl isomerase
Solyc12g013880.2	0.510492391	4.19804E-13	0.68344012	1.94246E-23	Origin of replication complex subunit 3
Solyc01g081610.3	0.509989993	9.30424E-05	0.477136156	0.00016959	Beta-hexosaminidase
Solyc03g044020.4	0.509971074	0.000424483	0.757419918	1.74875E-08	Condensin complex subunit 1 C-terminal domain-containing protein
Solyc06g050980.3	0.509532762	2.34349E-12	0.473160962	5.93933E-11	Ferritin
Solyc02g093620.2	0.509526322	0.000384509	0.779308459	8.19466E-09	Protein LOW PHOTOSYNTHET IC EFFICIENCY 1, chloroplastic
Solyc12g014040.1	0.509109141	0.003808061	1.088966637	9.56193E-12	Calmodulin-binding domain-containing protein
Solyc10g045630.2	0.508752647	0.014750554	0.832385508	1.95396E-05	Protein RETICULATA- RELATED 1, chloroplastic
Solyc04g015490.4	0.508531411	4.23771E-10	0.780027798	4.00669E-23	Mg-protoporphyrin IX chelataase
Solyc01g103960.3	0.507517688	2.63893E-05	0.753785005	4.82564E-11	DNA helicase
Solyc04g074990.3	0.506547573	1.28263E-05	0.962281597	7.15354E-19	Zinc-finger homeodomain protein 1
Solyc08g076730.4	0.506436349	2.02545E-14	0.6895205	2.44408E-26	Adenosine monophosphate- protein like
Solyc04g072032.1	0.506429183	3.06797E-05	0.314186412	0.010068828	Signal peptidase complex subunit 2
Solyc12g096990.2	0.506406819	0.009537185	0.776224285	1.97214E-05	Histone-lysine N- methyltransferase family member SUVH9-like
Solyc01g028810.3	0.505998532	3.62526E-12	0.605600082	2.82219E-17	RuBisCO large subunit-binding protein subunit beta, chloroplastic
Solyc01g008160.4	0.505673946	5.5674E-05	0.441153753	0.00029654	Protein SLOW GREEN 1, chloroplastic
Solyc02g062170.3	0.505591816	0.000323088	0.491840468	0.000271414	Chalcone-flavanone isomerase family protein
Solyc08g068050.3	0.505588908	0.000102899	0.376308444	0.003204922	DDT domain- containing protein
Solyc07g054760.1	0.505525787	0.001078408	0.342739365	0.02514594	Wound-responsive family protein
Solyc05g050970.4	0.505415498	1.84949E-08	0.441317054	7.76533E-07	transketolase
Solyc09g082510.3	0.505361944	1.55387E-08	0.823568358	1.27841E-21	NAB domain- containing protein
Solyc04g076560.3	0.505277101	2.26838E-11	0.559534979	2.85618E-14	Neuroguidin

Solyc01g068280.3	0.504676827	4.34244E-09	0.587817148	1.94929E-12	Protein CHROMATIN REMODELING 24
Solyc08g068150.4	0.504326833	4.51392E-09	1.004389022	6.45366E-34	BURP domain- containing protein
Solyc04g014400.4	0.504297666	0.004025444	0.58019792	0.000408634	Receptor-like protein 15
Solyc04g078050.3	0.504009972	1.2803E-07	0.602914467	7.09421E-11	RST domain- containing protein
Solyc02g080260.4	0.503621418	0.000161214	0.733022812	6.74215E-09	Homeobox-leucine zipper protein PROTODERMAL FACTOR 2
Solyc09g018850.3	0.503343537	0.000688171	0.33608724	0.021892201	Adenine DNA glycosylase
Solyc12g010670.1	0.503080194	0.001905696	0.682744744	7.12534E-06	E3 ubiquitin-protein ligase RMA
Solyc12g099800.2	0.5028065	2.25269E-06	0.509568309	8.58405E-07	Rhodanese- like/PpiC domain- containing protein 12, chloroplastic
Solyc06g072900.4	0.502678737	0.014702642	0.4246561	0.0312986	60S ribosomal protein L13
Solyc01g058160.3	0.502674719	0.000378137	0.986397735	2.59329E-14	Agenet domain- containing protein
Solyc03g121840.3	0.500675915	0.001589044	0.472588917	0.001895587	MYB transcription factor
Solyc01g080750.3	0.500234486	1.39799E-07	0.491203705	1.23286E-07	TOG domain- containing protein
Solyc09g065840.3	0.499952467	4.42531E-07	0.438538853	6.33491E-06	Single-stranded DNA-binding protein, ssb
Solyc07g066180.2	0.499841772	0.001688493	0.559849157	0.000219039	Putative WPP domain interacting protein 1
Solyc06g070970.3	0.499751654	7.24302E-08	0.415693977	4.82006E-06	Putative muscle M- line assembly protein unc-89-like
Solyc03g114640.4	0.499333213	1.173E-05	0.815207135	3.09884E-14	Peptidase S49 domain-containing protein
Solyc02g014360.3	0.499252354	0.000100653	0.622599483	3.18331E-07	DYW domain- containing protein
Solyc06g071640.3	0.498170637	2.36291E-09	0.424586489	2.93987E-07	Tryptophan aminotransferase- related protein 2
Solyc01g094290.3	0.498139955	1.01762E-05	0.661864514	1.16981E-09	K(+) efflux antiporter 2, chloroplastic
Solyc03g083400.3	0.496986133	4.69295E-05	0.392491908	0.001112231	CCT domain- containing protein
Solyc06g061090.3	0.496290858	0.000104314	0.455119721	0.000246498	TLDc domain- containing protein
Solyc02g093720.3	0.496086411	8.9856E-06	0.436421114	6.37535E-05	TPX2 C-terminal domain-containing protein
Solyc12g014210.3	0.496006479	0.006319645	0.546999211	0.001668891	UBP1-associated protein 2C
Solyc01g104640.3	0.495102638	6.15391E-08	0.480795187	6.86428E-08	Helicase ATP- binding domain- containing protein
Solyc01g105040.3	0.493839792	0.01461131	0.786508357	2.24294E-05	PORR domain- containing protein
Solyc07g045170.3	0.493297246	0.001004071	0.771865359	4.70008E-08	Kn1 C-terminal RWD domain- containing protein
Solyc06g068270.3	0.493235459	2.20231E-10	0.408633676	1.31966E-07	Codeine O- demethylase

Solyc08g082070.3	0.493175561	2.5532E-08	0.553304627	1.19082E-10	High mobility group B protein 6
Solyc07g061940.4	0.492524799	6.16415E-08	0.244068999	0.008920607	Acetolactate synthase
Solyc12g044290.2	0.492161114	0.003507916	0.817283444	1.93341E-07	Malonate--CoA ligase isoform X1
Solyc10g007840.3	0.491993732	6.7162E-07	0.475937877	8.37504E-07	Glutamyl-tRNA(Gln) amidotransferase subunit A, chloroplastic/mitochondrial
Solyc02g070390.3	0.490227896	3.26467E-07	0.738099047	4.26152E-16	Plastid transcriptionally active 12
Solyc01g086750.4	0.489925852	3.97915E-05	0.681800133	2.95283E-09	Clustered mitochondria protein homolog
Solyc05g006770.4	0.489900538	0.000159874	0.614233122	5.71367E-07	Protein kinase domain-containing protein
Solyc07g066040.1	0.489668487	1.56567E-06	0.376707995	0.000193189	RNA polymerase II elongation factor
Solyc03g025890.2	0.489505604	0.013322368	0.726537693	8.57092E-05	DNA mismatch repair protein
Solyc09g061870.3	0.489112084	1.49582E-05	0.481889002	1.18444E-05	Protein LATE FLOWERING
Solyc06g074730.4	0.489028774	0.029948938	0.938605365	2.22939E-06	Argonaute 5
Solyc01g009430.3	0.489007032	1.76179E-08	0.227085148	0.010693991	Histone deacetylase HDT1-like
Solyc09g090030.2	0.488274175	0.002406046	0.542695818	0.000362291	Histone-lysine N-methyltransferase ASHR2
Solyc10g078330.2	0.488241566	3.65735E-06	0.227344042	0.035481486	Cyclin N-terminal domain-containing protein
Solyc11g010960.2	0.488197483	2.03209E-07	0.771883835	1.56838E-17	Putative mannitol dehydrogenase
Solyc07g054210.3	0.488083705	1.46506E-11	0.372476739	2.72803E-07	NADPH-protochlorophyllide oxidoreductase
Solyc01g099530.3	0.487350205	0.033041735	1.152993836	7.97707E-09	Desiccation-related protein like
Solyc01g010520.3	0.487197143	4.70971E-10	0.469892921	9.25739E-10	Angiotensin-converting enzyme 2
Solyc09g009860.1	0.487171898	0.00447096	0.677347235	1.97961E-05	Glutaredoxin domain-containing protein
Solyc07g056540.3	0.487160878	2.74781E-11	0.511119249	1.39236E-12	(S)-2-hydroxy-acid oxidase
Solyc03g005260.3	0.487124521	2.09053E-10	0.569279232	2.06231E-14	sulfate adenylyltransferase
Solyc06g060270.4	0.487084483	7.98277E-05	0.736702226	2.09589E-10	DUF632 domain-containing protein
Solyc03g095180.3	0.486931553	0.00053301	0.443270864	0.00117228	superoxide dismutase
Solyc01g007990.4	0.4868835	0.003753601	0.506342583	0.001453521	Pkinase domain-containing protein/Stress-antifung domain-containing protein
Solyc03g120440.3	0.486587426	0.028976392	0.695087207	0.000583076	Cyclin-A2-4 like
Solyc07g049680.4	0.48566678	0.000193459	0.378257508	0.002955287	Condensin complex subunit 2
Solyc03g113090.3	0.485646013	2.60243E-06	0.366137175	0.000340205	Putative muscle M-line assembly protein unc-89-like

Solyc09g007200.4	0.485174804	0.000101973	0.604600679	3.3389E-07	Pentacotriptide-repeat region of PRORP domain-containing protein
Solyc01g057830.3	0.484627137	8.22205E-12	0.3945891	2.75809E-08	30S ribosomal protein S1, chloroplastic
Solyc09g092050.4	0.484321944	0.044988086	0.537158599	0.016772426	DYW domain-containing protein
Solyc03g113370.3	0.484009189	0.01296278	1.257443391	5.59993E-13	Ubiquitin thiolesterase/ zinc ion binding
Solyc11g006580.3	0.483991841	0.000196419	0.315237915	0.014392916	Mutator
Solyc09g074940.3	0.48355766	5.85701E-05	0.696412089	1.68386E-09	Translocase of chloroplast 159, chloroplastic
Solyc03g082690.3	0.483216298	0.044391094	0.585141334	0.008385039	RING-type E3 ubiquitin transferase
Solyc01g079520.3	0.482709352	0.000137275	0.721240476	1.68543E-09	DNA mismatch repair protein
Solyc01g010700.3	0.481737307	1.3526E-05	0.568939603	7.99401E-08	SNF1-related protein kinase regulatory subunit gamma-1-like
Solyc12g013710.2	0.480848322	6.09386E-12	0.443979843	1.84981E-10	NADPH-protochlorophyllide oxidoreductase
Solyc10g009280.4	0.480508461	7.89039E-06	0.218953961	0.047492275	GRF1-interacting factor 3
Solyc02g084830.4	0.480217752	0.035085266	1.136639021	7.41685E-09	DYW domain-containing protein
Solyc10g086660.2	0.479727689	6.23017E-06	0.68803578	7.0225E-12	Rop guanine nucleotide exchange factor 7-like
Solyc06g060910.2	0.479559374	0.012138351	0.939785611	4.40139E-08	Glycerol-3-phosphate transporter 4
Solyc10g084150.2	0.479213822	3.54332E-06	0.412114678	4.7885E-05	Cytokinin riboside 5'-monophosphate phosphoribohydrolase
Solyc12g042950.2	0.478547216	6.2714E-10	0.607504151	1.09367E-15	ADP _i ATP carrier protein
Solyc04g072460.3	0.478468127	3.24325E-07	0.27552606	0.0035643	Transcription factor TGA7
Solyc05g039950.2	0.478134523	0.001888675	1.180367174	7.59898E-18	Deacetylvindoline O-acetyltransferase-like
Solyc03g006850.3	0.47793717	0.001624851	0.486385225	0.000815067	RAB6-interacting golgin
Solyc02g089860.1	0.477818756	0.001759964	0.385015489	0.009569542	Elongation of fatty acids protein 3-like
Solyc09g007830.3	0.477310394	7.89276E-05	0.464876036	7.19618E-05	Cytokinin riboside 5'-monophosphate phosphoribohydrolase
Solyc11g044940.1	0.477094086	0.000154757	0.697610382	3.51559E-09	Serine/threonine-protein kinase-like protein ACR4
Solyc02g093300.3	0.477049807	3.49399E-05	0.615325319	2.50637E-08	DNA polymerase
Solyc11g069380.2	0.476723292	5.51918E-08	0.61181099	7.51357E-13	GcpE
Solyc11g012040.2	0.476517848	0.012667297	0.583398249	0.000983803	Ubiquitin-specific protease family C19-related protein
Solyc06g076640.3	0.476454465	1.43934E-09	0.288633712	0.000310274	Tubulin beta chain

Solyc12g049270.3	0.475762686	0.000534403	0.68332609	1.01536E-07	Developmentally-regulated G-protein 2
Solyc03g095300.4	0.475461354	0.001258593	0.290339278	0.04819365	C2 domain-containing protein
Solyc02g094640.4	0.475191265	5.02194E-10	0.488425436	9.87931E-11	acetate--CoA ligase
Solyc09g010810.3	0.474618622	6.09967E-05	0.58235868	2.07103E-07	Kinesin motor domain-containing protein
Solyc07g048030.4	0.474466125	0.001524642	0.680480216	1.61519E-06	Heterogeneous nuclear ribonucleoprotein 1
Solyc03g123430.4	0.474326644	0.030805049	0.419838309	0.044589632	AP2-like ethylene-responsive transcription factor AIL1
Solyc12g095780.2	0.474297439	6.46613E-06	0.544449711	8.99877E-08	Hydroxyproline-rich glycoprotein family protein
Solyc07g052350.3	0.474086573	1.88346E-06	0.604874764	4.07782E-10	Aconitate hydratase
Solyc02g070780.4	0.473916905	5.27182E-09	0.478292608	2.08172E-09	DNA replication licensing factor MCM3
Solyc01g080070.4	0.473696381	4.02666E-11	0.65002009	1.23495E-20	Heavy metal-associated isoprenylated plant protein 32
Solyc05g052010.2	0.47344828	0.000225004	0.389367192	0.002002793	Branchpoint-bridging protein
Solyc09g098040.3	0.473002609	4.02213E-09	0.629697348	8.50038E-16	Phosphoglucan, water dikinase, chloroplastic
Solyc08g006550.4	0.472997601	0.002152765	0.510681361	0.000449149	Rop guanine nucleotide exchange factor 5
Solyc11g065240.2	0.472557166	8.05894E-05	0.445204137	0.000124352	Saccharopine dehydrogenase NADP binding domain-containing protein
Solyc06g051940.4	0.472384745	0.016634583	1.160341357	3.37017E-11	protein-serine/threonine phosphatase
Solyc06g011530.3	0.472259537	0.037545106	1.114102786	4.46948E-08	Hydroxymethylglutaryl-CoA lyase, mitochondrial
Solyc06g066380.1	0.472173154	0.011225892	0.544765328	0.001752515	Pentatricopeptide repeat-containing protein
Solyc04g082900.4	0.471799728	0.000590269	0.473690504	0.000356723	Mitotic spindle checkpoint protein BUBR1
Solyc11g066840.3	0.471385213	1.0366E-08	0.271544998	0.001194547	Histone deacetylase
Solyc12g095870.3	0.471339607	0.003503182	0.371697542	0.01784141	Aurora kinase
Solyc06g053710.3	0.471205774	1.5758E-10	0.45458238	4.33729E-10	Ethylene receptor
Solyc06g005610.1	0.471080404	0.000827656	0.746489337	1.28262E-08	DVL domain-containing protein
Solyc10g074680.2	0.470881947	6.14077E-06	0.476793165	2.44799E-06	SCARECROW SCR
Solyc03g118870.4	0.470150026	1.20608E-05	0.460958465	1.12991E-05	PB1 domain-containing protein
Solyc09g008770.3	0.469875611	0.000995778	0.834173251	2.38441E-10	Embryonic protein DC-8-like
Solyc04g076820.1	0.469817668	5.22817E-07	0.231787706	0.015678807	PB1 domain-containing protein
Solyc05g006800.2	0.469704488	0.039357869	0.616848444	0.003276523	DYW domain-containing protein

Solyc10g080470.1	0.469316206	2.51429E-06	0.337474577	0.000638858	POU domain, class 2, transcription factor 2 like
Solyc08g081530.3	0.469134251	1.16638E-11	0.159279303	0.0289463	Monodehydroascorbate reductase
Solyc06g082190.3	0.468954046	0.010680198	0.542735751	0.00165179	Dual specificity protein kinase shkD
Solyc01g079750.3	0.468832948	7.2792E-06	0.518516091	2.61901E-07	Mitogen-activated protein kinase kinase NPK1
Solyc09g009770.3	0.468749284	1.56178E-05	0.379745733	0.000363568	IQ domain-containing protein IQM3-like
Solyc02g070770.3	0.468634937	0.000109395	0.469518298	5.98672E-05	3-beta hydroxysteroid dehydrogenase/isomerase
Solyc12g027870.1	0.468593257	7.06947E-05	0.403554329	0.000449479	Protein kinase domain-containing protein
Solyc06g005940.3	0.468405846	2.85625E-11	0.275606497	0.000120428	Protein disulfide-isomerase
Solyc04g078190.4	0.467958515	2.9809E-09	0.424340782	5.37112E-08	Soluble secretory phospholipase A2 receptor
Solyc02g083900.3	0.467860545	0.030336791	0.892209286	8.10164E-06	Transformation transcription domain-associated isoform X4
Solyc07g018300.3	0.467506524	0.001404093	0.305692342	0.034853685	Replication protein A C-terminal domain-containing protein
Solyc03g110880.4	0.467132674	3.05874E-06	0.618048557	1.46513E-10	DNA-directed RNA polymerase subunit beta
Solyc04g077060.3	0.466797763	4.63038E-07	0.588649354	4.53367E-11	K Homology domain-containing protein
Solyc02g094520.3	0.466757446	5.87045E-06	0.420608822	2.8434E-05	Histone-lysine N-methyltransferase
Solyc09g092510.3	0.466554096	0.000138504	0.470160252	6.60707E-05	LOB domain-containing protein (Fragment)
Solyc02g085220.4	0.466353961	0.04562645	0.758429748	0.000296368	Vacuolar sorting protein 39
Solyc04g054410.3	0.465337021	0.01355988	0.52702645	0.003075425	Regulation of nuclear pre-mRNA domain-containing protein 1B
Solyc08g076030.3	0.465123325	0.00129573	0.688867395	5.2464E-07	WD-40 repeat protein-like isoform 1
Solyc07g042560.4	0.465090635	0.002959362	0.467443249	0.001784445	Kinesin-like protein NACK1
Solyc06g083470.4	0.464632376	5.89541E-11	0.345629336	1.23966E-06	Senescence-associated protein 13
Solyc02g032870.4	0.464502869	0.002372841	0.595412465	2.92574E-05	Tyrosyl-DNA phosphodiesterase 2
Solyc02g092950.3	0.464483256	2.89964E-05	0.419258199	0.000108193	Microtubule-associated protein RP/EB family member 1C
Solyc03g025900.3	0.464235504	0.000187071	0.31303534	0.010933993	Flap endonuclease GEN-like 2
Solyc12g062250.2	0.464060966	9.00015E-11	0.693087676	5.10339E-24	Tyrosine-protein phosphatase

Solyc05g050630.4	0.463626421	0.001639233	0.952161299	4.93222E-12	domain-containing protein
Solyc01g091240.4	0.463451822	0.010374771	0.827251157	3.95886E-07	Clu domain-containing protein
Solyc03g005310.4	0.462300773	4.16328E-06	0.331019172	0.000884113	Chlororespiratory reduction 4
Solyc03g093140.3	0.462132045	3.56368E-07	0.482977177	4.2157E-08	Armadillo repeat-containing protein LFR
Solyc04g009180.3	0.462056824	3.05752E-05	0.44360963	3.87201E-05	Phosphate starvation-induced protein 3 isoform 1
Solyc02g082690.3	0.462022327	1.72557E-05	0.797097775	2.38539E-15	TCP domain-containing protein
Solyc12g005010.2	0.461974613	7.90909E-10	0.624878204	6.0075E-18	Lethal giant larvae (Lgl)-like C-terminal domain-containing protein
Solyc09g059240.3	0.461374051	0.017979247	0.57726744	0.001463479	CAP-Gly domain-containing linker 1
Solyc03g119350.3	0.461364642	0.000615661	0.793327726	9.92637E-11	Cytochrome P450, family 82, subfamily G, polypeptide 1
Solyc06g009220.4	0.460662664	3.30337E-06	0.596396427	4.17245E-10	Protein kinase domain-containing protein
Solyc01g006450.4	0.459500813	6.6827E-07	0.41996064	3.78675E-06	Isoamylase 3, chloroplastic
Solyc04g071340.5	0.459398334	0.000168349	0.460755507	8.27664E-05	Enoyl-ACP reductase
Solyc03g114380.4	0.459104868	2.96052E-05	0.410647198	0.000120469	fructose-bisphosphatase
Solyc01g097640.3	0.458849408	6.2751E-07	0.50637277	1.38253E-08	Kinesin motor domain-containing protein
Solyc12g014430.2	0.458467218	0.000610129	0.891288865	4.01323E-13	Bms1-type G domain-containing protein
Solyc02g085230.3	0.458389089	3.30925E-07	0.440134014	4.28983E-07	Cellulose synthase-like protein G3
Solyc07g064810.3	0.457144493	7.04157E-08	0.398670745	1.89394E-06	Nucleolar protein 6
Solyc03g111940.2	0.457007237	0.000775374	0.691173664	4.61392E-08	Imidazole glycerol phosphate synthase hisHF
Solyc02g086600.3	0.456841088	0.000425558	0.398366758	0.001515988	Putative psoralen synthase
Solyc04g008300.1	0.456567635	0.00232261	0.809724621	4.03777E-09	polyribonucleotide nucleotidyltransferase
Solyc02g068350.1	0.455866562	0.00054581	0.339575606	0.008757888	UbiB domain
Solyc10g080090.3	0.455805409	0.000910664	0.67388544	1.82346E-07	uroporphyrinogen-III synthase
Solyc06g074260.4	0.455715325	1.26507E-06	0.377920707	4.18358E-05	Zinc finger BED domain-containing protein
Solyc12g099010.3	0.455694477	0.000191802	0.650496757	1.73979E-08	DAYSLEEPER-like Pollen Ole e 1 allergen and extensin family protein
Solyc05g014790.3	0.455333656	2.314E-07	0.766704246	5.17716E-20	Inactive serine/threonine-protein kinase lvsG
Solyc05g054760.4	0.455031371	4.61026E-09	0.433101044	1.71633E-08	Lipoxygenase
Solyc08g061800.3	0.454995733	0.005422121	0.410256865	0.009153131	Dehydroascorbate reductase
					Apicidin F synthase

Solyc02g086090.4	0.454331445	3.8268E-08	0.513400874	1.05577E-10	mannose-6-phosphate isomerase
Solyc01g081490.3	0.454150252	5.86808E-08	0.634558155	3.06774E-15	RNA polymerase sigma factor
Solyc05g052150.4	0.454063177	1.26396E-06	0.219108383	0.02260193	ATP synthase F1 complex delta/epsilon subunit N-terminal domain-containing protein
Solyc02g094160.1	0.453853848	1.44632E-07	0.328130536	0.000140004	Ribonucleoside-diphosphate reductase small chain
Solyc02g082180.3	0.453765936	7.86851E-07	0.433538773	1.51299E-06	DNA replication licensing factor MCM6
Solyc06g075130.4	0.453432731	5.46817E-06	0.57977053	1.4149E-09	Protein ENHANCED DISEASE RESISTANCE 2-like
Solyc06g068290.1	0.453423374	0.019438718	0.464280834	0.010901808	Triphosphate tunnel metalloenzyme 3
Solyc04g012060.3	0.453154871	1.68933E-06	0.470026109	3.48253E-07	Ribonucleoside-diphosphate reductase
Solyc10g081770.3	0.452772917	0.011331726	0.340287836	0.04814508	START domain-containing protein
Solyc04g081950.4	0.452714833	0.002440149	0.734955047	7.26218E-08	Pentatricopeptide repeat-containing protein
Solyc02g071260.3	0.452524811	0.003156928	0.673686923	2.88851E-06	Phytochrome
Solyc01g100360.4	0.452470809	3.0595E-09	0.515520066	4.93222E-12	Lipoamide dehydrogenase 1
Solyc12g014140.3	0.451711872	0.000132222	0.696450768	2.05944E-10	Lanceolate
Solyc01g104490.3	0.450857416	0.00875934	0.702803471	1.13149E-05	separase
Solyc01g107640.3	0.450733906	3.59503E-10	0.200396082	0.007002553	Translocon at inner membrane of chloroplasts 21
Solyc03g019960.3	0.450665156	0.002078416	0.431369374	0.002094709	CDT1-like protein a, chloroplastic
Solyc01g090240.3	0.450634843	0.001837785	0.479272947	0.000503647	Serine/threonine-protein kinase D6PK
Solyc01g095010.4	0.450580456	3.05762E-05	0.317568304	0.002959609	Sphingoid long-chain bases kinase 2, mitochondrial
Solyc06g009400.3	0.450150384	6.19089E-09	0.317333486	4.54188E-05	Nitrogen regulatory protein P-II homolog
Solyc05g052190.4	0.44995033	2.04678E-08	0.387499925	8.57451E-07	Transcription elongation factor
Solyc06g007110.3	0.4497078	1.41043E-09	0.57828552	9.09909E-16	Smr domain-containing protein
Solyc02g081160.3	0.449265187	3.10877E-10	0.381539676	8.64315E-08	Pyrophosphate--fructose 6-phosphate 1-phosphotransferase subunit beta
Solyc12g100330.2	0.449230398	2.79042E-06	0.711672249	8.83487E-15	DNA (Cytosine-5)-methyltransferase CMT3
Solyc07g043460.3	0.449214049	3.10929E-08	0.357348789	9.34114E-06	Secologanin synthase-like
Solyc09g089580.4	0.448989852	0.010435486	0.409153236	0.014324315	1-aminocyclopropane-1-carboxylate oxidase homolog

Solyc07g066410.4	0.448961242	2.24084E-05	0.379592475	0.00026621	WD repeat-containing protein 75
Solyc12g088720.2	0.447472278	2.39788E-07	0.48844834	9.44104E-09	Polyadenylate-binding protein
Solyc11g010950.2	0.44715996	1.52547E-06	0.338276101	0.00022262	Elongator complex protein 4
Solyc09g092450.3	0.446820285	1.9357E-07	0.484729334	6.27735E-09	Probable acyl-activating enzyme 16, chloroplastic
Solyc06g083890.4	0.44656776	1.78786E-06	0.374841201	4.43615E-05	Pre-mRNA-splicing factor SLU7
Solyc03g121640.3	0.446517542	2.79205E-05	0.348769205	0.000920503	Chaperonin CPN60-like 2, mitochondrial
Solyc10g086030.2	0.445578721	6.8771E-12	0.533434636	4.32541E-17	Interactor of constitutive active ROPs 2, chloroplastic
Solyc10g055740.2	0.445267899	6.06487E-06	0.681084226	1.18567E-13	Lysine histidine transporter-like 8
Solyc08g075510.4	0.4450312	0.01979883	0.43355458	0.016214658	JmjC domain-containing protein
Solyc02g092320.2	0.444828992	0.044239547	0.986977286	6.65268E-07	Pentatricopeptide repeat-containing protein, chloroplastic
Solyc10g006000.4	0.444781842	0.000474802	0.674250247	1.23977E-08	DEK C-terminal domain-containing protein
Solyc03g121720.2	0.443936101	4.32661E-10	0.501452883	5.64741E-13	Glyoxylate/succinic semialdehyde reductase 2, chloroplastic
Solyc01g057760.4	0.44380788	0.000144845	0.444894699	9.1043E-05	DEAD-box ATP-dependent RNA helicase 40
Solyc07g018360.3	0.443729142	5.43503E-08	0.649784306	2.13244E-16	Elongation factor Ts, mitochondrial
Solyc09g005010.4	0.44338361	1.17974E-06	0.1965276	0.036467102	Importin N-terminal domain-containing protein
Solyc09g010420.4	0.443379882	1.10611E-07	0.328506892	8.02239E-05	Arginine biosynthesis bifunctional protein ArgJ, chloroplastic
Solyc08g007080.4	0.443215659	0.001118206	0.62518723	7.55989E-07	Inositol polyphosphate-related phosphatase domain-containing protein
Solyc06g062840.4	0.443112012	3.23774E-06	0.578405799	2.72559E-10	threonine synthase
Solyc01g080780.2	0.44261403	5.83462E-05	0.538830951	2.87911E-07	Translocase of chloroplast 159, chloroplastic
Solyc12g044620.2	0.442357482	0.003615683	0.367573721	0.011572582	2-oxoglutarate (2OG) and Fe(II)-dependent oxygenase
Solyc04g005830.3	0.442271143	0.004320896	0.602417038	2.25432E-05	superfamily protein AAA+ ATPase domain-containing protein
Solyc01g090690.4	0.442124945	0.002217217	0.678545557	6.81735E-07	Elongation factor G, mitochondrial
Solyc04g014730.4	0.441803645	0.002394488	0.492604356	0.000350786	Fumarylacetoacetase
Solyc04g015620.3	0.441301908	8.21095E-07	0.447053542	3.87087E-07	DUF642 domain-containing protein

Solyc02g093950.3	0.441242781	9.99516E-05	0.249672221	0.028910431	26S proteasome regulatory complex, subunit PSMD10
Solyc07g063310.3	0.441095232	5.21721E-05	0.403133437	0.000130923	Abscisic acid ABA receptor
Solyc03g117480.4	0.44104801	1.85086E-09	0.420155192	7.15601E-09	H(+)-exporting diphosphatase
Solyc02g080790.4	0.440843133	3.56459E-08	0.606465768	2.81319E-15	Deoxyhypusine synthase
Solyc11g006350.1	0.440755558	7.51669E-06	0.253077994	0.010601753	aspartate carbamoyltransferase
Solyc11g022400.1	0.440199435	0.002943927	0.755559161	3.92885E-08	C2 domain-containing protein
Solyc02g085100.3	0.439959145	1.98133E-07	0.409320951	8.71675E-07	glucose-6-phosphate 1-epimerase
Solyc12g044920.3	0.439482903	0.045722447	0.725412363	0.000215146	Phospholipid-transporting ATPase
Solyc12g006790.3	0.439363204	0.000224712	0.318961248	0.006425861	Argonaute/Dicer protein, PAZ
Solyc01g102740.3	0.439036888	0.016385598	0.638707368	0.000132056	NAC domain-containing protein
Solyc08g078470.4	0.438683111	0.00849251	0.634522473	3.62807E-05	FHA domain-containing protein
Solyc07g025530.1	0.438488392	0.01979883	0.536123709	0.002216295	S-adenosyl-L-methionine-dependent methyltransferases superfamily
Solyc04g009030.3	0.438086802	3.30358E-10	0.485798392	1.54602E-12	Glyceraldehyde-3-phosphate dehydrogenase
Solyc01g108610.3	0.4379363	0.003576317	0.542089265	0.000119808	Cyclin-dependent kinase inhibitor
Solyc04g074300.3	0.437833628	7.13192E-08	0.177859939	0.035470172	S5 DRBM domain-containing protein
Solyc09g065340.3	0.437437721	0.028817493	0.625867031	0.000822733	Increased DNA methylation like
Solyc03g007800.3	0.437260653	0.000205992	0.659949151	2.05108E-09	Timeless N-terminal domain-containing protein
Solyc03g006840.4	0.437044809	0.000250896	0.258507855	0.029927629	DUF4378 domain-containing protein/VARLMGL domain-containing protein
Solyc08g074740.3	0.436060508	0.010972416	0.876585192	1.21907E-08	Poly [ADP-ribose] polymerase
Solyc07g064480.1	0.435477234	0.037212571	0.570453035	0.003105086	tRNA-uridine aminocarboxypropyl transferase
Solyc11g062010.3	0.434997839	0.04732712	0.89182636	9.51089E-06	Chromatin structure-remodeling complex protein SYD
Solyc02g083350.4	0.434685122	0.000182197	0.476234017	2.41088E-05	DNA-directed RNA polymerase subunit
Solyc10g039190.2	0.433491269	1.34073E-06	0.403006405	4.73796E-06	Small-subunit processome Utp12 domain-containing protein
Solyc08g083030.4	0.433313253	2.05868E-05	0.301957626	0.002748486	Zinc finger matrin-type protein 1
Solyc05g054640.4	0.432788568	3.11131E-07	0.59113634	5.37601E-13	Putative 2-oxoglutarate dehydrogenase, mitochondrial-like
Solyc12g007140.3	0.432733105	0.001906887	0.454755578	0.000633907	DUF3741 domain-containing protein (Fragment)

Solyc01g067530.3	0.432359192	5.28056E-05	0.656711051	1.03313E-10	GTP-binding protein OBGc, chloroplastic
Solyc10g005280.1	0.432117806	1.60141E-05	0.468657528	1.07628E-06	Pentatricopeptide repeat-containing protein
Solyc03g098200.4	0.432087775	0.03579986	0.673714527	0.00035305	Homeodomain GLABROUS 11
Solyc02g014310.4	0.431812067	9.26082E-11	0.290870632	1.57395E-05	Nucleolin 2
Solyc07g007840.3	0.431522995	0.000107027	0.46307303	1.58044E-05	Spen paralogue and orthologue SPOC C-terminal domain-containing protein
Solyc09g074470.3	0.431521277	7.26662E-05	0.282820662	0.008851548	NAB domain-containing protein
Solyc02g088490.3	0.431134278	4.88701E-08	0.376944897	1.45041E-06	Saccharopine dehydrogenase NADP binding domain-containing protein
Solyc12g056940.2	0.430829116	0.006410187	0.769597238	2.01928E-07	acetyl-CoA carboxylase
Solyc06g073040.1	0.430542122	0.020417623	0.650751995	0.000152216	Transcription repressor
Solyc02g080570.3	0.430347512	0.000433013	0.889015709	5.59316E-15	Starch synthase
Solyc01g098630.3	0.429804763	0.001372811	0.313653933	0.017296474	39S ribosomal protein L45, mitochondrial
Solyc08g060920.4	0.429563662	0.000180197	0.479852091	1.1273E-05	SPX domain-containing protein
Solyc06g051930.3	0.429431211	6.36142E-05	0.675253242	1.54358E-11	pyruvate kinase
Solyc01g105160.4	0.42926174	2.58582E-08	0.440395664	5.19583E-09	P-type ATP-ase 1
Solyc02g084750.4	0.429174147	2.88895E-05	0.558093614	1.40611E-08	Methylthiotransferase
Solyc04g056410.3	0.429021073	0.002547646	0.837721707	7.70563E-11	Protein CHROMATIN REMODELING 25
Solyc02g069570.3	0.428781819	0.000130898	0.549564576	2.29495E-07	Pentatricopeptide repeat-containing protein
Solyc01g088380.3	0.428405035	0.00014043	0.559732971	1.12015E-07	DNA replication ATP-dependent helicase/nuclease
Solyc07g025380.3	0.427773636	9.89877E-05	0.645115261	3.51342E-10	DNA replication checkpoint mediator MRC1 domain-containing protein
Solyc07g007510.4	0.427743612	1.16177E-08	0.380026543	2.68297E-07	Triphosphate tunnel metalloenzyme 3
Solyc02g093180.3	0.427225428	0.000930008	0.799561852	9.81558E-12	HXXXD-type acyl-transferase family protein
Solyc11g042880.3	0.426871683	0.012575783	0.398569328	0.014736816	Group 2 isoform 2
Solyc03g032190.3	0.42578065	2.46365E-05	0.558324984	6.10029E-09	G2/mitotic-specific cyclin-2 isoform X2
Solyc09g064440.4	0.425563109	4.86835E-06	0.524174446	6.25212E-09	ABC-type xenobiotic transporter
Solyc02g071930.2	0.425487413	0.025601127	0.544170103	0.002070072	TFIIF-interacting CTD phosphatase, including NLI-interacting factor
Solyc03g120850.4	0.425197753	2.86394E-09	0.527451304	4.82856E-14	RuBisCO large subunit-binding protein subunit beta, chloroplastic

Solyc07g008910.3	0.423788891	2.86282E-05	0.600438817	2.8912E-10	Thioredoxin domain-containing protein
Solyc05g047590.4	0.423121694	9.02609E-05	0.810359287	3.95282E-16	Pectinesterase
Solyc04g051580.4	0.423097946	2.4286E-07	0.606305509	8.11281E-15	S-adenosylmethionine transporter
Solyc04g082320.3	0.422841845	0.003283697	0.642886333	1.79186E-06	Pentatricopeptide repeat-containing protein
Solyc08g081380.3	0.422757023	0.019885146	0.752990066	7.19593E-06	BTB/POZ domain-containing protein At1g63850
Solyc03g063680.3	0.422617654	0.016686124	0.548792521	0.000780789	C3HL domain class transcription factor isoform 1
Solyc08g076480.3	0.422559517	1.59343E-08	0.575493784	7.39512E-16	Plastoglobulin-1, chloroplastic
Solyc10g085100.2	0.42248046	0.000430229	0.516046848	5.52878E-06	Sulfoquinovosyl transferase SQD2
Solyc12g099360.2	0.422452212	0.026601542	0.4942486	0.005317171	Acyl-activating enzyme 7
Solyc03g118290.3	0.421916292	0.002984149	0.673432613	5.31036E-07	Auxin response factor
Solyc05g010670.3	0.421659105	1.4559E-08	0.663436007	2.47432E-20	Heat shock protein 90-5, chloroplastic
Solyc03g006970.1	0.42070165	2.65778E-10	0.405790117	7.37628E-10	Subtilisin-like protease
Solyc03g051900.4	0.420159391	4.71335E-07	0.649567453	2.64303E-16	rRNA biogenesis protein RRP5
Solyc12g098640.3	0.419997629	4.16796E-08	0.292231934	0.000144686	Cycloeucalenol cycloisomerase
Solyc02g088610.4	0.419857231	2.46541E-08	0.495814011	9.83645E-12	Chaperone protein ClpB3, chloroplastic
Solyc06g076700.1	0.419651587	8.17128E-05	0.556569591	3.55677E-08	Auxin transporter-like protein 2-like
Solyc07g063970.3	0.419075906	0.005568381	0.611408439	1.12512E-05	Dihydroflavonol-4-reductase-like isoform X1
Solyc03g034220.3	0.418845552	1.15951E-07	0.295139899	0.000203871	Ribulose biphosphate carboxylase small subunit, chloroplastic
Solyc09g020010.2	0.418546536	0.014625807	1.056226202	4.5961E-12	Mediator of RNA polymerase II transcription subunit 19a
Solyc04g049130.4	0.418523288	0.005578027	0.902513965	6.0472E-11	Iron-sulfur cluster biosynthesis family protein
Solyc01g094010.3	0.418248774	0.003987953	0.380285743	0.006340337	Alpha/beta hydrolase fold-3 domain-containing protein
Solyc03g117740.3	0.417795328	6.03356E-05	0.235033398	0.02502626	Nuclear protein (Fragment)
Solyc09g091280.4	0.417467163	7.45067E-05	0.539171678	9.22545E-08	Retinoblastoma-related protein isoform X1
Solyc04g081280.3	0.417460042	0.000215547	0.476647023	1.19644E-05	5'-3' exoribonuclease
Solyc03g115990.3	0.417452159	6.2439E-09	0.203606001	0.005706537	malate dehydrogenase
Solyc09g011830.4	0.417278513	3.2885E-08	0.609410859	3.90747E-17	Plastid transcriptionally active
Solyc08g066180.3	0.417238563	4.89448E-08	0.440448164	3.36436E-09	Haloacid dehalogenase-like

Solyc02g070670.4	0.417197897	3.24805E-06	0.355972779	5.42477E-05	hydrolase family protein CobW/HypB/UreG nucleotide-binding domain-containing protein
Solyc04g007560.3	0.417132778	3.26184E-06	0.410499992	2.77791E-06	ALG-2 interacting protein X
Solyc12g007010.2	0.416844843	1.71846E-08	0.395756808	5.26335E-08	Fe-S cluster assembly factor HCF101, chloroplastic
Solyc08g075530.3	0.416596571	4.57826E-06	0.540100554	7.90954E-10	Alpha-glucosidase 2
Solyc02g085250.4	0.416406316	3.81406E-05	0.45599366	2.79614E-06	Amine oxidase domain-containing protein
Solyc07g005020.3	0.416149003	4.09382E-06	0.623965948	3.97296E-13	DNA replication licensing factor MCM5
Solyc12g014490.3	0.41566272	4.12981E-05	0.307724261	0.002079061	Putative microtubule-associated protein 1-like
Solyc01g111590.4	0.415630992	0.001890428	0.265736387	0.045065475	Histone-binding protein RBBP4 N-terminal domain-containing protein
Solyc10g074880.3	0.415480445	8.13686E-06	0.369089374	4.81583E-05	Protein RETICULATA-RELATED 3, chloroplastic
Solyc08g076290.3	0.414987959	0.000526453	0.651496903	5.09635E-09	Plastidal glycolate/glycerate translocator 1, chloroplastic
Solyc12g096250.2	0.414935088	0.037443979	0.641378036	0.000385938	HXXXD-type acyl-transferase family protein
Solyc03g006420.4	0.414680714	0.000287734	0.720629308	1.95317E-11	Origin recognition complex subunit 1
Solyc07g042250.3	0.414327751	1.42614E-08	0.299814252	4.35318E-05	20 kDa chaperonin, chloroplastic
Solyc11g018550.4	0.413306913	4.16952E-07	0.281011591	0.000595224	L-ascorbate peroxidase
Solyc06g083520.3	0.413275962	8.30446E-06	0.302498378	0.000978643	Guanine nucleotide-binding protein-like NSN1
Solyc04g010260.3	0.413261298	1.74759E-05	0.665976649	3.88455E-13	Splicing factor 3B subunit 3
Solyc02g030130.4	0.413250652	0.000250663	0.553394984	1.86457E-07	Subtilisin-like protease SBT2,2
Solyc02g080330.4	0.412699081	8.99105E-08	0.595412447	9.95056E-16	Cytochrome P450, E-class, group I
Solyc08g006170.1	0.412197673	0.015513969	0.580078141	0.000256433	Pentatricopeptide repeat-containing protein
Solyc08g042050.3	0.4121847	4.43616E-07	0.609258085	1.00925E-14	RNA helicase
Solyc10g006290.3	0.412132711	1.34465E-06	0.200885711	0.021351948	Reactive Intermediate Deaminase A, chloroplastic
Solyc10g078680.3	0.412129833	0.001916948	0.389188539	0.002179731	FT-interacting protein 1
Solyc01g097800.3	0.411967747	0.000508658	0.428776983	0.000142259	DNA damage-repair/toleration protein DRT102

Solyc01g006280.3	0.411803805	2.58569E-09	0.436858109	1.3611E-10	formate-- tetrahydrofolate ligase
Solyc08g082400.1	0.411143829	8.18157E-06	0.592139236	2.46966E-11	NAD(P)H-quinone oxidoreductase subunit S, chloroplastic
Solyc08g061270.1	0.410576022	0.026410744	0.348514088	0.04874889	DUF1677 domain- containing protein (Fragment)
Solyc01g111990.3	0.410514361	6.32059E-05	0.701264644	4.86583E-13	Probable alanine-- tRNA ligase, chloroplastic
Solyc07g008880.3	0.409978963	0.00148208	0.709643501	5.78849E-09	Pre-mRNA- processing-splicing factor 8A
Solyc10g007050.3	0.40989055	4.12502E-07	0.343486304	1.61304E-05	Probable bifunctional methylthioribulose- 1-phosphate dehydratase/enolase- phosphatase E1
Solyc05g026560.3	0.409880265	1.69213E-06	0.714332424	1.16872E-18	ARM repeat superfamily protein
Solyc07g006810.3	0.409832698	0.00018481	0.501388021	1.64704E-06	Dethiobiotin synthase
Solyc02g092870.2	0.409510147	0.026815849	0.509405936	0.00310399	C2 N1'-type domain- containing protein
Solyc02g079770.3	0.40933838	2.33942E-08	0.487727882	6.44055E-12	DAG protein, chloroplastic
Solyc01g081510.4	0.40925237	0.001211488	0.405205859	0.00084001	3-hydroxyisobutyrate dehydrogenase-like 2, mitochondrial
Solyc10g024320.2	0.40908817	8.0278E-07	0.50589896	2.02546E-10	Lon protease homolog, mitochondrial
Solyc03g097160.4	0.408653335	8.80976E-05	0.320508488	0.001745352	U3 small nucleolar RNA-associated protein 13 C- terminal domain- containing protein
Solyc01g086930.4	0.408637454	0.009592513	0.43010325	0.003740663	Protein gamma response 1
Solyc11g072730.2	0.408332958	0.020513077	0.70798187	1.27291E-05	DNA-directed RNA polymerase subunit
Solyc03g117970.4	0.407544641	1.13616E-06	0.697800681	9.32057E-19	Poly [ADP-ribose] polymerase
Solyc07g008530.1	0.407478903	0.004922739	0.489191038	0.000344353	Tyrosine--tRNA ligase
Solyc01g103040.4	0.40700263	0.000137275	0.596004085	3.02536E-09	Spindle assembly checkpoint component MAD1
Solyc09g005740.3	0.406934417	2.33918E-05	0.464525563	4.87896E-07	Chloroplast lumen common family protein
Solyc01g100980.4	0.406735813	0.018797832	1.022233672	1.60909E-11	Polygalacturonase
Solyc03g095760.3	0.406648412	0.000146813	0.228125398	0.034355687	Rhodanese-like domain-containing protein 7
Solyc03g121610.3	0.40589885	3.08737E-05	0.647403793	2.92527E-12	Receptor-like serine/threonine- protein kinase ALE2
Solyc03g113450.4	0.405870873	2.04771E-05	0.272541008	0.00392304	LRR receptor-like serine/threonine- protein kinase FEI 2
Solyc12g005030.3	0.405845369	0.002611801	0.77457215	7.30161E-10	Calcium dependent protein kinase8

Solyc02g077990.3	0.405791121	1.2553E-07	0.270804214	0.000464614	30S ribosomal protein S5, chloroplastic
Solyc07g008860.3	0.405445371	2.10826E-05	0.279347902	0.003101556	Angio-associated migratory cell protein
Solyc12g095760.2	0.404924282	3.69049E-08	0.338943986	3.54103E-06	Pyrophosphate--fructose 6-phosphate 1-phosphotransferase subunit alpha
Solyc11g013110.2	0.404807943	0.048762182	0.620902542	0.000904293	Flavonol synthase
Solyc11g006710.2	0.404765603	4.48438E-07	0.421680817	7.7657E-08	Cationic amino acid transporter C-terminal domain-containing protein
Solyc07g005860.3	0.404216257	2.64591E-06	0.333086303	8.5554E-05	AUGMIN subunit 8
Solyc04g048900.3	0.404209278	0.035379268	0.454807282	0.010578529	Calreticulin
Solyc01g079860.3	0.40410939	0.000205882	0.338502577	0.001473139	ATP-dependent (S)-NAD(P)H-hydrate dehydratase
Solyc07g052980.3	0.404027095	2.92207E-08	0.371887477	2.60711E-07	Xyloglucan endotransglucosylase /hydrolase
Solyc03g083210.3	0.404020114	6.80467E-05	0.381600644	0.000103307	Protein DEFECTIVE IN MERISTEM SILENCING 3
Solyc07g016170.4	0.404019344	5.59925E-08	0.477159377	3.30948E-11	L-arabinokinase isoform X2
Solyc05g009460.3	0.403990979	3.86934E-05	0.44580601	2.25332E-06	WD repeat-containing 55
Solyc02g069090.3	0.403970738	6.8203E-10	0.499124478	7.19791E-15	Cathepsin B
Solyc02g068750.1	0.403839787	0.000883019	0.37673774	0.001372654	Probable tRNA N6-adenosine threonylcarbamoyltransferase
Solyc06g011450.3	0.40370657	1.32792E-05	0.415674173	4.21978E-06	Clathrin assembly protein At2g25430
Solyc04g055200.3	0.40356123	7.09655E-09	0.436782774	1.39785E-10	Asparagine synthetase [glutamine-hydrolyzing]
Solyc08g080550.1	0.40347853	0.002568096	0.704165271	1.43259E-08	Increased size exclusion limit 1a
Solyc02g089940.4	0.4031472	2.83449E-05	0.525861434	1.09316E-08	BEL1-like homeodomain protein 4
Solyc07g047860.4	0.402623559	0.000309548	0.622081931	3.30996E-09	Nuclear pore complex protein NUP133
Solyc09g090700.1	0.402564067	1.44004E-07	0.235444336	0.002400774	Succinate-semialdehyde dehydrogenase
Solyc02g069680.3	0.401806776	0.001811244	0.282180399	0.026418834	Vacuolar protein sorting-associated protein 2 homolog 2
Solyc06g054080.3	0.401586122	0.00012714	0.243509629	0.020113006	RNA polymerase II accessory factor
Solyc07g056020.3	0.401534156	0.000260923	0.691831675	3.332E-11	Tr-type G domain-containing protein
Solyc06g071350.4	0.401472711	0.006430532	0.676441156	9.57964E-07	BAH domain-containing protein
Solyc04g076960.4	0.401224849	0.000344621	0.418241233	8.69853E-05	Sucrose transporter

Solyc03g007050.3	0.401185422	0.003325746	0.681595131	6.2112E-08	LRR receptor-like serine/threonine-protein kinase ERL1
Solyc01g112280.3	0.400743941	1.23142E-08	0.302115783	1.69429E-05	N-acyl-aliphatic-L-amino acid amidohydrolase
Solyc09g076000.3	0.400594151	7.49254E-08	0.411297084	1.48634E-08	non-specific serine/threonine protein kinase
Solyc03g117010.4	0.400422105	3.67952E-05	0.455734769	1.04764E-06	Transcriptional regulator ATRX isoform X5
Solyc02g083250.3	0.400266796	5.19501E-08	0.658788702	7.7067E-21	Putative ganglioside-induced differentiation-associated protein 2-like
Solyc07g066280.3	0.400186917	5.36387E-05	0.323877633	0.00084546	Heat stress transcription factor A-1, putative isoform 1
Solyc06g073690.2	0.400161931	0.01337173	0.457182133	0.002559704	Transcription factor IIC 90kDa subunit N-terminal domain-containing protein
Solyc06g073540.4	0.399983349	7.11035E-07	0.45608751	6.87295E-09	Argonaute 4
Solyc03g096980.1	0.399974477	7.20925E-06	0.380605362	1.15145E-05	Alpha/beta hydrolase fold-3 domain-containing protein
Solyc09g059440.1	0.399811189	0.028490788	0.42205073	0.01363134	Cell division control protein 45 homolog
Solyc09g097980.4	0.399321161	0.007294636	0.454835073	0.001114984	Auxin-induced protein PCNT115-like
Solyc06g007610.2	0.398815343	1.44037E-07	0.208454772	0.007032813	Early tobacco anther 1
Solyc05g012325.1	0.398729505	0.050365318	0.645032622	0.000458076	Ureide permease
Solyc05g005810.4	0.398691654	1.33573E-05	0.641435817	9.38287E-14	Transcription factor MYC/MYB N-terminal domain-containing protein
Solyc01g080720.4	0.398586857	0.025332195	0.354935094	0.035746873	Pentacotriptide-repeat region of PRORP domain-containing protein
Solyc12g010380.3	0.398140989	0.000338155	0.735265131	5.36085E-13	adenylate kinase
Solyc04g078610.4	0.398075358	2.28515E-07	0.560959115	4.27488E-14	Kinesin-like protein KIN-4A isoform X2
Solyc10g083500.2	0.397923095	5.40981E-05	0.603704218	1.15891E-10	Serine/threonine-protein kinase KIPK2 isoform A
Solyc03g096000.3	0.397870898	0.004008969	0.687893469	1.17989E-07	Clathrin heavy chain
Solyc06g075340.4	0.39775071	0.000946826	0.618140443	5.83341E-08	carbamoyl-phosphate synthase (glutamine-hydrolyzing)
Solyc08g075580.3	0.397708677	9.55331E-05	0.396623191	5.29591E-05	DNA-directed RNA polymerase III subunit RPC6
Solyc04g072850.4	0.397571394	1.65403E-07	0.694517629	9.02311E-22	Probable beta-D-xylosidase 7
Solyc08g068330.3	0.396987555	5.05313E-07	0.303234914	0.000117746	Aspartate aminotransferase
Solyc05g043430.4	0.396949636	4.72026E-07	0.392080788	3.98852E-07	Carboxymethylenebutenolide, putative

Solyc07g017510.3	0.396693388	0.005059052	0.725718418	4.05344E-08	1-phosphatidylinositol-3-phosphate 5-kinase
Solyc03g111260.3	0.396616102	2.90847E-06	0.671455631	3.99695E-17	Putative Cycloeucaenol cycloisomerase
Solyc07g066600.3	0.396509995	2.37853E-07	0.259912644	0.000788638	Phosphoglycerate kinase
Solyc11g011370.2	0.39644971	0.014357737	0.48402001	0.001373158	Nuclear condensin complex subunit 3 C-terminal domain-containing protein
Solyc06g083040.3	0.396118907	4.82508E-06	0.655121519	7.35509E-16	Carboxypeptidase
Solyc01g098740.4	0.395886447	0.001998932	0.671439241	1.54587E-08	Probable serine/threonine-protein kinase PBL7
Solyc07g007590.1	0.395868313	0.006193935	0.345598059	0.013437365	Prephenate/arogenate dehydrogenase domain-containing protein
Solyc11g040370.2	0.395746562	2.51429E-06	0.240391943	0.004629192	Far upstream element-binding protein 2
Solyc11g069780.3	0.395162742	0.000997295	0.459711971	6.15013E-05	P-loop NTPase domain-containing protein LPA1 homolog 1
Solyc12g094710.2	0.394946439	0.000444154	0.284477795	0.01003539	AT-hook motif nuclear-localized protein
Solyc06g060140.4	0.394825775	0.000119766	0.408849839	3.54737E-05	Kinesin-like protein KIN-7C, mitochondrial
Solyc03g083280.4	0.394213306	3.71704E-05	0.258348497	0.006697859	Pentatricopeptide repeat-containing protein
Solyc05g023680.4	0.394133134	3.01124E-07	0.298870404	9.43565E-05	RING-type E3 ubiquitin transferase
Solyc01g079800.4	0.394031555	0.012607006	0.483593143	0.000969318	DEAD-box ATP-dependent RNA helicase 58, chloroplastic
Solyc04g079660.2	0.39376279	0.007414133	0.780071801	5.38358E-09	p450 monooxygenase
Solyc08g007000.3	0.393583784	0.006767705	0.573177608	2.25564E-05	PPM-type phosphatase domain-containing protein
Solyc05g056310.3	0.393276957	1.2112E-09	0.336824229	1.72619E-07	T-complex protein 1 subunit gamma
Solyc09g074930.3	0.392287159	9.69399E-09	0.300949242	1.13973E-05	Rubber elongation factor
Solyc07g044760.3	0.391833178	3.53411E-06	0.337699117	5.2764E-05	RNA helicase
Solyc02g087180.4	0.391440298	0.040903458	0.748555003	1.91078E-05	Mediator of RNA polymerase II transcription subunit 4
Solyc04g009560.3	0.391306802	9.91232E-08	0.446769439	4.14678E-10	Ypt/Rab-GAP domain of gyp1p superfamily protein isoform 3
Solyc03g120080.4	0.39111869	0.003434831	0.458368042	0.000289147	Periodic tryptophan protein 2
Solyc06g065010.4	0.39091778	1.77341E-05	0.337346229	0.000154408	GDSL esterase/lipase 1-like
Solyc07g064030.4	0.390902503	3.32321E-05	0.581416306	7.28146E-11	Kinesin-like protein KIN-14N isoform X2

Solyc02g092070.3	0.390720193	4.40884E-08	0.417036714	2.33754E-09	Growth-regulating factor
Solyc06g071330.4	0.390183983	7.99487E-06	0.279652687	0.001293476	Nucleobase-ascorbate transporter 6
Solyc06g061280.3	0.3899857	3.9237E-06	0.72931344	2.32791E-20	Cinnamoyl-CoA reductase-like SNL6
Solyc10g079160.1	0.389910858	0.041181383	0.7939977	3.20282E-06	Protein WHAT'S THIS FACTOR 9, mitochondrial
Solyc12g088220.2	0.38951811	0.002234378	0.869470876	9.87636E-14	Branched-chain-amino-acid aminotransferase
Solyc08g076220.3	0.389170003	7.98573E-08	0.659910128	2.83236E-21	Phosphoribulokinase
Solyc08g082710.3	0.389067493	2.53933E-05	0.455661135	3.04144E-07	ABL interactor-like protein 3
Solyc01g080840.3	0.388977213	1.6255E-05	0.622919496	5.07479E-13	Protein translocase subunit SecA
Solyc12g010840.2	0.388933457	3.23774E-08	0.340329466	1.12324E-06	Ketol-acid reductoisomerase
Solyc10g054440.3	0.388603407	7.08214E-06	0.390836033	4.17296E-06	Arginine decarboxylase
Solyc04g077150.3	0.388487042	4.63529E-06	0.283656463	0.000718817	Ergosterol biosynthetic protein 28
Solyc09g031650.3	0.388453388	0.01535543	0.540906248	0.000339729	ABI3-interacting protein 3
Solyc04g015330.3	0.387988622	0.002234378	0.642007347	3.49366E-08	Phosphoglycerate mutase family protein
Solyc11g040120.3	0.387638706	0.000271802	0.549161971	6.56892E-08	DNA replication licensing factor MCM2
Solyc08g076190.3	0.387635169	0.040653646	0.425079034	0.015781329	Protein SENSITIVE TO UV 2
Solyc05g006120.3	0.387400999	0.00427404	0.58371977	3.21273E-06	DNA polymerase
Solyc07g044930.3	0.387167569	0.005477342	0.512141803	8.97155E-05	RNA helicase
Solyc09g014490.4	0.386820198	4.91467E-06	0.29070137	0.000520874	Endochitinase A
Solyc02g062290.2	0.386761677	0.003727668	0.83033405	1.96484E-11	Heterogeneous nuclear ribonucleoprotein Q
Solyc07g053960.3	0.386603334	0.001163774	0.383440211	0.000751015	Ubiquitin-conjugating enzyme E2 38
Solyc06g071860.3	0.386284247	3.88421E-06	0.519054092	8.32178E-11	Zinc finger CCH domain-containing protein 43
Solyc01g057310.4	0.386131446	0.000573352	0.678214018	9.64133E-11	Kinesin-like protein KIN-12D isoform A
Solyc04g011580.4	0.385555439	3.35401E-05	0.622780205	1.7622E-12	Pumilio-like protein 3
Solyc04g063360.3	0.385253727	0.000189999	0.614681828	3.21297E-10	Cell division protease ftsH
Solyc03g119280.3	0.385104181	3.59485E-06	0.435661167	5.67707E-08	isogeny histidine--tRNA ligase
Solyc02g069410.4	0.384613696	0.005666719	0.435992014	0.00084001	Haloacid dehalogenase-like hydrolase domain-containing protein
Solyc02g093060.3	0.384528183	1.11853E-06	0.46124128	1.65191E-09	DUS-like FMN-binding domain-containing protein
Solyc07g041640.3	0.384445512	0.001926848	0.598459751	1.83672E-07	Growth-regulating factor
Solyc08g043140.4	0.38443984	0.001674571	0.336300914	0.004303875	ADP-ribosylation factor GTPase-

Solyc02g087280.3	0.384267083	0.004637788	0.378402316	0.003564633	activating protein AGD11
Solyc11g011420.3	0.383791488	1.18316E-07	0.432154328	7.00107E-10	Proton-dependent oligopeptide transport family protein
Solyc07g008250.3	0.383749781	0.000145119	0.257523622	0.010622124	peptidylprolyl isomerase
Solyc09g011850.4	0.383695987	0.000507402	0.460439823	1.14616E-05	EIN3-binding F-box protein 1
Solyc01g095740.4	0.383558058	1.05952E-05	0.493866331	3.59104E-09	Fructokinase-like 1, chloroplastic
Solyc11g065320.2	0.383374868	1.87148E-08	0.486334092	1.70417E-13	ATP-dependent RNA helicase
Solyc08g068920.4	0.382950455	0.009730419	0.475828251	0.000570867	Zinc finger CCH domain-containing protein 53-like
Solyc01g090750.3	0.382938723	4.91248E-08	0.240131218	0.000708666	ABC1 atypical kinase-like domain- containing protein
Solyc01g086710.4	0.382846016	0.000400103	0.445038307	1.67653E-05	T-complex protein 1 subunit alpha
Solyc01g058450.3	0.382666572	0.000316736	0.215167584	0.044351959	DNA-directed RNA polymerase subunit beta
Solyc11g010110.3	0.382493052	3.02158E-06	0.518904589	4.69652E-11	Flowering time control protein FCA
Solyc01g009990.3	0.382228793	1.272E-06	0.292391817	0.0002038	RNA cytosine-C(5)- methyltransferase NSUN2-like isoform X4
Solyc01g104590.3	0.382084875	1.99675E-07	0.182099959	0.015993828	Photosynthetic NDH subunit of luminal location 5, chloroplastic
Solyc04g082250.3	0.381977952	6.90111E-07	0.509184759	8.50939E-12	60S ribosomal protein L3
Solyc10g083310.2	0.381782849	0.002436882	0.629776925	5.97655E-08	FTSH protease 1
Solyc01g095730.4	0.381694366	0.007098424	0.593786965	7.76349E-06	Kinesin-like protein KIN-5C
Solyc08g082630.3	0.381105384	0.004480712	0.401216428	0.001565935	Poly(A) RNA polymerase
Solyc11g012020.2	0.38108153	0.006260948	0.524895505	5.54341E-05	Auxin response factor
Solyc01g079790.4	0.38081135	3.01533E-07	0.507030424	1.19701E-12	EPS15 homology domain 2
Solyc10g083170.2	0.380782219	0.0011197	0.678198301	3.10041E-10	Glucose-1- phosphate adenyltransferase
Solyc01g102510.4	0.380508495	0.002152765	0.392416961	0.001047307	Secoisolaricresinol dehydrogenase
Solyc03g118020.3	0.380440706	1.53215E-07	0.367596974	2.77461E-07	G- beta subunit (Contains WD40 repeats)
Solyc02g076720.3	0.380353731	0.000822692	0.62447963	5.96721E-09	Ribonuclease
Solyc09g009190.4	0.380333034	0.001249729	0.744898023	1.49567E-11	phosphoribosylform ylglycinamide synthase
Solyc02g070030.4	0.38008187	0.00343821	0.439936604	0.000340731	1,4-alpha-glucan branching enzyme
Solyc05g014690.3	0.379665777	0.040081533	0.585364254	0.000501134	Small RNA 2'-O- methyltransferase
Solyc08g082200.3	0.379617585	0.022111338	0.33020657	0.037306567	ATP-dependent DNA helicase Q-like 5
					DNA primase

Solyc01g095120.3	0.37952925	2.0192E-05	0.257595495	0.003566458	AB hydrolase-1 domain-containing protein
Solyc01g067790.3	0.379489104	0.018184765	0.731929811	5.69802E-07	BRCT domain-containing protein
Solyc02g091970.4	0.379394555	8.01657E-08	0.187459411	0.009435633	Branched-chain-amino-acid aminotransferase
Solyc01g079500.4	0.37933559	0.000379266	0.520913748	2.50734E-07	DNA replication licensing factor MCM7
Solyc02g094470.3	0.379311551	7.23669E-08	0.211097232	0.003265376	Mitochondrial phosphate transporter
Solyc04g007100.4	0.379140421	0.0077328	0.464318663	0.000503534	Serine/threonine-protein phosphatase 2A 65 kDa regulatory subunit A beta isoform
Solyc08g078530.4	0.379102262	0.001998932	0.589774054	3.77644E-07	Agnet domain-containing protein
Solyc09g090340.3	0.379077739	0.008290701	0.68274226	2.3986E-07	Serine-threonine kinase receptor-associated
Solyc07g043420.3	0.379040236	2.35295E-08	0.294332501	1.46298E-05	Hyoscyamine dioxygenase
Solyc11g062190.2	0.378918404	5.89165E-06	0.191270026	0.025387133	ADP/ATP translocase
Solyc04g082330.3	0.378523059	0.000335198	0.464530453	4.16084E-06	Bms1-type G domain-containing protein
Solyc04g076380.4	0.378450754	6.60921E-07	0.473477805	1.64453E-10	NADPH--cytochrome P450 reductase
Solyc01g067290.3	0.378262796	0.000435973	0.794283436	1.66473E-15	Divinyl chlorophyllide a 8-vinyl-reductase, chloroplastic
Solyc05g005480.2	0.37819666	2.17045E-06	0.723168213	4.44463E-22	2-methylene-furan-3-one reductase-like isoform X1
Solyc01g068160.4	0.377682048	1.43594E-05	0.442841199	1.11148E-07	L-cysteine desulhydrase
Solyc10g018520.1	0.377419789	3.24026E-07	0.430202272	2.13406E-09	HRDC domain-containing protein
Solyc12g036150.1	0.377341522	0.047206796	0.625901506	0.000305187	ABC-type xenobiotic transporter
Solyc07g055050.3	0.377201005	3.70674E-07	0.503886616	1.49134E-12	Protein CONSERVED ONLY IN THE GREEN LINEAGE
Solyc02g081910.2	0.377073716	0.001494486	0.485217228	1.41167E-05	160, chloroplastic DNA topoisomerase
Solyc03g059180.4	0.377041801	0.001146877	0.632959733	6.50035E-09	Calcium sensing receptor, chloroplastic
Solyc06g073550.3	0.376577132	0.000247015	0.496226267	4.436E-07	HTH La-type RNA-binding domain-containing protein
Solyc01g009050.3	0.376437944	3.04999E-06	0.324869	4.11569E-05	Molybdopterin biosynthesis protein CNX1
Solyc06g071920.4	0.376216322	3.55259E-07	0.188261416	0.012901783	Glyceraldehyde-3-phosphate dehydrogenase
Solyc04g076620.4	0.376164739	0.029752099	0.779758743	9.95625E-07	HECT-type E3 ubiquitin transferase

Solyc09g010550.4	0.37570301	0.003995778	0.447529196	0.000262296	Protein EMBRYO DEFECTIVE like
Solyc01g108200.3	0.375568492	0.046478363	0.403702097	0.022270386	Protein disulfide-isomerase SCO2
Solyc06g068550.4	0.37546708	0.000129578	0.860393546	5.7305E-22	Peptidase A1 domain-containing protein
Solyc02g088700.4	0.375430157	1.2176E-07	0.247460466	0.00053864	Mitochondrial-processing peptidase subunit beta, mitochondrial
Solyc02g071580.4	0.375227749	0.047932923	0.533856265	0.002033816	Subtilisin-like protease SBT5,6
Solyc03g095960.1	0.375225298	0.024384667	0.386163844	0.013857126	Pentacotriptide-repeat region of PRORP domain-containing protein
Solyc02g088000.3	0.375158343	0.001112388	0.629943257	5.14005E-09	Starch synthase, chloroplastic/amylo plastic
Solyc04g072260.3	0.375074045	0.037735731	0.982712349	1.90418E-09	Midasin
Solyc06g084250.4	0.374892451	5.10066E-05	0.598235041	5.01481E-12	ARM REPEAT PROTEIN INTERACTING WITH ABF2-like
Solyc01g094720.3	0.374828174	0.000445854	0.521511851	2.67001E-07	Ascorbate transporter, chloroplastic
Solyc09g065880.4	0.374365657	0.000161232	0.360980532	0.000171375	F-box/LRR-repeat protein 17
Solyc06g065520.3	0.374289809	4.5203E-07	0.290325266	8.46345E-05	T-complex protein 1 subunit eta
Solyc08g069030.4	0.37423102	5.13078E-08	0.407060597	1.56988E-09	Delta-aminolevulinic acid dehydratase
Solyc03g121440.4	0.374215408	1.49362E-06	0.562885578	3.22747E-14	Proline-rich receptor-like protein kinase PERK13
Solyc03g031780.4	0.374128519	0.034482915	0.34719238	0.03791801	Putative dolichyl-diphosphooligosacch aride--protein glycosyltransferase subunit 3B
Solyc07g066610.3	0.373964772	1.15633E-06	0.344114169	6.00408E-06	Phosphoglycerate kinase
Solyc12g099470.2	0.373366032	3.77496E-06	0.188315156	0.022292391	protein-synthesizing GTPase
Solyc04g015750.3	0.373309692	4.31716E-05	0.820068784	1.34983E-21	magnesium chelatase
Solyc07g048080.4	0.373274194	1.37054E-05	0.585320077	3.7466E-13	threonine--tRNA ligase
Solyc07g005930.4	0.373261025	0.001792983	0.485051783	1.81077E-05	DNA-directed RNA polymerase
Solyc07g064280.3	0.373154208	0.000830606	0.31667474	0.00363718	Tryptophan synthase
Solyc08g076720.4	0.37287778	0.01942425	0.648623025	7.60445E-06	Multidrug/pheromone exporter, MDR family, ABC transporter family isoform 1
Solyc04g082780.3	0.372700679	1.40348E-07	0.277934337	8.58699E-05	Cinnamoyl-CoA reductase 1-like
Solyc01g106750.2	0.37265534	0.008843635	0.490501288	0.000215537	Serine/threonine-protein kinase TOR
Solyc08g076370.3	0.372364016	0.005959474	0.598781582	1.98387E-06	Homeobox-leucine zipper protein ROC3
Solyc02g069970.4	0.372150079	0.000662694	0.712000691	2.19701E-12	Protein kinase domain-containing protein

Solyc01g097760.3	0.37208751	9.34297E-07	0.15624569	0.047273123	quinol--cytochrome-c reductase
Solyc12g094620.3	0.372045252	4.24607E-07	0.357660384	8.54968E-07	Catalase
Solyc10g078860.2	0.372019545	0.002318914	0.533781553	3.02827E-06	DNA-directed RNA polymerase subunit beta
Solyc06g069030.3	0.371959122	0.008599751	0.391538508	0.003589783	Microbial collagenase
Solyc06g072750.3	0.37189841	0.04000307	0.393109867	0.01990413	Heat stress transcription factor A-1
Solyc03g121320.3	0.371693263	0.007006814	0.493649279	0.000125175	PWWP domain-containing protein
Solyc07g019650.4	0.371506026	2.76243E-06	0.67033626	2.06649E-19	ribonuclease P
Solyc03g019890.3	0.371486943	3.17528E-05	0.519127866	1.56922E-09	Beta-galactosidase
Solyc04g082110.4	0.371328341	0.005208296	0.490703291	7.93667E-05	Rop guanine nucleotide exchange factor 1
Solyc02g091780.1	0.371196779	0.00208761	0.3672009	0.001454485	Kinesin motor domain-containing protein
Solyc01g104910.3	0.370727068	0.000184213	0.394183039	3.77369E-05	WRKY transcription factor 19
Solyc08g061910.4	0.370141575	0.009634256	0.561859684	2.47828E-05	Trihelix transcription factor gt-2
Solyc09g007340.4	0.369845231	0.001424165	0.457394649	3.07579E-05	PWWP domain-containing protein
Solyc10g086340.1	0.369813483	0.005521468	0.705487652	8.26317E-09	Kinesin-like protein KIN-5B
Solyc05g005670.1	0.369640389	0.006755162	0.515334694	5.47685E-05	RING-type E3 ubiquitin transferase
Solyc08g062920.3	0.369630152	0.002747493	0.532067718	5.64449E-06	Pre-tRNA nuclear export protein
Solyc07g062140.3	0.369255731	0.000331652	0.272754727	0.00704967	alpha,alpha-trehalose-phosphate synthase (UDP-forming)
Solyc01g111910.3	0.369097035	0.003824123	0.461382842	0.000138477	Transcriptional elongation regulator MINIYO
Solyc10g037900.1	0.368709079	0.01146735	0.740067835	3.09057E-08	Dihydroorotate dehydrogenase
Solyc03g007280.4	0.368588722	0.000579212	0.427230324	2.57273E-05	DnaJ subfamily B member like
Solyc05g054580.3	0.367745879	5.25554E-07	0.160007029	0.035028042	60S acidic ribosomal protein P0
Solyc01g080810.3	0.367628853	7.86914E-05	0.67902169	8.49558E-15	isoleucine--tRNA ligase
Solyc09g031780.3	0.367511605	1.24809E-06	0.529589965	4.16439E-13	TIC110, chloroplastic
Solyc09g074520.3	0.36746809	0.000112095	0.467106672	3.43365E-07	Protein TRANSPORT INHIBITOR RESPONSE 1
Solyc11g071320.2	0.367327456	1.04422E-06	0.237110837	0.001668366	Ribosomal protein L27
Solyc07g007670.3	0.367274954	4.67689E-07	0.557156731	1.60604E-15	Purple acid phosphatase
Solyc01g103050.3	0.366889115	2.57114E-05	0.544371336	7.72873E-11	Auxin response factor
Solyc01g111240.4	0.365613609	0.001309536	0.526769896	1.13215E-06	Translocase of chloroplast 120, chloroplastic-like
Solyc02g081200.1	0.365574419	0.011947138	0.592278077	1.16873E-05	Myosin assembly sexual cycle
Solyc07g047790.3	0.36537166	3.0674E-07	0.388764938	2.39228E-08	Heat shock protein 90-6, mitochondrial

Solyc02g079000.4	0.365241532	0.000232329	0.673982946	3.14565E-13	ATP-dependent zinc metalloprotease FTSH 12, chloroplastic
Solyc08g029220.3	0.36490257	0.001450651	0.492398189	5.12801E-06	Bifunctional 3-dehydroquinase dehydratase/shikimate dehydrogenase isoform 1
Solyc05g007270.4	0.364683409	0.011681408	0.415310232	0.002090544	Angiotensin-converting enzyme 2
Solyc02g094100.4	0.364366774	0.036716529	0.563024957	0.000394721	ATPase family AAA domain-containing protein FIGL1
Solyc09g092690.3	0.364177568	0.021112637	0.656104282	4.74431E-06	peptidylprolyl isomerase
Solyc03g026200.4	0.363908883	0.01291329	0.328524467	0.019040291	Protein COFACTOR ASSEMBLY OF COMPLEX C SUBUNIT B CCB2, chloroplastic
Solyc07g053820.3	0.363844223	0.019178314	0.443313933	0.00205421	Mitotic checkpoint serine/threonine-protein kinase BUB1
Solyc04g008710.4	0.363841804	0.000117611	0.243930866	0.009609878	Putative coiled-coil domain-containing protein 9-like (Fragment)
Solyc06g072700.3	0.36375591	5.58763E-08	0.148605267	0.032732946	HMA domain-containing protein
Solyc01g097460.3	0.363352546	8.70162E-05	0.206861324	0.026918109	ribose-5-phosphate isomerase
Solyc02g085470.3	0.363241493	0.005104565	0.309189274	0.013511461	Plant-specific TFIIB-related protein 1
Solyc03g123440.3	0.363106297	0.027336075	0.739353655	7.26804E-07	Transcriptional activator
Solyc02g038740.4	0.363072009	4.9101E-06	0.551379731	5.23024E-13	DEMETER-like 3-hydroxy-3-methylglutaryl coenzyme A reductase
Solyc09g072710.4	0.362903426	0.000893462	0.372310005	0.000372673	Phospholipid--sterol O-acyltransferase
Solyc08g067920.3	0.362320421	0.025289672	0.551175981	0.000254242	Enhancer of polycomb-like protein
Solyc07g042315.1	0.362254654	0.00012538	0.521191109	6.69007E-09	Plastid 3-keto-acyl-ACP synthase II-B
Solyc02g068760.4	0.361544943	0.000197055	0.370821589	7.27769E-05	Pentacotriptide-repeat region of PRORP domain-containing protein
Solyc12g043020.2	0.361501555	1.78249E-06	0.407849475	3.27361E-08	dihydroxy-acid dehydratase
Solyc10g083490.3	0.361394243	7.03229E-06	0.414320804	8.79158E-08	Cell division protein FtsZ
Solyc01g081300.4	0.361309459	0.004170352	0.432269386	0.000274939	phosphoribosylamin oimidazolesuccinocarboxamide synthase
Solyc03g098020.4	0.360856178	3.74159E-05	0.386592757	4.64461E-06	Monoacylglycerol lipase-like
Solyc12g006320.3	0.360834173	1.01237E-06	0.625848046	9.19726E-19	RNA helicase
Solyc12g005020.2	0.360608511	0.001360399	0.236419149	0.034771246	NEP1-interacting protein-like 1
Solyc01g057020.3	0.360491733	0.027031437	0.632046928	1.70116E-05	Protein TRIGALACTOSYL

Solyc10g008540.3	0.360436048	0.029094702	0.638243021	2.15888E-05	DIACYLGLYCEROL 4, chloroplastic
Solyc09g010800.5.1	0.360211605	1.71015E-05	0.253949209	0.002442924	Ras-associated and pleckstrin protein domain-containing
Solyc07g017760.1	0.359611693	0.02250032	0.787392579	3.20733E-08	Metallothionein-like protein type 2
Solyc03g044430.3	0.359457782	0.020980996	0.378804076	0.009942646	Pentatricopeptide repeat-containing protein
Solyc02g083130.4	0.359361857	4.33996E-05	0.282925098	0.000983584	Nicotinate phosphoribosyltransferase
Solyc11g008780.3	0.358965994	0.000266801	0.49223869	1.71919E-07	Regulator of Vps4 activity in the MVB pathway protein
Solyc08g042100.3	0.358413558	0.002720766	0.536121319	1.6002E-06	VALINE-TOLERANT 1
Solyc06g082100.4	0.358375164	0.002942279	0.582982985	2.8062E-07	Armadillo repeat-containing domain-containing protein
Solyc07g062650.4	0.35836813	1.06761E-07	0.188427689	0.006241374	U5 small nuclear ribonucleoprotein helicase
Solyc03g111600.4	0.35792953	0.021000813	0.332205703	0.023848943	Malate dehydrogenase
Solyc03g121580.3	0.357825193	7.35271E-05	0.186913701	0.040780322	DNA-(apurinic or apyrimidinic site) endonuclease
Solyc06g050120.3	0.357744625	1.03424E-06	0.210236798	0.004624834	WD-40 repeat-containing protein
Solyc01g006180.4	0.357318686	0.019371637	0.299361222	0.040453673	MSI4
Solyc01g087720.4	0.357285142	0.00024701	0.61981205	1.37904E-11	quinol--cytochrome-c reductase
Solyc12g009930.3	0.357189491	1.86835E-07	0.710219863	1.74296E-27	GTP-binding protein
Solyc01g089870.3	0.356717958	0.002153236	0.561300188	2.31187E-07	BRASSINAZOLE INSENSITIVE
Solyc03g113190.1	0.356402508	0.015417673	0.550526902	5.66887E-05	PALE GREEN 2, chloroplastic
Solyc06g084270.3	0.35625492	0.00056222	0.532355108	3.78432E-08	P-loop containing nucleoside triphosphate hydrolase
Solyc05g012390.4	0.355639343	2.11712E-05	0.50901323	1.57537E-10	Zeatin O-glucosyltransferase
Solyc03g118910.1	0.355546214	1.15008E-05	0.31067759	0.000101568	Pentatricopeptide repeat-containing protein
Solyc03g031760.4	0.355442073	1.20427E-05	0.501973897	5.84919E-11	C2 domain-containing protein
Solyc04g078940.3	0.355224276	5.96932E-06	0.320488133	2.89255E-05	DAR GTPase 3, chloroplastic
					Pentatricopeptide repeat-containing protein
					T-complex protein 1 subunit delta
					Homeobox-leucine zipper protein
					PROTODERMAL FACTOR 2
					Vacuolar import/degradation
					Vid27 C-terminal domain-containing protein

Solyc08g014060.4	0.355184138	3.81005E-07	0.2924596	2.18846E-05	Eukaryotic translation initiation factor 2A
Solyc02g081850.4	0.35513344	0.009667755	0.451409985	0.000483256	Cationic amino acid transporter C-terminal domain-containing protein
Solyc05g007730.4	0.35510451	0.0188315	0.382489092	0.006575321	Uncoupling protein 3
Solyc01g088080.3	0.355088443	4.18669E-05	0.332273776	9.22752E-05	CCT-theta
Solyc06g065360.3	0.354897531	0.037145796	0.688630587	7.74889E-06	Erythroid differentiation-related factor 1
Solyc01g067370.3	0.354627849	0.001784954	0.486204475	6.29436E-06	Lysine-rich protein (Fragment)
Solyc02g088760.2	0.354543802	3.4918E-06	0.37876602	3.64157E-07	Ribosomal protein L7/L12 C-terminal domain-containing protein
Solyc06g072300.4	0.354533217	0.001759964	0.475581686	1.08226E-05	Argonaute 1
Solyc03g063560.3	0.354508936	0.026347676	0.82062336	2.06982E-08	Glutamine amidotransferase type-2 domain-containing protein
Solyc01g106020.3	0.354489528	0.002154002	0.328232534	0.003249134	K Homology domain-containing protein
Solyc10g081830.3	0.35448182	0.000114442	0.244438594	0.006938634	Replication protein A C-terminal domain-containing protein
Solyc02g068640.3	0.354465477	0.000257206	0.322838358	0.000603386	Pyrroline-5-carboxylate reductase
Solyc06g071490.3	0.354447624	0.001534037	0.44750326	2.4531E-05	Serine/threonine-protein kinase ATM
Solyc06g068480.3	0.354434718	1.74583E-06	0.283034005	0.000113822	Protein LOW PSII ACCUMULATION 3, chloroplastic
Solyc02g067310.4	0.3544258	0.00090908	0.720878463	3.03349E-13	Zinc-finger homeodomain protein 9
Solyc03g120090.1	0.354425066	2.30902E-05	0.197705364	0.01909586	Pyridoxal 5'-phosphate synthase-like subunit PDX1,2
Solyc05g054350.3	0.354056875	2.85317E-06	0.430577627	3.66113E-09	AB hydrolase-1 domain-containing protein
Solyc03g117120.4	0.35362383	0.000921648	0.59160492	3.19356E-09	SUPPRESSOR OF AUXIN RESISTANCE 3
Solyc02g014150.4	0.353578393	2.85416E-06	0.426719386	5.38698E-09	Photosystem II stability/assembly factor
Solyc05g010240.4	0.353524806	0.000835051	0.520488697	1.36885E-07	Chaperonin-60 beta4
Solyc03g033480.4	0.353411448	0.012062377	0.387432473	0.003273854	SWR1 complex subunit 6
Solyc06g075150.3	0.353197662	0.004212187	0.472983603	3.4223E-05	Auxin response factor
Solyc12g098660.3	0.35316831	0.025871375	0.552286827	0.000122319	Pheophytinase, chloroplastic
Solyc12g056740.2	0.35315591	8.07351E-07	0.377826251	6.02345E-08	RNA helicase, DEAD-box type, Q motif protein
Solyc11g069500.2	0.353138957	8.03838E-06	0.52118058	4.30451E-12	Auxin response factor

Solyc02g078120.2	0.352682509	9.39027E-07	0.304517235	1.89602E-05	Eukaryotic translation initiation factor 3 subunit D
Solyc05g054720.3	0.352677747	2.13476E-05	0.295256643	0.000319004	Protein TIC 20-I, chloroplastic
Solyc10g081020.2	0.352618841	0.006597242	0.729718818	1.41615E-09	Transcription elongation factor spt6
Solyc05g012190.3	0.352500811	0.005940571	0.272575422	0.028516163	Cell division control protein 48 homolog B
Solyc03g019940.4	0.352310387	1.81977E-07	0.40041353	9.55929E-10	asparagine--tRNA ligase
Solyc05g053950.4	0.351750797	0.011476573	0.27612173	0.039981073	TBC1 domain family member 14 like
Solyc02g088830.4	0.351449721	0.008541052	0.280727134	0.030151897	Hydroxyproline-rich protein
Solyc07g064520.3	0.351445287	1.36681E-05	0.265313291	0.000854524	ATP-dependent RNA helicase
Solyc10g081510.2	0.351376159	9.0605E-06	0.20578785	0.01025262	5-methyltetrahydropteroyltriglutamate--homocysteine S-methyltransferase
Solyc05g006900.2	0.351051199	0.01134226	0.698258347	4.56687E-08	Glycine-rich protein, putative isoform 1
Solyc07g066430.3	0.350946908	0.000383671	0.621542507	1.4985E-11	OBG-type G domain-containing protein (Fragment)
Solyc12g099560.2	0.350913937	2.98739E-07	0.29186856	1.56047E-05	Methyltransferase domain-containing protein
Solyc07g054200.4	0.350849718	0.00076109	0.435129488	1.13058E-05	Pre-mRNA-processing factor 6
Solyc06g066310.3	0.350767074	0.002813659	0.32671344	0.003698285	phosphomevalonate kinase
Solyc09g007940.3	0.350200244	2.16051E-07	0.216550185	0.001488829	Adenosine kinase
Solyc04g071660.3	0.350143838	0.000283286	0.752491696	3.70078E-17	SAP domain-containing protein
Solyc01g088600.4	0.349945044	7.26662E-05	0.468424278	2.79589E-08	Protein TRIGALACTOSYL DIACYLGLYCEROL 4, chloroplastic
Solyc01g101030.4	0.349931342	0.019942047	0.410401944	0.003616989	FACT complex subunit
Solyc03g119080.4	0.349802179	0.00113703	0.526971535	1.72077E-07	Beta-glucosidase 44
Solyc12g099420.2	0.349741327	0.00015771	0.334757966	0.000168204	Condensin-2 complex subunit H2
Solyc06g075080.4	0.349579771	9.55331E-05	0.360280601	3.30538E-05	NAD(+) diphosphatase
Solyc03g115510.3	0.349531513	0.022058815	0.73913006	9.67242E-08	S phase cyclin A-associated protein in the endoplasmic reticulum N-terminal domain-containing protein
Solyc04g040220.3	0.349214623	0.009685961	0.417936285	0.000927206	Regulatory protein NPR5
Solyc08g082410.4	0.349041461	0.000965394	0.442526593	1.18949E-05	Zinc finger CCCH domain-containing protein 13
Solyc05g015510.3	0.349019312	0.019339786	0.294706871	0.0396195	Squamosa promoter-binding-like protein 12
Solyc11g072280.3	0.348889901	0.004640951	0.294342581	0.013349255	65-kDa microtubule-associated protein 3
Solyc01g087170.3	0.348449221	9.74711E-06	0.297158862	0.000136571	C3HL domain class transcription factor

Solyc10g074720.3	0.348337991	0.002327513	0.333750793	0.002345366	Cell division control protein 2 homolog C
Solyc01g068070.4	0.34807145	0.048293914	0.784030508	6.46769E-07	WD repeat-containing protein 6
Solyc10g039210.4	0.347937171	0.000303679	0.90459079	9.58844E-25	Cytochrome P450, family 82, subfamily C, polypeptide 4
Solyc12g019290.1	0.347649229	0.003366987	0.64135256	5.81133E-09	Pentacotriptide-repeat region of PRORP domain-containing protein
Solyc11g006680.3	0.347304726	8.96655E-06	0.47155574	2.8229E-10	Tetratricopeptide-like helical domain, Nucleotide-binding alpha-beta plait domain protein
Solyc02g094280.4	0.347035054	1.22481E-05	0.293257655	0.000185978	Metal-nicotianamine transporter YSL6
Solyc04g016290.3	0.346827354	0.022654453	0.685521027	6.27844E-07	Rho termination factor N-terminal domain-containing protein
Solyc04g051670.3	0.346826752	9.78095E-05	0.496741635	3.59104E-09	RNA cytidine acetyltransferase
Solyc11g008360.3	0.346730633	3.71937E-06	0.308731952	2.53889E-05	Ribosomal large subunit pseudouridine synthase B
Solyc03g112810.3	0.346430563	0.000767575	0.314592553	0.001561966	Mitochondrial import inner membrane translocase subunit Tim17/Tim22/Tim23 family protein
Solyc01g104060.3	0.34625522	0.011082351	0.308351733	0.018280991	Glycine cleavage T-protein aminomethyltransferase
Solyc11g012760.2	0.346240569	0.010537812	0.390425839	0.002188766	SAM-dependent MTase TRM10-type domain-containing protein
Solyc09g098290.3	0.34614985	1.30884E-06	0.53581297	3.79833E-15	Probably inactive leucine-rich repeat receptor-like protein kinase At3g28040
Solyc01g110440.5.1	0.345812753	0.000490172	0.481913959	3.78973E-07	Arginine decarboxylase
Solyc06g036330.1	0.345505175	0.001234366	0.276371563	0.007816926	Protein SAR DEFICIENT 4
Solyc06g076150.3	0.344963749	0.000620868	0.311165394	0.001529609	Eukaryotic translation initiation factor 3 subunit C
Solyc04g071010.4	0.344826968	0.000348729	0.578616128	9.64441E-11	Protein MITOFERRIN like 1, chloroplastic
Solyc07g062110.3	0.34481593	0.000148329	0.270009601	0.002384395	Intracellular protein transport protein USO1
Solyc11g008670.2	0.344440317	0.001034989	0.408484826	4.33459E-05	Chromatin assembly factor 1 subunit FAS1
Solyc02g068560.3	0.344365745	0.005961081	0.435639057	0.000249424	Protein CHROMATIN REMODELING 4
Solyc01g111420.3	0.344136681	0.00050946	0.333336728	0.00048782	Ribosomal protein L1

Solyc03g033990.1	0.344056949	0.011287634	0.302934096	0.019366094	Cytochrome c-type biogenesis protein CcmE
Solyc05g050980.3	0.344040389	0.001180569	0.427250944	1.9321E-05	3-phosphoshikimate 1-carboxyvinyltransferase
Solyc09g064840.4	0.343994945	0.013493405	0.458264643	0.000474925	CID domain-containing protein
Solyc02g091640.3	0.343798547	0.000153934	0.449959079	1.66988E-07	Endoribonuclease E
Solyc05g009470.4	0.343532966	0.000156103	0.776305157	7.32396E-20	Alpha-xylosidase 1
Solyc10g085550.3	0.343522813	1.74583E-06	0.354960174	4.50446E-07	phosphopyruvate hydratase
Solyc06g009520.3	0.34348743	0.00019865	0.42425595	1.71667E-06	S uncoupled 1
Solyc07g017640.2	0.343405369	0.032721597	0.640866203	1.00128E-05	Lariat debranching enzyme C-terminal domain-containing protein
Solyc10g038190.2	0.343110072	0.000493541	0.446792272	1.47566E-06	Serine/threonine-protein kinase D6PK
Solyc10g009410.1	0.342685015	0.030979347	0.330111058	0.028634346	Aspartyl protease family protein 2
Solyc03g122180.4	0.342548047	2.78334E-06	0.16420454	0.02828408	Oligouridylate-binding protein 1B-like
Solyc04g076220.3	0.342314812	0.000315625	0.222938653	0.018831225	AT-hook motif nuclear-localized protein
Solyc02g081920.3	0.342238142	8.94987E-05	0.382620253	5.40521E-06	Protein PLASTID TRANSCRIPTIONALLY ACTIVE 14
Solyc11g008150.3	0.342088135	0.001452368	0.464185845	5.81792E-06	Protein RNA-directed DNA methylation 3
Solyc03g096800.4	0.342065626	0.000105296	0.696872482	3.83645E-17	Membrane protein of ER body-like protein
Solyc02g076930.2	0.341877798	0.019137833	0.472030778	0.000430991	U-box domain-containing protein 7
Solyc04g077210.3	0.341436802	3.45652E-05	0.284890612	0.000434045	Homeotic protein knotted-1
Solyc04g015440.4	0.34137275	0.016321656	0.838513425	4.84924E-11	Pentatricopeptide repeat-containing protein at4g31850 chloroplastic
Solyc12g014080.2	0.341332052	0.00035598	0.283884249	0.002315553	RAB GTPase
Solyc10g081920.2	0.341307008	0.001202132	0.37157671	0.000258035	Coatomer subunit beta
Solyc03g019930.4	0.341175796	0.001380068	0.358234474	0.000419088	DUF1308 domain-containing protein (Fragment)
Solyc01g079090.4	0.341060126	2.6862E-06	0.271199741	0.000172161	Protoporphyrinogen oxidase
Solyc06g071790.3	0.340684645	3.6576E-07	0.545553503	2.33895E-17	RAB GTPase homolog E1B
Solyc01g091480.4	0.340512823	0.000155144	0.476799495	2.42297E-08	Armadillo repeat kinesin 2
Solyc04g077030.3	0.340187906	3.99313E-06	0.398598603	1.96662E-08	Xylulose kinase
Solyc03g098280.4	0.340125716	0.005465272	0.500381205	1.52771E-05	Argonaute 1
Solyc07g043570.3	0.339930793	1.69256E-05	0.535163208	5.62225E-13	NADP-dependent oxidoreductase domain-containing protein
Solyc10g006790.4	0.339430669	0.004314478	0.278954959	0.015678807	Probable serine/threonine-protein kinase abkC

Solyc01g097890.2	0.339083805	0.001643924	0.305851512	0.003360243	GLABROUS1 enhancer-binding protein family
Solyc07g039500.4	0.338970305	0.012442703	0.690398878	2.46585E-08	CRM-domain containing factor CFM3, chloroplastic/mitoch ondrial
Solyc04g050510.3	0.338807317	7.70382E-05	0.505710627	6.12969E-10	ILITYHIA
Solyc10g075020.3	0.338560099	0.000197056	0.197677181	0.030356942	Elongation factor P
Solyc06g076360.4	0.338044763	2.15215E-05	0.540858601	1.16664E-12	Chloroplast envelope protein translocase, IAP
Solyc04g008860.4	0.337997698	0.002983606	0.236308667	0.034403257	Protein arginine N- methyltransferase 6
Solyc05g010260.4	0.337828599	4.10422E-05	0.409352014	2.20967E-07	6-phosphogluconate dehydrogenase, decarboxylating
Solyc04g056390.3	0.3376313	6.136E-07	0.393525602	2.20955E-09	isopentenyl- diphosphate Delta- isomerase
Solyc10g080080.3	0.337506067	3.47213E-05	0.302828143	0.000151919	Thioredoxin reductase
Solyc10g074580.2	0.337439459	0.000117447	0.420931348	5.04511E-07	Virus resistant/susceptible lipocalin
Solyc06g050170.4	0.337438016	5.78444E-05	0.390742354	1.51768E-06	Potassium transporter
Solyc08g068310.3	0.337363633	5.18475E-05	0.296903326	0.000278469	La protein 1
Solyc04g082070.4	0.337144965	0.005870458	0.516202493	6.1203E-06	Pseudouridine synthase I TruA alpha/beta domain- containing protein
Solyc10g050890.2	0.337084391	4.2279E-06	0.233449682	0.001478561	Ferredoxin--nitrite reductase, chloroplastic
Solyc04g076430.3	0.33698618	0.006801148	0.743036885	5.19818E-11	Geranylgeranyl transferase type-2 subunit alpha
Solyc07g053750.1	0.336710082	0.002680894	0.5995523	1.23535E-08	Zinc finger CCH domain-containing protein 2
Solyc03g007410.4	0.336562861	0.027720865	0.725779994	7.36382E-08	Transcription factor SPEECHLESS
Solyc06g071960.4	0.336537939	8.24988E-05	0.252993841	0.00279179	Nucleoside diphosphate kinase
Solyc03g020020.3	0.33644162	0.006275106	0.510707511	1.0448E-05	Virilizer N-terminal domain-containing protein
Solyc06g007160.4	0.336406851	0.028821487	0.63359265	4.65951E-06	Internal alternative NAD(P)H- ubiquinone oxidoreductase A1, mitochondrial
Solyc11g069460.2	0.336155187	0.001819551	0.252015066	0.016991655	Double-stranded RNA-binding protein 2
Solyc09g008240.3	0.336087089	0.000178714	0.284125108	0.001264538	Putative ABC transporter Tap-like, P-loop containing nucleoside triphosphate hydrolase
Solyc11g065620.2	0.336040362	1.39809E-05	0.359235684	1.94471E-06	assimilatory sulfite reductase (ferredoxin)

Solyc03g114920.1	0.335973338	3.98815E-06	0.2629469	0.000260236	Pentatricopeptide repeat-containing protein PNM1, mitochondrial
Solyc02g085350.4	0.33582401	5.43252E-07	0.237802241	0.000404346	Succinate dehydrogenase [ubiquinone] flavoprotein subunit, mitochondrial
Solyc10g081240.3	0.335808302	3.19365E-05	0.287303475	0.000296122	GrpE protein homolog
Solyc02g037530.3	0.33571243	0.005209166	0.631369599	1.82007E-08	Auxin response factor
Solyc12g015910.1	0.335495908	0.005395341	0.477724508	2.27733E-05	SufE-like protein 1, chloroplastic/mitochondrial
Solyc04g074660.3	0.335428225	0.037545106	0.305979588	0.046115875	Folate-sensitive fragile site protein Fra10Ac1
Solyc11g020040.2	0.335341089	0.009898764	0.485644292	4.95596E-05	Molecular chaperones mortalin/PBP74/GRP75, HSP70 superfamily
Solyc07g032710.4	0.335162504	0.025545236	0.834743709	4.89744E-10	DNA/RNA helicase, ATP-dependent, DEAH-box type, conserved site
Solyc01g107200.4	0.334684924	0.008287106	0.556111239	2.17621E-06	QWRF motif-containing protein 2
Solyc06g066670.4	0.334591262	0.029751949	0.499963749	0.000332526	DNA helicase
Solyc03g112350.4	0.334575794	0.000548252	0.35608683	0.000131279	UvrABC system, subunit B
Solyc04g005310.3	0.334384083	0.000825789	0.201929827	0.042139491	Translin-associated protein X
Solyc03g006300.3	0.334158447	0.008930383	0.317929411	0.008689322	Receptor-like protein kinase HSL1
Solyc01g067630.3	0.333465785	1.17701E-05	0.4416304	1.21064E-09	NAD(P)-binding Rossmann-fold superfamily protein
Solyc10g037950.2	0.333415516	0.00733344	0.421161858	0.000308537	Non-haem dioxygenase N-terminal domain-containing protein
Solyc04g076860.3	0.333327033	0.000832252	0.49118584	1.53508E-07	Auxin-responsive protein IAA9-like isoform X1
Solyc10g006330.3	0.333319625	0.001632403	0.47597512	1.64558E-06	Protein PLASTID MOVEMENT IMPAIRED 1
Solyc03g121120.4	0.333228823	0.02213923	0.355440156	0.00961918	RecA family profile 1 domain-containing protein
Solyc04g078830.3	0.333142439	0.000342703	0.504862222	9.17977E-09	THO complex subunit 5B
Solyc09g009080.4	0.333100358	0.00017215	0.471254166	2.81583E-08	Repressor of silencing 1
Solyc01g096900.3	0.332814051	0.000238499	0.416815621	1.4164E-06	DNA topoisomerase (ATP-hydrolyzing)
Solyc03g005010.4	0.332538446	3.91464E-05	0.418338506	7.60611E-08	RNA methyltransferase pc1998
Solyc01g096390.4	0.332382649	0.000400401	0.522367226	3.94635E-09	DNA-directed RNA polymerase subunit
Solyc06g083760.3	0.332305558	0.001407941	0.53475771	4.62456E-08	Probable inactive histone-lysine N-

Solyc12g098740.2	0.332135417	0.001482405	0.350267441	0.00053195	methyltransferase SUVR2 isoform X1
Solyc08g005300.3	0.332036951	0.00344046	0.546263048	2.13663E-07	Clathrin interactor EPSIN 2
Solyc04g008840.3	0.331922411	0.000729634	0.215502444	0.025918147	Chaperone protein dnaJ 49
Solyc01g094760.3	0.33167245	0.044378401	0.537313681	0.000332819	FRIGIDA-like protein 3
Solyc04g058140.3	0.331532847	0.00038511	0.348437477	0.000102407	Origin of replication complex subunit 5
Solyc04g072780.4	0.331480548	1.09765E-05	0.255209953	0.000637651	GTP-binding protein OBGm, mitochondrial
Solyc01g102800.3	0.331127544	0.00074536	0.385548053	4.01157E-05	FCS-Like Zinc finger 6-like
Solyc11g005140.1	0.33112739	2.57125E-05	0.357662021	2.26236E-06	Histidine--tRNA ligase, cytoplasmic
Solyc02g086940.3	0.331115751	0.000104958	0.448109303	3.71522E-08	Pentatricopeptide repeat-containing protein
Solyc05g005160.3	0.331083493	1.06784E-05	0.186045394	0.014596293	TOG domain- containing protein
Solyc03g113630.3	0.330942619	0.002729856	0.638544458	4.00671E-10	ATP citrate synthase
Solyc05g012100.3	0.33070821	0.00029255	0.56723091	2.55675E-11	Plastid transcriptionally active 2
Solyc09g010840.1	0.330577274	1.45299E-05	0.217820359	0.004351081	Fructokinase-like 2, chloroplastic
Solyc10g085400.3	0.330231516	0.001982951	0.453725435	5.17984E-06	Phantastica
Solyc07g008350.3	0.330072289	6.42916E-05	0.180206903	0.030794557	ATP-grasp fold
Solyc05g005710.4	0.329989127	1.01659E-05	0.2627601	0.000392175	Mitochondrial outer membrane protein porin 6
Solyc07g066470.3	0.329808043	2.10868E-06	0.462531509	5.24382E-12	spermidine synthase
Solyc09g090980.3	0.329553039	8.67452E-06	0.506216977	7.48651E-13	hydroxymethylbilane synthase
Solyc02g090230.4	0.329317458	0.000416042	0.243275484	0.007850136	Pathogenesis-related protein STH-21
Solyc08g008030.3	0.329310399	0.000130968	0.296209818	0.000394721	Nuclear pore complex protein NUP58
Solyc02g093190.3	0.329226689	0.020613838	0.695007714	7.70437E-08	AT-hook motif nuclear-localized protein
Solyc10g086580.2	0.329051268	5.58614E-07	0.355306919	3.65462E-08	Histone-lysine N- methyltransferase CLF
Solyc04g078790.3	0.328952174	0.025469643	0.79499128	1.05514E-09	Ribulose bisphosphate carboxylase/oxygenase activase, chloroplastic
Solyc05g006130.4	0.328946044	0.001062898	0.526469761	1.32049E-08	Transcription factor HEC1
Solyc01g044558.1	0.328932574	0.029499498	0.430104849	0.002022266	DEAD-box ATP- dependent RNA helicase 22
Solyc12g010520.3	0.328590856	0.000142354	0.378197084	5.16704E-06	A-type cyclin
Solyc08g007560.3	0.328298061	0.006643653	0.233231623	0.048620404	Eukaryotic peptide chain release factor subunit 1-3
					AT-hook motif nuclear-localized protein

Solyc01g090880.3	0.328186163	5.84455E-06	0.271340716	0.000144183	YqgF/RNase H-like domain-containing protein
Solyc07g043050.1	0.328058811	7.32218E-05	0.392533292	6.68776E-07	UDP-glucose flavonoid 3-O-glucosyltransferase 6-like
Solyc03g118680.3	0.327935475	0.000167049	0.33622989	5.63939E-05	Zinc finger protein VAR3, chloroplastic
Solyc06g053320.4	0.32792633	0.002219133	0.527002746	1.5087E-07	Flowering time control protein FPA
Solyc04g080980.2	0.327869465	0.001035557	0.469317856	7.97477E-07	Coatomer subunit alpha
Solyc02g067210.3	0.327596052	0.002316884	0.363764613	0.00042703	RNA-binding KH domain-containing protein isoform 1
Solyc10g008110.4	0.327534277	2.7702E-05	0.461451929	8.53511E-10	Acyl-coenzyme A oxidase
Solyc04g007550.4	0.327483207	1.30908E-05	0.26622952	0.000356723	ATP synthase subunit beta
Solyc06g083420.3	0.327333006	0.03230935	0.447170063	0.001790045	Chromatin modification-related protein EAF1 B-like
Solyc07g047610.3	0.326989316	0.015241114	0.482307674	0.000113868	Transcriptional adapter
Solyc12g021340.3	0.326958175	9.09778E-05	0.378702609	2.36304E-06	Rhodanese-like domain-containing protein 11, chloroplastic
Solyc11g069950.2	0.326942916	0.000926975	0.205835321	0.035894312	ATP-dependent zinc metalloprotease FTSH 4, mitochondrial
Solyc01g104570.4	0.326780263	0.002823767	0.469835002	3.96105E-06	Kinetochore protein NDC80
Solyc03g006400.3	0.326200072	0.03997755	0.448570512	0.001841178	Serine/threonine-protein kinase HT1
Solyc03g115420.3	0.325716868	0.040865832	0.337205919	0.024538525	DUF295 domain-containing protein
Solyc02g071210.3	0.325552425	0.000379175	0.518541574	1.26886E-09	Cold-regulated 413 inner membrane protein 1, chloroplastic
Solyc04g064800.4	0.325410713	0.000387578	0.422752402	1.25171E-06	Zinc finger CCCH domain-containing protein 38
Solyc06g008740.3	0.325290161	0.001214603	0.2313266	0.018650045	Zinc finger CCCH domain-containing protein 32
Solyc07g043500.1	0.32495826	0.002190042	0.310946305	0.002430026	Glycosyltransferase
Solyc05g014400.4	0.324816172	0.003391624	0.457833325	9.00469E-06	RecQ-mediated genome instability protein 1
Solyc02g087290.3	0.324721016	3.36377E-05	0.459882088	5.29769E-10	Alpha-mannosidase
Solyc07g055210.3	0.324698834	1.57423E-05	0.294460989	6.79534E-05	Aspartate aminotransferase
Solyc12g008750.3	0.324658371	1.26277E-06	0.240044872	0.000325499	Splicing factor U2af large subunit
Solyc07g053440.4	0.324532548	0.016250881	0.697727216	1.58377E-08	Sodium/calcium exchanger family protein / calcium-binding EF hand family protein isoform 1
Solyc06g008210.4	0.324433083	0.004599626	0.331368789	0.002173826	RING-type E3 ubiquitin transferase BRCA1

Solyc11g069720.2	0.324021741	9.72027E-06	0.30339617	2.4826E-05	Cell division cycle protein 48 homolog
Solyc03g082960.2	0.323154875	9.74039E-05	0.36015789	6.24326E-06	protein-serine/threonine phosphatase
Solyc02g063090.3	0.323146908	6.14077E-06	0.241183647	0.000680845	T-complex protein 1 subunit zeta
Solyc08g076160.3	0.32305125	1.78959E-05	0.363847712	5.81748E-07	Extra-large guanine nucleotide-binding protein 3
Solyc01g110490.4	0.322715855	0.00186603	0.41825532	2.04555E-05	tRNA-dihydrouridine(47) synthase [NAD(P)(+)]
Solyc05g053470.3	0.322649575	0.000146176	0.257316983	0.002167678	GroEL-like equatorial domain superfamily
Solyc08g075840.3	0.322143915	0.007454023	0.538879028	1.55487E-06	Replication protein A subunit
Solyc10g047050.2	0.321982309	0.005640849	0.515602021	2.00271E-06	Dynamin-like protein ARC5
Solyc04g082400.3	0.321801337	0.000780972	0.54737025	1.02375E-09	1,4-alpha-glucan branching enzyme
Solyc09g010560.3	0.32174067	0.001408056	0.288261528	0.003235521	Oxoprolinase 1
Solyc05g054700.3	0.321681494	0.005193066	0.625270609	4.02788E-09	MAPK phosphatase
Solyc09g064800.3	0.32163255	0.010643736	0.630283098	4.62456E-08	Isoamylase 2, chloroplastic
Solyc10g007950.4	0.321364855	0.039833703	0.633774835	9.02884E-06	Trehalose-6-phosphate synthase component TPS1
Solyc03g112150.1	0.321132956	1.04321E-05	0.51211835	1.64429E-13	Elongation factor Tu
Solyc05g013380.3	0.320466661	9.02524E-05	0.257309225	0.00133528	alanine transaminase
Solyc02g024070.3	0.319959521	0.000970697	0.409304333	9.99864E-06	PHAVOLUTA-like HD-ZIPIII protein
Solyc05g044480.3	0.319643936	0.003295529	0.808818206	3.04379E-16	DNA repair protein RAD16
Solyc07g043600.4	0.319400096	0.000717557	0.501279274	1.43482E-08	Pentatricopeptide repeat-containing protein
Solyc08g080510.4	0.319292663	0.015518604	0.326532253	0.009121049	Replication factor C subunit 2
Solyc04g079790.3	0.318900714	1.1283E-05	0.424179112	1.32421E-09	30S ribosomal protein S9, chloroplastic
Solyc03g119930.1	0.318837352	0.007356148	0.232789036	0.045583181	Molybdate transporter 2
Solyc07g049480.3	0.318634305	0.00104992	0.403294159	1.27585E-05	Cleavage and polyadenylation specificity factor subunit 3-I
Solyc03g114960.4	0.318563581	0.003828747	0.456964654	9.69185E-06	Transporter associated with antigen processing protein 2 isoform 1
Solyc10g081470.2	0.318431479	0.001060438	0.337772274	0.000289891	Sterol regulatory element-binding protein site 2
Solyc03g118240.4	0.318038538	1.43594E-05	0.392809949	2.96982E-08	protease
Solyc02g081310.3	0.318028498	0.000188736	0.179756202	0.036079694	Magnesium-protoporphyrin IX methyltransferase C-terminal domain-containing protein 54S ribosomal protein L10, mitochondrial isoform X1

Solyc06g076950.3	0.317872672	0.00882752	0.317953831	0.005801569	Inositol 3-kinase
Solyc01g088020.3	0.31784741	0.008541052	0.403612999	0.00044169	Ancestral coatomer element 1 Sec16/Sec31 domain-containing protein
Solyc01g009340.4	0.317772706	0.027016581	0.302218612	0.026843483	Vacuolar ATPase assembly integral membrane protein VMA21 homolog
Solyc07g066390.1	0.317318371	0.016920928	0.658844546	5.01089E-08	Pentatricopeptide repeat-containing protein
Solyc10g017510.3	0.317233299	2.13663E-05	0.37755106	1.48989E-07	Premnaspirodiene oxygenase
Solyc11g006380.2	0.316628386	0.005871522	0.529421595	6.30536E-07	Pentacotriptide-repeat region of PRORP domain-containing protein
Solyc06g050837.1	0.316055404	0.048293914	0.663493815	3.15926E-06	Armadillo/beta-catenin repeat family protein
Solyc01g100280.4	0.31603726	0.043857618	0.517833932	0.000247404	ATP-dependent DNA helicase
Solyc05g025750.3	0.315754128	0.013294034	0.645694836	3.98482E-08	ATPase, V1 complex, subunit H
Solyc12g044400.3	0.315692335	0.00162884	0.637334214	7.39128E-12	Cell division protease ftsH isogeny 4
Solyc05g007470.4	0.315590924	2.245E-05	0.412967014	7.48619E-09	AAA+ ATPase domain-containing protein
Solyc09g075360.4	0.315536423	0.000115358	0.337546032	2.2643E-05	Endoglucanase
Solyc05g055350.3	0.315418064	0.000415219	0.476881644	1.03245E-08	TRNase Z TRZ2, chloroplastic
Solyc06g034390.1	0.31540307	0.011325525	0.400429693	0.000625968	EXORDIUM like 3
Solyc03g111390.4	0.315315314	0.000187643	0.390425008	1.30555E-06	Kelch domain-containing protein 4
Solyc04g081580.4	0.315174758	6.80033E-05	0.312717298	4.35318E-05	DEAD-box ATP-dependent RNA helicase 28
Solyc02g079415.1	0.315002941	0.000179594	0.386423036	1.54162E-06	25S rRNA (Cytosine-C(5))-methyltransferase nop2
Solyc12g087940.2	0.314690906	3.13387E-06	0.378600886	7.63419E-09	Aspartic proteinase nepenthesin-1
Solyc03g033610.1	0.314640738	0.018910428	0.370314306	0.00290032	Probable LRR receptor-like serine/threonine-protein kinase At4g36180
Solyc04g078600.3	0.314429214	0.000422234	0.224894751	0.010381221	LPS-assembly protein like
Solyc02g086458.1	0.31408601	0.001386553	0.454398656	1.12992E-06	Microtubule-associated protein futsch
Solyc11g006390.2	0.314067045	0.000908244	0.391046739	1.54646E-05	Nuclear pore complex protein NUP1
Solyc07g006030.4	0.313978272	0.039555675	0.710739542	3.20924E-07	Clu domain-containing protein
Solyc06g005800.3	0.313898853	6.72824E-05	0.342669285	6.44672E-06	Serine/threonine-protein phosphatase
Solyc03g121030.2	0.313705531	0.013784576	0.434648727	0.000215537	MMS19 nucleotide excision repair protein

Solyc07g062610.4	0.313388523	3.76658E-05	0.214133227	0.004649234	Putative Class I glutamine amidotransferase-like superfamily protein isoform 1
Solyc06g053920.4	0.313359076	0.004099178	0.335463635	0.001155637	Protein RNA-directed DNA methylation 3
Solyc04g008740.3	0.313329103	1.18788E-05	0.288064781	4.34249E-05	Pyruvate kinase
Solyc02g087400.1	0.313009522	3.86858E-05	0.236845145	0.00165694	Putative signal-recognition-particle GTPase
Solyc02g083810.4	0.312774259	2.86596E-06	0.401557508	5.50369E-10	Ferredoxin--NADP reductase, chloroplastic
Solyc03g119650.3	0.312645623	0.001509971	0.353952397	0.000188397	DENN domain and WD repeat-containing protein SCD1
Solyc07g056410.3	0.312074319	0.00208848	0.335326265	0.000460997	Leucine-rich repeat receptor-like serine/threonine-protein kinase At1g17230
Solyc01g066640.2	0.312008268	0.001241305	0.675184268	5.64042E-14	Sericin
Solyc10g083590.2	0.311989705	0.007843462	0.600713094	2.29799E-08	Polyadenylation and cleavage factor like RNA helicase
Solyc10g009070.3	0.311744697	2.72496E-05	0.294874016	4.78621E-05	Small subunit processome component 20 homolog
Solyc09g092240.3	0.311737823	0.013083003	0.691014142	1.64019E-09	SOSS complex subunit B homolog
Solyc12g014020.2	0.311659777	0.029791722	0.293887255	0.029699216	protein-serine/threonine phosphatase
Solyc12g063050.3	0.311573702	0.000169264	0.390009414	9.63929E-07	glutamate--tRNA ligase
Solyc01g112290.4	0.311554484	6.88015E-06	0.341866297	4.14462E-07	Mg-protoporphyrin IX chelata
Solyc10g008740.3	0.311530263	1.11897E-05	0.319803382	4.04472E-06	Splicing factor 3A subunit 1
Solyc02g081960.3	0.311477993	0.011806616	0.396927579	0.000682912	Translation factor GUF1 organellar chromatophore
Solyc07g053470.4	0.310711785	0.000144406	0.241205747	0.00270944	WD40-repeat-containing domain superfamily
Solyc08g081640.3	0.310696016	0.040552008	0.71185161	1.98057E-07	Probable serine/threonine-protein kinase cdc7
Solyc08g077990.3	0.3106646	0.013499088	0.24035913	0.047850204	Variant 4, udp-glycosyltransferase
Solyc10g005490.4	0.310648796	0.001964572	0.406349964	2.05014E-05	RNA-binding KH domain-containing protein RCF3
Solyc03g082980.3	0.310488842	2.67818E-05	0.354202586	6.82168E-07	NPF family transporter
Solyc05g005940.3	0.310429756	7.85898E-05	0.569788747	1.24944E-14	phosphoglycerate mutase (2,3-diphosphoglycerate-independent)
Solyc07g044840.3	0.310344739	5.43636E-06	0.207879507	0.002420806	COP1-interacting protein 7
Solyc12g049510.3	0.310338763	0.002505142	0.595250531	3.19656E-10	RNA helicase
Solyc09g007440.3	0.310132924	0.003489395	0.239932635	0.020076923	

Solyc01g106260.3	0.309704854	1.22481E-05	0.174420306	0.014735395	Mitochondrial HSO70 2
Solyc09g090520.3	0.309561752	0.002464706	0.255051615	0.010806766	Heterogeneous nuclear ribonucleoprotein 1-like
Solyc02g093370.2	0.309218895	6.60459E-06	0.253216927	0.000191776	Altered inheritance of mitochondria protein 32
Solyc01g096010.4	0.308975727	0.016981547	0.783357457	9.23793E-12	Embryo defective 1703
Solyc04g039620.2	0.308973705	0.03207733	0.480124012	0.000252173	Phosphoribosyl pyrophosphate synthase 3
Solyc07g021550.3	0.308961056	0.025594342	0.480994862	0.000155338	Protein EFFECTOR OF TRANSCRIPTION 2-like
Solyc05g014370.3	0.308892755	0.005460333	0.24451298	0.022989635	Mitotic spindle checkpoint protein MAD2
Solyc02g092480.4	0.308781843	3.47584E-06	0.409442625	1.86988E-10	BTB/POZ domain-containing protein NPY4-like isoform X1
Solyc08g081210.4	0.308662593	0.006629433	0.32553298	0.002563007	Mitogen-activated protein kinase kinase kinase YODA
Solyc04g008760.3	0.308600289	0.017386596	0.388646122	0.001370631	Homoserine kinase
Solyc07g005570.4	0.308535419	0.00029639	0.174165127	0.042884536	APO domain-containing protein
Solyc10g086240.2	0.308422011	0.037929477	0.335622605	0.015336826	Glycosyltransferase
Solyc04g079310.4	0.308247175	5.26415E-06	0.206672383	0.002289221	RNA-binding protein 47C
Solyc05g008270.3	0.308202155	0.022216067	0.302192695	0.018441016	Multicopper oxidase LPR1
Solyc09g014230.2	0.308139765	0.030519872	0.671556355	1.41449E-07	Putative peptide-transporting ATPase
Solyc03g065340.3	0.307756766	1.93876E-05	0.503140014	2.32693E-13	Alpha-1,4 glucan phosphorylase
Solyc04g074640.4	0.307728931	0.000962003	0.429467796	1.15944E-06	Thylakoid lumenal 29 kDa protein, chloroplastic
Solyc02g078580.1	0.307723023	0.001564074	0.203605085	0.034270019	Plus3 domain-containing protein
Solyc09g015670.3	0.307633547	0.000157043	0.450487331	4.63272E-09	Vacuolar-sorting receptor 1
Solyc04g049630.3	0.307303665	0.000177236	0.387889659	6.69951E-07	Acylamino-acid-releasing enzyme, putative
Solyc06g073720.3	0.307258824	0.000354461	0.273236439	0.001139403	Ethylene insensitive 3-like DNA-binding domain-containing protein
Solyc05g053930.4	0.30704124	0.000116642	0.394775268	1.89306E-07	Probable serine/threonine-protein kinase NAK
Solyc10g049710.2	0.306891356	4.57557E-06	0.321541087	8.74116E-07	ATP-dependent Clp protease proteolytic subunit
Solyc06g059960.4	0.306830631	0.002460687	0.437911551	4.35755E-06	Histone-lysine N-methyltransferase ASHH2
Solyc02g081290.4	0.306762656	0.000115923	0.309198773	6.2308E-05	DEAD-box ATP-dependent RNA helicase 21
Solyc08g062910.4	0.306589934	0.031101294	0.499972677	0.00015686	Elongation factor 2

Solyc08g006250.2	0.306374741	0.029483388	0.280572128	0.035371289	Copper transport protein
Solyc06g066570.4	0.306180569	0.001037381	0.296279106	0.000996988	RING-type E3 ubiquitin transferase (cysteine targeting)
Solyc05g056210.4	0.306089036	0.001229527	0.521786254	4.11675E-09	Methyltransferase-like protein 1
Solyc12g099260.2	0.305574602	2.22941E-05	0.154648916	0.0355891	ATP citrate synthase
Solyc02g085520.4	0.305407389	0.000387578	0.301386276	0.000293223	Adenylosuccinate synthetase, chloroplastic
Solyc05g012700.3	0.305084549	7.11886E-05	0.417451671	8.6242E-09	Glycine-tRNA ligase
Solyc09g010460.3	0.304817341	4.30893E-05	0.336483444	3.43274E-06	Eukaryotic translation initiation factor 3 subunit A
Solyc05g012620.4	0.304262354	0.000100454	0.347720083	3.55245E-06	Clp protease adapter protein ClpF, chloroplastic
Solyc04g009350.3	0.304003083	0.000755482	0.301559897	0.000520458	Imidazole acetol-phosphate transaminase
Solyc03g019800.4	0.303871923	0.012819626	0.44021085	0.000103887	RNA polymerase I termination factor
Solyc04g016510.3	0.303250516	0.000159603	0.432885136	1.35945E-08	U4/U6 small nuclear ribonucleoprotein
Solyc03g112070.4	0.3032095	0.000179009	0.19536461	0.015768234	PRP4-like protein
Solyc02g067320.3	0.303175892	0.001262007	0.467007969	1.17205E-07	D-3-phosphoglycerate dehydrogenase
Solyc09g009270.2	0.303013025	0.047441954	0.291901448	0.043359374	Zinc-finger homeodomain protein 9
Solyc01g080280.3	0.302712393	4.17081E-06	0.283374051	1.23734E-05	Tumor susceptibility gene 101 family protein
Solyc11g062070.3	0.302647523	0.001702501	0.481621423	8.59357E-08	Glutamine synthetase
Solyc03g093480.3	0.302042212	0.007706057	0.627768124	2.05523E-09	Outer envelope protein 80, chloroplastic
Solyc10g005110.3	0.301661509	3.38547E-05	0.329021595	3.22243E-06	BP28 C-terminal domain-containing protein
Solyc10g044670.3	0.301420866	0.00095924	0.473066616	4.74237E-08	coproporphyrinogen oxidase
Solyc12g095900.2	0.300949695	4.88267E-05	0.234300063	0.001270833	Phytochrome
Solyc07g042150.3	0.300931989	0.002607789	0.225016159	0.021038164	Protein EARLY FLOWERING 3
Solyc01g103010.4	0.300815187	0.013334501	0.478231563	2.55538E-05	Ubiquinone biosynthesis protein
Solyc06g065690.3	0.300294444	0.005898028	0.541694862	8.64315E-08	Cullin-associated NEDD8-dissociated protein 1 isoform A
Solyc08g016170.3	0.300253433	5.98853E-05	0.372692068	2.11875E-07	Serine/threonine protein phosphatase 2A regulatory subunit
Solyc09g007850.3	0.300016032	1.86268E-05	0.238252079	0.000617108	50 kDa ketoacyl-ACP synthase
Solyc06g060360.3	0.300012006	0.009280274	0.33324162	0.002215853	29 kDa ribonucleoprotein A, chloroplastic
Solyc02g086660.4	0.299395496	0.001333351	0.205740044	0.025685461	UspA domain-containing protein
					ATP-dependent RNA helicase-like protein DB10

Solyc02g089260.4	0.299372058	0.043857618	0.570178862	2.92574E-05	Auxin transport protein BIG
Solyc04g071940.3	0.299259848	0.000149507	0.183013851	0.020258641	Xanthoxin dehydrogenase
Solyc10g009490.2	0.299200577	0.001608517	0.396366177	1.06318E-05	Poly(A) RNA polymerase
Solyc03g119960.3	0.299065767	0.003986862	0.339106769	0.000547067	Root phototropism protein 3
Solyc05g005950.3	0.298827758	0.01622746	0.651475999	6.63677E-09	NPF family transporter
Solyc03g031820.4	0.298663265	0.001539134	0.298731367	0.000902283	Tyrosyl-DNA phosphodiesterase 1
Solyc01g106450.3	0.298645438	0.000499682	0.215284052	0.010681008	L-galactose dehydrogenase
Solyc10g083650.1	0.298608319	0.000171332	0.340860154	8.88693E-06	Glutaredoxin-dependent peroxiredoxin
Solyc12g009640.1	0.298538487	0.009842966	0.448474759	3.49268E-05	Zinc finger BED domain-containing protein
Solyc07g005510.3	0.298388722	6.21877E-05	0.478654647	1.28569E-11	DAYSLEEPER-like Plastidial delta-12 oleate desaturase
Solyc10g075160.1	0.298289545	3.9153E-05	0.495162591	5.12287E-13	Ferredoxin
Solyc02g036360.1	0.298239999	0.004866405	0.421421225	1.93955E-05	PB1 domain-containing protein
Solyc08g069010.4	0.297720596	0.013334501	0.383210186	0.000684671	Pentatricopeptide repeat-containing protein
Solyc01g006700.3	0.297428617	0.001095732	0.323858767	0.000190587	Donson
Solyc10g079930.1	0.297174477	0.000350441	0.350519713	9.29644E-06	Zeatin O-glucosyltransferase
Solyc06g017970.4	0.297064803	0.006437901	0.623020674	5.63663E-10	MATH domain-containing protein
Solyc03g113610.4	0.297040621	0.013559809	0.324368263	0.004054153	Polyribonucleotide 5'-hydroxyl-kinase
Solyc10g081460.2	0.296735193	0.000230075	0.50588898	3.66226E-11	Clp1 P-loop domain-containing protein
Solyc06g035450.4	0.296613532	7.57487E-05	0.428251692	2.59188E-09	Cationic amino acid transporter C-terminal domain-containing protein
Solyc04g051780.3	0.296083082	0.001403197	0.305335462	0.000577667	RNA helicase
Solyc06g051570.4	0.29608109	0.014108083	0.394729903	0.000468367	Probable 20S rRNA accumulation protein 4
Solyc09g063090.4	0.296044212	0.002471464	0.465507004	3.88243E-07	NF-X1-type zinc finger protein
Solyc01g100530.3	0.295836774	0.001970411	0.508081168	1.41164E-08	NFXL2
Solyc12g007310.3	0.295790053	5.26506E-05	0.485310486	2.07556E-12	Methyl-coenzyme M reductase II subunit gamma, putative
Solyc11g044250.3	0.29577021	0.00108411	0.442737823	1.3397E-07	Putative transmembrane protein cmp44E
Solyc06g005990.4	0.295582942	0.017458442	0.515648762	6.64121E-06	Lactoylglutathione lyase
Solyc09g011030.3	0.295540181	0.000493406	0.20097037	0.016679213	K(+) efflux antiporter 3, chloroplastic
Solyc01g106210.3	0.295176282	3.54803E-05	0.175515005	0.014682122	DExH-box ATP-dependent RNA helicase DExH11
					TOG domain-containing protein
					Mitochondrial HSO70 2

Solyc10g086760.2	0.295146019	0.000193137	0.176220227	0.026820224	Tubulin beta chain
Solyc06g071030.3	0.29514053	0.028687477	0.418717905	0.000708666	isochorismate synthase
Solyc10g086150.2	0.295083946	9.53659E-06	0.523098551	1.46404E-16	29 kDa ribonucleoprotein A, chloroplastic
Solyc08g006150.3	0.29451106	0.001759964	0.229727917	0.01305663	Gamma-glutamylcyclotransferase
Solyc11g039830.2	0.294402796	5.21902E-05	0.256623249	0.000322964	glycine--tRNA ligase
Solyc07g043170.4	0.294308028	0.000782526	0.516239311	1.69535E-10	Glycosyltransferase
Solyc03g119300.4	0.294191945	0.016691726	0.528147615	2.05738E-06	Zinc finger protein BRUTUS
Solyc09g092680.4	0.294084755	0.000620121	0.421443049	1.97585E-07	Protein transport protein SEC23
Solyc02g069620.4	0.29401516	0.003241835	0.474300648	3.51349E-07	ribose-5-phosphate isomerase
Solyc04g054140.4	0.293842142	0.013233981	0.561766226	2.81027E-07	E3 ubiquitin-protein ligase RKP
Solyc05g054240.3	0.293241485	0.006656209	0.310481188	0.002553832	Methyltransferase domain-containing protein
Solyc09g073000.3	0.293079826	5.18878E-05	0.252416058	0.000387846	Elongation factor Tu
Solyc05g015980.3	0.293074009	0.000205531	0.367932334	1.21505E-06	Gap junction beta-4 protein
Solyc02g061760.4	0.29305313	0.029377734	0.527905764	1.71727E-05	Protein DETOXIFICATION
Solyc06g060260.3	0.292893727	0.000149993	0.267359868	0.000386406	N-L-ascorbate peroxidase
Solyc08g081260.1	0.29266784	0.028442048	0.407739656	0.000866339	TIR domain-containing protein
Solyc06g052070.3	0.292284252	0.000139064	0.499598847	3.41407E-12	WD repeat-containing protein 44
Solyc08g082670.4	0.292178749	0.014691	0.988319177	1.7921E-20	Cellulose synthase-like protein G3
Solyc05g005640.4	0.291782215	0.008659054	0.535717148	1.84379E-07	Methyl-CpG-binding domain-containing protein 9
Solyc07g064970.4	0.291454788	2.83449E-05	0.336070558	6.23053E-07	Putative microtubule-associated protein 1-like
Solyc01g103750.4	0.29133906	1.35531E-05	0.237170644	0.000342705	ATP phosphoribosyltransferase
Solyc02g078260.3	0.291237586	0.035955826	0.605695019	1.92265E-06	DNA-directed RNA polymerase subunit beta
Solyc08g080670.1	0.291142019	0.000179524	0.182501183	0.019166924	Osmotin-like protein OSM15
Solyc09g074650.3	0.29113316	0.002585017	0.448128143	6.84563E-07	Prokaryotic-type class I peptide chain release factors domain-containing protein
Solyc01g103450.3	0.291099541	4.30107E-05	0.381858026	2.74128E-08	Molecular chaperones mortalin/PBP74/GRP75, HSP70 superfamily
Solyc12g042600.2	0.291024875	0.048569251	0.581650932	1.27585E-05	UDP-glycosyltransferase 73C2
Solyc05g005800.4	0.290988306	0.001140748	0.391875244	3.96585E-06	threonine--tRNA ligase

Solyc01g109830.3	0.290794207	0.001023751	0.407321351	1.00415E-06	Bifunctional dihydrofolate reductase-thymidylate synthase
Solyc03g116380.4	0.290674516	0.000778569	0.270731255	0.001186508	Small-subunit processome Utp12 domain-containing protein
Solyc05g056010.3	0.290370721	0.001415086	0.297323764	0.000632872	Aminotransferase-like plant mobile domain-containing protein
Solyc09g009020.3	0.290198834	3.58494E-05	0.162561925	0.022412903	phosphopyruvate hydratase
Solyc03g058190.3	0.290186229	0.009537185	0.543794428	1.56069E-07	Elongation factor TypA-like SVR3, chloroplastic
Solyc05g008350.3	0.290007264	0.000112717	0.525736835	9.05759E-14	Transporter, ABC superfamily (Breast cancer resistance protein)
Solyc02g080340.3	0.289990217	0.016752324	0.518167998	3.2467E-06	Patatin
Solyc01g097160.3	0.289959503	0.003462929	0.480543913	2.16061E-07	Renalase
Solyc08g081760.3	0.28995556	0.001962781	0.20624611	0.026046167	WRKY transcription factor 19
Solyc08g078430.4	0.289782483	0.000762649	0.247170743	0.003224823	U4/U6 small nuclear ribonucleoprotein Prp31 homolog
Solyc02g087800.3	0.289585556	0.040084581	0.374811738	0.004155271	Aldose 1-epimerase
Solyc04g074090.4	0.289559759	0.008878642	0.482153312	2.48754E-06	Nucleolar complex protein 3 homolog
Solyc09g083080.4	0.289461022	5.00674E-05	0.237756857	0.000736836	MAR-binding protein
Solyc05g006070.4	0.28925416	0.005004459	0.556954865	3.01945E-09	Putative RNA-binding motif, single-stranded-interacting protein 1
Solyc02g020980.4	0.289126017	0.000219166	0.342689695	5.40481E-06	4-alpha-glucanotransferase
Solyc05g047520.4	0.288987481	0.000662694	0.453062777	1.39561E-08	RNA helicase, ATP-dependent, SK12/DOB1 protein isoform 1
Solyc07g032100.3	0.288937137	0.002049841	0.369023408	3.6246E-05	Coatomer subunit alpha
Solyc03g007330.3	0.288553629	0.000525055	0.370742948	2.74783E-06	ATP-dependent zinc metalloprotease FTSH 11, chloroplastic/mitochondrial
Solyc10g005260.3	0.288517217	0.000185204	0.178987513	0.020901457	Polyadenylate-binding protein RBP45-like isoform X1
Solyc02g065300.1	0.288305157	0.002434194	0.44817708	6.00574E-07	leucine--tRNA ligase
Solyc04g009950.3	0.288026734	0.000622411	0.379505643	2.33146E-06	Cell division cycle 5-like protein
Solyc07g014640.3	0.287966292	0.009606114	0.297955158	0.004358567	Galacturonokinase
Solyc10g085630.3	0.287951809	0.001488654	0.295864396	0.000623708	3-hydroxyisobutyryl-CoA hydrolase
Solyc11g012670.1	0.28769263	0.001771627	0.529097234	6.19755E-10	Chloroplastic RNA-binding protein P67
Solyc01g097810.3	0.287571104	0.002012136	0.480815818	3.46313E-08	Zeta-carotene desaturase
Solyc03g114310.3	0.287360685	0.000192443	0.283240967	0.000144249	Serine/threonine-protein kinase HT1

Solyc03g031970.4	0.287312129	0.000156246	0.328224135	7.64875E-06	Auxin response factor
Solyc12g017260.2	0.287304465	0.00841308	0.379824715	0.000221456	mRNA decay factor PAT1 domain-containing protein
Solyc01g088370.3	0.287258434	9.96957E-06	0.29841969	2.69571E-06	Eukaryotic translation initiation factor 3 subunit B
Solyc03g063060.3	0.287036691	0.00393349	0.429831583	3.13738E-06	DUF565 domain-containing protein
Solyc07g025170.3	0.286577957	0.003503519	0.493078716	5.30327E-08	Exocyst complex component Sec3 PIP2-binding N-terminal domain-containing protein
Solyc07g052900.1	0.28653298	0.010199057	0.29593915	0.005187691	Storekeeper protein
Solyc02g080990.2	0.286246387	0.001090593	0.492020908	1.72106E-09	leucine--tRNA ligase
Solyc10g084770.3	0.286000132	0.001147313	0.336569027	5.85886E-05	Probable serine/threonine-protein kinase NAK
Solyc01g100500.3	0.285983226	9.62601E-05	0.213086876	0.003187256	Putative microfilament-associated protein 1-like
Solyc09g098260.3	0.285969903	0.026625087	0.599996883	2.83743E-07	Histone-lysine N-methyltransferase ATX2-like isoform X1
Solyc01g094190.3	0.2857311	0.01225034	0.360748368	0.000622157	RmlD-like substrate binding domain-containing protein
Solyc08g076910.3	0.285697681	0.041185949	0.408813902	0.001503755	Ubiquitin carboxyl-terminal hydrolase
Solyc02g082840.3	0.2851885	0.000120265	0.358949868	4.46706E-07	GRIP domain-containing protein
Solyc01g010460.4	0.285147384	0.048347672	0.77483691	1.03962E-09	Isoamylase N-terminal domain containing protein
Solyc03g026350.3	0.285002595	0.0005494	0.443790906	8.33729E-09	Zinc finger CCCH domain-containing protein 48
Solyc06g083770.4	0.284986268	0.040645574	0.294478626	0.023637675	GST C-terminal domain-containing protein
Solyc03g083090.4	0.284978799	0.002882361	0.408998974	4.92621E-06	Starch synthase, chloroplastic/amyloplastic
Solyc01g081010.4	0.284764496	1.15114E-05	0.277630454	1.33762E-05	Nucleolar GTP-binding protein 1
Solyc08g068340.3	0.284736256	0.000267331	0.264318537	0.000527028	Eukaryotic translation initiation factor 3 subunit L
Solyc05g054630.4	0.284681705	0.00923653	0.582333513	6.11942E-09	Elongator complex protein 1
Solyc10g006230.3	0.28466664	0.000667224	0.236878565	0.003944685	Chlorophyll a-b binding protein, chloroplastic
Solyc01g079450.3	0.284525784	0.007352863	0.383053095	0.000138779	Probable glutamyl endopeptidase, chloroplastic isoform X1
Solyc12g049410.3	0.284242074	0.008089121	0.506444385	3.4165E-07	Nuclear pore complex protein
Solyc09g092720.3	0.284203269	0.009789688	0.233534914	0.029612004	Glycine-rich protein 3 short isoform-like isoform X2
Solyc11g072430.3	0.284163207	0.001657049	0.47298395	2.08255E-08	tRNA ligase phosphodiesterase

Solyc08g007360.3	0.28414296	0.034369395	0.44275796	0.000387827	domain-containing protein
Solyc08g042130.2	0.283875346	0.029239668	0.303984748	0.013172347	Protein transport protein sec16
Solyc11g005950.2	0.283846631	0.003269127	0.211564157	0.024416794	PX domain-containing protein
Solyc09g010930.4	0.283739518	0.000295191	0.351406002	2.83412E-06	BTB/POZ domain-containing protein
Solyc08g048500.3	0.283726911	0.000243993	0.28249943	0.00015679	At2g13690
Solyc01g096870.4	0.28365045	0.000819776	0.407505355	3.90121E-07	Sanguinarine reductase
Solyc01g059880.3	0.283563032	0.000493901	0.220246136	0.005919814	KH domain-containing protein
Solyc02g093040.4	0.283170776	0.04008717	0.580316954	2.66623E-06	proline--tRNA ligase
Solyc03g119450.3	0.283154999	0.021036743	0.691196504	6.10028E-10	ATP citrate synthase
Solyc07g064310.2	0.283091107	0.023524628	0.303760132	0.009863036	Cysteine proteinase
Solyc06g084210.3	0.283063942	0.03674362	0.445377126	0.000404831	CRM-domain containing factor
Solyc01g108150.3	0.283020485	6.41859E-05	0.211818741	0.002563007	CFM3, chloroplastic/mitochondrial
Solyc09g082830.4	0.282991626	0.000215178	0.23037849	0.002163675	Protein phosphatase
Solyc08g041870.3	0.282854816	3.222E-05	0.225783691	0.000811532	Transport protein
Solyc03g112820.4	0.282790941	0.011248474	0.425030754	3.61252E-05	Sec24-like
Solyc05g040050.3	0.282698871	0.007081567	0.412706237	2.41113E-05	Probable quinone oxidoreductase
Solyc03g031720.3	0.282604633	0.000997001	0.244946399	0.003494976	Argonaute 10
Solyc01g090940.3	0.282555554	0.000363537	0.23546773	0.002235304	Aspartate aminotransferase
Solyc03g044190.3	0.282390668	0.001333783	0.192756151	0.025835249	U3 small nucleolar ribonucleoprotein
Solyc04g015580.3	0.282032341	0.013130321	0.452921972	1.51979E-05	protein MPP10
Solyc02g082870.4	0.281905558	0.019685026	0.271928882	0.017539755	J domain-containing protein
Solyc07g065310.3	0.281857656	0.000392904	0.273725636	0.000345839	Polyadenylate-binding protein
Solyc01g106430.3	0.281826985	5.89743E-05	0.226371501	0.001074717	RBP45-like isoform X1
Solyc12g013990.3	0.281748828	0.001186321	0.202245696	0.017442822	Phosphatidate cytidyltransferase
Solyc02g066950.4	0.281693439	0.000538866	0.415505504	5.78353E-08	Oxidoreductase
Solyc03g083310.4	0.280779823	0.013022942	0.232768205	0.032261522	TDA3
Solyc11g020780.2	0.280439433	0.000465139	0.356399756	3.00596E-06	Putative transmembrane protein
Solyc10g044840.2	0.280070943	0.006885767	0.288738425	0.003266924	cmp44E
Solyc11g072390.2	0.279916278	0.002341573	0.347192423	6.40269E-05	Acyl-activating enzyme 2
					DUF21 domain-containing protein,
					chloroplastic
					inorganic
					diphosphatase
					50S ribosomal
					protein L1
					alpha-amylase
					Zinc finger
					transcription factor
					YY1
					DCK/dGK-like
					deoxyribonucleoside
					kinase
					RNA-binding
					protein containing a
					PIN domain
					Something about
					silencing protein 10

Solyc02g082830.3	0.279625932	0.004300025	0.247845154	0.009084637	Phosphoserine aminotransferase
Solyc01g102410.3	0.279175207	0.002603505	0.424179042	1.20777E-06	glutamate--tRNA ligase
Solyc05g008630.4	0.279087208	0.000331652	0.359343359	1.21703E-06	polynucleotide adenyltransferase
Solyc11g028100.2	0.278970115	1.1737E-05	0.185630106	0.003655225	Elongation factor 1- gamma
Solyc01g111740.3	0.27851078	0.024458279	0.423355962	0.000173816	Nitrate regulatory gene2 protein-like
Solyc07g062730.1	0.278459574	0.00300335	0.299234135	0.000843354	Calmodulin-binding domain-containing protein
Solyc05g053240.4	0.278408213	0.02140587	0.689376103	3.04978E-10	Squamosa promoter- binding-like protein 1
Solyc08g067790.4	0.278068196	0.009039574	0.320519521	0.00158298	TFIIS central domain-containing protein
Solyc01g111120.4	0.278045481	3.59439E-05	0.170873793	0.011526689	Triosephosphate isomerase
Solyc08g066790.4	0.278028943	0.009526535	0.538070212	3.58086E-08	Phospholipase D
Solyc01g099230.3	0.277820144	0.033138195	0.356922592	0.003149199	RanBP2-type domain-containing protein
Solyc09g082800.3	0.277612156	0.003359871	0.453157305	2.7582E-07	Ras guanine nucleotide exchange factor L
Solyc10g079470.3	0.277549421	0.001443935	0.175203107	0.04370426	L-galactono-1,4- lactone dehydrogenase
Solyc01g097130.4	0.277248037	0.010444161	0.443153009	7.69222E-06	Pentatricopeptide repeat-containing protein
Solyc01g102540.3	0.27686049	0.002063133	0.420891586	5.12917E-07	Nuclear pore complex protein NUP160 domain- containing protein
Solyc07g039200.4	0.276821228	0.000861915	0.236376117	0.003505848	Glutamate-rich WD repeat-containing protein 1
Solyc03g097870.4	0.276805566	0.031220821	0.715954742	7.80585E-10	Bidirectional sugar transporter SWEET
Solyc01g057780.3	0.27646203	0.004090517	0.29152057	0.001461224	Zinc finger protein VAR3, chloroplastic
Solyc12g017510.2	0.276404433	0.000676805	0.514592155	6.52763E-12	RAP domain- containing protein
Solyc01g097030.3	0.276326146	0.017741714	0.310149894	0.004634598	Mutator transposase
Solyc06g066300.1	0.276184822	0.037202107	0.404198929	0.000936012	2-(3-amino-3- carboxypropyl)histidi ne synthase subunit 1
Solyc04g016360.3	0.276134074	0.000305342	0.24458252	0.00105639	S-formylglutathione hydrolase
Solyc05g005920.4	0.275752733	0.001900427	0.664990399	3.07864E-16	LATD/NIP
Solyc06g072660.4	0.275702251	0.014539258	0.421780833	5.848E-05	DEK C-terminal domain-containing protein
Solyc01g091500.3	0.27568192	0.040379563	0.398003396	0.001335965	Nucleoprotein TPR isoform X4
Solyc03g046450.3	0.275265757	0.043912259	0.43503613	0.000582734	Cell polarity protein mor2
Solyc01g105420.4	0.274918589	0.002319066	0.200032984	0.024079723	Phospho-2-dehydro- 3-deoxyheptonate aldolase
Solyc12g009310.2	0.274887763	0.044703168	0.328203574	0.009880748	Probable serine/threonine-

Solyc06g063230.3	0.27436999	0.004087035	0.258348023	0.005052683	protein kinase PBL17
Solyc05g018240.4	0.27429109	0.001993933	0.311835438	0.000203156	WD repeat-containing protein 49
Solyc01g097520.4	0.274128319	1.78448E-05	0.256972212	4.24408E-05	CRS2-associated factor 1, chloroplastic
Solyc05g017990.4	0.273778861	0.005169232	0.55376991	9.19803E-10	Annexin
Solyc02g091900.4	0.273649315	0.001745378	0.335158996	5.66887E-05	rRNA methyltransferase 1, mitochondrial
Solyc06g074180.3	0.273615963	0.003885423	0.197634237	0.033690266	cysteine desulfurase
Solyc03g095250.3	0.273546011	0.00988783	0.430543051	1.27772E-05	Cytochrome P450, family 87, subfamily A, polypeptide 6
Solyc09g065160.4	0.273492528	0.002467411	0.489119347	6.86758E-09	Serine/arginine repetitive matrix protein 2-like
Solyc09g031970.3	0.273351277	0.000180522	0.349547406	5.92245E-07	Probable transmembrane GTPase FZO-like, chloroplastic isoform X1
Solyc01g005250.4	0.273185823	9.08156E-05	0.223936414	0.001039963	Alpha-1,4 glucan phosphorylase
Solyc03g013630.4	0.273126389	0.011284309	0.483629482	8.72686E-07	aspartate-semialdehyde dehydrogenase
Solyc11g069610.3	0.272888665	0.019396725	0.292510133	0.007929225	Hexosyltransferase
Solyc08g061610.4	0.272643135	0.027164225	0.537692887	2.00543E-06	Helicase protein MOM1
Solyc06g084470.4	0.272440028	0.025745236	0.294728664	0.009889047	Copper-transporting ATPase paa2
Solyc08g079100.3	0.272244667	0.006759275	0.291428941	0.002162817	Auxin response factor
Solyc02g077280.4	0.272153131	0.01055172	0.442372029	7.07541E-06	Axial regulator YABBY 1
Solyc04g080600.3	0.272040635	0.0146533	0.588513097	7.60816E-09	Era-type G domain-containing protein
Solyc02g070790.3	0.271947142	0.000842632	0.271604352	0.000526261	Auxilin-like protein 1
Solyc08g005170.3	0.271662186	0.003078906	0.181554702	0.044823899	50 kDa ketoacyl-ACP synthase
Solyc06g008310.3	0.271564632	0.007364338	0.266045046	0.005838762	Heat shock factor protein HSF8
Solyc03g044330.1	0.271507533	0.00034925	0.284043316	0.000117814	Elongator complex protein 2
Solyc12g042990.3	0.271391473	0.007312577	0.364964799	0.000127365	Acetolactate synthase
Solyc02g014770.3	0.271374588	0.018160638	0.425447961	5.42122E-05	Btz domain-containing protein
Solyc05g053300.3	0.271287012	0.000634875	0.165260017	0.037805381	Protein CHROMATIN REMODELING 19
Solyc05g056290.4	0.27115522	0.002459348	0.245270401	0.004690796	Dihydrolipoyl dehydrogenase
Solyc03g095860.3	0.27083492	0.023120054	0.354287961	0.001418237	Biotin carboxyl carrier protein of acetyl-CoA carboxylase
Solyc03g031940.4	0.27073356	0.014639438	0.786330188	4.76E-15	MSP domain-containing protein
					Acyl-activating enzyme 5, peroxisomal

Solyc09g056160.4	0.27073217	0.000357532	0.286874824	7.98654E-05	Protein PEP-RELATED DEVELOPMENT ARRESTED 1, chloroplastic
Solyc08g077880.3	0.270723288	0.000106164	0.295262793	1.26687E-05	Light-harvesting complex-like protein 3 isotype 1, chloroplastic
Solyc09g059310.3	0.27070183	0.000214145	0.296640757	2.49206E-05	Putative ras GTPase-activating protein-binding protein 1-like
Solyc03g093260.3	0.270154318	0.003453659	0.466212341	3.9833E-08	SMC hinge domain-containing protein
Solyc02g069630.3	0.270061435	0.010595862	0.217790802	0.033444372	Subtilisin-like protease SBT2,2
Solyc07g064330.3	0.269839053	0.002316884	0.523009907	1.86431E-10	DNA-directed DNA polymerase family A palm domain-containing protein
Solyc05g009920.4	0.26962834	0.027393622	0.35930993	0.001376681	Arsenical pump ATPase
Solyc09g091690.1	0.269488158	0.041025061	0.674035211	6.27735E-09	F-box/kelch-repeat protein at3g23880
Solyc03g122040.4	0.269224987	0.002600415	0.511932016	7.63275E-10	COP1-interacting protein 7
Solyc01g098200.3	0.269163881	0.001735294	0.39734492	7.5054E-07	Vesicle-associated protein 1-2 isoform X1
Solyc12g095850.2	0.269132306	0.011115642	0.39784523	5.19921E-05	tryptophan--tRNA ligase
Solyc09g082560.4	0.268621929	0.000974136	0.254742341	0.001275999	IQ-DOMAIN 14
Solyc08g067090.4	0.268386562	0.000477855	0.199753615	0.008514588	Multidomain cyclophilin type peptidyl-prolyl cis-trans isomerase
Solyc07g008180.4	0.268167801	0.01336737	0.531567334	5.88283E-08	Axial regulator YABBY 5-like
Solyc01g073670.3	0.267924136	0.022036656	0.636082686	1.4698E-09	Major facilitator superfamily (MFS) profile domain-containing protein
Solyc11g006340.2	0.267767316	0.019885146	0.262473245	0.016277347	phosphoribosylamin oimidazole carboxylase
Solyc10g045310.2	0.267296533	0.006680113	0.228137525	0.016153469	Oxidoreductase/ transition metal ion binding protein
Solyc07g005810.3	0.267268602	0.00027424	0.212219904	0.003427313	Eukaryotic translation initiation factor
Solyc09g013080.3	0.267240886	0.000526453	0.44130309	1.3685E-09	acetyl-CoA carboxyltransferase
Solyc11g066110.2	0.26693929	7.89249E-05	0.279196474	2.19154E-05	Inner membrane protein PPF-1, chloroplastic
Solyc10g009570.3	0.266683343	0.001415086	0.254480406	0.001595341	Rhodanese-like domain-containing protein 4, chloroplastic
Solyc09g074420.4	0.266591758	0.000958924	0.414615978	4.70008E-08	Protease Do-like 2, chloroplastic
Solyc02g078610.4	0.265785358	0.000368739	0.225847768	0.001966945	Proline-rich spliceosome-associated family protein isoform 2

Solyc10g080350.3	0.265757436	0.00266906	0.337159417	5.54292E-05	DNA-directed RNA polymerase subunit
Solyc03g083440.4	0.265753601	0.005245643	0.35829117	7.39078E-05	glutamate synthase (NADH)
Solyc07g064950.3	0.265687992	0.002807842	0.535478718	7.51223E-11	peptidylprolyl isomerase
Solyc12g096190.2	0.265676783	0.003049601	0.315158122	0.000217514	tryptophan synthase
Solyc11g044310.2	0.265499652	0.001904279	0.235527378	0.004394284	Proline iminopeptidase
Solyc03g007100.3	0.265476114	0.011056385	0.554320407	7.28527E-09	Cleavage and polyadenylation specificity factor subunit 1
Solyc04g055120.3	0.265406033	0.031836441	0.562359378	6.52969E-07	Long-chain acyl-CoA transporter, ABC superfamily
Solyc11g071340.3	0.265211516	0.006767692	0.226626768	0.016354799	Protein kinase domain-containing protein
Solyc01g068100.4	0.265091772	0.013355641	0.372702725	0.000220939	Squamosa promoter-binding-like protein 1
Solyc08g081890.4	0.265061785	0.016490113	0.749877185	2.05756E-14	ABC-type xenobiotic transporter
Solyc05g009780.3	0.26483235	0.000954351	0.246184837	0.001566765	Methionine aminopeptidase
Solyc02g087640.3	0.264828726	0.041891993	0.302838998	0.012615775	Protein arginine methyltransferase
Solyc06g082370.4	0.264408689	0.023330897	0.278773547	0.011862044	NDUFAF7
Solyc08g067250.4	0.264302126	0.026859712	0.400363892	0.000238162	28S ribosomal protein S29, mitochondrial
Solyc01g100520.3	0.26390454	0.000668006	0.22228503	0.003419475	DNA cross-link repair protein SNM1
Solyc04g080340.3	0.26389239	0.000398682	0.390847815	2.88169E-08	ATP-dependent Clp protease proteolytic subunit
Solyc08g005190.4	0.263875119	0.00415634	0.474006366	3.07514E-08	tRNA 4-demethylwyosine synthase (AdoMet-dependent)
Solyc10g080180.3	0.263827366	0.016669681	0.384202549	0.000174588	Pre-mRNA-splicing factor CWC22 homolog
Solyc07g005580.4	0.263547212	0.029005677	0.439298544	6.65629E-05	U3 small nucleolar RNA-associated protein 18 homolog
Solyc05g026540.3	0.263105748	0.001897209	0.377720459	2.45639E-06	1-acyl-sn-glycerol-3-phosphate acyltransferase
Solyc12g019860.2	0.26310187	0.006651579	0.266676943	0.004156839	Transmembrane protein 214-A
Solyc01g088700.4	0.263066484	0.009749521	0.409669224	1.7935E-05	CCR4-NOT transcription complex subunit 3
Solyc01g008960.3	0.26298858	0.001871078	0.370162279	4.16144E-06	Eukaryotic translation initiation factor 4G
Solyc01g008170.3	0.262735615	0.004412986	0.251842879	0.004535893	Argonaute 4
Solyc08g061500.3	0.262545264	0.016362906	0.370654791	0.000276742	Zinc finger CCH domain-containing protein 17
Solyc06g053300.3	0.262513931	0.042065682	0.312018473	0.00941394	Myosin-15
					Polyadenylate-binding protein-interacting protein 11 isoform X1

Solyc01g096700.4	0.262483709	8.98762E-05	0.207662977	0.00173834	DnaJ homolog subfamily C member 2-like
Solyc02g090950.1	0.262421764	0.017495413	0.490660882	1.2277E-06	Transcription factor HEC2
Solyc01g105560.3	0.26233678	0.000151673	0.232809037	0.000597621	GTP cyclohydrolase II
Solyc09g011720.3	0.26233156	0.0031985	0.405177172	1.22361E-06	Tubby C-terminal domain-containing protein
Solyc03g058920.3	0.262039289	0.000122673	0.148606422	0.030773544	Mitochondrial outer membrane protein porin of 34 kDa
Solyc10g084690.2	0.261996257	0.018389998	0.331956951	0.001357741	Probable ADP-ribosylation factor GTPase-activating protein AGD6
Solyc03g098440.4	0.261858652	0.003259384	0.351282337	2.43895E-05	Hsp70-Hsp90 organizing protein 1
Solyc02g078830.4	0.261858221	0.005655231	0.211396534	0.021217735	P21-activated protein kinase-interacting protein 1-like
Solyc02g021760.3	0.261786758	0.016057707	0.270359174	0.008704472	30-kDa cleavage and polyadenylation specificity factor 30
Solyc03g052980.3	0.261759703	0.000544175	0.167101194	0.026738113	RNA helicase
Solyc04g079140.3	0.261656547	0.001063418	0.384222158	2.78957E-07	DUF829 domain-containing protein
Solyc12g015710.2	0.261632632	0.042176173	0.601196758	1.71357E-07	NOL1/NOP2/sun family protein / antitermination
Solyc06g065840.3	0.261531109	0.017131826	0.423203104	3.18585E-05	NusB domain-containing protein Trafficking protein particle complex II-specific subunit 120 homolog
Solyc06g072270.4	0.261528513	0.027067542	0.316732149	0.004054153	Myb-like protein O
Solyc05g032880.3	0.26147784	0.005493512	0.253200364	0.00483743	50S ribosomal protein L9, chloroplastic
Solyc12g035670.3	0.261381259	0.019693603	0.483902656	2.58146E-06	SAC3 family protein B isoform X1
Solyc08g081505.1	0.261380816	0.039258071	0.246574709	0.039139994	MuDR family transposase
Solyc07g014740.3	0.261318912	0.033100637	0.396585868	0.000356556	Sodium/metabolite cotransporter
Solyc03g083580.3	0.261281541	0.045155406	0.297850495	0.013830545	BASS4, chloroplastic
Solyc01g006130.4	0.26106195	0.002951401	0.218864817	0.010246273	Mitochondrial intermediate peptidase
Solyc07g066320.3	0.260727626	0.01699681	0.273318415	0.007754329	Protein EMBRYO SAC DEVELOPMENT ARREST 3, chloroplastic
Solyc01g086990.3	0.260587906	0.002952284	0.328312694	7.84866E-05	RecA family profile 2 domain-containing protein
Solyc08g079240.4	0.260559453	0.000337769	0.417521478	1.10945E-09	Pre-mRNA-splicing factor SYF1
Solyc02g091490.4	0.260262308	0.002833601	0.19039388	0.025885718	Ribosomal L22e protein family
					Probable fructokinase-6, chloroplastic

Solyc03g123530.4	0.260008513	0.006507386	0.327335664	0.000286623	CCAAT/enhancer-binding protein zeta-like isoform X1
Solyc08g062800.3	0.259994056	0.000112436	0.2194736	0.000927251	Eukaryotic initiation factor 4A
Solyc06g008160.4	0.259977958	0.004784694	0.364552545	2.38575E-05	Protein FLUORESCENT IN BLUE LIGHT, chloroplastic
Solyc06g059750.3	0.259975626	0.036261446	0.409103295	0.000374256	Transcriptional corepressor SEUSS
Solyc03g034200.3	0.259920064	0.01985913	0.341986013	0.001116295	K Homology domain-containing protein
Solyc08g074370.4	0.259866668	0.04162719	0.432756377	0.000232327	DDB1- and CUL4-associated factor homolog 1
Solyc07g063190.3	0.25979106	0.002017814	0.194187858	0.019095555	Thioredoxin domain-containing protein
Solyc01g079690.4	0.259749001	0.013784576	0.323007442	0.001041322	Transcription regulatory protein SNF2-like isoform X1
Solyc12g015880.2	0.259645288	0.000445454	0.263906571	0.000240134	Molecular chaperone Hsp90-1
Solyc12g055780.3	0.259504924	0.003000528	0.192165241	0.024827053	Poly(RC)-binding protein 1 isoform X1
Solyc02g083140.3	0.259115873	0.012219879	0.479627997	4.59956E-07	Ribonuclease E/G-like protein, chloroplastic
Solyc08g006660.2	0.258932296	0.032651151	0.499838984	5.42502E-06	Conserved oligomeric Golgi complex subunit 2
Solyc04g072770.4	0.258834137	0.012236294	0.272045393	0.005361667	TrmE-type G domain-containing protein
Solyc04g049720.4	0.258499787	0.006215845	0.389167771	8.32218E-06	Peptidase M1 leukotriene A4 hydrolase/aminopeptidase C-terminal domain-containing protein
Solyc08g081570.3	0.258456874	0.008452637	0.203196168	0.032569525	2-C-methyl-D-erythritol 2,4-cyclodiphosphate synthase
Solyc10g085280.1	0.258296294	0.004778009	0.350982995	4.23112E-05	UDP-glucose iridoid glucosyltransferase-like
Solyc11g066480.2	0.25809852	0.041554742	0.574316721	5.36889E-07	Increased dna methylation
Solyc06g050930.3	0.257915672	0.047645921	0.4119485	0.000545622	mannosyl-glycoprotein endo-beta-N-acetylglucosaminidase
Solyc10g007290.4	0.25790549	0.003637633	0.246437446	0.004094809	phosphoenolpyruvate carboxylase
Solyc06g073780.4	0.257247547	0.006856532	0.482812001	4.65471E-08	SMC hinge domain-containing protein
Solyc10g080700.2	0.256749059	0.002069444	0.320798355	5.4244E-05	Casein kinase
Solyc08g080370.3	0.256547501	0.004732846	0.238484996	0.006537287	acetylornithine transaminase
Solyc12g098830.2	0.256526319	0.0029661	0.432212802	6.53144E-08	5'-nucleotidase domain-containing protein 4 isoform X1

Solyc08g082530.4	0.25648435	0.000723194	0.481741209	1.019E-11	Probable inactive ATP-dependent zinc metalloprotease FTSH1, chloroplastic
Solyc06g059760.3	0.256375827	0.041414928	0.332598495	0.00464764	Transcriptional corepressor SEUSS
Solyc11g005250.3	0.256031253	0.014944633	0.573229083	2.44197E-09	SNF2 domain-containing protein / helicase domain-containing protein / F-box family protein isoform 3
Solyc07g054190.4	0.255692809	0.009749521	0.32135354	0.000506275	Lumazine-binding domain-containing protein
Solyc03g116680.3	0.255583908	0.00125758	0.24965866	0.001114984	Methyl-CpG-binding domain-containing protein 10
Solyc11g012110.2	0.255537734	0.000334399	0.172888587	0.014905119	Ribosomal protein L6 N-terminal domain-containing protein
Solyc11g040390.2	0.255182679	0.020980996	0.531471511	1.37079E-07	Bifunctional aspartokinasehomoserine dehydrogenase, chloroplastic
Solyc10g079010.3	0.255140853	0.016920928	0.444631201	6.83781E-06	Stress response protein NST1
Solyc11g072540.3	0.254911898	0.003174346	0.342466379	2.69006E-05	DDB1- and CUL4-associated factor 8
Solyc06g053600.4	0.254901235	0.022925846	0.419664261	4.55964E-05	Putative aldo-keto reductase isoform X1
Solyc01g009280.4	0.254841804	0.038350046	0.259755652	0.026228373	Serine/threonine-protein phosphatase
Solyc08g082850.3	0.254402501	0.002790054	0.353201654	1.19903E-05	General control non-repressible 3
Solyc03g006870.3	0.254383587	0.001237536	0.459744751	3.32863E-10	phosphoglucomutase (alpha-D-glucose-1,6-bisphosphate-dependent)
Solyc04g049670.4	0.254312698	0.004507627	0.423754294	4.12176E-07	Two-component response regulator-like PRR37
Solyc10g046930.3	0.254096282	0.001399533	0.357790475	1.9055E-06	Putative rRNA methyltransferase
Solyc11g044540.2	0.253887646	0.00140114	0.268195706	0.000437532	Citrate transporter-like domain-containing protein
Solyc02g069010.4	0.253553656	0.025533596	0.342802696	0.0011238	Inositol-1-monophosphatase
Solyc02g086890.3	0.253230455	0.008752578	0.394682113	1.16849E-05	Photosystem I assembly factor
Solyc11g072050.1	0.253006516	0.020443147	0.274375204	0.007456726	PSA3, chloroplastic F-box/WD-40 repeat-containing protein At5g21040
Solyc11g066870.3	0.252990607	0.000904591	0.456270921	1.71407E-10	MORN repeat-containing protein
Solyc03g058350.4	0.252986704	0.040871407	0.523710478	3.49223E-06	Eukaryotic translation initiation factor 5B
Solyc05g008780.4	0.252885849	0.039884783	0.545359131	1.10062E-06	Proton pump interactor 1
Solyc09g008280.2	0.252697458	0.007143278	0.214675863	0.019065485	S-adenosylmethionine synthase

Solyc07g032110.3	0.252645668	0.002655742	0.175560712	0.033546872	Clathrin binding protein
Solyc02g094590.3	0.25258453	0.017104051	0.507343366	1.562E-07	ATP-dependent DNA helicase At3g02060, chloroplastic
Solyc03g119970.3	0.252549916	0.00230908	0.293622256	0.000195773	ADP,ATP carrier protein
Solyc02g085640.4	0.252494054	0.001240481	0.237829931	0.001636709	Xaa-Pro aminopeptidase P
Solyc06g048970.3	0.252172326	0.041534862	0.326540894	0.004399838	Cation-transporting ATPase
Solyc12g007170.3	0.252113063	0.002404339	0.22476043	0.005305315	Peroxisomal fatty acid beta-oxidation multifunctional protein AIM1
Solyc08g076360.4	0.252035632	0.000592042	0.238187757	0.000842791	Tocopherol O-methyltransferase, chloroplastic
Solyc12g014190.2	0.251933475	0.034299795	0.331886667	0.002493751	Isopentenyltransferase
Solyc08g081900.4	0.251847962	0.005318499	0.290722761	0.000718283	Tr-type G domain-containing protein
Solyc11g008710.2	0.251776277	0.022383535	0.327569244	0.001457811	Probable 37S ribosomal protein S5, mitochondrial
Solyc12g049230.2	0.251650078	0.002048571	0.195847822	0.013992198	GBF-interacting protein 1 N-terminal domain-containing protein
Solyc12g100360.1	0.251326103	0.017378909	0.350313065	0.000412253	Calpain-type cysteine protease DEK1
Solyc06g007710.4	0.251312403	0.000662694	0.16627435	0.022741073	Mitochondrial import receptor subunit TOM40-1-like
Solyc11g013530.3	0.251160486	0.034651095	0.362273138	0.001066086	Histone-lysine n-methyltransferase atx1
Solyc10g009220.3	0.25115162	0.001010345	0.178432329	0.0179256	Heterogeneous nuclear ribonucleoprotein Q
Solyc05g016330.3	0.251066162	0.000930008	0.452783838	1.12078E-10	Cytochrome P450, chloroplastic
Solyc01g049650.3	0.250975699	0.001608517	0.255323482	0.00087599	Pyruvate kinase
Solyc10g085580.3	0.250675638	0.031278159	0.291719189	0.007374593	Embryo sac development arrest 7
Solyc07g066090.4	0.250393008	0.000592648	0.315681893	5.2312E-06	Phosphatidylinositol /phosphatidylcholine transfer protein SFH13
Solyc11g009020.2	0.250379904	0.002015056	0.32536442	2.04812E-05	Haloacid dehalogenase-like hydrolase domain-containing protein
Solyc07g056270.3	0.250374021	0.003550069	0.310030749	0.000140745	Protein kinase domain-containing protein
Solyc12g008630.2	0.25036461	0.000684538	0.193344923	0.007828577	Mitochondrial-processing peptidase subunit alpha
Solyc03g112230.4	0.250274472	0.019897292	0.378677521	0.00016497	Next to BRCA1 protein 1 protein
Solyc08g043170.4	0.250273074	0.001302132	0.351311479	1.9055E-06	Delta-1-pyrroline-5-carboxylate synthase
Solyc08g078320.3	0.250200651	0.023143522	0.5100106	4.12176E-07	High expression of osmotically responsive protein 1

Solyc09g009120.4	0.250037361	0.035792458	0.543888505	4.64488E-07	Polyadenylation and cleavage factor homolog 4 isoform X1
Solyc01g087670.3	0.249819656	0.022454615	0.377629247	0.0001985	U3 small nucleolar RNA-associated protein 21 homolog
Solyc07g005530.4	0.249407373	0.004022195	0.350517016	2.04897E-05	Ubiquitin carboxyl-terminal hydrolase
Solyc07g005390.3	0.24901852	0.000662694	0.464855667	1.0753E-11	Aldehyde dehydrogenase domain-containing protein
Solyc10g006890.4	0.248817221	0.002988815	0.324800428	4.03402E-05	WD repeat-containing protein 44
Solyc07g005830.3	0.248803226	0.009583946	0.308825413	0.000657977	Translation initiation factor IF-3
Solyc03g113780.3	0.248637035	0.002650579	0.292766627	0.000191038	NAD(P)H-hydrate epimerase
Solyc09g091580.3	0.248391859	0.032403638	0.316874304	0.003276523	UbiB domain protein
Solyc02g081730.3	0.248214269	0.006255918	0.218571891	0.012295332	3beta-hydroxysteroid-dehydrogenase/decarboxylase isoform 1
Solyc05g055000.4	0.248125661	0.004823157	0.354817793	1.46943E-05	cysteine desulfurase
Solyc10g007720.4	0.248026338	0.015025868	0.223334975	0.022515155	Conserved oligomeric Golgi complex subunit 5
Solyc06g082840.4	0.247922407	0.003111514	0.275687645	0.000614363	Auxilin-related protein 2
Solyc06g065210.4	0.247781313	0.00216375	0.202973641	0.009905493	Alkaline/neutral invertase
Solyc10g005920.4	0.247582242	0.020417623	0.456415462	3.55245E-06	Enhancer of mRNA-decapping protein 4 WD40 repeat region domain-containing protein
Solyc06g066730.3	0.24753054	0.012995535	0.35308542	0.00016097	Coatomer subunit beta'
Solyc10g085830.2	0.247511082	0.030936907	0.520684659	4.19363E-07	Caffeic acid 3-O-methyltransferase
Solyc01g104920.3	0.247196498	0.048658137	0.503870021	1.07712E-05	Vesicle-fusing ATPase
Solyc01g087750.4	0.247014461	0.00186603	0.271506301	0.000306714	Protein RETICULATA-RELATED 4, chloroplastic
Solyc11g020810.2	0.24698171	0.00090658	0.371005285	1.27532E-07	Putative rRNA methyltransferase
Solyc09g031600.2	0.24666501	0.043192765	0.409377375	0.000249512	Vacuolar protein sorting-associated protein 17, Vps
Solyc03g097260.4	0.246513052	0.012492983	0.325803825	0.000435151	Zinc finger PHD-type domain-containing protein
Solyc03g111850.3	0.246379842	0.000930008	0.227496926	0.001569933	indole-3-glycerol-phosphate synthase
Solyc01g068330.4	0.246197399	0.009747507	0.482851386	3.3615E-08	Cell division control protein 48 homolog C-like
Solyc04g071420.3	0.246102355	0.027225419	0.512757012	3.54715E-07	Thioredoxin-like fold domain-containing protein
					MRL7L, chloroplastic

Solyc05g009930.3	0.246017912	0.000816838	0.408885015	3.19356E-09	CHUP1, chloroplastic
Solyc02g085700.1	0.245977866	0.003443386	0.203464354	0.012308829	Geranyl diphosphate synthase large subunit
Solyc01g109850.3	0.245863025	0.000185911	0.155314546	0.018272867	Diaminopimelate decarboxylase
Solyc01g094800.4	0.245743987	0.030587558	0.399754431	0.000149665	ATP-dependent helicase BRM
Solyc11g044530.2	0.24569686	0.03156698	0.415133782	6.35455E-05	Probable plastid- lipid-associated protein 4, chloroplastic
Solyc01g079570.3	0.24562388	0.002092105	0.488225179	4.9284E-11	Probable beta-D- xylosidase 2
Solyc01g081520.3	0.245606527	0.000866988	0.380927927	3.78432E-08	UTP--glucose-1- phosphate uridylyltransferase
Solyc05g008460.4	0.245419684	0.001045347	0.255005831	0.000438317	ATP synthase subunit beta
Solyc09g075180.3	0.24496178	0.00131308	0.280658657	0.000124962	Blue-light photoreceptor PHR2
Solyc02g091000.4	0.244735051	0.017163115	0.370466825	8.66451E-05	Late embryogenesis abundant protein LEA-2 subgroup domain-containing protein
Solyc10g074700.2	0.244696246	0.007459673	0.294769163	0.000641304	ethanolamine- phosphate cytidylyltransferase
Solyc11g005020.3	0.244665612	0.001774207	0.33003798	8.25994E-06	Protein translocase subunit SecA
Solyc07g062600.4	0.244263263	0.020629278	0.374240112	0.000136577	Increased DNA methylation 1
Solyc09g018450.3	0.244187321	0.002980122	0.297824866	0.000148914	E1 ubiquitin- activating enzyme
Solyc04g080240.4	0.244059881	0.011212929	0.359539542	6.89533E-05	Essential for potexvirus accumulation 1
Solyc03g120230.3	0.244005459	0.045745889	0.405428611	0.000258143	MAR-binding filament-like protein 1-1 isoform X1
Solyc02g086930.4	0.243681487	0.0012717	0.199959999	0.007067554	Homeobox-leucine zipper protein
Solyc04g007280.3	0.243378692	0.001262816	0.219792227	0.002736791	Peptidase S59 domain-containing protein
Solyc05g009220.3	0.243351467	0.001897209	0.286318179	0.000130682	glutamine--tRNA ligase
Solyc03g043950.4	0.243196542	0.022689059	0.436945809	8.14323E-06	N-acetyl-glutamate synthase
Solyc03g083410.3	0.243020472	0.036363708	0.396296564	0.000203615	Histone-lysine N- methyltransferase ATX5-like isoform X2
Solyc07g045540.4	0.243019644	0.008729787	0.312790433	0.000308556	Glucose-6- phosphate 1- dehydrogenase
Solyc01g056570.3	0.242962876	0.033995924	0.410491622	0.000100667	Ankyrin repeat family protein / regulator of chromosome condensation (RCC1) family protein isoform 1
Solyc03g098230.3	0.242821267	0.000743143	0.300626633	1.05323E-05	Bifunctional D- cysteine desulphydrase/1-

Solyc04g045340.3	0.242747259	0.000469531	0.309322895	3.35349E-06	aminocyclopropane-1-carboxylate deaminase, mitochondrial phosphoglucomutase (alpha-D-glucose-1,6-bisphosphate-dependent)
Solyc12g043000.3	0.242698385	0.003079119	0.224377775	0.004799532	Coatomer subunit beta'
Solyc09g010510.4	0.242547647	0.009018151	0.562373745	3.73181E-11	Short-chain dehydrogenase TIC 32, chloroplastic
Solyc03g083240.4	0.242342573	0.025718116	0.47812049	1.44413E-06	Lysine-specific demethylase JM25
Solyc04g008700.3	0.242322062	0.007841066	0.347759707	4.39309E-05	Pre-mRNA-processing protein 40C
Solyc08g006640.3	0.242301413	0.00742133	0.292752887	0.000617494	monogalactosyldiacylglycerol synthase
Solyc01g111210.3	0.242007159	0.005841356	0.305351926	0.000200353	Amidase domain-containing protein
Solyc07g065470.4	0.241825639	0.035264169	0.234387453	0.030425275	Pyridoxal-5'-phosphate-dependent enzyme family protein
Solyc11g065870.3	0.241597116	0.014693937	0.328594333	0.000343977	GTPase Der
Solyc09g010950.3	0.241523985	0.003278277	0.159785196	0.049017333	Mitochondrial respiratory chain complexes assembly protein AFG3
Solyc09g008040.3	0.241516205	0.025091156	0.415606838	2.41121E-05	RNA polymerase sigma factor
Solyc02g021560.4	0.241479463	0.04322953	0.5943594	3.54992E-08	UBP1-associated protein 2C
Solyc04g008680.4	0.241437317	0.002535228	0.49853065	1.65699E-11	ATP/GTP-binding family protein, putative isoform 2
Solyc06g074890.1	0.241335146	0.026456352	0.319850261	0.001554173	Trigger factor ribosome-binding bacterial domain-containing protein
Solyc05g009850.4	0.241290193	0.01535543	0.415925615	5.78931E-06	Transcriptional repressor ILP1
Solyc06g073330.4	0.24106558	0.001361322	0.176673611	0.01742751	Lysine--tRNA ligase
Solyc08g077310.3	0.240864798	0.004897114	0.257405787	0.001708601	SUPPRESSOR OF ABI3-5
Solyc12g017540.2	0.240857753	0.033181646	0.260447585	0.014531237	Ankyrin repeat protein SKIP35
Solyc03g115050.3	0.240548803	0.006321136	0.399622021	7.93191E-07	Replication protein A subunit
Solyc03g115390.4	0.24028262	0.009537185	0.253258041	0.004024487	RNA helicase
Solyc01g111020.3	0.240133023	0.013752245	0.531243081	2.85488E-09	Pentacotriptide-repeat region of PRORP domain-containing protein
Solyc01g079330.3	0.239893199	0.001270082	0.321497239	4.38697E-06	DEAD-box ATP-dependent RNA helicase 24
Solyc03g118340.3	0.239685764	0.008923242	0.377781831	9.95641E-06	Clp R domain-containing protein
Solyc07g017860.3	0.239670501	0.001727741	0.294126267	5.33424E-05	acetate--CoA ligase
Solyc01g090200.4	0.239472322	0.000970661	0.328895488	1.8791E-06	glycine--tRNA ligase
Solyc12g010130.1	0.239360042	0.002656841	0.403391904	6.86428E-08	non-specific serine/threonine protein kinase

Solyc07g064350.3	0.239339508	0.030472645	0.346785256	0.000686254	Kri1-like C-terminal domain-containing protein
Solyc05g053810.3	0.239119945	0.000485936	0.181148933	0.007549037	Serine hydroxymethyltransferase
Solyc03g116870.3	0.238508795	0.00265294	0.340900806	5.03801E-06	Photosynthetic NDH subunit of subcomplex B 1, chloroplastic
Solyc11g066900.2	0.238392661	0.004021558	0.201955129	0.011898359	Nucleobase-ascorbate transporter 12
Solyc06g030570.3	0.238237142	0.007889848	0.320779259	0.000131228	Radical SAM core domain-containing protein
Solyc01g091630.3	0.238075522	0.027748592	0.397614016	7.17496E-05	Homeodomain/HO MEOBOX transcription factor
Solyc03g123750.3	0.238016644	0.016994107	0.321508099	0.000495551	Fungal lipase-like domain-containing protein
Solyc11g013170.2	0.237957238	0.000729634	0.139764183	0.04686355	Probable N-succinyl-diaminopimelate aminotransferase DapC
Solyc06g082793.1	0.23774918	0.009165095	0.197364029	0.025744384	Mitochondrial import receptor subunit TOM40-1-like
Solyc06g009780.4	0.23769069	0.003314772	0.189507056	0.016271458	Kinesin-like protein KIN-14I isoform X1
Solyc01g091780.4	0.237552454	0.035918426	0.215430862	0.045707317	Protein-ribulosamine 3-kinase, chloroplastic
Solyc03g095220.3	0.237412628	0.000686488	0.288327797	1.69906E-05	Translocase of chloroplast
Solyc01g057200.4	0.237170314	0.013128364	0.4392489	4.4488E-07	Pentatricopeptide repeat-containing protein
Solyc06g065650.3	0.237158997	0.004217149	0.256414933	0.001169956	Tify domain-containing protein
Solyc05g021530.3	0.237102908	0.029551721	0.487160328	4.96124E-07	Stromal antigen
Solyc11g066410.2	0.237075731	0.008705166	0.32398481	0.000146144	50S ribosomal protein L9, chloroplastic
Solyc06g083300.4	0.236838049	0.001025976	0.210238398	0.002842521	Putative ras GTPase-activating protein-binding protein 1-like
Solyc03g098110.4	0.236816854	0.003847091	0.275446619	0.000387421	AT-rich interactive domain-containing protein 1A (Fragment)
Solyc02g092230.3	0.23649912	0.021771757	0.231775373	0.017318617	Heptahelical transmembrane protein 4-like
Solyc05g041530.3	0.236464291	0.005589249	0.2230418	0.006514095	Hydrolase isoform X1
Solyc02g091280.3	0.236382913	0.003147861	0.232524371	0.002563642	ATP-dependent Clp protease proteolytic subunit
Solyc03g121980.3	0.236078317	0.000845307	0.213783445	0.001913338	Developmentally-regulated G-protein 2
Solyc03g025280.4	0.236035499	0.001428038	0.253057391	0.000361777	Putative transcription regulator SAP family

Solyc07g045160.3	0.23600159	0.031599514	0.300726086	0.002976572	ATP-dependent 6-phosphofructokinase
Solyc03g080010.3	0.235651578	0.006278271	0.357927719	9.00547E-06	DNA mismatch repair proteins mutS family domain-containing protein
Solyc09g064530.3	0.235626545	0.012107317	0.237923636	0.007691452	Auxin-responsive protein
Solyc02g086150.4	0.235615669	0.004242581	0.185627647	0.020394672	Chloroplastic group IIB intron splicing facilitator CRS2, chloroplastic
Solyc08g007770.4	0.235483031	0.021516718	0.657451193	3.43369E-13	PGR5-like protein 1A, chloroplastic
Solyc10g008980.4	0.235463835	0.001208967	0.368527605	8.86642E-08	Triose phosphate/phosphate translocator, chloroplastic
Solyc01g095040.3	0.235278398	0.002320788	0.184363338	0.014914618	C-terminal binding protein AN
Solyc11g006320.2	0.235173223	0.03294342	0.487800765	1.21839E-06	ubiquitinyl hydrolase 1
Solyc06g071040.4	0.235165097	0.015384237	0.337456644	0.000195416	YLP motif-containing protein 1
Solyc05g007930.3	0.235139948	0.017982596	0.448515591	5.64572E-07	Galectin domain-containing protein
Solyc01g068590.4	0.235137147	0.021112637	0.406561653	1.57989E-05	Paladin
Solyc08g068200.4	0.234821167	0.010066009	0.2746697	0.001340303	GTP-binding protein At2g22870
Solyc09g008840.4	0.234733549	0.015573248	0.218498309	0.01829437	Pyruvate kinase
Solyc03g115590.4	0.234604306	0.003695948	0.213007707	0.006054445	Putative dentin sialophosphoprotein-like
Solyc01g110290.3	0.234259501	0.007103374	0.319966951	9.1043E-05	Squalene synthase
Solyc03g078080.4	0.234195237	0.016522126	0.442082646	8.29538E-07	UMP kinase
Solyc09g007090.4	0.233996449	0.014377387	0.337689564	0.000137709	THO1-MOS11 C-terminal domain-containing protein
Solyc08g007950.3	0.233956779	0.019885146	0.508872153	2.28018E-08	S1 motif domain-containing protein
Solyc01g104480.4	0.233847518	0.004045942	0.36043744	2.0342E-06	Mediator of RNA polymerase II transcription subunit 1
Solyc06g074720.4	0.233769684	0.006428392	0.222951968	0.007130161	RNA-binding (RRM/RBD/RNP motifs) family protein isoform 1
Solyc09g098580.3	0.233754867	0.009436175	0.30828869	0.000267604	GTP diphosphokinase
Solyc04g064700.4	0.233707826	0.01969391	0.409768707	9.92605E-06	Transcription elongation factor SPT5
Solyc03g118170.3	0.233622654	0.000781169	0.175568875	0.010211724	glycine--tRNA ligase
Solyc12g096220.2	0.233616765	0.000753241	0.146359176	0.035045988	Rop guanine nucleotide exchange factor
Solyc01g100750.2	0.233532779	0.020189957	0.467220858	3.45222E-07	DUF538 domain-containing protein
Solyc04g077050.3	0.233396818	0.005870458	0.398309577	4.22096E-07	Amino acid transporter transmembrane domain-containing protein

Solyc01g010440.4	0.23331139	0.001440032	0.220996299	0.0018913	Putative ATP-dependent RNA helicase A-like
Solyc06g083980.3	0.233216135	0.017210941	0.400902544	7.971E-06	Transcription factor
Solyc01g096540.4	0.233176895	0.002666143	0.485017582	1.0312E-11	MHD1 domain-containing protein
Solyc08g007340.3	0.233159683	0.032914792	0.417863646	3.22193E-05	Protein transport protein sec16
Solyc08g065880.3	0.232894746	0.002505142	0.171098276	0.02348627	PiRNA biogenesis protein EXD1
Solyc06g053140.3	0.232744508	0.025545236	0.486475552	2.0218E-07	Rhodanese-like domain-containing protein 14, chloroplastic
Solyc01g102370.4	0.232615377	0.003801394	0.177858134	0.02267735	Flap endonuclease 1
Solyc03g113540.3	0.232535103	0.034902363	0.298791972	0.003310146	Dynein light chain
Solyc05g007960.4	0.232410848	0.002930918	0.306380906	3.64217E-05	O-fucosyltransferase family protein
Solyc02g091580.4	0.232370817	0.003718886	0.186315254	0.017498113	oligopeptidase A
Solyc02g065630.4	0.232058636	0.006957064	0.19394508	0.019732266	Sarcolemmal membrane-associated protein putative isoform 2
Solyc03g111030.3	0.231971182	0.001629467	0.281244529	5.42477E-05	Major capsid
Solyc11g012720.2	0.231765982	0.048099498	0.293907588	0.006173558	Trihelix transcription factor GT-2
Solyc07g049500.3	0.231725682	0.040615665	0.478740158	2.58259E-06	Argonaute 8
Solyc01g010130.4	0.231579775	0.005602729	0.333775939	1.61507E-05	Transcription factor bHLH49
Solyc11g039650.2	0.231236911	0.011058037	0.267579835	0.002011403	dynamain GTPase
Solyc03g112870.3	0.231077256	0.006782934	0.234920194	0.004107343	Phosphoenolpyruvate/phosphate translocator 1, chloroplastic
Solyc01g109990.4	0.231064154	0.015379298	0.354399238	6.05354E-05	RNA-binding protein 28-like isoform X1
Solyc01g103100.3	0.23102133	0.015978089	0.219114614	0.015697034	NADPH-dependent pterin aldehyde reductase
Solyc06g007980.4	0.23099366	0.005192632	0.176063749	0.030058994	Sterol 3-beta-glucosyltransferase UGT80A2
Solyc01g096490.3	0.230839541	0.04553363	0.356674136	0.000847751	RING-type E3 ubiquitin transferase
Solyc03g115370.3	0.230724912	0.01336737	0.242827065	0.006054445	Diacylglycerol kinase
Solyc07g063650.4	0.230570712	0.012442703	0.337300232	8.78783E-05	Ubiquitin carboxyl-terminal hydrolase
Solyc03g115100.4	0.230507085	0.01979883	0.30912721	0.0007394	Protein POLAR LOCALIZATION DURING ASYMMETRIC DIVISION AND REDISTRIBUTION
Solyc11g005170.2	0.23047673	0.003140032	0.154997974	0.045641292	Splicing factor isoform 1
Solyc02g090890.4	0.230398193	0.005853472	0.256430679	0.001235779	Zeaxanthin epoxidase, chloroplastic
Solyc01g068240.3	0.230217176	0.045042879	0.235776828	0.030029734	Ubiquitin carboxyl-terminal hydrolase
Solyc10g012030.4	0.229899901	0.02424895	0.309519818	0.00118403	Cell wall protein AWA1

Solyc07g056030.3	0.22966546	0.033100637	0.352982788	0.000424228	C3HC-type domain-containing protein
Solyc11g008770.2	0.229405408	0.021888197	0.376872555	4.47729E-05	Mitochondrial proton/calcium exchanger protein
Solyc01g110360.3	0.229054111	0.002327268	0.246287978	0.000692341	Fructose-bisphosphate aldolase
Solyc01g101020.4	0.228933711	0.017658167	0.349730497	0.000101394	FACT complex subunit
Solyc11g011470.2	0.228932877	0.001750047	0.170099127	0.018371029	NADH dehydrogenase [ubiquinone] iron-sulfur protein 1, mitochondrial
Solyc05g009530.3	0.228635257	0.005264159	0.287327401	0.000205724	Dihydrolipoamide acetyltransferase component of pyruvate dehydrogenase complex
Solyc04g071890.3	0.228433855	0.011738266	0.337496434	6.67329E-05	Peroxidase
Solyc06g068090.3	0.228247541	0.008530246	0.275641179	0.000845011	Phospholipase D
Solyc01g100570.4	0.228019727	0.000776158	0.193572697	0.003559402	Nucleolar protein 56
Solyc01g079680.3	0.227741336	0.00343159	0.327406024	6.879E-06	Ran GTPase activating protein 2
Solyc12g055800.3	0.227715193	0.019421469	0.386131947	2.03317E-05	V-type proton ATPase catalytic subunit A
Solyc02g081410.3	0.227507758	0.036135219	0.29681675	0.003383076	Beta-catenin-like protein 1 N-terminal domain-containing protein
Solyc06g048730.3	0.227470922	0.002017332	0.351149495	3.91472E-07	Uroporphyrinogen decarboxylase
Solyc12g020050.2	0.227378913	0.030651787	0.314752373	0.001314806	Pentatricopeptide repeat-containing protein, mitochondrial
Solyc07g053650.4	0.226906646	0.035075296	0.414071639	3.01307E-05	26S proteasome non-ATPase regulatory subunit 2 homolog
Solyc01g096040.4	0.226896926	0.004217149	0.273986088	0.000298138	Aspartyl protease family protein 2
Solyc07g052110.4	0.226798757	0.003414928	0.338791711	2.94004E-06	25S rRNA (Cytosine-C(5))-methyltransferase nop2
Solyc01g100650.3	0.226180202	0.003234264	0.248737785	0.000724154	Protein SUPPRESSOR OF QUENCHING 1, chloroplastic isoform X1
Solyc10g007690.3	0.226059822	0.00650813	0.474842585	4.50629E-10	Chlorophyll a-b binding protein, chloroplastic
Solyc11g066370.2	0.225997881	0.037589783	0.355339051	0.000380289	DNA ligase
Solyc11g011220.2	0.225973084	0.004676755	0.373511697	5.61306E-07	Transmembrane protein 214-A
Solyc01g095570.3	0.225856427	0.003721412	0.18029075	0.017334487	Mitochondrial adenine nucleotide transporter ADNT1
Solyc05g052350.3	0.225687242	0.035752799	0.583543822	5.56208E-10	Probable leucine-rich repeat receptor-like protein kinase IMK3

Solyc09g010030.3	0.225438014	0.02109374	0.229479913	0.013133077	Ribosomal protein L7/L12 C-terminal domain-containing protein
Solyc05g016030.3	0.225436097	0.021041711	0.297228684	0.001124307	S-acyltransferase
Solyc02g021360.3	0.225228317	0.015890119	0.412918876	1.5286E-06	Katanin p80 WD40 repeat-containing subunit B1 homolog
Solyc02g071180.3	0.224986812	0.01998096	0.242101644	0.008541021	GBF-interacting protein 1 N-terminal domain-containing protein
Solyc06g071100.4	0.22488322	0.016914914	0.242174063	0.007106211	Plasma membrane ATPase
Solyc09g031750.4	0.224695541	0.009479048	0.259926348	0.001515988	Sodium-dependent phosphate transport protein 1, chloroplastic
Solyc05g008450.3	0.224658679	0.016186751	0.293879812	0.000807516	Fruit protein like
Solyc07g006520.3	0.224613784	0.001527038	0.312377449	2.83412E-06	CpSecY
Solyc11g008700.2	0.224500885	0.014131055	0.253016422	0.003407511	Splicing factor U2AF-associated protein 2
Solyc03g115530.4	0.224369193	0.010022677	0.264742435	0.001226987	DNA annealing helicase and endonuclease ZRANB3
Solyc11g070170.2	0.224148135	0.033232463	0.386337247	5.89697E-05	Casein kinase I
Solyc05g013960.3	0.224058498	0.013930634	0.415001462	7.76553E-07	Oxysterol-binding protein-related protein 1D
Solyc06g069020.4	0.223937853	0.005140921	0.278097444	0.000262296	Eukaryotic peptide chain release factor
Solyc02g014350.4	0.223644104	0.025142366	0.481388953	1.04184E-07	GTP-binding subunit AAA+ ATPase domain-containing protein
Solyc09g098590.4	0.223631646	0.003007715	0.280417744	8.6392E-05	Sucrose synthase
Solyc12g089280.2	0.223509639	0.013030843	0.342340165	4.337E-05	5'-3' exoribonuclease
Solyc04g081030.3	0.22296262	0.049537466	0.396260143	0.000126399	Low temperature viability protein
Solyc02g071890.3	0.222797284	0.012702858	0.230003188	0.006693965	histidinol dehydrogenase
Solyc09g009430.3	0.222669908	0.002430646	0.292701705	2.16794E-05	Tubulin/FtsZ family protein isoform 1
Solyc08g015960.3	0.222527897	0.01745883	0.337974614	7.94396E-05	Aminoacyl tRNA synthase complex-interacting multifunctional protein 1
Solyc04g009650.4	0.222268192	0.019622244	0.24030168	0.007269768	Diphosphomevalonate decarboxylase
Solyc08g007180.3	0.222173567	0.024405263	0.351677267	0.000106407	Light-harvesting complex-like protein 3 isotype 1, chloroplastic
Solyc04g008240.3	0.222079632	0.011175162	0.213251647	0.011005246	RNA demethylase ALKBH10B
Solyc01g095670.4	0.221872797	0.015986078	0.217886097	0.013290934	Rhodanese-like domain-containing protein 4, chloroplastic
Solyc12g007090.2	0.221852005	0.010410797	0.249554682	0.002137522	Thermosome subunit gamma

Solyc09g075390.4	0.221715062	0.003885423	0.295181511	4.48774E-05	GTP diphosphokinase
Solyc04g054880.3	0.221542952	0.003347422	0.337973948	1.64563E-06	Nitrate regulatory gene2 protein-like
Solyc03g007170.3	0.22152357	0.016668966	0.223614296	0.010879176	Peptidyl-prolyl cis-trans isomerase FKBP53
Solyc12g043110.2	0.221319152	0.006926847	0.249947876	0.001402188	Heat shock 70 kDa protein 14
Solyc10g085220.3	0.221129171	0.006031345	0.186954865	0.01603584	Mitochondrial succinate-fumarate transporter 1
Solyc10g051310.2	0.221110201	0.003626453	0.380284778	7.41754E-08	ATP-dependent Clp protease proteolytic subunit
Solyc03g115240.4	0.220926298	0.002123121	0.276097941	5.11737E-05	RNA polymerase-associated protein LEO1
Solyc05g053100.3	0.220916581	0.002823767	0.261139169	0.000204899	Dihydrolipoyl dehydrogenase
Solyc12g008980.3	0.220382568	0.043304575	0.8110316	1.92169E-17	Lycopene epsilon-cyclase
Solyc10g084050.2	0.22013681	0.007976198	0.200627053	0.01254221	Cell division cycle protein 48 homolog
Solyc10g074470.3	0.220051753	0.025768562	0.294565699	0.00127818	DUF632 domain-containing protein
Solyc11g010480.2	0.219847088	0.032360393	0.602457118	4.12225E-11	Threonine endopeptidase
Solyc12g094490.2	0.219806768	0.040250588	0.306831635	0.002083694	Polyadenylation and cleavage factor homolog 4 isoform X1
Solyc04g076880.3	0.219120225	0.020173393	0.208575917	0.021625824	phosphoenolpyruvate carboxykinase (ATP)
Solyc02g081680.4	0.218822486	0.028442048	0.22344495	0.017667661	Nucleolar complex protein 2 homolog
Solyc11g010610.2	0.218638088	0.027149017	0.191091218	0.044227397	Mechanosensitive ion channel protein
Solyc06g068670.3	0.218583316	0.005769087	0.177175041	0.021847792	ACT domain-containing protein ACR
Solyc07g008670.3	0.218283104	0.015887344	0.37402856	8.10676E-06	Serine/arginine repetitive matrix protein 2 isoform 1
Solyc04g071310.3	0.218160074	0.031945869	0.21629385	0.024281336	Cdk-activating kinase assembly factor MAT1 centre domain-containing protein
Solyc08g066570.3	0.218130591	0.005088777	0.247553806	0.000837792	Ultraviolet-B receptor UVR8
Solyc09g074330.3	0.217980206	0.030448824	0.214996335	0.023783887	Homeobox domain-containing protein
Solyc11g007990.2	0.217758795	0.010954625	0.42880775	5.54E-08	Malate dehydrogenase [NADP], chloroplastic
Solyc04g082050.3	0.217600852	0.019093832	0.287888631	0.000975418	CRAL-TRIO lipid binding domain containing protein
Solyc08g081340.4	0.217302461	0.005169232	0.162903765	0.031892035	General transcription and DNA repair factor IIIH helicase subunit
Solyc01g099810.3	0.217144661	0.034237065	0.291496864	0.002139511	XPB1 Serine/arginine-rich-splicing factor like

Solyc05g054970.3	0.217036211	0.004584462	0.293667406	4.91204E-05	Ankyrin repeat domain-containing protein 13B
Solyc10g054870.3	0.216669151	0.006280977	0.218741508	0.003971694	Triosephosphate isomerase
Solyc10g081330.3	0.21663642	0.02965643	0.234391823	0.012877698	UBP1-associated protein 2B
Solyc05g053540.3	0.21660153	0.003580122	0.263153583	0.000181341	dihydroxy-acid dehydratase
Solyc11g020300.2	0.216381115	0.005940571	0.282283582	0.000144686	Protein TIC 40, chloroplastic
Solyc02g093080.3	0.216376361	0.026290436	0.204836947	0.027844847	Probable 2-oxoglutarate-dependent dioxygenase At3g50210
Solyc04g080730.3	0.216259201	0.006921562	0.553040243	2.55514E-14	Mitogen-activated protein kinase
Solyc09g057660.3	0.216231293	0.025924749	0.490096028	2.67149E-08	peptidylprolyl isomerase
Solyc12g019110.3	0.216163321	0.032727294	0.521224951	1.12967E-08	valine--tRNA ligase
Solyc05g052600.4	0.216148836	0.002666192	0.496955027	6.85135E-14	Sedoheptulose-1,7-bisphosphatase, chloroplastic
Solyc07g052240.3	0.215829008	0.004143188	0.155674593	0.035630682	L-ascorbate oxidase homolog
Solyc01g112060.4	0.215645862	0.01042461	0.19591924	0.015573198	Protein HIGH CHLOROPHYLL FLUORESCENCE PHENOTYPE 244, chloroplastic
Solyc04g079270.4	0.215427219	0.048892162	0.362429509	0.000306739	Sorting and assembly machinery component 50 homolog B-like
Solyc07g065050.4	0.214786066	0.033024804	0.226648041	0.017201251	Plastid-dividing ring protein
Solyc03g117890.3	0.214782566	0.00216375	0.329010728	6.37796E-07	ACT domain-containing protein
Solyc01g097860.4	0.214564993	0.006589887	0.225743254	0.002728232	ACR
Solyc11g071800.2	0.214368751	0.027545808	0.257166869	0.004678679	Myelin-associated oligodendrocyte basic protein
Solyc04g080010.4	0.214337976	0.003327327	0.35907396	1.46601E-07	Strictosidine synthase conserved region domain-containing protein
Solyc05g012270.3	0.21394773	0.006192065	0.16195712	0.033680166	Glycosyltransferase
Solyc11g072880.2	0.213743855	0.031474033	0.296181927	0.001450966	argininosuccinate synthase
Solyc04g005690.4	0.213584294	0.02255844	0.360245999	3.22866E-05	Cation-transporting P-type ATPase N-terminal domain-containing protein
Solyc03g005750.3	0.213118128	0.008657197	0.223196396	0.004142296	Splicing factor 3A subunit 1
Solyc12g009800.3	0.21302693	0.007976198	0.616215557	3.76562E-17	GBF-interacting protein 1 N-terminal domain-containing protein
Solyc01g006940.4	0.212960605	0.008522682	0.313755653	3.2772E-05	Purple acid phosphatase 33 kDa
Solyc07g045240.3	0.212897141	0.008731618	0.17206656	0.029613024	ribonucleoprotein, chloroplastic
					G-strand specific single-stranded

Solyc06g065710.3	0.212688973	0.006325467	0.180157117	0.017475325	telomere-binding protein 1
Solyc05g052200.4	0.212640296	0.008287106	0.315936301	2.69006E-05	Putative microtubule-associated protein futsch-like
Solyc12g096020.3	0.21256232	0.018335256	0.231135451	0.006592837	Probable inactive serine/threonine-protein kinase scy1 isoform X1
Solyc01g098030.4	0.212384883	0.007947703	0.22565129	0.003028259	protein-serine/threonine phosphatase
Solyc09g083130.3	0.21229942	0.01609904	0.168124831	0.050413299	Hydroxyproline-rich glycoprotein family protein
Solyc07g007040.4	0.211764021	0.002560226	0.275658574	3.49384E-05	acylaminoacyl-peptidase
Solyc01g109790.3	0.211612083	0.01427043	0.389816723	9.3437E-07	D111/G-patch domain-containing family protein
Solyc03g111050.3	0.211604286	0.00656789	0.44250562	4.20266E-10	Glucose-1-phosphate adenylyltransferase
Solyc03g122350.3	0.21159817	0.019940671	0.387175446	2.95349E-06	Protein PLASTID TRANSCRIPTIONALLY ACTIVE 10
Solyc09g011340.3	0.211571434	0.0368708	0.254774776	0.006942314	Cytochrome P450, family 76, subfamily C, polypeptide 4
Solyc09g090930.3	0.211465039	0.010194992	0.395070612	1.47164E-07	Protein RETICULATA, chloroplastic-like
Solyc04g076090.3	0.211236853	0.00344607	0.216712694	0.001771233	O-linked n-acetylglucosamine transferase, ogt
Solyc04g080900.3	0.211218671	0.038632401	0.216335584	0.024079723	Glucose-6-phosphate isomerase
Solyc05g006680.4	0.211038216	0.021260674	0.406985987	8.29327E-07	GTP-binding protein OBG2
Solyc02g083470.3	0.210952782	0.035756954	0.397146749	1.22978E-05	Hydroxyproline O-galactosyltransferase GALT6-like
Solyc11g068640.2	0.210888911	0.029343965	0.346253879	0.000111688	Pre-rRNA-processing protein esf1
Solyc08g048550.3	0.210651536	0.023518151	0.206103327	0.019192559	TPLATE
Solyc02g082850.3	0.210643542	0.047593699	0.368490888	0.000117897	Protease Do-like 5, chloroplastic
Solyc08g078300.4	0.210381794	0.011375545	0.336908655	1.09826E-05	serine O-acetyltransferase
Solyc02g014520.4	0.210248102	0.013739204	0.322757061	4.12487E-05	Homeobox-leucine zipper protein HAT4-like
Solyc08g016750.3	0.210237314	0.019744725	0.182733462	0.035039201	[Fructose-bisphosphate aldolase]-lysine N-methyltransferase, chloroplastic
Solyc06g054560.3	0.210112216	0.012902893	0.366081352	2.66668E-06	Pyruvate dehydrogenase E1 component subunit beta
					Chromatin-remodeling complex ATPase

Solyc03g032160.3	0.2094319	0.012301027	0.215211613	0.007119037	Ubiquitin domain-containing protein DSK2b
Solyc06g007120.3	0.209216469	0.017552112	0.393870892	9.57741E-07	Phosphoinositide phospholipase C
Solyc02g085000.3	0.208669836	0.02030295	0.259256222	0.001948506	Netrin receptor DCC
Solyc10g006800.4	0.208621152	0.030109042	0.404283323	3.97531E-06	Cyclic nucleotide-binding domain-containing protein
Solyc03g117040.3	0.208611444	0.001622749	0.197451645	0.002120571	Factor of DNA methylation 1-5/IDN2 domain-containing protein
Solyc02g080440.3	0.208604711	0.019864937	0.40994769	4.43961E-07	UPF0051 protein ABCI8, chloroplastic
Solyc02g050280.4	0.20810916	0.023039709	0.28743061	0.000739992	Helicase-like transcription factor CHR28
Solyc10g012370.3	0.208097095	0.007187848	0.173127785	0.020702505	Cysteine synthase
Solyc04g083160.2	0.207987461	0.026546854	0.410564828	1.17469E-06	Ent-kaurene oxidase, chloroplastic
Solyc01g105460.4	0.207943464	0.028736002	0.412192297	1.42271E-06	2-carboxy-1,4-naphthoquinone phytyltransferase, chloroplastic
Solyc05g006520.4	0.207888712	0.003626453	0.15124267	0.031799931	Pyruvate dehydrogenase E1 component subunit alpha
Solyc02g030080.4	0.2076291	0.004845304	0.18497367	0.009543162	Small-subunit processome Utp12 domain-containing protein
Solyc04g005080.3	0.207429815	0.006543538	0.16931248	0.022101201	Pyruvate dehydrogenase E1 component subunit alpha
Solyc01g098550.3	0.207023717	0.005889057	0.169115678	0.020083187	tryptophan synthase
Solyc07g063520.3	0.206635475	0.004295884	0.439351618	4.455E-11	Organic solute transporter subunit alpha/Transmembrane protein 184
Solyc02g094540.4	0.206539891	0.005100743	0.233733086	0.000862595	DEUBAD domain-containing protein
Solyc05g056220.3	0.205709422	0.03104507	0.50248271	6.55769E-09	Methyltransferase-like protein 1
Solyc08g067950.3	0.205595514	0.007381841	0.183030279	0.013756537	Ribosomal protein L17
Solyc03g123610.4	0.205562467	0.007143278	0.22649198	0.001896758	alanine transaminase
Solyc07g054820.4	0.205077347	0.013130321	0.247121203	0.00158298	Protein THYLAKOID FORMATION1, chloroplastic
Solyc03g114370.4	0.205019964	0.01535543	0.252439081	0.001518939	ATP-dependent RNA helicase
Solyc09g009940.3	0.204190338	0.003083773	0.20989121	0.001596535	SRP54-type proteins GTP-binding domain-containing protein
Solyc06g083190.4	0.204083336	0.007354552	0.366770015	2.36141E-07	peptidylprolyl isomerase
Solyc01g110990.2	0.204067012	0.023708377	0.343914484	3.43611E-05	RNA helicase
Solyc02g081170.4	0.204062925	0.023671936	0.253387413	0.002502796	Plastid-lipid-associated protein, chloroplastic

Solyc01g008970.4	0.204054147	0.024725028	0.306195388	0.000313685	UBP1-associated protein 2A
Solyc05g009980.4	0.203823546	0.020356355	0.338934173	3.33483E-05	Decapping 5
Solyc02g083340.4	0.203760974	0.014131055	0.345386784	6.41214E-06	Phospholipase D
Solyc05g055090.4	0.203141458	0.037649443	0.47138834	1.00217E-07	ubiquitinyl hydrolase 1
Solyc06g007760.4	0.202965999	0.004394604	0.200412253	0.003448934	Pheophorbide a oxygenase family protein
Solyc06g062670.3	0.202756163	0.043530893	0.444964703	8.28532E-07	Protein indeterminate-domain 7
Solyc01g080620.3	0.202366776	0.049223811	0.34419122	0.000239482	BTB/POZ domain-containing protein isoform 2
Solyc01g006970.4	0.202175848	0.027031437	0.336059987	6.61035E-05	RNA helicase
Solyc01g112150.3	0.201855452	0.03537284	0.274966212	0.00211069	SEC1 family transport protein SLY1
Solyc04g082820.4	0.20185404	0.021422201	0.184300732	0.028239871	AT-rich interactive domain-containing protein 5
Solyc04g007710.3	0.20134594	0.021828641	0.466931429	5.97442E-09	mitogen-activated protein kinase
Solyc04g072670.4	0.201147292	0.015155177	0.229601534	0.003528869	Apoptotic chromatin condensation inducer in the nucleus
Solyc02g077680.4	0.201052095	0.039946655	0.419203247	2.28893E-06	Alpha-1,4 glucan phosphorylase
Solyc10g062340.2	0.200603261	0.005999578	0.184161478	0.00888497	Heterogeneous nuclear ribonucleoprotein Q
Solyc06g065640.3	0.200394766	0.046465463	0.228720338	0.015966572	Transcriptional corepressor LEUNIG
Solyc04g009540.1	0.200233779	0.019767349	0.36884358	2.96971E-06	50S ribosomal protein L10, chloroplastic
Solyc12g021230.2	0.199708967	0.005428162	0.36718568	3.01885E-08	DNA gyrase subunit B
Solyc01g096570.3	0.199481697	0.004507627	0.180591966	0.007930534	ERI1
Solyc01g073770.2	0.199003108	0.048664125	0.205679479	0.030868016	exoribonuclease 2
Solyc04g005270.1	0.198973786	0.005228093	0.192506107	0.005080788	PRLI-interacting factor A
Solyc06g053400.3	0.198479959	0.00736734	0.311723942	5.98545E-06	1-phosphatidylinositol 4-kinase
Solyc12g006180.2	0.198255473	0.020356355	0.18861371	0.021176874	2-isopropylmalate synthase
Solyc01g005540.4	0.198229791	0.033270338	0.460436844	4.00586E-08	Heterogeneous nuclear ribonucleoprotein 1
Solyc06g083870.3	0.197811823	0.047905116	0.545774857	1.03177E-09	Lysine--tRNA ligase
Solyc09g014760.4	0.197669495	0.00698125	0.232211565	0.000862028	CRAL-TRIO domain-containing protein
Solyc08g075750.4	0.197547109	0.046618399	0.31026985	0.000685058	Chlorophyll synthase
Solyc01g108280.3	0.197274508	0.014272771	0.215420626	0.004827487	ATP-dependent Clp protease proteolytic subunit
					Serine/threonine-protein kinase SRK2E

Solyc11g044340.3	0.197198402	0.018310579	0.262488681	0.000753047	Pre-mRNA-processing protein 40A
Solyc06g084140.4	0.197000935	0.017570443	0.345921915	6.41214E-06	Sulfate/bicarbonate/oxalate exchanger and transporter sat-1
Solyc04g016240.3	0.196897654	0.035799137	0.352976778	3.94974E-05	Nuclear pore protein
Solyc02g080540.1	0.196614899	0.009265751	0.17182083	0.018924222	ATP-synt domain-containing protein
Solyc07g007120.3	0.196467245	0.044144452	0.297659054	0.000986857	Homeobox protein knotted-1-like 3
Solyc09g013100.3	0.196030755	0.03334163	0.373005615	7.39406E-06	Protein TIC 56, chloroplastic
Solyc05g007810.3	0.195778131	0.031926406	0.293980985	0.000505429	RNA-binding KH domain-containing protein RCF3
Solyc12g014440.2	0.195650916	0.042525283	0.190365962	0.037918354	Sialidase domain-containing protein
Solyc03g113500.4	0.195452648	0.025012665	0.260359662	0.001356545	DDT domain-containing protein
Solyc06g048470.4	0.195217322	0.021006858	0.379701101	8.04283E-07	Serine/arginine repetitive matrix protein 2-like
Solyc12g088700.1	0.194948851	0.023833839	0.24862821	0.001802507	Glycosyltransferase
Solyc02g082540.4	0.194535978	0.029074531	0.193455761	0.023165641	Calcium-binding EF hand family protein
Solyc09g005750.3	0.194484232	0.045737232	0.369483398	2.43467E-05	DUF3741 domain-containing protein (Fragment)
Solyc04g015450.3	0.194452887	0.009659512	0.35900267	2.29935E-07	Translation factor GUF1 homolog, chloroplastic
Solyc01g103720.4	0.194435363	0.031207525	0.393103963	1.89797E-06	Ribosome biogenesis protein BOP1 homolog
Solyc01g099100.4	0.194124086	0.006651579	0.323016092	1.21998E-06	Long-chain-fatty-acid--CoA ligase
Solyc08g074500.2	0.194036103	0.036842376	0.33999541	6.42127E-05	TATA-binding protein-associated factor BTAF1
Solyc03g083330.3	0.19397961	0.018184765	0.275964833	0.000267604	Putative dipeptidyl-peptidase IV
Solyc01g107550.3	0.193823859	0.011067641	0.205948629	0.004477056	transcription factor WD40-like family
Solyc11g072490.2	0.193738308	0.016924049	0.285867009	0.000138317	S-methyl-5-thioribose kinase
Solyc09g007110.3	0.193260373	0.028908249	0.385534871	1.56986E-06	Interactor of constitutive active ROPs 3
Solyc03g025150.4	0.192987684	0.017399373	0.344429452	3.68191E-06	Inactive receptor kinase
Solyc02g086910.4	0.192927646	0.021681699	0.236465312	0.002706041	Dentin sialophosphoprotein
Solyc02g072160.4	0.192689891	0.039716477	0.451937211	4.77133E-08	peptidylprolyl isomerase
Solyc07g061900.3	0.192232515	0.015556484	0.221689072	0.003308682	Protein HIGH CHLOROPHYLL FLUORESCENCE PHENOTYPE 173, chloroplastic
Solyc09g072990.3	0.191913153	0.007116311	0.225730731	0.000785725	50S ribosomal protein uL
Solyc04g079430.4	0.191489478	0.024484893	0.204364623	0.011378371	ATP-dependent RNA helicase
					Nucleobase-ascorbate transporter 3

Solyc07g005880.3	0.191295275	0.014245601	0.20639084	0.005356936	Replication factor C subunit 1
Solyc09g061430.3	0.190811086	0.024388482	0.170507024	0.035842745	CP-type G domain-containing protein
Solyc01g105340.4	0.190705319	0.00549488	0.188678932	0.004318759	Chaperone protein DnaJ
Solyc05g007130.4	0.190213262	0.044997586	0.185619286	0.03852851	Protein IQ-DOMAIN like
Solyc02g077090.4	0.189523302	0.014643989	0.316927789	9.58997E-06	CHUP1, chloroplastic
Solyc10g086190.3	0.189365879	0.00556651	0.153348536	0.02160089	Adenosine kinase
Solyc11g007690.3	0.189324821	0.018320991	0.20136347	0.008575637	Pyruvate kinase
Solyc03g025320.4	0.188995192	0.015574721	0.306270081	2.54158E-05	BAHD acyltransferase DCR
Solyc01g091080.3	0.188910799	0.036135246	0.311590767	0.000157699	Tubulin-folding cofactor D
Solyc01g087430.3	0.188737394	0.038704423	0.370376146	7.20075E-06	Putative histone-lysine N-methyltransferase chromatin regulator PHD family
Solyc09g055910.3	0.188565676	0.02512455	0.250124714	0.001419918	Probable D-amino acid oxidase PA4548
Solyc11g066990.2	0.188562755	0.037929477	0.24411414	0.003944685	XS domain-containing protein
Solyc10g085500.2	0.188066594	0.025303307	0.402886213	1.02796E-07	Cytochrome P450, E-class, group I
Solyc02g068910.3	0.187224139	0.03208761	0.243525958	0.002860412	Peptidase, trypsin-like serine and cysteine proteases
Solyc06g074220.3	0.18692001	0.025342634	0.16279555	0.042824099	OTU domain-containing protein
Solyc02g083590.3	0.186226762	0.023036564	0.190158566	0.014562592	3-dehydroquinate synthase, chloroplastic
Solyc01g102940.3	0.18603142	0.044735468	0.353267438	2.96488E-05	methionine S-methyltransferase
Solyc03g120280.1	0.185720084	0.011119697	0.188312	0.00692715	Nuclear pore complex protein NUP50A
Solyc11g006830.2	0.185647099	0.040551207	0.176396569	0.039222162	Hemerythrin/HHE cation-binding motif
Solyc03g123700.4	0.185439	0.037014039	0.347018315	1.52029E-05	Nuclease associated modular domain-containing protein
Solyc08g082620.3	0.184898047	0.026207959	0.235685641	0.002445244	Ketosynthase (KS) domain-containing protein
Solyc08g007990.3	0.183960785	0.016669681	0.214078622	0.003305958	RNA-binding protein NOB1
Solyc04g058090.3	0.183762164	0.016924534	0.268330957	0.000179161	phosphoribosylformylglycinamide cyclo-ligase
Solyc01g009090.3	0.1837122	0.020979677	0.254724587	0.000617494	Serrate RNA effector molecule
Solyc05g056260.2	0.183427669	0.016924534	0.181653331	0.013218621	Phenylalanyl-tRNA synthetase
Solyc09g007230.3	0.183236305	0.031065547	0.217320419	0.006529338	Zinc finger CCCH domain-containing protein 11
Solyc12g056080.2	0.183126257	0.023677209	0.263781081	0.000453432	Crooked neck-like protein 1
Solyc11g062270.2	0.182717048	0.019861777	0.175187856	0.019862247	Signal recognition particle subunit SRP72
Solyc04g058070.3	0.181708056	0.043108575	0.310592889	0.000144177	UDP-sugar pyrophosphorylase

Solyc03g025440.3	0.181576478	0.045547679	0.23990025	0.004256904	Putative receptor protein kinase
Solyc12g099320.2	0.180998912	0.028540107	0.384544749	2.8062E-07	Serine/threonine-protein phosphatase 4 regulatory subunit 3-like central domain-containing protein
Solyc01g102970.3	0.180369769	0.045433404	0.294115702	0.000381274	Squamous cell carcinoma antigen recognized by T-cells 3
Solyc09g090660.3	0.180235894	0.026195257	0.157767145	0.043932615	Pre-mRNA-processing factor 19
Solyc04g082090.3	0.18016828	0.049525871	0.229876157	0.006603945	Alpha-amylase
Solyc03g111840.3	0.179954099	0.02154373	0.244263922	0.000896361	31 kDa ribonucleoprotein, chloroplastic
Solyc03g117440.3	0.179430186	0.013784576	0.243087872	0.000349571	RNA helicase
Solyc01g087290.3	0.178954274	0.048658137	0.485738084	2.05874E-09	tRNA-dihydrouridine(20/20a) synthase isoform X1
Solyc04g008040.4	0.178764415	0.035660088	0.28754492	0.000249534	Myosin heavy chain, clone
Solyc01g107410.3	0.178488874	0.049273882	0.389221485	1.74131E-06	Pathogenesis-related homeodomain
Solyc04g049070.3	0.178091457	0.040989936	0.325551458	4.49433E-05	Probable glucan 1,3-alpha-glucosidase
Solyc10g006390.3	0.178009082	0.031963883	0.245671543	0.001447267	SMAD/FHA domain-containing protein isoform 5
Solyc07g053660.3	0.177950892	0.022181082	0.198028551	0.006771247	DDB1- and CUL4-associated factor 13
Solyc07g019530.3	0.17778407	0.016522699	0.167771138	0.017673576	Afadin-and alpha-actinin-binding protein
Solyc11g017250.2	0.177617518	0.04071798	0.278899935	0.000465137	Dihydrolipoamide acetyltransferase component of pyruvate dehydrogenase complex
Solyc05g018520.3	0.177493661	0.022402098	0.167716475	0.023817012	NADH-cytochrome b5 reductase
Solyc05g011920.3	0.177207408	0.016787033	0.217654646	0.001836224	ACT domain-containing protein
Solyc02g068100.3	0.177139566	0.042975964	0.18605464	0.024793273	ACR
Solyc06g019200.4	0.17682213	0.0290567	0.209173754	0.005899966	SWI/SNF complex component SNF12 homolog
Solyc06g063290.3	0.176227981	0.022033111	0.192160298	0.007781104	Zinc metalloprotease EGY2, chloroplastic
Solyc10g086220.2	0.176207565	0.039081314	0.345102127	9.35923E-06	FMN-binding split barrel
Solyc04g010220.3	0.175096572	0.031945869	0.221395146	0.003717417	12-oxophytodienoate reductase
Solyc01g066310.4	0.174821893	0.050161542	0.239236986	0.003906754	GRIP and coiled-coil domain-containing protein 2 isoform X2
Solyc03g005230.3	0.173409157	0.009102213	0.209545077	0.000898508	Acyl-CoA dehydrogenase IBR3
					2-methyl-6-phytyl-1,4-hydroquinone methyltransferase, chloroplastic

Solyc09g074510.3	0.172893105	0.023472866	0.165416229	0.023463021	Tubby-like F-box protein 3
Solyc04g005330.3	0.172694263	0.020373286	0.20703461	0.003218219	Periodic tryptophan protein 1
Solyc10g050110.1	0.172320256	0.046735348	0.441698467	1.43242E-08	Serine/Threonine kinase, plant-type protein, putative
Solyc05g046330.4	0.172144406	0.020898645	0.251077393	0.000296368	Dolichyl-diphosphooligosaccharide--protein glycosyltransferase subunit 2
Solyc11g008470.2	0.171675218	0.03156698	0.164051533	0.03116518	SART-1 family protein DOT2
Solyc07g053730.4	0.171482867	0.037776763	0.220131934	0.004053764	Nucleolar GTP-binding protein 1
Solyc11g069190.2	0.170746313	0.041025061	0.395830393	1.65403E-07	Auxin response factor
Solyc07g041870.3	0.170426462	0.044737498	0.261953951	0.000816531	Tubulin--tyrosine ligase-like protein 12
Solyc07g055320.4	0.170270184	0.024949204	0.219050573	0.002149356	Chloroplast protease
Solyc02g091560.3	0.170134613	0.013734485	0.240570951	0.000211557	Serine hydroxymethyltransferase
Solyc03g007590.4	0.169674239	0.025560789	0.230208538	0.001169956	FMN-binding split barrel
Solyc11g009080.2	0.169547316	0.017791812	0.189496226	0.005399557	Phospho-2-dehydro-3-deoxyheptonate aldolase
Solyc01g109700.3	0.169543285	0.022096803	0.28860504	2.43012E-05	Transcription factor bHLH63
Solyc11g007960.2	0.168942237	0.034285973	0.173980683	0.021865341	Acyl-CoA-binding domain-containing protein 4
Solyc03g114730.3	0.167971022	0.031501681	0.202148697	0.005964996	O-fucosyltransferase family protein
Solyc03g025530.3	0.167357697	0.029774195	0.233382239	0.001174092	SLH domain-containing protein
Solyc01g103230.3	0.167241317	0.044391094	0.282548552	0.000200868	Non-lysosomal glucosylceramidase
Solyc03g111180.3	0.166039653	0.041146661	0.17145712	0.025753585	Aspartyl aminopeptidase
Solyc12g009960.2	0.16590929	0.044053846	0.158679812	0.044329208	Eukaryotic translation initiation factor
Solyc01g109540.4	0.165298362	0.049568162	0.286534407	0.000216284	Coatomer subunit gamma
Solyc01g005240.4	0.165068856	0.038444364	0.309621011	2.10136E-05	aspartate kinase
Solyc02g021140.3	0.164161622	0.028193489	0.148860674	0.037721269	superoxide dismutase
Solyc01g103410.3	0.163793294	0.015986078	0.16802024	0.009833636	K Homology domain-containing protein
Solyc11g008870.2	0.162031983	0.050464537	0.269202341	0.000423861	Methylenetetrahydrofolate reductase
Solyc01g091620.3	0.159081095	0.046723448	0.323726935	7.9018E-06	non-specific serine/threonine protein kinase
Solyc08g082880.4	0.153405523	0.039699423	0.159608436	0.023034474	Methyltransferase-like protein 17,
Solyc05g009190.4	0.149283174	0.04621196	0.19731863	0.004535893	mitochondrial cysteine--tRNA ligase
Solyc01g104270.4	0.147867977	0.044347724	0.219585618	0.001240606	Protein RETICULATA-RELATED 1, chloroplastic

Solyc03g083970.3	0.147251086	0.035059336	0.140189625	0.036297081	BCL-2-associated athanogene 7
Solyc08g041890.4	0.141984295	0.048573581	0.135662932	0.048783194	Importin subunit alpha

Supplemental Table 7. List of common downregulated genes defined as the genes in SISGT3-ox lines 9 and 31 with F-test FDR value less than 0.05.

ID	Line 9 logFC	FDR	Line 31 logFC	FDR	Annotation
Solyc02g150124.1	-9.607260141	1.37185E-50	-6.6330088	7.16822E-54	Somatic embryogenesis receptor kinase 3A
Solyc10g009595.1	-7.368138807	1.89123E-77	-10.83183876	3.25156E-98	GAG-pre-integrase domain
Solyc08g065600.1	-7.102542547	1.36376E-77	-5.443267978	4.58109E-77	Vacuolar-processing enzyme
Solyc04g025560.4	-6.815587528	1.44902E-89	-6.012475674	1.12582E-95	ADP-ribosylation factor
Solyc10g150115.1	-6.78319578	1.22911E-69	-9.365233636	1.74335E-89	Ankyrin repeat-containing protein
Solyc10g038185.1	-5.84150707	6.66578E-29	-5.099787506	1.21403E-29	At5g02620 family Eukaryotic initiation factor 4A-3
Solyc07g008400.3	-5.629264603	1.6249E-63	-10.79811969	1.73076E-93	Receptor-like protein kinase ANXUR1
Solyc01g107950.2	-5.295025448	2.53698E-39	-4.03001215	2.53976E-34	Transcription factor bHLH95
Solyc01g108800.4	-4.796934768	2.5762E-101	-2.948031685	3.76316E-63	3-hydroxyisobutyryl-CoA hydrolase
Solyc03g044960.2	-4.433066112	3.90904E-45	-4.541987088	1.2422E-50	Calcium uniporter protein
Solyc10g008840.3	-4.395500847	6.2235E-58	-4.043309873	2.13247E-60	Putative small GTPase superfamily, P-loop containing nucleoside triphosphate hydrolase
Solyc11g011570.1	-3.96560302	9.75097E-27	-3.505182931	4.05773E-24	RING-H2 finger protein ATL36
Solyc09g014870.1	-3.722690004	4.87535E-20	-3.296175669	8.34116E-19	Copper transport protein
Solyc08g006280.2	-3.574990253	1.70269E-16	-2.593769393	3.05031E-11	B3 domain-containing protein
Solyc12g100150.2	-3.513571383	5.27486E-26	-3.800020023	8.60244E-31	REM15
Solyc07g040710.3	-3.27450499	3.76059E-31	-3.152937598	1.72862E-32	LOB domain-containing protein
Solyc03g005570.3	-3.215363183	3.42254E-32	-1.961628645	8.50038E-16	IQ domain-containing protein IQM1
Solyc07g032788.1	-3.142916509	2.03711E-32	-3.869079315	3.92495E-46	Transcription repressor MYB4
Solyc06g005320.1	-2.981005005	9.39056E-25	-3.051532999	6.82299E-29	Ketosynthase (KS) domain-containing protein
Solyc06g005330.3	-2.9264356	5.83792E-64	-2.766351811	3.24471E-60	Transcription factor MYB59
Solyc04g074850.3	-2.854357887	9.14323E-48	-2.86782635	6.99673E-51	Transcription factor MYB59
Solyc06g005310.3	-2.805474661	4.2866E-39	-3.130941262	1.5815E-48	Protein DETOXIFICATION
Solyc04g079240.3	-2.790823678	3.78273E-17	-1.422113363	2.57581E-06	Transcription factor MYB48
Solyc06g062920.3	-2.7561341	3.94057E-56	-1.684542906	1.23682E-26	Patatin
					Auxin-regulated dual specificity cytosolic kinase

Solyc07g044970.1	-2.722932184	2.81956E-32	-4.022610206	1.06666E-59	Pentatricopeptide repeat-containing protein mitochondrial isoform X2
Solyc04g056620.2	-2.680519889	8.7268E-14	-3.177933925	4.40517E-19	Auxin efflux carrier component
Solyc04g007750.4	-2.680253083	1.1991E-136	-2.174965177	3.81612E-98	Bet v I/Major latex protein domain-containing protein
Solyc06g005620.3	-2.670095429	4.10317E-74	-2.517019266	9.39895E-72	Zinc transporter
Solyc09g005400.3	-2.627685679	5.92478E-23	-1.333522648	1.15302E-08	Bet v I/Major latex protein domain-containing protein
Solyc04g076630.3	-2.620589333	9.76213E-21	-2.478636853	1.29002E-20	rhamnogalacturonan endolyase
Solyc11g071740.2	-2.610293307	3.11983E-14	-1.711113565	3.64587E-08	Regulator of gene silencing
Solyc04g014770.1	-2.580394862	2.21928E-44	-1.960635258	4.60914E-29	Transmembrane protein
Solyc07g008300.3	-2.574956163	2.96014E-26	-3.196758977	1.27511E-38	Choline monooxygenase, chloroplastic
Solyc01g103590.4	-2.420227553	1.0613E-16	-1.547189091	7.08804E-08	Metallothiol transferase
Solyc04g078340.3	-2.407110236	1.10868E-86	-2.356888537	1.00073E-87	Isoflavone 2'-hydroxylase-like
Solyc08g068610.3	-2.406278114	6.73811E-22	-1.731400624	9.29038E-15	Aromatic amino acid decarboxylase 2
Solyc04g071780.3	-2.391398309	1.16777E-28	-1.505619299	8.97653E-15	Flavonoid 3'-monooxygenase-like
Solyc01g102380.5.1	-2.363770579	9.98556E-44	-2.973032031	1.73975E-66	Nectarin-1
Solyc04g072110.4	-2.351466028	5.29703E-68	-2.796744601	6.40154E-94	Signal peptidase complex subunit 2
Solyc04g058100.3	-2.319289996	8.64296E-34	-3.551418962	2.02693E-69	Metallothionein-like protein type 2
Solyc01g079200.4	-2.314305327	1.1281E-21	-1.824003485	3.52006E-16	Gibberellin 2-beta-dioxygenase 2
Solyc09g014990.4	-2.300873148	1.65573E-62	-1.437796917	5.29398E-30	WRKY domain-containing protein
Solyc03g119250.4	-2.287485729	2.89336E-76	-1.772150563	4.14257E-52	Protein SAR DEFICIENT 1
Solyc04g011910.3	-2.272542016	1.81948E-31	-1.769269478	4.07959E-22	RIN4 pathogenic type III effector avirulence factor Avr cleavage site domain-containing protein
Solyc02g077370.1	-2.236570152	1.49276E-17	-2.176414276	1.07702E-18	Pathogenesis-related genes transcriptional activator PTI5-like
Solyc02g077060.2	-2.212985811	1.33129E-21	-1.851047181	3.28828E-18	RPW8 domain-containing protein (Fragment)
Solyc08g008280.3	-2.212464588	7.77044E-85	-1.294250786	3.91232E-35	WRKY domain-containing protein
Solyc01g080920.3	-2.195112898	2.60356E-12	-1.413304783	9.215E-07	U-box domain-containing protein
Solyc07g008240.3	-2.192796645	2.2734E-117	-2.287915452	1.1777E-129	Hemoglobin-2
Solyc03g083480.4	-2.188799867	1.61369E-27	-2.061114641	1.14864E-26	Membrane receptor 1

Solyc02g094000.1	-2.187759298	2.07505E-18	-1.912427619	2.97112E-16	Calcium-binding protein CML19
Solyc08g061920.3	-2.187467283	2.2572E-31	-2.248401353	2.70843E-35	cytokinin dehydrogenase
Solyc03g121230.3	-2.187425176	3.5006E-11	-1.628180436	1.79404E-07	Leucine-rich repeat receptor-like serine/threonine-protein kinase At2g19230
Solyc01g080680.3	-2.187352773	3.84365E-09	-2.267529373	3.63369E-10	Sugar transporter ERD6-like 16
Solyc05g009650.4	-2.186320308	5.05887E-12	-1.288402489	2.19882E-05	BZIP transcription factor family protein isoform 1
Solyc01g007010.2	-2.142367846	1.17511E-11	-1.286971277	1.15807E-05	U-box domain-containing protein
Solyc08g074490.4	-2.1375057	1.06711E-11	-1.456220949	1.18596E-06	Putative calcium-dependent protein kinase-like
Solyc11g073075.1	-2.108325549	2.68579E-21	-1.927513141	1.92875E-19	Zinc finger protein ZAT11
Solyc07g061930.1	-2.107238498	1.76159E-50	-1.714338377	9.6598E-37	Integral membrane single C2 domain protein
Solyc09g090005.1	-2.096089657	7.06085E-11	-2.563716851	1.12353E-15	Germin-like protein subfamily 1 member 7
Solyc04g077810.1	-2.091044004	5.31797E-28	-2.029286828	1.92867E-28	GPN-loop GTPase QQT1
Solyc01g006050.2	-2.081429755	1.99297E-11	-1.735961602	2.15312E-09	Proteinase inhibitor I4, serpin
Solyc07g007400.3	-2.069669508	1.34485E-14	-1.957282264	3.40187E-14	F-box/LRR-repeat protein 14 isoform X2
Solyc09g072750.2	-2.043500739	4.07567E-06	-1.28555826	0.002338168	Male specific sperm protein
Solyc11g010360.3	-2.032867854	1.0252E-15	-2.207998649	1.67675E-19	DUF617 domain-containing protein
Solyc02g091193.1	-2.030305114	1.14543E-11	-1.518000509	4.69995E-08	Transmembrane protein
Solyc06g060640.1	-2.018868207	8.2013E-163	-1.969554098	1.8552E-157	14 kDa proline-rich protein
Solyc07g007340.3	-2.018144044	2.2684E-116	-1.989935446	1.4633E-117	DC2,15-like Protein
Solyc10g086090.2	-2.015704982	1.02303E-58	-2.103296812	1.96296E-64	NUCLEAR FUSION DEFECTIVE 4
Solyc04g009960.3	-2.001393376	1.86648E-62	-2.078414557	1.50027E-70	Ethylene-responsive proteinase inhibitor 1
Solyc09g006005.1	-1.985342803	7.94784E-13	-1.566966976	1.20418E-09	Aromatic amino acid beta-eliminating lyase/threonine aldolase domain-containing protein
Solyc07g007170.3	-1.984085981	2.39335E-84	-1.908492748	7.96109E-81	Cytoplasmic small heat shock protein class I
Solyc09g092760.2	-1.975224888	1.10084E-13	-2.314878059	6.33007E-19	RING finger protein 165-like
					Cold and drought-regulated protein
					CORA-like isoform X1

Solyc01g014530.2	-1.963298244	8.42622E-11	-1.813012876	2.57403E-10	Bulb-type lectin domain-containing protein
Solyc12g099960.1	-1.954068706	1.3322E-105	-2.226371669	1.4296E-136	Ribosomal protein-related
Solyc08g075020.3	-1.943759372	6.75073E-70	-1.824630328	9.29503E-66	Pectin acetylesterase
Solyc08g082160.3	-1.938859284	5.24025E-25	-2.39977174	1.86742E-37	Inhibitor I9 domain-containing protein
Solyc08g080630.4	-1.932612117	4.88849E-40	-1.691004397	2.56141E-32	Ethylene-responsive proteinase inhibitor 1
Solyc03g019820.3	-1.91726312	6.61138E-79	-2.564410907	1.1814E-134	Aquaporin TIP3-2
Solyc10g054480.3	-1.909607111	1.64361E-09	-1.908595246	2.96997E-10	Berberine bridge enzyme-like
Solyc08g082110.4	-1.905435641	1.70603E-34	-1.454159708	1.64472E-22	WRKY domain-containing protein
Solyc04g014330.1	-1.894881745	3.18735E-16	-2.227825247	2.90759E-22	RNA-binding protein 12-like
Solyc04g078460.3	-1.880478715	8.78864E-42	-2.756731704	5.26269E-83	Isoaspartyl peptidase/L-asparaginase 2
Solyc07g008410.4	-1.877606853	5.52729E-25	-1.531083532	2.05898E-18	Protein DETOXIFICATION
Solyc02g090630.4	-1.871326214	1.67094E-30	-2.3024373	1.17383E-45	Patatin
Solyc06g062450.3	-1.857312449	4.74704E-08	-1.860446998	1.54493E-08	Leucine-rich repeat receptor-like protein kinase
Solyc10g017960.2	-1.840156412	1.73876E-48	-2.014842141	6.48202E-59	At2g19210 Phloem protein 2-A13
Solyc02g005340.4	-1.83407856	1.09655E-15	-2.082145247	1.16153E-20	Metal-nicotianamine transporter YSL7
Solyc04g008970.3	-1.811804262	3.53491E-33	-1.723764205	9.0493E-32	GRAM domain-containing protein
Solyc01g073720.2	-1.810773549	2.47984E-14	-1.967062933	3.92039E-17	Transcription termination factor like
Solyc06g007440.4	-1.806384276	1.10874E-59	-1.598957553	8.61546E-49	non-specific serine/threonine protein kinase
Solyc12g098110.1	-1.79492894	1.79501E-14	-1.301746829	2.33023E-09	S-protein homolog
Solyc04g007760.3	-1.79394158	4.26144E-28	-1.320175368	3.97186E-17	Bet v I/Major latex protein domain-containing protein
Solyc10g007600.3	-1.792209999	5.1497E-139	-2.361919991	1.4069E-232	(S)-2-hydroxy-acid oxidase
Solyc11g073055.1	-1.791208255	1.62009E-09	-2.118561194	2.35727E-13	Zinc finger protein 1
Solyc07g017980.1	-1.78247998	6.15896E-10	-1.696262252	6.3835E-10	Cornifin alpha-like
Solyc07g150104.1	-1.765683689	8.21329E-29	-1.761777605	1.44266E-29	Phytocyanin domain-containing protein
Solyc02g067750.4	-1.762183801	2.19554E-25	-1.479505755	1.61867E-19	Carbonic anhydrase
Solyc04g014320.1	-1.751455707	1.04785E-10	-1.864237107	2.23653E-12	RNA-binding protein 12-like
Solyc01g066520.3	-1.748833	1.0217E-106	-1.763422774	1.8272E-111	Dihydrolipoamide acetyltransferase component of pyruvate

Solyc04g008950.4	-1.745481455	6.89263E-19	-1.846402938	4.84559E-22	dehydrogenase complex
Solyc07g007410.4	-1.736853148	5.57733E-14	-1.194913677	4.43596E-08	GRAM domain-containing protein
Solyc01g007030.3	-1.730647736	3.01627E-20	-1.422128348	7.11083E-16	F-box-containing protein 1
Solyc07g009100.3	-1.72543704	5.83086E-12	-2.703203984	3.78464E-26	U-box domain-containing protein
Solyc02g036440.3	-1.72462914	2.12026E-20	-1.783027164	3.43002E-23	Defensin-like protein 19
Solyc12g098900.2	-1.715627891	6.5351E-60	-1.421712393	1.06454E-43	ALA-interacting subunit
Solyc06g072620.4	-1.704002949	1.76554E-28	-1.168379208	1.7731E-14	Embryonic protein DC-8
Solyc03g122340.3	-1.693321026	8.1428E-58	-1.294594344	5.88216E-37	Bidirectional sugar transporter SWEET
Solyc10g080130.3	-1.691656638	6.17132E-50	-2.765336205	1.2633E-121	Lipoxygenase
Solyc10g047170.2	-1.691245375	4.52747E-33	-1.425942534	3.80722E-25	Exosome complex component RRP43
Solyc06g005410.3	-1.671943127	7.5812E-13	-1.3362419	3.30525E-09	Sulfate transporter
Solyc01g005470.3	-1.671152005	1.95429E-11	-1.626958677	1.01657E-11	TMV resistance protein N
Solyc06g005465.1	-1.664424867	5.93135E-38	-1.881178778	4.08583E-48	Protein PLANT CADMIUM RESISTANCE 2-like
Solyc10g083420.2	-1.660898546	1.46614E-07	-1.56752743	2.38775E-07	Metallothionein-like protein type 2
Solyc01g015080.3	-1.658097064	5.91552E-17	-1.266227564	3.99665E-11	Uridine nucleosidase 1
Solyc01g102895.1	-1.652890469	2.50846E-19	-1.431350771	2.40324E-16	Peroxidase
Solyc03g083680.1	-1.643933021	2.02461E-19	-1.769962543	1.35295E-23	Germin-like protein subfamily 1 member 7
Solyc12g098620.2	-1.635218484	5.36987E-26	-1.219883399	3.82118E-16	Pseudouridine synthase
Solyc09g005830.1	-1.626445883	5.94825E-31	-1.477925044	1.55618E-27	Transcription factor bHLH77
Solyc03g095980.3	-1.626363455	1.47593E-09	-1.433671287	1.69354E-08	Exocyst complex subunit Exo70 C-terminal domain-containing protein
Solyc08g061490.3	-1.625108996	8.56888E-16	-1.02746493	3.31037E-07	Basic helix-loop-helix DNA-binding superfamily protein 51
Solyc08g079970.2	-1.624469367	7.68023E-09	-1.524198511	1.3249E-08	Oxidative stress 3
Solyc06g005480.3	-1.621927557	1.08239E-39	-1.301044983	1.4066E-28	Subtilisin-like protease fibronectin type-III domain-containing protein (Fragment)
Solyc02g088180.3	-1.617829144	3.92175E-23	-1.365313178	1.20259E-18	Plant-specific domain TIGR01615 family protein
Solyc06g035490.3	-1.613551094	2.1136E-66	-1.653405107	2.85004E-72	NAC domain-containing protein
Solyc02g071730.4	-1.612280643	1.69983E-14	-1.959679616	1.34721E-21	Transcription factor bHLH126 like
					Floral homeotic protein AGAMOUS

Solyc05g052880.4	-1.608357642	5.42351E-33	-1.326771214	1.09037E-23	Natural resistance-associated macrophage 1
Solyc02g080040.4	-1.606817223	1.30281E-40	-1.551743423	5.56369E-40	Cysteine-rich receptor-like protein kinase 29
Solyc08g007570.4	-1.605369218	7.16005E-08	-1.50344397	1.62844E-07	Basic-leucine zipper (BZIP) transcription factor family protein
Solyc07g006420.1	-1.588371266	1.58976E-09	-1.372396475	8.79158E-08	Transmembrane protein
Solyc02g077770.3	-1.564161505	4.86719E-16	-0.997044935	1.50886E-07	Trigger factor like
Solyc07g063020.3	-1.559353481	4.28113E-07	-1.82557207	1.02269E-09	Early nodulin-like protein 2
Solyc08g081470.3	-1.557413521	6.59239E-05	-0.997662435	0.007320959	Pectate lyase superfamily protein domain-containing protein
Solyc10g009140.3	-1.556913303	1.25924E-20	-0.993911069	3.9804E-10	Phosphoinositide-binding clathrin adaptor, N-terminal
Solyc03g078370.1	-1.556137045	1.60713E-09	-1.36435546	2.02331E-08	Receptor-like serine/threonine-protein kinase
Solyc04g074680.1	-1.555714814	1.04051E-09	-1.012190181	3.72315E-05	Avr9/Cf-9 rapidly elicited protein 75
Solyc12g013700.2	-1.546940995	3.4149E-90	-1.657368606	6.6262E-105	Stem-specific protein TSJT1
Solyc04g007580.1	-1.537105964	2.71163E-25	-1.87347025	1.76539E-37	DUF4228 domain-containing protein (Fragment)
Solyc03g005210.4	-1.536926595	1.8178E-08	-1.90997675	6.16346E-13	Alpha-amylase inhibitor
Solyc11g073120.2	-1.534240205	6.43601E-34	-1.243792137	4.20925E-23	Transcription factor MYB48
Solyc10g080460.2	-1.531613765	2.07415E-09	-1.138896323	2.85391E-06	HTH myb-type domain-containing protein
Solyc05g015300.4	-1.531333151	2.99896E-36	-1.65735111	1.15233E-42	BURP domain-containing protein
Solyc08g068770.3	-1.530466207	9.23184E-26	-1.823257584	6.56006E-37	Tyramine hydroxycinnamoyl transferase
Solyc03g096250.3	-1.523286018	1.10293E-20	-1.076670624	2.93729E-12	Yippee domain-containing protein
Solyc02g079240.1	-1.521076211	4.43676E-29	-2.355533212	3.43836E-65	Wound-responsive family protein
Solyc06g075100.3	-1.517222034	1.84479E-08	-1.313728922	2.43715E-07	Glycosyl transferase family 2 protein
Solyc07g062470.4	-1.514253434	2.89873E-21	-1.725808327	4.8729E-28	Protein LIGHT-DEPENDENT SHORT HYPOCOTYLS 10-like
Solyc01g105770.2	-1.508343861	2.51441E-09	-1.731735643	2.17742E-12	Periaxin
Solyc04g008960.3	-1.506165408	4.68022E-19	-1.508634397	6.10038E-20	GRAM domain-containing protein
Solyc11g005290.1	-1.501475346	3.04532E-14	-1.106127242	8.02215E-09	RING-type E3 ubiquitin transferase
Solyc10g086100.2	-1.497173848	7.71949E-29	-1.758617261	1.41096E-39	Inhibitor of trypsin and hageman factor

Solyc07g055670.1	-1.48790135	2.5548E-10	-1.733661721	4.80426E-14	Receptor-like serine/threonine-protein kinase Cupredoxin
Solyc05g050510.3	-1.485682852	5.49813E-12	-1.562495422	9.05759E-14	glutathione transferase
Solyc12g097080.2	-1.484878139	5.41913E-21	-1.239897256	1.4769E-15	Pleiotropic drug resistance protein 1
Solyc12g100190.2	-1.484057805	4.16601E-16	-1.290376666	1.42393E-13	Carbonic anhydrase
Solyc10g083890.2	-1.482866938	9.73491E-15	-1.183223187	1.39322E-10	GDSL esterase/lipase 5
Solyc12g049550.2	-1.480512759	2.72323E-15	-1.827182299	3.00795E-23	Cytochrome P450, family 72, subfamily C, polypeptide 1
Solyc07g055460.3	-1.475916079	3.90129E-08	-1.079984512	2.32934E-05	Xylose isomerase
Solyc07g006650.4	-1.475351567	9.55155E-96	-1.621113139	1.101E-115	Lrr receptor-like serinethreonine-protein kinase gso1
Solyc04g076450.1	-1.475251863	2.82494E-42	-1.440720852	3.13406E-42	Probable 2-oxoglutarate-dependent dioxygenase At3g111800
Solyc10g076660.2	-1.474139122	1.10824E-13	-1.636545585	2.08205E-17	Periaxin
Solyc01g105767.1	-1.471651069	8.78966E-06	-2.393221869	5.10054E-13	1-aminocyclopropane-1-carboxylate oxidase
Solyc06g060070.3	-1.46729643	2.02699E-18	-1.802038574	2.10508E-27	Seven transmembrane MLO family protein
Solyc11g069220.2	-1.451157823	9.5769E-21	-1.168966548	5.50297E-15	LOB domain-containing protein
Solyc06g082770.3	-1.450153693	4.12029E-06	-1.714255319	1.94031E-08	Ankyrin repeat-containing protein
Solyc01g088830.2	-1.44681183	8.65082E-07	-1.531237453	4.75634E-08	Cysteine protease
Solyc04g078540.4	-1.440097311	2.42809E-75	-1.408006636	1.8459E-72	Nucleolar and coiled-body phosphoprotein like
Solyc01g087180.4	-1.437777695	1.71926E-17	-1.085377354	2.89284E-11	Clade XII lectin receptor kinase
Solyc10g080510.1	-1.435539246	4.96154E-09	-1.419223242	2.60133E-09	Lipid-binding protein At4g00165
Solyc01g090965.1	-1.435124517	1.34664E-11	-1.677473141	7.67779E-16	MADS-box protein JOINTLESS-like isoform X3
Solyc01g105800.4	-1.434835001	4.05738E-06	-1.985061621	5.98431E-11	Tyramine hydroxycinnamoyl transferase
Solyc08g068790.3	-1.43462366	4.30895E-09	-1.422219747	1.13076E-09	Transcription factor bHLH51
Solyc06g051260.4	-1.434391087	9.91045E-07	-1.185253455	2.74606E-05	Transcription factor bHLH36
Solyc09g074805.1	-1.43104506	1.80149E-27	-1.071323679	4.3542E-17	Mutt domain protein
Solyc08g078210.3	-1.429319903	8.14371E-12	-1.086445424	5.88719E-08	Phytosulfokine-beta
Solyc10g081390.1	-1.424992007	2.6031E-08	-1.580140991	2.41773E-10	Lysine histidine transporter-like 8
Solyc01g111980.3	-1.417392557	1.79552E-47	-1.121142765	1.23076E-31	

Solyc01g103390.3	-1.409499653	2.2768E-66	-1.608921241	3.10314E-87	12-oxophytodienoate reductase-like protein
Solyc07g056090.1	-1.408905632	2.93286E-07	-1.840942574	7.36531E-12	Hydroxyproline-rich glycoprotein GAS31
Solyc01g109150.4	-1.406870685	5.92789E-06	-1.392526208	3.48955E-06	Allene oxide synthase
Solyc02g092460.3	-1.40330368	8.3461E-84	-1.798561367	8.5904E-137	BTB/POZ and TAZ domain-containing protein 4
Solyc10g081570.3	-1.403284793	1.12648E-06	-1.227893429	1.59164E-05	Probable serine/threonine-protein kinase roco5
Solyc08g016720.1	-1.402825107	1.63488E-19	-1.06368493	6.96808E-13	9-cis-epoxycarotenoid dioxygenase
Solyc06g060590.3	-1.400220961	3.6585E-25	-1.20529027	1.34994E-19	Bidirectional sugar transporter SWEET
Solyc11g011630.3	-1.395185286	1.68479E-08	-1.225745773	2.05296E-07	Auxin-responsive protein SAUR65
Solyc06g071890.3	-1.391239603	4.67096E-10	-1.385744465	1.37869E-10	Mitochondrial pyruvate carrier
Solyc06g062390.3	-1.384902926	4.70353E-15	-1.751356173	1.06399E-23	Stem 28 kDa glycoprotein-like
Solyc08g021820.3	-1.381017177	7.74894E-27	-1.52071412	4.86882E-33	Auxin-responsive protein
Solyc05g052370.3	-1.378074178	2.12666E-05	-1.472656384	2.39883E-06	Laccase
Solyc01g091700.4	-1.37734054	6.4826E-33	-1.507675399	4.77126E-41	Phloem protein 2-A13
Solyc02g084960.1	-1.375363439	9.99037E-06	-1.210729005	4.29655E-05	Putative Phosphatidic acid phosphatase family protein
Solyc03g113120.4	-1.367785861	1.36856E-09	-1.285335339	3.68113E-09	WRKY domain-containing protein
Solyc03g031450.3	-1.362082342	1.09461E-13	-1.208582582	7.28477E-12	BHLH domain-containing protein
Solyc03g116120.3	-1.361677815	1.03919E-43	-1.948459277	1.46764E-86	Glutathione S-transferase
Solyc02g071070.3	-1.361133116	1.61452E-16	-1.4516953	1.48931E-19	Cation/H(+) antiporter 18
Solyc03g113810.1	-1.359497487	2.05399E-05	-1.757626795	1.43692E-08	CDP-diacylglycerol-glycerol-3-phosphate phosphatidyltransferase
Solyc02g085010.1	-1.353979395	4.82001E-17	-1.170923867	2.87982E-14	GDP dissociation inhibitor family protein / RabGTPase activator family protein
Solyc07g007350.1	-1.353925545	8.03983E-34	-1.137728339	7.00263E-26	Sterile alpha motif, type 2
Solyc01g110710.3	-1.352989917	6.92273E-06	-1.121301592	9.02569E-05	Auxin-responsive protein SAUR21
Solyc06g066750.3	-1.351869659	3.90213E-07	-1.064900391	2.67031E-05	Thionin-like protein 2
Solyc11g018774.1	-1.350380379	8.28684E-09	-1.314914957	3.66936E-09	Peroxidase
Solyc07g017610.3	-1.347476682	6.86615E-77	-1.583816692	6.6921E-106	Alpha-aminoadipic semialdehyde synthase

Solyc09g064820.1	-1.345514392	1.95117E-08	-1.468041468	2.87331E-10	Circadian clock coupling factor ZGT
Solyc02g087090.4	-1.342551671	4.48508E-28	-1.469168741	9.00723E-35	Alpha-dioxygenase 1
Solyc08g005610.3	-1.341720426	4.17974E-34	-0.999395179	2.34119E-20	Abscisic acid 8'-hydroxylase 1
Solyc01g088160.4	-1.339203865	1.78758E-08	-1.362444087	4.51341E-09	cytokinin dehydrogenase
Solyc06g051680.1	-1.338870745	2.31886E-09	-1.744216067	2.46659E-15	Protein EARLY FLOWERING 4 domain-containing protein
Solyc04g076680.2	-1.338797793	2.60377E-38	-1.18505713	8.73529E-32	MADS-box transcription factor 23-like
Solyc02g068415.1	-1.338362592	4.4681E-11	-1.580633898	1.7136E-15	RING-type E3 ubiquitin transferase
Solyc08g068600.3	-1.331843233	9.41255E-09	-1.193225753	1.16738E-07	Aromatic amino acid decarboxylase 2
Solyc02g079460.1	-1.329110269	8.3519E-58	-1.110275486	1.57615E-41	FAD-linked oxidoreductase 1
Solyc01g096510.2	-1.325907161	6.15577E-10	-1.321127201	1.29762E-10	Sigma factor binding protein 1, chloroplastic-like
Solyc07g008620.1	-1.32157048	1.58796E-16	-1.177377924	2.05015E-14	EIX receptor 1
Solyc03g121540.3	-1.318838982	1.61401E-49	-1.758969365	4.88942E-86	Beta-galactosidase
Solyc12g009000.1	-1.308705009	2.21633E-26	-1.191633887	2.43591E-23	Salt responsive protein 2
Solyc07g007220.3	-1.305262149	5.90706E-22	-1.0771477	1.95417E-16	protein-serine/threonine phosphatase
Solyc08g068690.1	-1.304799783	8.85198E-19	-1.512503902	1.2205E-25	Tyramine hydroxycinnamoyl transferase
Solyc03g078330.1	-1.303890561	1.18544E-16	-1.45489377	4.02808E-21	3-ketoacyl-CoA synthase
Solyc06g005490.3	-1.303501708	2.66611E-34	-1.613262206	3.18482E-52	Triosphosphate isomerase-like protein type II
Solyc11g066400.1	-1.302917648	3.31031E-16	-1.235287112	8.11606E-16	Zinc finger protein ZAT5
Solyc06g071570.3	-1.295957472	2.91531E-08	-1.669320989	1.73094E-13	Solute carrier family 15 (Peptide/histidine transporter), member 3/4
Solyc01g095630.3	-1.295945152	4.89134E-38	-1.167458681	6.03722E-33	WRKY domain-containing protein
Solyc07g017570.2	-1.294894915	4.14974E-52	-1.786778799	9.4266E-97	Defensin-like protein 1
Solyc10g084980.3	-1.294397674	1.18356E-12	-1.104238096	1.62603E-10	Copper transport protein
Solyc06g051550.4	-1.287713249	2.70159E-17	-0.994857463	3.24559E-11	Transcription factor FER-LIKE IRON DEFICIENCY-INDUCED TRANSCRIPTION FACTOR
Solyc12g099860.2	-1.284971509	4.11125E-16	-1.063445256	6.06127E-12	DAR GTPase 2, mitochondrial
Solyc02g093070.3	-1.283088293	2.22873E-15	-1.320160728	1.63325E-17	Probable 2-oxoglutarate-dependent

Solyc10g086280.2	-1.280469176	1.49168E-35	-1.219258642	3.84674E-34	dioxygenase At3g50210 Ribosome biogenesis regulatory homolog
Solyc01g106060.3	-1.279109736	3.52107E-43	-1.506367433	2.71468E-60	Gamma-glutamyl peptidase 5-like
Solyc02g091920.3	-1.276304389	1.66712E-16	-2.191776354	1.12537E-44	Xyloglucan endotransglucosyla se/hydrolase
Solyc12g009290.1	-1.273338158	3.16972E-11	-1.266782913	1.14536E-11	Rho GTPase- activating protein gacM-like
Solyc07g008310.3	-1.268578095	1.42891E-13	-1.019494217	9.63061E-10	Choline monooxygenase, chloroplastic
Solyc03g026230.1	-1.262175838	4.25267E-23	-1.21623741	3.09293E-23	Protein DETOXIFICATI ON
Solyc12g100220.2	-1.25871736	9.17993E-07	-1.898402781	4.05988E-14	Short-chain type alcohol dehydrogenase
Solyc09g009560.2	-1.254317996	4.26657E-07	-1.665841296	4.18363E-12	Terminal flower 1
Solyc02g089620.3	-1.253804846	6.07495E-19	-1.271574889	3.29764E-20	Proline dehydrogenase
Solyc01g107170.2	-1.253082585	3.42568E-25	-1.541821594	3.09827E-38	Putative ATP- dependent Clp protease proteolytic subunit
Solyc08g061640.1	-1.252372804	0.028304978	-1.502594023	0.00564851	Transmembrane protein
Solyc07g008130.3	-1.245936039	4.67334E-35	-1.153471297	7.89343E-31	Dicyanin
Solyc04g077780.3	-1.244590055	3.81284E-84	-1.399898699	3.6305E-106	LIM zinc-binding domain-containing protein
Solyc03g082370.1	-1.239439877	1.27968E-25	-1.965887015	3.82897E-61	Avr9/Cf-9 rapidly elicited protein 65
Solyc03g097240.3	-1.233507243	4.97416E-19	-1.084050158	8.60524E-16	Chaperone J- domain superfamily
Solyc03g097500.3	-1.232547647	2.68343E-08	-1.711900036	2.71483E-15	Omega- hydroxypalmitate O-feruloyl transferase isoform X1
Solyc12g096480.1	-1.218468171	6.7068E-18	-1.27342342	2.1469E-20	Protein GLUTAMINE DUMPER 3
Solyc02g086300.4	-1.217496095	5.63827E-38	-1.340730352	5.58902E-47	Ntpr
Solyc02g064800.3	-1.21377039	9.95429E-60	-1.316286703	2.25095E-71	U2A'/phosphopro tein 32 family A C- terminal domain- containing protein
Solyc02g081990.3	-1.213329754	0.00042512	-1.14162575	0.000634808	Pectinesterase
Solyc06g073830.1	-1.209825112	4.4171E-06	-1.184056856	2.26675E-06	Regulator of gene silencing
Solyc11g012930.2	-1.207540344	1.70486E-29	-1.155329126	2.05483E-27	EamA domain- containing protein
Solyc03g115950.3	-1.20602227	1.78921E-17	-1.221808309	9.9175E-19	Putative Disulfide bond formation protein B 2
Solyc03g026000.4	-1.204308396	8.09104E-17	-1.640152386	1.92309E-30	Putative FAD- binding Berberine family protein
Solyc03g006620.3	-1.204294861	3.65559E-12	-1.38652674	1.84899E-16	Cotton fiber expressed protein

Solyc07g054060.3	-1.204189836	5.64455E-17	-1.136702077	5.19554E-16	Non-specific lipid-transfer protein 13
Solyc08g082680.3	-1.203577338	2.94458E-13	-1.070816693	3.2467E-11	RING-H2 zinc finger protein RHA4a
Solyc06g083130.4	-1.203090037	1.29062E-08	-1.076005454	1.22757E-07	dCTP pyrophosphatase 1
Solyc05g046290.3	-1.20124602	1.42909E-31	-1.219476677	9.61268E-34	Xyloglucan endotransglucosylase/hydrolase
Solyc10g008900.3	-1.200653094	3.16773E-06	-1.84590186	2.62731E-13	Dirigent protein (Fragment)
Solyc12g099590.1	-1.199608353	1.59738E-13	-1.226259261	5.38472E-15	Proline dehydrogenase 1, mitochondrial
Solyc03g114600.4	-1.197022872	2.1184E-39	-0.99497093	2.23387E-29	Alternaria stem canker resistance protein 1
Solyc04g078170.2	-1.193219151	0.000107027	-1.063086299	0.000264391	ARM-repeat/Tetratricopeptide repeat-like protein
Solyc02g071560.4	-1.192453682	2.35717E-06	-1.646203324	2.14044E-11	Subtilisin-like protease SBT5,6
Solyc08g066590.3	-1.190475177	1.19851E-10	-2.136054609	1.45669E-30	Root cap
Solyc02g076830.1	-1.190434622	5.11877E-17	-1.098606821	1.68949E-15	Epidermis-specific secreted glycoprotein EP1-like
Solyc08g083110.4	-1.18427068	1.64292E-34	-1.441804508	1.12462E-50	Methionine gamma-lyase
Solyc01g079940.4	-1.183423358	1.08952E-50	-1.095095712	3.05987E-44	Basic 7S globulin 2 small subunit
Solyc07g042510.3	-1.181698211	5.18879E-31	-1.065399613	3.31191E-27	Transmembrane BAX inhibitor motif-containing protein 4
Solyc07g026680.2	-1.181342551	1.52628E-32	-1.115975073	6.10349E-30	Transcription factor MYBS3
Solyc03g083730.1	-1.180996601	2.67542E-29	-2.13111322	9.65911E-89	Pectin methylesterase inhibitor protein 1
Solyc08g077080.1	-1.177662728	1.05665E-11	-1.361937775	5.80028E-16	Solanidine galactosyltransferase (Fragment)
Solyc02g070450.2	-1.17680657	1.8875E-06	-1.064193951	7.32487E-06	glucan endo-1,3-beta-D-glucosidase
Solyc10g007750.1	-1.173209936	7.13177E-12	-1.129066664	1.1619E-11	rRNA N-glycosidase
Solyc02g089170.4	-1.172484762	7.85401E-07	-1.257718141	4.991E-08	UDP-arabinopyranose mutase
Solyc12g015920.2	-1.165586072	5.78025E-05	-1.402658118	5.5842E-07	HMA domain-containing protein
Solyc10g083880.2	-1.161419164	1.68363E-44	-1.68573434	2.98964E-91	Tonoplast intrinsic protein
Solyc08g079930.2	-1.160230906	0.000556374	-1.910652765	5.10575E-09	Serine protease
Solyc03g120020.4	-1.158285586	5.75533E-12	-1.134184928	3.68698E-12	Boron transporter 4
Solyc01g080150.3	-1.152062453	4.73597E-08	-1.05609286	1.62473E-07	Adenylate isopentenyltransferase
Solyc01g109170.3	-1.145312348	8.36426E-58	-1.353361384	1.91355E-80	Cold-regulated 413 plasma membrane protein 2
Solyc09g014900.3	-1.144309058	3.77361E-20	-1.118146929	4.44594E-20	Tryptamine 5-hydrolase

Solyc05g055320.3	-1.144275948	4.62247E-05	-1.792503651	5.96467E-11	Peroxidase
Solyc05g006210.3	-1.140586545	1.94787E-06	-1.038203448	6.51957E-06	glucan endo-1,3- beta-D-glucosidase
Solyc01g104110.4	-1.140367443	1.23638E-31	-1.372168082	2.50097E-46	Glutelin type-A
Solyc08g068680.4	-1.136814354	0.000220178	-1.588092709	8.64526E-08	Aromatic amino acid decarboxylase 2
Solyc09g064160.3	-1.136548323	8.13378E-08	-1.051844701	2.52716E-07	Flavin-containing monooxygenase
Solyc09g065000.4	-1.136295245	2.56692E-18	-1.050211215	1.04666E-16	Basic 7S globulin 2 small subunit
Solyc04g007500.1	-1.135115167	3.19067E-14	-1.364382619	1.58176E-20	E3 ubiquitin- protein ligase RHA2A
Solyc03g113890.1	-1.134729536	1.72059E-05	-1.202402352	1.99502E-06	C2H2L domain class transcription factor
Solyc05g025820.4	-1.134038449	7.22785E-06	-1.225159868	3.71931E-07	Serine/threonine- protein kinase RIPK
Solyc09g089680.4	-1.128722053	1.76938E-22	-1.24122107	5.02441E-28	1- aminocyclopropan e-1-carboxylate oxidase-like protein
Solyc03g020010.1	-1.126829642	2.34579E-23	-1.23241008	2.61419E-28	Kunitz trypsin inhibitor 2
Solyc08g077810.2	-1.125353785	2.64037E-05	-1.604968699	6.63524E-10	Cationic amino acid transporter C- terminal domain- containing protein
Solyc10g084960.2	-1.125127528	5.06882E-07	-1.408330845	8.77304E-11	glutathione transferase
Solyc06g073583.1	-1.124690196	8.47443E-17	-1.435528892	1.8179E-27	Rhodanese-like domain-containing protein 19, mitochondrial
Solyc01g100010.3	-1.121375634	5.96592E-07	-1.550456751	9.2774E-13	Putative SKP1 interacting partner 3-related family protein (Fragment)
Solyc04g054690.3	-1.121166848	1.68074E-35	-1.290416756	6.40069E-48	L-ascorbate oxidase
Solyc06g076330.3	-1.120277388	1.80156E-09	-1.002009203	2.46585E-08	Laccase
Solyc05g052410.3	-1.1200554	7.49037E-07	-1.024866971	2.47707E-06	Dehydration- responsive element-binding protein 2C
Solyc04g077120.4	-1.119803902	7.666E-42	-0.993876199	5.92661E-35	Inositol- tetrakisphosphate 1-kinase
Solyc01g005680.4	-1.118693215	1.54946E-15	-1.231573371	1.64853E-19	Cytokinin riboside 5'-monophosphate phosphoribohydro lase
Solyc06g084170.3	-1.111567853	2.01999E-07	-1.258829821	1.24741E-09	Knottin scorpion toxin-like domain- containing protein
Solyc01g110660.4	-1.110185533	1.13324E-05	-1.348345967	3.17011E-08	Auxin-responsive protein SAUR21
Solyc03g046380.1	-1.108328817	5.37428E-07	-1.92005713	1.23688E-18	Seed maturation protein PM41
Solyc06g073590.3	-1.108134054	2.54914E-06	-1.532835177	2.23539E-11	Aquaporin
Solyc09g011190.1	-1.106026356	5.09804E-10	-1.153802358	2.81829E-11	Legume-specific protein

Solyc03g083770.1	-1.105241912	1.29604E-27	-1.288979068	1.29713E-37	Pectin methylesterase inhibitor protein 1
Solyc03g034230.3	-1.103945292	0.000235169	-1.601226175	2.78855E-08	Autophagy-related 2
Solyc06g072870.1	-1.099020757	1.49036E-09	-1.083434842	6.67068E-10	Glycosyltransferase
Solyc07g009290.3	-1.096532666	1.01029E-19	-1.070072671	5.88144E-20	Defensin-like protein 1
Solyc11g068710.3	-1.093497319	1.27535E-05	-1.820252934	1.07334E-13	F-box domain
Solyc03g083470.3	-1.093005756	1.10492E-15	-1.185633318	3.12287E-19	Rust resistance kinase Lr10-like
Solyc03g026050.3	-1.091220088	0.00140175	-2.129065144	1.81846E-10	Brother of FT and TFL1
Solyc03g043880.3	-1.089143608	3.07543E-11	-1.39380278	3.65455E-18	Branched-chain-amino-acid aminotransferase
Solyc01g073820.4	-1.08894275	2.11984E-05	-1.426492195	7.89934E-09	DC1 domain-containing protein
Solyc03g033360.3	-1.086953755	2.09282E-06	-1.465076377	5.16413E-11	Aspartyl protease family protein 1-like
Solyc10g085950.2	-1.085417441	0.000541591	-1.253770729	2.53478E-05	Protein ALUMINUM SENSITIVE 3
Solyc04g082420.3	-1.080283688	7.16741E-59	-1.095092706	2.73493E-61	BTB/POZ domain-containing protein isoform 1
Solyc02g071950.1	-1.077954935	3.97813E-16	-1.457174653	2.74497E-29	AT-hook motif nuclear-localized protein
Solyc08g068700.1	-1.077895863	1.82279E-19	-1.051369954	1.94359E-19	Tyramine hydroxycinnamoyl transferase
Solyc02g094860.3	-1.075785999	5.46433E-14	-1.332647927	1.51393E-21	Cytokinin hydroxylase
Solyc01g081600.3	-1.074883013	7.48375E-09	-1.268670217	1.79828E-12	Non-specific lipid-transfer protein
Solyc02g087520.3	-1.07316448	3.16004E-06	-1.468134531	4.82022E-11	Thaumatococcus
Solyc12g099160.2	-1.064157834	1.5252E-28	-1.188055849	1.18831E-36	Carboxypeptidase
Solyc05g006390.1	-1.060639907	1.00344E-14	-1.207360083	2.74869E-19	CDP-diacylglycerol-glycerol-3-phosphate phosphatidyltransferase
Solyc01g108030.4	-1.056571724	3.15862E-54	-1.240561845	3.26102E-75	methylcrotonoyl-CoA carboxylase
Solyc08g078870.3	-1.056233871	1.07278E-51	-1.192002776	4.96539E-66	p-rich protein EIG-I30
Solyc02g067190.4	-1.05401997	4.99055E-06	-1.986713387	4.0529E-18	Casparian strip membrane protein 3
Solyc10g009310.4	-1.051907105	0.000182336	-1.171037739	1.26622E-05	Cytochrome P450, family 78, subfamily A, polypeptide 6
Solyc01g067510.3	-1.051856106	1.56655E-28	-1.336311432	2.8088E-46	non-specific serine/threonine protein kinase
Solyc04g080540.2	-1.051373312	1.36144E-35	-1.11597846	2.66122E-40	Tat-binding like
Solyc08g079730.2	-1.049994366	4.3108E-14	-1.272366532	9.28124E-21	Protein DETOXIFICATION
Solyc02g083490.3	-1.049312211	5.91668E-08	-1.623859802	1.05188E-17	Peroxidase
Solyc12g010570.1	-1.049121401	1.33512E-08	-1.32072662	1.62757E-13	Tetraspanin-8

Solyc05g054250.1	-1.048798058	6.28044E-08	-1.05211648	1.27704E-08	Heavy metal-associated isoprenylated plant protein 20
Solyc09g075940.3	-1.046404579	4.80408E-12	-1.26122352	1.62251E-17	Amine oxidase
Solyc02g064980.1	-1.042870049	6.72013E-06	-1.053421084	2.27499E-06	Mitogen-activated protein kinase kinase npk1
Solyc02g081040.4	-1.039476553	8.26016E-08	-1.024313917	4.74947E-08	Chitin elicitor receptor kinase 1-like
Solyc04g040090.4	-1.031396604	4.77813E-05	-1.083558563	8.2776E-06	Strictosidine synthase conserved region domain-containing protein
Solyc04g005810.3	-1.031271134	9.40876E-10	-1.108561224	1.41622E-11	Thioredoxin domain-containing protein
Solyc02g032030.1	-1.030319938	3.29508E-06	-1.619101542	4.57054E-14	Dirigent protein (Fragment)
Solyc09g009830.3	-1.027494247	1.02198E-17	-1.502998628	6.86515E-37	Carbonic anhydrase
Solyc09g007730.4	-1.026683769	4.62691E-06	-1.057423442	6.43738E-07	Protein kinase domain-containing protein
Solyc01g087980.4	-1.025368997	2.07475E-21	-1.270648031	7.04346E-33	Rx N-terminal domain-containing protein
Solyc01g109895.1	-1.025306453	2.24829E-25	-0.996036919	2.51925E-24	Protein CASPARIAN STRIP INTEGRITY FACTOR 1
Solyc03g112100.3	-1.024025502	3.92016E-31	-1.025018846	3.39347E-32	High-affinity nitrate transporter
Solyc04g005040.1	-1.020736633	6.72481E-17	-1.122335201	1.00397E-20	Metalloendoproteinase 2-MMP
Solyc06g035960.3	-1.019496365	3.70986E-05	-1.211507053	2.39027E-07	4-coumarate--CoA ligase-like 10
Solyc05g041200.4	-1.019052906	1.14909E-37	-1.263241722	1.45598E-57	4-hydroxyphenylpyruvate dioxygenase
Solyc08g013930.4	-1.018994216	1.07359E-10	-1.04176818	1.81573E-11	Peroxidase
Solyc12g044330.2	-1.016232913	1.24923E-21	-1.582283894	1.41223E-50	Aquaporin
Solyc01g102290.3	-1.010411836	3.31136E-32	-1.196638284	5.86501E-45	Hydrophobic protein like
Solyc10g008150.1	-1.006778637	0.001118583	-1.131104932	0.000131781	Putative glutaredoxin-like, plant II, thioredoxin-like protein
Solyc01g098570.2	-1.005677736	4.37097E-12	-1.164899235	1.09297E-16	FAF domain-containing protein
Solyc08g079480.3	-1.005601444	9.4519E-05	-1.000785745	4.7885E-05	Homeodomain-interacting protein
Solyc12g007250.1	-1.003762237	0.000162714	-1.407176643	3.44193E-08	Xyloglucan endotransglucosylase/hydrolase
Solyc06g082240.2	-1.002355595	0.000114116	-1.782527104	1.64126E-12	Laccase
Solyc08g074690.3	-1.001905469	2.14989E-12	-1.403524083	1.16874E-23	catechol oxidase
Solyc03g093800.1	-1.001542653	0.000239643	-1.217754869	3.58943E-06	Glycine-rich cell wall structural protein 1

Solyc06g060600.3	-0.999989767	2.84545E-09	-1.785295851	9.7696E-27	Trehalose 6-phosphate phosphatase
Solyc06g005890.3	-0.999579023	5.39282E-24	-1.139624116	8.08966E-32	DUF674 domain-containing protein
Solyc01g107080.3	-0.999156077	2.07174E-24	-1.095586199	3.46271E-30	Anthranilate N-hydroxycinnamoyl/benzoyltransferase
Solyc06g005980.4	-0.999089495	2.48931E-11	-1.190628192	3.55816E-16	anthranilate synthase
Solyc07g043680.3	-0.998436933	1.53574E-05	-1.022314468	3.72119E-06	3-hydroxyisobutyryl-CoA hydrolase
Solyc03g034030.3	-0.997798047	0.00069773	-1.297675764	3.55815E-06	Ce-LEA
Solyc04g025650.3	-0.997345903	3.7671E-50	-1.021066186	1.04791E-53	Putative FAD/NAD(P)-binding domain protein
Solyc06g060700.1	-0.997256037	3.04451E-07	-1.515113931	1.02165E-15	Putative inactive serine/threonine-protein kinase-like
Solyc07g007130.1	-0.995905429	3.71419E-11	-1.350673511	5.1114E-20	Stress induced protein
Solyc04g009305.1	-0.994757355	8.62393E-08	-1.016156887	1.36944E-08	Endochitinase A
Solyc04g063350.3	-0.9912183	8.24154E-33	-1.045458561	1.55158E-37	Dehydrogenase E1 component domain-containing protein