



UNIVERSITAT DE
BARCELONA

Factores Gre de *Salmonella enterica* serovar Typhimurium, su papel en el control de la fisiología y patogenicidad

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Tabla Suplementaria 1

Diferencia de expresión de todos los genes de SV5015 en las cepas mutantes *greA*, *greB* y *greAgreB*, respecto a la cepa WT

ID	gene	Description	<i>greA</i> vs WT	<i>greB</i> vs WT	<i>greAgreB</i> vs WT
SL0001	-	Hypothetical Protein SL0001	-1,05	1,11	1,67
SL0002	<i>thrA</i>	Bifunctional aspartokinase/homoserine dehydrogenase 1	1,70	1,02	2,42
SL0003	<i>thrB</i>	Homoserine kinase	1,23	-1,09	1,15
SL0004	<i>thrC</i>	Threonine synthase	1,13	-1,11	-1,03
SL0005	<i>yaaA</i>	UPF0246 protein yaaA	1,04	1,17	-2,22
SL0006	<i>yaaJ</i>	Uncharacterized transporter yaaJ	1,24	1,13	1,12
SL0007	<i>tal1</i>	Transaldolase 1	1,02	-1,18	1,34
SL0008	<i>mog</i>	Molybdopterin adenyltransferase	1,33	1,02	2,27
SL0009	<i>yaaH</i>	Inner membrane protein yaaH	1,31	1,08	-1,16
SL0010	<i>yaaW</i>	UPF0174 protein yaaW	-1,14	1,06	1,09
SL0011	<i>yaal</i>	UPF0412 protein yaal	1,23	1,10	-1,14
SL0012	<i>dnaK</i>	Chaperone protein dnaK	1,05	1,13	2,97
SL0013	<i>dnaJ</i>	Chaperone protein dnaJ	-1,06	-1,09	2,03
SL0014	<i>ybdO</i>	Uncharacterized HTH-type transcriptional regulator ybdO	1,05	1,18	-1,02
SL0015	-	Hypothetical	-1,05	-1,02	1,02
SL0016	-	Hypothetical	1,02	-1,34	1,50
SL0017	<i>yqel</i>	Hypothetical	-1,11	-1,07	1,13
SL0018	<i>chiA</i>	Chitinase A	1,18	-1,04	1,36
SL0019	-	Hypothetical	1,33	-1,10	1,64
SL0020	<i>yaiV</i>	Uncharacterized protein yaiV	1,26	-1,33	-1,50
SL0021	<i>pilC</i>	Type-1 fimbrial protein, C chain	1,31	1,02	1,10
SL0022	<i>fimC</i>	Chaperone protein fimC	1,26	1,03	-1,03
SL0023	<i>ycbS</i>	Uncharacterized outer membrane usher protein ycbS	1,35	-1,10	1,59
SL0024	<i>fimH</i>	Protein fimH	1,16	-1,11	1,18
SL0025	<i>ycbU</i>	Uncharacterized fimbrial-like protein ycbU	1,46	1,48	-1,04
SL0026	<i>fimF</i>	Protein fimF	1,16	-1,21	1,31
SL0027	<i>ycbF</i>	Uncharacterized fimbrial chaperone ycbF	1,08	-1,30	1,22
SL0028	-	DSBA Oxidoreductase	1,20	-1,05	1,17
SL0029	-	Hypothetical	1,76	1,14	1,13
SL0030	<i>yqel</i>	Hypothetical	1,26	-1,05	-1,09
SL0031	<i>leuO</i>	Probable HTH-type transcriptional regulator leuO	-1,07	-1,03	1,27
SL0032	-	Hypothetical	-1,01	-1,02	1,21
SL0033	-	Arylsulfotransferase	-1,11	1,21	-1,02
SL0034	<i>yhcR</i>	Endonuclease yhcR	1,37	1,25	2,40
SL0035	<i>yfeN</i>	Uncharacterized protein yfeN	1,20	1,08	1,20
SL0036	<i>betC</i>	Choline-sulfatase	-1,04	-1,01	3,95
SL0037	<i>asIB</i>	Anaerobic sulfatase-maturing enzyme homolog AsIB	-1,23	1,05	1,34
SL0038	-	Hypothetical	1,10	1,18	1,54
SL0039	-	Arylsulfate Sulfotransferase	1,19	1,06	1,12
SL0040	<i>nhaA</i>	Na(+)/H(+) antiporter nhaA	-1,22	-1,40	-1,05
SL0041	<i>nhaR</i>	Transcriptional activator protein nhaR	-1,05	-1,34	-1,06
SL0042	<i>yicl</i>	Uncharacterized family 31 glucosidase ORF2	1,21	1,14	2,73
SL0043	<i>xyIP</i>	Putative xylose-proton symporter	1,11	-1,37	7,93
SL0044	<i>rpsT</i>	30S ribosomal protein S20	-1,21	1,09	-3,04

Tabla Suplementaria 1

Diferencia de expresión de todos los genes de SV5015 en las cepas mutantes *greA*, *greB* y *greAgreB*, respecto a la cepa WT

ID	gene	Description	<i>greA</i> vs WT	<i>greB</i> vs WT	<i>greAgreB</i> vs WT
SL0045	<i>yaaY</i>	Uncharacterized protein yaaY	1,11	-1,33	-1,13
SL0046	<i>ribF</i>	Riboflavin biosynthesis protein ribF	1,03	-1,03	-1,66
SL0047	<i>ileS</i>	Isoleucyl-tRNA synthetase	1,03	-1,25	1,37
SL0048	<i>lspA</i>	Lipoprotein signal peptidase	1,19	-1,11	1,55
SL0049	<i>fkpB</i>	FKBP-type 16 kDa peptidyl-prolyl cis-trans isomer	1,08	-1,04	1,25
SL0050	<i>ispH</i>	4-hydroxy-3-methylbut-2-enyl diphosphate reductase	1,21	1,24	1,10
SL0051	-	Hypothetical	1,06	-1,01	1,03
SL0052	<i>rihC</i>	Non-specific ribonucleoside hydrolase rihC	1,40	1,26	3,12
SL0053	<i>citB</i>	Transcriptional regulatory protein CitB	1,01	1,07	1,46
SL0054	<i>citA</i>	Sensor histidine kinase CitA	-1,01	1,15	1,46
SL0055	<i>oadB1</i>	Oxaloacetate decarboxylase beta chain 1	1,32	1,13	2,23
SL0056	<i>oadA</i>	Oxaloacetate decarboxylase alpha chain	1,21	-1,06	2,57
SL0057	<i>oadG1</i>	Probable oxaloacetate decarboxylase gamma chain	1,12	-1,07	4,14
SL0058	<i>citS</i>	Citrate-sodium symporter	-1,32	-1,22	3,02
SL0059	<i>citC</i>	[Citrate [pro-3S]-lyase] ligase	-1,20	-1,15	1,87
SL0060	<i>citD2</i>	Citrate lyase acyl carrier protein 2	-1,07	-1,12	1,73
SL0061	<i>citE</i>	Citrate lyase subunit beta	1,11	1,07	7,85
SL0062	<i>citF</i>	Citrate lyase alpha chain	1,37	1,12	5,71
SL0063	<i>citX</i>	Apo-citrate lyase phosphoribosyl-dephospho-CoA	1,02	-1,24	2,72
SL0064	<i>citG1</i>	Probable 2-(5"-triphosphoribosyl)-3"-dephosphococ	1,12	1,15	2,58
SL0065	<i>dapB</i>	Dihydrodipicolinate reductase	-1,24	1,02	-1,36
SL0066	-	Hypothetical	1,03	-1,28	-4,48
SL0067	<i>carA</i>	Carbamoyl-phosphate synthase small chain	-1,14	1,07	-1,37
SL0068	<i>carB</i>	Carbamoyl-phosphate synthase large chain	1,02	1,13	2,03
SL0069	<i>caiF</i>	Transcriptional activatory protein caiF	1,67	1,77	-1,26
SL0070	<i>caiE</i>	Carnitine operon protein caiE	1,75	1,12	1,38
SL0071	<i>caiD</i>	Carnitiny-CoA dehydratase	1,28	-1,04	2,23
SL0072	<i>caiC</i>	Probable crotonobetaine/carnitine-CoA ligase	1,28	1,02	-1,10
SL0073	<i>caiB</i>	Crotonobetainyl-CoA:carnitine CoA-transferase	1,39	-1,05	1,15
SL0074	<i>caiA</i>	Crotonobetainyl-CoA dehydrogenase	1,51	-1,22	1,33
SL0075	<i>caiT</i>	L-carnitine/gamma-butyrobetaine antiporter	1,15	-1,03	1,83
SL0076	<i>fixA</i>	Protein fixA	1,10	-1,07	1,64
SL0077	<i>fixB</i>	Protein fixB	1,38	1,19	1,73
SL0078	<i>fixC</i>	Protein fixC	1,35	1,10	1,71
SL0079	<i>fixX</i>	Ferredoxin-like protein fixX	1,50	-1,01	1,39
SL0080	<i>yaaU</i>	Putative metabolite transport protein yaaU	-1,00	1,00	-1,06
SL0081	<i>ygdl</i>	Uncharacterized lipoprotein ygdl	-1,38	1,04	-2,13
SL0082	-	Hypothetical	-1,34	1,37	-1,88
SL0083	<i>yhcN</i>	Hypothetical	-1,00	-1,12	1,61
SL0084	<i>gidJ</i>	Sulfatase	-1,07	1,03	1,35
SL0085	<i>caiD</i>	Hypothetical Protein caiD	1,44	1,28	1,84
SL0086	<i>kefF</i>	Glutathione-regulated potassium-efflux system ancillary protein kefF	1,02	-1,23	-1,15
SL0087	<i>kefC</i>	Glutathione-regulated potassium-efflux system protein kefC	1,10	1,22	1,62
SL0088	<i>folA</i>	Dihydrofolate reductase	-1,03	1,00	-1,63
SL0089	<i>apaH</i>	Bis(5"-nucleosyl)-tetraphosphatase, symmetrical	1,15	-1,16	1,04

Tabla Suplementaria 1Diferencia de expresión de todos los genes de SV5015 en las cepas mutantes *greA*, *greB* y *greAgreB*, respecto a la cepa WT

ID	gene	Description	<i>greA</i> vs WT	<i>greB</i> vs WT	<i>greAgreB</i> vs WT
SL0090	<i>apaG</i>	Protein ApaG	1,04	-1,15	-1,16
SL0091	<i>rsmA</i>	Ribosomal RNA small subunit methyltransferase A	-1,04	-1,11	-1,61
SL0092	<i>pdxA1</i>	4-hydroxythreonine-4-phosphate dehydrogenase 1	1,04	-1,17	-1,52
SL0093	<i>surA</i>	Chaperone surA	1,07	-1,07	-1,17
SL0094	<i>lptD</i>	LPS-assembly protein lptD	-1,06	-1,07	-1,25
SL0095	<i>djlA</i>	DnaJ-like protein djlA	-1,08	-1,10	-1,89
SL0096	<i>rluA</i>	Ribosomal large subunit pseudouridine synthase A	2,03	1,02	2,39
SL0097	<i>rapA</i>	RNA polymerase-associated protein rapA	1,91	-1,10	1,74
SL0098	<i>polB</i>	DNA polymerase II	-1,01	-1,09	-1,17
SL0099	<i>yggQ</i>	Hypothetical	1,26	1,05	-1,46
SL0100	-	Hypothetical	1,09	1,08	-1,24
SL0101	<i>araD</i>	L-ribulose-5-phosphate 4-epimerase	1,06	-1,14	1,65
SL0102	<i>araA</i>	L-arabinose isomerase	1,07	-1,06	2,50
SL0103	<i>araB</i>	Ribulokinase	1,02	-1,03	3,31
SL0104	<i>araC</i>	Arabinose operon regulatory protein	1,10	-1,07	10,58
SL0105	<i>yabl</i>	Inner membrane protein yabl	1,06	1,01	-1,17
SL0106	<i>thiQ</i>	Thiamine import ATP-binding protein ThiQ	1,10	-1,16	1,19
SL0107	<i>thiP</i>	Thiamine transport system permease protein thiP	-1,01	-1,07	1,13
SL0108	-	Hypothetical Protein SL0108	-1,08	-1,05	-1,49
SL0109	<i>sgrR</i>	HTH-type transcriptional regulator sgrR	1,10	1,09	1,28
SL0110	<i>leuD1</i>	3-isopropylmalate dehydratase small subunit 1	1,18	-1,08	2,28
SL0111	<i>leuC1</i>	3-isopropylmalate dehydratase large subunit 1	1,24	1,05	3,98
SL0112	<i>leuB</i>	3-isopropylmalate dehydrogenase	1,21	-1,08	3,10
SL0113	<i>leuA</i>	2-isopropylmalate synthase	1,12	1,12	1,81
SL0114	<i>leuL</i>	Hypothetical Protein leuL	1,02	1,37	1,14
SL0115	<i>leuO</i>	Probable HTH-type transcriptional regulator leuO	-1,27	1,23	-2,01
SL0116	<i>ilvI</i>	Acetolactate synthase isozyme 3 large subunit	1,01	-1,24	1,66
SL0117	<i>ilvH</i>	Acetolactate synthase isozyme 3 small subunit	-1,16	-1,05	1,43
SL0118	<i>fruR</i>	Fructose repressor	-1,13	-1,01	-1,58
SL0119	<i>mraZ</i>	Protein mraZ	1,12	1,13	-1,72
SL0120	<i>rsmH</i>	Ribosomal RNA small subunit methyltransferase H	1,04	1,01	-1,83
SL0121	<i>ftsL</i>	Cell division protein ftsL	1,06	1,04	-1,34
SL0122	<i>ftsI</i>	Peptidoglycan synthase ftsI	1,07	1,04	-1,35
SL0123	<i>murE</i>	UDP-N-acetylmuramoyl-L-alanyl-D-glutamate--2,6-diaminopimelate ligase	1,20	-1,07	-1,61
SL0124	<i>murF</i>	UDP-N-acetylmuramoyl-tripeptide--D-alanyl-D-alanine ligase	1,20	1,07	-1,46
SL0125	<i>mraY</i>	Phospho-N-acetylmuramoyl-pentapeptide-transferase	1,12	-1,09	-1,81
SL0126	<i>murD</i>	UDP-N-acetylmuramoylalanine--D-glutamate ligase	1,14	1,06	-1,26

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Diferencia de expresión de todos los genes de SV5015 en las cepas mutantes *greA*, *greB* y *greAgreB*, respecto a la cepa WT

ID	gene	Description	<i>greA</i> vs WT	<i>greB</i> vs WT	<i>greAgreB</i> vs WT
SL0127	<i>ftsW</i>	Cell division protein ftsW	1,16	1,07	-1,50
SL0128	<i>murG</i>	UDP-N-acetylglucosamine--N-acetylmuramyl-(pentapeptide) pyrophosphoryl-undecaprenol N-acetylglucosamine transferase	1,09	-1,07	-1,48
SL0129	<i>murC</i>	UDP-N-acetylmuramate--L-alanine ligase	1,10	1,01	-1,58
SL0130	<i>ddlB</i>	D-alanine--D-alanine ligase B	-1,16	-1,06	-1,48
SL0131	<i>ftsQ</i>	Cell division protein ftsQ	1,06	1,03	-1,32
SL0132	<i>ftsA</i>	Cell division protein ftsA	1,02	-1,03	-1,78
SL0133	<i>ftsZ</i>	Cell division protein ftsZ	-1,00	1,08	1,03
SL0134	<i>lpxC</i>	UDP-3-O-[3-hydroxymyristoyl] N-acetylglucosamine deacetylase	-1,08	1,11	-1,84
SL0135	<i>secM</i>	Secretion monitor	1,29	1,10	1,09
SL0136	<i>secA</i>	Protein translocase subunit secA	1,45	1,05	1,93
SL0137	<i>mutT</i>	Mutator mutT protein	1,11	-1,08	1,20
SL0138	<i>yacG</i>	UPF0243 zinc-binding protein yacG	-1,09	-1,01	1,04
SL0139	<i>yacF</i>	UPF0289 protein CKO_03274	-1,28	-1,14	-1,49
SL0140	<i>coaE</i>	Dephospho-CoA kinase	-1,16	1,05	-1,78
SL0141	<i>guaC</i>	GMP reductase	1,37	-1,09	1,22
SL0142	<i>hofC</i>	Protein transport protein hofC	1,16	1,15	1,01
SL0143	<i>hofB</i>	Protein transport protein hofB	-1,00	-1,08	2,18
SL0144	<i>ppdD</i>	Prepilin peptidase-dependent protein D	-1,04	1,06	2,04
SL0145	<i>nadC</i>	Nicotinate-nucleotide pyrophosphorylase [carboxylating]	1,00	-1,08	-1,77
SL0146	<i>ampD</i>	1,6-anhydro-N-acetylmuramyl-L-alanine amidase AmpD	-1,00	1,15	1,20
SL0147	<i>ampE</i>	Protein AmpE	-1,10	1,09	1,08
SL0148	-	Alpha-N-arabinofuranosidase 2	1,03	1,19	1,43
SL0149	<i>yicJ</i>	Inner membrane symporter yicJ	1,11	1,08	1,53
SL0150	<i>aroP</i>	Aromatic amino acid transport protein AroP	1,04	-1,07	2,45
SL0151	<i>pdhR</i>	Pyruvate dehydrogenase complex repressor	-1,06	-1,15	-2,74
SL0152	<i>aceE</i>	Pyruvate dehydrogenase E1 component	1,00	-1,19	1,91
SL0153	<i>aceF</i>	Dihydrolipoyllysine-residue acetyltransferase component of pyruvate dehydrogenase complex	1,13	-1,02	3,97
SL0154	<i>lpdA</i>	Dihydrolipoyl dehydrogenase	1,13	-1,04	2,79
SL0155	-	Hypothetical	1,09	1,62	-1,11
SL0156	-	Hypothetical	-1,01	-1,32	1,22
SL0157	<i>yacH</i>	Uncharacterized protein yacH	1,01	-1,02	-1,36
SL0158	<i>yacH</i>	Uncharacterized protein yacH	-1,14	1,22	-1,27
SL0159	<i>acnB</i>	Aconitate hydratase 2	1,07	-1,21	3,83
SL0160	-	Restriction Endonuclease	-1,11	-1,47	-2,18
SL0161	<i>yacL</i>	UPF0231 protein yacL	1,28	1,31	2,93
SL0162	<i>kdgT1</i>	2-keto-3-deoxygluconate permease 1	1,26	1,09	2,83
SL0163	<i>ygbK</i>	Uncharacterized protein HI_1011	1,23	-1,06	4,11
SL0164	<i>pdxA2</i>	4-hydroxythreonine-4-phosphate dehydrogenase 2	1,36	1,07	2,76
SL0165	<i>ygbI</i>	Uncharacterized HTH-type transcriptional regulator ygbI	1,10	-1,06	1,50

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Diferencia de expresión de todos los genes de SV5015 en las cepas mutantes *greA*, *greB* y *greAgreB*, respecto a la cepa WT

ID	gene	Description	<i>greA</i> vs WT	<i>greB</i> vs WT	<i>greAgreB</i> vs WT
SL0166	<i>speD</i>	S-adenosylmethionine decarboxylase proenzyme	-1,06	-1,33	-1,19
SL0167	<i>speE</i>	Spermidine synthase	-1,05	-1,18	-1,09
SL0168	<i>yacC</i>	Uncharacterized protein yacC	1,12	1,01	-1,74
SL0169	<i>cueO</i>	Blue copper oxidase cueO	1,02	-1,05	1,19
SL0170	<i>gcd</i>	Quinoprotein glucose dehydrogenase	-1,22	-1,09	1,72
SL0171	<i>hpt</i>	Hypoxanthine phosphoribosyltransferase	-1,02	1,03	-1,94
SL0172	<i>can</i>	Carbonic anhydrase 2	-1,06	-1,07	-1,38
SL0173	<i>yadG</i>	Uncharacterized ABC transporter ATP-binding protein yadG	1,04	-1,19	-1,05
SL0174	<i>yadH</i>	Inner membrane transport permease yadH	1,04	-1,17	1,19
SL0175	<i>lpfD</i>	Protein lpfD	1,32	1,03	1,20
SL0176	<i>lpfC</i>	Outer membrane usher protein lpfC	-1,08	-1,29	1,24
SL0177	<i>myfB</i>	Chaperone protein myfB	1,09	1,02	-1,21
SL0178	<i>fimF</i>	Fimbrial subunit type 1	1,05	-1,03	3,27
SL0179	<i>yadI</i>	Putative phosphotransferase enzyme IIA component yadI	1,54	1,63	1,28
SL0180	<i>yadE</i>	Uncharacterized protein yadE	-1,14	1,11	-2,44
SL0181	<i>panD</i>	Aspartate 1-decarboxylase	1,07	-1,12	-1,18
SL0182	<i>panC</i>	Pantothenate synthetase	-1,10	-1,29	-1,52
SL0183	<i>panB</i>	3-methyl-2-oxobutanoate hydroxymethyltransferase	1,18	1,27	-1,33
SL0184	<i>folK</i>	2-amino-4-hydroxy-6-hydroxymethyldihydropteridine pyrophosphokinase	1,08	1,01	-1,45
SL0185	<i>pcnB</i>	Poly(A) polymerase	-1,08	-1,04	-2,92
SL0186	<i>gluQ</i>	Glutamyl-Q tRNA(Asp) synthetase	-1,27	-1,04	-3,74
SL0187	<i>dksA</i>	DnaK suppressor protein	-1,08	1,05	1,21
SL0188	<i>sfsA</i>	Sugar fermentation stimulation protein A	-1,01	-1,18	1,04
SL0189	<i>ligT</i>	2'-5'-RNA ligase	1,01	-1,29	1,17
SL0190	<i>hrpB</i>	ATP-dependent RNA helicase hrpB	1,08	-1,05	1,07
SL0191	<i>mrcB</i>	Penicillin-binding protein 1B	1,13	1,15	1,29
SL0192	<i>fhuA</i>	Ferrichrome-iron receptor	-1,04	1,41	-2,51
SL0193	<i>fhuC</i>	Iron(3+)-hydroxamate import ATP-binding protein fhuC	-1,01	1,45	-1,42
SL0194	<i>fhuD</i>	Iron(3+)-hydroxamate-binding protein fhuD	1,23	1,59	-1,73
SL0195	<i>fhuB</i>	Iron(3+)-hydroxamate import system permease protein fhuB	-1,06	-1,19	-1,15
SL0196	<i>smfA</i>	Fimbria A protein	1,28	-1,06	3,38
SL0197	<i>yfcU</i>	Putative outer membrane usher protein yfcU	-1,10	-1,05	-1,11
SL0198	<i>yfcS</i>	Uncharacterized fimbrial chaperone yfcS	1,18	-1,13	1,31
SL0199	<i>yfcR</i>	Uncharacterized protein yfcR	1,14	1,01	1,30
SL0200	<i>yfcQ</i>	Uncharacterized fimbrial-like protein yfcQ	1,21	-1,13	-1,04
SL0201	<i>yfcP</i>	Uncharacterized fimbrial-like protein yfcP	1,04	-1,15	1,16
SL0202	<i>yadU</i>	Uncharacterized protein yadU	1,40	1,16	1,28
SL0203	<i>hemL</i>	Glutamate-1-semialdehyde 2,1-aminomutase	1,17	1,05	1,39
SL0204	<i>clcA</i>	H(+)/Cl(-) exchange transporter clcA	1,08	-1,01	-1,60
SL0205	<i>erpA</i>	Iron-sulfur cluster insertion protein erpA	-1,03	1,00	-1,55

Tabla Suplementaria 1

Diferencia de expresión de todos los genes de SV5015 en las cepas mutantes *greA*, *greB* y *greAgreB*, respecto a la cepa WT

ID	gene	Description	<i>greA</i> vs WT	<i>greB</i> vs WT	<i>greAgreB</i> vs WT
SL0206	<i>yadS</i>	UPF0126 inner membrane protein yadS	1,19	1,16	-1,37
SL0207	<i>btuF</i>	Vitamin B12-binding protein	-1,10	-1,42	-1,54
SL0208	<i>mtnN</i>	5'-methylthioadenosine/S-adenosylhomocysteine nucleosidase	1,10	-1,12	1,08
SL0209	<i>dgt</i>	Deoxyguanosinetriphosphate triphosphohydrolase	-1,16	-1,07	1,22
SL0210	<i>degP</i>	Protease do	-1,15	-1,21	1,54
SL0211	<i>cdaR</i>	Carbohydrate diacid regulator	-1,03	-1,04	4,32
SL0212	<i>yaeH</i>	UPF0325 protein ESA_03178	-1,12	-1,14	3,29
SL0213	<i>shiA</i>	Shikimate transporter	-1,19	1,05	-2,38
SL0214	<i>dapD</i>	2,3,4,5-tetrahydropyridine-2,6-dicarboxylate N-succinyltransferase	-1,01	-1,12	1,20
SL0215	<i>glnD</i>	[Protein-PII] uridylyltransferase	1,12	1,03	1,33
SL0216	<i>map</i>	Methionine aminopeptidase	1,05	-1,16	-1,26
SL0217	<i>rpsB</i>	30S ribosomal protein S2	-1,12	-1,08	-1,19
SL0218	<i>tsf</i>	Elongation factor Ts	1,05	-1,10	1,18
SL0219	<i>pyrH</i>	Uridylate kinase	1,14	-1,16	-1,05
SL0220	<i>frr</i>	Ribosome-recycling factor	1,02	-1,11	-1,14
SL0221	<i>dxr</i>	1-deoxy-D-xylulose 5-phosphate reductoisomerase	-1,00	-1,05	-2,21
SL0222	<i>uppS</i>	Undecaprenyl pyrophosphate synthase	-1,06	1,22	-2,18
SL0223	<i>cdsA</i>	Phosphatidate cytidyltransferase	1,14	1,07	-1,82
SL0224	<i>rseP</i>	Regulator of sigma E protease	-1,00	-1,06	-1,72
SL0225	<i>yaeT</i>	Outer membrane protein assembly factor yaeT	1,03	-1,07	1,15
SL0226	<i>skp</i>	Chaperone protein skp	-1,09	-1,29	-1,08
SL0227	<i>lpxD</i>	UDP-3-O-[3-hydroxymyristoyl] glucosamine N-acyltransferase	-1,12	-1,32	-1,68
SL0228	<i>fabZ</i>	(3R)-hydroxymyristoyl-[acyl-carrier-protein] dehydratase	-1,07	-1,06	-1,63
SL0229	<i>lpxA</i>	Acyl-[acyl-carrier-protein]-UDP-N-acetylglucosamine O-acyltransferase	-1,00	-1,12	-1,40
SL0230	<i>lpxB</i>	Lipid-A-disaccharide synthase	1,05	-1,20	-1,51
SL0231	<i>rnhB</i>	Ribonuclease HII	1,22	-1,26	-1,17
SL0232	<i>dnaE</i>	DNA polymerase III subunit alpha	1,23	-1,04	1,30
SL0233	<i>accA</i>	Acetyl-coenzyme A carboxylase carboxyl transferase subunit alpha	1,03	-1,02	-1,03
SL0234	-	Chitinase	1,07	1,01	1,25
SL0235	<i>ldcC</i>	Lysine decarboxylase, constitutive	1,13	1,05	1,10
SL0236	<i>yaeR</i>	Uncharacterized protein yaeR	1,09	-1,02	1,59
SL0237	<i>tilS</i>	tRNA(Ile)-lysine synthase	1,08	-1,02	-1,07
SL0238	<i>rof</i>	Protein rof	1,04	1,10	1,31
SL0239	<i>yaeP</i>	UPF0253 protein CKO_03176	1,09	1,29	1,59
SL0240	<i>yaeQ</i>	Uncharacterized protein yaeQ	-1,15	-1,01	-1,64
SL0241	<i>yaeJ</i>	Uncharacterized protein yaeJ	-1,22	-1,07	-1,74
SL0242	<i>nlpE</i>	Lipoprotein nlpE	1,09	1,07	-1,78
SL0243	<i>proS</i>	Prolyl-tRNA synthetase	-1,07	-1,13	-1,52
SL0244	<i>yaeB</i>	UPF0066 protein yaeB	1,15	1,05	-2,27
SL0245	<i>rscF</i>	Protein rscF	1,00	-1,08	-1,52
SL0246	<i>metQ</i>	D-methionine-binding lipoprotein metQ	-1,02	1,01	1,49
SL0247	<i>metI</i>	D-methionine transport system permease protein metI	-1,07	-1,27	-1,35

Tabla Suplementaria 1

Diferencia de expresión de todos los genes de SV5015 en las cepas mutantes *greA*, *greB* y *greAgreB*, respecto a la cepa WT

ID	gene	Description	<i>greA</i> vs WT	<i>greB</i> vs WT	<i>greAgreB</i> vs WT
SL0248	<i>metN1</i>	Methionine import ATP-binding protein MetN 1	1,06	-1,24	-1,87
SL0249	<i>gmhB</i>	D,D-heptose 1,7-bisphosphate phosphatase	-1,03	-1,16	-1,31
SL0250	<i>dkgB</i>	2,5-diketo-D-gluconic acid reductase B	1,07	-1,10	1,91
SL0251	<i>yafC</i>	Uncharacterized HTH-type transcriptional regulator yafC	1,35	1,14	1,45
SL0252	<i>ytbD</i>	Uncharacterized MFS-type transporter ytbD	1,11	-1,14	1,37
SL0253	<i>yafD</i>	UPF0294 protein Ent638_0743	1,17	-1,07	1,33
SL0254	<i>yafE</i>	Uncharacterized protein yafE	1,18	1,01	1,09
SL0255	<i>mltD</i>	Membrane-bound lytic murein transglycosylase D	-1,61	1,08	-6,32
SL0256	<i>gloB</i>	Hydroxyacylglutathione hydrolase	-1,07	-1,23	1,42
SL0257	<i>yafS</i>	Uncharacterized protein yafS	1,10	-1,03	1,20
SL0258	<i>rnhA</i>	Ribonuclease H	1,12	1,13	-1,42
SL0259	<i>dnaQ</i>	DNA polymerase III subunit epsilon	1,14	1,04	1,09
SL0260	-	Hypothetical	1,24	1,06	1,05
SL0261	-	Hypothetical	1,12	1,00	1,45
SL0262	-	Hypothetical	1,09	-1,00	1,24
SL0263	-	Hypothetical	1,11	-1,23	1,73
SL0264	-	Virulence Protein SciE Type	1,06	-1,17	1,86
SL0265	-	Cytoplasmic Protein	1,19	1,05	2,97
SL0266	<i>clpB</i>	Chaperone protein clpB	1,15	-1,36	3,43
SL0267	-	Hypothetical	1,22	1,04	3,82
SL0268	-	Hypothetical	1,09	-1,15	2,77
SL0269	-	Hypothetical Protein SL0269	1,14	1,01	1,44
SL0270	-	Cytoplasmic Protein	1,11	-1,00	1,02
SL0271	<i>hcp1</i>	Protein hcp1	1,14	1,07	1,85
SL0272	-	Cytoplasmic Protein	1,22	1,24	1,18
SL0273	-	Hypothetical	1,08	1,06	1,13
SL0274	<i>hcp1</i>	Protein hcp1	1,27	-1,27	-1,09
SL0275	-	Hypothetical	1,34	-1,06	1,02
SL0276	-	Hypothetical	1,12	-1,02	1,35
SL0277	<i>ytxE</i>	Uncharacterized 24.6 kDa protein in <i>ccpA</i> 3'region	1,07	1,24	1,55
SL0278	-	Hypothetical	1,62	1,42	1,64
SL0279	-	Hypothetical	1,03	1,10	1,07
SL0280	-	Hypothetical	1,27	1,04	1,88
SL0281	-	Cytoplasmic Protein	-1,09	-1,24	1,64
SL0282	-	Hypothetical	1,10	-1,17	1,66
SL0283	-	Hypothetical	1,05	-1,05	-1,11
SL0284	-	Hypothetical	1,09	-1,12	1,91
SL0285	-	Hypothetical	1,13	-1,20	1,10
SL0286	<i>rhsE</i>	Putative protein rhsE	-1,09	-1,10	-1,32
SL0287	<i>rhsE</i>	Putative protein rhsE	-1,02	1,22	-1,18
SL0288	-	Cytoplasmic Protein	1,12	1,14	1,52
SL0289	-	Phosphotriesterase	-1,00	-1,05	1,02
SL0290	<i>yjiW</i>	Hypothetical	1,12	1,09	-1,13
SL0291	-	Cytoplasmic Protein	1,14	1,47	1,14
SL0292	-	Hypothetical	1,16	1,29	-1,23

Tabla Suplementaria 1Diferencia de expresión de todos los genes de SV5015 en las cepas mutantes *greA*, *greB* y *greAgreB*, respecto a la cepa WT

ID	gene	Description	<i>greA</i> vs WT	<i>greB</i> vs WT	<i>greAgreB</i> vs WT
SL0293	-	Transposase	-1,05	1,26	1,05
SL0294	<i>yagA</i>	Insertion element IS407 uncharacterized 31.7 kDa protein	-1,11	-1,00	1,10
SL0295	-	Lipoprotein	-1,08	1,22	-1,63
SL0296	<i>aggD</i>	Chaperone protein AggD	1,20	1,07	-1,01
SL0297	<i>afaC</i>	Outer membrane usher protein AfaC	1,23	1,04	1,18
SL0298	-	Invasin Protein AfaD	1,15	1,07	1,14
SL0299	<i>yxkH</i>	Putative polysaccharide deacetylase yxkH	-1,28	1,01	-1,48
SL0300	<i>sinR</i>	Probable HTH-type transcriptional regulator sinR	-1,68	-1,43	-2,91
SL0301	-	Hypothetical	-1,19	1,22	-1,64
SL0302	-	Hypothetical	-1,47	1,23	-1,26
SL0303	-	Hypothetical	-1,04	1,09	1,11
SL0304	<i>yafV</i>	UPF0012 hydrolase yafV	1,05	1,10	1,98
SL0305	<i>fadE</i>	Acyl-coenzyme A dehydrogenase	-1,34	1,19	9,79
SL0306	<i>gmhA</i>	Phosphoheptose isomerase	1,03	-1,01	1,09
SL0307	<i>yafJ</i>	Putative glutamine amidotransferase yafJ	-1,01	-1,18	-1,10
SL0308	<i>yafK</i>	Putative L,D-transpeptidase YafK	1,10	1,11	-1,42
SL0309	<i>dinB</i>	DNA polymerase IV	1,05	1,08	1,26
SL0310	<i>ykfJ</i>	Uncharacterized protein ykfJ	-1,37	-1,03	-2,01
SL0311	<i>prfH</i>	Putative peptide chain release factor homolog	-1,04	-1,20	-1,91
SL0312	<i>pepD</i>	Aminoacyl-histidine dipeptidase	1,02	-1,14	1,31
SL0313	<i>gpt</i>	Xanthine phosphoribosyltransferase	1,09	1,06	-2,59
SL0314	<i>frsA</i>	Esterase frsA	1,13	1,20	1,61
SL0315	<i>crl</i>	Sigma factor-binding protein crl	1,19	1,17	2,15
SL0316	<i>phoE</i>	Outer membrane pore protein E	1,24	1,23	2,05
SL0317	<i>proB</i>	Glutamate 5-kinase	1,01	-1,26	-1,42
SL0318	<i>proA</i>	Gamma-glutamyl phosphate reductase	1,01	-1,26	1,46
SL0319	<i>insF1</i>	Transposase insF for insertion sequence IS3A	1,08	-1,10	1,51
SL0320	-	Glycerol Dehydratase Reactivation Factor Large Subunit	-1,12	-1,06	-1,23
SL0321	-	Glycerol Dehydratase Reactivation Factor Large Subunit	1,04	1,23	-1,17
SL0322	<i>yoaC</i>	Uncharacterized protein yoaC	1,20	1,21	1,81
SL0323	<i>ynfM</i>	Inner membrane transport protein ynfM	-1,19	-1,26	1,29
SL0324	<i>leuC2</i>	3-isopropylmalate dehydratase large subunit 2	-1,12	-1,33	1,41
SL0325	<i>leuD2</i>	3-isopropylmalate dehydratase small subunit 2	1,18	-1,21	-1,07
SL0326	<i>yisK</i>	Uncharacterized protein yisK	1,05	-1,20	-1,26
SL0327	<i>dehH1</i>	Haloacetate dehalogenase H-1	1,09	1,10	1,31
SL0328	<i>ttdR</i>	HTH-type transcriptional activator ttdR	1,12	1,05	1,13
SL0329	-	Hypothetical	-1,38	-1,10	-1,74
SL0330	-	Hypothetical	1,04	1,00	1,01
SL0331	<i>mrkB</i>	Chaperone protein mrkB	-1,13	-1,06	-1,12
SL0332	-	Hypothetical	1,14	-1,36	1,07
SL0333	<i>hifC</i>	Outer membrane usher protein hifC	1,17	1,17	-1,05
SL0334	<i>ecpD</i>	Chaperone protein ecpD	-1,46	-1,32	1,18

Tabla Suplementaria 1

Diferencia de expresión de todos los genes de SV5015 en las cepas mutantes *greA*, *greB* y *greAgreB*, respecto a la cepa WT

ID	gene	Description	<i>greA</i> vs WT	<i>greB</i> vs WT	<i>greAgreB</i> vs WT
SL0335	<i>F17a-A</i>	F17 fimbrial protein	-1,02	-1,06	-1,02
SL0336	-	Transmembrane Regulator	-1,37	-1,27	-3,98
SL0337	-	Periplasmic Protein	-1,33	-1,26	-2,23
SL0338	<i>rtn</i>	Protein rtn	-1,13	1,01	1,11
SL0339	-	Transmembrane Regulator	-1,15	1,05	1,28
SL0340	-	Hypothetical	-1,15	1,07	1,19
SL0341	<i>ail</i>	Attachment invasion locus protein	-1,07	-1,08	-1,19
SL0342	-	Response Regulator	1,13	-1,09	-1,38
SL0343	-	Hypothetical	1,10	-1,03	-1,84
SL0344	<i>yjel</i>	Uncharacterized protein yjel	1,27	1,26	3,73
SL0345	<i>oprM</i>	Outer membrane protein oprM	1,10	1,09	1,52
SL0346	<i>bepE</i>	Efflux pump membrane transporter BepE	1,15	1,05	1,76
SL0347	<i>mtrC</i>	Membrane fusion protein mtrC	-1,03	-1,30	1,36
SL0348	<i>actP</i>	Copper-transporting P-type ATPase	1,08	-1,11	4,15
SL0349	<i>hmrR</i>	HTH-type transcriptional regulator hmrR	1,16	1,30	2,01
SL0350	-	Conserved Hypothetical Protein	1,36	-1,02	2,36
SL0351	<i>yjhB</i>	Putative metabolite transport protein yjhB	-1,16	-1,13	2,18
SL0352	<i>mod</i>	Type III restriction-modification system StyLTI enzyme mod	-1,09	-1,12	1,15
SL0353	<i>res</i>	Type III restriction-modification system StyLTI enzyme res	1,14	1,07	2,64
SL0354	-	Hypothetical	-1,09	1,27	-1,59
SL0355	<i>cydA</i>	Cytochrome d ubiquinol oxidase subunit 1	-1,09	1,10	-1,82
SL0356	<i>appB</i>	Cytochrome bd-II oxidase subunit 2	1,10	1,07	1,19
SL0357	-	Hypothetical	1,07	1,01	1,18
SL0358	<i>pchR</i>	Regulatory protein pchR	1,16	1,19	-1,61
SL0359	<i>foxA</i>	Ferrioxamine B receptor	1,47	1,21	-1,08
SL0360	<i>yahN</i>	Uncharacterized membrane protein yahN	1,41	1,47	3,45
SL0361	<i>yahO</i>	Uncharacterized protein yahO	1,05	1,13	1,93
SL0362	<i>prpR</i>	Propionate catabolism operon regulatory protein	1,09	-1,04	2,42
SL0363	<i>prpB</i>	Methylisocitrate lyase	1,04	1,27	2,74
SL0364	<i>prpC</i>	2-methylcitrate synthase	-1,05	1,08	5,33
SL0365	<i>prpD</i>	2-methylcitrate dehydratase	1,05	-1,05	6,64
SL0366	<i>prpE</i>	Propionate--CoA ligase	1,23	-1,12	4,91
SL0367	<i>hemB</i>	Delta-aminolevulinic acid dehydratase	1,11	-1,02	-1,15
SL0368	<i>yaiT</i>	Uncharacterized protein yaiT	-1,07	1,07	-1,07
SL0369	<i>yaiV</i>	Uncharacterized protein yaiV	-1,01	1,14	-1,73
SL0370	<i>ampH</i>	Penicillin-binding protein AmpH	1,09	-1,05	-1,25
SL0371	<i>sbmA</i>	Protein sbmA	1,23	-1,04	-2,98
SL0372	<i>yaiW</i>	Uncharacterized protein yaiW	1,01	1,11	-2,53
SL0373	<i>yaiY</i>	Inner membrane protein yaiY	1,02	1,35	-1,95
SL0374	<i>yaiZ</i>	Uncharacterized protein yaiZ	1,39	1,18	2,44
SL0375	<i>ddlA</i>	D-alanine--D-alanine ligase A	1,06	-1,08	-1,04
SL0376	-	Extensin Family Protein	1,14	1,21	4,71
SL0377	<i>mdtG</i>	Multidrug resistance protein mdtG	1,08	-1,08	-2,63
SL0378	<i>iraP</i>	Anti-adaptor protein iraP	-1,20	1,30	1,32
SL0379	<i>psiF</i>	Phosphate starvation-inducible protein psiF	1,16	1,43	1,81
SL0380	<i>adrA</i>	Protein AdrA	1,05	1,02	1,03

Tabla Suplementaria 1

Diferencia de expresión de todos los genes de SV5015 en las cepas mutantes *greA*, *greB* y *greAgreB*, respecto a la cepa WT

ID	gene	Description	<i>greA</i> vs WT	<i>greB</i> vs WT	<i>greAgreB</i> vs WT
SL0381	<i>proC</i>	Pyrroline-5-carboxylate reductase	1,14	1,17	1,69
SL0382	<i>yail</i>	UPF0178 protein yail	-1,15	-1,06	-2,28
SL0383	<i>aroL</i>	Shikimate kinase 2	1,08	1,12	-1,44
SL0384	<i>yaiA</i>	Uncharacterized protein yaiA	-1,02	1,05	-1,36
SL0385	<i>aroM</i>	Protein AroM	-1,05	1,19	1,12
SL0386	<i>yaiE</i>	UPF0345 protein Ent638_0862	1,09	1,01	1,08
SL0387	<i>rdgC</i>	Recombination-associated protein rdgC	1,02	-1,04	-2,81
SL0388	<i>mak</i>	Fructokinase	1,01	-1,11	1,43
SL0389	<i>araJ</i>	Protein AraJ	1,21	1,06	1,25
SL0390	<i>sbcC</i>	Nuclease sbcCD subunit C	1,35	1,20	1,54
SL0391	<i>sbcD</i>	Nuclease sbcCD subunit D	1,16	1,08	-2,20
SL0392	<i>phoB</i>	Phosphate regulon transcriptional regulatory protein phoB	1,23	1,26	-1,43
SL0393	<i>phoR</i>	Phosphate regulon sensor protein phoR	1,52	1,35	-1,14
SL0394	<i>brnQ</i>	Branched-chain amino acid transport system 2 carrier protein	1,10	1,00	-1,30
SL0395	<i>proY</i>	Proline-specific permease proY	1,33	1,01	-2,05
SL0396	<i>malZ</i>	Maltodextrin glucosidase	-1,28	-1,40	-1,05
SL0397	<i>ahpC</i>	Probable peroxiredoxin	-1,02	1,14	-2,76
SL0398	<i>acpH</i>	Acyl carrier protein phosphodiesterase	1,08	1,10	-1,44
SL0399	<i>queA</i>	S-adenosylmethionine:tRNA ribosyltransferase-isomerase	-1,10	1,07	-2,69
SL0400	<i>tgt</i>	Queuine tRNA-ribosyltransferase	-1,13	-1,03	-1,43
SL0401	<i>yajC</i>	UPF0092 membrane protein yajC	-1,08	-1,11	-1,06
SL0402	<i>secD</i>	Protein-export membrane protein secD	1,00	-1,17	-1,54
SL0403	<i>secF</i>	Protein-export membrane protein secF	-1,00	-1,24	-1,07
SL0404	-	Glyoxalase/Bleomycin Resistance Protein/Dioxygenase	1,08	-1,03	-1,12
SL0405	<i>yobV</i>	Uncharacterized HTH-type transcriptional regulator yobV	1,22	-1,21	-1,56
SL0406	<i>yajD</i>	Uncharacterized protein yajD	-1,02	1,01	-1,42
SL0407	<i>tsx</i>	Nucleoside-specific channel-forming protein tsx	-1,09	-1,17	1,90
SL0408	<i>yajI</i>	Uncharacterized lipoprotein yajI	1,03	1,19	-1,41
SL0409	<i>nrdR</i>	Transcriptional repressor nrdR	1,04	-1,01	1,33
SL0410	<i>ribD</i>	Riboflavin biosynthesis protein ribD	-1,06	1,06	-1,16
SL0411	<i>ribH</i>	6,7-dimethyl-8-ribityllumazine synthase	1,02	1,07	1,27
SL0412	<i>nusB</i>	N utilization substance protein B homolog	-1,01	1,15	1,45
SL0413	<i>thiL</i>	Thiamine-monophosphate kinase	-1,04	-1,04	-1,04
SL0414	<i>pgpA</i>	Phosphatidylglycerophosphatase A	1,03	-1,11	-1,04
SL0415	<i>yajO</i>	Uncharacterized oxidoreductase yajO	1,20	1,41	2,32
SL0416	<i>dxs</i>	1-deoxy-D-xylulose-5-phosphate synthase	1,19	1,11	-1,64
SL0417	<i>ispA</i>	Geranyltranstransferase	1,05	-1,01	-1,64
SL0418	<i>xseB</i>	Exodeoxyribonuclease 7 small subunit	1,17	1,03	-1,23
SL0419	<i>thiI</i>	tRNA sulfurtransferase	1,08	-1,05	-2,71
SL0420	<i>phnV</i>	Putative 2-aminoethylphosphonate transport system permease protein phnV	1,01	1,17	-1,09
SL0421	<i>phnU</i>	Putative 2-aminoethylphosphonate transport system permease protein phnU	1,27	1,37	1,22
SL0422	<i>phnT</i>	Putative 2-aminoethylphosphonate import ATP-binding protein phnT	-1,02	1,13	1,21

Tabla Suplementaria 1

Diferencia de expresión de todos los genes de SV5015 en las cepas mutantes *greA*, *greB* y *greAgreB*, respecto a la cepa WT

ID	gene	Description	<i>greA</i> vs WT	<i>greB</i> vs WT	<i>greAgreB</i> vs WT
SL0423	<i>phnS</i>	Putative 2-aminoethylphosphonate-binding periplasmic protein	1,00	1,23	-1,27
SL0424	<i>phnR</i>	Putative transcriptional regulator of 2-aminoethylphosphonate degradation operons	1,09	1,02	1,25
SL0425	<i>phnW</i>	2-aminoethylphosphonate--pyruvate transaminase	-1,15	-1,04	1,07
SL0426	<i>phnX</i>	Phosphonoacetaldehyde hydrolase	1,15	-1,06	-1,17
SL0427	<i>thiJ</i>	Protein thiJ	1,07	-1,02	1,28
SL0428	<i>panE</i>	2-dehydropantoate 2-reductase	1,27	1,27	1,67
SL0429	<i>yajQ</i>	UPF0234 protein CKO_02735	1,34	1,12	1,49
SL0430	<i>yajR</i>	Inner membrane transport protein yajR	-1,07	1,01	-1,83
SL0431	<i>ybeT</i>	Hypothetical	-1,11	-1,21	1,68
SL0432	<i>ybeT</i>	Hypothetical	-1,10	-1,28	2,29
SL0433	<i>cyoE</i>	Protoheme IX farnesyltransferase	-1,12	-1,50	11,62
SL0434	<i>cyoD</i>	Cytochrome o ubiquinol oxidase protein cyoD	-1,20	-1,53	13,42
SL0435	<i>cyoC</i>	Cytochrome o ubiquinol oxidase subunit 3	-1,10	-1,60	13,28
SL0436	<i>cyoB</i>	Ubiquinol oxidase subunit 1	-1,08	-1,42	5,97
SL0437	<i>cyoA</i>	Ubiquinol oxidase subunit 2	-1,09	-1,17	6,05
SL0438	<i>ampG</i>	Protein AmpG	-1,13	-1,39	-1,37
SL0439	<i>yajG</i>	Uncharacterized lipoprotein yajG	-1,22	-1,13	-1,65
SL0440	<i>bolA</i>	Protein BolA	-1,15	1,16	1,95
SL0441	<i>tig</i>	Trigger factor	1,03	-1,11	-1,20
SL0442	<i>clpP</i>	ATP-dependent Clp protease proteolytic subunit	-1,01	-1,01	1,13
SL0443	<i>clpX</i>	ATP-dependent Clp protease ATP-binding subunit clpX	-1,02	-1,04	-1,38
SL0444	<i>lon</i>	Hypothetical Protein lon	1,07	1,06	2,44
SL0445	<i>hupB</i>	DNA-binding protein HU-beta	1,17	1,14	2,02
SL0446	<i>ppiD</i>	Peptidyl-prolyl cis-trans isomerase D	1,20	-1,11	-1,27
SL0447	<i>ybaV</i>	Uncharacterized protein ybaV	1,31	1,25	1,24
SL0448	<i>tesC</i>	Long-chain acyl-CoA thioesterase tesC	1,24	-1,05	1,33
SL0449	<i>queC</i>	7-cyano-7-deazaguanine synthase	1,00	-1,01	-2,53
SL0450	<i>ybaE</i>	Uncharacterized protein ybaE	1,13	1,12	6,33
SL0451	<i>cof</i>	HMP-PP phosphatase	-1,09	1,04	-1,13
SL0452	<i>cysM</i>	Cysteine synthase B	1,19	1,11	-1,12
SL0453	<i>ybaO</i>	Uncharacterized HTH-type transcriptional regulator ybaO	1,04	1,01	1,02
SL0454	<i>mdIA</i>	Multidrug resistance-like ATP-binding protein mdIA	1,13	-1,01	-1,09
SL0455	<i>mdIB</i>	Multidrug resistance-like ATP-binding protein mdIB	1,12	-1,04	1,28
SL0456	<i>glnK</i>	Nitrogen regulatory protein P-II 2	1,23	-1,09	-1,64
SL0457	<i>amtB</i>	Ammonia channel	1,19	1,20	1,32
SL0458	<i>tesB</i>	Acyl-CoA thioesterase 2	1,05	1,01	1,37
SL0459	<i>ybaY</i>	Uncharacterized lipoprotein ybaY	-1,00	1,07	-1,02
SL0460	<i>ybaZ</i>	Uncharacterized protein ybaZ	1,09	1,16	-1,82
SL0461	<i>ylaB</i>	Uncharacterized protein ylaB	1,20	1,16	-1,05
SL0462	<i>rpmE2</i>	50S ribosomal protein L31 type B	1,05	1,35	1,04
SL0463	<i>rpmJ</i>	50S ribosomal protein L36	1,07	1,36	1,01
SL0464	<i>ylaC</i>	Inner membrane protein ylaC	1,01	1,05	-1,11

Tabla Suplementaria 1

Diferencia de expresión de todos los genes de SV5015 en las cepas mutantes *greA*, *greB* y *greAgreB*, respecto a la cepa WT

ID	gene	Description	<i>greA</i> vs WT	<i>greB</i> vs WT	<i>greAgreB</i> vs WT
SL0465	<i>maa</i>	Maltose O-acetyltransferase	1,14	1,06	1,16
SL0466	<i>hha</i>	Hemolysin expression-modulating protein	-1,00	1,03	1,39
SL0467	<i>ybaJ</i>	Uncharacterized protein ybaJ	-1,02	1,05	1,33
SL0468	<i>acrB</i>	Acriflavine resistance protein B	1,30	1,12	1,43
SL0469	<i>acrA</i>	Acriflavine resistance protein A	1,02	-1,10	-1,37
SL0470	<i>acrR</i>	HTH-type transcriptional regulator AcrR	1,00	1,05	-1,48
SL0471	<i>kefA</i>	Potassium efflux system KefA	1,09	1,11	-1,42
SL0472	<i>yhgA</i>	Uncharacterized protein pSLT051	-1,04	-1,19	-1,11
SL0473	<i>ybaM</i>	Uncharacterized protein ybaM	1,03	-1,12	1,04
SL0474	<i>priC</i>	Primosomal replication protein N"	1,04	-1,08	1,21
SL0475	<i>ybaN</i>	Inner membrane protein ybaN	-1,06	1,22	-1,78
SL0476	<i>apt</i>	Adenine phosphoribosyltransferase	1,21	1,12	-1,45
SL0477	<i>dnaX</i>	DNA polymerase III subunit tau	1,04	1,09	-1,73
SL0478	<i>ybaB</i>	UPF0133 protein KPK_4227	1,22	-1,04	-1,11
SL0479	<i>recR</i>	Recombination protein recR	1,21	1,02	-1,38
SL0480	<i>htpG</i>	Chaperone protein htpG	1,08	-1,04	3,68
SL0481	<i>adk</i>	Adenylate kinase	-1,06	-1,07	-1,85
SL0482	<i>hemH</i>	Ferrochelataze	1,04	-1,00	-8,01
SL0483	<i>aes</i>	Acetyl esterase	1,02	1,08	-1,52
SL0484	<i>gsk</i>	Inosine-guanosine kinase	1,01	1,00	-2,02
SL0485	<i>ybaL</i>	Inner membrane protein ybaL	-1,08	-1,14	-1,70
SL0486	<i>fsr</i>	Fosmidomycin resistance protein	-1,06	-1,14	1,08
SL0487	<i>ushA</i>	Protein ushA	-1,05	-1,36	4,38
SL0488	<i>ybaK</i>	Cys-tRNA(Pro)/Cys-tRNA(Cys) deacylase ybaK	1,18	1,06	1,05
SL0489	<i>ybaP</i>	Uncharacterized protein ybaP	-1,07	1,01	-1,16
SL0490	-	Hypothetical	-1,01	1,08	1,07
SL0491	<i>copA</i>	Copper-exporting P-type ATPase A	1,09	1,03	1,74
SL0492	<i>cueR</i>	HTH-type transcriptional regulator cueR	1,11	1,17	1,11
SL0493	<i>ybbJ</i>	Inner membrane protein ybbJ	1,21	1,04	1,39
SL0494	<i>qmcA</i>	Protein qmcA	1,15	1,29	1,67
SL0495	<i>ybbL</i>	Uncharacterized ABC transporter A IP-binding protein vhhI	1,14	1,01	1,31
SL0496	<i>ybbM</i>	UPF0014 inner membrane protein ybbM	1,25	1,06	1,16
SL0497	<i>ybbN</i>	Uncharacterized protein ybbN	1,16	-1,06	1,46
SL0498	<i>ybbO</i>	Uncharacterized oxidoreductase ybbO	1,02	-1,08	-1,65
SL0499	<i>tesA</i>	Acyl-CoA thioesterase I	1,02	1,03	-1,45
SL0500	<i>ybbA</i>	Uncharacterized ABC transporter ATP-binding protein ybbA	1,09	-1,07	-1,15
SL0501	<i>ybbP</i>	Uncharacterized ABC transporter permease ybbP	1,26	-1,04	1,17
SL0502	-	Outer Membrane Protein	1,25	-1,12	2,30
SL0503	<i>metQ</i>	D-methionine-binding lipoprotein metQ	-1,21	-1,07	1,10
SL0504	<i>metN2</i>	Methionine import ATP-binding protein MetN 2	-1,32	-1,34	-1,78
SL0505	<i>metI</i>	Probable D-methionine transport system permease protein metI	-1,24	-1,04	-1,78
SL0506	<i>selU</i>	tRNA 2-selenouridine synthase	1,04	1,07	-1,28
SL0507	<i>allS</i>	HTH-type transcriptional activator AllS	1,23	1,15	7,16

Tabla Suplementaria 1

Diferencia de expresión de todos los genes de SV5015 en las cepas mutantes *greA*, *greB* y *greAgreB*, respecto a la cepa WT

ID	gene	Description	<i>greA</i> vs WT	<i>greB</i> vs WT	<i>greAgreB</i> vs WT
SL0508	<i>allA</i>	Ureidoglycolate hydrolase	-1,06	-1,21	2,65
SL0509	<i>allR</i>	HTH-type transcriptional repressor AllR	1,18	1,02	1,23
SL0510	<i>gcl</i>	Glyoxylate carboligase	1,65	-1,22	7,44
SL0511	<i>hyi</i>	Hydroxypyruvate isomerase	1,41	-1,11	10,16
SL0512	<i>glxR</i>	2-hydroxy-3-oxopropionate reductase	1,60	-1,03	5,13
SL0513	<i>yybO</i>	Uncharacterized transporter yybO	1,43	1,14	4,88
SL0514	<i>ybbV</i>	Cytoplasmic Protein	1,13	1,13	1,70
SL0515	<i>ybbW</i>	Putative allantoin permease	1,66	1,02	3,89
SL0516	<i>allB</i>	Allantoinase	1,05	1,11	2,94
SL0517	<i>ybbY</i>	Putative purine permease ybbY	-1,12	1,01	1,32
SL0518	<i>glxK</i>	Glycerate kinase 1	1,20	1,10	2,36
SL0519	<i>ylbA</i>	Uncharacterized protein ylbA	-1,04	-1,27	2,29
SL0520	<i>allC</i>	Allantoate amidohydrolase	-1,08	-1,17	3,13
SL0521	<i>allD</i>	Ureidoglycolate dehydrogenase	-1,04	-1,46	5,10
SL0522	<i>fdrA</i>	Protein fdrA	1,14	1,12	3,41
SL0523	<i>ylbE</i>	Uncharacterized protein ylbE	1,09	-1,20	3,61
SL0524	<i>ylbF</i>	Uncharacterized protein ylbF	1,09	-1,09	1,09
SL0525	<i>arcC</i>	Carbamate kinase	1,05	1,29	1,23
SL0526	<i>purK</i>	Phosphoribosylaminoimidazole carboxylase ATPase subunit	1,06	1,05	-1,87
SL0527	<i>purE</i>	Phosphoribosylaminoimidazole carboxylase catalytic subunit	1,17	1,38	-1,67
SL0528	<i>lpxH</i>	UDP-2,3-diacylglucosamine hydrolase	1,03	-1,11	-1,92
SL0529	<i>ppiB</i>	Peptidyl-prolyl cis-trans isomerase B	1,02	-1,14	-1,13
SL0530	<i>cysS</i>	CysteinyI-tRNA synthetase	-1,14	-1,15	-1,56
SL0531	-	Hypothetical	-1,03	-1,15	-1,06
SL0532	-	Hypothetical	-1,09	-1,06	-1,49
SL0533	<i>ybcI</i>	Inner membrane protein ybcI	-1,08	1,05	-2,95
SL0534	<i>ybcJ</i>	Uncharacterized protein ybcJ	-1,04	-1,13	-1,25
SL0535	<i>folD</i>	Bifunctional protein folD	1,04	1,00	-1,44
SL0536	<i>sfmA</i>	Fimbrial subunit type 1	-1,80	1,10	-9,56
SL0537	<i>fimI</i>	Putative fimbrin-like protein fimI	-2,48	-1,26	-17,41
SL0538	<i>fimC</i>	Chaperone protein fimC	-2,52	-1,37	-22,44
SL0539	<i>fimD</i>	Outer membrane usher protein fimD	-1,99	-1,09	-5,31
SL0540	<i>fimH</i>	Protein fimH	-1,50	-1,09	-2,74
SL0541	<i>fimF</i>	Fimbrial-like protein fimF	-1,19	-1,04	-1,45
SL0542	<i>fimZ</i>	Fimbriae Z protein	-1,27	1,09	-2,40
SL0543	<i>fimY</i>	Fimbriae Y protein	1,43	1,29	-2,23
SL0544	-	Hypothetical	-1,17	1,54	-2,09
SL0545	<i>fimW</i>	Fimbriae W protein	-1,39	1,23	-1,49
SL0546	<i>nisX1</i>	Transposase for insertion sequence element IS904	-1,03	1,07	1,47
SL0547	-	Hypothetical	-1,04	-1,41	-1,27
SL0548	<i>yfdH</i>	Bactoprenol glucosyl transferase homolog from prophage CPS-53	-1,04	-1,04	-1,99
SL0549	<i>yfdG</i>	Bactoprenol-linked glucose translocase homolog from prophage CPS-53	1,09	-1,03	-2,84
SL0550	<i>cusS</i>	Sensor kinase cusS	-1,04	1,09	-1,48

Tabla Suplementaria 1Diferencia de expresión de todos los genes de SV5015 en las cepas mutantes *greA*, *greB* y *greAgreB*, respecto a la cepa WT

ID	gene	Description	<i>greA</i> vs WT	<i>greB</i> vs WT	<i>greAgreB</i> vs WT
SL0551	<i>ykgD</i>	Uncharacterized HTH-type transcriptional regulator ykgD	1,16	1,20	3,20
SL0552	<i>ykgC</i>	Probable pyridine nucleotide-disulfide oxidoreductase ykgC	1,12	1,11	2,34
SL0553	<i>ykgI</i>	Uncharacterized protein ykgI	-1,13	1,01	-1,17
SL0554	<i>ykgB</i>	Inner membrane protein ykgB	-1,12	1,08	2,01
SL0555	-	Hypothetical	-1,19	1,19	-1,76
SL0556	<i>pheP</i>	Phenylalanine-specific permease	1,06	-1,04	-1,29
SL0557	<i>ybdG</i>	Uncharacterized protein ybdG	-1,07	-1,16	1,51
SL0558	<i>lip-1</i>	Lipase 1	1,12	1,17	1,79
SL0559	<i>levR</i>	Transcriptional regulatory protein levR	1,07	-1,01	2,64
SL0560	<i>frlB</i>	Fructosamine deglycase frlB	1,61	1,34	2,73
SL0561	<i>glmS</i>	Glucosamine--fructose-6-phosphate aminotransferase [isomerizing]	1,44	1,11	2,37
SL0562	<i>manZ</i>	Mannose permease IID component	1,02	-1,01	1,96
SL0563	<i>manY</i>	Mannose permease IIC component	1,13	1,43	1,67
SL0564	<i>manX</i>	PTS system mannose-specific EIIAB component	1,15	1,26	1,23
SL0565	<i>manX</i>	PTS System Fructocific IIA Component	1,10	-1,19	1,00
SL0566	<i>nfnB</i>	Oxygen-insensitive NAD(P)H nitroreductase	1,01	-1,13	2,14
SL0567	<i>ybdF</i>	Uncharacterized protein ybdF	-1,01	-1,14	1,04
SL0568	-	TetR Family Transcriptional Regulator	1,00	-1,04	-1,29
SL0569	<i>ramA</i>	Transcriptional activator ramA	1,31	1,08	-1,17
SL0570	<i>ybdJ</i>	Uncharacterized protein ybdJ	1,26	1,08	-1,27
SL0571	<i>ybdK</i>	Carboxylate-amine ligase ybdK	1,07	1,04	1,47
SL0572	<i>entD</i>	4'-phosphopantetheinyl transferase entD	1,07	1,60	1,10
SL0573	<i>fepA</i>	Ferrienterobactin receptor	-1,04	1,69	1,54
SL0574	<i>fes</i>	Enterochelin esterase	1,20	1,43	-1,26
SL0575	<i>ybdZ</i>	Uncharacterized protein ybdZ	1,07	1,17	1,03
SL0576	<i>entF</i>	Enterobactin synthase component F	1,49	1,21	1,25
SL0577	<i>fepE</i>	Ferric enterobactin transport protein fepE	1,02	-1,12	1,27
SL0578	<i>fepC</i>	Ferric enterobactin transport ATP-binding protein fepC	1,05	1,28	-1,40
SL0579	<i>fepG</i>	Ferric enterobactin transport system permease protein fepG	1,23	1,26	-1,50
SL0580	<i>fepD</i>	Ferric enterobactin transport system permease protein fepD	-1,03	1,00	-1,10
SL0581	<i>entS</i>	Enterobactin exporter entS	1,08	1,21	-1,05
SL0582	<i>fepB</i>	Ferrienterobactin-binding periplasmic protein	-1,16	1,09	-1,24
SL0583	<i>entC</i>	Isochorismate synthase entC	-1,05	1,72	-1,07
SL0584	<i>entE</i>	Enterobactin synthase component E	1,12	1,76	1,30
SL0585	<i>entB</i>	Isochorismatase	1,10	1,23	2,00
SL0586	<i>entA</i>	2,3-dihydro-2,3-dihydroxybenzoate dehydrogenase	1,11	-1,28	2,33
SL0587	<i>ybdB</i>	Esterase ybdB	-1,13	-1,04	2,26
SL0588	<i>cstA</i>	Carbon starvation protein A	-1,16	-1,23	9,48
SL0589	<i>ybdD</i>	Uncharacterized protein ybdD	-1,21	-1,30	9,97
SL0590	<i>ybdH</i>	Uncharacterized oxidoreductase ybdH	-1,04	-1,11	1,63
SL0591	<i>ybdL</i>	Aminotransferase ybdL	1,18	1,07	-1,15
SL0592	<i>ybdM</i>	Uncharacterized protein ybdM	1,15	-1,04	2,44
SL0593	<i>ybdN</i>	Uncharacterized protein ybdN	-1,07	-1,21	-1,24

Tabla Suplementaria 1Diferencia de expresión de todos los genes de SV5015 en las cepas mutantes *greA*, *greB* y *greAgreB*, respecto a la cepa WT

ID	gene	Description	<i>greA</i> vs WT	<i>greB</i> vs WT	<i>greAgreB</i> vs WT
SL0594	<i>ybdO</i>	Uncharacterized HTH-type transcriptional regulator ybdO	-1,14	-1,05	1,04
SL0595	<i>dsbG</i>	Thiol:disulfide interchange protein dsbG	1,09	-1,13	1,69
SL0596	<i>ahpC</i>	Alkyl hydroperoxide reductase subunit C	1,12	1,10	-2,32
SL0597	<i>ahpF</i>	Alkyl hydroperoxide reductase subunit F	-1,10	-1,02	-2,42
SL0598	<i>ynfl</i>	Cytoplasmic Chaperone rD Family Protein	1,33	1,02	-3,67
SL0599	<i>yyaE</i>	Probable oxidoreductase yyaE	1,16	1,09	-1,10
SL0600	<i>dmsB</i>	Anaerobic dimethyl sulfoxide reductase chain B	1,03	-1,04	-1,23
SL0601	<i>ynfH</i>	DMSO Reductase Anchor Subunit	1,48	-1,05	-1,09
SL0602	<i>uspG</i>	Universal stress protein G	1,17	1,45	1,37
SL0603	<i>ybdR</i>	Uncharacterized zinc-type alcohol dehydrogenase-like protein ybdR	1,40	1,34	1,93
SL0604	<i>rnk</i>	Regulator of nucleoside diphosphate kinase	1,33	1,18	1,48
SL0605	<i>rna</i>	Ribonuclease I	-1,07	1,13	-2,35
SL0606	<i>citT</i>	Citrate carrier	-1,20	1,14	-1,87
SL0607	<i>citG2</i>	Probable 2-(5"-triphosphoribosyl)-3'-dephosphocoenzyme-A synthase 2	-1,07	1,03	-1,25
SL0608	<i>citX</i>	Apo-citrate lyase phosphoribosyl-dephospho-CoA transferase	-1,04	-1,08	-1,87
SL0609	<i>citF</i>	Citrate lyase alpha chain	1,17	1,26	-1,61
SL0610	<i>citE</i>	Citrate lyase subunit beta	1,06	1,12	-2,50
SL0611	<i>citD1</i>	Citrate lyase acyl carrier protein 1	-1,06	1,09	-2,36
SL0612	<i>citC</i>	[Citrate [pro-3S]-lyase] ligase	-1,02	1,10	-2,47
SL0613	<i>dpiB</i>	Sensor histidine kinase DpiB	-1,09	1,19	-3,56
SL0614	<i>dpiA</i>	Transcriptional regulatory protein DpiA	1,03	1,04	-2,28
SL0615	<i>dcuC</i>	Anaerobic C4-dicarboxylate transporter dcuC	1,18	1,06	-2,87
SL0616	<i>crcA</i>	Protein crcA	-1,02	1,07	-6,65
SL0617	<i>cspE</i>	Cold shock-like protein cspE	-1,33	1,02	-2,78
SL0618	<i>crcB</i>	Protein crcB homolog	1,38	1,24	-1,21
SL0619	<i>ybeM</i>	UPF0012 hydrolase ybeM	1,12	1,37	1,07
SL0620	<i>tatE</i>	Sec-independent protein translocase protein tatE	-1,01	1,14	-2,04
SL0621	<i>lipA</i>	Lipoyl synthase	1,20	1,03	-1,65
SL0622	<i>ybeF</i>	Uncharacterized HTH-type transcriptional regulator ybeF	1,11	-1,05	-1,06
SL0623	<i>lipB</i>	Octanoyltransferase	1,05	-1,03	-1,53
SL0624	<i>ybeD</i>	UPF0250 protein Ent638_1166	1,11	1,28	-1,12
SL0625	<i>dacA</i>	D-alanyl-D-alanine carboxypeptidase dacA	-1,04	1,03	-2,41
SL0626	<i>rlpA</i>	Rare lipoprotein A	1,08	1,09	-1,04
SL0627	<i>mrdb</i>	Rod shape-determining protein rodA	1,21	-1,03	1,39
SL0628	<i>mrda</i>	Penicillin-binding protein 2	1,10	-1,05	-1,38
SL0629	<i>rlmH</i>	Ribosomal RNA large subunit methyltransferase H	-1,09	-1,08	-1,70
SL0630	<i>ybeB</i>	Uncharacterized protein ybeB	-1,19	-1,10	-1,91
SL0631	<i>cobC</i>	Alpha-ribazole phosphatase	-1,01	1,06	1,49
SL0632	<i>cobD</i>	Threonine-phosphate decarboxylase	1,21	1,26	1,02
SL0633	<i>nadD</i>	Probable nicotinate-nucleotide adenyltransferase	1,17	-1,04	-1,19
SL0634	<i>holA</i>	DNA polymerase III subunit delta	1,15	-1,07	-1,43

Tabla Suplementaria 1

Diferencia de expresión de todos los genes de SV5015 en las cepas mutantes *greA*, *greB* y *greAgreB*, respecto a la cepa WT

ID	gene	Description	<i>greA</i> vs WT	<i>greB</i> vs WT	<i>greAgreB</i> vs WT
SL0635	<i>lptE</i>	LPS-assembly lipoprotein lptE	1,05	-1,13	-1,20
SL0636	<i>leuS</i>	Leucyl-tRNA synthetase	1,07	-1,08	-1,44
SL0637	<i>uxaA</i>	SAF Domain-Containing Protein	1,26	-1,00	-7,34
SL0638	<i>uxaA</i>	Altronate hydrolase	1,24	-1,26	-5,57
SL0639	<i>kdgT2</i>	2-keto-3-deoxygluconate permease 2	1,23	1,24	-2,50
SL0640	<i>yqiR</i>	Putative sigma L-dependent transcriptional regulator yqiR	1,11	1,16	1,94
SL0641	<i>ybeL</i>	Uncharacterized protein ybeL	1,43	1,38	4,14
SL0642	<i>ybeQ</i>	Uncharacterized protein ybeQ	1,10	1,13	2,20
SL0643	<i>ybeR</i>	Uncharacterized protein ybeR	-1,39	-1,21	1,43
SL0644	<i>djlC</i>	Uncharacterized J domain-containing protein djlC	-1,25	-1,33	1,98
SL0645	<i>ybeU</i>	Uncharacterized protein ybeU	-1,32	-1,27	1,97
SL0646	<i>ybeU</i>	Uncharacterized protein ybeU	-1,29	-1,16	-1,14
SL0647	<i>djlC</i>	Uncharacterized J domain-containing protein djlC	-1,12	-1,19	-1,31
SL0648	<i>hscC</i>	Chaperone protein hscC	1,19	1,18	1,80
SL0649	-	Hypothetical	-1,06	1,02	2,03
SL0650	<i>rihA</i>	Pyrimidine-specific ribonucleoside hydrolase rihA	-1,07	-1,01	2,38
SL0651	<i>gltL</i>	Glutamate/aspartate transport ATP-binding protein gltL	-1,77	-2,15	8,59
SL0652	<i>gltK</i>	Glutamate/aspartate transport system permease protein gltK	-1,72	-2,00	8,36
SL0653	<i>gltJ</i>	Glutamate/aspartate transport system permease protein gltJ	-1,52	-1,47	5,50
SL0654	<i>gltI</i>	Glutamate/aspartate periplasmic-binding protein	-1,40	-1,20	6,78
SL0655	<i>Int</i>	Apolipoprotein N-acyltransferase	-1,21	-1,42	-2,17
SL0656	<i>corC</i>	Magnesium and cobalt efflux protein corC	-1,29	-1,29	-1,14
SL0657	<i>ybeY</i>	Putative metalloprotease ybeY	-1,05	-1,05	-1,29
SL0658	<i>ybeZ</i>	PhoH-like protein	-1,11	-1,24	-1,27
SL0659	<i>miaB</i>	(Dimethylallyl)adenosine tRNA methyltransferase miaB	1,06	1,03	-1,50
SL0660	<i>ubiF</i>	2-octaprenyl-3-methyl-6-methoxy-1,4-benzoquinol hydroxylase	1,46	1,20	2,78
SL0661	-	Hypothetical	1,37	1,23	1,51
SL0662	<i>asnB</i>	Asparagine synthetase B [glutamine-hydrolyzing]	-1,09	-1,12	1,62
SL0663	<i>nagD</i>	Protein nagD	1,05	-1,13	-1,32
SL0664	<i>nagC</i>	N-acetylglucosamine repressor	1,07	-1,13	-1,37
SL0665	<i>nagA</i>	N-acetylglucosamine-6-phosphate deacetylase	-1,01	-1,03	1,11
SL0666	<i>nagB</i>	Glucosamine-6-phosphate deaminase	1,12	1,19	1,15
SL0667	<i>nagE</i>	PTS system N-acetylglucosamine-specific EIICBA component	1,06	1,08	1,88
SL0668	<i>glnS</i>	Glutaminyl-tRNA synthetase	1,03	1,01	-1,52
SL0669	<i>ybfM</i>	Uncharacterized protein ybfM	-1,09	-1,10	2,74
SL0670	<i>ybfN</i>	Uncharacterized lipoprotein ybfN	1,01	-1,18	3,34
SL0671	<i>citA</i>	Citrate-proton symporter	-1,21	-1,15	2,57
SL0672	<i>citB</i>	Citrate utilization protein B	1,06	-1,08	3,82
SL0673	<i>ifcA</i>	Fumarate reductase flavoprotein subunit	-1,01	-1,07	2,24
SL0674	<i>nac</i>	Nitrogen assimilation regulatory protein nac	1,08	-1,12	-1,21
SL0675	<i>fur</i>	Ferric uptake regulation protein	1,00	1,07	-2,81
SL0676	<i>fldA</i>	Flavodoxin-1	-1,03	1,01	-1,98
SL0677	<i>ybfE</i>	Uncharacterized protein ybfE	1,32	1,22	-1,29

Tabla Suplementaria 1

Diferencia de expresión de todos los genes de SV5015 en las cepas mutantes *greA*, *greB* y *greAgreB*, respecto a la cepa WT

ID	gene	Description	<i>greA</i> vs WT	<i>greB</i> vs WT	<i>greAgreB</i> vs WT
SL0678	<i>ybfF</i>	Esterase ybfF	1,16	1,04	-1,32
SL0679	<i>seqA</i>	Protein seqA	-1,05	-1,03	-1,76
SL0680	<i>pgm</i>	Phosphoglucomutase	1,14	-1,04	1,35
SL0681	-	5-Nitroimidazole Antibiotic Resistance Protein	1,06	1,14	-5,70
SL0682	<i>potE</i>	Putrescine-ornithine antiporter	1,06	-1,20	-4,57
SL0683	<i>speF</i>	Ornithine decarboxylase, inducible	1,04	-1,26	-4,29
SL0684	<i>kdpE</i>	KDP operon transcriptional regulatory protein kdpE	-1,05	-1,01	1,34
SL0685	<i>kdpD</i>	Sensor protein kdpD	1,07	1,06	1,42
SL0686	<i>kdpC</i>	Potassium-transporting ATPase C chain	1,06	1,16	1,32
SL0687	<i>kdpB</i>	Potassium-transporting ATPase B chain	1,16	1,11	1,70
SL0688	<i>kdpA</i>	Potassium-transporting ATPase A chain	-1,01	-1,07	1,15
SL0689	<i>ybfA</i>	Uncharacterized protein ybfA	1,23	1,38	-1,11
SL0690	<i>phrB</i>	Deoxyribodipyrimidine photo-lyase	1,15	1,03	-1,55
SL0691	<i>dtpD</i>	Dipeptide permease D	1,38	-1,01	-2,14
SL0692	<i>ybgI</i>	UPF0135 protein ybgI	1,14	1,06	2,27
SL0693	<i>ybgJ</i>	Uncharacterized protein ybgJ	1,17	1,00	2,74
SL0694	<i>ybgK</i>	Uncharacterized protein ybgK	1,17	-1,07	2,38
SL0695	<i>ybgL</i>	UPF0271 protein ybgL	1,32	1,26	1,48
SL0696	-	Hypothetical	1,10	1,37	-1,72
SL0697	<i>fimB</i>	Type 1 fimbriae regulatory protein fimB	-1,14	-1,03	-1,63
SL0698	-	Hypothetical	1,23	1,03	1,00
SL0699	-	Hypothetical	-1,17	1,06	1,10
SL0700	<i>rfdD</i>	Probable UDP-galactopyranose mutase	1,29	1,34	-1,11
SL0701	<i>rfdD</i>	Probable UDP-galactopyranose mutase	1,07	1,04	-1,02
SL0702	-	Glycosyltransferase	-1,07	-1,10	1,03
SL0703	-	Glycosyltransferase	1,17	1,16	1,07
SL0704	<i>rfdD</i>	O-antigen export system permease protein rfdD	1,06	-1,06	1,07
SL0705	<i>rfdE</i>	O-antigen export system ATP-binding protein rfdE	1,04	-1,10	1,12
SL0706	<i>glfT2</i>	UDP-galactofuranosyl transferase GlfT2	1,08	1,08	1,25
SL0707	-	Hypothetical	1,02	1,07	1,06
SL0708	-	Hypothetical	1,14	-1,02	1,00
SL0709	-	Hypothetical	1,15	-1,07	-1,32
SL0710	<i>nei</i>	Endonuclease 8	1,01	-1,05	-1,01
SL0711	<i>abrB</i>	Protein AbrB	1,38	1,17	2,71
SL0712	<i>gltA</i>	Citrate synthase	1,06	-1,00	2,70
SL0713	-	Hypothetical	-1,31	-1,16	3,77
SL0714	<i>sdhC</i>	Succinate dehydrogenase cytochrome b556 subunit	-1,15	-1,23	8,34
SL0715	<i>sdhD</i>	Succinate dehydrogenase hydrophobic membrane anchor subunit	-1,10	-1,29	6,00
SL0716	<i>sdhA</i>	Succinate dehydrogenase flavoprotein subunit	-1,00	-1,20	8,19

Tabla Suplementaria 1

Diferencia de expresión de todos los genes de SV5015 en las cepas mutantes *greA*, *greB* y *greAgreB*, respecto a la cepa WT

ID	gene	Description	<i>greA</i> vs WT	<i>greB</i> vs WT	<i>greAgreB</i> vs WT
SL0717	<i>sdhB</i>	Succinate dehydrogenase iron-sulfur subunit	-1,01	-1,14	8,63
SL0718	<i>sucA</i>	2-oxoglutarate dehydrogenase E1 component	1,01	-1,26	2,25
SL0719	<i>sucB</i>	Dihydrolipoyllysine-residue succinyltransferase component of 2-oxoglutarate dehydrogenase complex	1,09	-1,10	2,41
SL0720	<i>sucC</i>	Succinyl-CoA ligase [ADP-forming] subunit beta	1,14	-1,24	3,54
SL0721	<i>sucD</i>	Succinyl-CoA ligase [ADP-forming] subunit alpha	1,10	-1,07	2,39
SL0722	<i>cydA</i>	Cytochrome d ubiquinol oxidase subunit 1	1,06	-1,03	1,13
SL0723	<i>cydB</i>	Cytochrome d ubiquinol oxidase subunit 2	1,03	-1,02	1,12
SL0724	<i>ybgT</i>	Uncharacterized protein ybgT	1,07	1,05	1,33
SL0725	<i>ybgE</i>	Uncharacterized protein ybgE	1,02	-1,21	1,07
SL0726	<i>ybgC</i>	Acyl-CoA thioester hydrolase ybgC	-1,13	1,13	-2,47
SL0727	<i>tolQ</i>	Protein tolQ	-1,29	-1,15	-2,54
SL0728	<i>tolR</i>	Protein tolR	-1,08	-1,01	-2,59
SL0729	<i>tolA</i>	Protein tolA	1,01	1,18	-2,07
SL0730	<i>tolB</i>	Protein tolB	1,03	1,05	1,45
SL0731	<i>pal</i>	Peptidoglycan-associated lipoprotein	-1,13	-1,02	1,75
SL0732	<i>ybgF</i>	Uncharacterized protein YbgF	-1,47	-1,22	1,06
SL0733	<i>nadA</i>	Quinolinolate synthase A	1,18	1,13	-1,61
SL0734	<i>pnuC</i>	Nicotinamide riboside transporter pnuC	1,26	1,02	1,31
SL0735	<i>zitB</i>	Zinc transporter zitB	1,30	1,07	1,95
SL0736	<i>ybgS</i>	Uncharacterized protein ybgS	1,23	1,34	-1,11
SL0737	<i>aroG</i>	Phospho-2-dehydro-3-deoxyheptonate aldolase, Phe-sensitive	1,10	-1,03	-1,14
SL0738	<i>fumB</i>	Fumarate hydratase class I, anaerobic	1,05	1,17	1,42
SL0739	<i>ttdA</i>	Putative fumarate hydratase subunit alpha	1,18	1,10	1,78
SL0740	<i>ywbl</i>	Uncharacterized HTH-type transcriptional regulator ywbl	1,10	1,17	3,02
SL0741	<i>yjiE</i>	Uncharacterized HTH-type transcriptional regulator yjiE	1,22	1,44	1,29
SL0742	<i>yfbS</i>	Uncharacterized transporter MJ0672	1,28	1,16	1,23
SL0743	<i>oadG3</i>	Oxaloacetate decarboxylase gamma chain 3	1,07	-1,07	1,60
SL0745	<i>oadB1</i>	Oxaloacetate decarboxylase beta chain 1	1,38	1,16	2,25
SL0746	<i>citG</i>	2-(5"-triphosphoribosyl)-3'-dephosphocoenzyme-A synthase	1,60	1,35	2,94
SL0747	<i>fecD</i>	Putative ABC transporter permease protein MJ0087	1,06	1,44	1,49
SL0748	<i>fhuC</i>	Iron(3+)-hydroxamate import ATP-binding protein fhuC	1,23	-1,06	1,00
SL0749	<i>gpmA</i>	2,3-bisphosphoglycerate-dependent phosphoglycerate mutase	1,08	1,01	1,94
SL0750	<i>galM</i>	Aldose 1-epimerase	1,18	-1,06	-1,02
SL0751	<i>galK</i>	Galactokinase	1,21	1,04	1,01
SL0752	<i>galT</i>	Galactose-1-phosphate uridylyltransferase	1,22	1,11	1,52
SL0753	<i>galE</i>	UDP-glucose 4-epimerase	1,12	1,17	2,06
SL0754	-	Hypothetical	1,17	1,03	-1,09

Tabla Suplementaria 1

Diferencia de expresión de todos los genes de SV5015 en las cepas mutantes *greA*, *greB* y *greAgreB*, respecto a la cepa WT

ID	gene	Description	<i>greA</i> vs WT	<i>greB</i> vs WT	<i>greAgreB</i> vs WT
SL0755	<i>modF</i>	Putative molybdenum transport ATP-binding protein modF	-1,11	-1,19	-1,25
SL0756	<i>modE</i>	Transcriptional regulator modE	-1,01	1,03	-1,08
SL0757	<i>ybhT</i>	Uncharacterized protein ybhT	1,09	1,18	-1,89
SL0758	<i>modA</i>	Molybdate-binding periplasmic protein	-1,45	1,09	-1,83
SL0759	<i>modB</i>	Molybdenum transport system permease protein modB	-1,30	-1,10	-1,93
SL0760	<i>modC</i>	Molybdenum import ATP-binding protein ModC	-1,14	-1,11	-2,39
SL0761	<i>ybhA</i>	Phosphatase ybhA	-1,04	-1,03	-1,04
SL0762	<i>pgl</i>	6-phosphogluconolactonase	1,19	1,08	2,28
SL0763	<i>ybhC</i>	Putative acyl-CoA thioester hydrolase ybhC	1,16	-1,13	1,36
SL0764	<i>hutI</i>	Imidazolonepropionase	1,16	1,05	3,21
SL0765	<i>hutG</i>	Formimidoylglutamase	1,08	-1,06	4,38
SL0766	<i>hutC</i>	Histidine utilization repressor	-1,14	-1,08	2,51
SL0767	<i>hutU</i>	Urocanate hydratase	-1,11	-1,18	21,16
SL0768	<i>hutH</i>	Histidine ammonia-lyase	-1,22	-1,51	18,07
SL0769	<i>ybhB</i>	UPF0098 protein ybhB	1,14	-1,07	1,83
SL0770	<i>bioA</i>	Adenosylmethionine-8-amino-7-oxononanoate aminotransferase	1,06	1,01	-1,01
SL0771	<i>bioB</i>	Biotin synthase	-1,22	-1,11	2,06
SL0772	<i>bioF</i>	8-amino-7-oxononanoate synthase	-1,01	-1,00	1,64
SL0773	<i>bioC</i>	Biotin synthesis protein BioC	1,36	1,15	1,31
SL0774	<i>bioD</i>	Dethiobiotin synthetase	1,44	-1,15	1,94
SL0775	<i>uvrB</i>	UvrABC system protein B	1,01	-1,01	-1,36
SL0776	<i>slrP</i>	E3 ubiquitin-protein ligase slrP	-1,49	-1,17	-6,12
SL0777	<i>ybhK</i>	UPF0052 protein ybhK	1,21	1,19	1,61
SL0778	<i>moaA</i>	Molybdenum cofactor biosynthesis protein A	1,04	1,26	-1,52
SL0779	<i>moaB</i>	Molybdenum cofactor biosynthesis protein B	1,17	1,24	1,86
SL0780	<i>moaC</i>	Molybdenum cofactor biosynthesis protein C	1,17	1,08	2,26
SL0781	<i>moaD</i>	Molybdopterin synthase sulfur carrier subunit	1,13	1,02	2,25
SL0782	<i>moaE</i>	Molybdopterin synthase catalytic subunit	1,38	1,21	2,41
SL0783	<i>ybhL</i>	Inner membrane protein ybhL	1,27	1,15	1,75
SL0784	<i>ybhM</i>	Uncharacterized protein ybhM	1,07	1,13	-1,09
SL0785	-	Inner Membrane Protein	-1,41	-1,08	-1,58
SL0786	-	Inner Membrane Protein	1,01	1,17	-1,12
SL0787	<i>ybhN</i>	Inner membrane protein ybhN	1,01	-1,08	-1,19
SL0788	<i>ybhO</i>	Putative cardiolipin synthase ybhO	-1,04	1,03	-1,29
SL0789	<i>ybhP</i>	Uncharacterized protein ybhP	1,04	1,12	-1,66
SL0790	<i>ybhQ</i>	Inner membrane protein ybhQ	1,34	1,59	1,17
SL0791	<i>ybhR</i>	Inner membrane transport permease ybhR	1,32	1,20	-1,03
SL0792	<i>ybhS</i>	Inner membrane transport permease ybhS	1,08	1,04	-1,21
SL0793	<i>ybhF</i>	Uncharacterized ABC transporter ATP-binding protein ybhF	-1,05	-1,08	-1,20
SL0794	<i>ybhG</i>	UPF0194 membrane protein CKO_02332	-1,05	1,04	-1,08
SL0795	<i>ybiH</i>	Uncharacterized HTH-type transcriptional regulator ybiH	-1,06	-1,03	1,60

Tabla Suplementaria 1

Diferencia de expresión de todos los genes de SV5015 en las cepas mutantes *greA*, *greB* y *greAgreB*, respecto a la cepa WT

ID	gene	Description	<i>greA</i> vs WT	<i>greB</i> vs WT	<i>greAgreB</i> vs WT
SL0796	<i>rhIE</i>	ATP-dependent RNA helicase rhIE	-1,30	-1,24	-4,28
SL0797	<i>dinG</i>	Probable ATP-dependent helicase dinG	-1,10	-1,05	-1,18
SL0798	<i>ybiB</i>	Uncharacterized protein ybiB	1,20	1,05	1,16
SL0799	<i>ybiJ</i>	Uncharacterized protein ybiJ	-1,05	-1,01	-3,65
SL0800	<i>ybil</i>	Uncharacterized protein ybil	1,15	1,02	1,03
SL0801	<i>rlmF</i>	Ribosomal RNA large subunit methyltransferase F	1,16	1,15	-1,03
SL0802	<i>ybiO</i>	Uncharacterized mscS family protein ybiO	1,05	1,09	1,44
SL0803	<i>glnQ</i>	Glutamine transport ATP-binding protein glnQ	-1,06	-1,33	2,29
SL0804	<i>glnP</i>	Glutamine transport system permease protein glnP	1,04	-1,28	1,78
SL0805	<i>glnH</i>	Glutamine-binding periplasmic protein	1,14	-1,22	3,68
SL0806	<i>dps</i>	DNA protection during starvation protein	1,06	1,11	-1,22
SL0807	<i>rhtA</i>	Inner membrane transporter rhtA	1,01	-1,06	-2,23
SL0808	<i>ompX</i>	Outer membrane protein X	-1,01	1,19	-2,41
SL0809	<i>ybiP</i>	Putative phosphoethanolamine transferase ybiP	1,17	1,15	-1,21
SL0810	<i>mntR</i>	Transcriptional regulator mntR	1,08	-1,10	-1,25
SL0811	<i>ybiR</i>	Inner membrane protein ybiR	1,23	1,01	-1,31
SL0812	<i>ybiS</i>	Probable L,D-transpeptidase YbiS	-1,04	1,02	-1,95
SL0813	<i>ybiT</i>	Uncharacterized ABC transporter ATP-binding protein ybiT	-1,23	1,08	-2,82
SL0814	-	Hypothetical	-1,47	-1,29	1,19
SL0815	<i>supH</i>	Sugar phosphatase supH	1,10	-1,04	-1,20
SL0816	<i>ybiT</i>	Hypothetical Protein ybiT	-1,19	1,08	-1,94
SL0817	<i>ybiU</i>	Uncharacterized protein ybiU	-1,13	-1,19	1,74
SL0818	<i>supH</i>	Sugar phosphatase supH	-1,11	-1,18	1,08
SL0819	<i>ybiW</i>	Putative formate acetyltransferase 3	1,08	1,27	1,45
SL0820	<i>ybiY</i>	Putative pyruvate formate-lyase 3-activating enzyme	1,12	1,77	1,49
SL0821	<i>moeB</i>	Sulfur carrier protein moaD adenylyltransferase	-1,00	-1,36	-1,21
SL0822	<i>moeA</i>	Molybdopterin molybdenumtransferase	1,08	-1,14	-1,52
SL0823	<i>iaaA</i>	Isoaspartyl peptidase	1,02	-1,05	1,76
SL0824	<i>gsiA</i>	Glutathione import ATP-binding protein gsiA	1,11	-1,26	2,57
SL0825	<i>gsiB</i>	Glutathione-binding protein gsiB	1,21	1,04	3,72
SL0826	<i>gsiC</i>	Glutathione transport system permease protein gsiC	1,27	1,11	2,09
SL0827	<i>gsiD</i>	Glutathione transport system permease protein gsiD	1,19	1,02	1,63
SL0828	<i>rimO</i>	Ribosomal protein S12 methylthiotransferase rimO	-1,00	1,12	-2,33
SL0829	<i>bssR</i>	Biofilm regulator BssR	1,61	2,18	2,38
SL0830	-	HpcH/Hpal Aldolase	-1,01	1,05	-1,52
SL0831	<i>etfB</i>	Electron transfer flavoprotein subunit beta	-1,24	-1,19	-1,39
SL0832	<i>etfA</i>	Electron transfer flavoprotein subunit alpha	1,14	1,01	-1,16
SL0833	<i>mmgC</i>	Acyl-CoA dehydrogenase	-1,28	1,20	-1,02
SL0834	<i>ydiS</i>	Electron transfer flavoprotein-ubiquinone oxidoreductase	-1,35	-1,00	1,20

Tabla Suplementaria 1

Diferencia de expresión de todos los genes de SV5015 en las cepas mutantes *greA*, *greB* y *greAgreB*, respecto a la cepa WT

ID	gene	Description	<i>greA</i> vs WT	<i>greB</i> vs WT	<i>greAgreB</i> vs WT
SL0835	<i>cysL</i>	HTH-type transcriptional regulator <i>cysL</i>	-1,55	1,10	-5,57
SL0836	<i>yxjC</i>	Uncharacterized transporter <i>yxjC</i>	-1,04	1,32	-2,37
SL0837	<i>ylil</i>	Soluble aldose sugar dehydrogenase <i>ylil</i>	1,14	1,03	1,35
SL0838	<i>yliJ</i>	Uncharacterized GST-like protein <i>yliJ</i>	1,04	-1,01	1,67
SL0839	<i>dacC</i>	D-alanyl-D-alanine carboxypeptidase <i>dacC</i>	1,07	1,23	2,58
SL0840	<i>deoR</i>	Deoxyribose operon repressor	1,00	1,10	-2,08
SL0841	<i>ybjG</i>	Putative undecaprenyl-diphosphatase <i>ybjG</i>	-1,08	1,12	-2,77
SL0842	<i>cmr</i>	Multidrug translocase <i>mdfA</i>	1,14	1,06	-1,45
SL0843	<i>ybjI</i>	Phosphatase <i>ybjI</i>	1,10	-1,03	1,33
SL0844	<i>ybjJ</i>	Inner membrane protein <i>ybjJ</i>	-1,10	-1,10	-1,13
SL0845	<i>ybjK</i>	Uncharacterized HTH-type transcriptional regulator <i>ybjK</i>	-1,08	1,01	-1,20
SL0846	<i>ybjL</i>	Putative transport protein <i>ybjL</i>	-1,04	1,02	-2,78
SL0847	<i>ybjM</i>	Inner membrane protein <i>ybjM</i>	1,05	1,11	-1,16
SL0848	<i>grxA</i>	Glutaredoxin-1	-1,19	-1,03	-1,99
SL0849	<i>ybjC</i>	Uncharacterized protein <i>ybjC</i>	1,04	1,12	-1,33
SL0850	<i>nfsA</i>	Oxygen-insensitive NADPH nitroreductase	1,04	-1,28	1,25
SL0851	<i>nfsA</i>	Oxygen-insensitive NADPH nitroreductase	1,15	-1,05	1,82
SL0852	<i>rimK</i>	Ribosomal protein S6 modification protein	-1,03	1,29	-1,72
SL0853	<i>ybjN</i>	Uncharacterized protein <i>ybjN</i>	-1,11	1,16	-1,64
SL0854	<i>potF</i>	Putrescine-binding periplasmic protein	1,10	1,26	3,91
SL0855	<i>potG</i>	Putrescine transport ATP-binding protein <i>potG</i>	1,38	1,04	2,73
SL0856	<i>potH</i>	Putrescine transport system permease protein <i>potH</i>	1,29	1,16	2,71
SL0857	<i>potI</i>	Putrescine transport system permease protein <i>potI</i>	-1,03	-1,11	1,46
SL0858	<i>ybjO</i>	Inner membrane protein <i>ybjO</i>	1,27	1,26	-1,85
SL0859	<i>rumB</i>	23S rRNA (uracil-5-)-methyltransferase <i>rumB</i>	1,19	1,21	-1,78
SL0860	<i>ulaA</i>	Ascorbate-specific permease IIC component <i>ulaA</i>	1,52	1,14	1,97
SL0861	<i>sgaB</i>	Phosphotransferase II B Component	1,03	1,15	1,59
SL0862	<i>yidJ</i>	Arylsulfatase	1,17	1,07	1,35
SL0863	<i>artJ</i>	ABC transporter arginine-binding protein 1	1,12	-1,15	1,37
SL0864	<i>artM</i>	Arginine ABC transporter permease protein <i>ArtM</i>	1,41	-1,04	-1,33
SL0865	<i>artQ</i>	Arginine ABC transporter permease protein <i>ArtQ</i>	1,27	-1,20	-1,15
SL0866	<i>artI</i>	Putative ABC transporter arginine-binding protein 2	1,30	1,06	1,20
SL0867	<i>artP</i>	Arginine transport ATP-binding protein <i>ArtP</i>	1,28	-1,01	-1,37
SL0868	<i>ybjP</i>	Uncharacterized lipoprotein <i>ybjP</i>	1,07	1,01	1,34
SL0869	<i>ybjQ</i>	UPF0145 protein Ent638_1382	1,04	1,29	1,25
SL0870	<i>amiD</i>	N-acetylmuramoyl-L-alanine amidase <i>AmiD</i>	-1,15	1,05	-1,04
SL0871	<i>ybjS</i>	Uncharacterized protein <i>ybjS</i>	-1,14	1,03	-2,45
SL0872	<i>ybjT</i>	Uncharacterized protein <i>ybjT</i>	1,04	-1,16	-1,01
SL0873	<i>ltaE</i>	Low specificity L-threonine aldolase	1,04	-1,05	1,14
SL0874	<i>poxB</i>	Pyruvate dehydrogenase [cytochrome]	-1,15	-1,06	-1,49

Tabla Suplementaria 1

Diferencia de expresión de todos los genes de SV5015 en las cepas mutantes *greA*, *greB* y *greAgreB*, respecto a la cepa WT

ID	gene	Description	<i>greA</i> vs WT	<i>greB</i> vs WT	<i>greAgreB</i> vs WT
SL0875	<i>hcr</i>	NADH oxidoreductase hcr	-1,01	-1,04	1,74
SL0876	<i>hcp</i>	Hydroxylamine reductase	1,05	1,23	2,63
SL0877	<i>ybjE</i>	Uncharacterized protein ybjE	-1,02	-1,17	-1,41
SL0878	<i>ybjD</i>	Uncharacterized protein ybjD	-1,03	-1,07	1,26
SL0879	<i>ybjX</i>	Uncharacterized protein ybjX	-1,58	1,10	-5,97
SL0880	<i>macA</i>	Macrolide-specific efflux protein macA	-1,09	1,04	-2,43
SL0881	<i>macB</i>	Macrolide export ATP-binding/permease protein macB	-1,11	-1,01	-1,49
SL0882	<i>cspD</i>	Cold shock-like protein cspD	1,06	1,16	1,09
SL0883	<i>clpS</i>	ATP-dependent Clp protease adapter protein clpS	-1,14	-1,01	-3,50
SL0884	<i>clpA</i>	ATP-dependent Clp protease ATP-binding subunit clpA	1,04	1,06	-1,23
SL0885	<i>tnpA1</i>	Transposase for insertion sequence element IS200	1,26	-1,00	-2,87
SL0886	<i>insF7</i>	Insertion element IS600 uncharacterized 31 kDa protein	-1,12	1,38	1,01
SL0887	-	Transposase	-1,15	1,21	1,21
SL0888	<i>ycaC</i>	Uncharacterized protein ycaC	1,10	1,07	2,29
SL0889	<i>yhhW</i>	Pirin-like protein PA2418	1,22	1,23	2,37
SL0890	<i>yafC</i>	Uncharacterized HTH-type transcriptional regulator HI_1364	1,06	-1,13	1,48
SL0891	<i>infA</i>	Translation initiation factor IF-1	1,15	-1,11	-1,25
SL0892	-	Inner Membrane Protein	1,14	1,22	-2,29
SL0893	<i>aat</i>	Leucyl/phenylalanyl-tRNA--protein transferase	1,20	1,07	1,08
SL0894	<i>cydC</i>	ATP-binding/permease protein cydC	1,18	1,01	1,34
SL0895	<i>cydD</i>	ATP-binding/permease protein cydD	1,01	-1,03	-2,02
SL0896	<i>trxB</i>	Thioredoxin reductase	1,04	-1,10	-1,49
SL0897	<i>lrp</i>	Leucine-responsive regulatory protein	-1,12	-1,16	1,30
SL0898	<i>ftsK</i>	DNA translocase ftsK	1,09	1,04	1,38
SL0899	<i>lolA</i>	Outer-membrane lipoprotein carrier protein	1,06	1,14	-1,11
SL0900	<i>rarA</i>	Replication-associated recombination protein A	1,06	1,13	-1,38
SL0901	<i>serS</i>	Seryl-tRNA synthetase	1,11	1,08	-1,13
SL0902	<i>dmsA</i>	Anaerobic dimethyl sulfoxide reductase chain A	1,13	1,10	-1,01
SL0903	<i>dmsB</i>	Anaerobic dimethyl sulfoxide reductase chain B	1,03	1,01	-1,07
SL0904	<i>dmsC</i>	Anaerobic dimethyl sulfoxide reductase chain C	1,17	1,08	-1,05
SL0905	<i>ycaD</i>	Uncharacterized MFS-type transporter ycaD	1,14	1,32	-1,80
SL0906	<i>ycaM</i>	Inner membrane transporter ycaM	-1,03	1,22	1,28
SL0907	<i>pflA</i>	Pyruvate formate-lyase 1-activating enzyme	1,08	1,14	-1,86
SL0908	-	Conserved Hypothetical Protein	1,22	1,31	-1,72
SL0909	<i>sopD2</i>	Secreted effector protein sopD2	-8,04	1,35	-3,81
SL0910	<i>pflB</i>	Formate acetyltransferase 1	1,10	1,06	-1,35
SL0911	<i>focA</i>	Probable formate transporter 1	-1,06	-1,08	-7,51
SL0912	<i>ycaO</i>	UPF0142 protein ycaO	-1,14	-1,04	-2,38
SL0913	<i>ycaP</i>	UPF0702 transmembrane protein ycaP	-1,06	-1,08	1,44
SL0914	<i>serC</i>	Phosphoserine aminotransferase	-1,00	-1,22	-1,35

Tabla Suplementaria 1

Diferencia de expresión de todos los genes de SV5015 en las cepas mutantes *greA*, *greB* y *greAgreB*, respecto a la cepa WT

ID	gene	Description	<i>greA</i> vs WT	<i>greB</i> vs WT	<i>greAgreB</i> vs WT
SL0915	<i>aroA</i>	3-phosphoshikimate 1-carboxyvinyltransferase	1,05	-1,23	-1,55
SL0916	<i>ycaL</i>	Uncharacterized metalloprotease ycaL	-1,00	-1,18	-1,17
SL0917	<i>cmk</i>	Cytidylate kinase	-1,13	1,12	-2,16
SL0918	<i>rpsA</i>	30S ribosomal protein S1	-1,06	-1,13	-1,22
SL0919	<i>ihfB</i>	Integration host factor subunit beta	-1,03	1,05	-1,01
SL0920	<i>ycaI</i>	Uncharacterized protein ycaI	-1,19	-1,09	-1,23
SL0921	<i>msbA</i>	Lipid A export ATP-binding/permease protein msbA	-1,08	-1,02	-2,20
SL0922	<i>lpxK</i>	Tetraacyldisaccharide 4'-kinase	-1,03	-1,33	-1,71
SL0923	<i>ycaQ</i>	Uncharacterized protein ycaQ	1,13	1,08	-1,18
SL0924	<i>ycaR</i>	UPF0434 protein CKO_02153	-1,00	-1,13	1,15
SL0925	<i>kdsB</i>	3-deoxy-manno-octulosonate cytidyltransferase	1,11	1,05	1,21
SL0926	<i>ycbJ</i>	Uncharacterized protein ycbJ	1,19	1,47	1,59
SL0927	<i>ycbC</i>	Uncharacterized protein ycbC	1,34	1,35	-1,02
SL0928	<i>smtA</i>	Protein smtA	1,02	-1,01	-1,62
SL0929	<i>mukF</i>	Chromosome partition protein mukF	-1,01	-1,09	-1,19
SL0930	<i>mukE</i>	Chromosome partition protein mukE	1,00	-1,21	1,05
SL0931	<i>mukB</i>	Chromosome partition protein mukB	1,03	1,14	2,29
SL0932	<i>ycbB</i>	Probable L,D-transpeptidase YcbB	1,43	1,18	1,44
SL0933	<i>ycbK</i>	Uncharacterized protein ycbK	-1,03	-1,01	-1,46
SL0934	<i>ycbL</i>	Uncharacterized protein ycbL	1,11	-1,13	-1,15
SL0935	<i>aspC</i>	Aspartate aminotransferase	1,11	-1,16	-1,03
SL0936	<i>ompF</i>	Outer membrane protein F	-1,25	-1,04	7,42
SL0937	<i>asnS</i>	Asparaginyl-tRNA synthetase	1,12	1,02	-1,25
SL0938	<i>lrp</i>	Uncharacterized HTH-type transcriptional regulator y4tD	1,13	1,13	1,11
SL0939	<i>dpaL</i>	Diaminopropionate ammonia-lyase	1,26	-1,27	3,64
SL0940	<i>yfIA</i>	Uncharacterized transporter yfIA	1,28	1,08	3,99
SL0941	<i>pncB</i>	Nicotinate phosphoribosyltransferase	1,02	1,01	-1,31
SL0942	<i>intQ</i>	Putative lambdoid prophage Qin defective integrase	1,06	-1,01	-1,04
SL0943	-	Excisionase	-1,05	-1,20	1,12
SL0944	-	Hypothetical	-1,09	1,11	1,03
SL0945	-	Hypothetical	-1,18	1,15	1,00
SL0946	<i>recE</i>	Exodeoxyribonuclease 8	-1,40	-1,10	-1,93
SL0947	-	Hypothetical	-1,95	-1,34	-1,41
SL0948	<i>ydaE</i>	Hypothetical	-2,04	-1,32	-1,12
SL0949	-	Hypothetical	-2,04	-1,24	-2,03
SL0950	<i>dicA</i>	Regulatory Protein	-1,10	-1,01	-1,44
SL0951	-	Gifsy-1 Prophage CI Protein	-1,47	1,16	-2,19
SL0952	<i>ydaU</i>	Uncharacterized protein ydaU	-2,00	-1,28	-1,62
SL0953	<i>ydaV</i>	Uncharacterized protein ydaV	-1,78	-1,35	1,15
SL0954	-	Hypothetical	-1,67	-1,31	-1,17
SL0955	-	Hypothetical	-1,46	-1,25	-1,10
SL0956	-	Hypothetical	-1,16	-1,12	-1,06
SL0957	<i>dinI</i>	DNA-damage-inducible protein I	-1,02	1,05	1,89
SL0958	-	Hypothetical	1,22	-1,02	-1,32

Tabla Suplementaria 1

Diferencia de expresión de todos los genes de SV5015 en las cepas mutantes *greA*, *greB* y *greAgreB*, respecto a la cepa WT

ID	gene	Description	<i>greA</i> vs WT	<i>greB</i> vs WT	<i>greAgreB</i> vs WT
SL0959	-	Hypothetical	-1,50	-1,04	-1,53
SL0960	-	Hypothetical	-1,65	-1,22	1,17
SL0961	<i>quuQ</i>	Antitermination protein Q homolog from lambdoid prophage Qin	1,11	1,12	1,93
SL0962	-	Hypothetical	-1,44	-1,02	-1,72
SL0963	-	Bacteriophage Protein	-1,44	-1,22	-2,18
SL0964	-	Hypothetical	1,03	-1,01	1,29
SL0965	-	Hypothetical	-1,87	-1,12	-2,25
SL0966	<i>arrD</i>	Probable lysozyme from lambdoid prophage DLP12	-1,77	-1,04	-3,53
SL0967	<i>rzpD</i>	Putative Rz endopeptidase from lambdoid prophage DLP12	-2,04	-1,37	-4,10
SL0968	-	Hypothetical	-2,15	-1,28	-3,14
SL0969	-	Phage Terminase Large Subunit	-1,39	-1,38	-2,08
SL0970	-	Hypothetical	-1,26	-1,15	-1,69
SL0971	-	Phage Portal Protein Lambda Family	-1,21	-1,36	-1,36
SL0972	<i>clpP1</i>	ATP-dependent Clp protease proteolytic subunit 1	-1,40	-1,21	-1,11
SL0973	-	Hypothetical	-2,06	-1,33	-2,53
SL0974	-	Hypothetical	-1,91	-1,39	-2,39
SL0975	-	Minor Tail Protein Z-Like	-1,91	-1,36	-2,19
SL0976	-	Minor Tail Protein U	-1,73	-1,28	-1,96
SL0977	-	Tail Protein V	-1,62	-1,44	-1,74
SL0978	-	Minor Tail Component Of Putative Prophage	-1,50	-1,12	-1,76
SL0979	-	Minor Tail Protein	-1,52	-1,14	-2,27
SL0980	-	Hypothetical	-1,32	-1,16	-1,76
SL0981	-	Minor Tail Protein	-1,22	-1,03	-1,58
SL0982	<i>ail</i>	Attachment invasion locus protein	1,00	1,26	1,48
SL0983	<i>sodC1</i>	Superoxide dismutase [Cu-Zn] 1	-1,01	1,19	1,13
SL0984	-	Phage Minor Tail Protein L	-1,39	-1,24	-2,05
SL0985	-	NLP/P60 Protein	-1,25	-1,23	-1,45
SL0986	-	Phage Tail Assembly Protein	1,01	-1,07	1,52
SL0987	-	Hocificity Protein J	-1,70	-1,15	-2,37
SL0988	<i>stfQ</i>	Side tail fiber protein homolog from lambdoid prophage Qin	-1,78	-1,55	-2,71
SL0989	<i>ycdD</i>	Tail fiber assembly protein homolog from lambdoid prophage Fels-1	-1,94	-1,45	-3,53
SL0990	-	Hypothetical	-2,79	-1,68	-6,38
SL0991	<i>ssel</i>	Secreted effector protein ssel	-1,56	1,29	-1,47
SL0992	-	Hypothetical Protein SL0992	-1,10	1,21	-1,08
SL0993	<i>yedK</i>	Uncharacterized protein yedK	-1,37	-1,07	-1,98
SL0994	-	Hypothetical	-1,83	-1,71	-3,96
SL0995	-	Prophage Encoded Virulence Factor	-2,02	-1,28	-1,84
SL0996	<i>msgA</i>	Virulence protein msgA	-1,48	-1,02	-5,56
SL0997	<i>pepN</i>	Aminopeptidase N	1,09	-1,07	1,56

Tabla Suplementaria 1

Diferencia de expresión de todos los genes de SV5015 en las cepas mutantes *greA*, *greB* y *greAgreB*, respecto a la cepa WT

ID	gene	Description	<i>greA</i> vs WT	<i>greB</i> vs WT	<i>greAgreB</i> vs WT
SL0998	<i>pyrD</i>	Dihydroorotate dehydrogenase	-1,09	1,06	-1,85
SL0999	<i>ycbW</i>	Uncharacterized protein ycbW	-1,29	-1,11	-3,12
SL1000	<i>ycbX</i>	Uncharacterized protein ycbX	-1,07	-1,09	-2,33
SL1001	<i>rlmL</i>	Ribosomal RNA large subunit methyltransferase L	-1,12	-1,04	-1,60
SL1002	<i>uup</i>	ABC transporter ATP-binding protein uup	1,02	1,05	1,07
SL1003	<i>pqiA</i>	Paraquat-inducible protein A	1,03	1,06	1,10
SL1004	<i>pqiB</i>	Paraquat-inducible protein B	-1,07	1,03	1,15
SL1005	<i>ymbA</i>	Uncharacterized lipoprotein ymbA	1,01	1,04	1,58
SL1006	<i>rmf</i>	Ribosome modulation factor	1,19	1,13	-1,47
SL1007	<i>fabA</i>	3-hydroxydecanoyl-[acyl-carrier-protein] dehydratase	1,13	-1,21	-1,03
SL1008	<i>ycbZ</i>	Putative protease La homolog	1,08	-1,33	-1,89
SL1009	<i>ycbG</i>	UPF0268 protein ycbG	1,16	1,10	1,15
SL1010	<i>ompA</i>	Outer membrane protein A	1,07	1,09	1,01
SL1011	<i>sulA</i>	Cell division inhibitor sulA	-1,19	-1,19	1,39
SL1012	<i>sxy</i>	Protein sxy	1,20	1,07	3,23
SL1013	<i>yccS</i>	Inner membrane protein yccS	1,19	-1,07	-1,03
SL1014	<i>yccF</i>	Inner membrane protein yccF	1,04	-1,03	-2,33
SL1015	<i>helD</i>	Helicase IV	1,18	1,04	1,57
SL1016	<i>mgsA</i>	Methylglyoxal synthase	1,08	1,22	2,85
SL1017	<i>yccT</i>	UPF0319 protein yccT	1,16	1,27	1,71
SL1018	<i>yccU</i>	Uncharacterized protein yccU	1,13	1,36	2,07
SL1019	<i>hspQ</i>	Heat shock protein hspQ	1,14	1,34	2,80
SL1020	<i>rlmI</i>	Ribosomal RNA large subunit methyltransferase I	-1,02	1,16	-1,01
SL1021	<i>ybcL</i>	UPF0098 protein ybcL	-1,04	1,11	1,51
SL1022	<i>ybcM</i>	Uncharacterized HTH-type transcriptional regulator ybcM	1,09	1,05	1,63
SL1023	<i>yccX</i>	Acylphosphatase	1,27	1,12	1,32
SL1024	<i>tusE</i>	Sulfurtransferase tusE	1,30	1,04	-1,42
SL1025	<i>yccA</i>	Inner membrane protein yccA	1,09	1,10	-1,06
SL1026	-	Hypothetical	-1,63	1,10	-3,52
SL1027	<i>pipB</i>	Secreted effector protein pipB	-2,78	1,16	-16,02
SL1028	-	Inner Membrane Protein	-2,14	-1,05	-47,98
SL1029	<i>sigE</i>	Chaperone protein sigE	-1,10	1,11	-8,91
SL1030	<i>sopB</i>	Inositol phosphate phosphatase sopB	-1,10	-1,03	-10,63
SL1031	-	Hypothetical	-1,65	-1,10	-1,75
SL1032	-	Hypothetical	-1,44	1,03	-1,49
SL1033	<i>pipD</i>	Probable dipeptidase	-1,10	1,62	1,52
SL1034	<i>yedV</i>	Putative sensor-like histidine kinase yedV	1,17	-1,04	-1,35
SL1035	<i>yedW</i>	Probable transcriptional regulatory protein yedW	1,08	-1,02	-1,21
SL1036	<i>yedX</i>	5-hydroxyisourate hydrolase	1,09	1,39	1,05
SL1037	<i>hpaC</i>	4-hydroxyphenylacetate 3-monooxygenase reductase component	1,26	-1,03	1,22
SL1038	<i>hpaB</i>	4-hydroxyphenylacetate 3-monooxygenase oxygenase component	1,05	1,14	1,75
SL1039	<i>hpcR</i>	Homoprotocatechuate degradative operon repressor	-1,21	1,04	1,55

Tabla Suplementaria 1

Diferencia de expresión de todos los genes de SV5015 en las cepas mutantes *greA*, *greB* y *greAgreB*, respecto a la cepa WT

ID	gene	Description	<i>greA</i> vs WT	<i>greB</i> vs WT	<i>greAgreB</i> vs WT
SL1040	<i>hpaG</i>	4-hydroxyphenylacetate degradation bifunctional isomerase/decarboxylase	-1,05	-1,11	7,56
SL1041	<i>hpcC</i>	5-carboxymethyl-2-hydroxymuconate semialdehyde dehydrogenase	1,01	-1,10	7,23
SL1042	<i>hpcB</i>	3,4-dihydroxyphenylacetate 2,3-dioxygenase	-1,01	-1,16	6,00
SL1043	<i>hpcD</i>	5-carboxymethyl-2-hydroxymuconate Delta-isomerase	-1,06	-1,20	5,31
SL1044	<i>hpcG</i>	2-oxo-hepta-3-ene-1,7-dioic acid hydratase	-1,17	-1,78	3,18
SL1045	<i>hpcH</i>	4-hydroxy-2-oxo-heptane-1,7-dioate aldolase	-1,41	-2,00	3,02
SL1046	<i>ttuB</i>	Putative tartrate transporter	1,13	-1,13	3,69
SL1047	<i>ydiP</i>	Transcriptional Regulator AraC Family	-1,04	-1,18	1,51
SL1048	<i>atsA</i>	Arylsulfatase	1,27	-1,06	2,97
SL1049	<i>iraM</i>	Anti-adapter protein iraM	-1,15	1,06	-2,94
SL1050	<i>cbpM</i>	Chaperone modulatory protein cbpM	1,03	1,11	1,67
SL1051	<i>cbpA</i>	Curved DNA-binding protein	1,11	1,22	1,33
SL1052	-	Metal Resistance Protein	1,01	1,11	-1,66
SL1053	<i>dsbD</i>	Thiol:disulfide interchange protein dsbD	1,27	1,11	1,62
SL1054	-	DSBA Oxidoreductase	1,40	1,09	1,73
SL1055	-	Thioredoxin-like protein HI_1115	1,60	1,17	1,18
SL1056	<i>agp</i>	Glucose-1-phosphatase	1,04	1,28	3,03
SL1057	<i>yccJ</i>	Uncharacterized protein yccJ	1,22	1,18	1,44
SL1058	<i>wrbA</i>	Flavoprotein wrbA	1,09	1,06	1,16
SL1059	<i>ymdF</i>	Uncharacterized protein ymdF	-1,04	1,56	-1,47
SL1060	<i>rutR</i>	HTH-type transcriptional regulator rutR	1,20	1,14	1,84
SL1061	-	Uncharacterized protein R02472	1,20	1,19	9,50
SL1062	<i>putA</i>	Bifunctional protein putA	1,76	1,51	77,71
SL1063	<i>putP</i>	Sodium/proline symporter	1,15	-1,25	12,16
SL1064	<i>phoH</i>	Protein phoH	-1,56	1,21	-1,69
SL1065	<i>yfeT</i>	Uncharacterized HTH-type transcriptional regulator HI_0143	-1,09	-1,13	-2,08
SL1066	<i>sglT</i>	Sodium/glucose cotransporter	1,15	-1,18	6,36
SL1067	<i>nanE1</i>	Putative N-acetylmannosamine-6-phosphate 2-epimerase 1	1,14	1,00	4,53
SL1068	<i>nanM</i>	N-acetylneuraminase epimerase	-1,44	-1,77	4,04
SL1069	<i>yiiY</i>	Uncharacterized protein yiiY	-1,43	-1,50	5,40
SL1070	<i>yjhB</i>	Putative metabolite transport protein yjhB	-1,31	-1,41	2,42
SL1071	<i>yjhC</i>	Uncharacterized oxidoreductase yjhC	1,01	1,08	1,52
SL1072	<i>ghrA</i>	Glyoxylate/hydroxypyruvate reductase A	1,21	-1,38	2,06
SL1073	<i>ycdX</i>	Putative hydrolase ycdX	1,12	-1,10	1,30
SL1074	<i>ycdY</i>	Uncharacterized protein ycdY	1,15	-1,11	1,32
SL1075	<i>ycdZ</i>	Inner membrane protein ycdZ	1,22	1,04	-1,57
SL1076	<i>csgG</i>	Curli production assembly/transport component csgG	1,28	1,21	-1,42
SL1077	<i>csgF</i>	Curli production assembly/transport component csgF	1,01	1,13	2,00
SL1078	<i>csgE</i>	Curli production assembly/transport component csgE	-1,37	-1,06	1,57
SL1079	<i>csgD</i>	Probable csgAB operon transcriptional regulatory protein	-1,18	-1,02	1,28
SL1080	<i>csgB</i>	Minor curlin subunit	1,10	1,11	1,08

Tabla Suplementaria 1

Diferencia de expresión de todos los genes de SV5015 en las cepas mutantes *greA*, *greB* y *greAgreB*, respecto a la cepa WT

ID	gene	Description	<i>greA</i> vs WT	<i>greB</i> vs WT	<i>greAgreB</i> vs WT
SL1081	<i>csgA</i>	Major curlin subunit	1,37	1,64	1,36
SL1082	<i>csgC</i>	Curli assembly protein <i>csgC</i>	-1,04	1,64	1,08
SL1083	<i>ymdA</i>	Uncharacterized protein <i>ymdA</i>	1,05	-1,09	3,20
SL1084	<i>ymdB</i>	UPF0189 protein <i>ymdB</i>	1,09	1,09	1,79
SL1085	<i>ymdC</i>	Uncharacterized protein <i>ymdC</i>	-1,03	-1,06	-1,20
SL1086	<i>mdoC</i>	Glucans biosynthesis protein C	1,21	1,22	-2,02
SL1087	<i>mdoG</i>	Glucans biosynthesis protein G	1,03	-1,12	-1,29
SL1088	<i>mdoH</i>	Glucans biosynthesis glucosyltransferase H	1,15	-1,14	-1,05
SL1089	<i>yceK</i>	Uncharacterized protein <i>yceK</i>	1,14	1,08	2,17
SL1090	<i>msyB</i>	Acidic protein <i>msyB</i>	1,23	1,20	2,50
SL1091	<i>mdtG</i>	Multidrug resistance protein <i>mdtG</i>	1,06	-1,11	-1,44
SL1092	<i>htrB</i>	Lipid A biosynthesis lauroyl acyltransferase	-1,04	-1,13	-2,37
SL1093	<i>yceA</i>	UPF0176 protein <i>yceA</i>	-1,02	1,13	-1,00
SL1094	<i>yceI</i>	UPF0312 protein Ent638_1570	1,15	1,28	1,32
SL1095	<i>yceJ</i>	Cytochrome b561 homolog 2	-1,07	1,07	1,24
SL1096	<i>yceO</i>	Hypothetical	1,30	-1,02	-1,09
SL1097	<i>solA</i>	N-methyl-L-tryptophan oxidase	1,26	-1,10	1,62
SL1098	<i>bssS</i>	Biofilm regulator <i>BssS</i>	1,09	1,49	1,53
SL1099	<i>dinI</i>	DNA-damage-inducible protein I	1,04	1,06	-1,08
SL1100	<i>pyrC</i>	Dihydroorotase	1,02	1,00	1,06
SL1101	<i>yceB</i>	Uncharacterized lipoprotein <i>yceB</i>	-1,02	1,07	-1,39
SL1102	<i>grxB</i>	Glutaredoxin-2	1,21	1,37	2,26
SL1103	<i>mdtH</i>	Multidrug resistance protein <i>mdtH</i>	1,13	1,19	-2,07
SL1104	<i>rimJ</i>	Ribosomal-protein-alanine acetyltransferase	1,23	1,04	2,57
SL1105	<i>yceH</i>	UPF0502 protein <i>yceH</i>	1,32	1,25	3,95
SL1106	<i>mviM</i>	Virulence factor <i>mviM</i>	1,26	1,13	2,46
SL1107	<i>mviN</i>	Virulence factor <i>mviN</i>	1,22	1,13	-2,09
SL1108	<i>flgN</i>	Flagella synthesis protein <i>flgN</i>	-1,10	1,19	-1,28
SL1109	<i>flgM</i>	Negative regulator of flagellin synthesis	1,15	1,33	1,22
SL1110	<i>flgA</i>	Flagella basal body P-ring formation protein <i>flgA</i>	1,52	1,11	3,45
SL1111	<i>flgB</i>	Flagellar basal-body rod protein <i>flgB</i>	-1,12	-1,27	1,24
SL1112	<i>flgC</i>	Flagellar basal-body rod protein <i>flgC</i>	-1,06	-1,28	1,31
SL1113	<i>flgD</i>	Basal-body rod modification protein <i>flgD</i>	-1,02	-1,13	1,85
SL1114	<i>flgE</i>	Flagellar hook protein <i>flgE</i>	1,02	-1,00	1,79
SL1115	<i>flgF</i>	Flagellar basal-body rod protein <i>flgF</i>	1,06	-1,01	2,09
SL1116	<i>flgG</i>	Flagellar basal-body rod protein <i>flgG</i>	1,03	1,01	2,14
SL1117	<i>flgH</i>	Flagellar L-ring protein	-1,07	-1,21	1,60
SL1118	<i>flgI</i>	Flagellar P-ring protein	-1,08	-1,21	1,10
SL1119	<i>flgJ</i>	Peptidoglycan hydrolase <i>flgJ</i>	1,02	-1,09	1,15
SL1120	<i>flgK</i>	Flagellar hook-associated protein 1	-1,10	1,09	-2,64
SL1121	<i>flgL</i>	Flagellar hook-associated protein 3	-1,00	1,12	-1,48
SL1122	<i>rne</i>	Ribonuclease E	1,17	-1,24	1,71

Tabla Suplementaria 1Diferencia de expresión de todos los genes de SV5015 en las cepas mutantes *greA*, *greB* y *greAgreB*, respecto a la cepa WT

ID	gene	Description	<i>greA</i> vs WT	<i>greB</i> vs WT	<i>greAgreB</i> vs WT
SL1123	<i>rluC</i>	Ribosomal large subunit pseudouridine synthase C	-1,05	1,01	-1,65
SL1124	<i>yiaF</i>	Uncharacterized protein yiaF	1,02	1,17	-1,14
SL1125	-	Hypothetical	1,18	1,20	1,18
SL1126	<i>yceF1</i>	Maf-like protein yceF 1	1,03	1,13	1,00
SL1127	<i>yceD</i>	Uncharacterized protein yceD	-1,09	-1,06	-1,86
SL1128	<i>rpmF</i>	50S ribosomal protein L32	-1,07	-1,00	-1,29
SL1129	<i>plsX</i>	Phosphate acyltransferase	-1,11	-1,30	-4,72
SL1130	<i>fabH</i>	3-oxoacyl-[acyl-carrier-protein] synthase 3	1,17	-1,08	-2,12
SL1131	<i>fabD</i>	Malonyl CoA-acyl carrier protein transacylase	1,19	-1,15	-1,16
SL1132	<i>fabG</i>	3-oxoacyl-[acyl-carrier-protein] reductase	1,04	-1,13	1,11
SL1133	<i>acpP</i>	Acyl carrier protein	-1,05	-1,10	-1,14
SL1134	<i>fabF</i>	3-oxoacyl-[acyl-carrier-protein] synthase 2	1,01	-1,11	-1,37
SL1135	<i>pabC</i>	Aminodeoxychorismate lyase	1,07	1,05	-1,36
SL1136	<i>yceG</i>	UPF0755 protein yceG	-1,03	1,08	-1,82
SL1137	<i>tmk</i>	Thymidylate kinase	1,04	1,05	-1,68
SL1138	<i>holB</i>	DNA polymerase III subunit delta'	1,08	-1,07	-1,61
SL1139	<i>ycfH</i>	Uncharacterized deoxyribonuclease ycfH	1,21	1,13	-1,00
SL1140	<i>ptsG</i>	PTS system glucose-specific EIICB component	1,55	1,07	1,22
SL1141	<i>fhuE</i>	FhuE receptor	-1,05	1,73	-1,38
SL1142	<i>hinT</i>	HIT-like protein hinT	-1,18	-1,37	-1,64
SL1143	<i>ycfL</i>	Uncharacterized protein ycfL	-1,26	-1,56	-1,81
SL1144	<i>ycfM</i>	Uncharacterized protein ycfM	-1,09	-1,39	-1,57
SL1145	<i>thiK</i>	Thiamine kinase	-1,06	-1,49	-1,77
SL1146	<i>nagZ</i>	Beta-hexosaminidase	-1,02	-1,25	-1,46
SL1147	<i>ycfP</i>	UPF0227 protein KPN78578_10770	1,03	1,05	1,22
SL1148	<i>ndh</i>	NADH dehydrogenase	1,22	1,36	-1,18
SL1149	<i>ycfJ</i>	Uncharacterized protein ycfJ	1,11	1,32	-1,57
SL1150	<i>ycfQ</i>	Uncharacterized HTH-type transcriptional regulator ycfQ	1,08	1,17	1,09
SL1151	<i>bhsA</i>	Multiple stress resistance protein BhsA	1,06	1,26	-2,12
SL1152	<i>ycfS</i>	Probable L,D-transpeptidase YcfS	1,30	1,09	1,35
SL1153	<i>mfd</i>	Transcription-repair-coupling factor	1,17	-1,08	1,32
SL1154	<i>lolC</i>	Lipoprotein-releasing system transmembrane protein lolC	1,20	1,01	-2,02
SL1155	<i>lolD</i>	Lipoprotein-releasing system ATP-binding protein LolD	-1,06	-1,14	-1,48
SL1156	<i>lolE</i>	Lipoprotein-releasing system transmembrane protein lolE	1,08	-1,20	-1,28
SL1157	<i>nagK</i>	N-acetyl-D-glucosamine kinase	1,37	1,05	1,62
SL1158	<i>npdA</i>	NAD-dependent deacetylase	1,23	1,12	1,91
SL1159	<i>potD</i>	Spermidine/putrescine-binding periplasmic protein	-1,16	-1,05	1,17
SL1160	<i>potC</i>	Spermidine/putrescine transport system permease protein potC	-1,49	-1,06	-2,92
SL1161	<i>sifA</i>	Secreted effector protein sifA	-15,51	-1,07	-3,57
SL1162	<i>potB</i>	Spermidine/putrescine transport system permease protein potB	-1,09	-1,09	-1,34

Tabla Suplementaria 1

Diferencia de expresión de todos los genes de SV5015 en las cepas mutantes *greA*, *greB* y *greAgreB*, respecto a la cepa WT

ID	gene	Description	<i>greA</i> vs WT	<i>greB</i> vs WT	<i>greAgreB</i> vs WT
SL1163	<i>potA</i>	Spermidine/putrescine import ATP-binding protein PotA	-1,04	1,03	-1,58
SL1164	<i>pepT</i>	Peptidase T	1,29	-1,08	1,30
SL1165	-	Hypothetical Protein SL1165	1,29	1,19	-1,75
SL1167	<i>ycfD</i>	Uncharacterized protein ycfD	1,03	-1,06	1,14
SL1168	<i>phoQ</i>	Virulence sensor histidine kinase phoQ	-1,28	-1,16	-2,17
SL1169	<i>phoP</i>	Virulence transcriptional regulatory protein phoP	-1,14	-1,01	-1,56
SL1170	<i>purB</i>	Adenylosuccinate lyase	1,12	-1,02	1,16
SL1171	<i>hflD</i>	High frequency lysogenization protein hflD	1,05	-1,07	-1,43
SL1172	<i>mnmA</i>	tRNA-specific 2-thiouridylase mnmA	1,06	1,12	-2,25
SL1173	<i>nudJ</i>	Phosphatase nudJ	1,12	-1,26	-1,75
SL1174	-	Hypothetical	1,37	1,07	-1,60
SL1175	<i>rluE</i>	Ribosomal large subunit pseudouridine synthase E	1,40	1,03	-1,80
SL1176	<i>icd</i>	Isocitrate dehydrogenase [NADP]	-1,06	-1,25	3,29
SL1177	-	Bacteriophage Protein	-2,96	1,17	-25,20
SL1178	-	Hypothetical Protein SL1178	-2,75	1,66	-7,87
SL1179	<i>envF</i>	Probable lipoprotein envF	-1,32	1,19	-2,17
SL1180	<i>msgA</i>	Virulence protein msgA	-1,13	1,20	-2,85
SL1181	<i>envE</i>	Probable lipoprotein envE	-1,28	1,13	-3,82
SL1182	<i>cspH</i>	Cold shock-like protein cspH	-1,05	1,31	-3,33
SL1183	<i>pagD</i>	Virulence protein pagD	-2,53	1,62	-6,00
SL1184	<i>pagC</i>	Virulence membrane protein pagC	-2,42	1,32	-11,99
SL1185	-	Lysozyme Inhibitor	-1,19	1,14	-1,75
SL1186	-	Hypothetical	-1,47	1,10	-4,22
SL1187	<i>ibp</i>	Small heat shock protein ibp	1,04	1,66	1,96
SL1188	-	Hypothetical	-1,14	1,37	-1,93
SL1189	<i>yodB</i>	Cytochrome b561 homolog 1	-1,39	-1,02	-2,27
SL1190	-	Outer Membrane Lipoprotein	-1,12	-1,27	-1,54
SL1191	<i>xp55</i>	Protein XP55	1,49	-1,02	3,96
SL1192	<i>dppB</i>	Putative peptide transport system permease protein BMEII0209	1,22	-1,42	2,88
SL1193	<i>nikC</i>	Putative peptide transport system permease protein BruAb2_1032	1,52	1,06	1,85
SL1194	<i>nikD</i>	Nickel import ATP-binding protein NikD	1,11	-1,20	2,65
SL1195	<i>potA</i>	Spermidine/putrescine import ATP-binding protein PotA	1,03	-1,05	1,79
SL1196	<i>ynal</i>	Uncharacterized mscS family protein aq_812	-1,24	-1,30	-1,80
SL1197	<i>yhjQ</i>	Uncharacterized cysteine-rich protein yhjQ	-1,10	1,44	1,79
SL1198	<i>yodA</i>	Metal-binding protein yodA	1,34	1,13	2,48
SL1199	<i>aadA</i>	Streptomycin 3"-adenylyltransferase	1,02	1,06	1,30
SL1200	-	Response Regulator	1,05	1,17	-1,02
SL1201	<i>ycgE</i>	Uncharacterized HTH-type transcriptional regulator ycgE	-1,06	1,11	-2,37
SL1202	<i>ymgB</i>	Hypothetical	1,03	1,02	1,84
SL1203	-	Hypothetical	-1,00	1,12	1,13
SL1204	<i>aroQ</i>	Monofunctional chorismate mutase	-2,19	1,16	-3,35
SL1205	<i>leuE</i>	Leucine efflux protein	-1,32	-1,11	-2,13

Tabla Suplementaria 1

Diferencia de expresión de todos los genes de SV5015 en las cepas mutantes *greA*, *greB* y *greAgreB*, respecto a la cepa WT

ID	gene	Description	<i>greA</i> vs WT	<i>greB</i> vs WT	<i>greAgreB</i> vs WT
SL1206	<i>yeaR</i>	Uncharacterized protein yeaR	1,24	1,24	-1,18
SL1207	<i>yoaG</i>	Protein yoaG	-1,47	-1,03	1,24
SL1208	-	Hypothetical	1,10	1,10	-1,19
SL1209	-	Hypothetical	1,08	1,25	-1,36
SL1210	<i>yeaQ</i>	UPF0410 protein yeaQ	1,29	1,32	1,44
SL1211	<i>yoaF</i>	Uncharacterized protein yoaF	-1,24	1,15	-1,61
SL1212	-	Hypothetical	-1,02	1,08	-1,41
SL1213	<i>yeaO</i>	Uncharacterized protein yeaO	1,29	1,26	-1,15
SL1214	<i>yeaN</i>	Inner membrane transport protein yeaN	-1,09	-1,08	-1,77
SL1215	<i>yeaM</i>	Uncharacterized HTH-type transcriptional regulator yeaM	1,05	-1,07	-1,20
SL1216	<i>yeaL</i>	UPF0756 membrane protein yeaL	1,06	-1,06	-2,55
SL1217	<i>yeaK</i>	Uncharacterized protein yeaK	-1,21	-1,22	-2,37
SL1218	<i>yeaJ</i>	Putative diguanylate cylase YeaJ	1,01	-1,01	-3,03
SL1219	<i>yeaH</i>	UPF0229 protein yeaH	-1,03	1,11	1,74
SL1220	<i>yeaG</i>	Uncharacterized protein yeaG	1,08	1,16	2,00
SL1221	<i>mipA</i>	MitA-interacting protein	-1,05	-1,11	-1,15
SL1222	<i>chuR</i>	Anaerobic sulfatase-maturing enzyme	-1,05	-1,07	-1,42
SL1223	<i>yeaE</i>	Uncharacterized protein yeaE	1,11	-1,20	2,25
SL1224	<i>yeaD</i>	Putative glucose-6-phosphate 1-epimerase	1,30	1,15	-1,83
SL1225	<i>gapA</i>	Glyceraldehyde-3-phosphate dehydrogenase A	1,12	1,10	1,00
SL1226	<i>msrB</i>	Peptide methionine sulfoxide reductase msrB	1,03	-1,04	2,56
SL1227	<i>yeaC</i>	Uncharacterized protein yeaC	1,32	1,05	3,00
SL1228	<i>pncA</i>	Pyrazinamidase/nicotinamidase	1,14	-1,19	1,79
SL1229	<i>ansA</i>	L-asparaginase 1	1,18	-1,26	1,40
SL1230	<i>sppA</i>	Protease 4	1,02	-1,38	1,48
SL1231	<i>ydjA</i>	Putative NAD(P)H nitroreductase ydjA	1,12	1,02	2,64
SL1232	<i>selD</i>	Selenide, water dikinase	1,11	-1,10	1,53
SL1233	<i>topB</i>	DNA topoisomerase 3	1,03	-1,26	-1,14
SL1234	<i>gdhA</i>	NADP-specific glutamate dehydrogenase	-1,02	-1,09	1,57
SL1235	<i>ynjH</i>	Uncharacterized protein ynjH	-1,26	1,19	-1,56
SL1236	<i>nudG</i>	CTP pyrophosphohydrolase	-1,29	1,22	-2,76
SL1237	<i>xthA</i>	Exodeoxyribonuclease III	-1,03	-1,08	-2,28
SL1238	<i>astC</i>	Succinylornithine transaminase	-1,30	-1,41	43,62
SL1239	<i>astA</i>	Arginine N-succinyltransferase	-1,37	-2,03	26,67
SL1240	<i>astD</i>	N-succinylglutamate 5-semialdehyde dehydrogenase	-1,43	-1,74	23,23
SL1241	<i>astB</i>	N-succinylarginine dihydrolase	-1,35	-1,81	14,27
SL1242	<i>astE</i>	Succinylglutamate desuccinylase	-1,19	-2,02	8,31
SL1243	<i>spy</i>	Spheroplast protein Y	-1,08	1,19	2,21
SL1244	<i>cho</i>	Excinuclease cho	-1,05	1,06	-1,55
SL1245	<i>nadE</i>	NH(3)-dependent NAD(+) synthetase	1,01	-1,08	1,74
SL1246	<i>osmE</i>	Osmotically-inducible lipoprotein E	1,19	1,23	1,08
SL1247	<i>chbB</i>	N,N'-diacetylchitobiose-specific phosphotransferase enzyme IIB component	-1,10	-1,11	2,05
SL1248	<i>chbC</i>	N,N'-diacetylchitobiose permease IIC component	1,03	-1,15	2,19

Tabla Suplementaria 1

Diferencia de expresión de todos los genes de SV5015 en las cepas mutantes *greA*, *greB* y *greAgreB*, respecto a la cepa WT

ID	gene	Description	<i>greA</i> vs WT	<i>greB</i> vs WT	<i>greAgreB</i> vs WT
SL1249	<i>chbA</i>	N,N'-diacetylchitobiose-specific phosphotransferase enzyme IIA component	1,23	1,14	1,09
SL1250	<i>chbR</i>	HTH-type transcriptional regulator chbR	1,06	-1,24	-1,16
SL1251	<i>chbF</i>	6-phospho-beta-glucosidase	1,41	-1,17	1,23
SL1252	<i>chbG</i>	UPF0249 protein chbG	1,05	1,00	1,37
SL1253	<i>katE</i>	Catalase HP11	1,27	1,20	1,83
SL1254	<i>cedA</i>	Cell division activator cedA	-1,16	1,10	-1,03
SL1255	<i>ydjN</i>	Uncharacterized symporter ydjN	-1,04	1,01	3,28
SL1256	<i>ydjM</i>	Inner membrane protein ydjM	-1,28	1,00	-1,23
SL1257	<i>yniC</i>	Phosphatase yniC	1,13	-1,14	1,05
SL1258	<i>yniB</i>	Uncharacterized protein yniB	1,05	1,08	1,13
SL1259	<i>yniA</i>	Uncharacterized protein yniA	1,23	1,38	3,45
SL1260	<i>ydiZ</i>	Uncharacterized protein ydiZ	1,11	1,07	1,91
SL1261	<i>pfkB</i>	6-phosphofructokinase isozyme 2	1,16	1,13	2,15
SL1262	<i>ydiY</i>	Uncharacterized protein ydiY	-1,13	1,09	-3,05
SL1263	-	Hypothetical	-1,90	-1,40	-12,64
SL1264	-	DNA/RNA Non-Specific Endonuclease	-2,17	1,18	-7,63
SL1265	<i>nucA</i>	Nuclease	-2,21	1,00	-13,64
SL1266	<i>rfc</i>	O-antigen polymerase	-1,22	1,02	-2,41
SL1267	<i>thrS</i>	Threonyl-tRNA synthetase	1,18	1,14	1,17
SL1268	<i>infC</i>	Translation initiation factor IF-3	1,00	-1,01	-1,48
SL1269	<i>rpml</i>	50S ribosomal protein L35	1,02	-1,08	-1,22
SL1270	<i>rplT</i>	50S ribosomal protein L20	-1,03	-1,01	-1,21
SL1271	<i>pheS</i>	Phenylalanyl-tRNA synthetase alpha chain	1,13	-1,09	1,09
SL1272	<i>pheT</i>	Phenylalanyl-tRNA synthetase beta chain	1,17	-1,02	1,94
SL1273	<i>ihfA</i>	Integration host factor subunit alpha	-1,07	1,06	-1,02
SL1274	<i>btuC</i>	Vitamin B12 import system permease protein BtuC	1,15	-1,11	-1,72
SL1275	<i>btuE</i>	Vitamin B12 transport periplasmic protein BtuE	1,08	-1,06	1,10
SL1276	<i>btuD</i>	Vitamin B12 import ATP-binding protein BtuD	1,04	-1,17	1,13
SL1277	<i>nlpC</i>	Probable lipoprotein nlpC	-1,06	-1,08	1,16
SL1278	<i>cdgR</i>	Cyclic di-GMP regulator cdgR	-1,08	1,07	-2,05
SL1279	<i>ydiU</i>	UPF0061 protein ydiU	1,07	1,09	1,55
SL1280	<i>ydiE</i>	Uncharacterized protein ydiE	1,21	1,48	-1,28
SL1281	<i>aroH</i>	Phospho-2-dehydro-3-deoxyheptonate aldolase, Trp-sensitive	1,15	1,01	-1,48
SL1282	<i>ydiA</i>	Putative phosphotransferase CKO_01727	1,09	-1,13	1,01
SL1283	<i>ppsA</i>	Phosphoenolpyruvate synthase	1,03	-1,18	4,30
SL1284	<i>fadK</i>	Short-chain-fatty-acid--CoA ligase	1,23	1,08	-1,08
SL1285	<i>ydiT</i>	Ferredoxin-like protein ydiT	1,10	-1,03	-1,11
SL1286	<i>ydiS</i>	Probable electron transfer flavoprotein-quinone oxidoreductase ydiS	-1,01	-1,04	-1,19
SL1287	<i>ydiR</i>	Putative electron transfer flavoprotein subunit ydiR	-1,32	1,23	-2,22
SL1288	<i>ydiQ</i>	Putative electron transfer flavoprotein subunit ydiQ	-1,05	-1,16	1,48
SL1289	<i>ydiP</i>	Uncharacterized HTH-type transcriptional regulator ydiP	-1,33	-1,19	1,27
SL1290	<i>ydiO</i>	Uncharacterized protein ydiO	1,09	1,12	1,78
SL1291	<i>ydiF</i>	Uncharacterized protein ydiF	1,35	1,01	4,23

Tabla Suplementaria 1

Diferencia de expresión de todos los genes de SV5015 en las cepas mutantes *greA*, *greB* y *greAgreB*, respecto a la cepa WT

ID	gene	Description	<i>greA</i> vs WT	<i>greB</i> vs WT	<i>greAgreB</i> vs WT
SL1292	<i>aroD</i>	3-dehydroquinase dehydratase	1,21	1,04	2,37
SL1293	<i>ydiB</i>	Quinate/shikimate dehydrogenase	-1,06	-1,22	2,17
SL1294	<i>ydiN</i>	Inner membrane transport protein ydiN	1,50	1,58	-2,01
SL1295	<i>ydiN</i>	Inner membrane transport protein ydiN	-1,07	-1,05	1,01
SL1296	<i>ydiM</i>	Inner membrane transport protein ydiM	1,00	1,43	-1,39
SL1297	<i>ydiL</i>	Uncharacterized protein ydiL	1,38	1,15	-2,44
SL1298	<i>ydiK</i>	UPF0118 inner membrane protein ydiK	1,09	1,11	1,09
SL1299	<i>ydiJ</i>	Uncharacterized protein ydiJ	1,10	-1,13	1,24
SL1300	<i>ydil</i>	Esterase ydil	1,11	-1,10	-1,01
SL1301	<i>ydiH</i>	Uncharacterized protein ydiH	1,19	1,08	1,10
SL1302	<i>ydjN</i>	Uncharacterized symporter ydjN	1,07	-1,02	6,96
SL1303	<i>sufA</i>	Protein sufA	1,22	1,43	4,08
SL1304	<i>sufB</i>	FeS cluster assembly protein sufB	1,17	1,13	2,10
SL1305	<i>sufC</i>	Probable ATP-dependent transporter sufC	1,18	1,21	1,30
SL1306	<i>sufD</i>	FeS cluster assembly protein sufD	1,21	1,07	1,35
SL1307	<i>sufS</i>	Cysteine desulfurase	1,37	1,11	1,34
SL1308	<i>sufE</i>	Cysteine desulfuration protein sufE	1,39	1,06	1,19
SL1309	<i>ynhG</i>	Probable L,D-transpeptidase YnhG	1,25	1,14	2,90
SL1310	<i>lpp2</i>	Major outer membrane lipoprotein 2	1,11	-1,10	-1,20
SL1311	<i>lpp1</i>	Major outer membrane lipoprotein 1	1,08	1,39	-1,48
SL1312	<i>pykF</i>	Pyruvate kinase I	1,08	1,01	-1,64
SL1313	<i>puuP</i>	Putrescine importer	-1,06	-1,08	4,25
SL1314	<i>pip</i>	Proline iminopeptidase	-1,21	-1,35	4,08
SL1315	-	Hypothetical	-1,21	-1,22	3,97
SL1316	<i>rbsK</i>	Ribokinase	-1,13	-1,17	8,68
SL1317	<i>ynfF</i>	Probable dimethyl sulfoxide reductase chain ynfF	1,20	1,42	-2,14
SL1318	-	Tetrathionate Reductase Subunit C	1,05	1,47	-2,98
SL1319	<i>nrfC</i>	Protein nrfC	1,01	1,19	-2,70
SL1320	<i>fixL</i>	Sensor protein fixL	1,42	1,12	2,21
SL1321	<i>fixJ</i>	Transcriptional regulatory protein fixJ	1,43	-1,07	1,20
SL1322	<i>ydhZ</i>	Uncharacterized protein ydhZ	1,52	-1,03	-1,02
SL1323	<i>ybgA</i>	Uncharacterized protein ybgA	1,18	1,12	2,23
SL1324	<i>mlrA</i>	HTH-type transcriptional regulator mlrA	-1,84	-1,14	-2,75
SL1325	<i>ssrB</i>	putative two-component response regulator	-2,38	1,26	-2,58
SL1326	<i>spiR</i>	Sensor kinase protein	-3,42	-1,01	-2,56
SL1327	<i>spiC</i>	Salmonella pathogenicity island protein C	-7,40	1,89	-7,03
SL1328	<i>yscC</i>	Yop proteins translocation protein C	-8,81	1,31	-6,06
SL1329	-	Type-III Secretion Protein	-5,18	-1,04	-7,92
SL1330	-	Secretion System Protein	-4,91	1,17	-4,88
SL1331	<i>sseA</i>	Type III secretion system chaperone sseA	-7,73	1,49	-3,08
SL1332	<i>sseB</i>	Secreted effector protein sseB	-6,60	1,31	-2,69
SL1333	-	Type III Secretion Low Calcium Response Chaperone LcrH/SycD	-5,68	1,13	-2,44
SL1334	<i>sseC</i>	Secreted effector protein sseC	-6,74	1,15	-2,37
SL1335	<i>sseD</i>	Secreted effector protein sseD	-5,29	1,33	-1,44
SL1336	<i>sseE</i>	Secreted Effector Protein	-4,59	1,21	-1,28
SL1337	<i>sscB</i>	Type III Secretion Chaperone	-5,73	1,14	-1,55
SL1338	<i>sseF</i>	Hypothetical	-2,64	-1,03	-1,30

Tabla Suplementaria 1

Diferencia de expresión de todos los genes de SV5015 en las cepas mutantes *greA*, *greB* y *greAgreB*, respecto a la cepa WT

ID	gene	Description	<i>greA</i> vs WT	<i>greB</i> vs WT	<i>greAgreB</i> vs WT
SL1339	<i>sseG</i>	Hypothetical	-2,53	-1,17	-1,36
SL1340	<i>ssaG</i>	Secretion System Apparatus SsaG	-4,80	1,60	-1,67
SL1341	-	Hypothetical	-14,29	1,75	-18,14
SL1342	-	Type III Secretion System Apparatus Protein	-14,52	1,76	-22,27
SL1343	<i>ssaJ</i>	Secretion system apparatus lipoprotein ssaJ	-15,99	1,46	-17,00
SL1344	-	Type III Secretion Apparatus	-11,83	1,31	-16,48
SL1345	<i>ssaK</i>	Secretion system apparatus protein ssaK	-11,43	1,32	-11,64
SL1346	<i>ssaL</i>	Secretion system apparatus protein ssaL	-8,55	1,37	-5,60
SL1347	<i>ssaM</i>	Secretion system apparatus protein ssaM	-8,23	1,24	-5,75
SL1348	<i>ssaV</i>	Secretion system apparatus protein ssaV	-2,98	1,24	-1,41
SL1349	<i>ssaN</i>	Probable secretion system apparatus ATP synthase ssaN	-3,19	1,27	1,14
SL1350	<i>ssaO</i>	Secretion system apparatus protein ssaO	-3,52	1,44	1,32
SL1351	<i>ssaP</i>	Secretion system apparatus protein ssaP	-2,62	1,21	-1,05
SL1352	<i>ssaQ</i>	Secretion system apparatus protein SsaQ	-2,23	1,24	1,11
SL1353	<i>yscR</i>	Virulence protein yscR	-8,10	1,79	-4,01
SL1354	<i>ssaS</i>	Secretion system apparatus protein SsaS	-11,20	1,36	-6,62
SL1355	<i>ssaT</i>	Secretion system apparatus protein ssaT	-4,96	1,26	-4,28
SL1356	<i>ssaU</i>	Secretion system apparatus protein ssaU	-1,39	-1,02	-1,11
SL1357	<i>mdtK</i>	Multidrug resistance protein mdtK	1,00	-1,11	-1,19
SL1358	<i>ribE</i>	Riboflavin synthase alpha chain	-1,24	1,07	-1,46
SL1359	<i>cfa</i>	Cyclopropane-fatty-acyl-phospholipid synthase	1,03	1,04	-1,59
SL1360	<i>ydhC</i>	Inner membrane transport protein ydhC	-1,19	-1,07	-24,59
SL1361	<i>ydhB</i>	Uncharacterized HTH-type transcriptional regulator ydhB	1,03	1,02	1,34
SL1362	<i>purR</i>	HTH-type transcriptional repressor purR	1,16	1,15	-1,81
SL1363	<i>sodB</i>	Superoxide dismutase [Fe]	1,20	1,31	1,63
SL1364	<i>ydhO</i>	Uncharacterized protein ydhO	-1,19	1,04	-2,16
SL1365	<i>grxD</i>	Glutaredoxin-4	-1,08	-1,05	1,16
SL1366	<i>rnt</i>	Ribonuclease T	1,06	-1,20	-2,27
SL1367	<i>gloA</i>	Lactoylglutathione lyase	1,09	-1,05	-1,06
SL1368	<i>nemA</i>	N-ethylmaleimide reductase	1,06	1,12	1,46
SL1369	<i>nemR</i>	HTH-type transcriptional repressor nemR	-1,03	-1,24	-1,51
SL1370	<i>ydhL</i>	Uncharacterized protein ydhL	-1,06	1,12	-1,08
SL1371	<i>ydhF</i>	Oxidoreductase ydhF	1,35	1,11	1,92
SL1372	<i>sodC</i>	Superoxide dismutase [Cu-Zn] 2	1,22	1,35	1,30
SL1373	<i>ydhK</i>	Uncharacterized transporter ydhK	1,15	1,14	-1,20
SL1374	<i>ydhJ</i>	Uncharacterized protein ydhJ	1,02	1,16	-1,76
SL1375	<i>ydhI</i>	Uncharacterized protein ydhI	1,10	1,20	-1,70
SL1376	<i>slyA</i>	Transcriptional regulator slyA	-1,20	1,17	-2,26
SL1377	<i>slyB</i>	Outer membrane lipoprotein slyB	1,10	1,19	1,38
SL1378	<i>anmK</i>	Anhydro-N-acetylmuramic acid kinase	1,04	1,03	1,05
SL1379	<i>mliC</i>	Membrane-bound lysozyme inhibitor of C-type lysozyme	1,05	1,19	-1,71
SL1380	<i>pdxH</i>	Pyridoxine/pyridoxamine 5'-phosphate oxidase	1,10	1,04	-2,30
SL1381	<i>tyrS</i>	Tyrosyl-tRNA synthetase	1,03	1,01	-1,82
SL1382	<i>pdxY</i>	Pyridoxamine kinase	-1,08	-1,37	-1,63
SL1383	<i>gst</i>	Glutathione S-transferase	1,30	1,18	2,14

Tabla Suplementaria 1

Diferencia de expresión de todos los genes de SV5015 en las cepas mutantes *greA*, *greB* y *greAgreB*, respecto a la cepa WT

ID	gene	Description	<i>greA</i> vs WT	<i>greB</i> vs WT	<i>greAgreB</i> vs WT
SL1384	<i>dtpA</i>	Dipeptide and tripeptide permease A	-1,18	1,13	-1,29
SL1385	<i>nth</i>	Endonuclease III	1,21	1,33	1,16
SL1386	<i>rnfE</i>	Electron transport complex protein rnfE	1,27	1,25	1,50
SL1387	<i>rnfG</i>	Electron transport complex protein rnfG	1,53	1,36	1,41
SL1388	<i>rnfD</i>	Electron transport complex protein rnfD	1,52	1,14	-1,07
SL1389	<i>rnfC</i>	Electron transport complex protein rnfC	1,50	1,10	-1,42
SL1390	<i>rnfB</i>	Electron transport complex protein rnfB	1,25	1,05	-1,58
SL1391	<i>rnfA</i>	Electron transport complex protein rnfA	1,23	1,06	-2,32
SL1392	<i>ydgK</i>	Inner membrane protein ydgK	-1,11	-1,15	-2,54
SL1393	<i>cnu</i>	OriC-binding nucleoid-associated protein	-1,19	1,07	-2,33
SL1394	<i>ydgJ</i>	Uncharacterized oxidoreductase ydgJ	1,06	1,02	1,50
SL1395	<i>add</i>	Adenosine deaminase	-2,04	1,21	-2,80
SL1396	<i>ydgA</i>	Protein ydgA	1,12	1,02	1,21
SL1397	<i>manA</i>	Mannose-6-phosphate isomerase	1,01	-1,07	-1,44
SL1398	<i>fumA</i>	Fumarate hydratase class I, aerobic	1,13	-1,26	5,66
SL1399	-	Hypothetical Protein SL1399	1,53	1,02	7,56
SL1400	<i>fumC</i>	Fumarate hydratase class II	1,16	1,05	4,75
SL1401	<i>tus</i>	DNA replication terminus site-binding protein	1,35	1,09	3,56
SL1402	<i>rstB</i>	Sensor protein rstB	1,05	-1,08	-1,68
SL1403	<i>aepA</i>	Exoenzymes regulatory protein AepA	1,09	1,15	1,51
SL1404	<i>ompS2</i>	Outer membrane protein S2	-1,25	1,15	2,01
SL1405	<i>rstA</i>	Transcriptional regulatory protein rstA	-1,14	1,08	-3,50
SL1406	<i>ydgC</i>	Inner membrane protein ydgC	1,20	1,03	-1,29
SL1407	<i>ydgl</i>	Putative arginine/ornithine antiporter	1,13	1,02	-1,11
SL1408	<i>ydgH</i>	Protein ydgH	-1,04	-1,11	-1,15
SL1409	<i>pntA</i>	NAD(P) transhydrogenase subunit alpha	1,20	-1,04	1,42
SL1410	<i>pntB</i>	NAD(P) transhydrogenase subunit beta	1,15	-1,13	1,41
SL1411	<i>tqsA</i>	AI-2 transport protein tqsA	-1,07	-1,09	-1,44
SL1412	<i>mdtJ</i>	Spermidine export protein mdtJ	1,12	-1,40	1,69
SL1413	<i>mdtI</i>	Spermidine export protein mdtI	1,25	-1,34	1,89
SL1414	<i>ydgD</i>	Uncharacterized serine protease ydgD	1,06	1,04	2,11
SL1415	<i>asr</i>	Acid shock protein	-1,07	1,37	-1,04
SL1416	<i>ynfM</i>	Inner membrane transport protein ynfM	1,05	1,24	-1,69
SL1417	<i>ynfL</i>	Uncharacterized HTH-type transcriptional regulator ynfL	1,01	-1,11	-1,02
SL1418	<i>mlc</i>	Protein mlc	1,28	1,06	1,71
SL1419	<i>ynfK</i>	Putative dethiobiotin synthetase	1,30	1,20	-1,52
SL1420	<i>clcB</i>	Voltage-gated ClC-type chloride channel clcB	1,53	1,23	-1,29
SL1421	<i>opuBA</i>	Choline transport ATP-binding protein opuBA	1,03	1,04	2,73
SL1422	<i>opuCB</i>	Glycine betaine/carnitine/choline transport system permease protein opuCB	1,01	-1,06	3,34
SL1423	<i>opuCC</i>	Glycine betaine/carnitine/choline-binding protein	1,02	-1,08	4,59
SL1424	<i>opuCB</i>	Glycine betaine/carnitine/choline transport system permease protein opuCB	-1,00	-1,03	3,48
SL1425	<i>dmsD</i>	Twin-arginine leader-binding protein dmsD	1,18	-1,01	-2,00
SL1426	<i>ynfH</i>	Anaerobic dimethyl sulfoxide reductase chain ynfH	1,19	1,02	-1,54

Tabla Suplementaria 1

Diferencia de expresión de todos los genes de SV5015 en las cepas mutantes *greA*, *greB* y *greAgreB*, respecto a la cepa WT

ID	gene	Description	<i>greA</i> vs WT	<i>greB</i> vs WT	<i>greAgreB</i> vs WT
SL1427	<i>dmsB</i>	Anaerobic dimethyl sulfoxide reductase chain B	-1,12	-1,19	-1,19
SL1428	<i>ynfF</i>	Probable dimethyl sulfoxide reductase chain ynfF	1,52	1,15	-1,23
SL1429	<i>ynfE</i>	Putative dimethyl sulfoxide reductase chain ynfE	1,13	1,33	1,31
SL1430	<i>ynfD</i>	Uncharacterized protein ynfD	1,28	1,31	1,63
SL1431	<i>ynfC</i>	UPF0257 lipoprotein ynfC	1,15	1,12	1,59
SL1432	<i>speG</i>	Spermidine N(1)-acetyltransferase	1,09	1,05	1,42
SL1433	<i>ynfB</i>	UPF0482 protein CKO_01577	1,12	1,17	1,43
SL1434	<i>ynfA</i>	UPF0060 membrane protein ynfA	-1,59	-1,09	-1,97
SL1435	<i>rspA</i>	Starvation-sensing protein rspA	-1,55	-1,73	7,90
SL1436	<i>rspB</i>	Starvation-sensing protein rspB	-1,23	-1,45	8,06
SL1437	<i>ydfJ</i>	Putative inner membrane metabolite transport protein ydfJ	-1,19	-1,35	4,11
SL1438	<i>ydfI</i>	Uncharacterized oxidoreductase ydfI	-1,01	-1,14	1,44
SL1439	<i>ydfZ</i>	Putative selenoprotein ydfZ	1,13	1,61	1,39
SL1440	<i>ydfH</i>	Uncharacterized HTH-type transcriptional regulator ydfH	1,01	-1,36	-1,42
SL1441	<i>ydfG</i>	NADP-dependent L-serine/L-allo-threonine dehydrogenase ydfG	1,11	-1,09	1,39
SL1442	<i>dcp</i>	Peptidyl-dipeptidase dcp	1,15	1,05	1,40
SL1443	<i>ymdF</i>	Uncharacterized protein ymdF	-1,27	1,29	-2,06
SL1444	<i>ydeJ</i>	Protein ydeJ	-1,13	1,04	-1,03
SL1445	<i>ydeI</i>	Uncharacterized protein ydeI	-1,08	1,40	-1,44
SL1446	<i>ydeE</i>	Uncharacterized MFS-type transporter ydeE	1,09	-1,09	-1,13
SL1447	<i>eamA</i>	Probable amino-acid metabolite efflux pump	-1,31	-1,18	-1,04
SL1448	<i>marB</i>	Multiple antibiotic resistance protein marB	-1,04	1,14	-1,08
SL1449	<i>marA</i>	Multiple antibiotic resistance protein marA	-1,05	-1,22	1,05
SL1450	<i>marR</i>	Multiple antibiotic resistance protein marR	-1,05	-1,20	-1,09
SL1451	<i>marC</i>	UPF0056 inner membrane protein marC	-1,01	1,17	-1,80
SL1452	<i>sotB</i>	Probable sugar efflux transporter	1,14	1,36	-3,01
SL1453	<i>yneJ</i>	Uncharacterized HTH-type transcriptional regulator yneJ	-1,00	1,02	-1,03
SL1454	<i>ynel</i>	Aldehyde dehydrogenase-like protein ynel	-1,03	1,04	-2,65
SL1455	<i>glsA2</i>	Glutaminase 2	1,01	-1,08	-2,29
SL1456	<i>yneG</i>	Uncharacterized protein yneG	1,13	1,05	-1,35
SL1457	<i>yneE</i>	UPF0187 protein yneE	-1,08	1,01	-2,75
SL1458	-	Hypothetical	-1,09	-1,02	1,19
SL1459	<i>ompC</i>	Outer membrane protein C	-1,17	1,00	2,18
SL1460	<i>hypA</i>	Hydrogenase nickel incorporation protein hypA	-1,33	-1,20	-1,28
SL1461	-	Hypothetical	-1,40	-1,53	-1,55
SL1462	<i>hoxQ</i>	Hydrogenase expression/formation protein hoxQ	-1,27	-1,50	-1,20
SL1463	<i>hyaE</i>	Hydrogenase-1 operon protein hyaE	-1,32	-1,31	1,16
SL1464	<i>hupF</i>	Hydrogenase expression/formation protein hupF	-1,30	-1,26	1,23
SL1465	<i>hoxM</i>	Hydrogenase expression/formation protein hoxM	-1,27	-1,14	1,27
SL1466	<i>hupZ</i>	Probable Ni/Fe-hydrogenase B-type cytochrome subunit	-1,22	-1,24	2,79

Tabla Suplementaria 1

Diferencia de expresión de todos los genes de SV5015 en las cepas mutantes *greA*, *greB* y *greAgreB*, respecto a la cepa WT

ID	gene	Description	<i>greA</i> vs WT	<i>greB</i> vs WT	<i>greAgreB</i> vs WT
SL1467	<i>hupB</i>	Uptake hydrogenase large subunit	-1,17	-1,17	3,66
SL1468	<i>hoxK</i>	Uptake hydrogenase small subunit	-1,12	-1,13	2,86
SL1469	<i>cbh</i>	Choloylglycine hydrolase	-1,26	1,27	-1,26
SL1470	<i>uxuR</i>	Uxu operon transcriptional regulator	-1,07	-1,05	1,17
SL1471	<i>rspB</i>	Uncharacterized zinc-type alcohol dehydrogenase-like protein HI_0053	-1,46	-1,07	2,30
SL1472	<i>exuT</i>	Hexuronate transporter	-1,63	-1,16	3,48
SL1473	-	Hypothetical	-2,52	1,11	-3,72
SL1474	<i>tetA</i>	Tetracycline resistance protein, class G	-1,36	-1,40	1,83
SL1475	<i>yhjG</i>	Uncharacterized aromatic compound monooxygenase yhjG	-1,14	-1,35	3,46
SL1476	-	MarR Family Transcriptional Regulator	-1,08	-1,08	2,15
SL1477	<i>queA</i>	S-adenosylmethionine:tRNA ribosyltransferase-isomerase	-1,49	1,25	-1,99
SL1478	<i>yjgH</i>	UPF0076 protein yjgH	1,25	1,32	-1,10
SL1479	<i>relE</i>	Toxin relE	-1,04	-1,11	-1,51
SL1480	-	Hypothetical	-1,32	-1,13	-1,09
SL1481	-	Hypothetical	1,23	1,09	1,77
SL1482	-	Cytoplasmic Protein	-1,07	-1,00	1,66
SL1483	-	Putative transposase y4bF	1,14	-1,09	-1,02
SL1484	-	Coiled-Coil Protein	-1,18	-2,93	-1,44
SL1485	<i>galS</i>	HTH-type transcriptional regulator galS	1,22	-1,83	-1,18
SL1486	-	Uncharacterized Na(+)/H(+) antiporter HI_1107	1,17	-1,49	2,21
SL1487	<i>patB</i>	Cystathionine beta-lyase patB	1,36	-1,26	1,52
SL1488	<i>glgX</i>	Glycogen operon protein glgX homolog	1,22	1,24	1,63
SL1489	<i>treY</i>	Maltooligosyl trehalose synthase	1,42	1,24	3,14
SL1490	<i>treZ</i>	Malto-oligosyltrehalose trehalohydrolase	1,24	1,06	1,87
SL1491	-	Hypothetical	1,20	-1,00	1,29
SL1492	<i>hdeB</i>	Protein hdeB	-1,07	-1,02	-1,20
SL1493	<i>osmC</i>	Peroxiredoxin osmC	1,09	1,24	1,01
SL1494	<i>bdm</i>	Protein bdm homolog	-1,04	1,05	-4,02
SL1495	<i>sra</i>	Stationary-phase-induced ribosome-associated protein	1,24	1,25	-1,76
SL1496	<i>sfcA</i>	NAD-dependent malic enzyme	1,20	-1,33	2,28
SL1497	<i>adhP</i>	Alcohol dehydrogenase, propanol-preferring	1,09	1,40	1,35
SL1498	<i>fdnI</i>	Formate dehydrogenase, nitrate-inducible, cytochrome b556(fdn) subunit	1,08	1,10	-1,34
SL1499	<i>fdnH</i>	Formate dehydrogenase, nitrate-inducible, iron-sulfur subunit	1,04	-1,07	-1,09
SL1500	<i>fdnG</i>	Formate dehydrogenase, nitrate-inducible, major subunit	-1,04	-1,46	-1,19
SL1501	<i>fdnG</i>	Formate dehydrogenase, nitrate-inducible, major subunit	-1,29	-2,04	1,12
SL1502	<i>yddG</i>	Inner membrane protein yddG	-1,10	-1,14	-1,55
SL1503	<i>ompD</i>	Outer membrane porin protein ompD	-1,00	-1,04	1,09
SL1504	-	Glutathione-Dependent Formaldehyde-Activating GFA	1,21	-1,06	1,03
SL1505	<i>smvA</i>	Methyl viologen resistance protein smvA	-1,22	-1,29	-2,99
SL1506	-	TetR Family Transcriptional Regulator	1,03	1,07	-1,02
SL1507	<i>narU</i>	Nitrite extrusion protein 2	1,27	1,03	11,11
SL1508	<i>narZ</i>	Respiratory nitrate reductase 2 alpha chain	1,02	1,04	6,46

Tabla Suplementaria 1

Diferencia de expresión de todos los genes de SV5015 en las cepas mutantes *greA*, *greB* y *greAgreB*, respecto a la cepa WT

ID	gene	Description	<i>greA</i> vs WT	<i>greB</i> vs WT	<i>greAgreB</i> vs WT
SL1509	<i>narY</i>	Respiratory nitrate reductase 2 beta chain	-1,04	1,09	5,04
SL1510	<i>narW</i>	Probable nitrate reductase molybdenum cofactor assembly chaperone NarW	1,11	1,04	4,15
SL1511	<i>narV</i>	Respiratory nitrate reductase 2 gamma chain	1,08	1,07	4,38
SL1512	<i>yddE</i>	Uncharacterized isomerase yddE	1,06	-1,16	1,27
SL1513	<i>nhoA</i>	N-hydroxyarylamine O-acetyltransferase	-1,08	-1,04	-2,40
SL1514	<i>steA</i>	Secreted effector protein steA	-1,31	1,49	-1,37
SL1515	<i>ansP</i>	L-asparagine permease	1,18	1,17	1,56
SL1516	<i>ygdR</i>	Uncharacterized lipoprotein ygdR	1,22	1,30	1,44
SL1517	<i>yncE</i>	Uncharacterized protein YncE	-1,02	1,25	-1,12
SL1518	<i>yncD</i>	Probable tonB-dependent receptor yncD	1,00	-1,27	1,97
SL1519	<i>mcbR</i>	HTH-type transcriptional regulator mcbR	-1,07	-1,28	1,04
SL1520	<i>yncB</i>	Putative NADP-dependent oxidoreductase yncB	1,13	-1,03	1,34
SL1521	<i>yncA</i>	Uncharacterized N-acetyltransferase yncA	1,17	-1,01	1,85
SL1522	<i>ydcZ</i>	Inner membrane protein ydcZ	1,28	1,03	1,40
SL1523	<i>ydcY</i>	Uncharacterized protein ydcY	1,08	1,20	1,61
SL1524	-	Hypothetical	1,17	-1,37	1,75
SL1525	-	Virulence Protein SrfB	1,49	-1,02	4,34
SL1526	-	Virulence Factor	1,42	-1,05	2,39
SL1527	<i>ydcX</i>	Uncharacterized protein ydcX	1,40	-1,13	1,79
SL1528	<i>ydcW</i>	Gamma-aminobutyraldehyde dehydrogenase	1,09	1,11	2,33
SL1529	<i>ydcR</i>	Uncharacterized HTH-type transcriptional regulator ydcR	-1,16	-1,03	-1,20
SL1530	<i>vanX</i>	D-alanyl-D-alanine dipeptidase	-1,40	1,07	-1,39
SL1531	-	D-Alanyl-D-Alanine Dipeptidase	-2,42	1,47	-4,95
SL1532	<i>sifB</i>	Secreted effector protein sifB	-6,21	1,85	-3,28
SL1533	<i>yncJ</i>	Uncharacterized protein yncJ	-4,14	1,63	-2,28
SL1534	<i>ydcP</i>	Uncharacterized protease ydcP	-1,07	1,06	-1,39
SL1535	<i>ydcN</i>	Uncharacterized HTH-type transcriptional regulator ydcN	1,34	1,05	1,50
SL1536	<i>ydcO</i>	Inner membrane protein ydcO	1,28	-1,18	1,53
SL1537	<i>ydcL</i>	Uncharacterized lipoprotein ydcL	1,44	-1,04	2,52
SL1538	<i>tehB</i>	Tellurite resistance protein tehB	1,27	1,03	1,79
SL1539	<i>tehA</i>	Tellurite resistance protein tehA	1,28	-1,12	-1,02
SL1540	<i>ydcK</i>	Uncharacterized acetyltransferase ydcK	1,13	-1,14	2,24
SL1541	<i>rimL</i>	Ribosomal-protein-serine acetyltransferase	1,16	1,11	2,07
SL1542	<i>sgcX</i>	Putative aminopeptidase sgcX	1,37	1,22	2,48
SL1543	<i>sgcB</i>	Putative phosphotransferase enzyme IIB component sgcB	1,16	1,24	2,02
SL1544	<i>sgcC</i>	Putative permease IIC component	1,24	1,20	2,09
SL1545	<i>sgcQ</i>	Putative sgc region protein sgcQ	1,06	1,05	1,32
SL1546	<i>sgcA</i>	Putative phosphotransferase IIA component sgcA	1,29	1,10	1,68
SL1547	<i>sgcE</i>	Protein sgcE	1,20	-1,01	1,40
SL1548	<i>sgcR</i>	Putative sgc region transcriptional regulator	1,14	-1,12	1,02
SL1549	<i>aacA7</i>	Aminoglycoside N(6')-acetyltransferase type 1	1,13	1,33	-1,22
SL1550	<i>lldD</i>	Lactate 2-monooxygenase	-1,01	-1,24	1,85

Tabla Suplementaria 1

Diferencia de expresión de todos los genes de SV5015 en las cepas mutantes *greA*, *greB* y *greAgreB*, respecto a la cepa WT

ID	gene	Description	<i>greA</i> vs WT	<i>greB</i> vs WT	<i>greAgreB</i> vs WT
SL1551	<i>ycel</i>	UPF0312 protein VPA0850	1,36	1,06	2,34
SL1552	<i>mdoD</i>	Glucans biosynthesis protein D	1,26	-1,10	1,48
SL1553	<i>pnbA</i>	Para-nitrobenzyl esterase	1,36	-1,32	3,07
SL1554	<i>ydcJ</i>	Uncharacterized protein ydcJ	1,30	1,10	9,60
SL1555	<i>ydcI</i>	Uncharacterized HTH-type transcriptional regulator ydcI	1,03	1,07	1,83
SL1556	<i>trg</i>	Methyl-accepting chemotaxis protein III	-1,26	-1,37	1,17
SL1557	<i>frmA</i>	S-(hydroxymethyl)glutathione dehydrogenase	1,23	1,06	1,77
SL1558	<i>yaiN</i>	Uncharacterized protein in bioA 5'region	1,03	-1,11	1,18
SL1559	<i>steB</i>	Secreted effector protein steB	-1,78	1,43	-16,75
SL1560	<i>tfpB</i>	Protein tfpB	-1,29	1,88	-2,37
SL1561	<i>sseJ</i>	Secreted effector protein sseJ	-4,43	1,67	-2,52
SL1562	-	Hypothetical	-1,22	1,44	-2,15
SL1563	<i>fliY</i>	Cystine-binding periplasmic protein	-1,39	1,05	-1,92
SL1564	<i>yecS</i>	Inner membrane amino-acid ABC transporter permease protein yecS	-1,20	1,15	-2,41
SL1565	<i>glnQ</i>	Glutamine transport ATP-binding protein glnQ	-1,24	1,22	-1,18
SL1566	<i>yecS</i>	Inner membrane amino-acid ABC transporter permease protein yecS	-1,06	1,32	-1,18
SL1567	-	Hypothetical	-1,43	1,20	-1,98
SL1568	<i>ybcY</i>	Putative uncharacterized protein ybcY	-1,17	-1,95	1,04
SL1569	<i>cybB</i>	Cytochrome b561	1,09	1,03	1,10
SL1570	<i>ydcF</i>	Protein ydcF	1,23	1,09	2,05
SL1571	<i>hrpA</i>	ATP-dependent RNA helicase hrpA	1,32	1,02	1,78
SL1572	<i>azoR</i>	FMN-dependent NADH-azoreductase	1,13	1,01	-1,67
SL1573	-	Glutathione-Dependent Formaldehyde-Activating GFA	1,15	1,18	-1,38
SL1574	<i>ydbL</i>	Uncharacterized protein ydbL	1,33	1,15	-1,40
SL1575	<i>ynbE</i>	Uncharacterized protein ynbE	1,29	1,09	-1,46
SL1576	<i>ydbH</i>	Uncharacterized protein ydbH	1,18	1,16	-1,21
SL1577	<i>ldhA</i>	D-lactate dehydrogenase	1,24	1,35	-1,30
SL1578	<i>hslJ</i>	Heat shock protein hslJ	1,22	1,18	-2,04
SL1579	<i>ydbJ</i>	Uncharacterized protein ydbJ	1,09	1,09	-1,02
SL1580	-	Hypothetical	1,03	1,12	1,02
SL1581	<i>ydbK</i>	Probable pyruvate-flavodoxin oxidoreductase	1,39	1,16	1,69
SL1582	<i>uspF</i>	Universal stress protein F	1,10	1,34	2,66
SL1583	<i>emrE</i>	Multidrug transporter emrE	1,24	-1,21	1,36
SL1584	<i>intR</i>	Putative lambdoid prophage Rac integrase	1,27	1,20	-1,05
SL1585	<i>ttcA</i>	tRNA 2-thiocytidine biosynthesis protein TtcA	-1,16	-1,22	-1,78
SL1586	<i>dbpA</i>	ATP-independent RNA helicase dbpA	-1,03	-1,02	-1,26
SL1587	<i>zntB</i>	Zinc transport protein zntB	1,20	1,22	1,00
SL1588	<i>tap</i>	Methyl-accepting chemotaxis protein IV	1,11	1,23	-1,08
SL1589	<i>ydaL</i>	Uncharacterized protein ydaL	-1,12	-1,09	1,39
SL1590	<i>ogt</i>	Methylated-DNA--protein-cysteine methyltransferase	-1,00	1,18	1,49
SL1591	<i>fnr</i>	Fumarate and nitrate reduction regulatory protein	1,03	1,12	-1,38
SL1592	<i>uspE</i>	Universal stress protein E	1,17	1,34	2,28

Tabla Suplementaria 1

Diferencia de expresión de todos los genes de SV5015 en las cepas mutantes *greA*, *greB* y *greAgreB*, respecto a la cepa WT

ID	gene	Description	<i>greA</i> vs WT	<i>greB</i> vs WT	<i>greAgreB</i> vs WT
SL1593	<i>ynaJ</i>	Uncharacterized protein ynaJ	1,25	1,00	2,94
SL1594	<i>ynal</i>	MscS family inner membrane protein ynal	-1,03	1,14	-1,63
SL1595	<i>ydcN</i>	XRE Family Transcriptional Regulator	-1,13	1,13	-1,04
SL1596	-	Hypothetical	-1,83	-1,18	-1,06
SL1597	<i>tpx</i>	Probable thiol peroxidase	-1,05	1,22	1,09
SL1598	-	Hypothetical	1,16	1,08	1,18
SL1599	<i>yeeJ</i>	Invasin	1,01	-1,40	-1,03
SL1600	-	Conserved Hypothetical Protein Exported Protein	-1,57	-1,56	-1,44
SL1601	-	Hypothetical Protein SL1601	1,07	1,17	-1,26
SL1602	-	Hypothetical	-1,76	1,08	-4,92
SL1603	<i>ygdR</i>	Outer Membrane Lipoprotein	1,19	1,24	-1,19
SL1604	<i>yjgJ</i>	Uncharacterized HTH-type transcriptional regulator yjgJ	1,34	1,11	1,87
SL1605	<i>yjgl</i>	Uncharacterized oxidoreductase yjgl	-1,23	-1,54	2,37
SL1606	<i>ytbE</i>	Uncharacterized oxidoreductase ytbE	-1,03	-1,11	1,35
SL1607	<i>yhjC</i>	Uncharacterized HTH-type transcriptional regulator yhjC	1,09	1,08	2,41
SL1608	-	NmrA Family Protein	1,10	1,07	1,90
SL1609	<i>mppA</i>	Periplasmic murein peptide-binding protein	1,15	1,00	1,82
SL1610	<i>mpaA</i>	Protein mpaA	1,01	-1,01	-1,08
SL1611	<i>ycjG</i>	L-Ala-D/L-Glu epimerase	1,29	-1,05	1,18
SL1612	<i>tpx</i>	Probable thiol peroxidase	-1,28	-1,22	2,53
SL1613	<i>tyrR</i>	Transcriptional regulatory protein tyrR	1,19	1,22	1,07
SL1614	<i>ycjF</i>	UPF0283 membrane protein ycjF	1,15	1,15	1,16
SL1615	<i>ycjX</i>	Uncharacterized protein ycjX	1,10	1,04	-1,58
SL1616	<i>pspE</i>	Thiosulfate sulfurtransferase PspE	-1,05	1,28	-1,14
SL1617	<i>pspD</i>	Phage shock protein D	-1,19	1,34	-2,02
SL1618	<i>pspC</i>	Phage shock protein C	-1,17	1,35	-1,96
SL1619	<i>pspB</i>	Phage shock protein B	-1,15	1,34	-2,10
SL1620	<i>pspA</i>	Phage shock protein A	-1,22	1,22	-1,75
SL1621	<i>pspF</i>	Psp operon transcriptional activator	1,09	-1,00	2,78
SL1622	<i>sapA</i>	Peptide transport periplasmic protein sapA	1,08	1,00	-1,31
SL1623	<i>sapB</i>	Peptide transport system permease protein sapB	1,10	1,16	-1,15
SL1624	<i>sapC</i>	Peptide transport system permease protein sapC	-1,02	-1,16	-1,08
SL1625	<i>sapD</i>	Peptide transport system ATP-binding protein sapD	1,16	1,09	1,22
SL1626	<i>sapF</i>	Peptide transport system ATP-binding protein sapF	1,26	1,14	1,42
SL1627	<i>ydiV</i>	Uncharacterized protein ydiV	1,20	-1,14	1,44
SL1628	<i>steC</i>	Secreted effector kinase steC	-5,23	1,46	-2,62
SL1629	-	Hypothetical A	1,31	1,13	1,19
SL1630	<i>ycjE</i>	Uncharacterized protein ycjE	-1,40	1,43	-1,95
SL1631	<i>fabI</i>	Enoyl-[acyl-carrier-protein] reductase [NADH]	-1,02	-1,02	-1,14
SL1632	<i>yciW</i>	Uncharacterized protein yciW	-1,03	-1,05	1,51
SL1633	<i>rnB</i>	Exoribonuclease 2	-1,15	-1,12	-1,78
SL1634	<i>gmr</i>	Protein gmr	1,07	1,04	2,42
SL1635	<i>yciZ</i>	UPF0509 protein yciZ	1,04	1,11	1,37

Tabla Suplementaria 1

Diferencia de expresión de todos los genes de SV5015 en las cepas mutantes *greA*, *greB* y *greAgreB*, respecto a la cepa WT

ID	gene	Description	<i>greA</i> vs WT	<i>greB</i> vs WT	<i>greAgreB</i> vs WT
SL1636	<i>yciT</i>	Uncharacterized HTH-type transcriptional regulator yciT	1,24	1,04	1,01
SL1637	<i>osmB</i>	Osmotically-inducible lipoprotein B	-1,30	1,02	-4,73
SL1638	<i>yciH</i>	Uncharacterized protein yciH	-1,06	1,16	-1,24
SL1639	<i>pyrF</i>	Orotidine 5'-phosphate decarboxylase	-1,46	1,05	-2,53
SL1640	<i>yciM</i>	Uncharacterized protein yciM	-1,08	1,06	-2,25
SL1641	<i>yciS</i>	Inner membrane protein yciS	1,01	1,08	-1,96
SL1642	<i>pgpB</i>	Phosphatidylglycerophosphatase B	1,06	-1,14	-1,16
SL1643	<i>ribA</i>	GTP cyclohydrolase-2	1,11	1,01	1,06
SL1644	<i>acnA</i>	Aconitate hydratase 1	1,18	1,02	3,38
SL1645	<i>cysB</i>	HTH-type transcriptional regulator cysB	-1,04	-1,01	-1,06
SL1646	<i>topA</i>	DNA topoisomerase 1	1,17	-1,11	1,64
SL1647	<i>yciN</i>	Protein yciN	1,14	1,16	1,22
SL1648	<i>sohB</i>	Probable protease sohB	1,02	1,02	-1,14
SL1649	<i>yciK</i>	Uncharacterized oxidoreductase yciK	1,05	1,03	2,60
SL1650	<i>btuR</i>	Cob(II)yrinic acid a,c-diamide adenosyltransferase	1,19	-1,12	2,90
SL1651	<i>rluB</i>	Ribosomal large subunit pseudouridine synthase B	1,06	1,06	-1,54
SL1652	<i>yciO</i>	Uncharacterized protein yciO	1,00	-1,17	-1,34
SL1653	<i>trpH</i>	Protein trpH	1,05	-1,11	-1,39
SL1654	<i>trpE</i>	Anthranilate synthase component 1	-1,14	1,12	1,50
SL1655	<i>trpD</i>	Anthranilate synthase component II	-1,04	1,09	2,35
SL1656	<i>trpC</i>	Tryptophan biosynthesis protein trpCF	-1,00	1,03	1,06
SL1657	<i>trpB</i>	Tryptophan synthase beta chain	1,10	1,16	1,33
SL1658	<i>trpA</i>	Tryptophan synthase alpha chain	1,10	1,12	1,48
SL1659	<i>ymdF</i>	Uncharacterized protein ymdF	-1,55	1,10	-3,54
SL1660	<i>yciF</i>	Protein yciF	-1,73	1,18	-3,65
SL1661	<i>yciE</i>	Protein yciE	-1,42	1,25	-3,21
SL1662	<i>katN</i>	Probable manganese catalase	-1,31	1,20	-2,83
SL1663	<i>ompW</i>	Outer membrane protein W	1,15	1,13	1,85
SL1664	<i>ykgJ</i>	Uncharacterized protein ykgJ	1,17	-1,05	1,52
SL1665	<i>yciC</i>	UPF0259 membrane protein CKO_01332	-1,01	-1,00	-1,69
SL1666	<i>ispZ</i>	Probable intracellular septation protein	-1,19	-1,16	-2,06
SL1667	<i>yciA</i>	Acyl-CoA thioester hydrolase yciA	-1,03	1,14	-1,66
SL1668	<i>tonB</i>	Protein tonB	1,07	1,31	-2,20
SL1669	<i>yciI</i>	Protein yciI	1,09	-1,09	-1,02
SL1670	<i>cls</i>	Cardiolipin synthase	1,06	1,03	-1,23
SL1671	<i>yciU</i>	UPF0263 protein CKO_01325	1,00	1,09	1,09
SL1672	-	Putative potassium channel protein RPA4233	1,11	1,16	1,03
SL1673	<i>oppF</i>	Oligopeptide transport ATP-binding protein oppF	1,18	1,00	2,57
SL1674	<i>oppD</i>	Oligopeptide transport ATP-binding protein oppD	1,01	-1,39	1,82
SL1675	<i>oppC</i>	Oligopeptide transport system permease protein oppC	-1,00	-1,64	1,62
SL1676	<i>oppB</i>	Oligopeptide transport system permease protein oppB	-1,10	-1,72	2,18
SL1677	<i>oppA</i>	Periplasmic oligopeptide-binding protein	-1,05	-1,22	3,54
SL1678	-	Hypothetical	-1,01	1,01	1,98
SL1679	<i>yhcE</i>	UPF0056 membrane protein yhcE	-1,34	1,25	-3,72

Tabla Suplementaria 1

Diferencia de expresión de todos los genes de SV5015 en las cepas mutantes *greA*, *greB* y *greAgreB*, respecto a la cepa WT

ID	gene	Description	<i>greA</i> vs WT	<i>greB</i> vs WT	<i>greAgreB</i> vs WT
SL1680	<i>adhE</i>	Aldehyde-alcohol dehydrogenase	1,16	1,23	-1,83
SL1681	<i>tdk</i>	Thymidine kinase	1,05	1,03	-1,56
SL1682	<i>hns</i>	DNA-binding protein H-NS	-1,03	1,01	-1,01
SL1683	<i>galU</i>	UTP--glucose-1-phosphate uridylyltransferase	1,10	1,04	-1,38
SL1684	<i>hnr</i>	Protein hnr	1,03	-1,21	-1,37
SL1685	<i>rssA</i>	NTE family protein rssA	-1,04	-1,21	-1,13
SL1686	<i>yehJ</i>	UPF0225 protein yehJ	-1,06	-1,10	-1,73
SL1687	<i>purU</i>	Formyltetrahydrofolate deformylase	1,08	-1,10	1,00
SL1688	<i>ybeQ</i>	Uncharacterized protein ybeQ	1,05	1,06	-1,04
SL1689	<i>narI</i>	Respiratory nitrate reductase 1 gamma chain	1,04	1,24	2,45
SL1690	<i>narJ</i>	Nitrate reductase molybdenum cofactor assembly chaperone NarJ	1,11	1,01	2,43
SL1691	<i>narH</i>	Respiratory nitrate reductase 1 beta chain	1,08	1,23	2,12
SL1692	<i>narG</i>	Respiratory nitrate reductase 1 alpha chain	1,06	1,07	2,24
SL1693	<i>narK</i>	Nitrite extrusion protein 1	1,03	-1,15	1,66
SL1694	<i>narX</i>	Nitrate/nitrite sensor protein narX	1,05	1,15	-1,63
SL1695	<i>narL</i>	Nitrate/nitrite response regulator protein narL	1,05	1,08	1,14
SL1696	<i>yehO</i>	Uncharacterized protein yehO	-1,07	-1,09	-2,00
SL1697	<i>yehN</i>	Protein yehN	1,10	1,15	-1,79
SL1698	<i>chaB</i>	Cation transport regulator chaB	-1,25	-1,04	-1,65
SL1699	<i>chaA</i>	Calcium/proton antiporter	1,01	-1,19	-1,28
SL1700	<i>kdsA</i>	2-dehydro-3-deoxyphosphooctonate aldolase	1,04	-1,07	1,34
SL1701	<i>sirB1</i>	Protein sirB1	-1,11	-1,15	-1,86
SL1702	<i>sirB2</i>	Protein sirB2	1,48	-1,03	-2,42
SL1703	<i>hemK</i>	Protein methyltransferase hemK	1,30	-1,09	-2,25
SL1704	<i>prfA</i>	Peptide chain release factor 1	1,21	1,09	-2,31
SL1705	<i>hemA</i>	Glutamyl-tRNA reductase	1,20	1,06	-1,44
SL1706	<i>lolB</i>	Outer-membrane lipoprotein lolB	-1,13	-1,15	-2,18
SL1707	<i>ispE</i>	4-diphosphocytidyl-2-C-methyl-D-erythritol kinase	-1,08	-1,03	-1,58
SL1708	<i>prs</i>	Ribose-phosphate pyrophosphokinase	-1,05	-1,15	-1,63
SL1709	<i>yehM</i>	Putative sulfate transporter yehM	1,40	-1,40	-1,06
SL1710	<i>yehH</i>	Uncharacterized protein yehH	1,38	1,30	3,18
SL1711	<i>pth</i>	Peptidyl-tRNA hydrolase	1,04	-1,01	-1,86
SL1712	<i>engD</i>	GTP-dependent nucleic acid-binding protein engD	-1,06	-1,30	-1,81
SL1713	-	Hypothetical	1,00	-1,05	1,11
SL1714	<i>hyaA</i>	Hydrogenase-1 small chain	-1,30	-2,04	-2,23
SL1715	<i>hyaB</i>	Hydrogenase-1 large chain	-1,05	-1,55	1,14
SL1716	<i>hyaC</i>	Probable Ni/Fe-hydrogenase 1 B-type cytochrome subunit	1,21	-1,28	1,10
SL1717	<i>hyaD</i>	Hydrogenase 1 maturation protease	1,11	-1,16	-1,03
SL1718	NA	NA	1,17	-1,10	1,15
SL1719	<i>hyaF</i>	Hydrogenase-1 operon protein hyaF	1,04	-1,10	1,07
SL1720	<i>appC</i>	Cytochrome bd-II oxidase subunit 1	1,09	-1,28	1,58
SL1721	<i>appB</i>	Cytochrome bd-II oxidase subunit 2	1,32	1,06	1,84
SL1722	<i>yccB</i>	Hypothetical Protein yccB	1,43	1,03	1,51
SL1723	<i>gdhA</i>	Glutamate dehydrogenase	1,13	-1,42	17,53

Tabla Suplementaria 1

Diferencia de expresión de todos los genes de SV5015 en las cepas mutantes *greA*, *greB* y *greAgreB*, respecto a la cepa WT

ID	gene	Description	<i>greA</i> vs WT	<i>greB</i> vs WT	<i>greAgreB</i> vs WT
SL1724	<i>treA</i>	Periplasmic trehalase	1,22	1,12	2,95
SL1725	<i>ymgE</i>	UPF0410 protein ymgE	1,21	1,23	1,62
SL1726	<i>ycgR</i>	Flagellar brake protein YcgR	-1,35	1,14	-5,01
SL1727	<i>emtA</i>	Endo-type membrane-bound lytic murein transglycosylase A	1,00	1,06	-2,10
SL1728	<i>ldcA</i>	Murein tetrapeptide carboxypeptidase	-1,05	1,06	-1,51
SL1729	<i>cvrA</i>	Cell volume regulation protein A	-1,03	1,01	-2,77
SL1730	<i>dadX</i>	Alanine racemase, catabolic	-1,27	-1,83	6,94
SL1731	<i>dadA</i>	D-amino acid dehydrogenase small subunit	-1,36	-1,36	9,25
SL1732	<i>ycgB</i>	Uncharacterized protein ycgB	-1,06	1,21	2,94
SL1733	<i>fadR</i>	Fatty acid metabolism regulator protein	1,07	-1,00	-1,36
SL1734	<i>nhaB</i>	Na(+)/H(+) antiporter nhaB	-1,32	-1,53	-1,59
SL1735	<i>dsbB</i>	Disulfide bond formation protein B	1,07	-1,14	-2,28
SL1736	<i>yeaR</i>	Uncharacterized protein yeaR	1,36	1,02	1,48
SL1737	<i>gns</i>	Protein gns	1,34	1,53	2,78
SL1738	-	Hypothetical Protein SL1738	-1,03	1,17	-1,08
SL1739	<i>ycgN</i>	UPF0260 protein CKO_01185	1,12	-1,08	-1,74
SL1740	<i>ycgM</i>	Uncharacterized protein ycgM	1,04	-1,04	-1,33
SL1741	<i>ycgL</i>	UPF0745 protein ycgL	-1,02	-1,00	-1,52
SL1742	<i>minC</i>	Probable septum site-determining protein minC	-1,29	-1,16	-4,10
SL1743	<i>minD</i>	Septum site-determining protein minD	-1,05	-1,05	1,29
SL1744	<i>minE</i>	Cell division topological specificity factor	-1,02	1,08	1,55
SL1745	<i>rnd</i>	Ribonuclease D	1,08	-1,05	-1,80
SL1747	<i>fadD</i>	Long-chain-fatty-acid--CoA ligase	1,07	1,29	-1,02
SL1748	<i>yeaY</i>	Uncharacterized lipoprotein yeaY	-1,02	1,19	-2,20
SL1749	<i>yeaZ</i>	M22 peptidase homolog yeaZ	-1,33	-1,49	-2,27
SL1750	<i>yoaA</i>	Probable ATP-dependent helicase yoaA	1,07	-1,06	-1,64
SL1751	<i>yoaB</i>	UPF0076 protein yoaB	1,13	-1,25	-1,30
SL1752	<i>yoaH</i>	UPF0181 protein yoaH	1,17	-1,05	-1,31
SL1753	<i>pabB</i>	Para-aminobenzoate synthase component 1	1,03	-1,14	-1,73
SL1754	<i>nudL</i>	Uncharacterized Nudix hydrolase nudL	1,10	-1,20	-1,15
SL1755	<i>sdaA</i>	L-serine dehydratase 1	1,18	-1,08	-1,20
SL1756	<i>yoaD</i>	Hypothetical Protein yoaD	-1,26	1,09	-1,01
SL1757	<i>yoaE</i>	UPF0053 inner membrane protein yoaE	1,07	1,08	1,45
SL1758	-	Cytoplasmic Protein	-1,12	1,19	-1,47
SL1759	<i>manX</i>	PTS system mannose-specific EIIAB component	1,35	1,22	-1,15
SL1760	<i>manY</i>	Mannose permease IIC component	1,08	1,00	-1,22
SL1761	<i>manZ</i>	Mannose permease IID component	1,46	1,17	-2,11
SL1762	<i>yobD</i>	UPF0266 membrane protein yobD	1,13	-1,35	-5,91
SL1763	<i>yebN</i>	UPF0059 membrane protein CKO_01156	1,08	-1,35	-2,84
SL1764	<i>rlmA</i>	Ribosomal RNA large subunit methyltransferase A	-1,09	1,06	-1,97
SL1765	<i>ftsI</i>	Peptidoglycan synthase ftsI	1,26	1,08	-1,60
SL1766	<i>cspC</i>	Cold shock-like protein cspC	-1,13	-1,17	-1,04
SL1767	<i>yobF</i>	Uncharacterized protein yobF	-1,17	-1,14	-1,31
SL1768	<i>yebO</i>	Uncharacterized protein yebO	-1,07	1,12	-3,12
SL1769	<i>mgrB</i>	Protein mgrB	1,02	1,21	-3,11

Tabla Suplementaria 1

Diferencia de expresión de todos los genes de SV5015 en las cepas mutantes *greA*, *greB* y *greAgreB*, respecto a la cepa WT

ID	gene	Description	<i>greA</i> vs WT	<i>greB</i> vs WT	<i>greAgreB</i> vs WT
SL1770	<i>yobH</i>	Uncharacterized protein yobH	-1,09	1,05	-2,58
SL1771	<i>kdgR</i>	Pectin degradation repressor protein kdgR	1,08	1,27	1,39
SL1772	<i>yebQ</i>	Uncharacterized transporter yebQ	-1,07	-1,23	-1,64
SL1773	<i>htpX</i>	Probable protease htpX homolog	1,18	1,07	1,83
SL1774	<i>prc</i>	Tail-specific protease	1,06	-1,13	-1,30
SL1775	<i>proQ</i>	ProP effector	-1,15	-1,16	-1,92
SL1776	<i>yebR</i>	Protein yebR	-1,06	-1,36	1,01
SL1777	<i>yebS</i>	Inner membrane protein yebS	-1,06	-1,02	-1,12
SL1778	<i>yebT</i>	Uncharacterized protein yebT	1,12	-1,04	1,14
SL1779	<i>rsmF</i>	Ribosomal RNA small subunit methyltransferase F	1,12	1,03	-2,70
SL1780	<i>yebV</i>	Uncharacterized protein yebV	-1,01	1,16	-2,02
SL1781	<i>yebW</i>	Uncharacterized protein yebW	1,16	1,23	-1,67
SL1782	<i>pphA</i>	Serine/threonine-protein phosphatase 1	-1,24	1,06	-4,92
SL1783	-	Hypothetical	-1,31	1,41	-8,58
SL1784	<i>sopE2</i>	Guanine nucleotide exchange factor sopE2	-1,51	1,15	-16,49
SL1785	<i>ycgX</i>	Uncharacterized protein ycgX	-1,44	1,14	-6,12
SL1786	-	Hypothetical	1,03	1,09	-2,05
SL1787	<i>bls</i>	Blasticidin-S acetyltransferase	-1,22	1,10	1,62
SL1788	-	Hypothetical Protein SL1788	1,09	1,35	-1,42
SL1789	-	Hypothetical	-1,11	1,18	1,33
SL1790	-	Transposase for insertion sequence element ISRM3	1,03	1,20	1,17
SL1791	<i>intE</i>	Prophage lambda integrase	-1,08	-1,08	-1,15
SL1792	-	Hypothetical	-1,04	1,18	-1,27
SL1793	<i>pagO</i>	Protein pagO	-1,97	1,23	-5,37
SL1794	-	Hypothetical	-2,21	1,11	-7,65
SL1795	-	Hypothetical	-1,97	1,32	-5,78
SL1796	<i>pinE</i>	DNA-invertase from lambdoid prophage e14	-1,46	-1,01	-1,82
SL1797	-	Hypothetical	-1,25	1,95	-1,96
SL1798	<i>insF1</i>	Hypothetical Protein insF1	-1,40	1,07	-1,34
SL1799	-	PagK-Like Protein	-2,12	1,45	-4,28
SL1800	<i>ycdD</i>	Tail fiber assembly protein homolog from lambdoid prophage Fels-1	-1,84	-1,23	-2,96
SL1801	-	Hypothetical	-1,02	1,08	-1,18
SL1802	-	Phage Membrane Protein	1,25	1,32	-1,26
SL1803	<i>rzpQ</i>	Uncharacterized protein rzpQ	1,37	1,00	-1,13
SL1804	-	Hypothetical	-1,63	-1,36	-3,58
SL1805	<i>recE</i>	Exodeoxyribonuclease 8	-1,14	1,20	-1,74
SL1806	<i>intE</i>	Prophage lambda integrase	1,05	1,01	2,88
SL1807	<i>yebY</i>	Uncharacterized protein yebY	-1,06	-1,13	-1,04
SL1808	<i>yebZ</i>	Inner membrane protein yebZ	-1,03	-1,37	1,32
SL1809	<i>yobA</i>	Protein yobA	1,01	-1,12	1,90
SL1810	<i>holE</i>	DNA polymerase III subunit theta	-1,04	-1,01	-1,04
SL1811	<i>yobB</i>	Uncharacterized protein yobB	1,12	-1,05	1,07
SL1812	<i>exoX</i>	Exodeoxyribonuclease 10	1,06	1,01	-1,16
SL1813	<i>ptrB</i>	Protease 2	1,03	1,08	-1,07
SL1814	<i>yebE</i>	Inner membrane protein yebE	1,18	1,04	1,17
SL1815	<i>yebF</i>	Protein yebF	-1,03	-1,01	1,27

Tabla Suplementaria 1

Diferencia de expresión de todos los genes de SV5015 en las cepas mutantes *greA*, *greB* y *greAgreB*, respecto a la cepa WT

ID	gene	Description	<i>greA</i> vs WT	<i>greB</i> vs WT	<i>greAgreB</i> vs WT
SL1816	<i>yebG</i>	Uncharacterized protein yebG	-1,01	1,10	1,37
SL1817	<i>purT</i>	Phosphoribosylglycinamide formyltransferase 2	1,03	1,17	-1,46
SL1818	<i>eda</i>	KHG/KDPG aldolase	1,16	-1,06	1,07
SL1819	<i>edd</i>	Phosphogluconate dehydratase	-1,05	-1,08	-5,50
SL1820	<i>zwf</i>	Glucose-6-phosphate 1-dehydrogenase	1,06	-1,18	-1,36
SL1821	<i>hexR</i>	HTH-type transcriptional regulator hexR	1,07	1,06	2,24
SL1822	<i>pykA</i>	Pyruvate kinase II	-1,09	-1,18	1,19
SL1823	<i>msbB1</i>	Lipid A biosynthesis (KDO)2-(lauroyl)-lipid IVA acyltransferase 1	1,03	-1,07	-1,29
SL1824	<i>yebA</i>	Uncharacterized metalloprotease yebA	-1,16	-1,12	-2,29
SL1825	<i>znuA</i>	High-affinity zinc uptake system protein znuA	-1,11	1,17	-1,50
SL1826	<i>znuC</i>	Zinc import ATP-binding protein ZnuC	1,38	1,24	-1,38
SL1827	<i>znuB</i>	High-affinity zinc uptake system membrane protein znuB	1,35	1,22	-1,75
SL1828	<i>ruvB</i>	Holliday junction ATP-dependent DNA helicase ruvB	1,01	-1,20	-1,03
SL1829	<i>ruvA</i>	Holliday junction ATP-dependent DNA helicase ruvA	-1,20	-1,07	-1,83
SL1830	-	Cytoplasmic Protein	1,11	1,10	-1,02
SL1831	-	Hypothetical	-1,20	-1,14	1,29
SL1832	<i>yebB</i>	Uncharacterized protein yebB	1,19	-1,00	1,21
SL1833	<i>ruvC</i>	Crossover junction endodeoxyribonuclease ruvC	1,13	-1,10	-1,05
SL1834	<i>yebC</i>	UPF0082 protein CKO_01097	1,18	1,04	1,34
SL1835	<i>nudB</i>	Dihydroneopterin triphosphate pyrophosphatase	1,03	-1,18	-1,14
SL1836	<i>aspS</i>	Aspartyl-tRNA synthetase	-1,17	-1,18	-1,56
SL1837	<i>yecD</i>	Uncharacterized isochorismatase family protein yecD	-1,02	-1,11	-1,37
SL1838	<i>yecE</i>	UPF0759 protein yecE	-1,10	-1,15	-1,29
SL1839	<i>yecN</i>	Inner membrane protein yecN	1,01	1,06	-1,49
SL1840	<i>cmoA</i>	tRNA (cmo5U34)-methyltransferase	-1,01	-1,08	-2,10
SL1841	<i>cmoB</i>	tRNA (mo5U34)-methyltransferase	-1,14	-1,08	-1,96
SL1842	<i>cutC</i>	Copper homeostasis protein cutC	-1,03	1,02	-1,01
SL1843	<i>yecM</i>	Protein yecM	-1,07	-1,06	-1,60
SL1844	<i>argS</i>	Arginyl-tRNA synthetase	-1,23	1,04	-3,31
SL1845	<i>mrdA</i>	Penicillin-binding protein 2	1,00	1,10	-1,56
SL1846	<i>yesR</i>	Unsaturated rhamnogalacturonyl hydrolase yesR	1,38	-1,05	1,01
SL1847	<i>flhE</i>	Flagellar protein flhE	1,54	1,25	1,81
SL1848	<i>flhA</i>	Flagellar biosynthesis protein flhA	1,16	-1,09	1,33
SL1849	<i>flhB</i>	Flagellar biosynthetic protein flhB	1,18	1,12	-1,23
SL1850	<i>cheZ</i>	Chemotaxis protein cheZ	-1,01	1,09	-2,12
SL1851	<i>cheY</i>	Chemotaxis protein cheY	-1,01	1,11	-2,17
SL1852	<i>cheB</i>	Chemotaxis response regulator protein-glutamate methylesterase	-1,12	1,10	-3,86
SL1853	<i>cheR</i>	Chemotaxis protein methyltransferase	-1,24	1,07	-3,83
SL1854	<i>tar</i>	Methyl-accepting chemotaxis protein II	-1,20	1,07	-2,19
SL1855	<i>cheW</i>	Chemotaxis protein cheW	1,17	1,25	-1,48
SL1856	<i>cheA</i>	Chemotaxis protein cheA	1,09	1,14	-1,79
SL1857	<i>motB</i>	Motility protein B	-1,29	1,06	-2,99

Tabla Suplementaria 1

Diferencia de expresión de todos los genes de SV5015 en las cepas mutantes *greA*, *greB* y *greAgreB*, respecto a la cepa WT

ID	gene	Description	<i>greA</i> vs WT	<i>greB</i> vs WT	<i>greAgreB</i> vs WT
SL1858	<i>motA</i>	Motility protein A	-1,20	1,23	-3,31
SL1859	<i>flhC</i>	Flagellar transcriptional activator flhC	-1,22	1,15	-3,09
SL1860	<i>flhD</i>	Transcriptional activator FlhD	-1,28	1,09	-3,17
SL1861	<i>uspC</i>	Universal stress protein C	1,20	1,43	1,74
SL1862	<i>otsA</i>	Alpha,alpha-trehalose-phosphate synthase [UDP-forming]	-1,06	1,03	1,27
SL1863	<i>otsB</i>	Trehalose-phosphate phosphatase	-1,14	1,02	-1,31
SL1864	<i>thiJ</i>	Protein thiJ	1,09	1,19	-1,01
SL1865	<i>ftnB</i>	Ferritin-like protein 2	1,16	1,07	3,10
SL1866	-	Hypothetical	-1,00	-1,56	-1,04
SL1867	<i>yecR</i>	Uncharacterized protein yecR	1,01	1,27	-1,43
SL1868	<i>ftnA</i>	Ferritin-1	-1,04	-1,07	1,49
SL1869	<i>yecH</i>	Uncharacterized protein yecH	1,05	-1,02	1,05
SL1870	<i>tyrP</i>	Tyrosine-specific transport protein	1,44	1,12	-1,98
SL1871	<i>yecA</i>	Uncharacterized protein yecA	1,52	1,20	1,80
SL1872	-	Hypothetical	-1,40	1,13	-4,52
SL1873	-	NLP/P60 Protein	-1,69	1,23	-1,65
SL1874	-	Hypothetical	-1,90	1,19	-4,78
SL1875	<i>pgsA</i>	CDP-diacylglycerol--glycerol-3-phosphate 3-phosphatidyltransferase	1,14	1,05	1,03
SL1876	<i>uvrC</i>	UvrABC system protein C	1,11	-1,11	-2,18
SL1877	<i>uvrY</i>	Response regulator uvrY	-1,01	1,05	-1,88
SL1878	<i>yecF</i>	Uncharacterized protein yecF	-1,09	1,13	-8,87
SL1879	<i>sdiA</i>	Regulatory protein sdiA	-1,09	1,23	-3,85
SL1880	<i>yecC</i>	Uncharacterized amino-acid ABC transporter ATP-binding protein yecC	1,29	1,23	-1,15
SL1881	<i>yecS</i>	Inner membrane amino-acid ABC transporter permease protein yecS	1,01	-1,12	-1,12
SL1882	<i>dcyD</i>	D-cysteine desulfhydrase	1,11	-1,03	1,15
SL1883	<i>fliY</i>	Cystine-binding periplasmic protein	-1,01	-1,03	-1,15
SL1884	<i>fliZ</i>	Protein fliZ	-1,05	-1,03	-1,25
SL1885	<i>fliA</i>	RNA polymerase sigma factor for flagellar operon	-1,12	-1,07	-1,39
SL1887	<i>fliB</i>	Lysine-N-methylase	-1,03	-1,10	-1,70
SL1888	<i>fliC</i>	Flagellin	-1,06	-1,01	-1,10
SL1889	<i>fliD</i>	Flagellar hook-associated protein 2	-1,07	1,01	-2,40
SL1890	<i>fliS</i>	Flagellar protein fliS	-1,30	-1,22	-3,14
SL1891	<i>fliT</i>	Flagellar protein fliT	-1,26	-1,14	-3,00
SL1892	<i>amyA</i>	Cytoplasmic alpha-amylase	1,06	-1,02	1,31
SL1893	<i>yedD</i>	Uncharacterized lipoprotein yedD	-1,07	-1,15	1,91
SL1894	<i>yedE</i>	UPF0394 inner membrane protein yedE	-1,04	-1,08	3,86
SL1895	<i>yedF</i>	UPF0033 protein yedF	1,16	1,05	3,15
SL1896	-	Hypothetical A	-1,92	-1,34	-3,36
SL1897	<i>fliE</i>	Flagellar hook-basal body complex protein fliE	1,01	-1,22	1,16
SL1898	<i>fliF</i>	Flagellar M-ring protein	1,04	-1,17	-1,12
SL1899	<i>fliG</i>	Flagellar motor switch protein FliG	1,11	-1,19	1,38
SL1900	<i>fliH</i>	Flagellar assembly protein fliH	1,19	-1,02	1,42
SL1901	<i>fliI</i>	Flagellum-specific ATP synthase	1,16	1,01	1,10
SL1902	<i>fliJ</i>	Flagellar fliJ protein	1,20	1,30	2,04
SL1903	<i>fliK</i>	Flagellar hook-length control protein	1,18	1,14	1,07

Tabla Suplementaria 1

Diferencia de expresión de todos los genes de SV5015 en las cepas mutantes *greA*, *greB* y *greAgreB*, respecto a la cepa WT

ID	gene	Description	<i>greA</i> vs WT	<i>greB</i> vs WT	<i>greAgreB</i> vs WT
SL1904	<i>fliL</i>	Flagellar protein FliL	1,10	-1,10	1,09
SL1905	<i>fliM</i>	Flagellar motor switch protein FliM	1,06	-1,05	1,05
SL1906	<i>fliN</i>	Flagellar motor switch protein FliN	1,04	-1,02	1,03
SL1907	<i>fliO</i>	Flagellar protein fliO	1,14	-1,20	-1,06
SL1908	<i>fliP</i>	Flagellar biosynthetic protein fliP	1,17	1,00	-1,19
SL1909	<i>fliQ</i>	Flagellar biosynthetic protein FliQ	1,15	1,14	-1,21
SL1910	<i>fliR</i>	Flagellar biosynthetic protein fliR	1,03	1,17	-1,37
SL1911	<i>rcsA</i>	Colanic acid capsular biosynthesis activation protein A	-1,16	1,36	-2,52
SL1912	<i>dsrB</i>	Protein dsrB	1,25	1,25	-1,15
SL1913	<i>yodD</i>	Uncharacterized protein yodD	1,28	1,20	1,33
SL1914	<i>yedP</i>	Putative mannosyl-3-phosphoglycerate phosphatase	1,55	-1,05	-1,26
SL1915	<i>yedQ</i>	Cellulose synthesis regulatory protein	-1,07	1,04	1,08
SL1916	<i>yodC</i>	Uncharacterized protein yodC	1,01	1,18	-1,18
SL1917	<i>yedI</i>	Inner membrane protein yedI	-1,20	-1,43	-1,63
SL1918	<i>yedA</i>	Uncharacterized inner membrane transporter yedA	1,17	-1,15	-1,17
SL1919	<i>vsr</i>	Very short patch repair protein	1,14	-1,07	-1,06
SL1920	<i>dcm</i>	DNA-cytosine methyltransferase	1,14	1,07	-1,21
SL1921	<i>yedJ</i>	Uncharacterized protein yedJ	1,03	-1,03	1,34
SL1922	<i>yedR</i>	Inner membrane protein yedR	1,03	1,36	-4,09
SL1923	<i>ompS1</i>	Outer membrane protein S1	1,31	1,22	2,32
SL1924	<i>cspJ</i>	Cold shock-like protein cspJ	-1,53	-1,31	-2,11
SL1925	<i>umuC</i>	Protein umuC	1,05	-1,11	1,47
SL1926	<i>umuD</i>	Protein umuD	1,28	1,20	1,75
SL1927	-	Hypothetical	-1,15	1,15	-1,93
SL1928	-	Cytoplasmic Protein	-5,33	1,56	-7,81
SL1929	<i>ycdD</i>	Tail fiber assembly protein homolog from lambdoid prophage Fels-1	-1,42	-1,05	-1,14
SL1930	<i>ycfK</i>	Uncharacterized protein ycfK	-1,22	-1,10	1,19
SL1931	<i>yfmQ</i>	Uncharacterized protein yfmQ in lambdoid prophage e14 region	-1,37	-1,11	-1,75
SL1932	<i>yfmP</i>	Putative protein yfmP	-1,69	-1,28	-1,79
SL1933	<i>yfmP</i>	Putative protein yfmP	-1,57	-1,19	-1,99
SL1934	-	Hypothetical	-1,55	-1,27	-1,83
SL1935	-	Mu-like prophage FluMu protein gp45	-1,51	-1,17	-1,68
SL1936	-	Tail Protein	-1,55	-1,14	-1,63
SL1937	-	Mu-like prophage FluMu DNA circulation protein	-1,24	-1,14	-1,61
SL1938	-	Phage Tail Tape Measure Protein	-1,35	-1,22	-1,27
SL1939	-	Hypothetical	-1,35	-1,30	-1,00
SL1940	-	Hypothetical	-1,33	-1,11	-1,05
SL1941	-	Mu-like prophage FluMu tail sheath protein	-1,38	-1,15	-1,70
SL1942	-	Hypothetical	-1,72	-1,22	-2,95
SL1943	-	Hypothetical	-1,68	-1,15	-2,74
SL1944	-	Hypothetical	-1,59	-1,10	-2,55
SL1945	-	Hypothetical	-1,56	-1,07	-2,73
SL1946	-	Hypothetical	-1,66	-1,10	-2,68
SL1947	-	Phage Capsid Protein	-1,49	-1,06	-1,80
SL1948	-	Phage Prohead Protease	-1,54	-1,04	-1,82

Tabla Suplementaria 1

Diferencia de expresión de todos los genes de SV5015 en las cepas mutantes *greA*, *greB* y *greAgreB*, respecto a la cepa WT

ID	gene	Description	<i>greA</i> vs WT	<i>greB</i> vs WT	<i>greAgreB</i> vs WT
SL1949	<i>yfmO</i>	Putative uncharacterized protein yfmO	-1,45	-1,07	-2,59
SL1950	<i>yfmN</i>	Uncharacterized protein yfmN	-1,38	-1,14	-3,34
SL1951	-	P27 Family Phage Terminase Small Subunit	-1,56	-1,17	-3,72
SL1952	-	Hypothetical	-1,58	-1,12	-3,08
SL1953	-	Hypothetical Protein SL1953	-1,40	-1,02	-2,20
SL1954	-	Hypothetical	-1,46	-1,09	-1,96
SL1955	<i>rzpD</i>	Putative Rz endopeptidase from lambdoid prophage DLP12	-1,36	-1,16	-3,37
SL1956	-	Uncharacterized protein HI_1415	-1,45	-1,11	-3,36
SL1957	-	Phage Holin Lambda Family	-1,42	-1,12	-3,53
SL1958	-	Hypothetical Protein SL1958	-1,02	1,09	-1,48
SL1959	-	Hypothetical	-1,39	-1,48	1,55
SL1960	<i>ydfU</i>	Uncharacterized protein ydfU	-1,08	-1,15	1,53
SL1961	-	Hypothetical	-1,00	1,06	2,40
SL1962	<i>yfdM</i>	Putative uncharacterized protein yfdM	-1,19	-1,23	2,13
SL1963	<i>yfdN</i>	Uncharacterized protein yfdN	-1,14	-1,13	2,23
SL1964	<i>yfdO</i>	Hypothetical	-1,30	-1,23	2,05
SL1965	-	Hypothetical	-1,31	-1,18	1,73
SL1966	<i>yfmL</i>	Uncharacterized protein yfmL	-1,50	-1,10	1,78
SL1967	-	Phage Repressor	-1,04	1,02	1,24
SL1968	<i>yfdP</i>	Uncharacterized protein yfdP	-1,03	1,04	2,99
SL1969	<i>yfdQ</i>	Uncharacterized protein yfdQ	-1,17	-1,09	3,27
SL1970	<i>yfdR</i>	Uncharacterized protein yfdR	-1,20	-1,18	2,48
SL1971	-	Hypothetical	-1,18	-1,23	2,22
SL1972	-	Hypothetical	-1,10	-1,10	2,63
SL1973	-	Hypothetical	1,03	-1,30	2,66
SL1974	-	Endodeoxyribonuclease	-1,19	-1,34	1,84
SL1975	-	Phage Protein	-1,23	-1,25	2,00
SL1976	<i>intE</i>	Phage Integrase Family Protein	-1,15	1,03	1,07
SL1977	<i>mtfA</i>	Protein mtfA	1,31	1,30	2,90
SL1978	<i>intB</i>	Putative prophage P4 integrase	1,91	1,28	1,21
SL1979	-	Hypothetical	1,30	1,15	1,57
SL1980	-	Hypothetical	1,02	-1,04	1,20
SL1981	-	Hypothetical	1,49	-1,05	1,66
SL1982	<i>ybeQ</i>	Uncharacterized protein ybeQ	-1,07	-1,42	1,44
SL1983	-	Hypothetical	1,05	-1,18	1,45
SL1984	-	Hypothetical	-1,01	1,05	-1,06
SL1985	-	Hypothetical	1,28	-1,06	1,50
SL1986	<i>amn</i>	AMP nucleosidase	1,16	1,00	1,80
SL1987	-	Hypothetical	1,10	1,21	-1,19
SL1988	-	Hypothetical Protein SL1988	1,13	1,16	-1,18
SL1989	-	Hypothetical	1,20	1,03	1,33
SL1990	<i>yeeO</i>	Uncharacterized transporter yeeO	-1,02	1,05	-1,42
SL1991	<i>erfK</i>	Probable L,D-transpeptidase ErfK/SrfK	1,09	1,16	1,73
SL1992	<i>cobT</i>	Nicotinate-nucleotide--dimethylbenzimidazole phosphoribosyltransferase	1,04	-1,15	-1,44
SL1993	<i>cobS</i>	Cobalamin synthase	-1,01	-1,29	-2,17

Tabla Suplementaria 1

Diferencia de expresión de todos los genes de SV5015 en las cepas mutantes *greA*, *greB* y *greAgreB*, respecto a la cepa WT

ID	gene	Description	<i>greA</i> vs WT	<i>greB</i> vs WT	<i>greAgreB</i> vs WT
SL1994	<i>cobU</i>	Bifunctional adenosylcobalamin biosynthesis protein cobU	1,05	-1,25	-1,90
SL1995	<i>cbiP</i>	Cobyric acid synthase	-1,02	-1,23	-1,59
SL1996	<i>cbiO</i>	Cobalt import ATP-binding protein CbiO	-1,16	-1,15	-1,67
SL1997	<i>cbiQ</i>	Cobalt transport protein cbiQ	-1,19	-1,26	-1,67
SL1998	<i>cbiN</i>	Cobalt transport protein cbiN	-1,21	-1,05	-1,36
SL1999	<i>cbiM</i>	Protein cbiM	-1,13	1,01	-1,38
SL2000	<i>cbiL</i>	Cobalt-precorrin-2 C(20)-methyltransferase	-1,22	-1,18	-1,39
SL2001	<i>cbiK</i>	Sirohydrochlorin cobaltochelatase	-1,14	-1,16	-1,61
SL2002	<i>cbiJ</i>	Cobalt-precorrin-6A reductase	-1,05	-1,31	-1,68
SL2003	<i>cbiH</i>	Cobalt-precorrin-3B C(17)-methyltransferase	-1,06	-1,26	-1,74
SL2004	<i>cbiG</i>	Protein cbiG	-1,04	-1,11	-1,59
SL2005	<i>cbiF</i>	Cobalt-precorrin-4 C(11)-methyltransferase	-1,01	-1,05	-1,53
SL2006	<i>cbiT</i>	Probable cobalt-precorrin-6Y C(15)-methyltransferase [decarboxylating]	1,08	1,11	-2,83
SL2007	<i>cbiE</i>	Probable cobalt-precorrin-6Y C(5)-methyltransferase	1,12	-1,05	-3,51
SL2008	<i>cbiD</i>	Putative cobalt-precorrin-6A synthase [deacetylating]	1,22	1,23	-2,77
SL2009	<i>cbiC</i>	Cobalt-precorrin-8X methylmutase	1,01	1,01	-2,23
SL2010	<i>cbiB</i>	Cobalamin biosynthesis protein cbiB	1,02	1,05	-3,16
SL2011	<i>cbiA</i>	Cobyric acid A,C-diamide synthase	1,11	1,33	-1,82
SL2012	<i>pocR</i>	Regulatory protein pocR	-1,01	1,50	1,34
SL2013	<i>pduF</i>	Propanediol diffusion facilitator	1,29	1,42	-3,03
SL2014	<i>pduA</i>	Propanediol utilization protein pduA	-1,43	1,42	-22,81
SL2015	<i>pduB</i>	Propanediol utilization protein pduB	-1,67	1,17	-40,16
SL2016	<i>pduC</i>	Propanediol dehydratase large subunit	-1,47	-1,07	-24,41
SL2017	<i>pduD</i>	Propanediol dehydratase medium subunit	-1,57	-1,14	-38,60
SL2018	<i>pduE</i>	Propanediol dehydratase small subunit	-1,75	-1,25	-66,46
SL2019	-	Glycerol Dehydratase Reactivation Factor Large Subunit	-1,77	-1,18	-53,01
SL2020	-	Hypothetical	-1,85	-1,16	-77,87
SL2021	<i>pduA</i>	Propanediol utilization protein pduA	-1,69	-1,19	-20,95
SL2022	-	Propanediol Utilization Protein PduK	-1,67	-1,31	-18,88
SL2023	-	Propanediol Utilization Protein	-2,00	-1,44	-25,45
SL2024	-	Propanediol Utilization Protein	-1,98	-1,30	-26,37
SL2025	<i>ccmL</i>	Carbon dioxide concentrating mechanism protein ccmL	-1,73	-1,23	-20,64
SL2026	-	Cob(I)yrinic acid a,c-diamide adenosyltransferase	-1,80	-1,25	-21,04
SL2027	<i>eutE</i>	Ethanolamine utilization protein eutE	-1,52	-1,18	-8,20
SL2028	<i>adh1</i>	NADPH-dependent butanol dehydrogenase	-1,56	-1,41	-9,36
SL2029	<i>rnfC</i>	Electron transport complex protein rnfC	-1,93	-1,59	-4,59
SL2030	<i>eutM</i>	Microcompartments Protein	-1,28	-1,28	-3,61
SL2031	<i>pduU</i>	Propanediol utilization protein pduU	-1,53	-1,36	-4,09
SL2032	<i>pduV</i>	Propanediol utilization protein pduV	-1,75	-1,80	-3,98
SL2033	<i>pduW</i>	Probable propionate kinase	-1,52	-1,24	-3,31
SL2034	-	Hypothetical	1,42	1,08	-2,41
SL2035	<i>yeeX</i>	UPF0265 protein Ent638_2575	1,03	-1,04	-1,75
SL2036	<i>yeeA</i>	Inner membrane protein yeeA	1,10	1,09	1,44
SL2037	<i>gyrl</i>	DNA gyrase inhibitory protein homolog	1,20	1,24	4,09

Tabla Suplementaria 1

Diferencia de expresión de todos los genes de SV5015 en las cepas mutantes *greA*, *greB* y *greAgreB*, respecto a la cepa WT

ID	gene	Description	<i>greA</i> vs WT	<i>greB</i> vs WT	<i>greAgreB</i> vs WT
SL2038	<i>dacD</i>	D-alanyl-D-alanine carboxypeptidase <i>dacD</i>	1,14	-1,00	-3,59
SL2039	<i>phsC</i>	Thiosulfate reductase cytochrome B subunit	1,30	1,05	-1,50
SL2040	<i>phsB</i>	Thiosulfate reductase electron transport protein <i>phsB</i>	1,32	-1,03	-1,80
SL2041	<i>phsA</i>	Thiosulfate reductase	1,31	1,07	-1,60
SL2042	<i>ybjQ</i>	Cytoplasmic Protein	-1,10	1,09	1,06
SL2043	<i>sopA</i>	E3 ubiquitin-protein ligase <i>SopA</i>	-1,29	-1,17	-11,05
SL2044	<i>sbcB</i>	Exodeoxyribonuclease I	-1,18	-1,39	-1,84
SL2045	<i>yeeF</i>	Inner membrane transport protein <i>yeeF</i>	1,13	1,09	-1,13
SL2046	<i>yeeY</i>	Uncharacterized HTH-type transcriptional regulatc	1,13	1,24	-1,04
SL2047	<i>yeeZ</i>	Protein <i>yeeZ</i>	1,05	1,09	1,38
SL2048	<i>hisG</i>	ATP phosphoribosyltransferase	1,19	1,02	1,90
SL2049	<i>hisD</i>	Histidinol dehydrogenase	1,16	-1,09	3,14
SL2050	<i>hisC</i>	Histidinol-phosphate aminotransferase	1,27	1,00	3,41
SL2051	<i>hisB</i>	Histidine biosynthesis bifunctional protein <i>hisB</i>	1,25	-1,13	2,86
SL2052	<i>hisH</i>	Imidazole glycerol phosphate synthase subunit <i>hisH</i>	1,21	-1,23	2,78
SL2053	<i>hisA</i>	1-(5-phosphoribosyl)-5-[(5-phosphoribosylamino)methylideneamino]imidazole-4-carboxamide isomerase	1,22	-1,18	2,60
SL2054	<i>hisF</i>	Imidazole glycerol phosphate synthase subunit <i>hisF</i>	1,31	-1,03	2,74
SL2055	<i>hisI</i>	Histidine biosynthesis bifunctional protein <i>hisIE</i>	1,21	-1,08	2,06
SL2056	<i>wzzB</i>	Chain length determinant protein	-1,51	1,00	-6,76
SL2057	<i>udg</i>	UDP-glucose 6-dehydrogenase	-1,82	1,07	-6,30
SL2058	<i>gnd</i>	6-phosphogluconate dehydrogenase, decarboxylating	1,10	-1,05	1,47
SL2059	<i>rfbP</i>	Undecaprenyl-phosphate galactose phosphotransferase	-1,05	1,05	-1,01
SL2060	<i>rfbK</i>	Phosphomannomutase	-1,01	-1,05	1,27
SL2061	<i>rfbM</i>	Mannose-1-phosphate guanylyltransferase <i>rfbM</i>	-1,12	-1,21	-1,23
SL2062	<i>rfbN</i>	O antigen biosynthesis rhamnosyltransferase <i>rfbN</i>	-1,07	-1,19	-1,11
SL2063	<i>rfbU</i>	Protein <i>rfbU</i>	-1,03	-1,14	-1,08
SL2064	<i>rfbV</i>	O antigen biosynthesis abequosyltransferase <i>rfbV</i>	-1,20	-1,07	-1,36
SL2065	<i>rfbX</i>	Putative O-antigen transporter	-1,06	-1,21	-1,11
SL2066	<i>rfbJ</i>	CDP-abequose synthase	-1,10	-1,12	1,51
SL2067	<i>rfbH</i>	Lipopolysaccharide biosynthesis protein <i>rfbH</i>	-1,01	-1,15	1,44
SL2068	<i>rfbG</i>	CDP-glucose 4,6-dehydratase	-1,01	-1,10	1,23
SL2069	<i>rfbF</i>	Glucose-1-phosphate cytidyltransferase	-1,03	-1,09	1,15
SL2070	<i>rfbI</i>	Protein <i>rfbI</i>	-1,12	-1,18	-1,20
SL2071	<i>rfbC</i>	dTDP-4-dehydrorhamnose 3,5-epimerase	-1,07	-1,17	-1,15
SL2072	<i>rmlA1</i>	Glucose-1-phosphate thymidyltransferase 1	1,07	-1,09	-1,25
SL2073	<i>rfbD</i>	dTDP-4-dehydrorhamnose reductase	1,05	-1,09	-1,38
SL2074	<i>rfbB</i>	dTDP-glucose 4,6-dehydratase	1,11	1,02	-1,81
SL2075	<i>galF</i>	UTP--glucose-1-phosphate uridyltransferase	1,03	1,11	-2,43
SL2076	<i>wcaM</i>	Colanic acid biosynthesis protein <i>wcaM</i>	1,19	1,01	1,65
SL2077	<i>wcaL</i>	Putative colanic acid biosynthesis glycosyltransferase <i>wcaL</i>	1,29	-1,03	3,22
SL2078	<i>wcaK</i>	Colanic acid biosynthesis protein <i>wcaK</i>	1,32	1,01	2,81

Tabla Suplementaria 1

Diferencia de expresión de todos los genes de SV5015 en las cepas mutantes *greA*, *greB* y *greAgreB*, respecto a la cepa WT

ID	gene	Description	<i>greA</i> vs WT	<i>greB</i> vs WT	<i>greAgreB</i> vs WT
SL2079	<i>wzxC</i>	Lipopolysaccharide biosynthesis protein wzxC	1,52	-1,11	1,29
SL2080	<i>wcaJ</i>	Putative colanic biosynthesis UDP-glucose lipid carrier transferase	1,15	-1,28	1,65
SL2081	<i>manB</i>	Phosphomannomutase	1,91	1,15	2,85
SL2082	<i>manC</i>	Mannose-1-phosphate guanylyltransferase manC	1,16	-1,09	1,21
SL2083	<i>wcaI</i>	Putative colanic acid biosynthesis glycosyl transferase wcaI	1,26	1,18	1,17
SL2084	<i>nudD</i>	GDP-mannose mannosyl hydrolase	1,37	1,36	1,67
SL2085	<i>fcl</i>	GDP-L-fucose synthase	1,07	1,07	1,11
SL2086	<i>gmd</i>	GDP-mannose 4,6-dehydratase	1,13	1,26	1,40
SL2087	<i>wcaF</i>	Putative colanic acid biosynthesis acetyltransferase wcaF	-1,05	1,46	-1,57
SL2088	<i>wcaE</i>	Putative colanic acid biosynthesis glycosyl transferase wcaE	-1,06	1,38	-1,15
SL2089	<i>wcaD</i>	Putative colanic acid polymerase	-1,09	-1,19	1,07
SL2090	<i>wcaC</i>	Putative colanic acid biosynthesis glycosyl transferase wcaC	-1,16	-1,09	1,13
SL2091	<i>wcaB</i>	Putative colanic acid biosynthesis acetyltransferase wcaB	1,35	-1,18	1,62
SL2092	<i>wcaA</i>	Putative colanic acid biosynthesis glycosyl transferase wcaA	1,08	1,00	1,47
SL2093	<i>wzc</i>	Tyrosine-protein kinase wzc	-1,05	1,00	-1,15
SL2094	<i>wzb</i>	Low molecular weight protein-tyrosine-phosphatase wzb	-1,29	1,11	-1,41
SL2095	<i>wza</i>	Putative polysaccharide export protein wza	-1,10	-1,18	-1,57
SL2096	<i>yegH</i>	UPF0053 protein yegH	-1,10	-1,03	-1,81
SL2097	<i>asmA</i>	Protein AsmA	1,12	-1,01	-1,01
SL2098	<i>dcd</i>	Deoxycytidine triphosphate deaminase	1,03	-1,02	1,07
SL2099	<i>udk</i>	Uridine kinase	1,19	1,20	-2,45
SL2100	<i>yegE</i>	Probable diguanylate cyclase YegE	1,04	1,26	-1,57
SL2101	<i>alkA</i>	DNA-3-methyladenine glycosylase 2	-1,19	-1,09	-1,18
SL2102	<i>yegD</i>	Uncharacterized chaperone protein yegD	-1,09	-1,01	-1,53
SL2103	<i>mdtA</i>	Multidrug resistance protein mdtA	-1,18	-1,07	-1,74
SL2104	<i>mdtB</i>	Multidrug resistance protein mdtB	1,25	1,14	-1,23
SL2105	<i>mdtC</i>	Multidrug resistance protein mdtC	1,03	1,22	-1,49
SL2106	<i>mdtD</i>	Putative multidrug resistance protein mdtD	1,11	1,19	-1,22
SL2107	<i>baeS</i>	Signal transduction histidine-protein kinase BaeS	-1,25	-1,02	-2,13
SL2108	<i>baeR</i>	Transcriptional regulatory protein BaeR	-1,30	-1,25	-1,58
SL2109	-	Hypothetical	-1,46	1,05	-1,60
SL2110	-	Hypothetical	-1,10	-1,17	-1,30
SL2111	-	Hypothetical	1,18	-1,11	1,24
SL2112	<i>yegQ</i>	Uncharacterized protease yegQ	-1,03	1,12	-2,43
SL2113	-	Hypothetical	-1,21	1,30	-1,00
SL2114	<i>cesT</i>	Tir chaperone	-3,66	1,12	-1,47
SL2115	-	Hypothetical	-4,46	1,33	-2,96
SL2116	-	Hypothetical	1,36	1,91	1,14
SL2117	<i>yegS</i>	Probable lipid kinase yegS	1,04	1,19	-1,63
SL2118	<i>fbaB</i>	Fructose-bisphosphate aldolase class 1	1,26	1,34	1,76
SL2119	<i>yegT</i>	Putative nucleoside transporter yegT	-1,23	-1,16	4,25
SL2120	<i>yegU</i>	Uncharacterized protein yegU	-1,16	-1,12	2,62

Tabla Suplementaria 1

Diferencia de expresión de todos los genes de SV5015 en las cepas mutantes *greA*, *greB* y *greAgreB*, respecto a la cepa WT

ID	gene	Description	<i>greA</i> vs WT	<i>greB</i> vs WT	<i>greAgreB</i> vs WT
SL2121	<i>yegV</i>	Uncharacterized sugar kinase yegV	-1,04	1,05	2,37
SL2122	<i>yegW</i>	Uncharacterized HTH-type transcriptional regulator yegW	1,13	1,07	1,37
SL2123	<i>thiD</i>	Hydroxymethylpyrimidine/phosphomethylpyrimidine kinase	1,28	1,23	1,66
SL2124	<i>thiM</i>	Hydroxyethylthiazole kinase	1,23	1,17	1,16
SL2125	<i>yohN</i>	Uncharacterized protein yohN	1,09	1,20	-1,05
SL2126	<i>yehA</i>	Uncharacterized protein yehA	-1,06	1,15	1,19
SL2127	<i>yehB</i>	Uncharacterized outer membrane usher protein yehB	1,10	-1,06	1,18
SL2128	<i>yehC</i>	Uncharacterized fimbrial chaperone yehC	1,00	-1,17	-2,06
SL2129	<i>yehD</i>	Uncharacterized protein yehD	1,02	1,12	-1,04
SL2130	<i>yehE</i>	Uncharacterized protein yehE	-1,84	-1,06	-15,13
SL2131	<i>mrp</i>	Protein mrp	-1,02	-1,04	-1,27
SL2132	<i>metG</i>	Methionyl-tRNA synthetase	-1,14	-1,04	-1,54
SL2133	<i>yehR</i>	Uncharacterized lipoprotein yehR	1,19	1,21	-1,32
SL2134	<i>yehR</i>	Uncharacterized lipoprotein Lmo0207	-1,12	-1,13	-1,68
SL2135	<i>yehS</i>	Uncharacterized protein yehS	1,04	-1,15	-2,30
SL2136	<i>yehT</i>	Uncharacterized response regulatory protein yehT	1,13	1,06	3,14
SL2137	<i>yehU</i>	Inner membrane protein yehU	-1,01	-1,03	1,50
SL2138	<i>mlrA</i>	HTH-type transcriptional regulator mlrA	1,15	1,35	1,56
SL2139	<i>yohO</i>	UPF0387 membrane protein yohO	1,34	1,07	1,32
SL2140	<i>yehW</i>	Putative osmoprotectant uptake system permease protein yehW	1,11	-1,18	1,23
SL2141	<i>yehX</i>	Putative osmoprotectant uptake system ATP-binding protein yehX	1,11	-1,15	1,32
SL2142	<i>yehY</i>	Putative osmoprotectant uptake system permease protein yehY	1,18	-1,15	1,39
SL2143	<i>osmF</i>	Putative osmoprotectant uptake system substrate-binding protein osmF	1,15	1,03	1,84
SL2144	<i>bglX</i>	Periplasmic beta-glucosidase	-1,13	-1,16	-1,14
SL2145	<i>dld</i>	D-lactate dehydrogenase	1,09	-1,07	2,01
SL2146	<i>pbpG</i>	D-alanyl-D-alanine endopeptidase	1,13	1,04	-1,75
SL2147	<i>yohC</i>	Inner membrane protein yohC	1,03	1,41	1,33
SL2148	<i>yohD</i>	Inner membrane protein yohD	1,02	1,11	1,33
SL2149	<i>yohF</i>	Uncharacterized oxidoreductase yohF	1,03	-1,00	1,55
SL2150	<i>mdtQ</i>	Multidrug resistance outer membrane protein mdtQ	-1,36	-1,08	-1,12
SL2151	<i>dusC</i>	tRNA-dihydrouridine synthase C	-1,11	-1,09	-1,92
SL2152	<i>mhbM</i>	3-hydroxybenzoate 6-hydroxylase	1,16	1,06	2,31
SL2153	<i>maiA</i>	Probable maleylacetoacetate isomerase	1,22	1,04	3,04
SL2154	<i>ycgM</i>	Uncharacterized protein PYRAB13970	-1,01	-1,03	3,97
SL2155	-	Gentisate 1 2-Dioxygenase	1,03	1,05	5,13
SL2156	<i>pcaK</i>	4-hydroxybenzoate transporter	-1,10	-1,02	2,29
SL2157	<i>gbpR</i>	HTH-type transcriptional regulator gbpR	-1,37	-1,28	2,35
SL2158	<i>yohJ</i>	UPF0299 membrane protein CKO_00648	1,00	1,05	-11,34
SL2159	<i>yohK</i>	Inner membrane protein yohK	1,04	-1,03	-12,19
SL2160	<i>cdd</i>	Cytidine deaminase	1,03	-1,06	-8,24
SL2161	<i>sanA</i>	Protein sanA	-1,10	-1,13	-1,16
SL2162	<i>yeiS</i>	Uncharacterized protein yeiS	1,00	-1,02	1,40
SL2163	<i>yeiT</i>	Uncharacterized oxidoreductase yeiT	-1,08	1,11	-1,15

Tabla Suplementaria 1

Diferencia de expresión de todos los genes de SV5015 en las cepas mutantes *greA*, *greB* y *greAgreB*, respecto a la cepa WT

ID	gene	Description	<i>greA</i> vs WT	<i>greB</i> vs WT	<i>greAgreB</i> vs WT
SL2164	<i>yeiA</i>	Uncharacterized protein yeiA	-1,11	1,13	-1,48
SL2165	<i>mgIC</i>	Galactoside transport system permease protein mgIC	1,03	-1,75	6,61
SL2166	<i>mgIA</i>	Galactose/methyl galactoside import ATP-binding protein MglA	-1,07	-1,75	11,23
SL2167	<i>mgIB</i>	D-galactose-binding periplasmic protein	1,09	-1,19	10,18
SL2168	<i>galS</i>	HTH-type transcriptional regulator galS	1,09	1,13	1,68
SL2169	<i>yeiB</i>	Uncharacterized protein yeiB	-1,10	-1,00	-4,93
SL2170	<i>folE</i>	GTP cyclohydrolase 1	1,10	1,04	-3,82
SL2171	<i>yeiG</i>	S-formylglutathione hydrolase yeiG	1,06	1,05	2,13
SL2172	-	Transcriptional Regulator	1,13	1,12	1,11
SL2173	<i>sdaA</i>	L-serine dehydratase 1	1,17	1,05	1,12
SL2174	<i>serB</i>	Phosphoserine phosphatase	-1,13	-1,26	1,96
SL2175	<i>uhpC</i>	Regulatory protein uhpC	1,13	-1,03	2,60
SL2176	<i>cirA</i>	Colicin I receptor	1,00	1,62	-1,86
SL2177	<i>lysP</i>	Lysine-specific permease	1,26	-1,12	-1,74
SL2178	<i>yeiE</i>	Uncharacterized HTH-type transcriptional regulator yeiE	1,09	1,05	1,42
SL2179	<i>yeiH</i>	UPF0324 inner membrane protein yeiH	1,13	1,21	-2,57
SL2180	<i>nfo</i>	Probable endonuclease 4	-1,23	-1,31	-1,63
SL2181	<i>fruA</i>	PTS system fructose-specific EIIBC component	1,17	1,23	-10,61
SL2182	<i>fruK</i>	1-phosphofructokinase	1,06	1,18	-8,46
SL2183	<i>fruB</i>	Multiphosphoryl transfer protein	-1,06	-1,02	-6,16
SL2184	<i>setB</i>	Sugar efflux transporter B	-1,25	-1,03	-5,41
SL2185	<i>ykgH</i>	Hypothetical	1,16	1,17	-1,63
SL2186	-	Hypothetical	1,19	-1,00	1,09
SL2187	<i>yeiW</i>	UPF0153 protein yeiW	1,15	1,16	-1,77
SL2188	<i>yeiP</i>	Elongation factor P-like protein	-1,08	-1,12	-1,18
SL2189	<i>yeiR</i>	Uncharacterized protein yeiR	-1,09	-1,15	1,23
SL2190	<i>yeiU</i>	Inner membrane protein yeiU	-1,14	1,09	-2,33
SL2191	<i>spr</i>	Lipoprotein spr	-1,35	1,17	-3,81
SL2192	<i>rtn</i>	Protein rtn	1,25	1,16	1,27
SL2193	<i>yejA</i>	Uncharacterized protein yejA	1,11	1,02	-1,49
SL2194	<i>yejB</i>	Inner membrane ABC transporter permease protein yejB	1,14	-1,03	-1,24
SL2195	<i>yejE</i>	Inner membrane ABC transporter permease protein yejE	1,12	1,10	-1,16
SL2196	<i>yejF</i>	Uncharacterized ABC transporter ATP-binding protein yejF	1,13	1,10	-1,05
SL2197	<i>yejG</i>	Uncharacterized protein yejG	-1,07	1,18	-1,41
SL2198	<i>bcr</i>	Bicyclomycin resistance protein	1,12	-1,27	-1,34
SL2199	<i>rsuA</i>	Ribosomal small subunit pseudouridine synthase A	1,17	1,00	-1,68
SL2200	<i>yejH</i>	Uncharacterized protein yejH	1,19	-1,15	1,04
SL2201	<i>rplY</i>	50S ribosomal protein L25	-1,05	1,01	-1,57
SL2202	-	Hypothetical	1,15	1,00	-1,02
SL2203	<i>ndpA</i>	Nucleoid-associated protein ndpA	1,12	1,03	-1,18
SL2204	<i>yejL</i>	UPF0352 protein yejL	-1,17	-1,16	-2,47
SL2205	<i>yejM</i>	Inner membrane protein yejM	1,01	-1,05	-2,01
SL2206	<i>umuD</i>	Protein umuD	-1,31	-1,09	-1,53
SL2207	<i>msgA</i>	Virulence protein msgA	-1,06	-1,35	-1,68

Tabla Suplementaria 1

Diferencia de expresión de todos los genes de SV5015 en las cepas mutantes *greA*, *greB* y *greAgreB*, respecto a la cepa WT

ID	gene	Description	<i>greA</i> vs WT	<i>greB</i> vs WT	<i>greAgreB</i> vs WT
SL2208	<i>yrhL</i>	Putative peptidoglycan O-acetyltransferase yrhL	-1,29	-1,71	1,10
SL2209	<i>yfdK</i>	Uncharacterized protein yfdK	1,03	1,10	1,10
SL2210	-	Hypothetical	1,09	1,13	1,19
SL2211	<i>ycfK</i>	Uncharacterized protein ycfK	1,01	1,01	-1,12
SL2212	-	Prohead Protease	1,04	1,13	-2,07
SL2213	-	Hypothetical	1,16	-1,13	-2,23
SL2214	<i>pifA</i>	KAP P-Loop Domain-Containing Protein	-1,29	-1,52	2,07
SL2215	<i>quuD</i>	Antitermination protein Q homolog from lambdoid prophage DLP12	-1,17	1,07	1,18
SL2216	<i>ydfU</i>	Uncharacterized protein ydfU	-1,13	-1,15	1,52
SL2217	<i>sspH2</i>	E3 ubiquitin-protein ligase sspH2	-1,06	-1,09	-1,54
SL2218	-	Bacteriophage Tail Fiber Assembly Protein	-1,32	1,01	-1,96
SL2219	<i>stfR</i>	Side Tail Fiber Protein	-1,38	1,13	-1,40
SL2220	-	Homolog Of Virulence Protein MsgA	-1,66	1,18	-2,64
SL2221	-	Conserved Hypothetical Protein	-2,49	1,39	-2,04
SL2222	<i>narP</i>	Nitrate/nitrite response regulator protein narP	-1,32	-1,28	-1,33
SL2223	<i>ccmH</i>	Cytochrome c-type biogenesis protein ccmH	-1,11	-1,13	1,27
SL2224	<i>ccmAE</i>	Putative bifunctional cytochrome c-type biogenesis protein ccmAE	-1,01	1,06	-1,66
SL2225	<i>napC</i>	Cytochrome c-type protein napC	1,06	-1,02	2,49
SL2226	<i>napB</i>	Diheme cytochrome c napB	1,06	-1,08	1,77
SL2227	<i>napH</i>	Ferredoxin-type protein napH	1,02	-1,02	2,21
SL2228	<i>napG</i>	Ferredoxin-type protein napG	1,15	-1,12	2,65
SL2229	<i>napA</i>	Periplasmic nitrate reductase	1,17	-1,04	3,48
SL2230	<i>napD</i>	Protein napD	1,12	-1,46	-1,16
SL2231	<i>napF</i>	Ferredoxin-type protein napF	1,18	1,31	1,09
SL2232	<i>eco</i>	Ecotin	1,16	1,13	1,64
SL2233	<i>yojI</i>	ABC transporter ATP-binding protein yojI	1,08	1,30	-1,74
SL2234	<i>alkB</i>	Alpha-ketoglutarate-dependent dioxygenase AlkB	1,16	1,26	1,76
SL2235	<i>ada</i>	Regulatory protein ada	1,17	1,27	1,84
SL2236	<i>apbE</i>	Thiamine biosynthesis lipoprotein ApbE	1,15	1,13	1,05
SL2237	<i>ompC</i>	Outer membrane protein C	1,00	1,02	-1,03
SL2238	<i>yojN</i>	Hypothetical Protein yojN	-1,02	1,15	-1,55
SL2239	<i>rcsB</i>	Capsular synthesis regulator component B	-1,03	1,12	-1,71
SL2240	<i>rscC</i>	Sensor protein rcsC	1,05	-1,28	-1,14
SL2241	<i>gyrA</i>	DNA gyrase subunit A	1,01	-1,21	-1,34
SL2242	<i>dgoD</i>	D-galactonate dehydratase	-1,07	1,11	1,84
SL2243	<i>ttuB</i>	Putative tartrate transporter	1,05	-1,13	3,31
SL2244	<i>ntaR</i>	Nta operon transcriptional regulator	1,14	-1,14	1,71
SL2245	<i>ubiG</i>	3-demethylubiquinone-9 3-methyltransferase	1,07	1,12	-1,29
SL2246	<i>nrdA</i>	Ribonucleoside-diphosphate reductase 1 subunit alpha	-1,04	-1,21	-1,72
SL2247	<i>nrdB</i>	Ribonucleoside-diphosphate reductase 1 subunit beta	1,08	-1,08	1,05
SL2248	<i>yfaE</i>	Uncharacterized ferredoxin-like protein yfaE	1,17	-1,21	-1,30
SL2249	<i>ywoG</i>	Uncharacterized MFS-type transporter ywoG	1,12	-1,04	-1,92

Tabla Suplementaria 1

Diferencia de expresión de todos los genes de SV5015 en las cepas mutantes *greA*, *greB* y *greAgreB*, respecto a la cepa WT

ID	gene	Description	<i>greA</i> vs WT	<i>greB</i> vs WT	<i>greAgreB</i> vs WT
SL2250	<i>yvbU</i>	Uncharacterized HTH-type transcriptional regulator yvbU	1,24	-1,04	1,11
SL2251	<i>glpQ</i>	Glycerophosphoryl diester phosphodiesterase	1,05	-1,09	-1,04
SL2252	<i>glpT</i>	Glycerol-3-phosphate transporter	1,00	-1,07	1,01
SL2253	<i>glpA</i>	Anaerobic glycerol-3-phosphate dehydrogenase subunit A	1,19	1,22	1,01
SL2254	<i>glpB</i>	Anaerobic glycerol-3-phosphate dehydrogenase subunit B	1,14	1,10	-1,11
SL2255	<i>glpC</i>	Anaerobic glycerol-3-phosphate dehydrogenase subunit C	1,09	1,04	-1,28
SL2256	<i>sseL</i>	Deubiquitinase sseL	-7,62	1,57	-9,57
SL2257	<i>cinA</i>	CinA-like protein	1,33	1,03	1,80
SL2258	<i>yfaU</i>	2-keto-3-deoxy-L-rhamnonate aldolase	1,38	1,15	1,99
SL2259	<i>yfaV</i>	Inner membrane transport protein yfaV	1,50	1,14	1,29
SL2260	<i>yfaW</i>	L-rhamnonate dehydratase	1,21	1,11	1,37
SL2261	<i>yfaX</i>	Uncharacterized HTH-type transcriptional regulator yfaX	1,42	1,43	2,53
SL2262	<i>cinA</i>	CinA-like protein	-1,07	-1,08	1,18
SL2263	<i>yfaZ</i>	Uncharacterized protein yfaZ	-1,21	-1,04	-1,52
SL2264	<i>nudI</i>	Nucleoside triphosphatase nudI	-1,16	-1,05	1,24
SL2265	<i>ais</i>	Lipopolysaccharide core heptose(II)-phosphate phosphatase	-1,34	1,08	-4,74
SL2266	<i>arnB</i>	UDP-4-amino-4-deoxy-L-arabinose--oxoglutarate aminotransferase	-1,29	1,15	-2,44
SL2267	<i>arnC</i>	Undecaprenyl-phosphate 4-deoxy-4-formamido-L-arabinose transferase	-1,49	-1,03	-2,05
SL2268	<i>arnA</i>	Bifunctional polymyxin resistance protein ArnA	-1,48	-1,12	-1,73
SL2269	<i>arnD</i>	Probable 4-deoxy-4-formamido-L-arabinose-phosphoundecaprenol deformylase ArnD	-1,35	-1,10	-2,06
SL2270	<i>arnT</i>	Undecaprenyl phosphate-alpha-4-amino-4-deoxy-L-arabinose arabinosyl transferase	-1,32	-1,01	-2,12
SL2271	<i>arnE</i>	Probable 4-amino-4-deoxy-L-arabinose-phosphoundecaprenol flippase subunit ArnE	1,11	1,37	-1,89
SL2272	<i>arnF</i>	Probable 4-amino-4-deoxy-L-arabinose-phosphoundecaprenol flippase subunit ArnF	-1,17	1,24	-2,31
SL2273	<i>pmrD</i>	Signal transduction protein pmrD	-1,12	1,28	-1,44
SL2274	<i>menE</i>	2-succinylbenzoate--CoA ligase	1,19	-1,15	-1,31
SL2275	<i>menC</i>	o-succinylbenzoate synthase	1,30	-1,10	1,05
SL2276	<i>menB</i>	Naphthoate synthase	1,21	-1,07	-1,01
SL2277	<i>menH</i>	2-succinyl-6-hydroxy-2,4-cyclohexadiene-1-carboxylate synthase	1,44	1,02	-2,59
SL2278	<i>menD</i>	2-succinyl-5-enolpyruvyl-6-hydroxy-3-cyclohexene-1-carboxylate synthase	1,09	1,20	-1,85
SL2279	<i>menF</i>	Menaquinone-specific isochorismate synthase	-1,00	-1,05	-2,16
SL2280	<i>elaB</i>	Protein elaB	-1,05	1,02	1,73
SL2281	<i>elaA</i>	Protein elaA	-1,04	1,01	1,91
SL2282	<i>rnz</i>	Ribonuclease Z	1,07	-1,19	1,08
SL2283	<i>cheV</i>	Chemotaxis protein cheV	-1,26	-1,24	-10,75
SL2284	<i>yfbK</i>	Uncharacterized protein yfbK	1,05	-1,11	-2,45
SL2285	<i>nuoN</i>	NADH-quinone oxidoreductase subunit N	1,11	-1,19	1,42

Tabla Suplementaria 1

Diferencia de expresión de todos los genes de SV5015 en las cepas mutantes *greA*, *greB* y *greAgreB*, respecto a la cepa WT

ID	gene	Description	<i>greA</i> vs WT	<i>greB</i> vs WT	<i>greAgreB</i> vs WT
SL2286	<i>nuoM</i>	NADH-quinone oxidoreductase subunit M	1,09	-1,07	1,38
SL2287	<i>nuoL</i>	NADH-quinone oxidoreductase subunit L	1,04	-1,10	1,99
SL2288	<i>nuoK</i>	NADH-quinone oxidoreductase subunit K	1,03	-1,13	2,30
SL2289	<i>nuoJ</i>	NADH-quinone oxidoreductase subunit J	1,08	-1,05	1,84
SL2290	<i>nuoI</i>	NADH-quinone oxidoreductase subunit I	1,02	-1,10	1,99
SL2291	<i>nuoH</i>	NADH-quinone oxidoreductase subunit H	1,09	-1,12	1,93
SL2292	<i>nuoG</i>	NADH-quinone oxidoreductase subunit G	1,01	-1,06	1,69
SL2293	<i>nuoF</i>	NADH-quinone oxidoreductase subunit F	1,13	-1,14	1,95
SL2294	<i>nuoE</i>	NADH-quinone oxidoreductase subunit E	1,06	-1,16	1,32
SL2295	<i>nuoC</i>	NADH-quinone oxidoreductase subunit C/D	-1,01	-1,26	-1,07
SL2296	<i>nuoB</i>	NADH-quinone oxidoreductase subunit B	1,01	-1,07	-1,27
SL2297	<i>nuoA</i>	NADH-quinone oxidoreductase subunit A	-1,05	-1,03	-1,37
SL2298	-	Hypothetical	-1,07	1,30	-1,86
SL2299	<i>lrhA</i>	Probable HTH-type transcriptional regulator LrhA	-1,35	1,08	-2,65
SL2300	<i>yfbQ</i>	Uncharacterized aminotransferase yfbQ	-1,15	-1,01	-1,62
SL2301	<i>yfbR</i>	UPF0207 protein KPK_1466	-1,06	-1,05	-1,02
SL2302	<i>yfbS</i>	Uncharacterized transporter yfbS	1,19	1,06	1,01
SL2303	<i>yfbT</i>	Phosphatase yfbT	1,11	1,04	-1,15
SL2304	<i>yfbU</i>	UPF0304 protein yfbU	1,03	1,02	1,13
SL2305	<i>yfbV</i>	UPF0208 membrane protein yfbV	-1,17	-1,00	-2,12
SL2306	<i>ackA</i>	Acetate kinase	-1,09	-1,09	-3,07
SL2307	<i>pta</i>	Phosphate acetyltransferase	1,04	-1,15	-1,77
SL2308	<i>yfcC</i>	Uncharacterized protein yfcC	1,14	-1,21	-2,45
SL2309	<i>dxs</i>	Putative transketolase C-terminal section	1,04	-1,22	1,97
SL2310	<i>tktA</i>	Putative transketolase N-terminal section	1,13	-1,04	1,67
SL2311	<i>ulaA</i>	Ascorbate-specific permease IIC component ulaA	1,08	-1,02	2,27
SL2312	-	Hypothetical	-1,02	-1,08	2,94
SL2313	<i>ulaC</i>	Ascorbate-specific phosphotransferase enzyme IIA component	-1,14	-1,17	3,39
SL2314	<i>gntR</i>	HTH-type transcriptional regulator gntR	1,29	1,15	1,45
SL2315	<i>yfcD</i>	Uncharacterized Nudix hydrolase yfcD	-1,07	-1,07	-1,28
SL2316	<i>yfcE</i>	Phosphodiesterase yfcE	-1,12	-1,14	-1,34
SL2317	<i>yfcF</i>	Uncharacterized GST-like protein yfcF	1,03	1,19	1,15
SL2318	<i>yfcG</i>	Uncharacterized GST-like protein yfcG	-1,05	-1,17	1,14
SL2319	<i>yfcH</i>	Epimerase family protein yfcH	1,40	1,21	1,77
SL2320	<i>hisP</i>	Histidine transport ATP-binding protein hisP	1,08	-1,10	1,04
SL2321	<i>hisM</i>	Histidine transport system permease protein hisM	1,13	-1,04	1,12
SL2322	<i>hisQ</i>	Histidine transport system permease protein hisQ	1,21	-1,07	1,08
SL2323	<i>hisJ</i>	Histidine-binding periplasmic protein	-1,05	-1,15	2,32
SL2324	<i>argT</i>	Lysine-arginine-ornithine-binding periplasmic protein	-1,15	1,01	7,89
SL2325	<i>ubiX</i>	3-octaprenyl-4-hydroxybenzoate carboxy-lyase	-1,04	-1,06	-1,66
SL2326	<i>rocC</i>	Amino-acid permease rocC	1,06	1,04	-1,18
SL2327	-	Amino Acid Racemase	1,18	1,13	2,86
SL2328	<i>xasA</i>	Uncharacterized transporter lpg1691	-1,05	1,15	1,86
SL2329	<i>lysA</i>	Diaminopimelate decarboxylase	1,22	1,48	1,50

Tabla Suplementaria 1

Diferencia de expresión de todos los genes de SV5015 en las cepas mutantes *greA*, *greB* y *greAgreB*, respecto a la cepa WT

ID	gene	Description	<i>greA</i> vs WT	<i>greB</i> vs WT	<i>greAgreB</i> vs WT
SL2330	<i>rocR</i>	Arginine utilization regulatory protein rocR	1,21	1,43	1,99
SL2331	<i>purF</i>	Amidophosphoribosyltransferase	-1,01	1,09	-1,24
SL2332	<i>cvpA</i>	Colicin V production protein	1,09	1,21	-1,46
SL2333	<i>dedD</i>	Protein dedD	-1,11	-1,08	-1,77
SL2334	<i>folC</i>	Bifunctional protein folC	-1,00	-1,11	-1,60
SL2335	<i>accD</i>	Acetyl-coenzyme A carboxylase carboxyl transferase subunit beta	1,16	1,20	-1,67
SL2336	<i>dedA</i>	Protein dedA	1,22	1,16	-1,32
SL2337	<i>truA</i>	tRNA pseudouridine synthase A	1,18	-1,11	-1,17
SL2338	<i>usg</i>	USG-1 protein	1,01	-1,05	-1,45
SL2339	<i>pdxB</i>	Erythronate-4-phosphate dehydrogenase	-1,02	-1,07	-2,04
SL2340	<i>flk</i>	Flagellar regulator flk	-1,01	1,03	-1,91
SL2341	<i>yfcJ</i>	UPF0226 membrane protein SARI_00527	-1,10	-1,09	-1,53
SL2342	-	Bacteriophage Protein	1,02	1,11	-1,38
SL2343	<i>sfsB</i>	Sugar fermentation stimulation protein B	1,04	-1,01	-1,02
SL2344	-	Hypothetical	1,13	1,02	1,06
SL2345	-	Hypothetical	1,05	1,01	1,06
SL2346	-	Uncharacterized 24.3 kDa protein	1,20	1,05	-1,17
SL2347	<i>fabB</i>	3-oxoacyl-[acyl-carrier-protein] synthase 1	-1,09	-1,26	1,11
SL2348	<i>mnmC</i>	tRNA 5-methylaminomethyl-2-thiouridine biosynthesis bifunctional protein mnmC	1,02	-1,02	1,03
SL2349	<i>yfcL</i>	Uncharacterized protein yfcL	1,12	1,02	-1,13
SL2350	<i>yfcM</i>	Uncharacterized protein yfcM	-1,06	-1,31	-1,11
SL2351	<i>yfcA</i>	UPF0721 transmembrane protein yfcA	-1,08	-1,19	-1,24
SL2352	<i>mepA</i>	Penicillin-insensitive murein endopeptidase	-1,08	-1,21	1,27
SL2353	<i>aroC</i>	Chorismate synthase	-1,10	-1,18	1,39
SL2354	<i>yfcB</i>	Uncharacterized adenine-specific methylase yfcB	-1,24	-1,13	-1,03
SL2355	<i>yfcN</i>	UPF0115 protein KPK_1418	1,36	1,06	-1,06
SL2356	<i>sixA</i>	Phosphohistidine phosphatase sixA	-1,03	1,16	-1,32
SL2357	<i>fadJ</i>	Fatty acid oxidation complex subunit alpha	-1,03	1,15	4,65
SL2358	<i>fadI</i>	3-ketoacyl-CoA thiolase	1,09	1,26	2,24
SL2359	<i>yfcZ</i>	UPF0381 protein yfcZ	1,02	1,31	-1,84
SL2360	<i>fadL</i>	Long-chain fatty acid transport protein	-1,14	1,08	7,09
SL2361	<i>mIaA</i>	Probable phospholipid-binding lipoprotein mIaA	-1,20	-1,07	-1,42
SL2362	<i>yfdC</i>	Inner membrane protein yfdC	1,06	1,22	1,40
SL2363	<i>pgtE</i>	Outer membrane protease E	-2,81	1,47	-2,42
SL2364	<i>pgtA</i>	Phosphoglycerate transport system transcriptional regulatory protein pgtA	1,10	1,00	-1,35
SL2365	<i>pgtB</i>	Phosphoglycerate transport system sensor protein pgtB	1,13	1,15	-1,88
SL2366	<i>pgtC</i>	Phosphoglycerate transport regulatory protein pgtC	1,25	1,46	1,18
SL2367	<i>pgtP</i>	Phosphoglycerate transporter protein	1,36	1,62	2,39
SL2368	<i>yfdY</i>	Uncharacterized protein yfdY	1,75	1,30	1,94
SL2369	<i>ddg</i>	Protein ddg	-1,46	-1,05	-11,56
SL2370	<i>yfdZ</i>	Uncharacterized aminotransferase yfdZ	1,11	1,12	1,13
SL2371	<i>glk</i>	Glucokinase	1,03	-1,07	1,06
SL2372	<i>yfeO</i>	Putative ion-transport protein yfeO	1,03	1,07	1,06
SL2373	<i>ipdC</i>	Indole-3-pyruvate decarboxylase	1,14	1,25	1,97

Tabla Suplementaria 1

Diferencia de expresión de todos los genes de SV5015 en las cepas mutantes *greA*, *greB* y *greAgreB*, respecto a la cepa WT

ID	gene	Description	<i>greA</i> vs WT	<i>greB</i> vs WT	<i>greAgreB</i> vs WT
SL2374	<i>yghZ</i>	Uncharacterized protein yghZ	1,19	1,27	1,19
SL2375	<i>ypeC</i>	Uncharacterized protein ypeC	1,03	1,16	-1,39
SL2376	<i>mntH</i>	Manganese transport protein mntH	1,04	1,05	-1,03
SL2377	<i>nupC</i>	Nucleoside permease nupC	-1,00	-1,03	1,23
SL2378	<i>yfeA</i>	Uncharacterized protein yfeA	-1,11	-1,04	-2,35
SL2379	<i>yfeC</i>	Uncharacterized protein yfeC	1,31	1,08	1,46
SL2380	<i>yfeD</i>	Uncharacterized protein yfeD	1,50	1,35	1,87
SL2381	<i>gltX</i>	Glutamyl-tRNA synthetase	1,02	-1,05	-1,53
SL2382	<i>xapR</i>	HTH-type transcriptional regulator xapR	1,15	-1,11	-1,19
SL2383	-	Hypothetical N	1,21	1,10	1,01
SL2384	<i>xapB</i>	Xanthosine permease	-1,16	1,29	-1,13
SL2385	<i>xapA</i>	Xanthosine phosphorylase	-1,25	1,08	-1,57
SL2386	<i>yfeN</i>	Uncharacterized protein yfeN	-1,13	-1,23	-1,03
SL2387	<i>yfeR</i>	Uncharacterized HTH-type transcriptional regulator yfeR	-1,09	-1,25	1,35
SL2388	<i>yfeH</i>	Uncharacterized protein yfeH	1,12	-1,04	-1,38
SL2389	<i>ypeB</i>	Uncharacterized protein ypeB	1,13	-1,08	1,08
SL2390	<i>ligA</i>	DNA ligase	1,06	-1,06	1,11
SL2391	<i>zipA</i>	Cell division protein zipA homolog	-1,15	1,20	-1,54
SL2392	<i>cysZ</i>	Protein cysZ homolog	1,04	1,21	-1,89
SL2393	<i>cysK</i>	Cysteine synthase A	1,11	1,01	2,16
SL2394	<i>ptsH</i>	Phosphocarrier protein HPr	-1,02	-1,12	-1,17
SL2395	<i>ptsI</i>	Phosphoenolpyruvate-protein phosphotransferase	1,05	1,00	-1,26
SL2396	<i>crr</i>	Glucose-specific phosphotransferase enzyme IIA component	1,08	1,02	1,16
SL2397	-	Hypothetical	1,07	1,16	1,03
SL2398	<i>pdxK</i>	Pyridoxine kinase	-1,19	1,11	1,25
SL2399	<i>ptsJ</i>	Putative transcriptional regulatory protein ptsJ	-1,34	-1,19	-1,19
SL2400	<i>yfeJ</i>	Putative glutamine amidotransferase-like protein yfeJ	-1,12	-1,05	1,75
SL2401	<i>yfeK</i>	Uncharacterized protein yfeK	1,12	1,03	1,15
SL2402	<i>yfeL</i>	Uncharacterized protein yfeL	1,15	1,23	-1,19
SL2403	<i>cysM</i>	Cysteine synthase B	1,20	1,19	1,54
SL2404	<i>cysA</i>	Sulfate/thiosulfate import ATP-binding protein cysA	1,55	1,39	12,67
SL2405	<i>cysW</i>	Sulfate transport system permease protein cysW	1,09	-1,12	6,01
SL2406	<i>cysU</i>	Sulfate transport system permease protein cysT	1,34	1,03	8,74
SL2407	<i>cysP</i>	Thiosulfate-binding protein	-1,07	-1,31	13,02
SL2408	<i>ucpA</i>	Oxidoreductase ucpA	1,35	1,16	3,08
SL2409	<i>yfeX</i>	Uncharacterized protein yfeX	1,30	1,04	-1,32
SL2410	<i>yfeY</i>	Uncharacterized protein yfeY	-1,10	-1,32	-1,20
SL2411	<i>yfeZ</i>	Inner membrane protein yfeZ	-1,01	-1,14	-1,29
SL2412	<i>ypeA</i>	Acetyltransferase ypeA	-1,05	-1,07	-1,48
SL2413	<i>amiA</i>	Probable N-acetylmuramoyl-L-alanine amidase AmiA	-1,12	-1,14	-1,89
SL2414	<i>hemF</i>	Coproporphyrinogen-III oxidase, aerobic	-1,12	-1,12	-1,84
SL2415	<i>ypfK</i>	Uncharacterized protein ypfK	1,47	1,24	-1,32
SL2416	<i>ypfL</i>	Uncharacterized protein ypfL	-1,08	-1,21	-1,34

Tabla Suplementaria 1

Diferencia de expresión de todos los genes de SV5015 en las cepas mutantes *greA*, *greB* y *greAgreB*, respecto a la cepa WT

ID	gene	Description	<i>greA</i> vs WT	<i>greB</i> vs WT	<i>greAgreB</i> vs WT
SL2417	<i>eutR</i>	HTH-type transcriptional regulator eutR	-1,01	-1,07	-1,22
SL2418	<i>eutK</i>	Ethanolamine utilization protein eutK	1,05	1,14	-1,20
SL2419	<i>eutL</i>	Ethanolamine utilization protein eutL	-1,08	1,11	1,13
SL2420	<i>eutC</i>	Ethanolamine ammonia-lyase light chain	-1,02	1,12	1,12
SL2421	<i>eutB</i>	Ethanolamine ammonia-lyase heavy chain	-1,03	1,10	1,27
SL2422	<i>eutA</i>	Ethanolamine utilization protein eutA	-1,25	-1,01	-1,05
SL2423	<i>eutH</i>	Ethanolamine utilization protein eutH	-1,11	1,21	-1,02
SL2424	<i>eutG</i>	Ethanolamine utilization protein eutG	-1,06	1,01	-1,09
SL2425	<i>eutJ</i>	Ethanolamine utilization protein eutJ	-1,15	1,18	-1,42
SL2426	<i>eutE</i>	Ethanolamine utilization protein eutE	-1,16	-1,07	-1,29
SL2427	<i>eutN</i>	Ethanolamine utilization protein eutN	-1,45	-1,19	-1,11
SL2428	<i>eutM</i>	Ethanolamine utilization protein eutM	-1,23	1,04	-1,05
SL2429	<i>eutD</i>	Ethanolamine utilization protein eutD	-1,14	-1,21	-1,39
SL2430	<i>eutT</i>	Ethanolamine utilization cobalamin adenosyltransferase	-1,46	-1,07	1,09
SL2431	<i>eutQ</i>	Ethanolamine utilization protein eutQ	-1,24	1,18	1,59
SL2432	<i>eutP</i>	Ethanolamine utilization protein eutP	-1,30	1,35	2,01
SL2433	<i>eutS</i>	Ethanolamine utilization protein eutS	-1,02	1,75	1,70
SL2435	<i>maeB</i>	NADP-dependent malic enzyme	1,15	-1,08	5,97
SL2436	<i>tal2</i>	Transaldolase 2	-1,04	-1,00	1,53
SL2437	<i>tktB</i>	Transketolase 2	1,18	1,11	2,01
SL2438	-	Hypothetical	-1,08	-1,04	-2,50
SL2439	<i>ypfG</i>	Uncharacterized protein ypfG	1,12	1,41	-2,79
SL2440	<i>nudK</i>	GDP-mannose pyrophosphatase nudK	-1,07	-1,10	-1,43
SL2441	<i>yfeW</i>	UPF0214 protein yfeW	-1,11	1,12	-1,61
SL2442	<i>aegA</i>	Protein AegA	-1,03	-1,06	1,13
SL2443	<i>narQ</i>	Nitrate/nitrite sensor protein narQ	1,17	1,31	-1,27
SL2444	<i>acrD</i>	Probable aminoglycoside efflux pump	1,30	-1,02	-1,21
SL2445	<i>yffB</i>	Protein yffB	-1,03	-1,26	-1,06
SL2446	<i>dapE</i>	Succinyl-diaminopimelate desuccinylase	-1,18	-1,27	-1,18
SL2447	-	UPF0370 protein YpsIP31758_1253	1,06	-1,02	1,21
SL2448	<i>ypfI</i>	Uncharacterized protein ypfI	1,22	1,07	1,11
SL2449	<i>ypfJ</i>	Uncharacterized protein ypfJ	-1,07	1,24	1,29
SL2450	<i>purC</i>	Phosphoribosylaminoimidazole-succinocarboxamide synthase	-1,06	-1,03	-1,20
SL2451	<i>nlpB</i>	Lipoprotein 34	-1,02	-1,34	-1,89
SL2452	<i>dapA</i>	Dihydrodipicolinate synthase	1,02	-1,21	-1,83
SL2453	<i>gcvR</i>	Glycine cleavage system transcriptional repressor	-1,13	-1,19	-1,08
SL2454	<i>bcp</i>	Putative peroxiredoxin bcp	-1,02	-1,18	1,33
SL2455	<i>garK</i>	Glycerate Kinase	1,12	-1,18	1,33
SL2456	<i>perM</i>	Putative permease perM	1,02	-1,04	-1,67
SL2457	<i>yfgC</i>	TPR repeat-containing protein yfgC	-1,01	1,07	-1,12
SL2458	<i>yfgD</i>	Uncharacterized protein yfgD	1,09	-1,02	1,19
SL2459	<i>hda</i>	DnaA-homolog protein hda	-1,01	1,00	-2,04
SL2460	<i>uraA</i>	Uracil permease	-1,07	-1,05	1,59
SL2461	<i>upp</i>	Uracil phosphoribosyltransferase	-1,02	1,28	-1,14
SL2462	<i>purM</i>	Phosphoribosylformylglycinamide cyclo-ligase	-1,04	1,28	-2,28

Tabla Suplementaria 1

Diferencia de expresión de todos los genes de SV5015 en las cepas mutantes *greA*, *greB* y *greAgreB*, respecto a la cepa WT

ID	gene	Description	<i>greA</i> vs WT	<i>greB</i> vs WT	<i>greAgreB</i> vs WT
SL2463	<i>purN</i>	Phosphoribosylglycinamide formyltransferase	1,14	1,09	-2,33
SL2464	<i>ppk</i>	Polyphosphate kinase	1,07	-1,05	1,32
SL2465	<i>ppx</i>	Exopolyphosphatase	1,03	-1,25	1,09
SL2466	<i>yfgF</i>	Inner membrane protein yfgF	-1,12	-1,02	-1,90
SL2467	-	Hypothetical	-1,23	-1,01	-3,33
SL2468	<i>yfgG</i>	Uncharacterized protein yfgG	1,01	1,01	-3,19
SL2469	-	Hypothetical	1,52	1,35	-2,17
SL2470	<i>insF1</i>	Transposase insF for insertion sequence IS3A	1,48	1,33	-1,86
SL2471	<i>guaA</i>	GMP synthase [glutamine-hydrolyzing]	1,01	1,02	-2,32
SL2472	<i>guaB</i>	Inosine-5'-monophosphate dehydrogenase	-1,09	1,02	-3,20
SL2473	<i>xseA</i>	Exodeoxyribonuclease 7 large subunit	-1,13	-1,03	-2,01
SL2474	<i>yuaQ</i>	Uncharacterized protein yuaQ	1,03	-1,02	1,78
SL2475	-	Invasin	1,34	1,31	1,32
SL2476	-	Invasin	1,00	-1,17	1,12
SL2477	-	Invasin	1,38	1,28	1,42
SL2478	-	Outer Membrane Protein	1,21	1,13	2,39
SL2479	<i>eae</i>	Intimin	1,06	1,22	-1,18
SL2480	<i>yfgJ</i>	Uncharacterized protein yfgJ	1,06	-1,08	-1,51
SL2481	<i>engA</i>	GTP-binding protein engA	1,09	1,02	-1,82
SL2482	<i>yfgL</i>	Lipoprotein yfgL	1,05	-1,15	-1,46
SL2483	<i>yfgM</i>	UPF0070 protein yfgM	1,06	-1,12	-1,65
SL2484	<i>hisS</i>	Histidyl-tRNA synthetase	-1,02	-1,10	-2,15
SL2485	<i>ispG</i>	4-hydroxy-3-methylbut-2-en-1-yl diphosphate synt	1,07	1,14	-1,05
SL2486	<i>rodZ</i>	Cytoskeleton protein rodZ	1,12	1,21	-1,60
SL2487	<i>rlmN</i>	Ribosomal RNA large subunit methyltransferase †	1,09	1,11	-1,53
SL2488	<i>ndk</i>	Nucleoside diphosphate kinase	1,18	1,01	6,14
SL2489	<i>ysaA</i>	Polyferredoxin	1,30	-1,29	-1,82
SL2490	<i>dmsC</i>	Anaerobic Dimethyl Sulfoxide Reductase Subunit	1,18	-1,42	1,02
SL2491	<i>dmsB</i>	Anaerobic dimethyl sulfoxide reductase chain B	1,14	1,30	1,48
SL2492	<i>dmsA</i>	Anaerobic dimethyl sulfoxide reductase chain A	1,29	1,11	1,33
SL2493	<i>pbpC</i>	Penicillin-binding protein 1C	-1,09	1,10	1,13
SL2494	<i>yfhM</i>	Uncharacterized lipoprotein yfhM	1,14	1,00	1,77
SL2495	<i>sseA</i>	3-mercaptopyruvate sulfurtransferase	1,08	1,25	2,90
SL2496	-	Hypothetical	-1,04	-1,03	1,87
SL2497	<i>sseB</i>	Protein sseB	1,00	-1,32	-1,12
SL2498	<i>pepB</i>	Peptidase B	1,08	-1,14	1,28
SL2499	<i>iscX</i>	Protein iscX	-1,02	-1,11	-1,11
SL2500	<i>fdx</i>	2Fe-2S ferredoxin	1,12	-1,04	-1,13
SL2501	<i>hscA</i>	Chaperone protein hscA	1,15	1,18	-1,76
SL2502	<i>hscB</i>	Co-chaperone protein hscB	1,01	1,05	-2,38
SL2503	<i>iscA</i>	Iron-binding protein iscA	1,00	1,12	-1,55
SL2504	<i>nifU</i>	NifU-like protein	-1,07	1,07	-1,53
SL2505	<i>iscS</i>	Cysteine desulfurase	-1,17	1,13	-1,99
SL2506	<i>iscR</i>	HTH-type transcriptional regulator iscR	-1,38	1,03	-3,23
SL2507	<i>trmJ</i>	tRNA (cytidine/uridine-2'-O-)-methyltransferase trr	1,39	1,02	-2,12
SL2508	<i>suhB</i>	Inositol-1-monophosphatase	-1,05	1,18	-1,86
SL2509	<i>yfhR</i>	Uncharacterized protein yfhR	1,05	1,19	-1,37
SL2510	<i>asrA</i>	Anaerobic sulfite reductase subunit A	1,36	1,67	-3,47

Tabla Suplementaria 1

Diferencia de expresión de todos los genes de SV5015 en las cepas mutantes *greA*, *greB* y *greAgreB*, respecto a la cepa WT

ID	gene	Description	<i>greA</i> vs WT	<i>greB</i> vs WT	<i>greAgreB</i> vs WT
SL2511	<i>asrB</i>	Anaerobic sulfite reductase subunit B	1,26	1,34	-3,42
SL2512	<i>asrC</i>	Anaerobic sulfite reductase subunit C	1,33	1,46	-2,90
SL2513	-	Putative nickel/cobalt efflux system HI_1248	1,07	-1,02	-1,36
SL2514	-	Uncharacterized protein HI_1249	1,01	-1,02	-1,22
SL2515	<i>csiE</i>	Stationary phase-inducible protein csiE	1,24	1,36	6,85
SL2516	<i>hcaT</i>	Probable 3-phenylpropionic acid transporter	1,01	1,14	-1,46
SL2517	<i>glyA1</i>	Serine hydroxymethyltransferase 1	1,10	-1,19	1,72
SL2518	<i>hmp</i>	Flavoheмоprotein	-1,07	1,11	5,21
SL2519	<i>cadC</i>	Transcriptional activator cadC	1,07	-1,02	-2,31
SL2520	<i>cadB</i>	Probable cadaverine/lysine antiporter	-1,10	-1,36	-1,44
SL2521	<i>cadA</i>	Lysine decarboxylase, inducible	1,46	-1,13	-4,98
SL2522	<i>yjdL</i>	Probable dipeptide and tripeptide permease YjdL	1,00	1,05	-6,76
SL2523	<i>glnB</i>	Nitrogen regulatory protein P-II 1	1,14	-1,08	-1,03
SL2524	<i>yfhA</i>	Uncharacterized protein yfhA	1,00	-1,15	-1,19
SL2525	<i>yfhG</i>	Uncharacterized protein yfhG	1,00	-1,04	-1,30
SL2526	<i>yfhK</i>	Putative sensor-like histidine kinase yfhK	1,10	1,02	-1,39
SL2527	<i>purL</i>	Phosphoribosylformylglycinamide synthase	1,27	1,43	2,08
SL2528	-	Periplasmic Protein	-1,24	1,06	-1,15
SL2529	<i>mltF</i>	Membrane-bound lytic murein transglycosylase F	1,08	1,17	-1,33
SL2530	<i>tadA</i>	tRNA-specific adenosine deaminase	1,24	1,16	-1,08
SL2531	<i>yfhB</i>	Uncharacterized protein yfhB	1,20	1,15	1,55
SL2532	<i>ybbF</i>	Putative PTS system EIIBC component ybbF	1,22	1,04	3,24
SL2533	<i>murQ</i>	N-acetylmuramic acid 6-phosphate etherase	1,17	1,02	3,66
SL2534	<i>yfhH</i>	Uncharacterized HTH-type transcriptional regulator yfhH	1,05	1,24	1,49
SL2535	<i>panE</i>	Putative 2-dehydropantoate 2-reductase	-1,09	1,19	1,16
SL2536	<i>yhjX</i>	Inner membrane protein yhjX	1,39	1,15	-1,02
SL2537	<i>cynR</i>	HTH-type transcriptional regulator cynR	-1,02	1,05	3,05
SL2538	<i>yfhL</i>	Uncharacterized ferredoxin-like protein yfhL	-1,32	1,11	-2,31
SL2539	<i>acpS</i>	Holo-[acyl-carrier-protein] synthase	1,26	1,14	1,68
SL2540	<i>pdxJ</i>	Pyridoxine 5'-phosphate synthase	1,18	1,08	1,68
SL2541	<i>recO</i>	DNA repair protein recO	1,01	-1,16	-1,97
SL2542	<i>era</i>	GTP-binding protein era homolog	-1,00	-1,09	-2,18
SL2543	<i>rnc</i>	Ribonuclease 3	-1,05	1,00	-2,47
SL2544	<i>lepB</i>	Signal peptidase I	1,00	-1,08	-1,23
SL2545	<i>lepA</i>	GTP-binding protein lepA	-1,01	-1,07	-1,93
SL2546	-	Hypothetical	-1,55	-1,09	-2,58
SL2547	-	Gifsy-1 Prophage Protein	-1,66	1,41	-1,59
SL2548	-	Hypothetical Protein SL2548	-1,50	-1,10	-3,48
SL2549	-	PagK-Like Protein	-2,08	1,46	-4,10
SL2550	<i>ycdD</i>	Tail fiber assembly protein homolog from lambdoid prophage Fels-1	-2,76	-1,35	-4,98
SL2551	-	Appr-1-P Processing Domain-Containing Protein	-2,46	-1,34	-4,76
SL2552	<i>stfQ</i>	Side tail fiber protein homolog from lambdoid prophage Qin	-1,74	-1,12	-3,35

Tabla Suplementaria 1

Diferencia de expresión de todos los genes de SV5015 en las cepas mutantes *greA*, *greB* y *greAgreB*, respecto a la cepa WT

ID	gene	Description	<i>greA</i> vs WT	<i>greB</i> vs WT	<i>greAgreB</i> vs WT
SL2553	-	Hocificity Protein J	-2,46	-1,12	-11,08
SL2554	-	Phage Tail Assembly Protein	-1,31	-1,13	-2,08
SL2555	-	NLP/P60 Protein	-1,80	-1,35	-3,95
SL2556	-	Phage Minor Tail Protein L	-1,54	-1,16	-2,63
SL2557	-	Minor Tail Protein	-1,77	-1,25	-2,28
SL2558	-	Hypothetical	-1,46	-1,20	-2,18
SL2559	-	Minor Tail Protein	-1,81	-1,02	-4,83
SL2560	-	Minor Tail Component Of Putative Prophage	-2,14	-1,10	-5,25
SL2561	-	Tail Protein V	-1,60	1,04	-2,80
SL2562	-	Minor Tail Protein U	-1,71	-1,09	-2,81
SL2563	<i>ydcM</i>	Putative transposase in <i>snaA-snaB</i> intergenic region	-1,48	1,01	-2,39
SL2564	-	Phage Tail Component	-1,67	-1,02	-3,00
SL2565	-	Tail Attachment Protein	-2,08	-1,12	-2,67
SL2566	-	DNA Packaging-Like Protein	-1,95	-1,02	-3,76
SL2567	-	P21 prophage-derived major head protein	-1,99	-1,10	-4,91
SL2568	-	Head Decoration Protein	-1,94	-1,06	-4,48
SL2569	<i>sppA</i>	Putative signal peptide peptidase <i>sppA</i>	-2,37	-1,11	-10,71
SL2570	-	Lambda Family Phage Portal Protein	-2,15	-1,13	-6,06
SL2571	-	Lambda prophage-derived head-to-tail joining protein W	-2,13	-1,13	-2,93
SL2572	<i>tfaD</i>	Putative tail fiber assembly protein homolog from lambdoid prophage DLP12	-2,40	-1,07	-4,71
SL2573	<i>nohA</i>	P21 prophage-derived terminase small subunit	-2,45	-1,05	-8,60
SL2574	<i>ycgK</i>	Uncharacterized protein <i>ycgK</i>	-1,07	1,23	1,70
SL2575	<i>rzpD</i>	Putative Rz endopeptidase from lambdoid prophage DLP12	-2,15	-1,02	-5,68
SL2576	<i>arrD</i>	Probable lysozyme from lambdoid prophage DLP12	-1,78	-1,03	-3,56
SL2577	-	Hypothetical	-1,85	-1,13	-2,26
SL2578	-	Hypothetical	1,66	1,60	2,10
SL2579	-	Phage Antitermination Protein Q	-1,28	1,02	-1,85
SL2580	<i>ylcG</i>	Hypothetical	-1,25	-1,06	-1,88
SL2581	-	Hypothetical	-1,49	1,00	-1,50
SL2582	-	Hypothetical	1,21	1,00	-1,38
SL2583	-	Hypothetical	1,01	1,10	2,16
SL2585	-	Hypothetical Protein SL2585	-1,24	-1,09	-1,29
SL2586	-	Hypothetical	-1,29	-1,18	-1,44
SL2587	-	Hypothetical	-1,37	-1,15	-1,11
SL2588	-	Methyltransferase	-1,46	-1,40	-1,13
SL2589	-	Hypothetical	-1,41	-1,37	-1,10
SL2590	-	Hypothetical	-1,40	-1,20	-1,41
SL2591	<i>yfdO</i>	Uncharacterized protein <i>yfdO</i>	-1,65	-1,21	-1,87
SL2592	-	Gifsy-1 Prophage CI Protein	-1,28	1,28	-2,12
SL2593	-	Hypothetical	1,06	-1,17	-1,45
SL2594	-	ATPase Domain-Containing Protein	-1,18	-1,08	-1,26
SL2595	-	Hypothetical	-1,09	1,33	-1,90
SL2596	-	Hypothetical	-1,72	-1,01	-2,41
SL2597	<i>recE</i>	Exodeoxyribonuclease 8	-1,33	1,01	-2,59

Tabla Suplementaria 1

Diferencia de expresión de todos los genes de SV5015 en las cepas mutantes *greA*, *greB* y *greAgreB*, respecto a la cepa WT

ID	gene	Description	<i>greA</i> vs WT	<i>greB</i> vs WT	<i>greAgreB</i> vs WT
SL2598	-	Hypothetical	-1,10	1,08	1,03
SL2599	-	Excisionase-Like Protein	-1,10	1,07	-1,22
SL2600	<i>intB</i>	Putative prophage P4 integrase	1,38	-1,17	1,90
SL2601	<i>rseC</i>	Sigma-E factor regulatory protein rseC	-1,20	-1,22	-1,48
SL2602	<i>rseB</i>	Sigma-E factor regulatory protein rseB	-1,23	-1,41	-2,07
SL2603	<i>rseA</i>	Sigma-E factor negative regulatory protein	-1,13	-1,10	-1,64
SL2604	<i>rpoE</i>	RNA polymerase sigma-E factor	-1,10	-1,09	-2,10
SL2605	<i>nadB</i>	L-aspartate oxidase	1,16	-1,03	-1,25
SL2606	<i>yfiC</i>	tRNA (adenine-N(6)-)-methyltransferase	1,02	-1,03	-1,28
SL2607	<i>srmB</i>	ATP-dependent RNA helicase srmB	1,17	1,17	1,31
SL2608	<i>yfiE</i>	Uncharacterized HTH-type transcriptional regulator yfiE	1,09	1,00	-1,59
SL2609	<i>eamB</i>	Cysteine/O-acetylserine efflux protein	1,53	1,05	-7,15
SL2610	<i>grcA</i>	Autonomous glycyl radical cofactor	1,06	1,11	-2,16
SL2611	<i>ung</i>	Uracil-DNA glycosylase	1,02	-1,17	-1,32
SL2612	<i>yfiF</i>	Uncharacterized tRNA/rRNA methyltransferase yfiF	1,19	1,12	-1,33
SL2613	<i>trxC</i>	Thioredoxin-2	-1,10	1,03	-2,37
SL2614	<i>yfiP</i>	DTW domain-containing protein yfiP	1,07	1,06	-1,87
SL2615	<i>yfiQ</i>	Uncharacterized protein yfiQ	1,10	1,07	1,60
SL2616	<i>pssA</i>	CDP-diacylglycerol--serine O-phosphatidyltransferase	-1,08	-1,17	-1,34
SL2617	<i>yfiM</i>	Uncharacterized protein yfiM	1,04	-1,02	-1,15
SL2618	<i>kgfP</i>	Alpha-ketoglutarate permease	1,23	1,05	2,63
SL2619	-	Hypothetical	-1,21	-1,07	1,51
SL2620	<i>clpB</i>	Chaperone protein clpB	1,03	1,15	2,60
SL2621	<i>yfiH</i>	UPF0124 protein yfiH	1,06	1,28	-1,05
SL2622	<i>rluD</i>	Ribosomal large subunit pseudouridine synthase D	-1,02	-1,09	-2,26
SL2623	<i>yfiO</i>	UPF0169 lipoprotein yfiO	-1,30	-1,33	-2,41
SL2624	<i>raiA</i>	Ribosome-associated inhibitor A	1,15	1,42	2,90
SL2625	<i>pheA</i>	P-protein	1,11	-1,21	2,88
SL2626	<i>yvrE</i>	Uncharacterized protein yvrE	-1,07	-1,20	1,03
SL2627	<i>tyrA</i>	T-protein	1,04	-1,10	-1,01
SL2628	<i>aroF</i>	Phospho-2-dehydro-3-deoxyheptonate aldolase, Tyr-sensitive	-1,06	1,13	-1,14
SL2629	<i>yfiR</i>	Uncharacterized protein yfiR	1,09	1,07	-1,77
SL2630	<i>yfiN</i>	Probable diguanylate cyclase YfiN	-1,01	1,18	-2,63
SL2631	<i>xerD</i>	Integrase	-1,25	-1,33	1,42
SL2632	<i>yebY</i>	Hypothetical Protein yebY	-1,17	-1,23	1,54
SL2633	-	Putative uncharacterized protein ORFI in retron EC67	-1,23	-1,42	1,34
SL2634	-	Hypothetical	-1,23	-1,02	-1,05
SL2635	-	Putative uncharacterized protein ORFB in retron EC67	-1,04	1,39	1,34
SL2636	-	Hypothetical	-1,13	-1,22	-1,01
SL2637	-	Putative uncharacterized protein ORFC-like in prophage region	1,30	1,03	1,65
SL2638	-	Hypothetical	1,69	-1,36	1,46
SL2639	<i>traR</i>	Hypothetical	1,30	-1,28	1,23
SL2640	-	Hypothetical Protein SL2640	1,13	1,04	2,32

Tabla Suplementaria 1

Diferencia de expresión de todos los genes de SV5015 en las cepas mutantes *greA*, *greB* y *greAgreB*, respecto a la cepa WT

ID	gene	Description	<i>greA</i> vs WT	<i>greB</i> vs WT	<i>greAgreB</i> vs WT
SL2641	-	Probable replication endonuclease from prophage-like region 1	1,11	-1,02	1,25
SL2642	-	P2 GpU Family Protein	1,12	1,01	1,36
SL2643	<i>b2083</i>	Late Control D Family Protein	1,00	1,21	1,42
SL2644	-	Hypothetical Protein SL2644	-1,01	-1,02	1,42
SL2645	<i>ogrK</i>	Prophage P2 OGR protein	-1,06	-1,04	-1,04
SL2646	<i>rplS</i>	50S ribosomal protein L19	-1,07	-1,16	1,03
SL2647	<i>trmD</i>	tRNA (guanine-N(1)-)-methyltransferase	-1,02	-1,02	-1,06
SL2648	<i>rimM</i>	Ribosome maturation factor rimM	-1,12	-1,12	-1,13
SL2649	<i>rpsP</i>	30S ribosomal protein S16	-1,09	-1,12	-1,58
SL2650	<i>ffh</i>	Signal recognition particle protein	1,17	1,02	-1,78
SL2651	<i>ypjD</i>	Inner membrane protein ypjD	-1,17	1,04	-2,45
SL2652	<i>yfjD</i>	UPF0053 inner membrane protein yfjD	-1,25	-1,36	-2,50
SL2653	-	Hypothetical	1,10	1,06	-1,30
SL2654	<i>grpE</i>	Protein grpE	-1,10	-1,23	1,66
SL2655	<i>ppnK</i>	Probable inorganic polyphosphate/ATP-NAD kinase	1,05	-1,08	1,03
SL2656	<i>recN</i>	DNA repair protein recN	1,01	1,17	1,58
SL2657	<i>smpA</i>	Small protein A	-1,12	-1,01	-1,24
SL2658	<i>rnfH</i>	Protein rnfH	-1,03	-1,05	1,02
SL2659	<i>yfjG</i>	UPF0083 protein yfjG	1,01	1,01	-1,10
SL2660	<i>smpB</i>	SsrA-binding protein	1,03	-1,10	-1,04
SL2661	-	Hypothetical	1,09	1,29	1,11
SL2662	<i>bepC</i>	Outer membrane efflux protein BepC	1,15	1,22	1,07
SL2663	<i>apxIB</i>	Toxin RTX-I translocation ATP-binding protein	1,06	-1,10	-1,12
SL2664	<i>cyaD</i>	Protein cyaD	-1,03	-1,10	1,21
SL2665	<i>ogrK</i>	Prophage P2 OGR protein	1,40	1,13	-1,21
SL2666	<i>b2083</i>	Late Control D Family Protein	1,20	-1,03	1,28
SL2667	-	P2 GpU Family Protein	1,20	-1,18	1,51
SL2668	-	Hypothetical	-1,04	-1,38	1,28
SL2669	-	Hypothetical	-1,14	-1,17	1,39
SL2670	-	Phage Tail Protein	-1,20	-1,34	1,88
SL2671	-	Phage Tail Tube Protein	-1,05	-1,24	1,33
SL2672	-	Phage Tail Sheath Protein	-1,39	-1,04	-1,13
SL2673	<i>pinE</i>	DNA-invertase from lambdoid prophage e14	-1,32	1,11	-3,80
SL2674	<i>sopE</i>	Guanine nucleotide exchange factor sopE	-1,33	-1,03	-27,69
SL2675	<i>ycdD</i>	Tail fiber assembly protein homolog from lambdoid prophage Fels-1	-1,12	1,28	1,64
SL2676	-	Hypothetical	1,16	1,09	1,99
SL2677	-	Phage Tail Protein I	-1,40	-1,44	1,33
SL2678	-	Baseplate J Family Protein	-1,01	-1,03	1,50
SL2679	-	GPW/Gp25 Family Protein	1,15	-1,26	1,80
SL2680	-	Phage Baseplate Assembly Protein V	-1,25	-1,24	1,48
SL2681	-	Phage Virion Morphogenesis Protein	1,15	1,16	1,02
SL2682	-	P2 Phage Tail Completion R Family Protein	1,21	-1,31	1,92
SL2683	-	Fels-2 Prophage Protein	1,12	1,04	1,96
SL2684	-	Hypothetical	1,15	1,21	1,47
SL2685	-	Hypothetical	1,34	1,28	1,69

Tabla Suplementaria 1

Diferencia de expresión de todos los genes de SV5015 en las cepas mutantes *greA*, *greB* y *greAgreB*, respecto a la cepa WT

ID	gene	Description	<i>greA</i> vs WT	<i>greB</i> vs WT	<i>greAgreB</i> vs WT
SL2686	<i>arrD</i>	Probable lysozyme from lambdoid prophage DLP12	-1,11	-1,03	1,75
SL2687	-	Secretion Protein	-1,19	-1,21	1,09
SL2688	-	Tail X Family Protein	-1,12	-1,26	-1,05
SL2689	-	Head Completion Protein	1,01	-1,10	1,08
SL2690	-	Phage Small Terminase Subunit	-1,06	-1,42	1,35
SL2691	-	P2 Family Phage Capsid Protein	-1,15	1,15	1,62
SL2692	-	Phage Capsid Scaffolding Protein	-1,21	1,06	1,63
SL2693	-	Hypothetical	-1,24	-1,18	1,19
SL2694	-	Putative uncharacterized protein ORF5 in retron EC67	-1,11	-1,34	-1,11
SL2695	<i>smf</i>	Protein smf	-1,04	-1,23	2,11
SL2696	-	Hypothetical	-1,12	-1,39	3,87
SL2697	-	Hypothetical	-1,30	-1,61	-2,19
SL2698	-	Hypothetical	-1,37	-1,48	-1,52
SL2699	<i>dinI</i>	DinI-like protein in retron EC67	-1,23	-1,04	1,76
SL2700	-	Hypothetical	1,04	1,39	1,93
SL2701	-	Probable replication endonuclease from prophage-like region	-1,01	-1,19	1,23
SL2702	<i>dam</i>	Retron EC67 DNA adenine methylase	-1,58	-1,11	-1,61
SL2703	<i>ybil</i>	Hypothetical	-2,29	-1,54	-1,69
SL2704	-	Putative uncharacterized protein ORFC-like in prophage region	-3,07	-1,35	-3,46
SL2705	-	Hypothetical	-1,95	-1,09	-1,79
SL2706	-	Putative uncharacterized protein ORFB in retron EC67	-1,15	-1,01	-1,87
SL2707	-	Phage Regulatory Protein	-1,22	-1,17	1,14
SL2708	-	Putative uncharacterized protein ORFI in retron EC67	-1,16	-1,34	1,57
SL2709	<i>xerD</i>	Tyrosine recombinase xerD	-1,14	-1,37	2,01
SL2710	<i>yopC</i>	SPBc2 prophage-derived uncharacterized protein yopC	-1,34	-1,52	3,11
SL2711	-	Hypothetical Protein SL2711	1,04	1,01	1,07
SL2712	<i>intA</i>	Prophage CP4-57 integrase	-1,10	-1,19	2,48
SL2713	-	Hypothetical	-1,41	-2,00	1,55
SL2714	-	Hypothetical Protein SL2714	-1,15	-1,28	1,66
SL2715	-	Hypothetical Protein SL2715	1,01	-1,13	2,19
SL2716	-	Phage Polarity Suppression Protein	-1,15	-1,03	1,47
SL2717	<i>ogrK</i>	Prophage P2 OGR protein	-1,16	1,01	1,29
SL2718	-	Hypothetical	1,39	-1,04	1,93
SL2719	-	Hypothetical	1,01	-1,31	3,69
SL2720	-	Hypothetical	1,12	-1,38	3,04
SL2721	-	P4 prophage-derived uncharacterized protein t2655	1,33	-1,17	2,87
SL2722	<i>traC</i>	DNA primase traC	1,07	-1,27	4,29
SL2723	<i>intA</i>	Prophage CP4-57 integrase	1,26	1,78	6,56
SL2724	<i>intA</i>	Integrase	1,18	1,34	3,40
SL2725	-	Hypothetical Protein SL2725	-1,05	-1,06	1,65
SL2726	-	Hypothetical	-1,35	-1,30	-2,11
SL2727	-	Hypothetical	-1,12	-1,08	1,54
SL2728	-	Cytoplasmic Protein	1,30	1,54	1,38
SL2729	-	Hypothetical	-1,20	-1,31	1,40

Tabla Suplementaria 1

Diferencia de expresión de todos los genes de SV5015 en las cepas mutantes *greA*, *greB* y *greAgreB*, respecto a la cepa WT

ID	gene	Description	<i>greA</i> vs WT	<i>greB</i> vs WT	<i>greAgreB</i> vs WT
SL2730	-	ATPase	-1,12	-1,32	-1,06
SL2731	-	Hypothetical	-1,17	-1,77	-1,37
SL2732	-	Transcriptional Regulator XRE Family	-1,13	1,15	1,05
SL2733	<i>sfsB</i>	Sugar fermentation stimulation protein B	-1,18	-1,03	-1,30
SL2734	<i>srlA</i>	Glucitol/sorbitol permease IIC component	-1,20	1,26	-1,03
SL2735	<i>srlB</i>	Glucitol/sorbitol-specific phosphotransferase enzyme IIA component	-1,20	1,36	1,28
SL2736	<i>srlE</i>	Glucitol/sorbitol-specific phosphotransferase enzyme IIB component	-1,21	1,05	-1,38
SL2737	<i>yrbE</i>	Uncharacterized oxidoreductase yrbE	-1,04	1,11	-1,22
SL2738	-	Hypothetical	1,02	-1,52	-1,08
SL2739	<i>hxlA</i>	3-hexulose-6-phosphate synthase	1,52	2,29	1,14
SL2740	<i>hxlB</i>	3-hexulose-6-phosphate isomerase	1,22	-1,18	2,93
SL2741	-	Glucose-6-Phosphate Isomerase	1,26	1,00	2,42
SL2742	<i>ptsG</i>	PTS system glucose-specific EIICBA component	-1,15	1,29	1,46
SL2743	<i>sgrR</i>	HTH-type transcriptional regulator sgrR	1,10	1,41	3,19
SL2744	-	Hypothetical	1,10	-1,12	1,13
SL2745	-	Hypothetical	1,08	1,11	1,30
SL2746	-	Hypothetical	1,16	1,38	1,44
SL2747	<i>intA</i>	Prophage CP4-57 integrase	-1,07	1,00	2,76
SL2748	-	Hypothetical Protein SL2748	1,00	1,12	1,42
SL2749	-	Hypothetical Protein SL2749	1,03	1,23	1,10
SL2750	<i>lcrS</i>	Low calcium response locus protein S	-1,00	1,09	1,46
SL2751	-	Hypothetical	-1,28	-1,51	1,36
SL2752	-	Hypothetical	-1,22	-1,83	1,68
SL2753	<i>insE1</i>	Transposase insE for insertion sequence IS3A	-1,34	-1,04	1,46
SL2754	<i>insF1</i>	Transposase insF for insertion sequence IS3A	-1,11	-1,24	-1,12
SL2755	<i>fljA</i>	Repressor of phase 1 flagellin gene	-12,65	-4,66	-15,85
SL2756	<i>fljB</i>	Phase 2 flagellin	-2,40	-1,63	-1,84
SL2757	NA	NA	-1,36	-1,03	-1,06
SL2758	-	Hypothetical	-1,39	1,54	-5,31
SL2759	<i>ygaD</i>	Putative multidrug export ATP-binding/permease protein ygaD	1,36	1,74	-2,78
SL2760	<i>fes</i>	Enterochelin esterase	1,04	-1,11	-2,90
SL2761	<i>besA</i>	Ferri-bacillibactin esterase BesA	1,04	-1,33	-1,58
SL2762	<i>pfeA</i>	Ferric enterobactin receptor	1,09	1,02	-1,57
SL2763	<i>pipB2</i>	Secreted effector protein pipB2	-1,78	1,18	-1,57
SL2764	<i>ybjX</i>	Uncharacterized protein ybjX	-1,45	1,10	-4,33
SL2765	-	Hypothetical	-1,67	-1,35	-3,63
SL2766	-	Hypothetical	-1,47	1,04	-2,82
SL2767	<i>hoxN</i>	High-affinity nickel transport protein	1,02	1,31	-1,93
SL2768	<i>qseC</i>	Sensor protein qseC	-1,13	-1,40	7,27
SL2769	<i>tctD</i>	Transcriptional regulatory protein tctD	1,03	1,08	13,84
SL2770	<i>yfIP</i>	UPF0065 protein yfIP	-1,24	-1,43	3,01
SL2771	-	Hypothetical	-1,06	-1,07	4,00
SL2772	-	Uncharacterized 52.8 kDa protein in TAR-I ttuC' 3'region	-1,08	-1,11	1,94

Tabla Suplementaria 1

Diferencia de expresión de todos los genes de SV5015 en las cepas mutantes *greA*, *greB* y *greAgreB*, respecto a la cepa WT

ID	gene	Description	<i>greA</i> vs WT	<i>greB</i> vs WT	<i>greAgreB</i> vs WT
SL2773	<i>csiD</i>	Protein csiD	-1,27	-1,17	11,87
SL2774	<i>ygaF</i>	Uncharacterized protein ygaF	-1,30	-1,54	9,95
SL2775	<i>gabD</i>	Succinate-semialdehyde dehydrogenase [NADP+]	-1,31	-1,53	12,61
SL2776	<i>gabT</i>	4-aminobutyrate aminotransferase	-1,37	-1,66	7,78
SL2777	<i>gabP</i>	GABA permease	-1,46	-1,56	6,21
SL2778	<i>ygaE</i>	Uncharacterized HTH-type transcriptional regulator ygaE	-1,10	-1,43	1,31
SL2779	<i>ygaU</i>	Uncharacterized protein ygaU	1,15	1,30	-1,15
SL2780	<i>yqaE</i>	UPF0057 membrane protein yqaE	1,08	1,20	1,76
SL2781	<i>ygaV</i>	Probable HTH-type transcriptional regulator ygaV	1,07	-1,13	-1,45
SL2782	<i>ygaP</i>	Inner membrane protein ygaP	1,00	1,15	-1,09
SL2783	<i>stpA</i>	DNA-binding protein stpA	-1,14	-1,00	-10,03
SL2784	<i>ygaW</i>	Uncharacterized protein ygaW	1,29	1,21	-3,82
SL2785	<i>ygaC</i>	Uncharacterized protein ygaC	-1,02	1,22	-2,25
SL2786	<i>ygaM</i>	Uncharacterized protein ygaM	1,24	1,24	1,23
SL2787	<i>mocR</i>	Probable rhizopine catabolism regulatory protein mocR	1,16	1,01	2,22
SL2788	<i>ydfG</i>	Uncharacterized protein ydfG	-1,03	-1,05	1,63
SL2789	-	Hypothetical	-1,05	-1,08	1,22
SL2790	<i>nrdH</i>	Glutaredoxin-like protein nrdH	1,05	1,10	1,70
SL2791	<i>nrdI</i>	Protein nrdI	1,01	1,49	1,53
SL2792	<i>nrdE</i>	Ribonucleoside-diphosphate reductase 2 subunit alpha	1,18	1,02	1,34
SL2793	<i>nrdF</i>	Ribonucleoside-diphosphate reductase 2 subunit beta	1,20	1,11	-1,08
SL2794	<i>proV</i>	Glycine betaine/L-proline transport ATP-binding protein proV	-1,29	-1,26	-1,46
SL2795	<i>proW</i>	Glycine betaine/L-proline transport system permease protein proW	-1,40	-1,38	1,20
SL2796	<i>proX</i>	Glycine betaine-binding periplasmic protein	-1,35	-1,23	1,67
SL2797	<i>ygaY</i>	Uncharacterized transporter ygaY	1,08	-1,03	-1,64
SL2798	<i>mprA</i>	Transcriptional repressor mprA	1,24	-1,17	-1,41
SL2799	<i>emrA</i>	Multidrug resistance protein A	1,29	-1,18	-1,51
SL2800	<i>emrB</i>	Multidrug resistance protein B	1,31	-1,42	-1,73
SL2801	-	Glycoporin	1,06	-1,06	1,97
SL2802	<i>luxS</i>	S-ribosylhomocysteine lyase	1,32	1,26	1,48
SL2803	<i>gshA</i>	Glutamate--cysteine ligase	1,06	-1,17	-1,18
SL2804	<i>yqaA</i>	Inner membrane protein yqaA	1,17	-1,22	-1,45
SL2805	<i>yqaB</i>	Phosphatase yqaB	1,08	-1,09	-1,39
SL2806	<i>csrA</i>	Carbon storage regulator homolog	1,06	-1,05	1,64
SL2807	<i>alaS</i>	Alanyl-tRNA synthetase	1,02	-1,30	1,48
SL2808	<i>recX</i>	Regulatory protein recX	1,21	1,00	-1,07
SL2809	<i>recA</i>	Protein recA	1,01	-1,13	1,52
SL2810	<i>ygaD</i>	Protein ygaD	1,04	-1,10	1,12
SL2811	<i>mltB</i>	Membrane-bound lytic murein transglycosylase B	-1,06	1,06	-1,34
SL2812	<i>srlA</i>	Glucitol/sorbitol permease IIC component	1,04	-1,17	-1,24
SL2813	<i>srlE</i>	Glucitol/sorbitol-specific phosphotransferase enzyme IIB component	1,16	-1,09	-1,59

Tabla Suplementaria 1

Diferencia de expresión de todos los genes de SV5015 en las cepas mutantes *greA*, *greB* y *greAgreB*, respecto a la cepa WT

ID	gene	Description	<i>greA</i> vs WT	<i>greB</i> vs WT	<i>greAgreB</i> vs WT
SL2814	<i>srlB</i>	Glucitol/sorbitol-specific phosphotransferase enzyme IIA component	1,10	-1,54	-2,28
SL2815	<i>srlD</i>	Sorbitol-6-phosphate 2-dehydrogenase	1,14	-1,24	-2,47
SL2816	<i>gutM</i>	Glucitol operon activator protein	-1,01	-1,27	-2,46
SL2817	<i>srlR</i>	Glucitol operon repressor	1,03	-1,08	-1,09
SL2818	<i>gutQ</i>	Protein gutQ	1,05	1,00	1,43
SL2819	<i>norR</i>	Anaerobic nitric oxide reductase transcription regulator norR	1,09	-1,01	1,54
SL2820	<i>norV</i>	Anaerobic nitric oxide reductase flavorubredoxin	-1,13	-1,12	-1,20
SL2821	<i>norW</i>	Nitric oxide reductase FIRd-NAD(+) reductase	-1,02	-1,22	1,44
SL2822	<i>hypF</i>	Carbamoyltransferase hypF	1,07	-1,10	-1,24
SL2823	<i>hydN</i>	Electron transport protein hydN	1,30	1,10	-7,66
SL2824	-	Conserved Hypothetical Protein	1,03	-1,10	1,96
SL2825	<i>hycl</i>	Hydrogenase 3 maturation protease	1,09	1,09	2,56
SL2826	<i>hycH</i>	Formate hydrogenlyase maturation protein hycH	1,04	1,06	2,01
SL2827	<i>hycG</i>	Formate hydrogenlyase subunit 7	-1,01	-1,12	1,94
SL2828	<i>hycF</i>	Formate hydrogenlyase subunit 6	1,02	-1,87	1,32
SL2829	<i>hycE</i>	Formate hydrogenlyase subunit 5	1,21	-1,35	-1,05
SL2830	<i>hycD</i>	Formate hydrogenlyase subunit 4	1,03	-1,07	-1,88
SL2831	<i>hycC</i>	Formate hydrogenlyase subunit 3	1,05	-1,28	-3,72
SL2832	<i>hycB</i>	Formate hydrogenlyase subunit 2	-1,10	1,04	-4,92
SL2833	<i>hycA</i>	Formate hydrogenlyase regulatory protein hycA	1,02	-1,01	-7,96
SL2834	<i>hypA</i>	Protein hypA	1,20	1,19	-1,62
SL2835	<i>hypB</i>	Hydrogenase isoenzymes nickel incorporation protein hypB	1,30	1,11	-1,01
SL2836	<i>hypC</i>	Hydrogenase isoenzymes formation protein hypC	1,26	1,15	-1,09
SL2837	<i>hypD</i>	Hydrogenase isoenzymes formation protein hypD	1,16	-1,05	-1,60
SL2838	<i>hypE</i>	Hydrogenase isoenzymes formation protein hypE	1,17	-1,26	-2,56
SL2839	<i>fhIA</i>	Formate hydrogenlyase transcriptional activator	1,22	-1,02	-2,24
SL2840	<i>ygbA</i>	Uncharacterized protein ygbA	-1,15	-1,20	1,17
SL2841	<i>znuA</i>	Uncharacterized periplasmic iron-binding protein HI_0362	-1,06	1,64	-1,87
SL2842	<i>sitB</i>	Chelated iron transport system membrane protein yfeB	-1,24	1,40	-1,80
SL2843	<i>sitC</i>	Chelated iron transport system membrane protein yfeC	-1,07	1,45	-1,60
SL2844	<i>sitD</i>	Probable iron transport system membrane protein HI_0359	-1,18	-1,12	-3,87
SL2845	<i>yopJ</i>	Effector protein yopJ	-1,36	-1,29	-5,48
SL2846	-	Hypothetical	-1,39	-1,66	-14,85
SL2847	<i>sirC</i>	Transcriptional regulator sirC	-1,41	-1,61	-10,80
SL2848	-	Hypothetical	-1,56	-1,22	-20,93
SL2849	<i>orgB</i>	Oxygen-regulated invasion protein orgB	-1,44	-1,20	-9,10
SL2850	<i>orgA</i>	Oxygen-regulated invasion protein orgA	-1,49	-1,26	-21,71
SL2851	<i>prgK</i>	Lipoprotein prgK	-1,30	-1,14	-8,73
SL2852	<i>prgJ</i>	Protein prgJ	-1,22	-1,08	-8,23

Tabla Suplementaria 1

Diferencia de expresión de todos los genes de SV5015 en las cepas mutantes *greA*, *greB* y *greAgreB*, respecto a la cepa WT

ID	gene	Description	<i>greA</i> vs WT	<i>greB</i> vs WT	<i>greAgreB</i> vs WT
SL2853	<i>prgI</i>	Protein prgI	-1,13	-1,02	-4,71
SL2854	<i>prgH</i>	Protein prgH	-1,36	1,09	-18,46
SL2855	<i>hilD</i>	Transcriptional regulator hilD	-1,39	-1,07	-5,63
SL2856	<i>hilA</i>	Transcriptional regulator hilA	-1,26	-1,38	-10,34
SL2857	<i>iagB</i>	Invasion protein iagB	-1,27	-1,07	-7,09
SL2858	<i>sptP</i>	Secreted effector protein sptP	-1,24	-1,03	-5,53
SL2859	<i>sicP</i>	Chaperone protein sicP	-1,35	-1,14	-8,37
SL2860	<i>iacP</i>	Probable acyl carrier protein iacP	-1,30	-1,10	-21,34
SL2861	<i>sipA</i>	Cell invasion protein sipA	-1,25	-1,06	-15,35
SL2862	<i>sipD</i>	Cell invasion protein sipD	-1,13	1,02	-18,49
SL2863	<i>sipC</i>	Cell invasion protein sipC	-1,10	1,01	-6,21
SL2864	<i>sipB</i>	Cell invasion protein sipB	-1,11	1,03	-7,20
SL2865	<i>sicA</i>	Chaperone protein sicA	-1,10	1,09	-8,04
SL2866	<i>spaS</i>	Surface presentation of antigens protein spaS	-1,42	-1,39	-21,68
SL2867	<i>spaR</i>	Surface presentation of antigens protein spaR	-1,55	-1,58	-22,12
SL2868	<i>spaQ</i>	Surface presentation of antigens protein SpaQ	-1,54	-1,38	-32,11
SL2869	<i>spaP</i>	Surface presentation of antigens protein spaP	-1,68	-1,43	-29,30
SL2870	<i>spaO</i>	Surface presentation of antigens protein SpaO	-1,28	-1,25	-14,14
SL2871	<i>spaN</i>	Surface presentation of antigens protein spaN	-1,17	-1,10	-9,31
SL2872	<i>spaM</i>	Surface presentation of antigens protein spaM	-1,29	-1,40	-10,63
SL2873	<i>spaL</i>	Probable ATP synthase spaL	-1,29	-1,41	-10,53
SL2874	<i>spaK</i>	Surface presentation of antigens protein spaK	-1,15	-1,03	-6,61
SL2875	<i>invA</i>	Invasion protein invA	-1,27	-1,01	-12,89
SL2876	<i>invE</i>	Invasion protein invE	-1,30	-1,14	-20,75
SL2877	<i>invG</i>	Protein invG	-1,17	-1,02	-8,31
SL2878	<i>invF</i>	Invasion protein invF	-1,17	1,06	-8,31
SL2879	<i>invH</i>	Invasion lipoprotein invH	-1,50	-1,13	-10,98
SL2880	-	Hypothetical	-1,50	1,10	-2,45
SL2881	-	Hypothetical	-1,52	-1,00	-3,47
SL2882	-	Cytoplasmic Protein	1,09	1,39	-1,04
SL2883	-	Hypothetical Protein SL2883	-1,10	1,10	-1,04
SL2884	-	Hypothetical	1,38	1,30	6,08
SL2885	-	GCN5-Related N-Acetyltransferase	1,09	1,04	5,08
SL2886	<i>pphB</i>	Serine/threonine-protein phosphatase 2	1,22	-1,08	-1,32
SL2887	-	Phage Integrase Family Protein	1,28	1,05	-1,09
SL2888	<i>mutS</i>	DNA mismatch repair protein mutS	1,14	-1,09	1,95
SL2889	-	Hypothetical	1,24	-1,08	1,32
SL2890	<i>yhcA</i>	Uncharacterized MFS-type transporter yhcA	1,02	-1,38	1,39
SL2891	<i>ptxR</i>	HTH-type transcriptional regulator ptxR	1,24	1,21	1,34
SL2892	<i>ygbN</i>	Uncharacterized permease HI_1015	1,20	-1,09	3,82
SL2893	<i>rffG</i>	Uncharacterized protein HI_1014	1,10	1,17	4,43
SL2894	<i>ygbM</i>	Protein ygbM	-1,09	-1,22	4,27
SL2895	<i>ygbL</i>	Putative aldolase class 2 protein ygbL	1,05	1,07	5,99
SL2896	<i>ygbK</i>	Uncharacterized protein ygbK	-1,09	1,24	7,13

Tabla Suplementaria 1

Diferencia de expresión de todos los genes de SV5015 en las cepas mutantes *greA*, *greB* y *greAgreB*, respecto a la cepa WT

ID	gene	Description	<i>greA</i> vs WT	<i>greB</i> vs WT	<i>greAgreB</i> vs WT
SL2897	<i>ygbJ</i>	Uncharacterized oxidoreductase ygbJ	-1,09	1,34	6,18
SL2898	<i>ygbI</i>	Uncharacterized HTH-type transcriptional regulator ygbI	-1,00	-1,17	1,08
SL2899	<i>hosA</i>	Transcriptional regulator hosA	-1,10	1,09	2,00
SL2900	<i>pad1</i>	Probable aromatic acid decarboxylase	1,01	1,13	-1,35
SL2901	<i>vdcC</i>	Protein vdcC	-1,01	-1,00	1,52
SL2902	<i>bsdD</i>	Phenolic acid decarboxylase subunit D	1,70	1,16	1,11
SL2903	<i>rpoS</i>	RNA polymerase sigma factor rpoS	1,17	1,12	2,05
SL2904	<i>nlpD</i>	Lipoprotein nlpD	1,13	1,13	1,07
SL2905	<i>pcm</i>	Protein-L-isoaspartate O-methyltransferase	1,25	-1,14	-1,25
SL2906	<i>surE</i>	Multifunctional protein surE	1,29	-1,19	1,17
SL2907	<i>truD</i>	tRNA pseudouridine synthase D	1,18	-1,14	1,17
SL2908	<i>ispF</i>	2-C-methyl-D-erythritol 2,4-cyclodiphosphate synthase	1,20	-1,09	1,39
SL2909	<i>ispD</i>	2-C-methyl-D-erythritol 4-phosphate cytidyltransferase	1,09	-1,21	-1,34
SL2910	<i>ftsB</i>	Cell division protein ftsB homolog	1,01	-1,03	-1,79
SL2911	<i>ygbE</i>	Inner membrane protein ygbE	-1,18	1,12	2,47
SL2912	<i>cysC</i>	Adenylyl-sulfate kinase	-1,09	-1,01	9,51
SL2913	<i>cysN</i>	Sulfate adenylyltransferase subunit 1	1,04	1,00	11,16
SL2914	<i>cysD</i>	Sulfate adenylyltransferase subunit 2	1,00	-1,20	4,76
SL2915	<i>iap</i>	Alkaline phosphatase isozyme conversion protein	-1,08	-1,03	-3,91
SL2916	<i>ygbF</i>	Uncharacterized protein ygbF	1,09	-1,11	-1,41
SL2917	<i>ygbT</i>	Uncharacterized protein ygbT	1,14	-1,39	-1,25
SL2918	<i>ygcH</i>	Uncharacterized protein ygcH	1,06	-1,16	-1,11
SL2919	<i>ygcl</i>	Uncharacterized protein ygcl	1,06	-1,23	-1,25
SL2920	<i>ygcJ</i>	Uncharacterized protein ygcJ	1,07	-1,02	-1,02
SL2921	-	Hypothetical	1,05	1,04	-1,02
SL2922	<i>ygcl</i>	Uncharacterized protein ygcL	1,14	-1,13	-1,28
SL2923	<i>ygcb</i>	Uncharacterized protein ygcB	1,43	1,36	1,33
SL2924	<i>sopD</i>	Secreted effector protein sopD	-1,52	1,19	-23,34
SL2925	<i>cysH</i>	Phosphoadenosine phosphosulfate reductase	1,07	-1,06	5,34
SL2926	<i>cysI</i>	Sulfite reductase [NADPH] hemoprotein beta-component	1,12	-1,02	6,16
SL2927	<i>cysJ</i>	Sulfite reductase [NADPH] flavoprotein alpha-component	-1,07	-1,06	4,34
SL2928	<i>queD</i>	6-carboxy-5,6,7,8-tetrahydropterin synthase	-1,10	1,06	-2,01
SL2929	-	Uncharacterized protein MJ0301	1,10	1,29	2,23
SL2930	<i>ygcf</i>	7-carboxy-7-deazaguanine synthase homolog	-1,05	-1,22	-1,51
SL2931	<i>eno</i>	Enolase	1,03	-1,03	-1,02
SL2932	<i>pyrG</i>	CTP synthase	1,04	1,04	-1,59
SL2933	<i>mazG</i>	Protein mazG	-1,03	-1,15	-1,57
SL2934	-	Hypothetical Protein SL2934	1,65	1,22	-1,46
SL2935	-	Plasmid Stabilization System	1,59	1,08	-1,43
SL2936	-	Hypothetical	1,30	1,22	1,07
SL2937	<i>relA</i>	GTP pyrophosphokinase	1,03	1,10	1,02
SL2938	<i>rumA</i>	23S rRNA (uracil-5-)-methyltransferase rumA	1,06	1,18	-1,26

Tabla Suplementaria 1

Diferencia de expresión de todos los genes de SV5015 en las cepas mutantes *greA*, *greB* y *greAgreB*, respecto a la cepa WT

ID	gene	Description	<i>greA</i> vs WT	<i>greB</i> vs WT	<i>greAgreB</i> vs WT
SL2939	<i>barA</i>	Signal transduction histidine-protein kinase BarA	1,13	1,08	-1,56
SL2940	<i>garK</i>	Glycerate kinase 2	1,24	1,22	1,41
SL2941	<i>gudD</i>	Glucarate dehydratase	1,21	1,12	1,87
SL2942	<i>gudX</i>	Glucarate dehydratase-related protein	1,19	1,10	3,30
SL2943	<i>gudP</i>	Probable glucarate transporter	1,30	1,14	5,33
SL2944	<i>yqcA</i>	Uncharacterized protein yqcA	1,22	1,26	1,32
SL2945	<i>truC</i>	tRNA pseudouridine synthase C	1,10	-1,02	-1,70
SL2946	<i>yqcC</i>	Uncharacterized protein yqcC	1,31	-1,09	-2,86
SL2947	<i>syd</i>	Protein syd	1,11	1,11	-1,78
SL2948	<i>queF</i>	NADPH-dependent 7-cyano-7-deazaguanine reductase	1,02	-1,08	-1,01
SL2949	<i>ygdH</i>	LOG family protein ygdH	1,08	-1,08	2,16
SL2950	<i>sdaC</i>	Serine transporter	-1,20	-1,09	2,59
SL2951	<i>sdaB</i>	L-serine dehydratase 2	1,12	-1,07	3,60
SL2952	<i>xni</i>	Uncharacterized exonuclease xni	-1,08	-1,15	-1,33
SL2953	<i>fucO</i>	Lactaldehyde reductase	1,09	-1,04	3,10
SL2954	<i>fucA</i>	L-fuculose phosphate aldolase	-1,08	1,00	2,94
SL2955	<i>fucP</i>	L-fucose-proton symporter	-1,13	-1,08	1,34
SL2956	<i>fucl</i>	L-fucose isomerase	1,14	1,10	1,26
SL2957	<i>fucK</i>	L-fuculokinase	1,14	-1,01	1,42
SL2958	<i>fucU</i>	L-fucose mutarotase	1,07	-1,01	1,75
SL2959	<i>fucR</i>	L-fucose operon activator	-1,02	1,03	2,02
SL2960	<i>rlmM</i>	Ribosomal RNA large subunit methyltransferase M	-1,10	1,02	-1,55
SL2961	<i>ygdD</i>	UPF0382 inner membrane protein ygdD	-1,18	-1,02	-2,47
SL2962	<i>gcvA</i>	Glycine cleavage system transcriptional activator	-1,22	1,12	-2,75
SL2963	<i>ygdI</i>	Uncharacterized lipoprotein ygdI	1,09	1,12	1,07
SL2964	<i>csdA</i>	Cysteine sulfinatase desulfinate	1,14	-1,03	-1,26
SL2965	<i>ygdK</i>	Uncharacterized sufE-like protein ygdK	1,09	-1,11	-1,14
SL2966	<i>rarD</i>	Protein rarD	1,25	-1,32	-1,38
SL2967	<i>ygdL</i>	Uncharacterized protein ygdL	1,18	-1,13	-1,42
SL2968	<i>mltA</i>	Membrane-bound lytic murein transglycosylase A	1,08	-1,08	-1,72
SL2969	<i>amiC</i>	N-acetylmuramoyl-L-alanine amidase AmiC	-1,05	1,02	-1,99
SL2970	<i>argA</i>	Amino-acid acetyltransferase	1,15	1,23	1,35
SL2971	<i>recD</i>	Exodeoxyribonuclease V alpha chain	1,37	1,13	1,45
SL2972	<i>recB</i>	Exodeoxyribonuclease V beta chain	1,06	-1,17	1,66
SL2973	<i>ptrA</i>	Protease 3	-1,07	-1,13	-1,01
SL2974	<i>recC</i>	Exodeoxyribonuclease V gamma chain	1,13	-1,02	1,69
SL2975	<i>ppdC</i>	Prepilin peptidase-dependent protein C	-1,06	-1,24	1,05
SL2976	<i>ygdB</i>	Uncharacterized protein ygdB	-1,29	-1,22	1,21
SL2977	<i>ppdB</i>	Prepilin peptidase-dependent protein B	-1,28	-1,11	2,36
SL2978	<i>ppdA</i>	Prepilin peptidase-dependent protein A	1,03	-1,14	1,23
SL2979	<i>thyA</i>	Thymidylate synthase	1,04	-1,03	-2,07
SL2980	<i>lgt</i>	Prolipoprotein diacylglycerol transferase	1,05	1,05	-1,72
SL2981	<i>ptsP</i>	Phosphoenolpyruvate-protein phosphotransferase ptsP	1,02	1,03	-1,57
SL2982	<i>rppH</i>	RNA pyrophosphohydrolase	1,05	1,11	-1,15

Tabla Suplementaria 1

Diferencia de expresión de todos los genes de SV5015 en las cepas mutantes *greA*, *greB* y *greAgreB*, respecto a la cepa WT

ID	gene	Description	<i>greA</i> vs WT	<i>greB</i> vs WT	<i>greAgreB</i> vs WT
SL2983	<i>mutH</i>	DNA mismatch repair protein mutH	1,14	1,11	1,09
SL2984	<i>ygdQ</i>	UPF0053 inner membrane protein ygdQ	-1,22	1,03	-4,13
SL2985	<i>ygdR</i>	Uncharacterized lipoprotein ygdR	1,33	1,27	1,09
SL2986	<i>tas</i>	Protein tas	1,24	1,14	1,51
SL2987	<i>lplT</i>	Lysophospholipid transporter lplT	1,07	-1,16	-1,08
SL2988	<i>aas</i>	Bifunctional protein aas	-1,09	-1,20	1,05
SL2989	<i>galR</i>	HTH-type transcriptional regulator galR	1,11	1,01	1,65
SL2990	<i>ascG</i>	HTH-type transcriptional regulator AscG	1,02	1,06	1,43
SL2991	<i>lysA</i>	Diaminopimelate decarboxylase	-1,27	-1,55	-1,32
SL2992	<i>lysR</i>	Transcriptional activator protein lysR	1,01	-1,06	1,56
SL2993	<i>ygeA</i>	Uncharacterized protein ygeA	-1,04	-1,17	1,38
SL2994	<i>araE</i>	Arabinose-proton symporter	1,49	1,34	4,71
SL2995	<i>kduD</i>	2-dehydro-3-deoxy-D-gluconate 5-dehydrogenase	-1,23	-1,27	2,87
SL2996	<i>kduI</i>	4-deoxy-L-threo-5-hexosulose-uronate ketol-isomerase	-1,33	-1,48	3,46
SL2997	<i>yqeF</i>	Probable acetyl-CoA acetyltransferase	-1,08	-1,04	4,20
SL2998	<i>allS</i>	HTH-type transcriptional activator AllS	1,11	1,11	1,19
SL2999	-	Hypothetical	1,97	1,21	-2,88
SL3000	<i>yqeG</i>	Inner membrane transport protein yqeG	1,04	-1,02	-3,13
SL3001	<i>rcnR</i>	Transcriptional repressor rcnR	1,00	1,27	1,49
SL3002	<i>rcnA</i>	Nickel/cobalt efflux system rcnA	-1,42	1,01	-1,42
SL3003	-	Hypothetical	1,04	1,06	1,52
SL3004	-	Hypothetical	-1,13	1,02	1,48
SL3005	-	Hypothetical	-1,00	-1,09	-1,07
SL3006	<i>papD</i>	Chaperone protein papD	-1,08	1,06	-1,04
SL3007	<i>yqiG</i>	Putative outer membrane usher protein yqiG	-1,06	-1,24	1,08
SL3008	<i>ybgD</i>	Uncharacterized fimbrial-like protein ybgD	1,50	1,10	2,60
SL3009	<i>yfdX</i>	Protein yfdX	-1,07	1,09	1,74
SL3010	<i>pagC</i>	Virulence membrane protein pagC	-1,03	1,16	2,46
SL3011	-	Uncharacterized protein HI_0947	1,04	-1,16	-1,51
SL3012	-	Uncharacterized protein CP0246	1,04	-1,02	1,36
SL3013	-	Hypothetical	-1,10	1,33	1,67
SL3014	<i>ygeR</i>	Uncharacterized lipoprotein ygeR	-1,07	-1,05	-1,43
SL3015	<i>idi</i>	Isopentenyl-diphosphate Delta-isomerase	1,17	1,02	-1,13
SL3016	<i>lysS</i>	Lysyl-tRNA synthetase	1,15	-1,01	1,28
SL3017	<i>prfB</i>	Peptide chain release factor 2	-1,09	-1,04	-2,12
SL3018	<i>recJ</i>	Single-stranded-DNA-specific exonuclease recJ	1,08	-1,43	-1,08
SL3019	<i>dsbC</i>	Thiol:disulfide interchange protein dsbC	-1,02	-1,29	1,28
SL3020	<i>xerD</i>	Tyrosine recombinase xerD	1,06	-1,13	1,06
SL3021	<i>fldB</i>	Flavodoxin-2	1,29	-1,03	1,05
SL3022	<i>ygfX</i>	Uncharacterized protein ygfX	1,12	-1,04	1,09
SL3023	<i>ygfY</i>	UPF0350 protein ygfY	1,15	1,07	1,21
SL3024	<i>ygfZ</i>	tRNA-modifying protein ygfZ	-1,05	-1,11	1,47
SL3025	<i>yqfA</i>	UPF0073 inner membrane protein yqfA	-1,01	1,19	1,34
SL3026	<i>yqfB</i>	UPF0267 protein yqfB	1,20	1,27	2,53
SL3027	<i>bglA</i>	6-phospho-beta-glucosidase BglA	1,09	-1,02	-1,14
SL3028	-	Hypothetical	1,21	1,12	1,22

Tabla Suplementaria 1

Diferencia de expresión de todos los genes de SV5015 en las cepas mutantes *greA*, *greB* y *greAgreB*, respecto a la cepa WT

ID	gene	Description	<i>greA</i> vs WT	<i>greB</i> vs WT	<i>greAgreB</i> vs WT
SL3029	<i>gcvP</i>	Glycine dehydrogenase [decarboxylating]	1,38	-1,19	1,01
SL3030	<i>gcvH</i>	Glycine cleavage system H protein	1,32	-1,13	-1,04
SL3031	<i>gcvT</i>	Aminomethyltransferase	1,11	-1,23	-1,08
SL3032	<i>visC</i>	Protein visC	1,09	-1,04	-1,29
SL3033	<i>ubiH</i>	2-octaprenyl-6-methoxyphenol hydroxylase	1,05	-1,07	1,15
SL3034	<i>pepP</i>	Xaa-Pro aminopeptidase	1,11	1,07	1,37
SL3035	<i>ygfB</i>	UPF0149 protein ygfB	-1,02	1,02	-1,06
SL3036	<i>zapA</i>	Cell division protein zapA	-1,00	-1,04	-1,20
SL3037	<i>ygfA</i>	Uncharacterized protein ygfA	1,32	1,15	-1,05
SL3038	<i>serA</i>	D-3-phosphoglycerate dehydrogenase	-1,06	-1,12	1,08
SL3039	<i>rpiA</i>	Ribose-5-phosphate isomerase A	-1,05	-1,14	1,40
SL3040	<i>iciA</i>	Chromosome initiation inhibitor	1,05	1,14	-1,29
SL3041	<i>yggE</i>	Uncharacterized protein yggE	-1,05	1,12	-2,34
SL3042	<i>argO</i>	Arginine exporter protein ArgO	1,04	-1,23	-1,49
SL3043	<i>mscS</i>	Small-conductance mechanosensitive channel	-1,11	-1,26	1,21
SL3044	<i>fbaA</i>	Fructose-bisphosphate aldolase class 2	1,11	-1,03	-1,08
SL3045	<i>pgk</i>	Phosphoglycerate kinase	1,14	1,01	-1,19
SL3046	<i>epd</i>	D-erythrose-4-phosphate dehydrogenase	1,30	1,04	-1,68
SL3047	<i>glmU</i>	Bifunctional protein glmU	1,17	-1,15	1,59
SL3048	-	Hypothetical	1,34	-1,23	3,16
SL3049	-	Permease Protein Of ABC-Type Cobalt Transporter	1,38	-1,21	2,71
SL3050	<i>cbiO1</i>	Cobalt import ATP-binding protein CbiO 1	1,19	-1,37	2,22
SL3051	<i>cbiO</i>	Cobalt import ATP-binding protein CbiO	1,32	-1,15	2,12
SL3052	<i>tktA</i>	Transketolase 1	1,10	-1,15	1,90
SL3053	<i>yggG</i>	Uncharacterized metalloprotease yggG	1,06	1,13	-1,48
SL3054	<i>speB</i>	Agmatinase	1,37	1,21	1,21
SL3055	<i>yisY</i>	AB hydrolase superfamily protein yisY	-1,26	1,14	-1,41
SL3056	<i>yjgK</i>	Uncharacterized protein yjgK	1,15	1,08	1,21
SL3057	<i>yjmC</i>	Uncharacterized oxidoreductase yjmC	1,12	-1,35	2,33
SL3058	<i>yjjN</i>	Uncharacterized zinc-type alcohol dehydrogenase-like protein yjjN	-1,14	-1,30	2,01
SL3059	<i>uxuB</i>	D-mannonate oxidoreductase	-1,09	-1,19	3,52
SL3060	<i>uxuR</i>	Uxu operon regulator	1,11	-1,10	1,27
SL3061	-	Hypothetical	-1,16	1,17	-1,17
SL3062	<i>speA</i>	Biosynthetic arginine decarboxylase	1,19	1,11	1,06
SL3063	<i>yqgB</i>	Hypothetical	1,17	1,17	-1,64
SL3064	<i>yqgD</i>	Uncharacterized protein yqgD	-1,10	1,08	-4,69
SL3065	<i>metK</i>	S-adenosylmethionine synthase	-1,11	-1,17	-2,26
SL3066	<i>galP</i>	Galactose-proton symporter	-1,31	1,06	1,25
SL3067	<i>sprT</i>	Protein sprT	1,15	-1,27	-1,42
SL3068	<i>endA</i>	Endonuclease-1	-1,20	-1,03	-1,06
SL3069	<i>rsmE</i>	Ribosomal RNA small subunit methyltransferase E	1,00	-1,02	-1,62
SL3070	<i>gshB</i>	Glutathione synthetase	1,18	1,02	1,07
SL3071	<i>yqgE</i>	UPF0301 protein yqgE	-1,16	-1,21	-1,74
SL3072	<i>yqgF</i>	Putative Holliday junction resolvase	1,02	-1,14	-1,46
SL3073	-	Hypothetical	1,07	-1,07	-1,49
SL3074	<i>yggR</i>	Uncharacterized protein yggR	-1,04	1,08	1,41

Tabla Suplementaria 1

Diferencia de expresión de todos los genes de SV5015 en las cepas mutantes *greA*, *greB* y *greAgreB*, respecto a la cepa WT

ID	gene	Description	<i>greA</i> vs WT	<i>greB</i> vs WT	<i>greAgreB</i> vs WT
SL3075	<i>yggS</i>	UPF0001 protein yggS	-1,04	-1,03	-1,69
SL3076	<i>yggT</i>	Uncharacterized protein yggT	1,05	-1,10	-1,26
SL3077	<i>yggU</i>	UPF0235 protein CKO_04329	-1,01	-1,16	-1,35
SL3078	<i>rdgB</i>	Nucleoside-triphosphatase rdgB	1,09	-1,18	-1,08
SL3079	<i>yggW</i>	Oxygen-independent coproporphyrinogen-III oxidase-like protein yggW	1,01	-1,28	-1,16
SL3080	<i>yggM</i>	Uncharacterized protein yggM	1,70	-1,04	2,39
SL3081	<i>ansB</i>	L-asparaginase 2	1,62	1,25	4,33
SL3082	<i>yggN</i>	Uncharacterized protein yggN	-1,17	-1,12	-1,33
SL3083	<i>yggL</i>	Uncharacterized protein yggL	-1,06	1,05	-1,01
SL3084	<i>trmB</i>	tRNA (guanine-N(7)-)-methyltransferase	-1,07	1,16	-1,30
SL3085	<i>mutY</i>	A/G-specific adenine glycosylase	-1,13	-1,16	-2,32
SL3086	<i>yggX</i>	Probable Fe(2+)-trafficking protein	-1,09	-1,11	-1,47
SL3087	<i>mltC</i>	Membrane-bound lytic murein transglycosylase C	1,06	-1,11	-1,16
SL3088	<i>nupG</i>	Nucleoside permease nupG	1,14	1,19	2,45
SL3089	<i>speC</i>	Ornithine decarboxylase, constitutive	1,05	1,15	1,12
SL3090	<i>yqgA</i>	Uncharacterized protein yqgA	1,17	-1,09	-1,71
SL3091	-	Virulence protein STM3117	1,01	-1,12	-1,24
SL3092	<i>cat2</i>	4-hydroxybutyrate coenzyme A transferase	1,04	-1,02	-1,05
SL3093	<i>maoC</i>	MaoC Domain Protein Dehydratase	1,16	1,28	1,10
SL3094	<i>citE</i>	Citrate lyase subunit beta	1,04	1,22	1,96
SL3095	<i>budR</i>	HTH-type transcriptional regulator BudR	1,05	-1,27	2,43
SL3096	<i>atsA</i>	Arylsulfatase	1,00	-1,12	1,54
SL3097	<i>atsB</i>	Anaerobic sulfatase-maturing enzyme	-1,33	-1,08	-1,13
SL3098	<i>moaR</i>	Monoamine regulon transcriptional regulator	1,11	1,43	2,42
SL3099	-	Hypothetical	-1,08	1,03	-1,09
SL3100	<i>steT</i>	Serine/threonine exchanger steT	1,09	1,15	1,20
SL3101	-	Hypothetical	-1,14	-1,19	1,09
SL3102	<i>puuB</i>	Gamma-glutamylputrescine oxidoreductase	-1,00	1,30	-1,36
SL3103	<i>feaB</i>	Phenylacetaldehyde dehydrogenase	1,10	1,20	1,04
SL3104	<i>iraD</i>	Anti-adapter protein iraD	1,41	1,15	1,59
SL3105	-	Hypothetical	1,68	1,43	1,34
SL3106	-	Polysaccharide Deacetylase	-1,96	1,79	-1,43
SL3107	<i>yhcX</i>	UPF0012 hydrolase yhcX	-1,88	1,67	-1,60
SL3108	<i>exuT</i>	Hexuronate transporter	1,24	1,15	4,36
SL3109	<i>uxuA</i>	Mannonate dehydratase	1,21	-1,08	3,06
SL3110	<i>uxuB</i>	D-mannonate oxidoreductase	1,20	-1,03	2,95
SL3111	<i>uxaC</i>	Uronate isomerase	1,15	1,04	2,61
SL3112	<i>bdlA</i>	Biofilm dispersion protein BdlA	-1,33	-1,01	-3,40
SL3113	<i>gsp</i>	Bifunctional glutathionylspermidine synthetase/amidase	1,15	1,10	-1,05
SL3114	<i>yghU</i>	Uncharacterized GST-like protein yghU	1,14	1,17	1,53
SL3115	-	Uncharacterized protein PM1146	1,29	-1,06	1,11
SL3116	-	Uncharacterized protein HI_1472	1,11	-1,19	1,15
SL3117	<i>hybG</i>	Hydrogenase-2 operon protein hybG	1,36	1,19	-1,33
SL3118	<i>hybF</i>	Probable hydrogenase nickel incorporation protein hybF	1,23	-1,08	-1,50
SL3119	<i>hybE</i>	Hydrogenase-2 operon protein hybE	1,32	-1,18	-1,14

Tabla Suplementaria 1

Diferencia de expresión de todos los genes de SV5015 en las cepas mutantes *greA*, *greB* y *greAgreB*, respecto a la cepa WT

ID	gene	Description	<i>greA</i> vs WT	<i>greB</i> vs WT	<i>greAgreB</i> vs WT
SL3120	<i>hybD</i>	Hydrogenase 2 maturation protease	1,32	-1,08	1,10
SL3121	<i>hybC</i>	Hydrogenase-2 large chain	1,30	-1,15	1,08
SL3122	<i>hybB</i>	Probable Ni/Fe-hydrogenase 2 b-type cytochrome subunit	1,27	-1,23	1,09
SL3123	<i>hybA</i>	Hydrogenase-2 operon protein <i>hybA</i>	1,28	1,02	1,14
SL3124	<i>hybO</i>	Hydrogenase-2 small chain	1,17	1,08	1,11
SL3125	<i>yghW</i>	Uncharacterized protein <i>yghW</i>	-1,36	1,16	-6,35
SL3126	<i>tse</i>	Methyl-accepting chemotaxis serine transducer	-1,55	1,00	-8,28
SL3127	<i>yqhA</i>	UPF0114 protein <i>yqhA</i>	-1,01	1,09	-1,62
SL3128	-	Hypothetical	-1,27	1,12	-2,72
SL3129	-	Hypothetical	-1,27	1,09	-5,12
SL3130	-	Hypothetical	-1,43	-1,26	-7,27
SL3131	<i>yghA</i>	Uncharacterized oxidoreductase <i>yghA</i>	1,05	-1,10	1,44
SL3132	<i>exbD</i>	Biopolymer transport protein <i>exbD</i>	1,20	1,13	-2,14
SL3133	<i>exbB</i>	Biopolymer transport protein <i>exbB</i>	1,04	1,15	-2,24
SL3134	<i>b3007</i> ;	Hypothetical	1,31	1,37	1,27
SL3135	<i>metC</i>	Cystathionine beta-lyase	1,16	-1,09	1,31
SL3136	<i>yghB</i>	Inner membrane protein <i>yghB</i>	1,14	1,16	-1,44
SL3137	<i>yqhC</i>	Uncharacterized HTH-type transcriptional regulator <i>yqhC</i>	1,26	1,08	1,10
SL3138	<i>yqhD</i>	Alcohol dehydrogenase <i>yqhD</i>	1,07	1,14	2,16
SL3139	<i>dkgA</i>	2,5-diketo-D-gluconic acid reductase A	1,07	1,06	1,93
SL3140	<i>yflS</i>	Putative malate transporter <i>yflS</i>	-1,24	1,14	-1,79
SL3141	-	Uncharacterized HIT-like protein MJ0866	1,07	1,02	1,05
SL3142	<i>ygiQ</i>	UPF0313 protein <i>ygiQ</i>	-1,38	1,18	-2,01
SL3143	<i>yiiZ</i>	Uncharacterized protein <i>yiiZ</i>	-1,25	-1,05	7,98
SL3144	-	C4-Dicarboxylate Transport System Permease Small Protein	-1,43	-1,29	6,19
SL3145	<i>ygiK</i>	Uncharacterized protein <i>ygiK</i>	-1,14	-1,20	3,14
SL3146	<i>sufI</i>	Protein <i>sufI</i>	-1,04	-1,14	-1,20
SL3147	<i>plsC</i>	1-acyl-sn-glycerol-3-phosphate acyltransferase	1,06	-1,03	-1,30
SL3148	<i>parC</i>	DNA topoisomerase 4 subunit A	-1,27	-1,10	-1,77
SL3149	<i>ygiV</i>	Probable transcriptional regulator <i>ygiV</i>	1,05	1,07	1,08
SL3150	<i>ygiW</i>	Protein <i>ygiW</i>	1,35	1,23	1,98
SL3151	<i>qseB</i>	Transcriptional regulatory protein <i>qseB</i>	1,02	-1,14	1,24
SL3152	<i>qseC</i>	Sensor protein <i>qseC</i>	-1,02	-1,14	-1,20
SL3153	<i>mdaB</i>	Modulator of drug activity B	1,06	-1,01	1,10
SL3154	<i>ygiN</i>	Probable quinol monooxygenase <i>ygiN</i>	1,26	1,03	1,26
SL3155	<i>parE</i>	DNA topoisomerase 4 subunit B	1,03	-1,09	-1,53
SL3156	<i>yqiA</i>	Esterase <i>yqiA</i>	1,19	-1,05	-1,30
SL3157	<i>icc</i>	Protein <i>icc</i>	1,18	1,07	-1,06
SL3158	<i>yqiB</i>	Uncharacterized protein <i>yqiB</i>	-1,05	-1,11	-1,25
SL3159	<i>nudF</i>	ADP-ribose pyrophosphatase	-1,05	-1,02	-1,31
SL3160	<i>tolC</i>	Outer membrane protein <i>tolC</i>	1,05	1,09	1,41
SL3161	<i>ygiB</i>	UPF0441 protein <i>ygiB</i>	1,07	1,00	1,69
SL3162	<i>ygiC</i>	Uncharacterized protein <i>ygiC</i>	1,05	-1,07	1,38
SL3163	<i>ygiD</i>	Uncharacterized protein <i>ygiD</i>	-2,08	1,12	-9,28
SL3164	<i>zupT</i>	Zinc transporter <i>zupT</i>	1,44	1,26	1,25

Tabla Suplementaria 1

Diferencia de expresión de todos los genes de SV5015 en las cepas mutantes *greA*, *greB* y *greAgreB*, respecto a la cepa WT

ID	gene	Description	<i>greA</i> vs WT	<i>greB</i> vs WT	<i>greAgreB</i> vs WT
SL3165	-	Arylsulfotransferase	-1,13	-1,15	3,35
SL3166	<i>dsbA</i>	Thiol:disulfide interchange protein dsbA	-1,19	-1,13	3,06
SL3167	<i>dsbB</i>	Putative protein-disulfide oxidoreductase	-1,31	-1,22	3,38
SL3168	<i>ribB</i>	3,4-dihydroxy-2-butanone 4-phosphate synthase	-1,31	-1,05	-1,73
SL3169	<i>yqiC</i>	Uncharacterized protein yqiC	1,05	1,12	1,42
SL3170	<i>glgS</i>	Glycogen synthesis protein glgS	1,26	1,60	2,05
SL3171	<i>yqiJ</i>	Inner membrane protein yqiJ	-1,24	-1,07	-1,03
SL3172	<i>yqiK</i>	Inner membrane protein yqiK	1,17	-1,05	-1,06
SL3173	<i>hldE</i>	Bifunctional protein hldE	-1,02	1,00	-1,17
SL3174	<i>glnE</i>	Glutamate-ammonia-ligase adenylyltransferase	1,08	-1,07	1,51
SL3175	<i>ygiF</i>	Uncharacterized protein ygiF	1,13	-1,04	-1,19
SL3176	<i>ygiM</i>	Uncharacterized protein ygiM	-1,23	1,09	-3,56
SL3177	<i>cca</i>	Multifunctional CCA protein	1,07	1,08	-1,52
SL3178	<i>uppP</i>	Undecaprenyl-diphosphatase	-1,19	-1,11	-2,21
SL3179	<i>folB</i>	Dihydroneopterin aldolase	-1,39	-1,02	-2,66
SL3180	<i>plsY</i>	Glycerol-3-phosphate acyltransferase	1,05	1,13	-1,24
SL3181	-	Hypothetical	1,11	1,16	-1,38
SL3182	<i>gcp</i>	Probable O-sialoglycoprotein endopeptidase	-1,07	1,10	-1,62
SL3183	<i>rpsU</i>	30S ribosomal protein S21	-1,10	1,23	-3,63
SL3184	<i>dnaG</i>	DNA primase	-1,03	1,12	-2,31
SL3185	<i>rpoD</i>	RNA polymerase sigma factor rpoD	1,08	1,07	-1,10
SL3186	<i>mug</i>	G/U mismatch-specific DNA glycosylase	1,13	1,13	1,95
SL3187	<i>yqiH</i>	Uncharacterized protein yqiH	-1,04	1,14	-1,17
SL3188	<i>yqiI</i>	Uncharacterized protein yqiI	1,06	1,32	1,63
SL3189	<i>tse</i>	Methyl-accepting chemotaxis serine transducer	-1,38	-1,15	-3,94
SL3190	<i>aer</i>	Aerotaxis receptor	-1,22	-1,40	1,59
SL3191	<i>patA</i>	Putrescine aminotransferase	-1,03	1,04	1,44
SL3192	<i>fadH</i>	2,4-dienoyl-CoA reductase [NADPH]	-1,06	1,12	6,90
SL3193	<i>rlmG</i>	Ribosomal RNA large subunit methyltransferase G	-1,01	1,07	-1,52
SL3194	<i>ygjP</i>	Uncharacterized protein ygjP	1,09	-1,07	-1,26
SL3195	<i>ygjQ</i>	Uncharacterized protein ygjQ	1,06	1,09	-1,69
SL3196	<i>ygjR</i>	Uncharacterized oxidoreductase ygjR	1,34	1,05	2,00
SL3197	<i>alx</i>	Inner membrane protein alx	-1,24	-1,08	-2,21
SL3198	<i>sstT</i>	Serine/threonine transporter sstT	-1,05	1,04	2,88
SL3199	<i>yqjA</i>	Inner membrane protein yqjA	-1,37	1,17	-2,94
SL3200	<i>yqjB</i>	Uncharacterized protein yqjB	-1,21	1,17	-3,22
SL3201	<i>yqjC</i>	Protein yqjC	1,03	1,18	1,23
SL3202	<i>yqjE</i>	Inner membrane protein yqjE	1,09	1,06	1,66
SL3203	<i>yqjK</i>	Uncharacterized protein yqjK	1,06	1,07	1,64
SL3204	<i>yqjF</i>	Inner membrane protein yqjF	1,44	-1,13	1,13
SL3205	<i>yqjG</i>	Uncharacterized protein yqjG	1,10	1,08	2,48
SL3206	<i>yhaH</i>	Inner membrane protein yhaH	1,01	-1,06	1,28
SL3207	<i>yhaJ</i>	Uncharacterized HTH-type transcriptional regulator yhaJ	1,03	1,08	-1,27
SL3208	<i>yhaK</i>	Pirin-like protein yhaK	1,23	1,30	1,40
SL3209	<i>yhaL</i>	Hypothetical Protein yhaL	1,20	1,49	5,32

Tabla Suplementaria 1

Diferencia de expresión de todos los genes de SV5015 en las cepas mutantes *greA*, *greB* y *greAgreB*, respecto a la cepa WT

ID	gene	Description	<i>greA</i> vs WT	<i>greB</i> vs WT	<i>greAgreB</i> vs WT
SL3210	<i>yhaM</i>	UPF0597 protein yhaM	1,20	1,14	1,14
SL3211	<i>yhaO</i>	Inner membrane transport protein yhaO	1,06	1,03	2,15
SL3212	<i>tdcG</i>	L-serine dehydratase tdcG	1,10	1,03	-1,55
SL3213	<i>tdcE</i>	Keto-acid formate acetyltransferase	1,10	1,00	-1,87
SL3214	<i>tdcD</i>	Propionate kinase	1,02	1,22	-2,52
SL3215	<i>tdcC</i>	Threonine/serine transporter tdcC	-1,13	1,19	-1,88
SL3216	<i>tdcB</i>	Threonine dehydratase catabolic	-1,26	1,33	-2,06
SL3217	<i>tdcA</i>	HTH-type transcriptional regulator tdcA	1,55	1,55	5,57
SL3218	-	Hypothetical	1,02	1,00	-1,10
SL3219	-	Hypothetical	1,00	1,33	-1,22
SL3220	<i>garK</i>	Glycerate kinase 2	1,09	-1,07	1,56
SL3221	<i>garR</i>	2-hydroxy-3-oxopropionate reductase	1,25	1,22	1,72
SL3222	<i>garL</i>	5-keto-4-deoxy-D-glucarate aldolase	1,27	1,19	2,25
SL3223	<i>garD</i>	D-galactarate dehydratase	1,28	1,27	2,13
SL3224	<i>ydjE</i>	Uncharacterized sugar kinase ydjE	-1,04	1,04	1,97
SL3225	<i>glpR</i>	Glycerol-3-phosphate regulon repressor	1,07	1,08	1,57
SL3226	<i>gatY</i>	D-tagatose-1,6-bisphosphate aldolase subunit gatY	1,03	1,06	-1,57
SL3227	<i>fruK</i>	1-phosphofructokinase	-1,26	-1,39	-2,73
SL3228	<i>fruA</i>	PTS system fructose-specific EIIABC component	-1,11	-1,19	-2,11
SL3229	<i>fruB</i>	Multiphosphoryl transfer protein	-1,34	-1,41	-2,50
SL3230	<i>gatZ</i>	D-tagatose-1,6-bisphosphate aldolase subunit gatZ	1,04	-1,33	-1,67
SL3231	<i>gatA</i>	Galactitol-specific phosphotransferase enzyme IIA component	-1,31	-1,28	1,01
SL3232	<i>gatB</i>	Galactitol-specific phosphotransferase enzyme IIB component	-1,11	-1,16	2,08
SL3233	<i>gatC</i>	Galactitol permease IIC component	1,08	1,01	2,52
SL3234	<i>gatD</i>	Galactitol-1-phosphate 5-dehydrogenase	1,13	1,02	1,05
SL3235	<i>gatR</i>	Galactitol utilization operon repressor	1,07	-1,04	4,26
SL3236	<i>rsml</i>	Ribosomal RNA small subunit methyltransferase I	1,10	1,14	-1,68
SL3237	<i>yraM</i>	Uncharacterized protein yraM	1,02	1,01	-1,63
SL3238	<i>yraN</i>	UPF0102 protein yraN	1,13	1,05	-1,85
SL3239	<i>diaA</i>	DnaA initiator-associating protein diaA	-1,01	1,01	-1,47
SL3240	<i>yraP</i>	Uncharacterized protein yraP	-1,08	-1,05	-1,02
SL3241	<i>yraR</i>	Uncharacterized protein yraR	1,09	1,11	1,04
SL3242	<i>yhbO</i>	Protein yhbO	-1,00	1,02	1,40
SL3243	<i>yhbP</i>	UPF0306 protein yhbP	1,20	1,07	-1,26
SL3244	<i>yhbQ</i>	UPF0213 protein yhbQ	1,15	-1,02	-1,15
SL3245	<i>yhbS</i>	Uncharacterized N-acetyltransferase yhbS	1,22	1,28	1,37
SL3246	<i>yhbT</i>	Uncharacterized protein yhbT	1,27	1,33	1,57
SL3247	<i>yhbU</i>	Uncharacterized protease yhbU	-1,02	-1,27	-1,56
SL3248	<i>yhbV</i>	Uncharacterized protein yhbV	1,09	-1,84	1,05
SL3249	<i>yhbW</i>	Uncharacterized protein yhbW	-1,37	-1,38	2,08
SL3250	<i>yafK</i>	Putative L,D-transpeptidase YafK	-1,02	1,18	1,09
SL3251	-	Conserved Hypothetical Protein	-1,02	-1,10	1,01
SL3252	<i>mtr</i>	Tryptophan-specific transport protein	-1,22	-1,07	-2,62
SL3253	<i>deaD</i>	Cold-shock DEAD box protein A	-1,04	-1,06	-8,59
SL3254	<i>nlpI</i>	Lipoprotein nlpI	-1,06	-1,00	-1,86

Tabla Suplementaria 1

Diferencia de expresión de todos los genes de SV5015 en las cepas mutantes *greA*, *greB* y *greAgreB*, respecto a la cepa WT

ID	gene	Description	<i>greA</i> vs WT	<i>greB</i> vs WT	<i>greAgreB</i> vs WT
SL3255	<i>pnf</i>	Polyribonucleotide nucleotidyltransferase	1,11	1,01	-1,21
SL3256	<i>rpsO</i>	30S ribosomal protein S15	-1,05	-1,03	-1,45
SL3257	<i>truB</i>	tRNA pseudouridine synthase B	1,10	-1,14	-1,30
SL3258	<i>rbfA</i>	Ribosome-binding factor A	1,11	1,01	-1,06
SL3259	<i>infB</i>	Translation initiation factor IF-2	1,09	1,01	-1,02
SL3260	<i>nusA</i>	Transcription elongation protein nusA	-1,14	-1,12	-1,59
SL3261	<i>rimP</i>	Ribosome maturation factor rimP	-1,28	-1,08	-2,79
SL3262	<i>argG</i>	Argininosuccinate synthase	1,23	-1,12	1,18
SL3263	-	Hypothetical	-1,04	1,35	-2,48
SL3264	<i>secG</i>	Protein-export membrane protein secG	-1,16	1,05	-2,46
SL3265	<i>glmM</i>	Phosphoglucosamine mutase	1,20	-1,20	1,41
SL3266	<i>folP</i>	Dihydropteroate synthase	1,18	-1,10	1,24
SL3268	<i>ftsH</i>	Cell division protease ftsH	1,27	-1,11	-1,54
SL3269	<i>rlmE</i>	Ribosomal RNA large subunit methyltransferase E	1,72	1,13	-1,17
SL3270	<i>yhbY</i>	RNA-binding protein yhbY	2,18	1,01	1,19
SL3271	<i>greA</i>	Transcription elongation factor greA	-97,36	1,03	-320,40
SL3272	<i>dacB</i>	D-alanyl-D-alanine carboxypeptidase dacB	1,05	1,04	-1,86
SL3273	<i>obg</i>	GTPase obg	1,05	1,03	-1,81
SL3274	<i>yhbE</i>	Uncharacterized inner membrane transporter yhbE	-1,01	-1,08	-1,81
SL3275	<i>rpmA</i>	50S ribosomal protein L27	-1,33	-1,01	-3,03
SL3276	<i>rplU</i>	50S ribosomal protein L21	-1,20	1,03	-2,51
SL3277	<i>ispB</i>	Octaprenyl-diphosphate synthase	-1,05	1,08	1,08
SL3278	<i>sfsB</i>	Sugar fermentation stimulation protein B	1,17	1,05	1,06
SL3279	<i>murA</i>	UDP-N-acetylglucosamine 1-carboxyvinyltransferase	1,00	-1,11	-1,36
SL3280	<i>yrbA</i>	Uncharacterized protein yrbA	1,01	1,03	-1,97
SL3281	<i>mlaB</i>	Probable phospholipid ABC transporter-binding protein mlaB	1,05	1,03	-1,21
SL3282	<i>mlaC</i>	Probable phospholipid-binding protein mlaC	-1,00	-1,03	-1,08
SL3283	<i>mlaD</i>	Probable phospholipid ABC transporter-binding protein mlaD	-1,08	-1,15	-1,29
SL3284	<i>mlaE</i>	Probable phospholipid ABC transporter permease protein mlaE	-1,15	-1,10	-1,98
SL3285	<i>mlaF</i>	Probable phospholipid import ATP-binding protein mlaF	-1,19	1,00	-1,85
SL3286	<i>yrbG</i>	Inner membrane protein yrbG	1,01	1,15	-1,82
SL3287	<i>kdsD</i>	Arabinose 5-phosphate isomerase	1,08	-1,02	-1,81
SL3288	<i>kdsC</i>	3-deoxy-D-manno-octulosonate 8-phosphate phosphatase	1,02	-1,12	-1,34
SL3289	<i>lptC</i>	Lipopolysaccharide export system protein lptC	1,06	-1,02	-1,19
SL3290	<i>lptA</i>	Lipopolysaccharide export system protein lptA	1,06	-1,07	-1,12
SL3291	<i>lptB</i>	Lipopolysaccharide export system ATP-binding protein lptB	1,06	-1,05	-1,08
SL3292	<i>rpoN</i>	RNA polymerase sigma-54 factor	1,01	-1,04	-1,21
SL3293	<i>yhbH</i>	Probable sigma(54) modulation protein	1,24	1,43	2,78
SL3294	<i>ptsN</i>	Nitrogen regulatory protein	1,19	1,06	2,57
SL3295	<i>yhbJ</i>	UPF0042 nucleotide-binding protein PC1_0271	1,16	-1,02	1,54
SL3296	<i>ptsO</i>	Phosphocarrier protein NPr	1,21	-1,07	1,52

Tabla Suplementaria 1Diferencia de expresión de todos los genes de SV5015 en las cepas mutantes *greA*, *greB* y *greAgreB*, respecto a la cepa WT

ID	gene	Description	<i>greA</i> vs WT	<i>greB</i> vs WT	<i>greAgreB</i> vs WT
SL3297	<i>yrbL</i>	Uncharacterized protein yrbL	1,26	1,34	1,76
SL3298	<i>mtgA</i>	Monofunctional biosynthetic peptidoglycan transglycosylase	1,03	-1,19	1,29
SL3299	<i>elbB</i>	Enhancing lycopene biosynthesis protein 2	1,17	1,12	1,58
SL3300	<i>arcB</i>	Aerobic respiration control sensor protein ArcB	1,17	-1,00	1,22
SL3301	<i>yhcC</i>	Uncharacterized protein yhcC	1,03	1,15	-3,69
SL3302	<i>gltB</i>	Glutamate synthase [NADPH] large chain	1,27	1,12	2,44
SL3303	<i>gltD</i>	Glutamate synthase [NADPH] small chain	1,26	1,03	2,37
SL3304	<i>yhcG</i>	Uncharacterized protein yhcG	-1,30	1,05	1,35
SL3305	<i>codB</i>	Cytosine permease	-1,49	1,05	-1,80
SL3306	<i>codA</i>	Cytosine deaminase	-1,15	1,09	-1,13
SL3307	<i>yhcH</i>	Uncharacterized protein yhcH	1,60	1,04	2,30
SL3308	<i>nanK</i>	N-acetylmannosamine kinase	1,30	-1,18	2,02
SL3309	<i>nanE2</i>	Putative N-acetylmannosamine-6-phosphate 2-epimerase 2	1,27	-1,23	1,86
SL3310	<i>nanT1</i>	Putative sialic acid transporter 1	1,28	-1,14	1,56
SL3311	<i>nanA</i>	N-acetylneuraminase lyase	1,50	-1,09	1,42
SL3312	<i>nanR</i>	Transcriptional regulator nanR	1,06	-1,03	1,09
SL3313	<i>sspB</i>	Stringent starvation protein B	-1,27	-1,08	-2,06
SL3314	<i>sspA</i>	Stringent starvation protein A	-1,25	-1,02	-2,69
SL3315	-	Hypothetical	1,27	1,27	1,19
SL3316	<i>rpsL</i>	30S ribosomal protein S9	-1,09	1,04	-1,76
SL3317	<i>rplM</i>	50S ribosomal protein L13	1,02	1,09	-1,82
SL3318	<i>yhcM</i>	Uncharacterized protein yhcM	-1,05	-1,10	-2,14
SL3319	<i>yhcB</i>	Putative cytochrome d ubiquinol oxidase subunit 3	-1,08	-1,05	-1,13
SL3320	<i>degQ</i>	Protease degQ	-1,00	-1,03	1,32
SL3321	<i>degS</i>	Protease degS	1,07	1,12	-1,63
SL3322	<i>citG1</i>	Probable 2-(5"-triphosphoribosyl)-3'-dephosphocoenzyme-A synthase 1	1,39	1,09	2,38
SL3323	<i>oadB1</i>	Oxaloacetate decarboxylase beta chain 1	1,31	1,17	1,88
SL3324	<i>oadA</i>	Oxaloacetate decarboxylase alpha chain	1,21	-1,05	2,42
SL3325	<i>oadG2</i>	Oxaloacetate decarboxylase gamma chain 2	1,13	1,03	1,71
SL3326	<i>ttdB</i>	L(+)-tartrate dehydratase subunit beta	1,24	-1,32	3,29
SL3327	<i>ttDA</i>	L(+)-tartrate dehydratase subunit alpha	1,12	-1,23	4,25
SL3328	<i>yfbS</i>	Uncharacterized transporter MJ0672	1,00	-1,49	3,26
SL3329	<i>ydfH</i>	GntR Family Transcriptional Regulator	1,04	-1,00	-1,58
SL3330	<i>pdhR</i>	GntR Family Transcriptional Regulator	-1,09	-1,03	-2,07
SL3331	<i>mdh</i>	Malate dehydrogenase	1,18	-1,00	4,77
SL3332	<i>argR</i>	Arginine repressor	1,14	1,17	1,30
SL3333	<i>yhcN</i>	Uncharacterized protein yhcN	1,33	1,28	-1,85
SL3334	<i>yhcN</i>	Uncharacterized protein yhcN	1,29	1,14	1,12
SL3335	<i>yhcO</i>	Uncharacterized protein yhcO	1,30	1,51	5,06
SL3336	<i>aaeB</i>	p-hydroxybenzoic acid efflux pump subunit AaeB	1,15	1,02	-1,34
SL3337	<i>aaeA</i>	p-hydroxybenzoic acid efflux pump subunit AaeA	1,08	-1,01	-1,10
SL3338	<i>aaeX</i>	Protein AaeX	1,10	1,09	-1,09
SL3339	<i>aaeR</i>	HTH-type transcriptional activator AaeR	-1,02	-1,07	1,38
SL3340	<i>tldD</i>	Protein tldD	1,18	-1,01	1,00

Tabla Suplementaria 1

Diferencia de expresión de todos los genes de SV5015 en las cepas mutantes *greA*, *greB* y *greAgreB*, respecto a la cepa WT

ID	gene	Description	<i>greA</i> vs WT	<i>greB</i> vs WT	<i>greAgreB</i> vs WT
SL3341	<i>yhdP</i>	Uncharacterized protein yhdP	-1,01	1,01	-1,09
SL3342	<i>rng</i>	Ribonuclease G	-1,02	-1,07	-1,18
SL3343	<i>yceF2</i>	Maf-like protein yceF 2	1,02	-1,03	-1,43
SL3344	<i>mreD</i>	Rod shape-determining protein mreD	1,12	1,18	-1,73
SL3345	<i>mreC</i>	Rod shape-determining protein mreC	-1,06	-1,07	-1,95
SL3346	<i>mreB</i>	Rod shape-determining protein mreB	-1,11	1,01	-2,43
SL3347	-	Conserved Hypothetical Protein	-1,08	1,03	-1,96
SL3348	<i>yhdA</i>	Hypothetical Protein yhdA	-1,15	1,08	-1,75
SL3349	<i>yhdH</i>	Putative quinone oxidoreductase yhdH	1,02	1,07	-1,22
SL3350	<i>yedY</i>	Sulfoxide reductase catalytic subunit yedY	1,06	-1,03	2,85
SL3351	<i>yedZ</i>	Sulfoxide reductase heme-binding subunit yedZ	1,06	-1,04	1,31
SL3352	<i>accB</i>	Biotin carboxyl carrier protein of acetyl-CoA carboxylase	-1,09	-1,16	-1,12
SL3353	<i>accC</i>	Biotin carboxylase	1,06	-1,20	1,22
SL3354	<i>yhdT</i>	Uncharacterized protein yhdT	1,09	1,17	-2,38
SL3355	<i>panF</i>	Sodium/pantothenate symporter	-1,04	1,01	-1,53
SL3356	<i>prmA</i>	Ribosomal protein L11 methyltransferase	1,00	-1,14	-1,03
SL3357	<i>dusB</i>	tRNA-dihydrouridine synthase B	-1,42	-1,03	-3,85
SL3358	<i>fis</i>	DNA-binding protein fis	-1,24	-1,03	-3,28
SL3359	<i>yhdJ</i>	Uncharacterized adenine-specific methylase yhdJ	-1,16	-1,02	-1,96
SL3360	<i>yhdU</i>	Uncharacterized protein yhdU	1,12	1,23	1,74
SL3361	<i>yciR</i>	Uncharacterized signaling protein PA1727	1,28	1,10	1,25
SL3362	<i>envR</i>	Probable <i>acrEF/envCD</i> operon repressor	1,05	-1,01	1,01
SL3363	<i>acrE</i>	Acriflavine resistance protein E	1,26	1,10	-2,58
SL3364	<i>acrF</i>	Acriflavine resistance protein F	1,36	1,06	-1,32
SL3365	<i>yhdV</i>	Uncharacterized protein yhdV	-1,10	1,10	-1,29
SL3366	<i>yrdA</i>	Protein yrdA	-1,05	-1,08	1,35
SL3367	<i>yrdB</i>	Uncharacterized protein yrdB	1,14	-1,05	-1,02
SL3368	<i>aroE</i>	Shikimate dehydrogenase	1,03	-1,01	-1,24
SL3369	<i>rimN</i>	Putative ribosome maturation factor rimN	1,01	-1,07	-1,53
SL3370	<i>yrdD</i>	Uncharacterized protein yrdD	1,05	-1,03	-1,21
SL3371	<i>smg</i>	Protein smg	1,09	1,19	1,55
SL3372	<i>smf</i>	Protein smf	1,11	1,06	1,60
SL3373	<i>def</i>	Peptide deformylase	1,02	1,07	-2,19
SL3374	<i>fmt</i>	Methionyl-tRNA formyltransferase	-1,06	-1,16	-3,52
SL3375	<i>rsmB</i>	Ribosomal RNA small subunit methyltransferase B	-1,04	-1,17	-4,60
SL3376	<i>trkA</i>	Trk system potassium uptake protein trkA	1,04	-1,01	-2,57
SL3377	<i>mscL</i>	Large-conductance mechanosensitive channel	1,05	1,26	1,93
SL3378	<i>yhdL</i>	Uncharacterized protein yhdL	-1,03	1,16	-1,02
SL3379	<i>zntR</i>	HTH-type transcriptional regulator zntR	-1,14	1,11	-1,16
SL3380	<i>yhdN</i>	Uncharacterized protein yhdN	-1,01	1,19	-1,34
SL3381	<i>rplQ</i>	50S ribosomal protein L17	1,07	-1,23	1,27
SL3382	<i>rpoA</i>	DNA-directed RNA polymerase subunit alpha	-1,02	-1,15	-1,01
SL3383	<i>rpsD</i>	30S ribosomal protein S4	-1,04	-1,11	-1,14
SL3384	<i>rpsK</i>	30S ribosomal protein S11	-1,07	-1,12	-1,17
SL3385	<i>rpsM</i>	30S ribosomal protein S13	-1,17	-1,16	-1,28

Tabla Suplementaria 1Diferencia de expresión de todos los genes de SV5015 en las cepas mutantes *greA*, *greB* y *greAgreB*, respecto a la cepa WT

ID	gene	Description	<i>greA</i> vs WT	<i>greB</i> vs WT	<i>greAgreB</i> vs WT
SL3386	<i>rpmJ1</i>	50S ribosomal protein L36 1	-1,03	-1,09	-1,21
SL3387	<i>secY</i>	Preprotein translocase subunit secY	-1,01	-1,08	-1,03
SL3388	<i>rplO</i>	50S ribosomal protein L15	1,06	1,08	1,18
SL3389	<i>rpmD</i>	50S ribosomal protein L30	1,04	1,07	1,19
SL3390	<i>rpsE</i>	30S ribosomal protein S5	1,08	1,09	1,06
SL3391	<i>rplR</i>	50S ribosomal protein L18	1,04	1,09	1,14
SL3392	<i>rplF</i>	50S ribosomal protein L6	1,02	1,01	-1,02
SL3393	<i>rpsH</i>	30S ribosomal protein S8	-1,06	-1,02	1,00
SL3394	<i>rpsN</i>	30S ribosomal protein S14	1,01	1,09	1,09
SL3395	<i>rplE</i>	50S ribosomal protein L5	-1,08	-1,01	-1,06
SL3396	<i>rplX</i>	50S ribosomal protein L24	-1,07	1,06	-1,04
SL3397	<i>rplN</i>	50S ribosomal protein L14	-1,08	1,05	-1,34
SL3398	<i>rpsQ</i>	30S ribosomal protein S17	1,24	1,10	1,40
SL3399	<i>rpmC</i>	50S ribosomal protein L29	1,25	1,15	1,55
SL3400	<i>rplP</i>	50S ribosomal protein L16	1,21	1,19	1,29
SL3401	<i>rpsC</i>	30S ribosomal protein S3	1,17	1,11	1,31
SL3402	<i>rplV</i>	50S ribosomal protein L22	1,19	1,12	1,18
SL3403	<i>rpsS</i>	30S ribosomal protein S19	1,16	1,10	1,10
SL3404	<i>rplB</i>	50S ribosomal protein L2	1,12	1,08	1,06
SL3405	<i>rplW</i>	50S ribosomal protein L23	1,09	1,05	-1,02
SL3406	<i>rplD</i>	50S ribosomal protein L4	1,07	1,06	-1,13
SL3407	<i>rplC</i>	50S ribosomal protein L3	1,02	1,08	-1,30
SL3408	<i>rpsJ</i>	30S ribosomal protein S10	-1,00	1,16	-1,67
SL3409	<i>hopD</i>	Leader peptidase hopD	1,10	1,19	-1,26
SL3410	<i>bfr</i>	Bacterioferritin	1,06	1,17	1,20
SL3411	<i>bfd</i>	Bacterioferritin-associated ferredoxin	-1,31	1,29	-4,45
SL3412	<i>tuf1</i>	Elongation factor Tu 1	1,00	-1,05	1,22
SL3413	<i>fusA</i>	Elongation factor G	1,06	1,02	1,08
SL3414	<i>rpsG</i>	30S ribosomal protein S7	-1,04	1,05	-1,20
SL3415	<i>rpsL</i>	30S ribosomal protein S12	-1,19	-1,02	-1,43
SL3416	<i>tusB</i>	Protein tusB	1,16	1,05	-1,60
SL3417	<i>tusC</i>	Protein tusC	1,23	1,10	-1,59
SL3418	<i>tusD</i>	Sulfurtransferase tusD	1,10	-1,03	-1,96
SL3419	<i>yheO</i>	Uncharacterized protein yheO	-1,04	1,03	-3,74
SL3420	<i>fkpA</i>	FKBP-type peptidyl-prolyl cis-trans isomerase fkpA	-1,28	-1,11	-2,76
SL3421	<i>slyX</i>	Protein slyX	1,15	1,18	-1,44
SL3422	<i>slyD</i>	FKBP-type peptidyl-prolyl cis-trans isomerase slyD	-1,09	-1,14	1,20
SL3423	<i>yheV</i>	Uncharacterized protein yheV	1,00	1,04	1,36
SL3424	<i>kefB</i>	Glutathione-regulated potassium-efflux system protein kefB	-1,06	1,09	1,04
SL3425	<i>kefG</i>	Glutathione-regulated potassium-efflux system ancillary protein kefG	-1,08	1,31	1,23
SL3426	<i>yheS</i>	Uncharacterized ABC transporter ATP-binding protein yheS	-1,06	-1,12	-1,43
SL3427	-	ABC Transporter ATPase	1,05	1,01	2,68
SL3428	<i>ydhR</i>	Putative monooxygenase ydhR	1,17	1,08	2,59
SL3429	<i>yheT</i>	Putative esterase yheT	-1,03	-1,18	-1,19
SL3430	<i>yheU</i>	UPF0270 protein yheU	1,15	1,10	-1,10

Tabla Suplementaria 1

Diferencia de expresión de todos los genes de SV5015 en las cepas mutantes *greA*, *greB* y *greAgreB*, respecto a la cepa WT

ID	gene	Description	<i>greA</i> vs WT	<i>greB</i> vs WT	<i>greAgreB</i> vs WT
SL3431	<i>prkB</i>	Probable phosphoribulokinase	1,06	-1,03	1,07
SL3432	<i>yhfA</i>	Protein yhfA	1,21	1,18	-1,19
SL3433	<i>crp</i>	Catabolite gene activator	-1,04	-1,17	1,36
SL3434	<i>yhfK</i>	Uncharacterized protein yhfK	1,20	1,03	1,21
SL3435	<i>argD</i>	Acetylornithine/succinyldiaminopimelate aminotransferase	1,04	-1,02	-1,17
SL3436	<i>pabA</i>	Para-aminobenzoate synthase glutamine amidotransferase component II	1,04	1,06	-1,29
SL3437	<i>fic</i>	Probable adenosine monophosphate-protein transferase fic	1,20	1,17	2,17
SL3438	<i>yhfG</i>	Uncharacterized protein yhfG	1,03	1,16	1,79
SL3439	<i>ppiA</i>	Peptidyl-prolyl cis-trans isomerase A	1,14	1,03	-1,43
SL3440	<i>tsgA</i>	Protein tsgA	-1,26	1,12	-2,99
SL3441	<i>nirB</i>	Nitrite reductase [NAD(P)H] large subunit	-1,07	1,83	-3,09
SL3442	<i>nirD</i>	Nitrite reductase [NAD(P)H] small subunit	1,11	1,18	-6,95
SL3443	<i>nirC</i>	Probable nitrite transporter	1,18	1,04	-5,91
SL3444	<i>cysG</i>	Siroheme synthase	1,23	1,22	-1,43
SL3445	<i>bigA</i>	Putative surface-exposed virulence protein BigA	-1,05	1,21	-1,05
SL3447	<i>yhfL</i>	Uncharacterized protein yhfL	1,04	-1,07	1,08
SL3448	<i>trpS</i>	Tryptophanyl-tRNA synthetase	-1,00	-1,19	1,24
SL3449	<i>gph</i>	Phosphoglycolate phosphatase	1,04	-1,27	1,41
SL3450	<i>rpe</i>	Ribulose-phosphate 3-epimerase	1,20	-1,03	1,73
SL3451	<i>dam</i>	DNA adenine methylase	1,08	1,02	-1,44
SL3452	<i>damX</i>	Protein damX	1,02	-1,01	-1,07
SL3453	<i>aroB</i>	3-dehydroquinate synthase	1,04	1,00	-1,47
SL3454	<i>aroK</i>	Shikimate kinase 1	-1,05	1,01	-1,65
SL3455	<i>hofQ</i>	Protein transport protein hofQ	1,04	-1,06	1,25
SL3456	<i>yrfA</i>	Uncharacterized protein yrfA	-1,06	1,19	2,46
SL3457	<i>yrfB</i>	Uncharacterized protein yrfB	-1,09	-1,15	1,22
SL3458	<i>yrfC</i>	Uncharacterized protein yrfC	-1,00	-1,17	1,82
SL3459	<i>yrfD</i>	Uncharacterized protein yrfD	1,07	-1,11	1,24
SL3460	<i>mrcA</i>	Penicillin-binding protein 1A	-1,02	1,05	1,15
SL3461	<i>nudE</i>	ADP compounds hydrolase nudE	1,26	1,16	-1,44
SL3462	<i>yrfF</i>	Putative membrane protein igaA homolog	1,02	1,06	-1,63
SL3463	<i>yrfG</i>	Uncharacterized protein yrfG	1,03	1,02	-1,35
SL3464	<i>hslR</i>	Heat shock protein 15	1,09	1,09	1,06
SL3465	<i>hslO</i>	33 kDa chaperonin	1,19	-1,00	1,18
SL3466	<i>yhgE</i>	Uncharacterized protein yhgE	1,01	-1,01	-1,16
SL3467	<i>pckA</i>	Phosphoenolpyruvate carboxykinase [ATP]	1,09	1,02	1,83
SL3468	<i>envZ</i>	Osmolarity sensor protein envZ	-1,07	-1,61	-2,23
SL3469	<i>ompR</i>	Transcriptional regulatory protein ompR	-1,01	-1,61	-1,66
SL3470	<i>greB</i>	Transcription elongation factor greB	1,06	-22,80	-59,94
SL3471	<i>yhgF</i>	Protein yhgF	-1,23	2,01	-1,52
SL3472	<i>feoA</i>	Ferrous iron transport protein A	-1,03	1,53	-3,17
SL3473	<i>feoB</i>	Ferrous iron transport protein B	-1,06	1,43	-3,20
SL3474	<i>feoC</i>	Ferrous iron transport protein C	-1,20	1,24	-2,73
SL3475	<i>yfcl</i>	Uncharacterized protein yfcl	1,11	1,08	1,36
SL3476	<i>bioH</i>	Carboxylesterase BioH	1,06	-1,05	1,02
SL3477	<i>gntX</i>	Protein gntX	-1,06	-1,35	1,60

Tabla Suplementaria 1

Diferencia de expresión de todos los genes de SV5015 en las cepas mutantes *greA*, *greB* y *greAgreB*, respecto a la cepa WT

ID	gene	Description	<i>greA</i> vs WT	<i>greB</i> vs WT	<i>greAgreB</i> vs WT
SL3478	<i>nfuA</i>	Fe/S biogenesis protein nfuA	-1,09	1,10	1,58
SL3479	<i>gntT</i>	High-affinity gluconate transporter	1,06	-1,22	2,22
SL3480	<i>malQ</i>	4-alpha-gluconotransferase	1,13	-1,11	-1,38
SL3481	<i>malP</i>	Maltodextrin phosphorylase	-1,20	-1,30	-1,12
SL3482	<i>malT</i>	HTH-type transcriptional regulator malT	1,22	1,26	5,14
SL3483	<i>yafQ</i>	Uncharacterized protein yafQ	1,27	1,24	1,97
SL3484	<i>dinJ</i>	DNA-damage-inducible protein J	1,04	1,37	2,15
SL3485	<i>rtcA</i>	Probable RNA 3'-terminal phosphate cyclase	-1,07	1,48	1,57
SL3486	<i>rtcB</i>	Protein rtcB	-1,08	1,43	1,15
SL3487	<i>rsr</i>	60 kDa SS-A/Ro ribonucleoprotein homolog	-1,06	1,27	-1,48
SL3488	<i>rtcR</i>	Transcriptional regulatory protein rtcR	1,22	1,02	1,33
SL3489	<i>glpR</i>	Glycerol-3-phosphate regulon repressor	1,24	1,06	-1,34
SL3490	<i>glpR</i>	Glycerol-3-phosphate regulon repressor	-1,04	-1,18	-1,84
SL3491	<i>glpG</i>	Rhomboid protease glpG	-1,03	-1,07	-2,04
SL3492	<i>glpE</i>	Thiosulfate sulfurtransferase glpE	-1,16	-1,10	-1,50
SL3493	<i>glpD</i>	Aerobic glycerol-3-phosphate dehydrogenase	-1,04	1,03	-1,26
SL3494	<i>ybbD</i>	Hypothetical	1,14	-1,06	-1,01
SL3495	<i>pstS1</i>	Phosphate-binding protein pstS 1	1,13	1,12	1,20
SL3496	<i>gldA</i>	Glycerol dehydrogenase	1,11	1,21	1,77
SL3497	<i>ttuB</i>	Putative tartrate transporter	1,09	1,05	2,60
SL3498	<i>ilvD</i>	Dihydroxy-acid dehydratase	1,02	1,08	3,10
SL3499	<i>yjhH</i>	Uncharacterized protein yjhH	1,14	1,00	1,97
SL3500	<i>yfaX</i>	Uncharacterized HTH-type transcriptional regulator yfaX	1,21	1,01	1,63
SL3501	<i>glgP</i>	Glycogen phosphorylase	1,13	1,02	1,04
SL3502	<i>glgA</i>	Glycogen synthase	1,17	1,09	1,32
SL3503	<i>glgC</i>	Glucose-1-phosphate adenylyltransferase	1,25	1,15	2,20
SL3504	<i>glgX</i>	Glycogen debranching enzyme	1,17	-1,13	2,04
SL3505	<i>glgB</i>	1,4-alpha-glucon-branching enzyme	1,20	-1,03	2,35
SL3506	<i>asd</i>	Aspartate-semialdehyde dehydrogenase	1,08	-1,30	1,45
SL3507	<i>gntU</i>	Low-affinity gluconate transporter	1,00	1,03	-1,61
SL3508	<i>gntK</i>	Thermoresistant gluconokinase	1,02	-1,24	-1,84
SL3509	<i>gntR</i>	HTH-type transcriptional regulator gntR	1,10	1,13	-1,14
SL3510	<i>yhhW</i>	Protein yhhW	1,23	1,22	1,35
SL3511	<i>yhhX</i>	Uncharacterized oxidoreductase yhhX	1,20	1,01	1,09
SL3512	<i>yhhY</i>	Uncharacterized N-acetyltransferase yhhY	-1,08	-1,11	-1,09
SL3513	<i>rbsK</i>	Ribokinase	-1,18	1,03	-2,44
SL3514	-	Hypothetical	-1,08	1,27	-3,60
SL3515	-	Hypothetical	-1,08	-1,01	-2,67
SL3516	<i>php</i>	Phosphotriesterase homology protein	1,01	-1,07	-2,76
SL3517	<i>ggt</i>	Gamma-glutamyltranspeptidase	1,08	1,06	1,29
SL3518	<i>yhhA</i>	Uncharacterized protein yhhA	1,13	1,56	2,39
SL3519	<i>ugpQ</i>	Glycerophosphoryl diester phosphodiesterase	1,18	1,30	2,41
SL3520	<i>ugpC</i>	sn-glycerol-3-phosphate import ATP-binding protein UgpC	1,20	-1,48	4,06
SL3521	<i>ugpE</i>	sn-glycerol-3-phosphate transport system permease protein ugpE	1,12	-1,72	3,15

Tabla Suplementaria 1

Diferencia de expresión de todos los genes de SV5015 en las cepas mutantes *greA*, *greB* y *greAgreB*, respecto a la cepa WT

ID	gene	Description	<i>greA</i> vs WT	<i>greB</i> vs WT	<i>greAgreB</i> vs WT
SL3522	<i>ugpA</i>	sn-glycerol-3-phosphate transport system permease protein <i>ugpA</i>	1,32	-1,43	3,48
SL3523	<i>ugpB</i>	sn-glycerol-3-phosphate-binding periplasmic protein <i>ugpB</i>	1,27	1,10	12,09
SL3524	-	Death On Curing Protein	1,38	1,12	4,53
SL3525	<i>yhhV</i>	Uncharacterized protein <i>yhhV</i>	1,35	1,25	4,30
SL3526	<i>livF</i>	High-affinity branched-chain amino acid transport ATP-binding protein <i>livF</i>	-1,11	-1,23	1,18
SL3527	<i>livG</i>	High-affinity branched-chain amino acid transport ATP-binding protein <i>livG</i>	1,15	-1,02	1,46
SL3528	<i>livM</i>	High-affinity branched-chain amino acid transport system permease protein <i>livM</i>	1,17	1,10	1,34
SL3529	<i>livH</i>	High-affinity branched-chain amino acid transport system permease protein <i>livH</i>	1,05	1,02	1,40
SL3530	<i>livK</i>	Leucine-specific-binding protein	1,17	-1,03	1,58
SL3531	<i>yhhK</i>	Uncharacterized protein <i>yhhK</i>	1,08	1,20	-1,11
SL3532	<i>livJ</i>	Leu/Ile/Val-binding protein	-1,06	1,01	2,72
SL3533	<i>rpoH</i>	RNA polymerase sigma-32 factor	1,09	1,05	-1,16
SL3534	<i>ftsX</i>	Cell division protein <i>ftsX</i>	1,16	1,03	-1,17
SL3535	<i>ftsE</i>	Cell division ATP-binding protein <i>ftsE</i>	-1,01	-1,06	-1,65
SL3536	<i>ftsY</i>	Cell division protein <i>ftsY</i>	1,05	1,09	-2,07
SL3537	<i>rsmD</i>	Ribosomal RNA small subunit methyltransferase D	1,15	-1,06	-1,13
SL3538	<i>yhhL</i>	Uncharacterized protein <i>yhhL</i>	1,03	-1,05	1,06
SL3539	<i>yhhM</i>	Uncharacterized protein <i>yhhM</i>	-1,03	-1,10	1,03
SL3540	<i>yhhN</i>	Uncharacterized membrane protein <i>yhhN</i>	1,19	1,35	-1,05
SL3541	<i>zntA</i>	Lead, cadmium, zinc and mercury-transporting ATPase	-1,06	1,04	3,05
SL3542	<i>tcp</i>	Methyl-accepting chemotaxis citrate transducer	1,12	1,11	-2,21
SL3543	<i>tusA</i>	Sulfurtransferase <i>tusA</i>	-1,02	-1,15	-11,47
SL3544	<i>yhhQ</i>	Inner membrane protein <i>yhhQ</i>	-1,29	1,01	-4,91
SL3545	<i>dcrB</i>	Protein <i>dcrB</i>	1,06	1,12	1,00
SL3546	<i>yhhS</i>	UPF0226 membrane protein SEN3404	1,78	1,40	1,31
SL3547	<i>yhhT</i>	UPF0118 inner membrane protein <i>yhhT</i>	-1,01	1,00	1,20
SL3548	<i>acpT</i>	4'-phosphopantetheinyl transferase <i>AcpT</i>	1,09	1,04	-1,20
SL3549	<i>nikR</i>	Nickel-responsive regulator	1,05	-1,15	-1,22
SL3550	<i>yhhJ</i>	Inner membrane transport permease <i>yhhJ</i>	1,11	1,06	1,42
SL3551	<i>yhiH</i>	Uncharacterized ABC transporter ATP-binding protein <i>yhiH</i>	1,05	1,06	1,02
SL3552	<i>yhil</i>	Uncharacterized protein <i>yhil</i>	1,18	1,31	2,20
SL3553	<i>yhiN</i>	Uncharacterized protein <i>yhiN</i>	1,13	1,13	-1,15
SL3554	<i>pitA</i>	Low-affinity inorganic phosphate transporter 1	-1,11	1,02	-1,94
SL3555	<i>uspB</i>	Universal stress protein B	1,18	1,24	2,84
SL3556	<i>uspA</i>	Universal stress protein A	1,17	1,22	1,87
SL3557	<i>dtpB</i>	Dipeptide and tripeptide permease B	1,53	1,11	3,02
SL3558	<i>yhiQ</i>	UPF0341 protein <i>yhiQ</i>	1,16	-1,23	-1,20
SL3559	<i>prlC</i>	Oligopeptidase A	1,01	-1,10	-2,03
SL3560	<i>phoC</i>	Major phosphate-irrepressible acid phosphatase	-1,39	1,43	-1,61
SL3561	<i>yhiR</i>	Uncharacterized protein <i>yhiR</i>	1,04	1,01	-2,11
SL3562	<i>gor</i>	Glutathione reductase	1,06	-1,03	-1,25

Tabla Suplementaria 1

Diferencia de expresión de todos los genes de SV5015 en las cepas mutantes *greA*, *greB* y *greAgreB*, respecto a la cepa WT

ID	gene	Description	<i>greA</i> vs WT	<i>greB</i> vs WT	<i>greAgreB</i> vs WT
SL3563	<i>ansB</i>	L-asparaginase	1,21	-1,48	32,54
SL3564	<i>dcuB</i>	Anaerobic C4-dicarboxylate transporter <i>dcuB</i>	1,27	-1,59	55,06
SL3565	<i>frlD</i>	Fructosamine kinase <i>frlD</i>	-1,09	-1,71	33,42
SL3566	<i>frlB</i>	Fructosamine deglycase <i>frlB</i>	1,36	-1,39	33,98
SL3567	<i>yvoA</i>	HTH-type transcriptional repressor <i>yvoA</i>	-1,22	1,02	1,81
SL3568	<i>treF</i>	Cytoplasmic trehalase	-1,04	1,07	-1,18
SL3569	-	Hypothetical	1,19	1,25	3,95
SL3570	-	Conserved Hypothetical Protein	-1,27	1,16	-1,38
SL3571	<i>yhjB</i>	Putative HTH-type transcriptional regulator <i>yhjB</i>	-1,50	1,26	-3,03
SL3572	<i>yhjC</i>	Uncharacterized HTH-type transcriptional regulator <i>yhjC</i>	1,07	-1,06	2,24
SL3573	<i>yhjD</i>	Inner membrane protein <i>yhjD</i>	-1,04	-1,11	1,18
SL3574	<i>yhjE</i>	Inner membrane metabolite transport protein <i>yhjE</i>	1,03	-1,05	1,26
SL3575	<i>yhjG</i>	Uncharacterized protein <i>yhjG</i>	1,15	1,14	1,60
SL3576	<i>yhjH</i>	Cyclic di-GMP phosphodiesterase <i>YhjH</i>	-1,44	1,20	-5,37
SL3577	<i>kdgK</i>	2-dehydro-3-deoxygluconokinase	1,12	-1,08	4,32
SL3578	<i>yhjJ</i>	Protein <i>yhjJ</i>	-1,09	-1,03	-1,58
SL3579	<i>dctA</i>	C4-dicarboxylate transport protein	-1,06	-1,17	14,63
SL3580	<i>yhjK</i>	Protein <i>YhjK</i>	1,24	1,26	-1,14
SL3581	<i>bcsC</i>	Cellulose synthase operon protein C	1,05	1,15	1,52
SL3582	<i>bcsZ</i>	Endoglucanase	1,04	-1,05	1,26
SL3583	<i>bcsB</i>	Cyclic di-GMP-binding protein	1,05	1,03	1,43
SL3584	<i>bcsA</i>	Cellulose synthase catalytic subunit [UDP-forming]	1,03	-1,05	-1,13
SL3585	<i>yhjQ</i>	Uncharacterized protein <i>yhjQ</i>	-1,10	1,03	1,17
SL3586	<i>yhjR</i>	Uncharacterized protein <i>yhjR</i>	-1,14	1,05	1,44
SL3587	<i>yhjS</i>	Uncharacterized protein <i>yhjS</i>	1,06	1,02	-1,15
SL3588	<i>yhjT</i>	Uncharacterized protein <i>yhjT</i>	1,15	1,07	1,02
SL3589	<i>yhjU</i>	Uncharacterized protein <i>yhjU</i>	1,12	-1,07	-1,15
SL3590	-	Hypothetical Protein SL3590	1,75	1,19	-1,82
SL3591	<i>yhjV</i>	Inner membrane transport protein <i>yhjV</i>	-1,12	1,08	-1,37
SL3592	<i>dppF</i>	Dipeptide transport ATP-binding protein <i>dppF</i>	1,36	-1,21	1,31
SL3593	<i>dppD</i>	Dipeptide transport ATP-binding protein <i>dppD</i>	1,21	-1,35	1,11
SL3594	<i>dppC</i>	Dipeptide transport system permease protein <i>dppC</i>	1,01	-1,55	-1,14
SL3595	<i>dppB</i>	Dipeptide transport system permease protein <i>dppB</i>	-1,01	-1,46	-1,12
SL3596	<i>dppA</i>	Periplasmic dipeptide transport protein	1,12	1,02	3,36
SL3597	<i>puck</i>	Uric acid permease <i>puck</i>	-1,06	-1,03	1,16
SL3598	-	Hypothetical	-1,38	-1,04	-2,34
SL3599	<i>celR</i>	HTH-type transcriptional regulator <i>celR</i>	-1,08	-1,03	-1,87
SL3600	<i>eptB</i>	Phosphoethanolamine transferase <i>eptB</i>	1,22	-1,11	-1,14
SL3601	<i>lpfE</i>	Protein <i>lpfE</i>	1,05	1,02	-1,41
SL3602	<i>lpfD</i>	Protein <i>lpfD</i>	1,02	1,13	-1,49
SL3603	<i>lpfD</i>	Protein <i>lpfD</i>	1,20	1,19	-1,39
SL3604	<i>lpfC</i>	Outer membrane usher protein <i>lpfC</i>	1,04	1,00	-1,06
SL3605	<i>lpfB</i>	Chaperone protein <i>lpfB</i>	-1,23	-1,01	-1,51

Tabla Suplementaria 1

Diferencia de expresión de todos los genes de SV5015 en las cepas mutantes *greA*, *greB* y *greAgreB*, respecto a la cepa WT

ID	gene	Description	<i>greA</i> vs WT	<i>greB</i> vs WT	<i>greAgreB</i> vs WT
SL3606	<i>lpfA</i>	Long polar fimbria protein A	-1,01	1,01	1,37
SL3607	<i>yhjY</i>	Uncharacterized protein yhjY	1,40	1,22	1,62
SL3608	<i>tag</i>	DNA-3-methyladenine glycosylase 1	1,17	-1,05	2,24
SL3609	<i>yiaC</i>	Uncharacterized N-acetyltransferase yiaC	1,15	-1,16	2,67
SL3610	<i>bisC</i>	Biotin sulfoxide reductase	1,13	-1,03	1,22
SL3611	<i>yiaD</i>	Inner membrane lipoprotein yiaD	1,04	1,14	-1,05
SL3612	<i>ghrB</i>	Glyoxylate/hydroxypyruvate reductase B	1,26	1,11	2,04
SL3613	<i>yiaF</i>	Uncharacterized protein yiaF	1,03	-1,02	1,25
SL3614	<i>yiaG</i>	Uncharacterized HTH-type transcriptional regulator yiaG	-1,01	-1,08	1,04
SL3615	<i>cspA</i>	Cold shock protein cspA	-1,20	-1,57	-2,91
SL3616	-	Hypothetical	-1,20	-1,12	-1,35
SL3617	-	GCN5-Related N-Acetyltransferase	-1,10	-1,24	-1,11
SL3618	-	Hypothetical	-1,06	-1,29	1,08
SL3619	<i>yafP</i>	Uncharacterized N-acetyltransferase yafP	-1,56	-1,18	-1,27
SL3620	<i>glyS</i>	Glycyl-tRNA synthetase beta subunit	1,12	-1,22	1,44
SL3621	<i>glyQ</i>	Glycyl-tRNA synthetase alpha subunit	1,05	1,04	-1,06
SL3622	<i>ysaB</i>	Uncharacterized lipoprotein ysaB	1,13	1,04	1,05
SL3623	<i>yiaH</i>	Inner membrane protein yiaH	-1,03	1,20	-1,18
SL3624	<i>yiaB</i>	Hypothetical	1,14	1,35	-1,30
SL3625	<i>xylB</i>	Xylulose kinase	1,11	1,10	2,26
SL3626	<i>xylA</i>	Xylose isomerase	-1,06	-1,04	2,26
SL3627	<i>xylR</i>	Xylose operon regulatory protein	-1,07	-1,01	1,05
SL3628	<i>bax</i>	Protein bax	-1,39	1,03	-9,21
SL3629	<i>malS</i>	Alpha-amylase	-1,19	-1,41	-1,72
SL3630	<i>avtA</i>	Valine--pyruvate aminotransferase	1,04	1,23	-1,04
SL3631	<i>ysaA</i>	Putative electron transport protein ysaA	1,28	1,09	1,85
SL3632	<i>yiaJ</i>	HTH-type transcriptional regulator yiaJ	1,17	-1,09	1,12
SL3633	<i>dlgD</i>	2,3-diketo-L-gulonate reductase	1,01	-1,07	4,51
SL3634	<i>yiaL</i>	Protein yiaL	1,49	1,24	1,71
SL3635	-	Hypothetical	1,09	1,12	2,38
SL3636	<i>yiaM</i>	2,3-diketo-L-gulonate TRAP transporter small permease protein yiaM	-1,20	-1,30	1,42
SL3637	<i>yiaN</i>	2,3-diketo-L-gulonate TRAP transporter large permease protein yiaN	-1,05	-1,38	2,40
SL3638	<i>yiaO</i>	2,3-diketo-L-gulonate-binding periplasmic protein yiaO	1,36	1,16	4,21
SL3639	<i>lyx</i>	L-xylulose/3-keto-L-gulonate kinase	1,14	1,11	2,70
SL3640	<i>sgbH</i>	3-keto-L-gulonate-6-phosphate decarboxylase sgbH	1,01	1,11	1,51
SL3641	<i>sgbU</i>	Putative L-ribulose-5-phosphate 3-epimerase sgbU	1,45	1,69	3,77
SL3642	<i>sgbE</i>	L-ribulose-5-phosphate 4-epimerase sgbE	1,07	1,33	1,93
SL3643	<i>yisR</i>	Uncharacterized HTH-type transcriptional regulator yisR	1,24	-1,19	4,41
SL3644	-	Hypothetical	1,18	-1,02	4,20
SL3645	<i>aldB</i>	Aldehyde dehydrogenase B	1,01	1,23	2,38
SL3646	<i>yajF</i>	Uncharacterized protein CPE0188	1,16	-1,04	1,47
SL3647	<i>selB</i>	Selenocysteine-specific elongation factor	-1,02	-1,04	1,24
SL3648	<i>selA</i>	L-seryl-tRNA(Sec) selenium transferase	1,30	1,25	1,52
SL3649	<i>yibF</i>	Uncharacterized GST-like protein yibF	1,10	1,09	2,65

Tabla Suplementaria 1

Diferencia de expresión de todos los genes de SV5015 en las cepas mutantes *greA*, *greB* y *greAgreB*, respecto a la cepa WT

ID	gene	Description	<i>greA</i> vs WT	<i>greB</i> vs WT	<i>greAgreB</i> vs WT
SL3650	<i>mtIA</i>	PTS system mannitol-specific EIICBA component	1,02	-1,03	3,05
SL3651	<i>mtID</i>	Mannitol-1-phosphate 5-dehydrogenase	1,16	1,20	1,95
SL3652	<i>mtIR</i>	Mannitol operon repressor	1,20	1,06	1,57
SL3653	<i>yibT</i>	Uncharacterized protein yibT	1,13	1,35	5,71
SL3654	<i>yibL</i>	Uncharacterized protein yibL	1,24	1,27	1,29
SL3655	-	Hypothetical	-1,00	1,02	1,20
SL3656	<i>yadA</i>	Adhesin yadA	1,10	1,17	1,97
SL3657	<i>lldP</i>	L-lactate permease	-1,29	-1,01	1,85
SL3658	<i>lldR</i>	Putative L-lactate dehydrogenase operon regulatory protein	-1,51	-1,00	2,62
SL3659	<i>lldD</i>	L-lactate dehydrogenase [cytochrome]	-1,46	-1,28	3,49
SL3660	<i>yibK</i>	Uncharacterized tRNA/rRNA methyltransferase yibK	1,16	-1,13	-1,22
SL3661	<i>idnR</i>	HTH-type transcriptional regulator idnR	-1,07	1,06	-1,58
SL3662	<i>mdIA</i>	Mandelate racemase	1,18	1,01	4,34
SL3663	<i>gudP</i>	Probable glucarate transporter	1,43	1,22	4,44
SL3664	-	MFS Transporter ACS Family Glucarate Transporter	1,26	1,18	1,32
SL3665	<i>cysE</i>	Serine acetyltransferase	1,17	-1,08	1,18
SL3666	<i>gpsA</i>	Glycerol-3-phosphate dehydrogenase [NAD(P)+]	1,10	-1,12	1,76
SL3667	<i>secB</i>	Protein-export protein secB	1,01	-1,10	1,68
SL3668	<i>grxC</i>	Glutaredoxin-3	1,17	1,04	1,35
SL3669	<i>yibN</i>	Uncharacterized protein yibN	1,01	1,01	1,35
SL3670	<i>gpml</i>	2,3-bisphosphoglycerate-independent phosphoglycerate mutase	-1,03	1,15	-3,23
SL3671	<i>yibP</i>	Uncharacterized protein yibP	-1,07	-1,17	-2,15
SL3672	<i>yibQ</i>	Uncharacterized protein yibQ	1,06	-1,12	-1,51
SL3673	<i>yibD</i>	Uncharacterized glycosyltransferase yibD	1,21	1,20	-1,75
SL3674	<i>tdh</i>	L-threonine 3-dehydrogenase	1,25	-1,10	3,79
SL3675	<i>kbl</i>	Putative 8-amino-7-oxononanoate synthase/2-amino-3-ketobutyrate coenzyme A ligase	1,06	-1,25	2,94
SL3676	<i>hldD</i>	ADP-L-glycero-D-manno-heptose-6-epimerase	1,23	1,05	1,15
SL3677	<i>rfaF</i>	ADP-heptose--LPS heptosyltransferase 2	1,22	-1,06	-1,25
SL3678	<i>rfaC</i>	Lipopolysaccharide heptosyltransferase 1	1,03	-1,22	-1,52
SL3679	<i>rfaL</i>	O-antigen ligase	1,05	-1,12	-1,69
SL3680	<i>waaK</i>	Lipopolysaccharide 1,2-N-acetylglucosaminetransferase	-1,13	-1,02	-1,32
SL3681	<i>rfaZ</i>	Lipopolysaccharide core biosynthesis protein rfaZ	-1,08	1,02	-1,55
SL3682	<i>rfaY</i>	Lipopolysaccharide core heptose(II) kinase rfaY	-1,19	-1,21	-1,46
SL3683	<i>rfaJ</i>	Lipopolysaccharide 1,2-glucosyltransferase	-1,13	1,05	1,04
SL3684	<i>rfaI</i>	Lipopolysaccharide 1,3-galactosyltransferase	-1,29	-1,02	-1,23
SL3685	<i>rfaB</i>	Lipopolysaccharide 1,6-galactosyltransferase	-1,13	1,07	-1,41
SL3686	<i>yibR</i>	Uncharacterized protein yibR	1,03	1,09	-1,10
SL3687	<i>rfaP</i>	Lipopolysaccharide core heptose(I) kinase rfaP	-1,00	1,01	-1,17

Tabla Suplementaria 1

Diferencia de expresión de todos los genes de SV5015 en las cepas mutantes *greA*, *greB* y *greAgreB*, respecto a la cepa WT

ID	gene	Description	<i>greA</i> vs WT	<i>greB</i> vs WT	<i>greAgreB</i> vs WT
SL3688	<i>rfaG</i>	Lipopolysaccharide core biosynthesis protein rfaG	-1,03	1,06	-1,58
SL3689	<i>rfaQ</i>	Lipopolysaccharide core heptosyltransferase rfaQ	-1,02	-1,01	-2,00
SL3690	<i>waaA</i>	3-deoxy-D-manno-octulosonic-acid transferase	-1,02	-1,06	-1,20
SL3691	<i>coaD</i>	Phosphopantetheine adenylyltransferase	-1,07	-1,08	-1,13
SL3692	<i>mutM</i>	Formamidopyrimidine-DNA glycosylase	1,10	-1,13	1,30
SL3693	<i>rpmG</i>	50S ribosomal protein L33	-1,22	-1,15	-1,66
SL3694	<i>rpmB</i>	50S ribosomal protein L28	-1,17	-1,08	-1,52
SL3695	<i>yicR</i>	UPF0758 protein yicR	-1,04	1,06	3,41
SL3696	<i>coaBC</i>	Coenzyme A biosynthesis bifunctional protein coaBC	1,06	1,03	-1,43
SL3697	<i>dut</i>	Deoxyuridine 5'-triphosphate nucleotidohydrolase	1,04	-1,17	-1,22
SL3698	<i>slmA</i>	HTH-type protein slmA	1,06	-1,18	-1,22
SL3699	<i>pyrE</i>	Orotate phosphoribosyltransferase	1,22	-1,17	1,04
SL3700	<i>rph</i>	Ribonuclease PH	1,16	1,06	-2,20
SL3701	<i>yicC</i>	UPF0701 protein yicC	-1,05	-1,02	-1,31
SL3702	<i>ybeF</i>	LysR Family Transcriptional Regulator	1,15	1,10	1,01
SL3703	<i>ycbL</i>	Metallo-beta-lactamase L1	1,29	-1,10	2,03
SL3704	<i>yicG</i>	UPF0126 inner membrane protein yicG	1,20	1,15	-3,47
SL3705	<i>ligB</i>	DNA ligase B	1,16	-1,05	1,50
SL3706	<i>gmk</i>	Guanylate kinase	1,02	-1,02	-1,31
SL3707	<i>rpoZ</i>	DNA-directed RNA polymerase subunit omega	1,02	1,01	-1,17
SL3708	<i>spoT</i>	Guanosine-3',5'-bis(diphosphate) 3'-pyrophosphohydrolase	1,01	-1,03	-1,35
SL3709	<i>trmH</i>	tRNA guanosine-2'-O-methyltransferase	1,33	1,12	-1,01
SL3710	<i>recG</i>	ATP-dependent DNA helicase recG	1,16	1,01	1,07
SL3711	-	Cytoplasmic Protein	1,50	-1,09	5,37
SL3712	<i>gltS</i>	Sodium/glutamate symport carrier protein	1,44	1,03	5,98
SL3713	<i>xanP</i>	Xanthine permease XanP	1,26	1,27	1,11
SL3714	<i>yicH</i>	Uncharacterized protein yicH	1,11	-1,08	2,92
SL3715	<i>yicI</i>	Alpha-xylosidase	1,25	1,16	1,98
SL3716	<i>yicJ</i>	Inner membrane symporter yicJ	1,23	-1,03	2,54
SL3717	-	Hypothetical	1,14	1,45	1,06
SL3718	-	Hypothetical	1,15	1,13	1,96
SL3719	-	Hypothetical	1,54	1,07	1,50
SL3720	-	Hypothetical	1,02	1,06	1,59
SL3721	-	Hypothetical Protein SL3721	1,06	1,02	1,16
SL3722	<i>yqeH</i>	Uncharacterized protein yqeH	-1,02	-1,00	-1,09
SL3723	<i>yuaQ</i>	Uncharacterized protein yuaQ	-1,03	1,04	1,72
SL3724	<i>yqeJ</i>	Uncharacterized protein yqeJ	-1,14	1,08	-1,10
SL3725	<i>yqeI</i>	Uncharacterized protein yqeI	1,18	1,05	-1,40
SL3726	<i>ycaC</i>	Uncharacterized protein ycaC	1,41	1,43	-1,31
SL3727	-	Hypothetical	-1,20	1,15	-1,14
SL3728	<i>mgtB</i>	Magnesium-transporting ATPase, P-type 1	-1,69	1,21	-4,80
SL3729	<i>mgtC</i>	Protein mgtC	-1,98	1,06	-24,09
SL3730	<i>yicL</i>	Uncharacterized inner membrane transporter yicL	-1,04	-1,10	-1,08
SL3731	<i>yfcl</i>	Uncharacterized protein yfcl	-1,03	1,11	1,97

Tabla Suplementaria 1

Diferencia de expresión de todos los genes de SV5015 en las cepas mutantes *greA*, *greB* y *greAgreB*, respecto a la cepa WT

ID	gene	Description	<i>greA</i> vs WT	<i>greB</i> vs WT	<i>greAgreB</i> vs WT
SL3732	-	Hypothetical	1,12	-1,04	1,45
SL3733	<i>selA</i>	Uncharacterized protein mlr3804	1,25	1,07	1,61
SL3734	<i>manZ</i>	Mannose permease IID component	1,12	1,23	1,61
SL3735	<i>agaC</i>	N-acetylgalactosamine permease IIC component 1	-1,04	1,05	1,30
SL3736	<i>levE</i>	Fructose-specific phosphotransferase enzyme IIB component	-1,04	1,28	1,42
SL3737	<i>manX</i>	PTS System Fructose Subfamily IIA Component	1,07	1,25	1,20
SL3738	<i>levR</i>	Transcriptional regulatory protein levR	1,15	1,07	2,12
SL3739	<i>yicS</i>	Uncharacterized protein yicS	1,08	1,19	1,22
SL3740	<i>gmuD</i>	6-phospho-beta-glucosidase gmuD	1,31	1,12	2,95
SL3741	<i>nepl</i>	Purine ribonucleoside efflux pump nepl	1,49	1,04	-1,01
SL3742	<i>nepl</i>	Purine ribonucleoside efflux pump nepl	1,26	-1,01	-4,69
SL3743	-	Hypothetical	1,50	1,54	3,57
SL3744	<i>yiaG</i>	Transcriptional Regulator XRE Family	1,35	1,35	3,84
SL3745	<i>ptsH</i>	Conserved Hypothetical Protein	1,45	-1,39	1,17
SL3746	<i>kbaY</i>	D-tagatose-1,6-bisphosphate aldolase subunit kbaY	1,12	-1,15	1,10
SL3747	<i>glpK</i>	Glycerol kinase	1,22	-1,62	-1,07
SL3748	<i>gatC</i>	Galactitol permease IIC component	1,05	-1,02	1,08
SL3749	<i>gatB</i>	Galactitol-specific phosphotransferase enzyme IIB component	1,11	-1,10	1,16
SL3750	<i>gatA</i>	PTS IIA-Like Nitrogen-Regulatory Protein PtsN	1,08	-1,01	1,99
SL3751	<i>mngR</i>	Mannosyl-D-glycerate transport/metabolism system repressor mngR	1,24	1,41	3,65
SL3752	<i>yicN</i>	Uncharacterized protein yicN	-1,14	1,05	1,11
SL3753	<i>uhpT</i>	Hexose phosphate transport protein	-1,82	1,08	1,42
SL3754	<i>uhpC</i>	Regulatory protein uhpC	1,05	-1,02	1,36
SL3755	<i>uhpB</i>	Sensor protein uhpB	-1,24	-1,12	-1,28
SL3756	<i>uhpA</i>	Transcriptional regulatory protein uhpA	-1,11	1,19	-2,39
SL3757	-	Hypothetical	1,24	1,05	3,49
SL3758	<i>fucP</i>	L-fucose-proton symporter	1,25	-1,02	3,39
SL3759	<i>rbsK</i>	Ribokinase	1,14	1,11	3,60
SL3760	<i>deoR</i>	Deoxyribose operon repressor	1,28	-1,00	2,51
SL3761	<i>ilvN</i>	Acetolactate synthase isozyme 1 small subunit	1,53	1,09	4,96
SL3762	<i>ilvB</i>	Acetolactate synthase isozyme 1 large subunit	1,51	1,08	5,91
SL3763	-	Hypothetical Protein SL3763	-1,35	1,19	-1,84
SL3764	-	Hypothetical Protein SL3764	-1,12	-1,42	1,09
SL3765	-	Hypothetical	1,04	-1,00	-1,13
SL3766	<i>emrD</i>	Multidrug resistance protein D	1,14	1,12	-1,94
SL3767	-	Hypothetical	1,23	-1,00	2,32
SL3768	<i>dsdC</i>	HTH-type transcriptional regulator dsdC	1,47	1,01	3,96
SL3769	<i>dsdX</i>	DsdX permease	1,23	1,23	2,10
SL3770	<i>dsdA</i>	D-serine dehydratase	1,35	1,12	1,53
SL3771	<i>yidF</i>	Uncharacterized protein yidF	1,14	1,11	1,26
SL3772	<i>yidG</i>	Inner membrane protein yidG	1,06	-1,11	1,37
SL3773	<i>yidH</i>	Inner membrane protein yidH	-1,13	-1,16	1,28

Tabla Suplementaria 1

Diferencia de expresión de todos los genes de SV5015 en las cepas mutantes *greA*, *greB* y *greAgreB*, respecto a la cepa WT

ID	gene	Description	<i>greA</i> vs WT	<i>greB</i> vs WT	<i>greAgreB</i> vs WT
SL3774	<i>yidE</i>	Putative transport protein CKO_00031	1,42	1,43	5,60
SL3775	<i>ibpB</i>	Small heat shock protein ibpB	-1,03	1,20	1,19
SL3776	<i>ibpA</i>	Small heat shock protein ibpA	1,29	1,47	3,13
SL3777	<i>yidQ</i>	Uncharacterized protein yidQ	1,12	1,01	1,43
SL3778	<i>yidR</i>	Uncharacterized protein yidR	1,01	-1,03	-1,25
SL3779	<i>ccmH</i>	Cytochrome c-type biogenesis protein ccmH	-1,06	-1,18	1,55
SL3780	<i>(dsbE1)</i>	Thiol:disulfide interchange protein dsbE	-1,04	-1,10	1,10
SL3781	<i>ccmF</i>	Cytochrome c-type biogenesis protein ccmF	1,05	1,00	1,13
SL3782	<i>ccmE1</i>	Cytochrome c-type biogenesis protein ccmE 1	1,08	1,15	-1,29
SL3783	<i>ccmC</i>	Heme exporter protein C	1,15	1,14	-1,37
SL3784	<i>ccmB</i>	Heme exporter protein B	-1,16	-1,17	-1,76
SL3785	<i>ccmAE</i>	Putative bifunctional cytochrome c-type biogenesis protein ccmAE	-1,10	-1,05	-1,67
SL3786	<i>yhjA</i>	Probable cytochrome c peroxidase	-1,07	-1,11	-2,69
SL3787	<i>torD</i>	Chaperone protein torD	1,07	-1,04	-1,40
SL3788	<i>torA</i>	Trimethylamine-N-oxide reductase	1,25	1,11	-1,03
SL3789	<i>torC</i>	Cytochrome c-type protein torC	1,30	-1,04	-3,23
SL3790	<i>torR</i>	TorCAD operon transcriptional regulatory protein torR	1,28	-1,04	4,44
SL3791	<i>torT</i>	Periplasmic protein torT	1,10	1,18	-1,04
SL3792	<i>torS</i>	Sensor protein torS	1,02	1,09	-1,15
SL3793	<i>dgoT</i>	D-galactonate transporter	1,67	1,10	2,84
SL3794	<i>dgoD1</i>	D-galactonate dehydratase 1	1,47	1,07	3,20
SL3795	<i>dgoA</i>	2-dehydro-3-deoxy-6-phosphogalactonate aldolase	1,43	1,31	2,97
SL3796	<i>dgoK</i>	2-dehydro-3-deoxygalactonokinase	1,05	-1,14	2,37
SL3797	<i>dgoR</i>	Galactonate operon transcriptional repressor	-1,02	-1,09	2,58
SL3798	<i>yidA</i>	Phosphatase yidA	-1,12	-1,09	-1,43
SL3799	<i>gudP</i>	Probable glucarate transporter	-1,03	-1,11	4,70
SL3800	<i>dgoD</i>	D-galactonate dehydratase	-1,02	1,03	3,13
SL3801	<i>ybhD</i>	Uncharacterized HTH-type transcriptional regulator ybhD	1,43	1,16	4,56
SL3802	<i>gyrB</i>	DNA gyrase subunit B	1,25	1,01	-1,25
SL3803	<i>recF</i>	DNA replication and repair protein recF	1,22	-1,05	-1,14
SL3804	<i>dnaN</i>	DNA polymerase III subunit beta	1,04	-1,06	-1,04
SL3805	<i>dnaA</i>	Chromosomal replication initiator protein dnaA	1,02	1,07	-2,05
SL3806	<i>rpmH</i>	50S ribosomal protein L34	-1,09	1,07	-2,20
SL3807	<i>rnpA</i>	Ribonuclease P protein component	-1,08	1,00	-2,10
SL3808	<i>hlyA</i>	Putative alpha-hemolysin	1,03	1,17	-1,89
SL3809	<i>oxaA</i>	Inner membrane protein oxaA	-1,06	-1,15	-1,97
SL3810	<i>mnmE</i>	tRNA modification GTPase mnmE	1,17	1,06	1,05
SL3811	<i>intA</i>	Prophage CP4-57 integrase	-1,46	-1,21	-1,99
SL3812	-	Inner Membrane Protein	-1,07	-1,24	-1,04
SL3813	-	RNA-directed DNA polymerase from retron EC86	1,13	1,02	1,24
SL3814	<i>mdtL</i>	Multidrug resistance protein mdtL	1,00	-1,06	-3,71
SL3815	<i>yidZ</i>	HTH-type transcriptional regulator yidZ	1,31	1,12	-1,14

Tabla Suplementaria 1

Diferencia de expresión de todos los genes de SV5015 en las cepas mutantes *greA*, *greB* y *greAgreB*, respecto a la cepa WT

ID	gene	Description	<i>greA</i> vs WT	<i>greB</i> vs WT	<i>greAgreB</i> vs WT
SL3816	<i>yieE</i>	Uncharacterized protein yieE	1,11	1,24	1,12
SL3817	<i>yieF</i>	Uncharacterized protein yieF	1,12	1,01	1,77
SL3818	<i>purP</i>	Probable adenine permease PurP	-1,18	1,00	-2,73
SL3819	<i>yieH</i>	Phosphatase yieH	-1,19	-1,09	-1,14
SL3820	<i>phoU</i>	Phosphate transport system protein phoU	1,33	1,41	1,44
SL3821	<i>pstB</i>	Phosphate import ATP-binding protein pstB	1,16	1,39	1,28
SL3822	<i>pstA</i>	Phosphate transport system permease protein pstA	1,29	1,49	1,34
SL3823	<i>pstC</i>	Phosphate transport system permease protein pstC	1,19	1,33	1,12
SL3824	<i>pstS</i>	Phosphate-binding protein pstS	1,01	1,24	-1,35
SL3825	<i>fruA</i>	PTS system fructose-specific EIIBC component	1,11	-1,03	1,58
SL3826	<i>ydiB</i>	Shikimate 5-dehydrogenase-like protein HI_0607	-1,07	-1,52	-1,37
SL3827	<i>sgrR</i>	HTH-type transcriptional regulator sgrR	1,01	-1,23	2,56
SL3828	<i>glmS</i>	Glucosamine--fructose-6-phosphate aminotransferase [isomerizing]	1,09	-1,06	1,67
SL3829	<i>glmU</i>	Bifunctional protein glmU	1,06	-1,08	-1,27
SL3830	-	Hypothetical	1,25	-1,04	1,15
SL3831	<i>atpC</i>	ATP synthase epsilon chain	1,19	1,07	3,56
SL3832	<i>atpD</i>	ATP synthase subunit beta	1,06	-1,12	1,94
SL3833	<i>atpG</i>	ATP synthase gamma chain	1,01	-1,31	2,51
SL3834	<i>atpA</i>	ATP synthase subunit alpha	1,08	-1,18	2,05
SL3835	<i>atpH</i>	ATP synthase subunit delta	-1,05	-1,17	2,01
SL3836	<i>atpF</i>	ATP synthase subunit b	-1,01	-1,14	1,60
SL3837	<i>atpE</i>	ATP synthase subunit c	1,06	-1,03	1,18
SL3838	<i>atpB</i>	ATP synthase subunit a	-1,10	-1,03	-1,38
SL3839	<i>atpI</i>	ATP synthase protein I	-1,12	-1,00	-1,22
SL3840	<i>rsmG</i>	Ribosomal RNA small subunit methyltransferase G	1,11	1,07	-1,02
SL3841	<i>mnmG</i>	tRNA uridine 5-carboxymethylaminomethyl modification enzyme mnmG	-1,01	-1,03	-1,70
SL3842	<i>mioC</i>	Protein mioC	1,08	1,05	-2,43
SL3843	<i>asnC</i>	Regulatory protein AsnC	-1,05	-1,20	1,36
SL3844	<i>asnA</i>	Aspartate--ammonia ligase	1,22	1,01	1,33
SL3845	<i>viaA</i>	Protein viaA	1,27	-1,09	-1,09
SL3846	<i>ravA</i>	ATPase ravA	1,17	-1,00	1,27
SL3847	<i>kup</i>	Low affinity potassium transport system protein kup	1,09	1,20	-1,78
SL3848	<i>rbsD</i>	D-ribose pyranase	-2,94	-1,06	-2,87
SL3849	<i>rbsA1</i>	Ribose import ATP-binding protein RbsA 1	-3,09	-1,10	-2,95
SL3850	<i>rbsC</i>	Ribose transport system permease protein rbsC	-1,26	1,14	-1,57
SL3851	<i>rbsB</i>	D-ribose-binding periplasmic protein	1,20	1,08	2,16
SL3852	<i>rbsK</i>	Ribokinase	1,14	1,02	1,87
SL3853	<i>rbsR</i>	Ribose operon repressor	1,27	-1,00	1,35
SL3854	<i>hsrA</i>	Probable transport protein hsrA	1,41	1,06	1,30
SL3855	<i>hsrA</i>	Probable transport protein hsrA	1,08	-1,00	1,26
SL3856	<i>hsrA</i>	Probable transport protein hsrA	1,29	-1,03	1,71
SL3857	<i>yieP</i>	Uncharacterized HTH-type transcriptional regulator yieP	1,21	-1,02	2,53

Tabla Suplementaria 1

Diferencia de expresión de todos los genes de SV5015 en las cepas mutantes *greA*, *greB* y *greAgreB*, respecto a la cepa WT

ID	gene	Description	<i>greA</i> vs WT	<i>greB</i> vs WT	<i>greAgreB</i> vs WT
SL3858	<i>hdfR</i>	HTH-type transcriptional regulator hdfR	-1,08	-1,32	-1,31
SL3859	<i>yifE</i>	UPF0438 protein yifE	1,10	1,25	1,55
SL3860	<i>yifB</i>	Uncharacterized protein yifB	-1,06	-1,12	-1,00
SL3861	<i>ilvG</i>	Acetolactate synthase isozyme 2 large subunit	-1,19	1,08	3,17
SL3862	<i>ilvM</i>	Acetolactate synthase isozyme 2 small subunit	-1,01	1,08	5,19
SL3863	<i>ilvE</i>	Branched-chain-amino-acid aminotransferase	1,05	-1,06	1,95
SL3864	<i>ilvD</i>	Dihydroxy-acid dehydratase	1,26	-1,03	1,90
SL3865	<i>ilvA</i>	Threonine dehydratase biosynthetic	1,35	-1,06	2,36
SL3866	-	Hypothetical	1,39	1,25	1,32
SL3867	-	Hypothetical	1,40	1,35	1,58
SL3868	<i>ilvY</i>	HTH-type transcriptional regulator ilvY	1,01	1,05	1,85
SL3869	<i>ilvC</i>	Ketol-acid reductoisomerase	1,31	1,17	-1,25
SL3870	<i>ppiC</i>	Peptidyl-prolyl cis-trans isomerase C	1,19	-1,33	-1,35
SL3871	-	Inner Membrane Protein	1,23	-1,17	1,45
SL3872	<i>rep</i>	ATP-dependent DNA helicase rep	1,13	1,08	-1,14
SL3873	<i>gppA</i>	Guanosine-5'-triphosphate,3'-diphosphate pyrophosphatase	-1,03	-1,19	-2,09
SL3874	<i>rhIB</i>	ATP-dependent RNA helicase rhIB	-1,08	-1,34	-2,45
SL3875	<i>trxA</i>	Thioredoxin-1	-1,08	1,03	-1,73
SL3876	<i>rho</i>	Transcription termination factor rho	-1,08	1,01	-3,61
SL3877	<i>wecA</i>	Undecaprenyl-phosphate alpha-N-acetylglucosaminyl 1-phosphate transferase	1,10	1,13	-1,83
SL3878	<i>wzzE</i>	Lipopolysaccharide biosynthesis protein wzzE	1,03	1,14	-1,65
SL3879	<i>wecB</i>	UDP-N-acetylglucosamine 2-epimerase	1,13	-1,03	-1,57
SL3880	<i>wecC</i>	UDP-N-acetyl-D-mannosamine dehydrogenase	1,16	-1,05	-1,04
SL3881	<i>rffG</i>	dTDP-glucose 4,6-dehydratase 2	1,27	1,01	1,15
SL3882	<i>rmlA2</i>	Glucose-1-phosphate thymidyltransferase 2	1,44	1,03	1,21
SL3883	<i>rffC</i>	Lipopolysaccharide biosynthesis protein rffC	1,17	1,00	1,03
SL3884	<i>rffA</i>	Lipopolysaccharide biosynthesis protein rffA	1,17	1,08	1,04
SL3885	<i>wzxE</i>	Protein wzxE	-1,02	-1,18	-1,66
SL3886	<i>wecF</i>	4-alpha-L-fucosyltransferase	-1,00	-1,11	-1,46
SL3887	<i>wzyE</i>	Putative ECA polymerase	1,26	-1,02	-1,03
SL3888	<i>wecG</i>	Probable UDP-N-acetyl-D-mannosaminuronic acid transferase	1,38	1,03	1,38
SL3889	<i>yifK</i>	Probable transport protein yifK	-1,19	-1,24	1,60
SL3890	<i>hemY</i>	Protein hemY	1,13	-1,21	1,19
SL3891	<i>hemX</i>	Putative uroporphyrinogen-III C-methyltransferase	1,04	-1,12	1,07
SL3892	<i>hemD</i>	Uroporphyrinogen-III synthase	1,17	1,06	1,05
SL3893	<i>hemC</i>	Porphobilinogen deaminase	1,21	1,07	1,24
SL3894	<i>cyaA</i>	Adenylate cyclase	-1,09	1,05	-2,83
SL3895	-	Inner Membrane Protein	1,68	-1,13	-1,09
SL3896	-	Hypothetical	1,28	1,27	-1,02
SL3897	-	Hypothetical	1,36	1,14	1,06

Tabla Suplementaria 1

Diferencia de expresión de todos los genes de SV5015 en las cepas mutantes *greA*, *greB* y *greAgreB*, respecto a la cepa WT

ID	gene	Description	<i>greA</i> vs WT	<i>greB</i> vs WT	<i>greAgreB</i> vs WT
SL3898	<i>cyaY</i>	Protein <i>cyaY</i>	1,17	-1,02	1,87
SL3899	-	Hypothetical	1,58	1,44	-1,02
SL3900	<i>yifL</i>	Uncharacterized lipoprotein <i>yifL</i>	1,26	-1,02	1,22
SL3901	<i>dapF</i>	Diaminopimelate epimerase	1,05	-1,06	-1,03
SL3902	<i>yigA</i>	Uncharacterized protein <i>yigA</i>	1,05	-1,09	-1,22
SL3903	<i>xerC</i>	Tyrosine recombinase <i>xerC</i>	-1,10	-1,39	-2,00
SL3904	<i>yigB</i>	Uncharacterized protein <i>yigB</i>	-1,03	-1,26	-1,61
SL3905	<i>uvrD</i>	DNA helicase II	1,03	1,06	-1,16
SL3906	<i>corA</i>	Magnesium transport protein <i>corA</i>	-1,33	1,07	-3,08
SL3907	<i>yigF</i>	Uncharacterized protein <i>yigF</i>	-1,18	1,24	-1,78
SL3908	<i>yigG</i>	Inner membrane protein <i>yigG</i>	1,30	-1,03	-1,57
SL3909	<i>rarD</i>	Protein <i>rarD</i>	1,18	-1,21	-1,16
SL3910	<i>yigI</i>	Uncharacterized protein <i>yigI</i>	1,07	1,31	1,75
SL3911	<i>pldA</i>	Phospholipase A1	1,17	1,01	-1,24
SL3912	<i>recQ</i>	ATP-dependent DNA helicase <i>recQ</i>	1,04	-1,01	-1,48
SL3913	<i>rhtC</i>	Threonine efflux protein	1,01	-1,12	-1,17
SL3914	<i>rhtB</i>	Homoserine/homoserine lactone efflux protein	-1,08	1,14	1,18
SL3915	<i>pldB</i>	Lysophospholipase L2	1,08	-1,08	-1,25
SL3916	<i>yigL</i>	Uncharacterized protein <i>yigL</i>	-1,14	-1,18	-1,39
SL3917	<i>yigM</i>	Uncharacterized membrane protein <i>yigM</i>	-1,10	-1,11	-1,15
SL3918	<i>metR</i>	HTH-type transcriptional regulator <i>metR</i>	-1,10	1,08	-1,14
SL3919	<i>metE</i>	5-methyltetrahydropteroyltryglutamate--homocysteine methyltransferase	-1,17	1,10	1,57
SL3920	<i>aslB</i>	Anaerobic sulfatase-maturing enzyme homolog <i>AslB</i>	1,04	-1,23	1,00
SL3921	<i>ysgA</i>	Putative carboxymethylenebutenolidase	1,12	1,04	1,88
SL3922	<i>udp</i>	Uridine phosphorylase	1,14	1,17	-1,01
SL3923	<i>rmuC</i>	DNA recombination protein <i>rmuC</i>	1,12	1,12	1,55
SL3924	<i>ubiE</i>	Ubiquinone/menaquinone biosynthesis methyltransferase <i>ubiE</i>	1,04	-1,14	1,13
SL3925	<i>yigP</i>	Uncharacterized protein <i>yigP</i>	-1,02	-1,21	1,12
SL3926	<i>ubiB</i>	Probable ubiquinone biosynthesis protein <i>ubiB</i>	1,10	-1,13	-1,04
SL3927	<i>tatA</i>	Sec-independent protein translocase protein <i>tatA</i>	1,04	1,09	-1,31
SL3928	<i>tatB</i>	Sec-independent protein translocase protein <i>tatB</i> homolog	-1,00	-1,02	-1,45
SL3929	<i>tatC</i>	Sec-independent protein translocase protein <i>tatC</i>	1,04	-1,01	-1,94
SL3930	<i>tatD</i>	Deoxyribonuclease <i>tatD</i>	1,06	-1,12	1,11
SL3931	<i>rfaH</i>	Transcriptional activator <i>rfaH</i>	1,18	1,02	-1,05
SL3932	<i>ubiD</i>	3-octaprenyl-4-hydroxybenzoate carboxy-lyase	1,11	-1,15	1,09
SL3933	<i>fre</i>	NAD(P)H-flavin reductase	1,13	-1,28	1,26
SL3934	-	Arylsulfotransferase	1,16	-1,10	1,80
SL3935	<i>fadA</i>	3-ketoacyl-CoA thiolase	-1,12	-1,11	23,14
SL3936	<i>fadB</i>	Fatty acid oxidation complex subunit alpha	-1,07	1,23	22,96
SL3937	<i>pepQ</i>	Xaa-Pro dipeptidase	1,10	-1,28	1,74
SL3938	<i>yigZ</i>	IMPACT family member <i>yigZ</i>	1,24	-1,35	1,04
SL3939	<i>trkH</i>	Trk system potassium uptake protein <i>trkH</i>	1,12	-1,17	-1,11
SL3940	<i>hemG</i>	Protoporphyrinogen oxidase	1,04	-1,16	1,26

Tabla Suplementaria 1

Diferencia de expresión de todos los genes de SV5015 en las cepas mutantes *greA*, *greB* y *greAgreB*, respecto a la cepa WT

ID	gene	Description	<i>greA</i> vs WT	<i>greB</i> vs WT	<i>greAgreB</i> vs WT
SL3941	<i>mobB</i>	Molybdopterin-guanine dinucleotide biosynthesis protein B	1,11	1,07	-1,12
SL3942	<i>mobA</i>	Molybdopterin-guanine dinucleotide biosynthesis protein A	1,16	1,02	1,40
SL3943	<i>yihD</i>	Protein yihD	1,06	1,15	1,44
SL3944	<i>rdoA</i>	Protein rdoA	1,04	-1,11	-1,43
SL3945	<i>dsbA</i>	Thiol:disulfide interchange protein dsbA	-1,13	-1,13	-1,36
SL3946	<i>yihG</i>	Probable acyltransferase yihG	1,08	1,05	-1,62
SL3947	<i>polA</i>	DNA polymerase I	1,21	1,18	1,89
SL3948	<i>engB</i>	Probable GTP-binding protein engB	1,03	1,02	-1,17
SL3949	-	Hypothetical	1,26	1,85	-1,15
SL3950	<i>yihI</i>	UPF0241 protein yihI	1,04	-1,00	-1,10
SL3951	<i>hemN</i>	Oxygen-independent coproporphyrinogen-III oxidase	1,07	-1,04	-1,39
SL3952	<i>glnG</i>	Nitrogen regulation protein NR(I)	1,25	1,22	1,05
SL3953	<i>glnL</i>	Nitrogen regulation protein NR(II)	1,34	1,24	-1,29
SL3954	<i>glnA</i>	Glutamine synthetase	1,18	1,24	-1,77
SL3955	<i>typA</i>	GTP-binding protein TypA/BipA	1,11	1,08	-2,44
SL3956	<i>ybhA</i>	Phosphatase ybhA	1,07	-1,16	-1,26
SL3957	-	Hypothetical	1,12	-1,26	-1,38
SL3958	<i>hemN</i>	Oxygen-independent coproporphyrinogen-III oxidase	-1,16	1,10	-1,13
SL3959	-	Hypothetical	-1,02	1,08	1,01
SL3960	-	Hypothetical	1,17	1,03	-1,15
SL3961	-	Hypothetical	-1,19	-1,13	2,67
SL3962	<i>ompL</i>	Porin ompL	1,29	-1,12	3,58
SL3963	<i>yihO</i>	Uncharacterized symporter yihO	1,17	-1,02	2,27
SL3964	<i>yihP</i>	Inner membrane symporter yihP	1,33	-1,13	2,70
SL3965	<i>yihQ</i>	Alpha-glucosidase yihQ	1,27	-1,07	2,10
SL3966	<i>yihR</i>	Uncharacterized protein yihR	1,04	-1,09	2,30
SL3967	<i>yihS</i>	Uncharacterized sugar isomerase yihS	1,06	-1,19	4,13
SL3968	<i>yihT</i>	Uncharacterized aldolase yihT	-1,06	-1,69	4,63
SL3969	<i>yihU</i>	Uncharacterized oxidoreductase yihU	1,17	-1,17	6,23
SL3970	<i>yihV</i>	Uncharacterized sugar kinase yihV	1,18	1,10	3,37
SL3971	<i>yihW</i>	Uncharacterized HTH-type transcriptional regulator yihW	1,26	1,03	1,91
SL3972	<i>yihX</i>	Phosphatase yihX	-1,02	1,08	1,47
SL3973	<i>rbn</i>	UPF0761 membrane protein CKO_03126	-1,14	1,01	1,32
SL3974	<i>dtd</i>	D-tyrosyl-tRNA(Tyr) deacylase	-1,26	-1,10	-1,02
SL3975	<i>yiiD</i>	Uncharacterized protein yiiD	-1,11	-1,05	1,07
SL3976	<i>ygjM</i>	Uncharacterized HTH-type transcriptional regulator ygjM	-1,08	-1,10	1,37
SL3977	<i>ygjN</i>	Uncharacterized protein ygjN	1,03	-1,00	2,34
SL3978	<i>est</i>	Esterase	1,17	-1,01	3,87
SL3979	<i>higB-2</i>	Toxin higB-2	-1,03	-1,15	2,12
SL3980	-	Transcriptional Regulator XRE Family	1,06	-1,11	2,21
SL3981	<i>fdhE</i>	Protein fdhE homolog	1,02	-1,18	-1,21
SL3982	<i>fdol</i>	Formate dehydrogenase, cytochrome b556(fdo) subunit	-1,02	-1,26	-1,34
SL3983	<i>fdoH</i>	Formate dehydrogenase-O iron-sulfur subunit	1,08	-1,06	-1,06
SL3984	<i>fdoG</i>	Formate dehydrogenase-O major subunit	1,02	-1,14	-1,05

Tabla Suplementaria 1

Diferencia de expresión de todos los genes de SV5015 en las cepas mutantes *greA*, *greB* y *greAgreB*, respecto a la cepa WT

ID	gene	Description	<i>greA</i> vs WT	<i>greB</i> vs WT	<i>greAgreB</i> vs WT
SL3985	<i>fdoG</i>	Formate dehydrogenase-O major subunit	1,04	-1,04	1,60
SL3986	<i>fdhD</i>	Protein fdhD	-1,04	1,08	-2,32
SL3987	<i>yiiG</i>	Uncharacterized protein yiiG	1,04	1,24	-1,39
SL3988	<i>yiiG</i>	Uncharacterized protein yiiG	1,13	1,01	-1,05
SL3989	-	Hypothetical	1,02	1,17	-2,15
SL3990	<i>azlC</i>	Branched-chain amino acid transport protein AzlC	1,15	1,12	-1,79
SL3991	<i>ydcN</i>	Uncharacterized HTH-type transcriptional regulator ydcN	1,17	-1,07	-1,24
SL3992	<i>rhaM</i>	L-rhamnose mutarotase	1,89	1,14	1,46
SL3993	<i>yiaY</i>	Probable alcohol dehydrogenase	1,63	1,51	1,98
SL3994	<i>rhaD</i>	Rhamnulose-1-phosphate aldolase	1,14	-1,20	1,83
SL3995	<i>rhaA</i>	L-rhamnose isomerase	1,07	-1,37	1,98
SL3996	<i>rhaB</i>	Rhamnulokinase	-1,11	-1,01	-1,07
SL3997	<i>rhaS</i>	HTH-type transcriptional activator rhaS	1,24	1,44	7,48
SL3998	<i>rhaR</i>	HTH-type transcriptional activator rhaR	1,11	1,18	3,48
SL3999	<i>rhaT</i>	L-rhamnose-proton symporter	1,19	1,02	-1,11
SL4000	<i>yiiY</i>	Uncharacterized protein yiiY	1,02	1,16	1,86
SL4001	<i>ygiK</i>	Uncharacterized protein ygiK	-1,01	1,03	1,67
SL4002	<i>yiaM</i>	Tripartite ATP-Independent Periplasmic Transporter DctQ	-1,04	1,51	1,31
SL4003	<i>yiiZ</i>	Uncharacterized protein yiiZ	-1,08	1,29	1,03
SL4004	<i>sodA</i>	Superoxide dismutase [Mn]	-1,10	1,08	-1,33
SL4005	<i>yiiM</i>	Protein yiiM	1,09	1,00	1,29
SL4006	-	Hypothetical	-1,00	-1,05	1,04
SL4007	<i>cpxA</i>	Sensor protein cpxA	-1,06	-1,14	-1,08
SL4008	<i>cpxR</i>	Transcriptional regulatory protein cpxR	-1,02	-1,03	1,21
SL4009	<i>cpxP</i>	Periplasmic protein cpxP	-1,04	1,07	-1,82
SL4010	<i>fiE</i>	Cation-efflux pump fieF	1,13	1,02	-1,45
SL4011	<i>pfkA</i>	6-phosphofructokinase isozyme 1	1,21	1,16	-1,27
SL4012	<i>sbp</i>	Sulfate-binding protein	1,43	1,13	3,15
SL4013	<i>cdh</i>	CDP-diacylglycerol pyrophosphatase	-1,17	1,28	1,07
SL4014	<i>yagG</i>	Uncharacterized symporter yagG	1,30	1,22	6,83
SL4015	<i>scrK</i>	Fructokinase	1,32	1,14	7,32
SL4016	<i>yegU</i>	Uncharacterized protein yegU	1,37	1,16	4,60
SL4017	<i>mngR</i>	Mannosyl-D-glycerate transport/metabolism system repressor mngR	1,04	-1,07	1,12
SL4018	-	Hypothetical	-1,08	1,22	-2,00
SL4019	<i>cdh</i>	CDP-diacylglycerol pyrophosphatase	1,01	1,06	2,10
SL4020	-	Conserved Hypothetical Protein	1,21	1,00	3,55
SL4021	<i>lsrK</i>	Autoinducer 2 kinase lsrK	1,15	-1,14	5,12
SL4022	<i>lsrR</i>	Transcriptional regulator lsrR	1,07	1,15	5,81
SL4023	<i>lsrA</i>	Autoinducer 2 import ATP-binding protein lsrA	-1,19	1,31	49,79
SL4024	<i>lsrC</i>	Autoinducer 2 import system permease protein lsrC	-1,24	-1,20	18,13
SL4025	<i>lsrD</i>	Autoinducer 2 import system permease protein lsrD	-1,14	-1,11	9,85
SL4026	<i>lsrB</i>	Autoinducer 2-binding protein lsrB	1,24	1,13	1,79
SL4027	<i>lsrF</i>	Uncharacterized aldolase lsrF	1,32	-1,03	1,54

Tabla Suplementaria 1

Diferencia de expresión de todos los genes de SV5015 en las cepas mutantes *greA*, *greB* y *greAgreB*, respecto a la cepa WT

ID	gene	Description	<i>greA</i> vs WT	<i>greB</i> vs WT	<i>greAgreB</i> vs WT
SL4028	<i>lsrG</i>	Autoinducer 2-degrading protein <i>lsrG</i>	1,15	1,16	1,93
SL4029	<i>lsrE</i>	Putative epimerase <i>lsrE</i>	1,24	1,12	1,81
SL4030	<i>tpiA</i>	Triosephosphate isomerase	1,09	-1,02	-1,21
SL4031	<i>yiiQ</i>	Uncharacterized protein <i>yiiQ</i>	-1,07	-1,45	-1,65
SL4032	<i>yiiR</i>	Uncharacterized protein <i>yiiR</i>	1,13	-1,04	-1,00
SL4033	<i>fpr</i>	Ferredoxin--NADP reductase	1,10	-1,01	1,18
SL4034	<i>glpX</i>	Fructose-1,6-bisphosphatase class 2	-1,05	-1,50	2,09
SL4035	<i>glpK</i>	Glycerol kinase	1,02	-1,03	1,80
SL4036	<i>glpF</i>	Glycerol uptake facilitator protein	1,03	-1,01	2,43
SL4037	<i>zapB</i>	Cell division protein <i>zapB</i>	1,02	1,16	1,53
SL4038	<i>rraA</i>	Regulator of ribonuclease activity A	1,00	1,03	-1,20
SL4039	<i>menA</i>	1,4-dihydroxy-2-naphthoate octaprenyltransferase	1,07	-1,01	-2,24
SL4040	<i>hslU</i>	ATP-dependent protease ATPase subunit <i>HslU</i>	-1,06	-1,05	1,42
SL4041	<i>hslV</i>	ATP-dependent protease subunit <i>HslV</i>	-1,08	-1,10	1,22
SL4042	<i>ftsN</i>	Cell division protein <i>ftsN</i>	1,18	-1,05	-1,62
SL4043	<i>cytR</i>	HTH-type transcriptional repressor <i>cytR</i>	1,14	-1,01	1,21
SL4044	<i>priA</i>	Primosomal protein N'	-1,12	1,14	-1,99
SL4045	<i>rpmE</i>	50S ribosomal protein L31	1,09	-1,01	1,41
SL4046	-	Hypothetical	1,25	1,08	-1,08
SL4047	-	Arylsulfate Sulfotransferase	1,05	-1,06	2,61
SL4048	<i>metJ</i>	Met repressor	-1,09	1,05	-1,21
SL4049	<i>metB</i>	Cystathionine gamma-synthase	1,01	-1,07	-1,71
SL4050	<i>metL</i>	Bifunctional aspartokinase/homoserine dehydrogenase 2	1,03	-1,23	1,29
SL4051	<i>mscS</i>	Small-conductance mechanosensitive channel	-1,15	-1,06	-1,26
SL4052	-	Hypothetical	-1,00	1,04	1,03
SL4053	-	Hypothetical	1,04	1,06	1,48
SL4054	<i>yfkN</i>	Trifunctional nucleotide phosphoesterase protein <i>yfkN</i>	-1,07	1,12	1,50
SL4055	<i>metF</i>	5,10-methylenetetrahydrofolate reductase	-1,37	1,02	-3,35
SL4056	<i>katG1</i>	Catalase-peroxidase 1	1,05	1,00	-3,75
SL4057	<i>yijF</i>	Uncharacterized protein <i>yijF</i>	1,33	-1,25	-8,02
SL4058	<i>gldA</i>	Glycerol dehydrogenase	1,31	1,46	1,87
SL4059	<i>fsa</i>	Probable fructose-6-phosphate aldolase	1,25	1,13	1,52
SL4060	<i>ptsA</i>	Multiphosphoryl transfer protein 2	1,41	1,33	2,52
SL4061	<i>frwC</i>	Fructose-like permease IIC component 2	1,36	1,35	5,71
SL4062	<i>frwB</i>	Fructose-like phosphotransferase enzyme IIB component 2	1,36	1,10	3,40
SL4063	<i>pflD</i>	Formate acetyltransferase 2	1,17	1,11	1,92
SL4064	<i>pflC</i>	Pyruvate formate-lyase 2-activating enzyme	1,09	1,09	1,42
SL4065	<i>frwD</i>	Fructose-like phosphotransferase enzyme IIB component 3	1,18	1,16	1,56
SL4066	<i>yijO</i>	Uncharacterized HTH-type transcriptional regulator <i>yijO</i>	-1,05	1,06	-1,42
SL4067	-	Hypothetical Protein SL4067	1,03	-1,15	-1,08
SL4068	<i>cptA</i>	Phosphoethanolamine transferase <i>cptA</i>	1,02	-1,03	-1,64
SL4069	<i>ppc</i>	Phosphoenolpyruvate carboxylase	1,10	-1,19	-1,26
SL4070	<i>argE</i>	Acetylornithine deacetylase	1,28	1,11	1,47

Tabla Suplementaria 1

Diferencia de expresión de todos los genes de SV5015 en las cepas mutantes *greA*, *greB* y *greAgreB*, respecto a la cepa WT

ID	gene	Description	<i>greA</i> vs WT	<i>greB</i> vs WT	<i>greAgreB</i> vs WT
SL4071	<i>argC</i>	N-acetyl-gamma-glutamyl-phosphate reductase	1,16	1,06	1,02
SL4072	<i>argB</i>	Acetylglutamate kinase	1,24	1,15	1,50
SL4073	<i>argH</i>	Argininosuccinate lyase	1,16	-1,09	1,31
SL4074	<i>oxyR</i>	Hydrogen peroxide-inducible genes activator	1,12	-1,03	1,71
SL4075	<i>sthA</i>	Soluble pyridine nucleotide transhydrogenase	-1,05	-1,16	2,56
SL4076	<i>fabR</i>	HTH-type transcriptional repressor fabR	1,15	1,08	1,35
SL4077	<i>yijD</i>	Inner membrane protein yijD	1,30	1,09	1,88
SL4078	<i>trmA</i>	tRNA (uracil-5-)-methyltransferase	1,06	1,07	-1,99
SL4079	<i>btuB</i>	Vitamin B12 transporter BtuB	1,05	-1,52	1,63
SL4080	<i>murl</i>	Glutamate racemase	1,09	-1,21	-1,15
SL4081	<i>murB</i>	UDP-N-acetylenolpyruvoylglucosamine reductase	1,18	1,02	-1,41
SL4082	<i>birA</i>	Bifunctional protein BirA	1,11	1,12	-1,12
SL4083	<i>coaA</i>	Pantothenate kinase	1,11	1,12	-1,48
SL4084	-	Hypothetical	-1,28	1,01	-1,17
SL4085	<i>tuf1</i>	Elongation factor Tu 1	1,00	-1,02	1,25
SL4086	<i>secE</i>	Preprotein translocase subunit secE	1,05	-1,06	-1,38
SL4087	<i>nusG</i>	Transcription antitermination protein nusG	1,10	1,00	-1,23
SL4088	<i>rplK</i>	50S ribosomal protein L11	-1,04	1,03	-1,15
SL4089	<i>rplA</i>	50S ribosomal protein L1	-1,16	-1,09	-1,13
SL4090	<i>rplJ</i>	50S ribosomal protein L10	-1,07	-1,10	-1,03
SL4091	<i>rplL</i>	50S ribosomal protein L7/L12	-1,16	-1,21	-1,13
SL4092	<i>rpoB</i>	DNA-directed RNA polymerase subunit beta	1,12	-1,09	1,63
SL4093	<i>rpoC</i>	DNA-directed RNA polymerase subunit beta'	1,17	1,01	2,04
SL4094	-	Inner Membrane Protein	1,20	-1,18	1,11
SL4095	-	Hypothetical	1,49	1,09	1,16
SL4096	-	Cytoplasmic Protein	1,01	-1,19	1,15
SL4097	-	Hypothetical	-1,33	1,16	-1,09
SL4098	<i>thiH</i>	Dehydroglycine synthase	1,23	1,13	3,47
SL4099	<i>thiG</i>	Thiazole synthase	1,42	1,35	4,86
SL4100	<i>thiS</i>	Sulfur carrier protein ThiS	1,69	1,23	3,53
SL4101	<i>thiF</i>	Sulfur carrier protein ThiS adenyllyltransferase	1,43	-1,04	4,02
SL4102	<i>thiE</i>	Thiamine-phosphate pyrophosphorylase	1,31	-1,10	3,49
SL4103	<i>thiC</i>	Phosphomethylpyrimidine synthase	1,36	1,01	3,16
SL4104	<i>rsd</i>	Regulator of sigma D	-1,03	1,26	3,58
SL4105	<i>nudC</i>	NADH pyrophosphatase	1,06	-1,02	-1,03
SL4106	<i>hemE</i>	Uroporphyrinogen decarboxylase	1,14	-1,03	1,49
SL4107	<i>nfi</i>	Endonuclease V	1,15	1,05	1,57
SL4108	<i>yjaG</i>	Uncharacterized protein yjaG	1,03	-1,08	-1,21
SL4109	<i>hupA</i>	DNA-binding protein HU-alpha	1,02	1,03	1,33
SL4110	<i>yjaH</i>	Uncharacterized protein yjaH	-1,07	-1,27	-1,23
SL4111	<i>zraP</i>	Zinc resistance-associated protein	1,57	1,64	-2,57
SL4112	<i>zraS</i>	Sensor protein zraS	1,18	-1,03	2,34
SL4113	<i>zraR</i>	Transcriptional regulatory protein zraR	1,24	1,03	1,88
SL4114	<i>purD</i>	Phosphoribosylamine--glycine ligase	1,17	1,22	1,20

Tabla Suplementaria 1

Diferencia de expresión de todos los genes de SV5015 en las cepas mutantes *greA*, *greB* y *greAgreB*, respecto a la cepa WT

ID	gene	Description	<i>greA</i> vs WT	<i>greB</i> vs WT	<i>greAgreB</i> vs WT
SL4115	<i>purH</i>	Bifunctional purine biosynthesis protein purH	1,20	1,28	-1,65
SL4116	<i>yjaB</i>	Uncharacterized N-acetyltransferase yjaB	1,14	1,30	1,56
SL4117	<i>metA</i>	Homoserine O-succinyltransferase	-1,22	-1,04	1,07
SL4118	<i>aceB</i>	Malate synthase A	-1,09	-1,09	7,52
SL4119	<i>aceA</i>	Isocitrate lyase	-1,27	-1,09	4,68
SL4120	<i>aceK</i>	Isocitrate dehydrogenase kinase/phosphatase	-1,00	-1,11	1,52
SL4121	-	Hypothetical	-1,13	-1,65	2,21
SL4122	<i>iclR</i>	Acetate operon repressor	-1,08	-1,37	2,81
SL4123	<i>metH</i>	Methionine synthase	1,12	-1,18	1,58
SL4124	<i>yjbB</i>	Uncharacterized protein yjbB	1,09	1,02	2,28
SL4125	<i>pepE</i>	Peptidase E	1,06	1,02	-1,03
SL4126	-	Hypothetical Protein SL4126	1,19	1,18	-1,40
SL4127	<i>yaiL</i>	Uncharacterized protein yaiL	1,02	-1,01	-1,24
SL4128	<i>rluF</i>	Ribosomal large subunit pseudouridine synthase F	-1,03	-1,06	-1,26
SL4129	<i>yjbD</i>	Uncharacterized protein yjbD	1,19	1,03	-1,05
SL4130	<i>yocS</i>	Uncharacterized sodium-dependent transporter yocS	-1,25	1,02	1,11
SL4131	-	Hypothetical	1,02	-1,17	-4,83
SL4132	-	Inner Membrane Protein	1,25	-1,02	1,36
SL4133	-	Hypothetical	1,16	-1,42	1,39
SL4134	-	Cytoplasmic Protein	-1,01	-1,23	2,11
SL4135	<i>stfR</i>	Tail Fiber Protein	-1,17	-1,22	1,52
SL4136	-	Phage Tail Protein	-1,11	-1,03	-1,18
SL4137	-	Baseplate J Family Protein	-1,19	-1,08	-1,03
SL4138	-	Phage Baseplate Protein	1,01	-1,01	-1,05
SL4139	-	Hypothetical	-1,05	-1,20	-1,01
SL4140	<i>gtrB</i>	Sfil prophage-derived bactoprenol glucosyl transferase	-1,15	1,03	-2,31
SL4141	<i>yfdG</i>	Bactoprenol-linked glucose translocase homolog from prophage CPS-53	-1,12	1,08	-1,20
SL4142	-	Phage Baseplate Assembly Protein V	1,32	1,09	3,49
SL4143	-	Late Control D Family Protein	1,23	-1,09	2,56
SL4144	-	Bacteriophage Tail Fibre Protein	1,42	1,06	2,50
SL4145	-	Hypothetical	1,19	-1,01	2,10
SL4146	-	Phage Tail Protein	1,06	-1,16	2,84
SL4147	-	Hypothetical	1,02	1,02	2,44
SL4148	-	Phage Tail Tube Protein	-1,14	-1,20	1,89
SL4149	-	Phage Tail Sheath Protein	-1,25	-1,08	1,74
SL4150	-	Cytoplasmic Protein	-1,87	-1,84	1,29
SL4151	-	Hypothetical	1,11	1,02	1,09
SL4152	-	Hypothetical	1,03	1,34	-1,00
SL4153	-	Lytic Transglycosylase Catalytic	-1,11	1,16	-1,03
SL4154	-	Phage-Related Membrane Protein	-1,05	-1,15	1,01
SL4155	<i>rdgB</i>	DNA-binding protein rdgB	1,05	1,28	1,77
SL4156	<i>lysC</i>	Lysine-sensitive aspartokinase 3	1,13	-1,15	1,32
SL4157	<i>pgi</i>	Glucose-6-phosphate isomerase	1,07	-1,05	-1,07
SL4158	<i>yjbE</i>	Hypothetical Protein yjbE	1,01	1,52	-1,65
SL4159	<i>yjbF</i>	Uncharacterized lipoprotein yjbF	-1,15	1,05	-2,28

Tabla Suplementaria 1

Diferencia de expresión de todos los genes de SV5015 en las cepas mutantes *greA*, *greB* y *greAgreB*, respecto a la cepa WT

ID	gene	Description	<i>greA</i> vs WT	<i>greB</i> vs WT	<i>greAgreB</i> vs WT
SL4160	<i>yjbG</i>	Uncharacterized protein yjbG	-1,01	1,05	-1,70
SL4161	<i>yjbH</i>	Uncharacterized lipoprotein yjbH	1,01	1,17	1,01
SL4162	<i>psiE</i>	Protein psiE	-1,22	1,16	-3,30
SL4163	<i>malG</i>	Maltose transport system permease protein malG	1,10	-1,08	-1,02
SL4164	<i>malF</i>	Maltose transport system permease protein malF	-1,01	-1,23	1,14
SL4165	-	Hypothetical Protein SL4165	-1,19	-1,46	2,30
SL4166	<i>malE</i>	Maltose-binding periplasmic protein	1,01	-1,39	1,50
SL4167	<i>malK</i>	Maltose/maltodextrin import ATP-binding protein MalK	-1,91	-2,04	1,67
SL4168	<i>lamB</i>	Maltoporin	1,51	-1,15	1,50
SL4169	<i>malM</i>	Maltose operon periplasmic protein	1,12	-1,38	1,06
SL4170	<i>ubiC</i>	Chorismate--pyruvate lyase	1,29	1,13	2,11
SL4171	<i>ubiA</i>	4-hydroxybenzoate octaprenyltransferase	1,15	1,06	1,87
SL4172	<i>plsB</i>	Glycerol-3-phosphate acyltransferase	1,13	-1,22	1,12
SL4173	<i>dgkA</i>	Diacylglycerol kinase	1,10	1,09	1,00
SL4174	<i>lexA</i>	LexA repressor	1,13	1,16	2,28
SL4175	<i>dinF</i>	DNA-damage-inducible protein F	1,24	1,02	1,06
SL4176	<i>yjbJ</i>	UPF0337 protein yjbJ	1,07	1,14	1,09
SL4177	<i>zur</i>	Zinc uptake regulation protein	1,09	-1,04	-1,02
SL4178	-	Hypothetical	-1,15	-1,08	1,91
SL4179	<i>dusA</i>	tRNA-dihydrouridine synthase A	-1,03	1,03	-1,05
SL4180	<i>pspG</i>	Phage shock protein G	-1,04	1,32	-2,02
SL4181	<i>qorA</i>	Quinone oxidoreductase 1	1,22	1,36	1,83
SL4182	<i>dnaB</i>	Replicative DNA helicase	-1,13	-1,19	-1,60
SL4183	<i>alr</i>	Alanine racemase, biosynthetic	1,08	-1,24	-1,05
SL4184	<i>tyrB</i>	Aromatic-amino-acid aminotransferase	1,01	-1,23	-1,32
SL4185	<i>aphA</i>	Class B acid phosphatase	-1,19	-1,10	2,41
SL4186	<i>yjbQ</i>	UPF0047 protein yjbQ	-1,05	1,12	1,38
SL4187	<i>yjbR</i>	Uncharacterized protein yjbR	-1,13	1,03	1,34
SL4188	-	Hypothetical	-1,09	-1,20	-1,77
SL4189	-	Lipoprotein	-1,08	-1,17	-1,87
SL4190	<i>uvrA</i>	UvrABC system protein A	1,03	-1,05	1,17
SL4191	-	Cytoplasmic Protein	-1,16	1,03	-2,80
SL4192	<i>ssb</i>	Single-stranded DNA-binding protein	1,12	1,21	1,12
SL4193	-	Hypothetical	-2,30	-1,86	-26,54
SL4194	-	Integral Membrane Protein	-2,14	-1,76	-26,23
SL4195	<i>tolC</i>	Outer membrane protein tolC	-2,10	-1,38	-22,66
SL4196	<i>prtE</i>	Proteases secretion protein prtE	-1,96	-1,42	-31,87
SL4197	-	Hypothetical	-1,31	1,08	-18,80
SL4198	<i>lktB</i>	Leukotoxin translocation ATP-binding protein lktB	-2,25	-1,23	-46,89
SL4199	<i>yjcB</i>	Uncharacterized protein yjcB	-1,49	1,15	-9,86
SL4200	<i>yjcC</i>	Uncharacterized protein yjcC	-1,93	1,10	-3,42
SL4201	<i>soxS</i>	Regulatory protein soxS	-1,57	-1,10	-3,63
SL4202	<i>soxR</i>	Redox-sensitive transcriptional activator soxR	-1,46	1,07	-1,86
SL4203	<i>yfcG</i>	Glutathione S-Transferase	-1,02	1,15	1,19
SL4204	<i>yjcD</i>	Putative permease yjcD	-1,08	1,19	-1,70

Tabla Suplementaria 1

Diferencia de expresión de todos los genes de SV5015 en las cepas mutantes *greA*, *greB* y *greAgreB*, respecto a la cepa WT

ID	gene	Description	<i>greA</i> vs WT	<i>greB</i> vs WT	<i>greAgreB</i> vs WT
SL4205	<i>yjcE</i>	Uncharacterized Na(+)/H(+) exchanger <i>yjcE</i>	-1,16	-1,16	-1,01
SL4206	<i>ywbl</i>	Uncharacterized HTH-type transcriptional regulator <i>ywbl</i>	1,14	1,30	1,69
SL4207	<i>cidA</i>	Holin-like protein <i>cidA</i>	-1,10	-1,01	-19,38
SL4208	<i>ywbG</i>	Uncharacterized protein <i>ywbG</i>	-1,18	-1,29	-19,43
SL4209	<i>actP</i>	Cation/acetate symporter <i>ActP</i>	-1,02	-1,45	13,02
SL4210	<i>yjcH</i>	Inner membrane protein <i>yjcH</i>	1,08	-1,46	39,97
SL4211	<i>acs</i>	Acetyl-coenzyme A synthetase	-1,26	-1,40	21,68
SL4212	-	Hypothetical	-1,04	1,03	3,32
SL4213	<i>nrfA</i>	Cytochrome c-552	1,17	1,40	2,13
SL4214	<i>nrfB</i>	Cytochrome c-type protein <i>nrfB</i>	-1,22	1,05	-1,02
SL4215	<i>nrfC</i>	Protein <i>nrfC</i>	-1,24	-1,09	1,02
SL4216	<i>nrfD</i>	Protein <i>nrfD</i>	-1,03	-1,05	1,25
SL4217	<i>nrfE</i>	Cytochrome c-type biogenesis protein <i>nrfE</i>	1,29	-1,04	-1,23
SL4218	<i>nrfG</i>	Formate-dependent nitrite reductase complex subunit <i>nrfG</i>	-1,07	-1,30	1,15
SL4219	<i>gltP</i>	Proton glutamate symport protein	1,19	-1,33	1,90
SL4220	<i>yjcO</i>	Uncharacterized protein <i>yjcO</i>	1,19	-1,20	-1,21
SL4221	<i>fdhF</i>	Formate dehydrogenase H	1,16	1,06	-2,29
SL4222	<i>fdhF</i>	Formate dehydrogenase H	1,09	1,13	-1,41
SL4223	-	Aspartyl/Asparaginyl Beta-Hydroxylase	-1,30	-1,13	1,36
SL4224	<i>phnO</i>	Protein <i>phnO</i>	-1,11	1,42	-1,27
SL4225	<i>phnB</i>	Protein <i>phnB</i>	-1,31	1,07	1,45
SL4226	<i>phnA</i>	Protein <i>phnA</i>	-1,16	-1,10	-1,36
SL4227	<i>proP</i>	Proline/betaine transporter	1,16	1,04	-1,52
SL4228	<i>basS</i>	Sensor protein <i>BasS</i>	-1,09	1,01	1,26
SL4229	<i>basR</i>	Transcriptional regulatory protein <i>BasR</i>	-1,05	1,01	1,31
SL4230	<i>eptA</i>	Phosphoethanolamine transferase <i>eptA</i>	-1,20	-1,09	-1,50
SL4231	<i>adiC</i>	Arginine/agmatine antiporter	-1,10	-1,77	-4,64
SL4232	<i>adiY</i>	HTH-type transcriptional regulator <i>AdiY</i>	-1,09	-1,40	-1,87
SL4233	<i>adiA</i>	Biodegradative arginine decarboxylase	-1,06	-1,33	-1,43
SL4234	<i>melR</i>	Melibiose operon regulatory protein	1,19	1,12	6,19
SL4235	<i>melA</i>	Alpha-galactosidase	1,88	-1,50	1,48
SL4236	<i>melB</i>	Melibiose carrier protein	2,07	-1,79	1,46
SL4237	<i>fumB</i>	Fumarate hydratase class I, anaerobic	1,18	-1,01	-1,84
SL4238	<i>dcuB</i>	Anaerobic C4-dicarboxylate transporter <i>dcuB</i>	1,02	1,56	-11,02
SL4239	-	Hypothetical	-1,18	1,39	-24,27
SL4240	<i>dcuR</i>	Transcriptional regulatory protein <i>dcuR</i>	-1,14	1,03	-1,93
SL4241	<i>dcuS</i>	Sensor protein <i>dcuS</i>	-1,01	1,10	-1,12
SL4242	<i>dmsA</i>	Anaerobic dimethyl sulfoxide reductase chain A	1,26	1,22	1,35
SL4243	<i>dmsB</i>	Anaerobic dimethyl sulfoxide reductase chain B	1,33	1,15	-1,05
SL4244	<i>ynfH</i>	Anaerobic dimethyl sulfoxide reductase chain <i>ynfH</i>	1,47	1,20	-1,08
SL4245	<i>dmsD</i>	Twin-arginine leader-binding protein <i>dmsD</i>	1,43	1,15	-1,43
SL4246	-	Hypothetical	1,06	-1,04	-1,13
SL4247	<i>yjiK</i>	Uncharacterized protein <i>yjiK</i>	-1,74	1,10	-24,46
SL4248	-	Hypothetical	-2,43	-1,91	-28,20
SL4249	-	Cytoplasmic Protein	-3,07	-2,48	-41,36

Tabla Suplementaria 1

Diferencia de expresión de todos los genes de SV5015 en las cepas mutantes *greA*, *greB* y *greAgreB*, respecto a la cepa WT

ID	gene	Description	<i>greA</i> vs WT	<i>greB</i> vs WT	<i>greAgreB</i> vs WT
SL4250	<i>yjjQ</i>	GerE Family Regulatory Protein	-3,14	-2,47	-60,33
SL4251	<i>sirC</i>	Transcriptional regulator sirC	-2,64	-1,89	-47,96
SL4252	-	Hypothetical	-1,52	1,12	-5,47
SL4253	-	Hypothetical	-1,44	1,09	-2,43
SL4254	-	GCN5-Related N-Acetyltransferase	-1,27	-1,09	-1,07
SL4255	<i>phoN</i>	Non-specific acid phosphatase	-1,91	1,07	-1,76
SL4256	-	Ail And OmpX Homolog	1,07	1,11	1,05
SL4257	-	Hypothetical	1,04	1,05	1,55
SL4258	<i>ybbI</i>	Transcriptional Regulator MerR Family	1,17	1,28	-1,49
SL4259	<i>yjdC</i>	HTH-type transcriptional regulator yjdC	-1,06	-1,07	-1,27
SL4260	<i>dsbD</i>	Thiol:disulfide interchange protein dsbD	-1,04	-1,45	-2,77
SL4261	<i>cutA</i>	Divalent-cation tolerance protein cutA	-1,04	-1,19	-2,17
SL4262	<i>dcuA</i>	Anaerobic C4-dicarboxylate transporter dcuA	1,09	1,16	-1,12
SL4263	<i>aspA</i>	Aspartate ammonia-lyase	1,15	1,12	1,10
SL4264	<i>fxsA</i>	UPF0716 protein fxsA	1,17	1,56	1,15
SL4265	<i>yjeH</i>	Inner membrane protein yjeH	1,13	1,35	-1,28
SL4266	<i>groS</i>	10 kDa chaperonin	1,19	1,04	3,79
SL4267	<i>groL</i>	60 kDa chaperonin	1,17	-1,02	2,58
SL4268	<i>yjeI</i>	Uncharacterized protein yjeI	1,21	1,13	1,63
SL4269	<i>yjeJ</i>	Uncharacterized protein yjeJ	1,15	1,14	-1,60
SL4270	<i>yjeK</i>	Uncharacterized KamA family protein YjeK	1,08	1,01	-2,15
SL4271	<i>efp</i>	Elongation factor P	-1,21	-1,17	-1,58
SL4272	<i>ecnA</i>	Entericidin A	-1,07	-1,04	-1,90
SL4273	<i>ecnB</i>	Entericidin B	1,14	1,42	1,10
SL4274	<i>ecnR</i>	Transcriptional regulatory protein entR	1,10	-1,03	1,11
SL4275	<i>sugE</i>	Quaternary ammonium compound-resistance protein sugE	1,26	1,09	1,17
SL4276	<i>blc</i>	Outer membrane lipoprotein blc	1,12	1,12	1,48
SL4277	<i>frdD</i>	Fumarate reductase subunit D	1,29	1,10	1,42
SL4278	<i>frdC</i>	Fumarate reductase subunit C	1,27	1,02	1,31
SL4279	<i>frdB</i>	Fumarate reductase iron-sulfur subunit	1,16	-1,07	1,17
SL4280	<i>frdA</i>	Fumarate reductase flavoprotein subunit	1,23	1,01	1,01
SL4281	<i>yjeA</i>	Uncharacterized protein YjeA	-1,18	-1,30	-2,31
SL4282	<i>yjeM</i>	Inner membrane transporter yjeM	-1,01	-1,06	-3,47
SL4283	<i>yjeO</i>	Inner membrane protein yjeO	1,07	-1,19	-1,41
SL4284	<i>yjeP</i>	Uncharacterized mscS family protein yjeP	1,03	-1,03	-1,04
SL4285	<i>psd</i>	Phosphatidylserine decarboxylase proenzyme	1,06	-1,08	1,10
SL4286	<i>rsgA</i>	Putative ribosome biogenesis GTPase RsgA	1,02	-1,14	-1,44
SL4287	<i>orn</i>	Oligoribonuclease	1,24	-1,10	1,07
SL4288	<i>artJ</i>	ABC transporter arginine-binding protein 1	-1,14	-1,08	1,16
SL4289	<i>yjeS</i>	Putative electron transport protein yjeS	1,02	1,05	-1,37
SL4290	<i>yjeF</i>	Uncharacterized protein yjeF	1,18	1,09	1,63
SL4291	<i>yjeE</i>	UPF0079 ATP-binding protein yjeE	-1,03	1,01	1,21
SL4292	<i>amiB</i>	N-acetylmuramoyl-L-alanine amidase AmiB	1,06	1,09	1,16
SL4293	<i>mutL</i>	DNA mismatch repair protein mutL	1,10	1,03	1,12
SL4294	<i>miaA</i>	tRNA dimethylallyltransferase	-1,06	1,01	1,15

Tabla Suplementaria 1

Diferencia de expresión de todos los genes de SV5015 en las cepas mutantes *greA*, *greB* y *greAgreB*, respecto a la cepa WT

ID	gene	Description	<i>greA</i> vs WT	<i>greB</i> vs WT	<i>greAgreB</i> vs WT
SL4295	<i>hfq</i>	Protein hfq	-1,03	-1,05	1,14
SL4296	<i>hflX</i>	GTP-binding protein hflX	-1,01	-1,10	-1,06
SL4297	<i>hflK</i>	Protein hflK	-1,04	-1,15	-1,11
SL4298	<i>hflC</i>	Protein hflC	-1,06	-1,18	1,03
SL4299	<i>purA</i>	Adenylosuccinate synthetase	-1,02	1,06	-1,82
SL4300	<i>nsrR</i>	HTH-type transcriptional repressor nsrR	1,06	-1,04	-1,32
SL4301	<i>rnr</i>	Ribonuclease R	1,06	-1,05	1,39
SL4302	<i>rlmB</i>	23S rRNA (guanosine-2'-O-)-methyltransferase rlmB	1,24	-1,15	-1,15
SL4303	<i>yjfl</i>	Uncharacterized protein yjfl	1,10	1,14	1,34
SL4304	<i>yjfJ</i>	Uncharacterized protein YjfJ	-1,06	-1,06	1,23
SL4305	-	Resembles Potassium Channels	1,02	-1,33	-1,00
SL4306	<i>yjfK</i>	Uncharacterized protein yjfK	-1,09	-1,32	-1,08
SL4307	<i>yjfL</i>	UPF0719 inner membrane protein yjfL	1,14	1,09	-1,51
SL4308	<i>yjfM</i>	Uncharacterized protein yjfM	1,15	1,01	-1,01
SL4309	<i>yjfC</i>	Uncharacterized protein yjfC	1,11	1,01	1,18
SL4310	<i>aidB</i>	Protein AidB	1,35	1,22	9,60
SL4311	<i>yjfN</i>	Uncharacterized protein yjfN	1,41	1,24	6,64
SL4312	<i>bsmA</i>	Lipoprotein BsmA	1,31	1,21	5,00
SL4313	<i>yjfP</i>	Esterase yjfP	1,04	1,03	2,55
SL4314	<i>ulaR</i>	HTH-type transcriptional regulator ulaR	1,06	-1,12	1,59
SL4315	<i>ulaG</i>	Probable L-ascorbate-6-phosphate lactonase ulaG	1,10	1,15	2,27
SL4316	<i>ulaA</i>	Ascorbate-specific permease IIC component ulaA	1,34	1,14	9,06
SL4317	<i>ulaB</i>	Ascorbate-specific phosphotransferase enzyme IIB component	1,29	1,06	6,92
SL4318	<i>ulaC</i>	Ascorbate-specific phosphotransferase enzyme IIA component	1,14	-1,11	5,04
SL4319	<i>ulaD</i>	3-keto-L-gulonate-6-phosphate decarboxylase ulaD	1,23	-1,49	3,02
SL4320	<i>ulaE</i>	L-ribulose-5-phosphate 3-epimerase ulaE	1,06	-1,20	2,25
SL4321	<i>ulaF</i>	L-ribulose-5-phosphate 4-epimerase ulaF	1,15	-1,17	1,83
SL4322	<i>yjfY</i>	Uncharacterized protein yjfY	-1,07	1,32	1,19
SL4323	-	Hypothetical	-1,04	1,46	-1,78
SL4324	<i>rpsF</i>	30S ribosomal protein S6	-1,05	1,10	-1,18
SL4325	<i>priB</i>	Primosomal replication protein n	-1,01	1,08	-1,19
SL4326	<i>rpsR</i>	30S ribosomal protein S18	-1,07	1,09	-1,02
SL4327	<i>rplI</i>	50S ribosomal protein L9	-1,15	1,10	-2,28
SL4328	<i>ydeD</i>	Hypothetical	1,10	-1,19	-1,35
SL4329	<i>ytfB</i>	Uncharacterized protein ytfB	1,24	1,19	2,09
SL4330	<i>fkIB</i>	FKBP-type 22 kDa peptidyl-prolyl cis-trans isomerase	-1,24	-1,10	-1,74
SL4331	<i>cycA</i>	D-serine/D-alanine/glycine transporter	-1,18	-1,15	1,35
SL4332	<i>ytfE</i>	Regulator of cell morphogenesis and NO signaling	1,10	-1,06	1,10
SL4333	<i>ytfF</i>	Inner membrane protein ytfF	1,15	1,22	2,16
SL4334	<i>qorB</i>	Quinone oxidoreductase 2	1,06	1,26	2,70
SL4335	<i>ytfH</i>	Uncharacterized HTH-type transcriptional regulator ytfH	1,48	-1,03	1,53
SL4336	<i>cpdB</i>	2',3'-cyclic-nucleotide 2'-phosphodiesterase/3'-nucleotidase	1,31	1,04	4,00

Tabla Suplementaria 1

Diferencia de expresión de todos los genes de SV5015 en las cepas mutantes *greA*, *greB* y *greAgreB*, respecto a la cepa WT

ID	gene	Description	<i>greA</i> vs WT	<i>greB</i> vs WT	<i>greAgreB</i> vs WT
SL4337	<i>cysQ</i>	3'(2'),5'-bisphosphate nucleotidase <i>cysQ</i>	-1,02	1,00	2,40
SL4338	<i>ytfJ</i>	Uncharacterized protein <i>ytfJ</i>	-1,19	1,16	2,51
SL4339	<i>ytfK</i>	Uncharacterized protein <i>ytfK</i>	-1,34	-1,01	-1,39
SL4340	<i>ytfL</i>	UPF0053 inner membrane protein <i>ytfL</i>	-1,12	-1,16	-2,96
SL4341	<i>msrA</i>	Peptide methionine sulfoxide reductase <i>msrA</i>	-1,09	1,23	2,87
SL4342	<i>ytfM</i>	Uncharacterized protein <i>ytfM</i>	1,10	1,05	1,13
SL4343	<i>ytfN</i>	Uncharacterized protein <i>ytfN</i>	1,12	-1,02	1,29
SL4344	<i>ytfP</i>	Gamma-glutamylcyclotransferase family protein <i>ytfP</i>	1,04	-1,06	-1,02
SL4345	<i>dgoT</i>	D-galactonate transporter	1,08	-1,01	-1,16
SL4346	-	Dihydroorotase	-1,26	-1,06	1,08
SL4347	<i>ppa</i>	Inorganic pyrophosphatase	1,01	-1,10	-1,03
SL4348	<i>fbp</i>	Fructose-1,6-bisphosphatase class 1	1,02	1,02	1,65
SL4349	<i>mpl</i>	UDP-N-acetylmuramate:L-alanyl-gamma-D-glutamyl-meso-diaminopimelate ligase	-1,08	-1,13	-1,53
SL4350	<i>hexR</i>	Uncharacterized HTH-type transcriptional regulator HI_0143	-1,08	1,02	-2,14
SL4351	<i>xylE</i>	D-xylose-proton symporter	1,00	-1,60	7,99
SL4352	<i>xylE</i>	D-xylose-proton symporter	1,12	1,12	2,71
SL4353	<i>iolB</i>	5-deoxy-glucuronate isomerase	1,33	1,06	3,00
SL4354	<i>iolA1</i>	Methylmalonate semialdehyde dehydrogenase [acylating] 1	1,29	1,10	3,93
SL4355	<i>ydiP</i>	Uncharacterized HTH-type transcriptional regulator <i>ydiP</i>	1,09	1,48	6,37
SL4356	<i>iolE</i>	Inosose dehydratase	1,14	1,10	1,85
SL4357	<i>iolG</i>	Inositol 2-dehydrogenase	1,01	1,06	1,65
SL4358	-	Glucan Endo-1 6-Beta-Glucosidase	-1,01	1,13	1,05
SL4359	<i>iolI</i>	Inosose isomerase	1,20	-1,01	2,12
SL4360	<i>yfcJ</i>	UPF0226 protein STM4428	-1,00	-1,20	1,54
SL4361	<i>iolC</i>	5-dehydro-2-deoxygluconokinase	1,02	-1,26	5,41
SL4362	<i>iolD1</i>	3D-(3,5/4)-trihydroxycyclohexane-1,2-dione hydrolase 1	1,04	-1,38	5,81
SL4363	<i>yrbE</i>	Uncharacterized oxidoreductase <i>yrbE</i>	1,39	1,20	1,51
SL4364	<i>csbX</i>	Alpha-ketoglutarate permease	-1,08	-1,49	1,78
SL4365	-	Xylose Isomerase Domain-Containing Protein	1,03	-1,04	2,81
SL4366	<i>iolH</i>	Protein <i>iolH</i>	1,00	-1,15	2,02
SL4367	<i>yjgA</i>	UPF0307 protein CKO_03595	1,03	1,14	1,12
SL4368	<i>pmbA</i>	Protein <i>pmbA</i>	1,15	1,11	1,63
SL4369	<i>cybC</i>	Soluble cytochrome b562	1,05	1,04	2,03
SL4370	-	Hypothetical	1,33	1,33	1,44
SL4371	-	Hypothetical	1,37	1,18	2,22
SL4372	-	Hypothetical	1,39	1,09	2,71
SL4373	-	Hypothetical	1,09	1,02	2,64
SL4374	-	Hypothetical	1,13	1,07	2,36
SL4375	-	Dihydroorotase	1,22	-1,08	2,21
SL4376	<i>selA</i>	Uncharacterized protein <i>mlr3804</i>	1,21	1,00	2,54
SL4377	-	Hypothetical	1,23	-1,01	2,59
SL4378	<i>licR</i>	Probable <i>licABCH</i> operon regulator	1,21	-1,02	1,93
SL4379	<i>relB</i>	Antitoxin <i>RelB</i>	1,21	-1,08	1,73
SL4380	<i>relE</i>	Toxin <i>relE</i>	1,29	-1,05	1,90

Tabla Suplementaria 1

Diferencia de expresión de todos los genes de SV5015 en las cepas mutantes *greA*, *greB* y *greAgreB*, respecto a la cepa WT

ID	gene	Description	<i>greA</i> vs WT	<i>greB</i> vs WT	<i>greAgreB</i> vs WT
SL4381	<i>nrdG</i>	Anaerobic ribonucleoside-triphosphate reductase-activating protein	1,27	-1,20	-2,24
SL4382	<i>nrdD</i>	Anaerobic ribonucleoside-triphosphate reductase	1,27	-1,05	-2,21
SL4383	-	Hypothetical	-1,17	-1,08	-1,04
SL4384	<i>treC</i>	Trehalose-6-phosphate hydrolase	-1,16	1,06	2,06
SL4385	<i>treB</i>	PTS system trehalose-specific EIIBC component	1,06	1,34	2,48
SL4386	<i>treR</i>	HTH-type transcriptional regulator treR	1,14	1,13	-1,37
SL4387	<i>mgtA</i>	Magnesium-transporting ATPase, P-type 1	-1,61	1,04	-2,08
SL4388	-	Conserved Hypothetical Protein	-1,13	1,10	1,27
SL4389	<i>yjgF</i>	UPF0076 protein yjgF	1,14	1,10	1,61
SL4390	<i>pyrI</i>	Aspartate carbamoyltransferase regulatory chain	-1,03	1,14	1,05
SL4391	<i>pyrB</i>	Aspartate carbamoyltransferase	-1,10	1,18	-1,15
SL4392	<i>pyrL</i>	PyrBI operon leader peptide	1,52	1,01	-1,50
SL4393	<i>argR</i>	Arginine repressor	2,49	1,35	-1,35
SL4394	<i>yfcC</i>	Uncharacterized protein HI_0594	2,59	1,62	-1,71
SL4395	<i>arcB</i>	Ornithine carbamoyltransferase, catabolic	2,46	1,57	-1,54
SL4396	<i>arcC</i>	Carbamate kinase	2,65	1,92	-1,01
SL4397	<i>arcA</i>	Arginine deiminase	2,65	2,16	1,41
SL4398	<i>yjgK</i>	Uncharacterized protein yjgK	-1,06	1,23	1,78
SL4399	<i>argI</i>	Ornithine carbamoyltransferase	-1,00	-1,08	1,10
SL4400	<i>yjgD</i>	Uncharacterized protein yjgD	1,08	1,05	1,16
SL4401	<i>miaE</i>	tRNA-(ms[2]io[6]A)-hydroxylase	1,03	-1,17	1,05
SL4402	<i>ytgA</i>	Uncharacterized protein ytgA	1,31	-1,20	2,30
SL4403	<i>yjgM</i>	Uncharacterized N-acetyltransferase yjgM	1,34	1,16	1,19
SL4404	<i>yjgN</i>	Inner membrane protein yjgN	1,05	1,18	1,02
SL4405	<i>valS</i>	Valyl-tRNA synthetase	1,17	-1,07	1,33
SL4406	<i>holC</i>	DNA polymerase III subunit chi	1,13	-1,20	2,20
SL4407	<i>pepA</i>	Probable cytosol aminopeptidase	1,17	-1,08	2,78
SL4408	-	Cytoplasmic Protein	-1,15	-1,33	1,45
SL4409	<i>lptF</i>	Lipopolysaccharide export system permease protein lptF	1,08	1,01	-1,52
SL4410	<i>lptG</i>	Lipopolysaccharide export system permease protein lptG	1,05	-1,05	-1,23
SL4411	<i>idnR</i>	HTH-type transcriptional regulator idnR	1,35	1,01	1,64
SL4412	<i>idnT</i>	Gnt-II system L-idonate transporter	1,58	-1,02	3,38
SL4413	<i>idnO</i>	Gluconate 5-dehydrogenase	1,50	-1,24	3,80
SL4414	<i>idnD</i>	L-idonate 5-dehydrogenase	1,71	-1,04	4,59
SL4415	<i>idnK</i>	Thermosensitive gluconokinase	1,14	1,03	2,28
SL4416	<i>yjgB</i>	Uncharacterized zinc-type alcohol dehydrogenase-like protein yjgB	-1,01	-1,02	1,77
SL4417	<i>intZ</i>	Integrase Family Protein	1,11	1,09	-1,17
SL4418	<i>yjhR</i>	Putative uncharacterized protein yjhR	1,07	-1,02	1,78
SL4419	-	Restriction Endonuclease	1,20	1,05	2,21
SL4420	<i>lon</i>	Hypothetical	1,23	1,12	1,32
SL4421	-	Hypothetical	1,14	1,07	-1,10
SL4422	-	Hypothetical	-1,11	-1,18	-1,06
SL4423	-	ABC-Type Transporter	-1,08	-1,02	-1,07
SL4424	-	Hypothetical	-1,19	-1,21	1,38

Tabla Suplementaria 1

Diferencia de expresión de todos los genes de SV5015 en las cepas mutantes *greA*, *greB* y *greAgreB*, respecto a la cepa WT

ID	gene	Description	<i>greA</i> vs WT	<i>greB</i> vs WT	<i>greAgreB</i> vs WT
SL4425	-	Hypothetical	1,20	-1,00	1,64
SL4426	-	Hypothetical	-1,10	-1,06	-1,78
SL4427	-	Hypothetical	-1,18	-1,09	-1,76
SL4428	-	Molybdopterin-Guanine Dinucleotide Biosynthesis Protein A	1,14	1,05	-1,32
SL4429	<i>yeeN</i>	UPF0082 protein LACR_0237	1,08	-1,07	-2,10
SL4430	<i>yjhP</i>	Uncharacterized protein yjhP	1,27	1,18	2,26
SL4431	-	UPF0386 protein KPN78578_02510	1,35	1,24	2,78
SL4432	-	Hypothetical	1,23	-1,30	1,88
SL4433	-	Hypothetical	1,01	-1,05	1,27
SL4434	-	Hypothetical	-2,10	1,20	-4,98
SL4435	-	Hypothetical	-1,43	1,10	-2,04
SL4436	<i>yczH</i>	Uncharacterized protein yczH	-1,08	1,14	-1,14
SL4437	<i>uxuR</i>	Uxu operon transcriptional regulator	1,16	1,14	1,19
SL4438	<i>trpS</i>	Tryptophanyl-tRNA synthetase	-1,02	-1,11	2,21
SL4439	-	Hypothetical	1,24	1,06	1,14
SL4440	-	Hypothetical	-1,08	1,06	-1,25
SL4441	<i>ygeA</i>	Uncharacterized protein in p <i>nlA</i> 3' region	1,23	1,02	1,24
SL4442	<i>yjiE</i>	Uncharacterized HTH-type transcriptional regulator yjiE	1,02	-1,47	-1,51
SL4443	<i>iadA</i>	Isoaspartyl dipeptidase	-1,05	-1,05	-1,36
SL4444	<i>yjiG</i>	Inner membrane protein yjiG	-1,18	-1,18	-1,21
SL4445	<i>yjiH</i>	Uncharacterized protein yjiH	-1,15	-1,14	-1,23
SL4446	<i>yjiJ</i>	Uncharacterized protein yjiJ	-1,01	1,15	-1,48
SL4447	<i>yjiN</i>	Uncharacterized protein yjiN	-1,02	1,01	-1,08
SL4448	<i>mdtM</i>	Multidrug resistance protein mdtM	1,16	1,17	-1,50
SL4449	<i>yfcl</i>	Uncharacterized protein yfcl	-1,00	-1,12	1,52
SL4450	<i>ssdA</i>	Succinate-semialdehyde dehydrogenase [NADP+]	1,49	1,45	2,77
SL4451	-	Hypothetical	1,32	-1,32	2,30
SL4452	<i>yjiS</i>	Hypothetical	1,19	1,14	1,25
SL4453	-	Hypothetical	1,00	-1,48	1,01
SL4454	<i>symE</i>	Endoribonuclease symE	1,23	1,19	1,72
SL4455	<i>hsdS</i>	Type-1 restriction enzyme StySJI specificity protein	-1,21	-1,46	1,35
SL4456	<i>hsdM</i>	Type I restriction enzyme EcoKI M protein	1,01	-1,00	1,28
SL4457	<i>hsdR</i>	Type I restriction enzyme EcoKI R protein	1,09	1,02	2,34
SL4458	<i>mrr</i>	Mrr restriction system protein	1,03	-1,00	1,62
SL4459	-	Hypothetical	1,29	1,33	2,48
SL4460	-	Hypothetical	1,26	1,49	3,02
SL4461	<i>yjiA</i>	Uncharacterized GTP-binding protein yjiA	1,13	-1,10	-1,01
SL4462	<i>yjiX</i>	Uncharacterized protein yjiX	-1,09	-1,08	-2,97
SL4463	<i>yjiY</i>	Inner membrane protein yjiY	1,11	1,19	-18,87
SL4464	<i>tsr</i>	Methyl-accepting chemotaxis protein I	-1,03	-1,00	-2,50
SL4465	<i>levR</i>	Transcriptional regulatory protein levR	1,19	1,17	1,99
SL4466	<i>manX</i>	PTS System Fructosic IIA Component	2,51	1,25	13,66
SL4467	<i>manX</i>	Probable phosphotransferase enzyme IIB component M6_Spy0801	1,80	-1,22	15,83
SL4468	<i>agaC</i>	N-acetylgalactosamine permease IIC component 1	2,23	-1,04	17,29
SL4469	<i>manZ</i>	Mannose permease IID component	2,24	1,09	14,20

Tabla Suplementaria 1

Diferencia de expresión de todos los genes de SV5015 en las cepas mutantes *greA*, *greB* y *greAgreB*, respecto a la cepa WT

ID	gene	Description	<i>greA</i> vs WT	<i>greB</i> vs WT	<i>greAgreB</i> vs WT
SL4470	<i>glmS</i>	Glucosamine--fructose-6-phosphate aminotransferase [isomerizing]	3,29	1,02	23,21
SL4471	<i>frlB</i>	Fructosamine deglycase frlB	2,57	1,34	14,58
SL4472	<i>mdoB</i>	Phosphoglycerol transferase I	-1,11	1,10	-1,77
SL4473	<i>yjjA</i>	Uncharacterized protein yjjA	1,05	1,00	1,04
SL4474	<i>dnaC</i>	DNA replication protein dnaC	1,14	1,15	1,14
SL4475	<i>dnaT</i>	Primosomal protein 1	1,18	1,09	-1,13
SL4476	<i>yjjB</i>	UPF0442 protein CKO_03436	1,21	1,11	-1,14
SL4477	<i>yjjP</i>	Inner membrane protein yjjP	1,09	1,20	-1,52
SL4478	<i>yjjQ</i>	Uncharacterized protein yjjQ	1,09	-1,10	-1,06
SL4479	<i>bglJ</i>	Transcriptional activator protein BglJ	1,07	1,19	1,30
SL4480	<i>ywhH</i>	Uncharacterized protein ywhH	1,03	-1,01	1,39
SL4481	<i>fhuF</i>	Ferric iron reductase protein fhuF	-1,00	1,47	-1,23
SL4482	<i>ycdT</i>	Inner membrane protein ycdT	1,19	1,00	-1,60
SL4483	<i>yjjZ</i>	Uncharacterized protein yjjZ	1,27	1,39	-1,41
SL4484	<i>rsmC</i>	Ribosomal RNA small subunit methyltransferase C	1,03	-1,07	-2,63
SL4485	<i>holD</i>	DNA polymerase III subunit psi	1,17	1,00	-1,63
SL4486	<i>rimI</i>	Ribosomal-protein-alanine acetyltransferase	1,14	-1,06	-1,63
SL4487	<i>yjjG</i>	5'-nucleotidase yjjG	1,20	-1,04	-1,72
SL4488	<i>prfC</i>	Peptide chain release factor 3	1,24	-1,03	-1,48
SL4489	<i>osmY</i>	Osmotically-inducible protein Y	-1,01	1,05	1,32
SL4490	<i>yjjU</i>	Uncharacterized protein yjjU	1,01	-1,15	-1,16
SL4491	<i>yjjV</i>	Uncharacterized deoxyribonuclease yjjV	1,11	-1,21	-1,06
SL4492	<i>yjjW</i>	Uncharacterized protein yjjW	1,36	-1,05	1,57
SL4493	<i>yjjI</i>	Uncharacterized protein yjjI	1,25	1,08	1,64
SL4494	<i>deoC</i>	Deoxyribose-phosphate aldolase	1,13	1,21	-1,06
SL4495	<i>deoA</i>	Thymidine phosphorylase	1,25	1,01	1,17
SL4496	<i>deoB</i>	Phosphopentomutase	-1,09	-1,00	-2,17
SL4497	<i>deoD</i>	Purine nucleoside phosphorylase deoD-type	-1,03	1,03	-1,71
SL4498	-	Hypothetical	1,14	1,15	-1,84
SL4499	<i>yhcD</i>	Uncharacterized outer membrane usher protein yhcD	1,16	1,10	-1,23
SL4500	<i>yhcA</i>	Uncharacterized fimbrial chaperone yhcA	-1,65	-1,01	-1,99
SL4501	<i>yhcF</i>	Uncharacterized protein yhcF	-1,19	-1,05	-1,12
SL4502	<i>yhcF</i>	Uncharacterized protein yhcF	-1,04	1,05	1,30
SL4503	<i>lplA</i>	Lipoate-protein ligase A	1,08	1,08	1,37
SL4504	<i>smp</i>	Protein smp	1,03	1,18	-1,38
SL4505	<i>serB</i>	Phosphoserine phosphatase	-1,05	-1,07	-1,08
SL4506	<i>radA</i>	DNA repair protein radA	1,16	-1,11	1,24
SL4507	<i>nadR</i>	Transcriptional regulator nadR	1,31	1,10	1,59
SL4508	<i>yjjK</i>	Uncharacterized ABC transporter ATP-binding protein yjjK	1,04	-1,18	1,54
SL4509	<i>slt</i>	Soluble lytic murein transglycosylase	1,26	-1,04	2,00
SL4510	<i>trpR</i>	Trp operon repressor	1,10	-1,25	2,05
SL4511	<i>yjjX</i>	UPF0244 protein yjjX	1,01	-1,12	-1,16
SL4512	<i>gpmB</i>	Probable phosphoglycerate mutase gpmB	-1,08	-1,00	-1,44
SL4513	<i>rob</i>	Right origin-binding protein	1,14	1,05	-1,09
SL4514	<i>creA</i>	Protein creA	-1,02	-1,00	1,42

Tabla Suplementaria 1

Diferencia de expresión de todos los genes de SV5015 en las cepas mutantes *greA*, *greB* y *greAgreB*, respecto a la cepa WT

ID	gene	Description	<i>greA</i> vs WT	<i>greB</i> vs WT	<i>greAgreB</i> vs WT
SL4515	<i>creB</i>	Transcriptional regulatory protein creB	1,16	-1,05	1,27
SL4516	<i>creC</i>	Sensor protein creC	1,16	-1,11	-1,09
SL4517	<i>creD</i>	Inner membrane protein creD	1,15	1,14	1,43
SL4518	-	Adhesin	1,13	-1,12	-1,05
SL4519	<i>fimG</i>	Hypothetical	1,11	1,29	-1,21
SL4520	<i>lpfC</i>	Outer membrane usher protein lpfC	-1,14	1,09	1,09
SL4521	<i>fimC</i>	Chaperone protein fimC	-1,08	1,03	-1,14
SL4522	<i>ydeS</i>	Uncharacterized fimbrial-like protein ydeS	-1,01	-1,27	1,08
SL4523	<i>yaiV</i>	Uncharacterized protein yaiV	1,04	1,03	1,18
SL4524	-	Hypothetical	1,46	1,20	-1,49
SL4525	<i>arcA</i>	Aerobic respiration control protein ArcA	-1,03	-1,02	-1,27
SL4526	<i>yjiY</i>	Uncharacterized protein yjiY	1,03	1,04	-1,07
SL4527	<i>lasT</i>	Uncharacterized tRNA/rRNA methyltransferase lasT	-1,01	-1,05	-1,02
SLP1_0001	<i>finO</i>	Fertility inhibition protein	1,13	-1,03	1,63
SLP1_0002	<i>traX</i>	Protein traX	1,33	-1,05	1,08
SLP1_0003	<i>tral</i>	Protein tral	1,12	1,04	-1,00
SLP1_0004	<i>trbH</i>	Protein trbH	1,32	-1,04	1,18
SLP1_0005	-	Uncharacterized protein CP0246	1,55	1,23	1,63
SLP1_0006	-	Uncharacterized protein HI_0947	1,32	1,09	1,42
SLP1_0007	<i>traD</i>	Protein traD	1,23	-1,03	-1,08
SLP1_0008	<i>traT</i>	TraT complement resistance protein	1,02	-1,06	1,22
SLP1_0009	-	Surface Exclusion Inner Membrane Protein TraS	-1,02	1,07	1,52
SLP1_0010	<i>traG</i>	Protein traG	1,08	1,03	1,65
SLP1_0011	<i>traH</i>	Protein traH	1,04	-1,15	1,93
SLP1_0012	<i>trbB</i>	Protein trbB	-1,03	-1,11	1,88
SLP1_0013	<i>traQ</i>	Protein traQ	1,07	-1,04	2,12
SLP1_0014	<i>traF</i>	Protein traF	1,16	1,02	1,57
SLP1_0015	<i>trbE</i>	Conjugative Transfer Protein	1,35	1,20	1,57
SLP1_0016	<i>traN</i>	Protein traN	1,12	-1,00	1,43
SLP1_0017	<i>trbC</i>	Periplasmic protein trbC	1,14	-1,03	1,34
SLP1_0018	-	Conjugative Transfer Protein	1,17	-1,00	1,19
SLP1_0019	<i>traU</i>	Protein traU	1,36	1,08	1,75
SLP1_0020	<i>traW</i>	Protein traW	1,25	1,02	1,70
SLP1_0021	<i>trbI</i>	Protein trbI	1,07	-1,21	1,91
SLP1_0022	<i>traC</i>	Protein traC	1,31	-1,11	2,12
SLP1_0023	-	Conjugative Transfer	1,16	-1,40	1,62
SLP1_0024	<i>traR</i>	Protein TraR	1,25	-1,14	1,96
SLP1_0025	<i>traV</i>	Protein TraV	1,03	-1,17	2,31
SLP1_0026	<i>trbD</i>	Conjugal Transfer Protein TrbD	1,16	1,24	2,84
SLP1_0027	<i>traP</i>	Protein traP	1,25	1,23	1,36
SLP1_0028	<i>traB</i>	Protein traB	1,11	-1,17	1,54
SLP1_0029	<i>traK</i>	TraK lipoprotein	1,28	1,07	1,39
SLP1_0030	<i>traE</i>	Protein traE	1,30	-1,03	-1,55
SLP1_0031	<i>traL</i>	Protein traL	1,45	-1,19	-1,36
SLP1_0032	<i>traA</i>	Pilin	1,94	1,28	1,53
SLP1_0033	<i>traY</i>	Protein traY	1,64	1,27	1,20
SLP1_0034	<i>traJ</i>	Protein traJ	1,09	1,03	1,13

Tabla Suplementaria 1

Diferencia de expresión de todos los genes de SV5015 en las cepas mutantes *greA*, *greB* y *greAgreB*, respecto a la cepa WT

ID	gene	Description	<i>greA</i> vs WT	<i>greB</i> vs WT	<i>greAgreB</i> vs WT
SLP1_0035	<i>traM</i>	Protein traM	1,13	1,08	1,57
SLP1_0036	X	X polypeptide	-1,13	1,03	1,02
SLP1_0037	<i>psiA</i>	Protein psiA	-1,06	1,04	1,84
SLP1_0038	<i>psiB</i>	Protein psiB	1,15	1,22	1,74
SLP1_0039	<i>yubM</i>	Uncharacterized protein yubM	-1,01	-1,02	2,75
SLP1_0040	<i>yubL</i>	UPF0401 protein yubL	1,02	-1,14	1,20
SLP1_0041	<i>ssb2</i>	Single-stranded DNA-binding protein 2	1,07	1,13	1,62
SLP1_0042	<i>holE</i>	DNA polymerase III subunit theta	1,22	1,14	-1,46
SLP1_0043	-	Hypothetical	1,34	1,21	2,35
SLP1_0044	<i>yubl</i>	Putative antirestriction protein Yubl	-1,04	-1,01	1,50
SLP1_0045	-	Uncharacterized protein yubG	1,05	1,33	1,62
SLP1_0047	-	Hypothetical	1,20	1,34	1,85
SLP1_0048	<i>yubE</i>	Uncharacterized protein YubE	1,05	1,21	1,26
SLP1_0049	<i>yubD</i>	Putative methylase yubD	-1,13	-1,14	-1,03
SLP1_0050	-	Cytoplasmic Protein	-1,04	-1,11	-1,09
SLP1_0051	-	Hypothetical	-1,00	-1,07	-1,44
SLP1_0052	<i>samA</i>	Protein samA	1,10	1,07	1,43
SLP1_0053	<i>samB</i>	Protein samB	1,05	1,04	1,75
SLP1_0054	<i>parB</i>	Plasmid Partition par B protein	1,09	1,12	5,19
SLP1_0055	<i>parA</i>	Plasmid partition protein A	-1,14	-1,37	5,75
SLP1_0056	<i>yfcl</i>	Uncharacterized protein pSLT051	1,11	1,07	-1,41
SLP1_0057	-	Cytoplasmic Protein	1,14	-1,02	2,77
SLP1_0058	-	Uncharacterized protein pSLT049	1,01	-1,09	2,85
SLP1_0059	-	Myosin Heavy Chain Gizzard Smooth	-1,00	1,14	2,65
SLP1_0060	-	Hypothetical	-1,13	-1,24	-1,05
SLP1_0061	<i>yadF</i>	Carbonic anhydrase	-1,12	-1,02	-1,50
SLP1_0062	<i>pinE</i>	Integrase-like protein y4IS	1,07	-1,16	-1,13
SLP1_0063	-	Transposase	1,19	-1,09	1,20
SLP1_0064	-	AAA ATPase	1,06	1,11	1,04
SLP1_0065	-	Insertion element IS630 uncharacterized 39 kDa protein	1,15	1,14	-2,02
SLP1_0066	<i>spvR</i>	Virulence genes transcriptional activator	-1,09	1,04	-1,11
SLP1_0067	<i>spvA</i>	28.1 kDa virulence protein	-1,35	1,10	-6,22
SLP1_0068	<i>spvB</i>	65 kDa virulence protein	-1,39	1,03	-12,28
SLP1_0069	<i>spvC</i>	27.5 kDa virulence protein	-1,59	-1,30	-34,55
SLP1_0070	<i>spvD</i>	Virulence protein vsdE	-1,34	-1,34	-10,27
SLP1_0071	-	Transposase	1,40	1,13	-1,16
SLP1_0072	<i>vsdF</i>	Virulence protein vsdF	1,03	-1,06	-1,01
SLP1_0073	<i>yeeJ</i>	Uncharacterized protein yeeJ	1,24	1,19	-1,24
SLP1_0074	-	Hypothetical	1,02	1,29	1,02
SLP1_0075	<i>yahA</i>	Cyclic di-GMP phosphodiesterase yahA	-1,06	-1,03	1,11
SLP1_0076	<i>resD</i>	Resolvase	1,05	-1,01	1,75
SLP1_0077	-	Cytoplasmic Protein	-1,01	-1,14	2,14
SLP1_0078	-	Hypothetical	1,07	-1,04	1,97
SLP1_0079	<i>ccdB</i>	Cytotoxic protein CcdB	-1,01	-1,01	2,35
SLP1_0080	<i>ccdA</i>	Protein CcdA	1,08	1,02	2,95
SLP1_0081	-	Hypothetical	1,13	1,25	1,04
SLP1_0082	-	Cytoplasmic Protein	1,18	1,10	-1,64
SLP1_0083	-	Replication Protein	-1,18	-1,18	-1,36

Tabla Suplementaria 1

Diferencia de expresión de todos los genes de SV5015 en las cepas mutantes *greA*, *greB* y *greAgreB*, respecto a la cepa WT

ID	gene	Description	<i>greA</i> vs WT	<i>greB</i> vs WT	<i>greAgreB</i> vs WT
SLP1_0084	<i>repA</i>	RepFIB replication protein A	-1,12	-1,14	-1,34
SLP1_0085	<i>ygiW</i>	Protein ygiW	-1,22	1,02	-1,32
SLP1_0086	<i>papB</i>	Major pilu subunit operon regulatory protein papB	1,95	2,29	-1,65
SLP1_0087	<i>fedA</i>	F107 fimbrial protein	1,31	1,36	2,72
SLP1_0088	<i>pefC</i>	Outer membrane usher protein pefC	-1,08	-1,29	1,62
SLP1_0089	<i>fanE</i>	Chaperone protein fanE	1,14	1,08	1,90
SLP1_0090	-	Outer Membrane Protein	1,25	-1,11	1,49
SLP1_0091	-	Hypothetical	-1,02	1,01	-1,21
SLP1_0092	-	Regulatory Protein	1,16	1,07	-1,34
SLP1_0093	<i>rcsB</i>	GerE Family Regulatory Protein	1,21	1,09	-1,15
SLP1_0094	<i>dsbA</i>	Thiol:disulfide interchange protein DsbA	1,31	1,16	1,19
SLP1_0095	<i>yjiK</i>	Uncharacterized protein yjiK	1,43	1,02	-1,05
SLP1_0096	<i>pagC</i>	Virulence membrane protein pagC	1,40	1,04	2,84
SLP1_0097	<i>gadX</i>	HTH-type transcriptional regulator gadX	1,27	1,05	1,55
SLP1_0098	<i>yjiK</i>	Outer Membrane Protein	1,20	1,14	-1,06
SLP1_0099	<i>repA</i>	Replication initiation protein	1,13	1,06	-1,50
SLP1_0100	-	Hypothetical Protein SLP1_0100	1,17	1,10	-1,80
SLP1_0101	-	DNA Replication Protein	1,15	1,16	-1,67
SLP1_0102	<i>repA2</i>	Replication regulatory protein repA2	1,11	1,30	-1,15
SLP1_0103	-	Endonuclease	1,38	1,17	-1,05
SLP1_0104	-	DSBA Oxidoreductase	1,33	1,21	1,41
SLP2_0001	-	Hypothetical Protein SLP2_0001	1,13	-1,02	-1,30
SLP2_0002	<i>repA</i>	Replication initiation protein	1,03	-1,04	-1,35
SLP2_0003	-	Hypothetical	1,01	1,12	4,59
SLP2_0004	-	Addiction Module Antitoxin	1,09	1,15	3,55
SLP2_0005	<i>dnaQ</i>	Uncharacterized protein pSLT049	1,03	1,28	4,21
SLP2_0006	-	Hypothetical	1,03	1,12	1,99
SLP2_0007	-	Hypothetical Protein SLP2_0007	-1,01	1,06	1,08
SLP2_0008	-	Hypothetical	-1,55	-1,08	1,80
SLP2_0009	-	Hypothetical	-1,52	-1,18	2,29
SLP2_0010	-	Hypothetical	-1,35	-1,13	1,97
SLP2_0011	-	Uncharacterized protein in cib 5' region	1,10	1,08	5,04
SLP2_0012	<i>cib</i>	Colicin-Ib	1,33	1,46	4,20
SLP2_0013	-	Colicin-Ib immunity protein	1,05	1,29	1,03
SLP2_0014	-	Hypothetical	1,39	1,43	1,40
SLP2_0015	-	Hypothetical	-1,09	-1,09	2,04
SLP2_0016	-	Hypothetical	-1,09	-1,31	2,65
SLP2_0017	<i>resD</i>	Resolvase	-1,24	-1,45	2,37
SLP2_0018	-	Hypothetical Protein SLP2_0018	1,07	-1,23	1,31
SLP2_0019	-	Hypothetical	-1,09	-1,30	1,91
SLP2_0020	-	Hypothetical	-1,03	-1,12	2,26
SLP2_0021	<i>parM</i>	Plasmid segregation protein parM	-1,10	-1,09	1,42
SLP2_0022	-	Plasmid Stability Protein	-1,00	-1,03	1,35
SLP2_0023	<i>impC</i>	Protein impC	1,09	-1,01	1,02
SLP2_0024	<i>yuaZ</i>	Uncharacterized protein yuaZ	1,14	1,10	-1,22
SLP2_0025	<i>yubA</i>	Uncharacterized protein YubA	1,62	1,38	1,16
SLP2_0026	<i>yubC</i>	Uncharacterized protein yubC	1,13	1,01	1,06
SLP2_0027	<i>yubD</i>	Putative methylase yubD	1,36	1,79	1,34

Tabla Suplementaria 1

Diferencia de expresión de todos los genes de SV5015 en las cepas mutantes *greA*, *greB* y *greAgreB*, respecto a la cepa WT

ID	gene	Description	<i>greA</i> vs WT	<i>greB</i> vs WT	<i>greAgreB</i> vs WT
SLP2_0028	<i>yubE</i>	Uncharacterized protein YubE	1,70	1,53	1,58
SLP2_0029	<i>yubF</i>	Uncharacterized protein yubF	1,32	1,06	2,34
SLP2_0030	-	Uncharacterized protein yubG	1,40	1,39	2,83
SLP2_0031	<i>yubH</i>	Uncharacterized protein yubH	-1,04	-1,23	2,24
SLP2_0032	<i>yubl</i>	Putative antirestriction protein Yubl	1,27	1,21	3,00
SLP2_0033	<i>yubJ</i>	Uncharacterized protein yubJ	1,06	1,04	3,01
SLP2_0034	-	Hypothetical	-1,22	-1,07	-1,11
SLP2_0035	<i>ssb</i>	Plasmid-derived single-stranded DNA-binding protein	1,09	-1,03	1,94
SLP2_0036	<i>yubM</i>	Uncharacterized protein yubM	1,09	1,12	2,51
SLP2_0037	<i>psiB</i>	Protein psiB	1,24	1,17	4,39
SLP2_0038	<i>psiA</i>	Protein psiA	1,23	1,09	5,34
SLP2_0039	-	Hypothetical	1,36	1,11	4,78
SLP2_0040	<i>yubH</i>	Uncharacterized protein yubH	1,69	-1,07	1,54
SLP2_0041	-	Antirestriction Protein	1,09	1,14	1,32
SLP2_0042	-	Hypothetical	1,28	1,06	-1,52
SLP2_0043	-	Hypothetical	1,14	1,21	1,31
SLP2_0044	<i>yfcl</i>	Uncharacterized protein pSLT051	1,09	1,07	2,09
SLP2_0045	-	Hypothetical	1,04	1,15	-1,28
SLP2_0047	-	Hypothetical	1,23	1,21	1,13
SLP2_0048	-	Hypothetical	1,06	-1,14	-1,02
SLP2_0049	<i>tral</i>	Protein tral	-1,13	-1,33	1,29
SLP2_0050	-	Hypothetical	1,09	-1,04	1,21
SLP2_0051	-	Hypothetical	1,11	-1,00	-1,08
SLP2_0052	-	Hypothetical	1,32	1,13	1,12
SLP2_0053	-	Plasmid Stability Protein	-1,16	1,88	-1,40
SLP2_0054	<i>pndA</i>	Protein pndA	-1,02	1,41	1,04
SLP2_0055	<i>exc</i>	Exclusion-determining protein	-1,00	1,12	1,84
SLP2_0056	-	Hypothetical	1,14	-1,04	-1,58
SLP2_0057	-	TraX-Like Protein	1,03	1,08	-1,63
SLP2_0058	-	Hypothetical	1,23	1,04	1,37
SLP2_0059	-	Conjugal Transfer Protein	1,13	-1,00	1,21
SLP2_0060	-	Hypothetical	1,20	-1,00	1,15
SLP2_0061	-	Hypothetical	1,09	-1,03	-1,33
SLP2_0062	-	Hypothetical	1,13	1,12	-1,40
SLP2_0063	-	Hypothetical	1,03	1,08	-2,42
SLP2_0064	-	TraQ Protein	1,13	1,18	-2,04
SLP2_0065	-	TraP Protein	1,08	1,10	-1,20
SLP2_0066	-	Hypothetical	1,15	-1,09	-1,56
SLP2_0067	-	Hypothetical	1,11	-1,23	-1,77
SLP2_0068	-	Hypothetical	1,07	-1,06	-1,50
SLP2_0069	-	TraL Protein	1,12	1,13	-1,02
SLP2_0070	-	DNA Primase	1,09	1,02	-1,10
SLP2_0072	<i>pld</i>	Phospholipase D	1,21	-1,04	1,35
SLP2_0073	-	Hypothetical	1,17	-1,14	1,26
SLP2_0074	<i>yggR</i>	Uncharacterized protein yggR	1,21	-1,03	1,40
SLP2_0075	-	Hypothetical	1,19	-1,02	1,05
SLP2_0076	-	TraH Protein	1,30	1,12	1,00

Tabla Suplementaria 1

Diferencia de expresión de todos los genes de SV5015 en las cepas mutantes *greA*, *greB* y *greAgreB*, respecto a la cepa WT

ID	gene	Description	<i>greA</i> vs WT	<i>greB</i> vs WT	<i>greAgreB</i> vs WT
SLP2_0077	<i>ais</i>	Lipopolysaccharide core heptose(II)-phosphate phosphatase	1,11	-1,28	-1,20
SLP2_0078	-	Hypothetical	1,48	1,07	3,93
SLP2_0079	-	Hypothetical	1,29	1,13	3,02
SLP2_0080	<i>rci</i>	Shufflon-specific DNA recombinase	1,18	-1,04	1,03
SLP2_0081	-	Shufflon protein B'	1,21	1,09	-1,69
SLP2_0082	-	Shufflon protein B	1,15	-1,01	-1,73
SLP2_0083	-	Shufflon protein A	1,09	1,00	-1,36
SLP2_0085	-	Shufflon protein A'	-1,01	-1,16	-1,58
SLP2_0086	-	Prepilin Peptidase	-1,08	-1,21	-3,05
SLP2_0087	<i>pbl</i>	Peptidoglycan-binding-like protein	1,09	1,03	-2,03
SLP2_0088	-	Type IV Prepilin	1,22	1,23	-1,32
SLP2_0089	-	Type II Secretion System Protein	1,10	-1,04	-1,36
SLP2_0090	<i>tcpT</i>	Toxin coregulated pilus biosynthesis protein T	1,06	-1,15	-1,05
SLP2_0091	-	Pilus Assembly Protein	1,06	-1,16	-1,20
SLP2_0092	-	Hypothetical	1,08	-1,16	-1,03
SLP2_0093	<i>bfpB</i>	Outer membrane lipoprotein BfpB	1,11	-1,11	-1,05
SLP2_0094	-	PilM Protein	1,14	1,01	-1,07
SLP2_0095	-	Hypothetical	1,19	1,15	1,08
SLP2_0096	-	Hypothetical	1,03	-1,10	-1,20
SLP2_0097	-	Hypothetical	1,07	1,04	1,36
SLP2_0098	-	Hypothetical	1,19	-1,08	-1,06
SLP2_0100	-	Hypothetical	1,09	1,12	-1,06
SLP2_0101	-	Conjugal Transfer Protein	1,28	-1,05	1,40
SLP2_0102	-	Transcription Antitermination Factor	1,08	1,21	1,08
SLP2_0103	-	Hypothetical Protein SLP2_0103	1,36	1,25	-1,22
SLP3_0001	<i>sullI</i>	Dihydropteroate synthase type-2	1,09	1,00	-2,14
SLP3_0002	-	Hypothetical	1,11	1,30	1,22
SLP3_0003	-	Replication C Family Protein	1,36	1,12	1,20
SLP3_0004	<i>repA</i>	Regulatory protein repA	1,20	1,20	2,05
SLP3_0005	-	Hypothetical Protein SLP3_0005	1,08	1,10	2,21
SLP3_0006	-	Hypothetical Protein SLP3_0006	1,15	1,23	2,23
SLP3_0007	<i>mobA</i>	Mobilization protein A	1,27	1,09	2,75
SLP3_0008	<i>mobA</i>	Mobilization protein A	1,39	1,26	2,71
SLP3_0009	<i>mobB</i>	Mobilization protein B	1,30	1,14	2,64
SLP3_0010	-	Uncharacterized mobilization operon protein F	1,21	-1,06	1,25
SLP3_0011	<i>mobC</i>	Mobilization protein C	1,12	1,04	3,03
SLP3_0012	-	Transposase	1,18	-1,07	-1,23
SLP3_0013	<i>str</i>	Streptomycin 3"-kinase	1,14	-1,10	-1,52
SLP3_0014	<i>aphE</i>	Streptomycin 3"-kinase	1,05	-1,04	-1,38

Tabla suplementaria 2Genes afectados en las cepas mutantes *greA*, *greB* y *greAgreB* respecto a la cepa WT

ID	gene	Description	greA vs WT	greB vs WT	greAgreB vs WT
SL0002	<i>thrA</i>	Bifunctional aspartokinase/homoserine dehydrogenase 1	1,70	1,02	2,42
SL0005	<i>yaaA</i>	UPF0246 protein yaaA	1,04	1,17	-2,22
SL0008	<i>mog</i>	Molybdopterin adenyllyltransferase	1,33	1,02	2,27
SL0012	<i>dnaK</i>	Chaperone protein dnaK	1,05	1,13	2,97
SL0013	<i>dnaJ</i>	Chaperone protein dnaJ	-1,06	-1,09	2,03
SL0034	<i>yhcR</i>	Endonuclease yhcR	1,37	1,25	2,40
SL0036	<i>betC</i>	Choline-sulfatase	-1,04	-1,01	3,95
SL0042	<i>yicI</i>	Uncharacterized family 31 glucosidase ORF2	1,21	1,14	2,73
SL0043	<i>xylP</i>	putative sodium galactoside symporter	1,11	-1,37	7,93
SL0044	<i>rpsT</i>	30S ribosomal protein S20	-1,21	1,09	-3,04
SL0052	<i>rihC</i>	Non-specific ribonucleoside hydrolase rihC	1,40	1,26	3,12
SL0055	<i>oadB1</i>	Oxaloacetate decarboxylase beta chain 1	1,32	1,13	2,23
SL0056	<i>oadA</i>	Oxaloacetate decarboxylase alpha chain	1,21	-1,06	2,57
SL0057	<i>oadG1</i>	Probable oxaloacetate decarboxylase gamma chain 1	1,12	-1,07	4,14
SL0058	<i>citC</i>	Citrate-sodium symporter	-1,32	-1,22	3,02
SL0061	<i>citE</i>	Citrate lyase subunit beta	1,11	1,07	7,85
SL0064	<i>citG1</i>	Probable 2-(5"-triphosphoribosyl)-3'-dephosphocoenzyme-A synthase 1	1,12	1,15	2,58
SL0066	-	putative viral protein	1,03	-1,28	-4,48
SL0068	<i>carB</i>	Carbamoyl-phosphate synthase large chain	1,02	1,13	2,03
SL0071	<i>caiD</i>	Carnitiny-CoA dehydratase	1,28	-1,04	2,23
SL0081	<i>ygdl</i>	Uncharacterized lipoprotein ygdl	-1,38	1,04	-2,13
SL0096	<i>rluA</i>	Ribosomal large subunit pseudouridine synthase A	2,03	1,02	2,39
SL0102	<i>araA</i>	L-arabinose isomerase	1,07	-1,06	2,50
SL0103	<i>araB</i>	Ribulokinase	1,02	-1,03	3,31
SL0104	<i>araC</i>	Arabinose operon regulatory protein	1,10	-1,07	10,58
SL0110	<i>leuD</i>	3-isopropylmalate dehydratase small subunit 1	1,18	-1,08	2,28
SL0111	<i>leuC</i>	3-isopropylmalate dehydratase large subunit 1	1,24	1,05	3,98
SL0112	<i>leuB</i>	3-isopropylmalate dehydrogenase	1,21	-1,08	3,10
SL0115	<i>leuO</i>	Probable HTH-type transcriptional regulator leuO	-1,27	1,23	-2,01
SL0143	<i>hofB</i>	Protein transport protein hofB	-1,00	-1,08	2,18
SL0144	<i>ppdD</i>	Prepilin peptidase-dependent protein D	-1,04	1,06	2,04
SL0150	<i>aroP</i>	Aromatic amino acid transport protein AroP	1,04	-1,07	2,45
SL0151	<i>pdhR</i>	Pyruvate dehydrogenase complex repressor	-1,06	-1,15	-2,74
SL0153	<i>aceF</i>	Dihydrolipoyllysine-residue acetyltransferase component of pyruvate dehydrogenase complex	1,13	-1,02	3,97
SL0154	<i>lpdA</i>	Dihydrolipoyl dehydrogenase	1,13	-1,04	2,79
SL0159	<i>acnB</i>	Aconitate hydratase 2	1,07	-1,21	3,83
SL0160	-	Restriction Endonuclease	-1,11	-1,47	-2,18
SL0161	<i>yacL</i>	UPF0231 protein yacL	1,28	1,31	2,93
SL0163	<i>ygbK</i>	Uncharacterized protein HI_1011	1,23	-1,06	4,11
SL0164	<i>pdxA2</i>	4-hydroxythreonine-4-phosphate dehydrogenase 2	1,36	1,07	2,76

Tabla suplementaria 2

 Genes afectados en las cepas mutantes *greA*, *greB* y *greAgreB* respecto a la cepa WT

ID	gene	Description	greA vs WT	greB vs WT	greAgreB vs WT
SL0178	<i>fimF</i>	Fimbrial subunit type 1	1,05	-1,03	3,27
SL0180	<i>yadE</i>	Uncharacterized protein yadE	-1,14	1,11	-2,44
SL0185	<i>pcnB</i>	Poly(A) polymerase	-1,08	-1,04	-2,92
SL0186	<i>yadB</i>	glutamyl-tRNA synthetase	-1,27	-1,04	-3,74
SL0192	<i>fhuA</i>	Ferrichrome-iron receptor	-1,04	1,41	-2,51
SL0196	<i>stfA</i>	Fimbria A protein	1,28	-1,06	3,38
SL0211	<i>cdaR</i>	Carbohydrate diacid regulator	-1,03	-1,04	4,32
SL0212	<i>yaeH</i>	UPF0325 protein ESA_03178	-1,12	-1,14	3,29
SL0213	<i>shiA</i>	Shikimate transporter	-1,19	1,05	-2,38
SL0221	<i>dxr</i>	1-deoxy-D-xylulose 5-phosphate reductoisomerase	-1,00	-1,05	-2,21
SL0222	<i>uppS</i>	Undecaprenyl pyrophosphate synthase	-1,06	1,22	-2,18
SL0244	<i>yaeB</i>	UPF0066 protein yaeB	1,15	1,05	-2,27
SL0255	<i>mltD</i>	Membrane-bound lytic murein transglycosylase D	-1,61	1,08	-6,32
SL0265	<i>sciF</i>	Cytoplasmic Protein	1,19	1,05	2,97
SL0266	<i>clpB</i>	Chaperone protein clpB	1,15	-1,36	3,43
SL0267	<i>sciH</i>	Hypothetical	1,22	1,04	3,82
SL0268	<i>scil</i>	Hypothetical	1,09	-1,15	2,77
SL0300	<i>sinR</i>	Probable HTH-type transcriptional regulator sinR	-1,68	-1,43	-2,91
SL0305	<i>fadE</i>	Acyl-coenzyme A dehydrogenase	-1,34	1,19	9,79
SL0310	<i>ykfJ</i>	Uncharacterized protein ykfJ (pseudo)	-1,37	-1,03	-2,01
SL0313	<i>gpt</i>	Xanthine phosphoribosyltransferase	1,09	1,06	-2,59
SL0315	<i>crl</i>	Sigma factor-binding protein crl	1,19	1,17	2,15
SL0316	<i>phoE</i>	Outer membrane pore protein E	1,24	1,23	2,05
SL0336	-	Transmembrane Regulator	-1,37	-1,27	-3,98
SL0337	-	Periplasmic Protein	-1,33	-1,26	-2,23
SL0344	<i>yjeI</i>	Uncharacterized protein yjeI	1,27	1,26	3,73
SL0348	<i>actP</i>	Copper-transporting P-type ATPase	1,08	-1,11	4,15
SL0349	<i>hmrR</i>	HTH-type transcriptional regulator hmrR	1,16	1,30	2,01
SL0350	-	putative copper chaperone	1,36	-1,02	2,36
SL0351	<i>yjhB</i>	Putative metabolite transport protein yjhB	-1,16	-1,13	2,18
SL0353	<i>res</i>	Type III restriction-modification system StyLTI enzyme res	1,14	1,07	2,64
SL0360	<i>yahN</i>	Uncharacterized membrane protein yahN	1,41	1,47	3,45
SL0362	<i>prpR</i>	Propionate catabolism operon regulatory protein	1,09	-1,04	2,42
SL0363	<i>prpB</i>	Methylisocitrate lyase	1,04	1,27	2,74
SL0364	<i>prpC</i>	2-methylcitrate synthase	-1,05	1,08	5,33
SL0365	<i>prpD</i>	2-methylcitrate dehydratase	1,05	-1,05	6,64
SL0366	<i>prpE</i>	Propionate--CoA ligase	1,23	-1,12	4,91
SL0371	<i>sbmA</i>	Protein sbmA	1,23	-1,04	-2,98
SL0372	<i>yaiW</i>	Uncharacterized protein yaiW	1,01	1,11	-2,53
SL0374	<i>yaiZ</i>	Uncharacterized protein yaiZ	1,39	1,18	2,44
SL0376	-	Extensin Family Protein	1,14	1,21	4,71
SL0377	<i>mdtG</i>	Multidrug resistance protein mdtG	1,08	-1,08	-2,63

Tabla suplementaria 2Genes afectados en las cepas mutantes *greA*, *greB* y *greAgreB* respecto a la cepa WT

ID	gene	Description	greA vs WT	greB vs WT	greAgreB vs WT
SL0382	<i>yail</i>	UPF0178 protein yail	-1,15	-1,06	-2,28
SL0387	<i>rdgC</i>	Recombination-associated protein rdgC	1,02	-1,04	-2,81
SL0391	<i>sbcD</i>	Nuclease sbcCD subunit D	1,16	1,08	-2,20
SL0395	<i>proY</i>	Proline-specific permease proY	1,33	1,01	-2,05
SL0397	<i>ahpC</i>	Probable peroxiredoxin	-1,02	1,14	-2,76
SL0399	<i>queA</i>	S-adenosylmethionine:tRNA ribosyltransferase-isomerase	-1,10	1,07	-2,69
SL0415	<i>yajO</i>	Uncharacterized oxidoreductase yajO	1,20	1,41	2,32
SL0419	<i>thil</i>	tRNA sulfurtransferase	1,08	-1,05	-2,71
SL0432	<i>ybeT</i>	Hypothetical	-1,10	-1,28	2,29
SL0433	<i>cyoE</i>	Protoheme IX farnesyltransferase	-1,12	-1,50	11,62
SL0434	<i>cyoD</i>	Cytochrome o ubiquinol oxidase protein cyoD	-1,20	-1,53	13,42
SL0435	<i>cyoC</i>	Cytochrome o ubiquinol oxidase subunit 3	-1,10	-1,60	13,28
SL0436	<i>cyoB</i>	Ubiquinol oxidase subunit 1	-1,08	-1,42	5,97
SL0437	<i>cyoA</i>	Ubiquinol oxidase subunit 2	-1,09	-1,17	6,05
SL0444	<i>lon</i>	Hypothetical Protein lon	1,07	1,06	2,44
SL0445	<i>hupB</i>	DNA-binding protein HU-beta	1,17	1,14	2,02
SL0449	<i>queC</i>	7-cyano-7-deazaguanine synthase (putative aluminum resistance protein)	1,00	-1,01	-2,53
SL0450	<i>ybaE</i>	Uncharacterized protein ybaE	1,13	1,12	6,33
SL0480	<i>htpG</i>	Chaperone protein htpG	1,08	-1,04	3,68
SL0482	<i>hemH</i>	Ferrochelatase	1,04	-1,00	-8,01
SL0484	<i>gsk</i>	Inosine-guanosine kinase	1,01	1,00	-2,02
SL0487	<i>ushA</i>	Protein ushA	-1,05	-1,36	4,38
SL0502	-	Outer Membrane Protein	1,25	-1,12	2,30
SL0507	<i>allS</i>	lysR family transcriptional regulator	1,23	1,15	7,16
SL0508	<i>allA</i>	Ureidoglycolate hydrolase	-1,06	-1,21	2,65
SL0510	<i>gcl</i>	Glyoxylate carboligase	1,65	-1,22	7,44
SL0511	<i>gip</i>	Hydroxypyruvate isomerase	1,41	-1,11	10,16
SL0512	<i>glxR</i>	2-hydroxy-3-oxopropionate reductase	1,60	-1,03	5,13
SL0513	<i>yybO</i>	metabolite transport protein	1,43	1,14	4,88
SL0515	<i>ybbW</i>	Putative allantoin permease	1,66	1,02	3,89
SL0516	<i>allB</i>	Allantoinase	1,05	1,11	2,94
SL0518	<i>glxK</i>	Glycerate kinase 1	1,20	1,10	2,36
SL0519	<i>ylbA</i>	Uncharacterized protein ylbA	-1,04	-1,27	2,29
SL0520	<i>allC</i>	Allantoate amidohydrolase	-1,08	-1,17	3,13
SL0521	<i>allD</i>	Ureidoglycolate dehydrogenase	-1,04	-1,46	5,10
SL0522	<i>fdrA</i>	Protein fdrA	1,14	1,12	3,41
SL0523	<i>ylbE</i>	Uncharacterized protein ylbE	1,09	-1,20	3,61
SL0533	<i>ybcI</i>	Inner membrane protein ybcI	-1,08	1,05	-2,95
SL0536	<i>fimA</i>	Fimbrial subunit type 1	-1,80	1,10	-9,56
SL0537	<i>fimI</i>	Putative fimbrin-like protein fimI	-2,48	-1,26	-17,41
SL0538	<i>fimC</i>	Chaperone protein fimC	-2,52	-1,37	-22,44
SL0539	<i>fimD</i>	Outer membrane usher protein fimD	-1,99	-1,09	-5,31
SL0540	<i>fimH</i>	Protein fimH	-1,50	-1,09	-2,74
SL0542	<i>fimZ</i>	Fimbriae Z protein	-1,27	1,09	-2,40
SL0543	<i>fimY</i>	Fimbriae Y protein	1,43	1,29	-2,23

Tabla suplementaria 2Genes afectados en las cepas mutantes *greA*, *greB* y *greAgreB* respecto a la cepa WT

ID	gene	Description	<i>greA</i> vs WT	<i>greB</i> vs WT	<i>greAgreB</i> vs WT
SL0544	-	putative diguanylate cyclase/phosphodiesterase	-1,17	1,54	-2,09
SL0548	<i>yfdH</i>	Bactoprenol glucosyl transferase homolog from prophage CPS-53	-1,04	-1,04	-1,99
SL0549	<i>gtrA</i>	Bactoprenol-linked glucose translocase homolog from prophage CPS-53	1,09	-1,03	-2,84
SL0551	<i>ykgD</i>	Uncharacterized HTH-type transcriptional regulator ykgD	1,16	1,20	3,20
SL0552	<i>ykgC</i>	Probable pyridine nucleotide-disulfide oxidoreductase ykgC	1,12	1,11	2,34
SL0554	<i>ykgB</i>	Inner membrane protein ykgB	-1,12	1,08	2,01
SL0559	<i>levR</i>	Transcriptional regulatory protein levR	1,07	-1,01	2,64
SL0560	<i>frlB</i>	Fructosamine deglycase frlB	1,61	1,34	2,73
SL0566	<i>nfnB</i>	Oxygen-insensitive NAD(P)H nitroreductase	1,01	-1,13	2,14
SL0585	<i>entB</i>	Isochorismatase	1,10	1,23	2,00
SL0586	<i>entA</i>	2,3-dihydro-2,3-dihydroxybenzoate dehydrogenase	1,11	-1,28	2,33
SL0587	<i>ybdB</i>	Esterase ybdB	-1,13	-1,04	2,26
SL0588	<i>cstA</i>	Carbon starvation protein A	-1,16	-1,23	9,48
SL0589	<i>ybdD</i>	Uncharacterized protein ybdD	-1,21	-1,30	9,97
SL0592	<i>ybdM</i>	Uncharacterized protein ybdM	1,15	-1,04	2,44
SL0596	<i>ahpC</i>	Alkyl hydroperoxide reductase subunit C	1,12	1,10	-2,32
SL0597	<i>ahpF</i>	Alkyl hydroperoxide reductase subunit F	-1,10	-1,02	-2,42
SL0598	<i>ynfl</i>	Cytoplasmic Chaperone rD Family Protein	1,33	1,02	-3,67
SL0605	<i>rna</i>	Ribonuclease I	-1,07	1,13	-2,35
SL0610	<i>citE</i>	Citrate lyase subunit beta	1,06	1,12	-2,50
SL0611	<i>citD</i>	Citrate lyase acyl carrier protein 1	-1,06	1,09	-2,36
SL0612	<i>citC</i>	[Citrate [pro-3S]-lyase] ligase	-1,02	1,10	-2,47
SL0613	<i>dpiB</i>	Sensor histidine kinase DpiB	-1,09	1,19	-3,56
SL0614	<i>dpiA</i>	Transcriptional regulatory protein DpiA	1,03	1,04	-2,28
SL0615	<i>dcuC</i>	Anaerobic C4-dicarboxylate transporter dcuC	1,18	1,06	-2,87
SL0616	<i>pagP</i>	antimicrobial peptide resistance and lipid A acylation protein	-1,02	1,07	-6,65
SL0617	<i>cspE</i>	Cold shock-like protein cspE	-1,33	1,02	-2,78
SL0620	<i>tatE</i>	Sec-independent protein translocase protein tatE	-1,01	1,14	-2,04
SL0625	<i>dacA</i>	D-alanyl-D-alanine carboxypeptidase dacA	-1,04	1,03	-2,41
SL0637	-	putative hydrolase N-terminus	1,26	-1,00	-7,34
SL0638	<i>uxaA</i>	putative hydrolase C-terminus	1,24	-1,26	-5,57
SL0639	<i>kdgT2</i>	2-keto-3-deoxygluconate permease 2	1,23	1,24	-2,50
SL0641	<i>ybeL</i>	Uncharacterized protein ybeL	1,43	1,38	4,14
SL0642	<i>ybeQ</i>	Uncharacterized protein ybeQ	1,10	1,13	2,20
SL0644	<i>ybeS</i>	putative molecular chaperone, DnaJ family	-1,25	-1,33	1,98
SL0649	-	Hypothetical	-1,06	1,02	2,03
SL0650	<i>rihA</i>	Pyrimidine-specific ribonucleoside hydrolase rihA	-1,07	-1,01	2,38
SL0651	<i>gltL</i>	Glutamate/aspartate transport ATP-binding protein gltL	-1,77	-2,15	8,59
SL0652	<i>gltK</i>	Glutamate/aspartate transport system permease protein gltK	-1,72	-2,00	8,36

Tabla suplementaria 2Genes afectados en las cepas mutantes *greA*, *greB* y *greAgreB* respecto a la cepa WT

ID	gene	Description	greA vs WT	greB vs WT	greAgreB vs WT
SL0653	<i>gltJ</i>	Glutamate/aspartate transport system permease protein gltJ	-1,52	-1,47	5,50
SL0654	<i>gltI</i>	Glutamate/aspartate periplasmic-binding protein	-1,40	-1,20	6,78
SL0655	<i>Int</i>	Apolipoprotein N-acyltransferase	-1,21	-1,42	-2,17
SL0660	<i>ubiF</i>	2-octaprenyl-3-methyl-6-methoxy-1,4-benzoquinol hydroxylase	1,46	1,20	2,78
SL0669	<i>ybfM</i>	Uncharacterized protein ybfM	-1,09	-1,10	2,74
SL0670	<i>ybfN</i>	Uncharacterized lipoprotein ybfN	1,01	-1,18	3,34
SL0671	<i>citA</i>	Citrate-proton symporter	-1,21	-1,15	2,57
SL0672	<i>citB</i>	Citrate utilization protein B	1,06	-1,08	3,82
SL0673	<i>ifcA</i>	Fumarate reductase flavoprotein subunit	-1,01	-1,07	2,24
SL0675	<i>fur</i>	Ferric uptake regulation protein	1,00	1,07	-2,81
SL0676	<i>fldA</i>	Flavodoxin-1	-1,03	1,01	-1,98
SL0681	-	5-Nitroimidazole Antibiotic Resistance Protein	1,06	1,14	-5,70
SL0682	<i>potE</i>	Putrescine-ornithine antiporter	1,06	-1,20	-4,57
SL0683	<i>speF</i>	Ornithine decarboxylase, inducible	1,04	-1,26	-4,29
SL0691	<i>dtpD</i>	Dipeptide permease D	1,38	-1,01	-2,14
SL0692	<i>ybgI</i>	UPF0135 protein ybgI	1,14	1,06	2,27
SL0693	<i>ybgJ</i>	Uncharacterized protein ybgJ	1,17	1,00	2,74
SL0694	<i>ybgK</i>	Uncharacterized protein ybgK	1,17	-1,07	2,38
SL0711	<i>abrB</i>	Protein AbrB	1,38	1,17	2,71
SL0712	<i>gltA</i>	Citrate synthase	1,06	-1,00	2,70
SL0713	-	Hypothetical	-1,31	-1,16	3,77
SL0714	<i>sdhC</i>	Succinate dehydrogenase cytochrome b556 subunit	-1,15	-1,23	8,34
SL0715	<i>sdhD</i>	Succinate dehydrogenase hydrophobic membrane anchor subunit	-1,10	-1,29	6,00
SL0716	<i>sdhA</i>	Succinate dehydrogenase flavoprotein subunit	-1,00	-1,20	8,19
SL0717	<i>sdhB</i>	Succinate dehydrogenase iron-sulfur subunit	-1,01	-1,14	8,63
SL0718	<i>sucA</i>	2-oxoglutarate dehydrogenase E1 component	1,01	-1,26	2,25
SL0719	<i>sucB</i>	Dihydropolyllysine-residue succinyltransferase component of 2-oxoglutarate dehydrogenase complex	1,09	-1,10	2,41
SL0720	<i>sucC</i>	Succinyl-CoA ligase [ADP-forming] subunit beta	1,14	-1,24	3,54
SL0721	<i>sucD</i>	Succinyl-CoA ligase [ADP-forming] subunit alpha	1,10	-1,07	2,39
SL0726	<i>ybgC</i>	Acyl-CoA thioester hydrolase ybgC	-1,13	1,13	-2,47
SL0727	<i>tolQ</i>	Protein tolQ	-1,29	-1,15	-2,54
SL0728	<i>tolR</i>	Protein tolR	-1,08	-1,01	-2,59
SL0729	<i>tolA</i>	Protein tolA	1,01	1,18	-2,07
SL0740	<i>ywbl</i>	Uncharacterized HTH-type transcriptional regulator ywbl	1,10	1,17	3,02
SL0745	<i>oadB2</i>	Oxaloacetate decarboxylase beta chain	1,38	1,16	2,25
SL0746	<i>citG</i>	2-(5"-triphosphoribosyl)-3'-dephosphocoenzyme-A synthase	1,60	1,35	2,94
SL0753	<i>galE</i>	UDP-glucose 4-epimerase	1,12	1,17	2,06
SL0760	<i>modC</i>	Molybdenum import ATP-binding protein ModC	-1,14	-1,11	-2,39

Tabla suplementaria 2Genes afectados en las cepas mutantes *greA*, *greB* y *greAgreB* respecto a la cepa WT

ID	gene	Description	greA vs WT	greB vs WT	greAgreB vs WT
SL0762	<i>ybhE</i>	putative 3-carboxymuconate cyclase	1,19	1,08	2,28
SL0764	<i>hutI</i>	Imidazolonepropionase	1,16	1,05	3,21
SL0765	<i>hutG</i>	Formimidoylglutamase	1,08	-1,06	4,38
SL0766	<i>hutC</i>	Histidine utilization repressor	-1,14	-1,08	2,51
SL0767	<i>hutU</i>	Urocanate hydratase	-1,11	-1,18	21,16
SL0768	<i>hutH</i>	Histidine ammonia-lyase	-1,22	-1,51	18,07
SL0771	<i>bioB</i>	Biotin synthase	-1,22	-1,11	2,06
SL0776	<i>slrP</i>	E3 ubiquitin-protein ligase slrP	-1,49	-1,17	-6,12
SL0780	<i>moaC</i>	Molybdenum cofactor biosynthesis protein C	1,17	1,08	2,26
SL0781	<i>moaD</i>	Molybdopterin synthase sulfur carrier subunit	1,13	1,02	2,25
SL0782	<i>moaE</i>	Molybdopterin synthase catalytic subunit	1,38	1,21	2,41
SL0796	<i>rhIE</i>	ATP-dependent RNA helicase rhIE	-1,30	-1,24	-4,28
SL0799	<i>ybiJ</i>	Uncharacterized protein ybiJ	-1,05	-1,01	-3,65
SL0803	<i>glnQ</i>	Glutamine transport ATP-binding protein glnQ	-1,06	-1,33	2,29
SL0805	<i>glnH</i>	Glutamine-binding periplasmic protein	1,14	-1,22	3,68
SL0807	<i>ybiF</i>	Inner membrane transporter rhtA	1,01	-1,06	-2,23
SL0808	<i>ompX</i>	Outer membrane protein X	-1,01	1,19	-2,41
SL0813	<i>ybiT</i>	Uncharacterized ABC transporter ATP-binding protein ybiT	-1,23	1,08	-2,82
SL0824	<i>gsiA</i>	Glutathione import ATP-binding protein gsiA	1,11	-1,26	2,57
SL0825	<i>gsiB</i>	Glutathione-binding protein gsiB	1,21	1,04	3,72
SL0826	<i>gsiC</i>	Glutathione transport system permease protein gsiC	1,27	1,11	2,09
SL0828	<i>yliG</i>	putative Fe-S oxidoreductases family 1	-1,00	1,12	-2,33
SL0829	<i>bssR</i>	Biofilm regulator BssR	1,61	2,18	2,38
SL0835	<i>cysL</i>	HTH-type transcriptional regulator cysL	-1,55	1,10	-5,57
SL0836	<i>yxjC</i>	Uncharacterized transporter yxjC	-1,04	1,32	-2,37
SL0839	<i>dacC</i>	D-alanyl-D-alanine carboxypeptidase dacC	1,07	1,23	2,58
SL0840	<i>deoR</i>	Deoxyribose operon repressor	1,00	1,10	-2,08
SL0841	<i>ybjG</i>	Putative undecaprenyl-diphosphatase ybjG	-1,08	1,12	-2,77
SL0846	<i>ybjL</i>	Putative transport protein ybjL	-1,04	1,02	-2,78
SL0848	<i>grxA</i>	Glutaredoxin-1	-1,19	-1,03	-1,99
SL0854	<i>potF</i>	Putrescine-binding periplasmic protein	1,10	1,26	3,91
SL0855	<i>potG</i>	Putrescine transport ATP-binding protein potG	1,38	1,04	2,73
SL0856	<i>potH</i>	Putrescine transport system permease protein potH	1,29	1,16	2,71
SL0871	<i>ybjS</i>	putative nucleoside-diphosphate-sugar epimerase	-1,14	1,03	-2,45
SL0876	<i>hcp</i>	Hydroxylamine reductase	1,05	1,23	2,63
SL0879	<i>ybjX</i>	Uncharacterized protein ybjX	-1,58	1,10	-5,97
SL0880	<i>macA</i>	Macrolide-specific efflux protein macA	-1,09	1,04	-2,43
SL0883	<i>clpS</i>	ATP-dependent Clp protease adapter protein clpS	-1,14	-1,01	-3,50
SL0885	<i>tnpA1</i>	Transposase for insertion sequence element IS1541	1,26	-1,00	-2,87
SL0888	<i>ycaC</i>	Uncharacterized protein ycaC	1,10	1,07	2,29

Tabla suplementaria 2

Genes afectados en las cepas mutantes *greA*, *greB* y *greAgreB* respecto a la cepa WT

ID	gene	Description	greA vs WT	greB vs WT	greAgreB vs WT
SL0889	<i>yhhW</i>	Pirin-like protein PA2418	1,22	1,23	2,37
SL0892	-	Inner Membrane Protein	1,14	1,22	-2,29
SL0895	<i>cydD</i>	ATP-binding/permease protein cydD	1,01	-1,03	-2,02
SL0909	<i>sopD2</i>	Secreted effector protein sopD2	-8,04	1,35	-3,81
SL0911	<i>focA</i>	Probable formate transporter 1	-1,06	-1,08	-7,51
SL0912	<i>ycaO</i>	UPF0142 protein ycaO	-1,14	-1,04	-2,38
SL0917	<i>cmk</i>	Cytidylate kinase	-1,13	1,12	-2,16
SL0921	<i>msbA</i>	Lipid A export ATP-binding/permease protein mshA	-1,08	-1,02	-2,20
SL0931	<i>mukB</i>	Chromosome partition protein mukB	1,03	1,14	2,29
SL0936	<i>ompF</i>	Outer membrane protein F	-1,25	-1,04	7,42
SL0939	<i>dpaL</i>	Diaminopropionate ammonia-lyase	1,26	-1,27	3,64
SL0940	<i>yflA</i>	putative transcriptional regulator, Lrp family	1,28	1,08	3,99
SL0948	<i>ydaE</i>	Hypothetical	-2,04	-1,32	-1,12
SL0949	-	Hypothetical	-2,04	-1,24	-2,03
SL0951	<i>C1</i>	Gifsy-2 Prophage CI Protein	-1,47	1,16	-2,19
SL0952	<i>ydaU</i>	Gifsy-2 replication Protein O	-2,00	-1,28	-1,62
SL0963	-	Bacteriophage Protein	-1,44	-1,22	-2,18
SL0965	<i>gtgA</i>	putative bacteriophage encoded virulence protein	-1,87	-1,12	-2,25
SL0966	<i>nucD</i>	Probable lysozyme from lambdoid prophage DLP12	-1,77	-1,04	-3,53
SL0967	<i>rzpD</i>	Putative Rz endopeptidase from lambdoid prophage DLP12	-2,04	-1,37	-4,10
SL0968	-	Hypothetical	-2,15	-1,28	-3,14
SL0969	-	Phage Terminase Large Subunit	-1,39	-1,38	-2,08
SL0973	-	putative RecA/RadA recombinase	-2,06	-1,33	-2,53
SL0974	-	ATP-binding sugartransporter-like protein	-1,91	-1,39	-2,39
SL0975	-	Minor Tail Protein Z-Like	-1,91	-1,36	-2,19
SL0979	-	Minor Tail Protein	-1,52	-1,14	-2,27
SL0984	-	Phage Minor Tail Protein L	-1,39	-1,24	-2,05
SL0987	-	Hocificity Protein J	-1,70	-1,15	-2,37
SL0988	<i>stfQ</i>	Side tail fiber protein homolog from lambdoid prophage Qin	-1,78	-1,55	-2,71
SL0989	<i>ycdD</i>	Tail fiber assembly protein homolog from lambdoid prophage Fels-1	-1,94	-1,45	-3,53
SL0990	-	Hypothetical (pseudo)	-2,79	-1,68	-6,38
SL0993	<i>yedK</i>	Uncharacterized protein yedK (gtgD)	-1,37	-1,07	-1,98
SL0994	-	Hypothetical	-1,83	-1,71	-3,96
SL0995	<i>gtgE</i>	Prophage Encoded Virulence Factor	-2,02	-1,28	-1,84
SL0996	<i>msgA</i>	Virulence protein msgA (gtgF)	-1,48	-1,02	-5,56
SL0999	<i>ycbW</i>	Uncharacterized protein ycbW	-1,29	-1,11	-3,12
SL1000	<i>ycbX</i>	Putative iron-sulfur protein	-1,07	-1,09	-2,33
SL1012	<i>yccR</i>	putative DNA transformation protein	1,20	1,07	3,23
SL1014	<i>yccF</i>	Inner membrane protein yccF	1,04	-1,03	-2,33
SL1016	<i>mgsA</i>	Methylglyoxal synthase	1,08	1,22	2,85
SL1018	<i>yccU</i>	Uncharacterized protein yccU	1,13	1,36	2,07
SL1019	<i>yccV</i>	putative inner membrane protein	1,14	1,34	2,80
SL1026	<i>pipA</i>	Hypothetical	-1,63	1,10	-3,52
SL1027	<i>pipB</i>	Secreted effector protein pipB	-2,78	1,16	-16,02
SL1028	-	Inner Membrane Protein	-2,14	-1,05	-47,98

Tabla suplementaria 2Genes afectados en las cepas mutantes *greA*, *greB* y *greAgreB* respecto a la cepa WT

ID	gene	Description	greA vs WT	greB vs WT	greAgreB vs WT
SL1029	<i>pipC</i>	cell invasion protein	-1,10	1,11	-8,91
SL1030	<i>sopB</i>	Inositol phosphate phosphatase sopB	-1,10	-1,03	-10,63
SL1040	<i>hpaG</i>	4-hydroxyphenylacetate degradation bifunctional isomerase/decarboxylase	-1,05	-1,11	7,56
SL1041	<i>hpcC</i>	5-carboxymethyl-2-hydroxymuconate semialdehyde dehydrogenase	1,01	-1,10	7,23
SL1042	<i>hpcB</i>	3,4-dihydroxyphenylacetate 2,3-dioxygenase	-1,01	-1,16	6,00
SL1043	<i>hpcD</i>	5-carboxymethyl-2-hydroxymuconate Delta-isomerase	-1,06	-1,20	5,31
SL1044	<i>hpcG</i>	2-oxo-hepta-3-ene-1,7-dioic acid hydratase	-1,17	-1,78	3,18
SL1045	<i>hpcH</i>	4-hydroxy-2-oxo-heptane-1,7-dioate aldolase	-1,41	-2,00	3,02
SL1046	<i>hpaX</i>	putative 4-hydroxyphenylacetate permease	1,13	-1,13	3,69
SL1049	<i>iraM</i>	Anti-adaptor protein iraM	-1,15	1,06	-2,94
SL1056	<i>agp</i>	Glucose-1-phosphatase	1,04	1,28	3,03
SL1061	-	Uncharacterized protein R02472	1,20	1,19	9,50
SL1062	<i>putA</i>	Bifunctional protein putA	1,76	1,51	77,71
SL1063	<i>putP</i>	Sodium/proline symporter	1,15	-1,25	12,16
SL1065	<i>yfeT</i>	Uncharacterized HTH-type transcriptional regulator HI_0143	-1,09	-1,13	-2,08
SL1066	<i>sgIT</i>	Sodium/glucose cotransporter	1,15	-1,18	6,36
SL1067	<i>nanE1</i>	Putative N-acetylmannosamine-6-phosphate 2-epimerase 1	1,14	1,00	4,53
SL1068	<i>nanM</i>	N-acetylneuraminate epimerase	-1,44	-1,77	4,04
SL1069	<i>yiiY</i>	Uncharacterized protein yiiY	-1,43	-1,50	5,40
SL1070	<i>yjhB</i>	Putative metabolite transport protein yjhB	-1,31	-1,41	2,42
SL1077	<i>csgF</i>	Curli production assembly/transport component csgF	1,01	1,13	2,00
SL1083	<i>ymdA</i>	Uncharacterized protein ymdA	1,05	-1,09	3,20
SL1086	<i>mdoC</i>	Glucans biosynthesis protein C	1,21	1,22	-2,02
SL1089	<i>yceK</i>	Uncharacterized protein yceK	1,14	1,08	2,17
SL1090	<i>msyB</i>	Acidic protein msyB	1,23	1,20	2,50
SL1092	<i>htrB</i>	Lipid A biosynthesis lauroyl acyltransferase	-1,04	-1,13	-2,37
SL1102	<i>grxB</i>	Glutaredoxin-2	1,21	1,37	2,26
SL1103	<i>mdtH</i>	Multidrug resistance protein mdtH	1,13	1,19	-2,07
SL1104	<i>rimJ</i>	Ribosomal-protein-alanine acetyltransferase	1,23	1,04	2,57
SL1105	<i>yceH</i>	UPF0502 protein yceH	1,32	1,25	3,95
SL1106	<i>mviM</i>	Virulence factor mviM	1,26	1,13	2,46
SL1107	<i>mviN</i>	Virulence factor mviN	1,22	1,13	-2,09
SL1110	<i>flgA</i>	Flagella basal body P-ring formation protein flgA	1,52	1,11	3,45
SL1115	<i>flgF</i>	Flagellar basal-body rod protein flgF	1,06	-1,01	2,09
SL1116	<i>flgG</i>	Flagellar basal-body rod protein flgG	1,03	1,01	2,14
SL1120	<i>flgK</i>	Flagellar hook-associated protein 1	-1,10	1,09	-2,64
SL1129	<i>plsX</i>	Phosphate acyltransferase	-1,11	-1,30	-4,72
SL1130	<i>fabH</i>	3-oxoacyl-[acyl-carrier-protein] synthase 3	1,17	-1,08	-2,12
SL1151	<i>bhsA</i>	Multiple stress resistance protein BhsA	1,06	1,26	-2,12
SL1154	<i>lolC</i>	Lipoprotein-releasing system transmembrane protein lolC	1,20	1,01	-2,02

Tabla suplementaria 2Genes afectados en las cepas mutantes *greA*, *greB* y *greAgreB* respecto a la cepa WT

ID	gene	Description	greA vs WT	greB vs WT	greAgreB vs WT
SL1160	<i>potC</i>	Spermidine/putrescine transport system permease protein potC	-1,49	-1,06	-2,92
SL1161	<i>sifA</i>	Secreted effector protein sifA	-15,51	-1,07	-3,57
SL1168	<i>phoQ</i>	Virulence sensor histidine kinase phoQ	-1,28	-1,16	-2,17
SL1172	<i>trmU</i>	tRNA-specific 2-thiouridylase mnma	1,06	1,12	-2,25
SL1176	<i>icdA</i>	Isocitrate dehydrogenase [NADP]	-1,06	-1,25	3,29
SL1177	-	Bacteriophage Protein	-2,96	1,17	-25,20
SL1178	-	Hypothetical Protein SL1178	-2,75	1,66	-7,87
SL1179	<i>envF</i>	Probable lipoprotein envF	-1,32	1,19	-2,17
SL1180	<i>msgA</i>	Virulence protein msgA	-1,13	1,20	-2,85
SL1181	<i>envE</i>	Probable lipoprotein envE	-1,28	1,13	-3,82
SL1182	<i>cspH</i>	Cold shock-like protein cspH	-1,05	1,31	-3,33
SL1183	<i>pagD</i>	Virulence protein pagD	-2,53	1,62	-6,00
SL1184	<i>pagC</i>	Virulence membrane protein pagC	-2,42	1,32	-11,99
SL1186	-	Hypothetical	-1,47	1,10	-4,22
SL1189	<i>yodB</i>	Cytochrome b561 homolog 1	-1,39	-1,02	-2,27
SL1191	<i>xp55</i>	Protein XP55	1,49	-1,02	3,96
SL1192	<i>dppB</i>	Putative peptide transport system permease protein BMEII0209	1,22	-1,42	2,88
SL1194	<i>nikD</i>	Nickel import ATP-binding protein NikD	1,11	-1,20	2,65
SL1198	<i>yodA</i>	Metal-binding protein yodA	1,34	1,13	2,48
SL1201	<i>ycgE</i>	Uncharacterized HTH-type transcriptional regulator ycgE	-1,06	1,11	-2,37
SL1204	<i>aroQ</i>	Monofunctional chorismate mutase	-2,19	1,16	-3,35
SL1205	<i>leuE</i>	Leucine efflux protein	-1,32	-1,11	-2,13
SL1216	<i>yeaL</i>	UPF0756 membrane protein yeaL	1,06	-1,06	-2,55
SL1217	<i>yeaK</i>	Uncharacterized protein yeaK	-1,21	-1,22	-2,37
SL1218	<i>yeaJ</i>	Putative diguanylate cylase YeaJ	1,01	-1,01	-3,03
SL1220	<i>yeaG</i>	Uncharacterized protein yeaG	1,08	1,16	2,00
SL1226	<i>msrB</i>	Peptide methionine sulfoxide reductase msrB	1,03	-1,04	2,56
SL1227	<i>yeaC</i>	Uncharacterized protein yeaC	1,32	1,05	3,00
SL1236	<i>nudG</i>	CTP pyrophosphohydrolase	-1,29	1,22	-2,76
SL1237	<i>xthA</i>	Exodeoxyribonuclease III	-1,03	-1,08	-2,28
SL1238	<i>astC</i>	Succinylornithine transaminase	-1,30	-1,41	43,62
SL1239	<i>astA</i>	Arginine N-succinyltransferase	-1,37	-2,03	26,67
SL1240	<i>astD</i>	N-succinylglutamate 5-semialdehyde dehydrogenase	-1,43	-1,74	23,23
SL1241	<i>astB</i>	N-succinylarginine dihydrolase	-1,35	-1,81	14,27
SL1242	<i>astE</i>	Succinylglutamate desuccinylase	-1,19	-2,02	8,31
SL1243	<i>spy</i>	Spheroplast protein Y	-1,08	1,19	2,21
SL1247	<i>celA</i>	N,N'-diacetylchitobiose-specific phosphotransferase enzyme IIB component	-1,10	-1,11	2,05
SL1248	<i>celB</i>	N,N'-diacetylchitobiose permease IIC component	1,03	-1,15	2,19
SL1255	<i>ydjN</i>	Uncharacterized symporter ydjN	-1,04	1,01	3,28
SL1259	<i>yniA</i>	Uncharacterized protein yniA	1,23	1,38	3,45
SL1261	<i>pfkB</i>	6-phosphofructokinase isozyme 2	1,16	1,13	2,15
SL1262	<i>ydiY</i>	Uncharacterized protein ydiY	-1,13	1,09	-3,05
SL1263	-	Hypothetical	-1,90	-1,40	-12,64

Tabla suplementaria 2

 Genes afectados en las cepas mutantes *greA*, *greB* y *greAgreB* respecto a la cepa WT

ID	gene	Description	<i>greA</i> vs WT	<i>greB</i> vs WT	<i>greAgreB</i> vs WT
SL1264	-	DNA/RNA Non-Specific Endonuclease	-2,17	1,18	-7,63
SL1265	<i>nucA</i>	Nuclease	-2,21	1,00	-13,64
SL1266	<i>rfc</i>	O-antigen polymerase	-1,22	1,02	-2,41
SL1278	<i>cdgR</i>	Cyclic di-GMP regulator <i>cdgR</i>	-1,08	1,07	-2,05
SL1283	<i>ppsA</i>	Phosphoenolpyruvate synthase	1,03	-1,18	4,30
SL1287	<i>ydiR</i>	Putative electron transfer flavoprotein subunit <i>ydiR</i>	-1,32	1,23	-2,22
SL1291	<i>ydiF</i>	Uncharacterized protein <i>ydiF</i>	1,35	1,01	4,23
SL1292	<i>aroD</i>	3-dehydroquininate dehydratase	1,21	1,04	2,37
SL1293	<i>ydiB</i>	Quinate/shikimate dehydrogenase	-1,06	-1,22	2,17
SL1294	<i>ydiN</i>	Inner membrane transport protein <i>ydiN</i>	1,50	1,58	-2,01
SL1297	<i>ydiL</i>	Uncharacterized protein <i>ydiL</i>	1,38	1,15	-2,44
SL1302	<i>ydjN</i>	Uncharacterized symporter <i>ydjN</i>	1,07	-1,02	6,96
SL1303	<i>sufA</i>	Protein <i>sufA</i>	1,22	1,43	4,08
SL1304	<i>sufB</i>	FeS cluster assembly protein <i>sufB</i>	1,17	1,13	2,10
SL1309	<i>ynhG</i>	Probable L,D-transpeptidase <i>YnhG</i>	1,25	1,14	2,90
SL1313	<i>puuP</i>	Putrescine importer	-1,06	-1,08	4,25
SL1314	<i>pip</i>	Proline iminopeptidase	-1,21	-1,35	4,08
SL1315	-	Hypothetical	-1,21	-1,22	3,97
SL1316	<i>rbsK</i>	Ribokinase	-1,13	-1,17	8,68
SL1317	<i>ttrA</i>	tetrathionate reductase subunit A	1,20	1,42	-2,14
SL1318	<i>ttrC</i>	Tetrathionate Reductase Subunit C	1,05	1,47	-2,98
SL1319	<i>ttrB</i>	Tetrathionate Reductase Subunit B	1,01	1,19	-2,70
SL1320	<i>ttrS</i>	Sensor protein	1,42	1,12	2,21
SL1323	<i>ybgA</i>	Uncharacterized protein <i>ybgA</i>	1,18	1,12	2,23
SL1324	<i>mlrA</i>	HTH-type transcriptional regulator <i>mlrA</i>	-1,84	-1,14	-2,75
SL1325	<i>ssrB</i>	putative two-component response regulator	-2,38	1,26	-2,58
SL1326	<i>spiR</i>	Sensor kinase protein	-3,42	-1,01	-2,56
SL1327	<i>spiC</i>	Salmonella pathogenicity island protein C	-7,40	1,89	-7,03
SL1328	<i>spiA</i>	Yop proteins translocation protein C	-8,81	1,31	-6,06
SL1329	<i>ssaD</i>	Type-III Secretion Protein	-5,18	-1,04	-7,92
SL1330	-	Secretion System Protein	-4,91	1,17	-4,88
SL1331	<i>sseA</i>	Type III secretion system chaperone <i>sseA</i>	-7,73	1,49	-3,08
SL1332	<i>sseB</i>	Secreted effector protein <i>sseB</i>	-6,60	1,31	-2,69
SL1333	<i>ssaA</i>	Type III Secretion Low Calcium Response Chaperone <i>LcrH/SycD</i>	-5,68	1,13	-2,44
SL1334	<i>sseC</i>	Secreted effector protein <i>sseC</i>	-6,74	1,15	-2,37
SL1335	<i>sseD</i>	Secreted effector protein <i>sseD</i>	-5,29	1,33	-1,44
SL1336	<i>sseE</i>	Secreted Effector Protein	-4,59	1,21	-1,28
SL1337	<i>sscB</i>	Type III Secretion Chaperone	-5,73	1,14	-1,55
SL1338	<i>sseF</i>	Hypothetical	-2,64	-1,03	-1,30
SL1339	<i>sseG</i>	Hypothetical	-2,53	-1,17	-1,36
SL1340	<i>ssaG</i>	Secretion System Apparatus <i>SsaG</i>	-4,80	1,60	-1,67
SL1341	<i>ssaH</i>	Hypothetical	-14,29	1,75	-18,14
SL1342	<i>ssaI</i>	Type III Secretion System Apparatus Protein	-14,52	1,76	-22,27

Tabla suplementaria 2

Genes afectados en las cepas mutantes *greA*, *greB* y *greAgreB* respecto a la cepa WT

ID	gene	Description	<i>greA</i> vs WT	<i>greB</i> vs WT	<i>greAgreB</i> vs WT
SL1343	<i>ssaJ</i>	Secretion system apparatus lipoprotein ssaJ	-15,99	1,46	-17,00
SL1344	-	Type III Secretion Apparatus	-11,83	1,31	-16,48
SL1345	<i>ssaK</i>	Secretion system apparatus protein ssaK	-11,43	1,32	-11,64
SL1346	<i>ssaL</i>	Secretion system apparatus protein ssaL	-8,55	1,37	-5,60
SL1347	<i>ssaM</i>	Secretion system apparatus protein ssaM	-8,23	1,24	-5,75
SL1348	<i>ssaV</i>	Secretion system apparatus protein ssaV	-2,98	1,24	-1,41
SL1349	<i>ssaN</i>	Probable secretion system apparatus ATP synthase ssaN	-3,19	1,27	1,14
SL1350	<i>ssaO</i>	Secretion system apparatus protein ssaO	-3,52	1,44	1,32
SL1351	<i>ssaP</i>	Secretion system apparatus protein ssaP	-2,62	1,21	-1,05
SL1352	<i>ssaQ</i>	Secretion system apparatus protein SsaQ	-2,23	1,24	1,11
SL1353	<i>yscR</i>	Virulence protein yscR	-8,10	1,79	-4,01
SL1354	<i>ssaS</i>	Secretion system apparatus protein SsaS	-11,20	1,36	-6,62
SL1355	<i>ssaT</i>	Secretion system apparatus protein ssaT	-4,96	1,26	-4,28
SL1360	<i>ydhC</i>	Inner membrane transport protein ydhC	-1,19	-1,07	-24,59
SL1364	<i>ydhO</i>	Uncharacterized protein ydhO	-1,19	1,04	-2,16
SL1366	<i>rnt</i>	Ribonuclease T	1,06	-1,20	-2,27
SL1376	<i>slyA</i>	Transcriptional regulator slyA	-1,20	1,17	-2,26
SL1380	<i>pdxH</i>	Pyridoxine/pyridoxamine 5'-phosphate oxidase	1,10	1,04	-2,30
SL1383	<i>gst</i>	Glutathione S-transferase	1,30	1,18	2,14
SL1391	<i>rnfA</i>	Electron transport complex protein rnfA	1,23	1,06	-2,32
SL1392	<i>ydgK</i>	Inner membrane protein ydgK	-1,11	-1,15	-2,54
SL1393	<i>cnu</i>	OriC-binding nucleoid-associated protein	-1,19	1,07	-2,33
SL1395	<i>add</i>	Adenosine deaminase	-2,04	1,21	-2,80
SL1398	<i>fumA</i>	Fumarate hydratase class I, aerobic	1,13	-1,26	5,66
SL1399	-	Hypothetical Protein SL1399	1,53	1,02	7,56
SL1400	<i>fumC</i>	Fumarate hydratase class II	1,16	1,05	4,75
SL1401	<i>tus</i>	DNA replication terminus site-binding protein	1,35	1,09	3,56
SL1404	<i>ompN</i>	Outer membrane protein N	-1,25	1,15	2,01
SL1405	<i>rstA</i>	Transcriptional regulatory protein rstA	-1,14	1,08	-3,50
SL1414	<i>ydgD</i>	Uncharacterized serine protease ydgD	1,06	1,04	2,11
SL1421	<i>opuBA</i>	Choline transport ATP-binding protein opuBA	1,03	1,04	2,73
SL1422	<i>opuCB</i>	Glycine betaine/carnitine/choline transport system permease protein opuCB	1,01	-1,06	3,34
SL1423	<i>opuCC</i>	Glycine betaine/carnitine/choline-binding protein	1,02	-1,08	4,59
SL1424	<i>opuCB</i>	Glycine betaine/carnitine/choline transport system permease protein opuCB	-1,00	-1,03	3,48
SL1425	<i>dmsD</i>	Twin-arginine leader-binding protein dmsD	1,18	-1,01	-2,00
SL1435	<i>rspA</i>	Starvation-sensing protein rspA	-1,55	-1,73	7,90
SL1436	<i>rspB</i>	Starvation-sensing protein rspB	-1,23	-1,45	8,06
SL1437	<i>ydfJ</i>	Putative inner membrane metabolite transport protein ydfJ	-1,19	-1,35	4,11
SL1443	<i>ymdF</i>	Uncharacterized protein ymdF	-1,27	1,29	-2,06
SL1452	<i>sotB</i>	Probable sugar efflux transporter	1,14	1,36	-3,01
SL1454	<i>ynel</i>	Aldehyde dehydrogenase-like protein ynel	-1,03	1,04	-2,65
SL1455	<i>glsA2</i>	Glutaminase 2	1,01	-1,08	-2,29

Tabla suplementaria 2Genes afectados en las cepas mutantes *greA*, *greB* y *greAgreB* respecto a la cepa WT

ID	gene	Description	greA vs WT	greB vs WT	greAgreB vs WT
SL1457	<i>yneE</i>	UPF0187 protein yneE	-1,08	1,01	-2,75
SL1459	<i>ompC</i>	Outer membrane protein C	-1,17	1,00	2,18
SL1466	<i>hupZ</i>	Probable Ni/Fe-hydrogenase B-type cytochrome subunit	-1,22	-1,24	2,79
SL1467	<i>hupB</i>	Uptake hydrogenase large subunit	-1,17	-1,17	3,66
SL1468	<i>hoxK</i>	Uptake hydrogenase small subunit	-1,12	-1,13	2,86
SL1471	<i>rspB</i>	Uncharacterized zinc-type alcohol dehydrogenase-like protein HI_0053	-1,46	-1,07	2,30
SL1472	<i>exuT</i>	Hexuronate transporter	-1,63	-1,16	3,48
SL1473	<i>pqaA</i>	PhoPQ-activated protein	-2,52	1,11	-3,72
SL1475	<i>yhjG</i>	Uncharacterized aromatic compound monooxygenase yhjG	-1,14	-1,35	3,46
SL1476	-	MarR Family Transcriptional Regulator	-1,08	-1,08	2,15
SL1477	<i>queA</i>	S-adenosylmethionine:tRNA ribosyltransferase-isomerase	-1,49	1,25	-1,99
SL1484	-	Coiled-Coil Protein	-1,18	-2,93	-1,44
SL1486	-	Uncharacterized Na(+)/H(+) antiporter HI_1107	1,17	-1,49	2,21
SL1489	<i>treY</i>	Maltooligosyl trehalose synthase	1,42	1,24	3,14
SL1494	<i>bdm</i>	Protein bdm homolog	-1,04	1,05	-4,02
SL1496	<i>sfcA</i>	NAD-dependent malic enzyme	1,20	-1,33	2,28
SL1505	<i>smvA</i>	Methyl viologen resistance protein smvA	-1,22	-1,29	-2,99
SL1507	<i>narU</i>	Nitrite extrusion protein 2	1,27	1,03	11,11
SL1508	<i>narZ</i>	Respiratory nitrate reductase 2 alpha chain	1,02	1,04	6,46
SL1509	<i>narY</i>	Respiratory nitrate reductase 2 beta chain	-1,04	1,09	5,04
SL1510	<i>narW</i>	Probable nitrate reductase molybdenum cofactor assembly chaperone NarW	1,11	1,04	4,15
SL1511	<i>narV</i>	Respiratory nitrate reductase 2 gamma chain	1,08	1,07	4,38
SL1513	<i>nhoA</i>	N-hydroxyarylamine O-acetyltransferase	-1,08	-1,04	-2,40
SL1525	<i>srfB</i>	Virulence Protein SrfB	1,49	-1,02	4,34
SL1526	<i>srfC</i>	Virulence Factor	1,42	-1,05	2,39
SL1528	<i>ydcW</i>	Gamma-aminobutyraldehyde dehydrogenase	1,09	1,11	2,33
SL1531	<i>ugtL</i>	D-Alanyl-D-Alanine Dipeptidase	-2,42	1,47	-4,95
SL1532	<i>sifB</i>	Secreted effector protein sifB	-6,21	1,85	-3,28
SL1533	<i>yncJ</i>	Uncharacterized protein yncJ	-4,14	1,63	-2,28
SL1537	<i>ydcL</i>	Uncharacterized lipoprotein ydcL	1,44	-1,04	2,52
SL1540	<i>ydcK</i>	Uncharacterized acetyltransferase ydcK	1,13	-1,14	2,24
SL1541	<i>rimL</i>	Ribosomal-protein-serine acetyltransferase	1,16	1,11	2,07
SL1542	<i>sgcX</i>	Putative aminopeptidase sgcX	1,37	1,22	2,48
SL1543	<i>sgcB</i>	Putative phosphotransferase enzyme IIB component sgcB	1,16	1,24	2,02
SL1544	<i>sgcC</i>	Putative permease IIC component	1,24	1,20	2,09
SL1551	<i>yceI</i>	UPF0312 protein VPA0850	1,36	1,06	2,34
SL1553	<i>pnbA</i>	Para-nitrobenzyl esterase	1,36	-1,32	3,07
SL1554	<i>ydcJ</i>	Uncharacterized protein ydcJ	1,30	1,10	9,60
SL1559	<i>steB</i>	Secreted effector protein steB	-1,78	1,43	-16,75
SL1560	<i>tfpB</i>	Protein tfpB	-1,29	1,88	-2,37
SL1561	<i>sseJ</i>	Secreted effector protein sseJ	-4,43	1,67	-2,52

Tabla suplementaria 2Genes afectados en las cepas mutantes *greA*, *greB* y *greAgreB* respecto a la cepa WT

ID	gene	Description	greA vs WT	greB vs WT	greAgreB vs WT
SL1562	-	Hypothetical	-1,22	1,44	-2,15
SL1564	<i>yecS</i>	Inner membrane amino-acid ABC transporter permease protein yecS	-1,20	1,15	-2,41
SL1567	-	Hypothetical	-1,43	1,20	-1,98
SL1570	<i>ycdF</i>	Protein ycdF	1,23	1,09	2,05
SL1578	<i>hslJ</i>	Heat shock protein hslJ	1,22	1,18	-2,04
SL1582	<i>uspF</i>	Universal stress protein F	1,10	1,34	2,66
SL1592	<i>uspE</i>	Universal stress protein E	1,17	1,34	2,28
SL1593	<i>ynaJ</i>	Uncharacterized protein ynaJ	1,25	1,00	2,94
SL1602	-	Hypothetical	-1,76	1,08	-4,92
SL1607	<i>yhjC</i>	Uncharacterized HTH-type transcriptional regulator yhjC	1,09	1,08	2,41
SL1612	<i>tpx</i>	Probable thiol peroxidase	-1,28	-1,22	2,53
SL1617	<i>pspD</i>	Phage shock protein D	-1,19	1,34	-2,02
SL1619	<i>pspB</i>	Phage shock protein B	-1,15	1,34	-2,10
SL1621	<i>pspF</i>	Psp operon transcriptional activator	1,09	-1,00	2,78
SL1628	<i>steC</i>	Secreted effector kinase steC	-5,23	1,46	-2,62
SL1634	<i>yciR</i>	putative PAS/PAC domain protein	1,07	1,04	2,42
SL1637	<i>osmB</i>	Osmotically-inducible lipoprotein B	-1,30	1,02	-4,73
SL1639	<i>pyrF</i>	Orotidine 5'-phosphate decarboxylase	-1,46	1,05	-2,53
SL1640	<i>yciM</i>	Uncharacterized protein yciM	-1,08	1,06	-2,25
SL1644	<i>acnA</i>	Aconitate hydratase 1	1,18	1,02	3,38
SL1650	<i>btuR</i>	Cob(II)yrinic acid a,c-diamide adenosyltransferase	1,19	-1,12	2,90
SL1655	<i>trpD</i>	Anthranilate synthase component II	-1,04	1,09	2,35
SL1659	<i>ymdF</i>	Uncharacterized protein ymdF	-1,55	1,10	-3,54
SL1660	<i>yciF</i>	Protein yciF	-1,73	1,18	-3,65
SL1661	<i>yciE</i>	Protein yciE	-1,42	1,25	-3,21
SL1662	<i>katN</i>	Probable manganese catalase	-1,31	1,20	-2,83
SL1666	<i>ispZ</i>	Probable intracellular septation protein	-1,19	-1,16	-2,06
SL1668	<i>tonB</i>	Protein tonB	1,07	1,31	-2,20
SL1673	<i>oppF</i>	Oligopeptide transport ATP-binding protein oppF	1,18	1,00	2,57
SL1676	<i>oppB</i>	Oligopeptide transport system permease protein oppB	-1,10	-1,72	2,18
SL1677	<i>oppA</i>	Periplasmic oligopeptide-binding protein	-1,05	-1,22	3,54
SL1678	-	Hypothetical	-1,01	1,01	1,98
SL1679	<i>yhcE</i>	UPF0056 membrane protein yhcE	-1,34	1,25	-3,72
SL1689	<i>narI</i>	Respiratory nitrate reductase 1 gamma chain	1,04	1,24	2,45
SL1690	<i>narJ</i>	Nitrate reductase molybdenum cofactor assembly chaperone NarJ	1,11	1,01	2,43
SL1691	<i>narH</i>	Respiratory nitrate reductase 1 beta chain	1,08	1,23	2,12
SL1692	<i>narG</i>	Respiratory nitrate reductase 1 alpha chain	1,06	1,07	2,24
SL1696	<i>yhcO</i>	Uncharacterized protein yhcO	-1,07	-1,09	-2,00
SL1702	<i>sirB2</i>	Protein sirB2	1,48	-1,03	-2,42
SL1703	<i>hemK</i>	Protein methyltransferase hemK	1,30	-1,09	-2,25
SL1704	<i>prfA</i>	Peptide chain release factor 1	1,21	1,09	-2,31
SL1706	<i>lolB</i>	Outer-membrane lipoprotein lolB	-1,13	-1,15	-2,18
SL1710	<i>yhcH</i>	Uncharacterized protein yhcH	1,38	1,30	3,18

Tabla suplementaria 2Genes afectados en las cepas mutantes *greA*, *greB* y *greAgreB* respecto a la cepa WT

ID	gene	Description	greA vs WT	greB vs WT	greAgreB vs WT
SL1714	<i>hyaA</i>	Hydrogenase-1 small chain	-1,30	-2,04	-2,23
SL1723	<i>gdhA</i>	Glutamate dehydrogenase	1,13	-1,42	17,53
SL1724	<i>treA</i>	Periplasmic trehalase	1,22	1,12	2,95
SL1726	<i>ycgR</i>	Flagellar brake protein YcgR	-1,35	1,14	-5,01
SL1727	<i>emtA</i>	Endo-type membrane-bound lytic murein transglycosylase A	1,00	1,06	-2,10
SL1727	<i>emtA</i>	Endo-type membrane-bound lytic murein transglycosylase A	1,00	1,06	-2,10
SL1729	<i>cvrA</i>	Cell volume regulation protein A	-1,03	1,01	-2,77
SL1730	<i>dadX</i>	Alanine racemase, catabolic	-1,27	-1,83	6,94
SL1731	<i>dadA</i>	D-amino acid dehydrogenase small subunit	-1,36	-1,36	9,25
SL1732	<i>ycgB</i>	Uncharacterized protein ycgB	-1,06	1,21	2,94
SL1735	<i>dsbB</i>	Disulfide bond formation protein B	1,07	-1,14	-2,28
SL1737	<i>gns</i>	Protein gns	1,34	1,53	2,78
SL1742	<i>minC</i>	Probable septum site-determining protein minC	-1,29	-1,16	-4,10
SL1748	<i>yeaY</i>	Uncharacterized lipoprotein yeaY	-1,02	1,19	-2,20
SL1749	<i>yeaZ</i>	M22 peptidase homolog yeaZ	-1,33	-1,49	-2,27
SL1761	<i>manZ</i>	Mannose permease IID component	1,46	1,17	-2,11
SL1762	<i>yobD</i>	UPF0266 membrane protein yobD	1,13	-1,35	-5,91
SL1763	<i>yebN</i>	UPF0059 membrane protein CKO_01156	1,08	-1,35	-2,84
SL1768	<i>yebO</i>	Uncharacterized protein yebO	-1,07	1,12	-3,12
SL1769	<i>mgrB</i>	Protein mgrB	1,02	1,21	-3,11
SL1770	<i>yobH</i>	Uncharacterized protein yobH	-1,09	1,05	-2,58
SL1779	<i>yebU</i>	Ribosomal RNA small subunit methyltransferase F	1,12	1,03	-2,70
SL1780	<i>yebV</i>	Uncharacterized protein yebV	-1,01	1,16	-2,02
SL1782	<i>pphA</i>	Serine/threonine-protein phosphatase 1	-1,24	1,06	-4,92
SL1783	-	Hypothetical	-1,31	1,41	-8,58
SL1784	<i>sopE2</i>	Guanine nucleotide exchange factor sopE2	-1,51	1,15	-16,49
SL1785	<i>ycgX</i>	Uncharacterized protein ycgX	-1,44	1,14	-6,12
SL1786	-	Hypothetical	1,03	1,09	-2,05
SL1793	<i>pagO</i>	Protein pagO	-1,97	1,23	-5,37
SL1794	-	Hypothetical	-2,21	1,11	-7,65
SL1795	-	Hypothetical	-1,97	1,32	-5,78
SL1799	<i>pagK</i>	bacteriophage encoded pagK (phoPQ-activated protein)	-2,12	1,45	-4,28
SL1800	<i>ycdD</i>	Tail fiber assembly protein homolog from lambdoid prophage Fels-1	-1,84	-1,23	-2,96
SL1804	-	Hypothetical	-1,63	-1,36	-3,58
SL1806	<i>intE</i>	Prophage lambda integrase	1,05	1,01	2,88
SL1819	<i>edd</i>	Phosphogluconate dehydratase	-1,05	-1,08	-5,50
SL1821	<i>hexR</i>	HTH-type transcriptional regulator hexR	1,07	1,06	2,24
SL1824	<i>yebA</i>	Uncharacterized metalloprotease yebA	-1,16	-1,12	-2,29
SL1840	<i>cmoA</i>	tRNA (cmo5U34)-methyltransferase	-1,01	-1,08	-2,10
SL1844	<i>argS</i>	Arginyl-tRNA synthetase	-1,23	1,04	-3,31
SL1850	<i>cheZ</i>	Chemotaxis protein cheZ	-1,01	1,09	-2,12
SL1851	<i>cheY</i>	Chemotaxis protein cheY	-1,01	1,11	-2,17

Tabla suplementaria 2Genes afectados en las cepas mutantes *greA*, *greB* y *greAgreB* respecto a la cepa WT

ID	gene	Description	<i>greA</i> vs WT	<i>greB</i> vs WT	<i>greAgreB</i> vs WT
SL1852	<i>cheB</i>	Chemotaxis response regulator protein-glutamate methyltransferase	-1,12	1,10	-3,86
SL1853	<i>cheR</i>	Chemotaxis protein methyltransferase	-1,24	1,07	-3,83
SL1854	<i>tar</i>	Methyl-accepting chemotaxis protein II	-1,20	1,07	-2,19
SL1857	<i>motB</i>	Motility protein B	-1,29	1,06	-2,99
SL1858	<i>motA</i>	Motility protein A	-1,20	1,23	-3,31
SL1859	<i>flhC</i>	Flagellar transcriptional activator flhC	-1,22	1,15	-3,09
SL1860	<i>flhD</i>	Transcriptional activator FlhD	-1,28	1,09	-3,17
SL1865	<i>ftnB</i>	Ferritin-like protein 2	1,16	1,07	3,10
SL1870	<i>tyrP</i>	Tyrosine-specific transport protein	1,44	1,12	-1,98
SL1872	-	Hypothetical	-1,40	1,13	-4,52
SL1874	-	Hypothetical	-1,90	1,19	-4,78
SL1876	<i>uvrC</i>	UvrABC system protein C	1,11	-1,11	-2,18
SL1878	<i>yecF</i>	Uncharacterized protein yecF	-1,09	1,13	-8,87
SL1879	<i>sdiA</i>	Regulatory protein sdiA	-1,09	1,23	-3,85
SL1889	<i>fliD</i>	Flagellar hook-associated protein 2	-1,07	1,01	-2,40
SL1890	<i>fliS</i>	Flagellar protein fliS	-1,30	-1,22	-3,14
SL1891	<i>fliT</i>	Flagellar protein fliT	-1,26	-1,14	-3,00
SL1894	<i>yedE</i>	UPF0394 inner membrane protein yedE	-1,04	-1,08	3,86
SL1895	<i>yedF</i>	UPF0033 protein yedF	1,16	1,05	3,15
SL1896	-	putative 50S ribosomal protein	-1,92	-1,34	-3,36
SL1902	<i>fliJ</i>	Flagellar fliJ protein	1,20	1,30	2,04
SL1911	<i>rcaA</i>	Colanic acid capsular biosynthesis activation protein A	-1,16	1,36	-2,52
SL1922	<i>yedR</i>	Inner membrane protein yedR	1,03	1,36	-4,09
SL1923	<i>ompS1</i>	Outer membrane protein S1	1,31	1,22	2,32
SL1924	<i>cspB</i>	Cold shock-like protein cspB	-1,53	-1,31	-2,11
SL1928	-	Cytoplasmic Protein	-5,33	1,56	-7,81
SL1933	<i>ymfP</i>	Putative protein ymfP	-1,57	-1,19	-1,99
SL1942	-	Hypothetical	-1,72	-1,22	-2,95
SL1943	-	Hypothetical	-1,68	-1,15	-2,74
SL1944	-	Hypothetical	-1,59	-1,10	-2,55
SL1945	-	Hypothetical	-1,56	-1,07	-2,73
SL1946	-	Hypothetical	-1,66	-1,10	-2,68
SL1949	<i>ymfO</i>	Putative uncharacterized protein ymfO	-1,45	-1,07	-2,59
SL1950	<i>ymfN</i>	Uncharacterized protein ymfN	-1,38	-1,14	-3,34
SL1951	-	P27 Family Phage Terminase Small Subunit	-1,56	-1,17	-3,72
SL1952	-	Hypothetical	-1,58	-1,12	-3,08
SL1953	-	Hypothetical Protein SL1953	-1,40	-1,02	-2,20
SL1955	<i>rzpD</i>	Putative Rz endopeptidase from lambdoid prophage DLP12	-1,36	-1,16	-3,37
SL1956	-	Uncharacterized protein HI_1415	-1,45	-1,11	-3,36
SL1957	-	Phage Holin Lambda Family	-1,42	-1,12	-3,53
SL1961	-	Hypothetical	-1,00	1,06	2,40
SL1962	<i>yfdM</i>	Putative uncharacterized protein yfdM	-1,19	-1,23	2,13
SL1963	<i>yfdN</i>	Uncharacterized protein yfdN	-1,14	-1,13	2,23
SL1964	<i>yfdO</i>	Hypothetical	-1,30	-1,23	2,05

Tabla suplementaria 2

 Genes afectados en las cepas mutantes *greA*, *greB* y *greAgreB* respecto a la cepa WT

ID	gene	Description	<i>greA</i> vs WT	<i>greB</i> vs WT	<i>greAgreB</i> vs WT
SL1968	<i>yfdP</i>	Uncharacterized protein yfdP	-1,03	1,04	2,99
SL1969	<i>yfdQ</i>	Uncharacterized protein yfdQ	-1,17	-1,09	3,27
SL1970	<i>yfdR</i>	Uncharacterized protein yfdR	-1,20	-1,18	2,48
SL1971	-	Hypothetical	-1,18	-1,23	2,22
SL1972	-	Hypothetical	-1,10	-1,10	2,63
SL1973	-	Hypothetical	1,03	-1,30	2,66
SL1975	-	Phage Protein	-1,23	-1,25	2,00
SL1977	<i>mtfA</i>	Protein mtfA	1,31	1,30	2,90
SL1993	<i>cobS</i>	Cobalamin synthase	-1,01	-1,29	-2,17
SL2006	<i>cbiT</i>	Probable cobalt-precorrin-6Y C(15)-methyltransferase [decarboxylating]	1,08	1,11	-2,83
SL2007	<i>cbiE</i>	Probable cobalt-precorrin-6Y C(5)-methyltransferase	1,12	-1,05	-3,51
SL2008	<i>cbiD</i>	Putative cobalt-precorrin-6A synthase [deacetylating]	1,22	1,23	-2,77
SL2009	<i>cbiC</i>	Cobalt-precorrin-8X methylmutase	1,01	1,01	-2,23
SL2010	<i>cbiB</i>	Cobalamin biosynthesis protein cbiB	1,02	1,05	-3,16
SL2013	<i>pduF</i>	Propanediol diffusion facilitator	1,29	1,42	-3,03
SL2014	<i>pduA</i>	Propanediol utilization protein pduA	-1,43	1,42	-22,81
SL2015	<i>pduB</i>	Propanediol utilization protein pduB	-1,67	1,17	-40,16
SL2017	<i>pduD</i>	Propanediol dehydratase medium subunit	-1,57	-1,14	-38,60
SL2018	<i>pduE</i>	Propanediol dehydratase small subunit	-1,75	-1,25	-66,46
SL2019	<i>pduG</i>	propanediol utilization protein	-1,77	-1,18	-53,01
SL2020	<i>pduH</i>	propanediol utilization protein	-1,85	-1,16	-77,87
SL2021	<i>pduJ</i>	propanediol utilization protein	-1,69	-1,19	-20,95
SL2022	<i>pduK</i>	propanediol utilization protein	-1,67	-1,31	-18,88
SL2023	<i>pduL</i>	propanediol utilization protein	-2,00	-1,44	-25,45
SL2024	<i>pduM</i>	propanediol utilization protein	-1,98	-1,30	-26,37
SL2025	<i>pduN</i>	propanediol utilization protein	-1,73	-1,23	-20,64
SL2026	<i>pduO</i>	propanediol utilization protein	-1,80	-1,25	-21,04
SL2027	<i>pduP</i>	putative CoA-dependent proprionaldehyde dehydrogenase	-1,52	-1,18	-8,20
SL2028	<i>pduQ</i>	putative propanol dehydrogenase	-1,56	-1,41	-9,36
SL2029	<i>pduS</i>	propanediol utilization ferredoxin	-1,93	-1,59	-4,59
SL2030	<i>pduT</i>	putative propanediol utilization protein	-1,28	-1,28	-3,61
SL2031	<i>pduU</i>	putative propanediol utilization protein PduU	-1,53	-1,36	-4,09
SL2032	<i>pduV</i>	putative propanediol utilization protein PduV	-1,75	-1,80	-3,98
SL2033	<i>pduW</i>	Acetokinase	-1,52	-1,24	-3,31
SL2034	<i>pduX</i>	putative propanediol utilization protein	1,42	1,08	-2,41
SL2037	<i>gyrI</i>	DNA gyrase inhibitory protein homolog	1,20	1,24	4,09
SL2038	<i>dacD</i>	D-alanyl-D-alanine carboxypeptidase dacD	1,14	-1,00	-3,59
SL2043	<i>sopA</i>	E3 ubiquitin-protein ligase SopA	-1,29	-1,17	-11,05
SL2049	<i>hisD</i>	Histidinol dehydrogenase	1,16	-1,09	3,14
SL2050	<i>hisC</i>	Histidinol-phosphate aminotransferase	1,27	1,00	3,41
SL2051	<i>hisB</i>	Histidine biosynthesis bifunctional protein hisB	1,25	-1,13	2,86
SL2052	<i>hisH</i>	Imidazole glycerol phosphate synthase subunit hisH	1,21	-1,23	2,78

Tabla suplementaria 2Genes afectados en las cepas mutantes *greA*, *greB* y *greAgreB* respecto a la cepa WT

ID	gene	Description	greA vs WT	greB vs WT	greAgreB vs WT
SL2053	<i>hisA</i>	1-(5-phosphoribosyl)-5-[(5-phosphoribosylamino)methylideneamino]imidazole-4-carboxamide isomerase	1,22	-1,18	2,60
SL2054	<i>hisF</i>	Imidazole glycerol phosphate synthase subunit hisF	1,31	-1,03	2,74
SL2055	<i>hisI</i>	Histidine biosynthesis bifunctional protein hisIE	1,21	-1,08	2,06
SL2056	<i>wzzB</i>	Chain length determinant protein	-1,51	1,00	-6,76
SL2057	<i>udg</i>	UDP-glucose 6-dehydrogenase	-1,82	1,07	-6,30
SL2075	<i>galF</i>	UTP--glucose-1-phosphate uridylyltransferase	1,03	1,11	-2,43
SL2077	<i>wcaL</i>	Putative colanic acid biosynthesis glycosyltransferase wcaL	1,29	-1,03	3,22
SL2078	<i>wcaK</i>	Colanic acid biosynthesis protein wcaK	1,32	1,01	2,81
SL2081	<i>cpsG</i>	phosphomannomutase	1,91	1,15	2,85
SL2099	<i>udk</i>	Uridine kinase	1,19	1,20	-2,45
SL2107	<i>baeS</i>	Signal transduction histidine-protein kinase BaeS	-1,25	-1,02	-2,13
SL2112	<i>yegQ</i>	Uncharacterized protease yegQ	-1,03	1,12	-2,43
SL2114	<i>cesT</i>	Tir chaperone	-3,66	1,12	-1,47
SL2115	-	Hypothetical	-4,46	1,33	-2,96
SL2119	<i>yegT</i>	Putative nucleoside transporter yegT	-1,23	-1,16	4,25
SL2120	<i>yegU</i>	Uncharacterized protein yegU	-1,16	-1,12	2,62
SL2121	<i>yegV</i>	Uncharacterized sugar kinase yegV	-1,04	1,05	2,37
SL2128	<i>yehC</i>	Uncharacterized fimbrial chaperone yehC	1,00	-1,17	-2,06
SL2130	<i>yehE</i>	Uncharacterized protein yehE	-1,84	-1,06	-15,13
SL2135	<i>yehS</i>	Uncharacterized protein yehS	1,04	-1,15	-2,30
SL2136	<i>yehT</i>	Uncharacterized response regulatory protein yehT	1,13	1,06	3,14
SL2145	<i>dld</i>	D-lactate dehydrogenase	1,09	-1,07	2,01
SL2152	<i>mhbM</i>	3-hydroxybenzoate 6-hydroxylase	1,16	1,06	2,31
SL2153	<i>maiA</i>	Probable maleylacetoacetate isomerase	1,22	1,04	3,04
SL2154	<i>ycgM</i>	Uncharacterized protein PYRAB13970	-1,01	-1,03	3,97
SL2155	<i>gtdA</i>	Gentisate 1 2-Dioxygenase	1,03	1,05	5,13
SL2156	<i>pcaK</i>	4-hydroxybenzoate transporter	-1,10	-1,02	2,29
SL2157	<i>gbpR</i>	HTH-type transcriptional regulator gbpR	-1,37	-1,28	2,35
SL2158	<i>yohJ</i>	UPF0299 membrane protein CKO_00648	1,00	1,05	-11,34
SL2159	<i>yohK</i>	Inner membrane protein yohK	1,04	-1,03	-12,19
SL2160	<i>cdd</i>	Cytidine deaminase	1,03	-1,06	-8,24
SL2165	<i>mgIC</i>	Galactoside transport system permease protein mgIC	1,03	-1,75	6,61
SL2166	<i>mgIA</i>	Galactose/methyl galactoside import ATP-binding protein MglA	-1,07	-1,75	11,23
SL2167	<i>mgIB</i>	D-galactose-binding periplasmic protein	1,09	-1,19	10,18
SL2169	<i>yeiB</i>	Uncharacterized protein yeiB	-1,10	-1,00	-4,93
SL2170	<i>folE</i>	GTP cyclohydrolase 1	1,10	1,04	-3,82
SL2175	<i>uhpC</i>	Regulatory protein uhpC	1,13	-1,03	2,60
SL2179	<i>yeiH</i>	UPF0324 inner membrane protein yeiH	1,13	1,21	-2,57
SL2181	<i>fruA</i>	PTS system fructose-specific EIIBC component	1,17	1,23	-10,61
SL2182	<i>fruK</i>	1-phosphofructokinase	1,06	1,18	-8,46

Tabla suplementaria 2Genes afectados en las cepas mutantes *greA*, *greB* y *greAgreB* respecto a la cepa WT

ID	gene	Description	greA vs WT	greB vs WT	greAgreB vs WT
SL2183	<i>fruB</i>	Multiphosphoryl transfer protein	-1,06	-1,02	-6,16
SL2184	<i>setB</i>	Sugar efflux transporter B	-1,25	-1,03	-5,41
SL2190	<i>yeiU</i>	Inner membrane protein yeiU	-1,14	1,09	-2,33
SL2191	<i>spr</i>	Lipoprotein spr	-1,35	1,17	-3,81
SL2204	<i>yejL</i>	UPF0352 protein yejL	-1,17	-1,16	-2,47
SL2205	<i>yejM</i>	Inner membrane protein yejM	1,01	-1,05	-2,01
SL2212	-	Prohead Protease	1,04	1,13	-2,07
SL2212	-	Prohead Protease	1,04	1,13	-2,07
SL2213	-	Hypothetical	1,16	-1,13	-2,23
SL2214	<i>pifA</i>	KAP P-Loop Domain-Containing Protein	-1,29	-1,52	2,07
SL2220	-	Homolog Of Virulence Protein MsgA	-1,66	1,18	-2,64
SL2221	-	Conserved Hypothetical Protein	-2,49	1,39	-2,04
SL2225	<i>napC</i>	Cytochrome c-type protein napC	1,06	-1,02	2,49
SL2227	<i>napH</i>	Ferredoxin-type protein napH	1,02	-1,02	2,21
SL2228	<i>napG</i>	Ferredoxin-type protein napG	1,15	-1,12	2,65
SL2229	<i>napA</i>	Periplasmic nitrate reductase	1,17	-1,04	3,48
SL2243	<i>ttuB</i>	Putative tartrate transporter	1,05	-1,13	3,31
SL2256	<i>sseL</i>	Deubiquitinase sseL	-7,62	1,57	-9,57
SL2258	<i>yfaU</i>	2-keto-3-deoxy-L-rhamnonate aldolase	1,38	1,15	1,99
SL2261	<i>yfaX</i>	Uncharacterized HTH-type transcriptional regulator yfaX	1,42	1,43	2,53
SL2265	<i>ais</i>	Lipopolysaccharide core heptose(II)-phosphate phosphatase	-1,34	1,08	-4,74
SL2266	<i>arnB</i>	UDP-4-amino-4-deoxy-L-arabinose--oxoglutarate aminotransferase	-1,29	1,15	-2,44
SL2267	<i>arnC</i>	Undecaprenyl-phosphate 4-deoxy-4-formamido-L-arabinose transferase	-1,49	-1,03	-2,05
SL2269	<i>arnD</i>	Probable 4-deoxy-4-formamido-L-arabinose-phosphoundecaprenol deformylase ArnD	-1,35	-1,10	-2,06
SL2270	<i>arnT</i>	Undecaprenyl phosphate-alpha-4-amino-4-deoxy-L-arabinose arabinosyl transferase	-1,32	-1,01	-2,12
SL2272	<i>arnF</i>	Probable 4-amino-4-deoxy-L-arabinose-phosphoundecaprenol flippase subunit ArnF	-1,17	1,24	-2,31
SL2277	<i>menH</i>	2-succinyl-6-hydroxy-2,4-cyclohexadiene-1-carboxylate synthase	1,44	1,02	-2,59
SL2279	<i>menF</i>	Menaquinone-specific isochorismate synthase	-1,00	-1,05	-2,16
SL2283	<i>cheV</i>	Chemotaxis protein cheV	-1,26	-1,24	-10,75
SL2284	<i>yfbK</i>	Uncharacterized protein yfbK	1,05	-1,11	-2,45
SL2287	<i>nuoL</i>	NADH-quinone oxidoreductase subunit L	1,04	-1,10	1,99
SL2288	<i>nuoK</i>	NADH-quinone oxidoreductase subunit K	1,03	-1,13	2,30
SL2290	<i>nuoI</i>	NADH-quinone oxidoreductase subunit I	1,02	-1,10	1,99
SL2299	<i>IrhA</i>	Probable HTH-type transcriptional regulator IrhA	-1,35	1,08	-2,65
SL2305	<i>yfbV</i>	UPF0208 membrane protein yfbV	-1,17	-1,00	-2,12
SL2306	<i>ackA</i>	Acetate kinase	-1,09	-1,09	-3,07

Tabla suplementaria 2Genes afectados en las cepas mutantes *greA*, *greB* y *greAgreB* respecto a la cepa WT

ID	gene	Description	greA vs WT	greB vs WT	greAgreB vs WT
SL2308	<i>yfcC</i>	Uncharacterized protein yfcC	1,14	-1,21	-2,45
SL2311	<i>ulaA</i>	Ascorbate-specific permease IIC component ulaA	1,08	-1,02	2,27
SL2312	<i>ulaB</i>	putative sugar phosphotransferase component IIB	-1,02	-1,08	2,94
SL2313	<i>ulaC</i>	Ascorbate-specific phosphotransferase enzyme IIA component	-1,14	-1,17	3,39
SL2323	<i>hisJ</i>	Histidine-binding periplasmic protein	-1,05	-1,15	2,32
SL2324	<i>argT</i>	Lysine-arginine-ornithine-binding periplasmic protein	-1,15	1,01	7,89
SL2327	-	Amino Acid Racemase	1,18	1,13	2,86
SL2330	<i>rocR</i>	Arginine utilization regulatory protein rocR	1,21	1,43	1,99
SL2339	<i>pdxB</i>	Erythronate-4-phosphate dehydrogenase	-1,02	-1,07	-2,04
SL2357	<i>fadJ</i>	Fatty acid oxidation complex subunit alpha	-1,03	1,15	4,65
SL2360	<i>fadL</i>	Long-chain fatty acid transport protein	-1,14	1,08	7,09
SL2363	<i>pgtE</i>	Outer membrane protease E	-2,81	1,47	-2,42
SL2367	<i>pgtP</i>	Phosphoglycerate transporter protein	1,36	1,62	2,39
SL2369	<i>ddg</i>	Protein ddg	-1,46	-1,05	-11,56
SL2378	<i>yfeA</i>	Uncharacterized protein yfeA	-1,11	-1,04	-2,35
SL2393	<i>cysK</i>	Cysteine synthase A	1,11	1,01	2,16
SL2404	<i>cysA</i>	Sulfate/thiosulfate import ATP-binding protein cysA	1,55	1,39	12,67
SL2405	<i>cysW</i>	Sulfate transport system permease protein cysW	1,09	-1,12	6,01
SL2406	<i>cysU</i>	Sulfate transport system permease protein cysT	1,34	1,03	8,74
SL2407	<i>cysP</i>	Thiosulfate-binding protein	-1,07	-1,31	13,02
SL2408	<i>ucpA</i>	Oxidoreductase ucpA	1,35	1,16	3,08
SL2432	<i>eutP</i>	Ethanolamine utilization protein eutP	-1,30	1,35	2,01
SL2435	<i>maeB</i>	NADP-dependent malic enzyme	1,15	-1,08	5,97
SL2437	<i>tktB</i>	Transketolase 2	1,18	1,11	2,01
SL2438	-	Hypothetical	-1,08	-1,04	-2,50
SL2439	<i>ypfG</i>	Uncharacterized protein ypfG	1,12	1,41	-2,79
SL2459	<i>hda</i>	DnaA-homolog protein hda	-1,01	1,00	-2,04
SL2462	<i>purM</i>	Phosphoribosylformylglycinamide cyclo-ligase	-1,04	1,28	-2,28
SL2463	<i>purN</i>	Phosphoribosylglycinamide formyltransferase	1,14	1,09	-2,33
SL2467	-	Hypothetical	-1,23	-1,01	-3,33
SL2468	<i>yfgG</i>	Uncharacterized protein yfgG	1,01	1,01	-3,19
SL2469	-	Hypothetical	1,52	1,35	-2,17
SL2471	<i>guaA</i>	GMP synthase [glutamine-hydrolyzing]	1,01	1,02	-2,32
SL2472	<i>guaB</i>	Inosine-5'-monophosphate dehydrogenase	-1,09	1,02	-3,20
SL2473	<i>xseA</i>	Exodeoxyribonuclease 7 large subunit	-1,13	-1,03	-2,01
SL2478	<i>sinI</i>	Outer Membrane Protein	1,21	1,13	2,39
SL2484	<i>hisS</i>	Histidyl-tRNA synthetase	-1,02	-1,10	-2,15
SL2488	<i>ndk</i>	Nucleoside diphosphate kinase	1,18	1,01	6,14
SL2495	<i>sseA</i>	3-mercaptopyruvate sulfurtransferase	1,08	1,25	2,90
SL2502	<i>hscB</i>	Co-chaperone protein hscB	1,01	1,05	-2,38

Tabla suplementaria 2Genes afectados en las cepas mutantes *greA*, *greB* y *greAgreB* respecto a la cepa WT

ID	gene	Description	greA vs WT	greB vs WT	greAgreB vs WT
SL2505	<i>iscS</i>	Cysteine desulfurase	-1,17	1,13	-1,99
SL2506	<i>iscR</i>	HTH-type transcriptional regulator <i>iscR</i>	-1,38	1,03	-3,23
SL2507	<i>trmJ</i>	tRNA (cytidine/uridine-2'-O-)-methyltransferase <i>trmJ</i>	1,39	1,02	-2,12
SL2510	<i>asrA</i>	Anaerobic sulfite reductase subunit A	1,36	1,67	-3,47
SL2511	<i>asrB</i>	Anaerobic sulfite reductase subunit B	1,26	1,34	-3,42
SL2512	<i>asrC</i>	Anaerobic sulfite reductase subunit C	1,33	1,46	-2,90
SL2515	<i>csiE</i>	Stationary phase-inducible protein <i>csiE</i>	1,24	1,36	6,85
SL2518	<i>hmpA</i>	Flavoheмоprotein	-1,07	1,11	5,21
SL2519	<i>cadC</i>	Transcriptional activator <i>cadC</i>	1,07	-1,02	-2,31
SL2521	<i>cadA</i>	Lysine decarboxylase, inducible	1,46	-1,13	-4,98
SL2522	<i>yjdL</i>	Probable dipeptide and tripeptide permease <i>YjdL</i>	1,00	1,05	-6,76
SL2527	<i>purL</i>	Phosphoribosylformylglycinamide synthase	1,27	1,43	2,08
SL2532	<i>ybbF</i>	Putative PTS system EIIBC component <i>ybbF</i>	1,22	1,04	3,24
SL2533	<i>murQ</i>	N-acetylmuramic acid 6-phosphate etherase	1,17	1,02	3,66
SL2537	<i>cynR</i>	HTH-type transcriptional regulator <i>cynR</i>	-1,02	1,05	3,05
SL2538	<i>yfhL</i>	Uncharacterized ferredoxin-like protein <i>yfhL</i>	-1,32	1,11	-2,31
SL2542	<i>era</i>	GTP-binding protein <i>era</i> homolog	-1,00	-1,09	-2,18
SL2543	<i>rnc</i>	Ribonuclease 3	-1,05	1,00	-2,47
SL2546	<i>gogB</i>	Hypothetical	-1,55	-1,09	-2,58
SL2548	-	Hypothetical Protein SL2548	-1,50	-1,10	-3,48
SL2549	-	PagK-Like Protein	-2,08	1,46	-4,10
SL2550	<i>ycdD</i>	Tail fiber assembly protein homolog from lambdoid prophage Fels-1	-2,76	-1,35	-4,98
SL2551	-	Appr-1-P Processing Domain-Containing Protein	-2,46	-1,34	-4,76
SL2552	<i>stfQ</i>	Side tail fiber protein homolog from lambdoid prophage Qin	-1,74	-1,12	-3,35
SL2553	-	Hocificity Protein J	-2,46	-1,12	-11,08
SL2554	-	Phage Tail Assembly Protein	-1,31	-1,13	-2,08
SL2555	-	NLP/P60 Protein	-1,80	-1,35	-3,95
SL2556	-	Phage Minor Tail Protein L	-1,54	-1,16	-2,63
SL2557	-	Minor Tail Protein	-1,77	-1,25	-2,28
SL2558	-	Hypothetical	-1,46	-1,20	-2,18
SL2559	-	Minor Tail Protein	-1,81	-1,02	-4,83
SL2560	-	Minor Tail Component Of Putative Prophage	-2,14	-1,10	-5,25
SL2561	-	Tail Protein V	-1,60	1,04	-2,80
SL2562	-	Minor Tail Protein U	-1,71	-1,09	-2,81
SL2563	<i>gipA</i>	Putative transposase in <i>snaA-snaB</i> intergenic region	-1,48	1,01	-2,39
SL2564	-	Phage Tail Component	-1,67	-1,02	-3,00
SL2565	-	Tail Attachment Protein	-2,08	-1,12	-2,67
SL2566	-	DNA Packaging-Like Protein	-1,95	-1,02	-3,76
SL2567	-	P21 prophage-derived major head protein	-1,99	-1,10	-4,91
SL2568	-	Head Decoration Protein	-1,94	-1,06	-4,48
SL2569	<i>sppA</i>	Putative signal peptide peptidase <i>sppA</i>	-2,37	-1,11	-10,71
SL2570	-	Lambda Family Phage Portal Protein	-2,15	-1,13	-6,06

Tabla suplementaria 2Genes afectados en las cepas mutantes *greA*, *greB* y *greAgreB* respecto a la cepa WT

ID	gene	Description	<i>greA</i> vs WT	<i>greB</i> vs WT	<i>greAgreB</i> vs WT
SL2571	-	Lambda prophage-derived head-to-tail joining protein W	-2,13	-1,13	-2,93
SL2572	<i>tfaD</i>	Putative tail fiber assembly protein homolog from lambdoid prophage DLP12	-2,40	-1,07	-4,71
SL2573	<i>nohA</i>	P21 prophage-derived terminase small subunit	-2,45	-1,05	-8,60
SL2575	<i>rzpD</i>	Putative Rz endopeptidase from lambdoid prophage DLP12	-2,15	-1,02	-5,68
SL2576	<i>arrD</i>	Probable lysozyme from lambdoid prophage DLP12	-1,78	-1,03	-3,56
SL2577	-	Hypothetical	-1,85	-1,13	-2,26
SL2578	-	Hypothetical	1,66	1,60	2,10
SL2583	-	Hypothetical	1,01	1,10	2,16
SL2592	-	Gifsy-1 Prophage CI Protein	-1,28	1,28	-2,12
SL2596	-	Hypothetical	-1,72	-1,01	-2,41
SL2597	<i>recE</i>	Exodeoxyribonuclease 8	-1,33	1,01	-2,59
SL2602	<i>rseB</i>	Sigma-E factor regulatory protein rseB	-1,23	-1,41	-2,07
SL2604	<i>rpoE</i>	RNA polymerase sigma-E factor	-1,10	-1,09	-2,10
SL2609	<i>eamB</i>	Cysteine/O-acetylserine efflux protein	1,53	1,05	-7,15
SL2610	<i>grcA</i>	Autonomous glycyl radical cofactor	1,06	1,11	-2,16
SL2613	<i>trxC</i>	Thioredoxin-2	-1,10	1,03	-2,37
SL2618	<i>kgtP</i>	Alpha-ketoglutarate permease	1,23	1,05	2,63
SL2620	<i>clpB</i>	Chaperone protein clpB	1,03	1,15	2,60
SL2622	<i>rluD</i>	Ribosomal large subunit pseudouridine synthase D	-1,02	-1,09	-2,26
SL2623	<i>yfiO</i>	UPF0169 lipoprotein yfiO	-1,30	-1,33	-2,41
SL2624	<i>raiA</i>	Ribosome-associated inhibitor A	1,15	1,42	2,90
SL2625	<i>pheA</i>	P-protein	1,11	-1,21	2,88
SL2630	<i>yfiN</i>	Probable diguanylate cyclase YfiN	-1,01	1,18	-2,63
SL2640	-	Hypothetical Protein SL2640	1,13	1,04	2,32
SL2651	<i>corE</i>	putative cytochrome c-type biogenesis protein	-1,17	1,04	-2,45
SL2652	<i>corB</i>	putative membrane protein	-1,25	-1,36	-2,50
SL2673	<i>pinE</i>	DNA-invertase from lambdoid prophage e14	-1,32	1,11	-3,80
SL2674	<i>sopE</i>	Guanine nucleotide exchange factor sopE	-1,33	-1,03	-27,69
SL2676	-	Hypothetical	1,16	1,09	1,99
SL2695	<i>smf</i>	Protein smf	-1,04	-1,23	2,11
SL2696	-	Hypothetical	-1,12	-1,39	3,87
SL2697	-	Hypothetical	-1,30	-1,61	-2,19
SL2703	<i>ybil</i>	Hypothetical (similar a P2p38)	-2,29	-1,54	-1,69
SL2704	-	Putative uncharacterized protein ORFC-like in prophage region	-3,07	-1,35	-3,46
SL2709	<i>xerD</i>	Tyrosine recombinase xerD	-1,14	-1,37	2,01
SL2710	<i>yopC</i>	SPBc2 prophage-derived uncharacterized protein yopC	-1,34	-1,52	3,11
SL2712	<i>intA</i>	Prophage CP4-57 integrase	-1,10	-1,19	2,48
SL2713	-	Hypothetical	-1,41	-2,00	1,55
SL2715	-	Hypothetical Protein SL2715	1,01	-1,13	2,19
SL2719	-	Hypothetical	1,01	-1,31	3,69
SL2720	-	Hypothetical	1,12	-1,38	3,04

Tabla suplementaria 2Genes afectados en las cepas mutantes *greA*, *greB* y *greAgreB* respecto a la cepa WT

ID	gene	Description	<i>greA</i> vs WT	<i>greB</i> vs WT	<i>greAgreB</i> vs WT
SL2721	-	P4 prophage-derived uncharacterized protein t2655	1,33	-1,17	2,87
SL2722	<i>traC</i>	DNA primase traC	1,07	-1,27	4,29
SL2723	<i>intA</i>	Prophage CP4-57 integrase	1,26	1,78	6,56
SL2724	<i>intA</i>	Integrase	1,18	1,34	3,40
SL2726	-	Hypothetical	-1,35	-1,30	-2,11
SL2740	<i>hxlB</i>	3-hexulose-6-phosphate isomerase	1,22	-1,18	2,93
SL2741	-	Glucose-6-Phosphate Isomerase	1,26	1,00	2,42
SL2743	<i>sgrR</i>	HTH-type transcriptional regulator sgrR	1,10	1,41	3,19
SL2747	<i>intA</i>	Prophage CP4-57 integrase	-1,07	1,00	2,76
SL2755	<i>fljA</i>	Repressor of phase 1 flagellin gene	-12,65	-4,66	-15,85
SL2756	<i>fljB</i>	Phase 2 flagellin	-2,40	-1,63	-1,84
SL2756	<i>fljB</i>	Phase 2 flagellin	-2,40	-1,63	-1,84
SL2758	<i>iroB</i>	putative glycosyltransferase	-1,39	1,54	-5,31
SL2759	<i>iroC</i>	Putative multidrug export ATP-binding/permease protein	1,36	1,74	-2,78
SL2760	<i>iroD</i>	Enterochelin esterase	1,04	-1,11	-2,90
SL2764	<i>ybjX</i>	Uncharacterized protein ybjX	-1,45	1,10	-4,33
SL2765	<i>mig-14</i>	putative transcriptional regulator	-1,67	-1,35	-3,63
SL2766	-	Hypothetical	-1,47	1,04	-2,82
SL2768	<i>tctE</i>	Sensor protein tctE	-1,13	-1,40	7,27
SL2769	<i>tctD</i>	Transcriptional regulatory protein tctD	1,03	1,08	13,84
SL2770	<i>yflP</i>	UPF0065 protein yflP	-1,24	-1,43	3,01
SL2771	-	Hypothetical	-1,06	-1,07	4,00
SL2773	<i>csiD</i>	Protein csiD	-1,27	-1,17	11,87
SL2774	<i>ygaF</i>	Uncharacterized protein ygaF	-1,30	-1,54	9,95
SL2775	<i>gabD</i>	Succinate-semialdehyde dehydrogenase [NADP+]	-1,31	-1,53	12,61
SL2776	<i>gabT</i>	4-aminobutyrate aminotransferase	-1,37	-1,66	7,78
SL2777	<i>gabP</i>	GABA permease	-1,46	-1,56	6,21
SL2783	<i>stpA</i>	DNA-binding protein stpA	-1,14	-1,00	-10,03
SL2784	<i>ygaW</i>	Uncharacterized protein ygaW	1,29	1,21	-3,82
SL2785	<i>ygaC</i>	Uncharacterized protein ygaC	-1,02	1,22	-2,25
SL2787	<i>mocR</i>	Probable rhizopine catabolism regulatory protein mocR	1,16	1,01	2,22
SL2814	<i>srlB</i>	Glucitol/sorbitol-specific phosphotransferase enzyme IIA component	1,10	-1,54	-2,28
SL2815	<i>srlD</i>	Sorbitol-6-phosphate 2-dehydrogenase	1,14	-1,24	-2,47
SL2816	<i>gutM</i>	Glucitol operon activator protein	-1,01	-1,27	-2,46
SL2823	<i>hydN</i>	Electron transport protein hydN	1,30	1,10	-7,66
SL2825	<i>hycl</i>	Hydrogenase 3 maturation protease	1,09	1,09	2,56
SL2826	<i>hychH</i>	Formate hydrogenlyase maturation protein hychH	1,04	1,06	2,01
SL2831	<i>hycC</i>	Formate hydrogenlyase subunit 3	1,05	-1,28	-3,72
SL2832	<i>hycB</i>	Formate hydrogenlyase subunit 2	-1,10	1,04	-4,92
SL2833	<i>hycA</i>	Formate hydrogenlyase regulatory protein hycA	1,02	-1,01	-7,96
SL2838	<i>hypE</i>	Hydrogenase isoenzymes formation protein hypE	1,17	-1,26	-2,56

Tabla suplementaria 2

 Genes afectados en las cepas mutantes *greA*, *greB* y *greAgreB* respecto a la cepa WT

ID	gene	Description	greA vs WT	greB vs WT	greAgreB vs WT
SL2839	<i>fhIA</i>	Formate hydrogenlyase transcriptional activator	1,22	-1,02	-2,24
SL2844	<i>sitD</i>	Probable iron transport system membrane protein HI_0359	-1,18	-1,12	-3,87
SL2845	<i>yopJ</i>	Effector protein yopJ	-1,36	-1,29	-5,48
SL2846	<i>sprB</i>	AraC family transcriptional regulator	-1,39	-1,66	-14,85
SL2847	<i>sirC</i>	Transcriptional regulator sirC	-1,41	-1,61	-10,80
SL2848	-	Hypothetical	-1,56	-1,22	-20,93
SL2849	<i>orgB</i>	Oxygen-regulated invasion protein orgB	-1,44	-1,20	-9,10
SL2850	<i>orgA</i>	Oxygen-regulated invasion protein orgA	-1,49	-1,26	-21,71
SL2851	<i>prgK</i>	Lipoprotein prgK	-1,30	-1,14	-8,73
SL2852	<i>prgJ</i>	Protein prgJ	-1,22	-1,08	-8,23
SL2853	<i>prgI</i>	Protein prgI	-1,13	-1,02	-4,71
SL2854	<i>prgH</i>	Protein prgH	-1,36	1,09	-18,46
SL2855	<i>hilD</i>	Transcriptional regulator hilD	-1,39	-1,07	-5,63
SL2856	<i>hilA</i>	Transcriptional regulator hilA	-1,26	-1,38	-10,34
SL2857	<i>iagB</i>	Invasion protein iagB	-1,27	-1,07	-7,09
SL2858	<i>sptP</i>	Secreted effector protein sptP	-1,24	-1,03	-5,53
SL2859	<i>sicP</i>	Chaperone protein sicP	-1,35	-1,14	-8,37
SL2860	<i>iacP</i>	Probable acyl carrier protein iacP	-1,30	-1,10	-21,34
SL2861	<i>sipA</i>	Cell invasion protein sipA	-1,25	-1,06	-15,35
SL2862	<i>sipD</i>	Cell invasion protein sipD	-1,13	1,02	-18,49
SL2863	<i>sipC</i>	Cell invasion protein sipC	-1,10	1,01	-6,21
SL2864	<i>sipB</i>	Cell invasion protein sipB	-1,11	1,03	-7,20
SL2865	<i>sicA</i>	Chaperone protein sicA	-1,10	1,09	-8,04
SL2866	<i>spaS</i>	Surface presentation of antigens protein spaS	-1,42	-1,39	-21,68
SL2867	<i>spaR</i>	Surface presentation of antigens protein spaR	-1,55	-1,58	-22,12
SL2868	<i>spaQ</i>	Surface presentation of antigens protein SpaQ	-1,54	-1,38	-32,11
SL2869	<i>spaP</i>	Surface presentation of antigens protein spaP	-1,68	-1,43	-29,30
SL2870	<i>spaO</i>	Surface presentation of antigens protein SpaO	-1,28	-1,25	-14,14
SL2871	<i>spaN</i>	Surface presentation of antigens protein spaN	-1,17	-1,10	-9,31
SL2872	<i>spaM</i>	Surface presentation of antigens protein spaM	-1,29	-1,40	-10,63
SL2873	<i>spaL</i>	Probable ATP synthase spaL	-1,29	-1,41	-10,53
SL2874	<i>spaK</i>	Surface presentation of antigens protein spaK	-1,15	-1,03	-6,61
SL2875	<i>invA</i>	Invasion protein invA	-1,27	-1,01	-12,89
SL2876	<i>invE</i>	Invasion protein invE	-1,30	-1,14	-20,75
SL2877	<i>invG</i>	Protein invG	-1,17	-1,02	-8,31
SL2878	<i>invF</i>	Invasion protein invF	-1,17	1,06	-8,31
SL2879	<i>invH</i>	Invasion lipoprotein invH	-1,50	-1,13	-10,98
SL2880	-	Hypothetical	-1,50	1,10	-2,45
SL2881	-	Hypothetical	-1,52	-1,00	-3,47
SL2884	-	Hypothetical	1,38	1,30	6,08
SL2885	-	GCN5-Related N-Acetyltransferase	1,09	1,04	5,08

Tabla suplementaria 2Genes afectados en las cepas mutantes *greA*, *greB* y *greAgreB* respecto a la cepa WT

ID	gene	Description	greA vs WT	greB vs WT	greAgreB vs WT
SL2892	<i>ygbN</i>	Uncharacterized permease HI_1015	1,20	-1,09	3,82
SL2893	<i>rffG</i>	Uncharacterized protein HI_1014	1,10	1,17	4,43
SL2894	<i>ygbM</i>	Protein ygbM	-1,09	-1,22	4,27
SL2895	<i>ygbL</i>	Putative aldolase class 2 protein ygbL	1,05	1,07	5,99
SL2896	<i>ygbK</i>	Uncharacterized protein ygbK	-1,09	1,24	7,13
SL2897	<i>ygbJ</i>	Uncharacterized oxidoreductase ygbJ	-1,09	1,34	6,18
SL2899	<i>slyA</i>	Transcriptional regulator	-1,10	1,09	2,00
SL2903	<i>rpoS</i>	RNA polymerase sigma factor rpoS	1,17	1,12	2,05
SL2911	<i>ygbE</i>	Inner membrane protein ygbE	-1,18	1,12	2,47
SL2912	<i>cysC</i>	Adenylyl-sulfate kinase	-1,09	-1,01	9,51
SL2913	<i>cysN</i>	Sulfate adenylyltransferase subunit 1	1,04	1,00	11,16
SL2914	<i>cysD</i>	Sulfate adenylyltransferase subunit 2	1,00	-1,20	4,76
SL2915	<i>iap</i>	Alkaline phosphatase isozyme conversion protein	-1,08	-1,03	-3,91
SL2924	<i>sopD</i>	Secreted effector protein sopD	-1,52	1,19	-23,34
SL2925	<i>cysH</i>	Phosphoadenosine phosphosulfate reductase	1,07	-1,06	5,34
SL2926	<i>cysI</i>	Sulfite reductase [NADPH] hemoprotein beta-component	1,12	-1,02	6,16
SL2927	<i>cysJ</i>	Sulfite reductase [NADPH] flavoprotein alpha-component	-1,07	-1,06	4,34
SL2928	<i>queD</i>	6-carboxy-5,6,7,8-tetrahydropterin synthase	-1,10	1,06	-2,01
SL2929	-	Uncharacterized protein MJ0301	1,10	1,29	2,23
SL2942	<i>gudX</i>	Glucarate dehydratase-related protein	1,19	1,10	3,30
SL2943	<i>gudP</i>	Probable glucarate transporter	1,30	1,14	5,33
SL2946	<i>yqcC</i>	Uncharacterized protein yqcC	1,31	-1,09	-2,86
SL2949	<i>ygdH</i>	LOG family protein ygdH	1,08	-1,08	2,16
SL2949	<i>ygdH</i>	LOG family protein ygdH	1,08	-1,08	2,16
SL2950	<i>sdaC</i>	Serine transporter	-1,20	-1,09	2,59
SL2951	<i>sdaB</i>	L-serine dehydratase 2	1,12	-1,07	3,60
SL2953	<i>fucO</i>	Lactaldehyde reductase	1,09	-1,04	3,10
SL2954	<i>fucA</i>	L-fuculose phosphate aldolase	-1,08	1,00	2,94
SL2959	<i>fucR</i>	L-fucose operon activator	-1,02	1,03	2,02
SL2961	<i>ygdD</i>	UPF0382 inner membrane protein ygdD	-1,18	-1,02	-2,47
SL2962	<i>gcvA</i>	Glycine cleavage system transcriptional activator	-1,22	1,12	-2,75
SL2969	<i>amiC</i>	N-acetylmuramoyl-L-alanine amidase AmiC	-1,05	1,02	-1,99
SL2977	<i>ppdB</i>	Prepilin peptidase-dependent protein B	-1,28	-1,11	2,36
SL2979	<i>thyA</i>	Thymidylate synthase	1,04	-1,03	-2,07
SL2984	<i>ygdQ</i>	UPF0053 inner membrane protein ygdQ	-1,22	1,03	-4,13
SL2994	<i>araE</i>	Arabinose-proton symporter	1,49	1,34	4,71
SL2996	<i>kdul</i>	4-deoxy-L-threo-5-hexosulose-uronate ketol-isomerase	-1,33	-1,48	3,46
SL2997	<i>yqeF</i>	Probable acetyl-CoA acetyltransferase	-1,08	-1,04	4,20
SL2999	-	Hypothetical	1,97	1,21	-2,88
SL3000	<i>yqeG</i>	Inner membrane transport protein yqeG	1,04	-1,02	-3,13
SL3008	<i>stdA</i>	Uncharacterized fimbrial-like protein ybgD	1,50	1,10	2,60
SL3010	-	Virulence membrane protein	-1,03	1,16	2,46

Tabla suplementaria 2Genes afectados en las cepas mutantes *greA*, *greB* y *greAgreB* respecto a la cepa WT

ID	gene	Description	greA vs WT	greB vs WT	greAgreB vs WT
SL3017	<i>prfB</i>	Peptide chain release factor 2	-1,09	-1,04	-2,12
SL3026	<i>yqfB</i>	UPF0267 protein yqfB	1,20	1,27	2,53
SL3041	<i>yggE</i>	Uncharacterized protein yggE	-1,05	1,12	-2,34
SL3048	-	Hypothetical	1,34	-1,23	3,16
SL3049	-	Permease Protein Of ABC-Type Cobalt Transporter	1,38	-1,21	2,71
SL3050	<i>cbiO1</i>	Cobalt import ATP-binding protein CbiO 1	1,19	-1,37	2,22
SL3051	<i>cbiO</i>	Cobalt import ATP-binding protein CbiO	1,32	-1,15	2,12
SL3057	<i>yjmC</i>	Uncharacterized oxidoreductase yjmC	1,12	-1,35	2,33
SL3058	<i>yjjN</i>	Uncharacterized zinc-type alcohol dehydrogenase-like protein yjjN	-1,14	-1,30	2,01
SL3059	<i>uxuB</i>	D-mannonate oxidoreductase	-1,09	-1,19	3,52
SL3064	<i>yqgD</i>	Uncharacterized protein yqgD	-1,10	1,08	-4,69
SL3065	<i>metK</i>	S-adenosylmethionine synthase	-1,11	-1,17	-2,26
SL3080	<i>yggM</i>	Uncharacterized protein yggM	1,70	-1,04	2,39
SL3081	<i>ansB</i>	L-asparaginase 2	1,62	1,25	4,33
SL3085	<i>mutY</i>	A/G-specific adenine glycosylase	-1,13	-1,16	-2,32
SL3088	<i>nupG</i>	Nucleoside permease nupG	1,14	1,19	2,45
SL3095	<i>budR</i>	HTH-type transcriptional regulator BudR	1,05	-1,27	2,43
SL3098	<i>moaR</i>	Monoamine regulon transcriptional regulator	1,11	1,43	2,42
SL3108	<i>exuT</i>	Hexuronate transporter	1,24	1,15	4,36
ID	gene	Description	greA vs WT	greB vs WT	greAgreB vs WT
SL3109	<i>uxuA</i>	Mannonate dehydratase	1,21	-1,08	3,06
SL3110	<i>uxuB</i>	D-mannonate oxidoreductase	1,20	-1,03	2,95
SL3111	<i>uxaC</i>	Uronate isomerase	1,15	1,04	2,61
SL3112	<i>bdlA</i>	Biofilm dispersion protein BdlA	-1,33	-1,01	-3,40
SL3125	<i>yghW</i>	Uncharacterized protein yghW	-1,36	1,16	-6,35
SL3126	<i>tse</i>	Methyl-accepting chemotaxis serine transducer	-1,55	1,00	-8,28
SL3128	-	Hypothetical	-1,27	1,12	-2,72
SL3129	-	Hypothetical	-1,27	1,09	-5,12
SL3130	-	Hypothetical	-1,43	-1,26	-7,27
SL3132	<i>exbD</i>	Biopolymer transport protein exbD	1,20	1,13	-2,14
SL3133	<i>exbB</i>	Biopolymer transport protein exbB	1,04	1,15	-2,24
SL3138	<i>yqhD</i>	Alcohol dehydrogenase yqhD	1,07	1,14	2,16
SL3142	<i>ygiQ</i>	UPF0313 protein ygiQ	-1,38	1,18	-2,01
SL3143	<i>yjiZ</i>	Uncharacterized protein yjiZ	-1,25	-1,05	7,98
SL3144	-	C4-Dicarboxylate Transport System Permease Small Protein	-1,43	-1,29	6,19
SL3145	<i>ygiK</i>	Uncharacterized protein ygiK	-1,14	-1,20	3,14
SL3150	<i>ygiW</i>	Protein ygiW	1,35	1,23	1,98
SL3163	<i>ygiD</i>	Uncharacterized protein ygiD	-2,08	1,12	-9,28
SL3165	-	Arylsulfotransferase	-1,13	-1,15	3,35
SL3166	<i>dsbA</i>	Thiol:disulfide interchange protein dsbA	-1,19	-1,13	3,06
SL3167	<i>dsbB</i>	Putative protein-disulfide oxidoreductase	-1,31	-1,22	3,38
SL3170	<i>glgS</i>	Glycogen synthesis protein glgS	1,26	1,60	2,05
SL3176	<i>ygiM</i>	Uncharacterized protein ygiM	-1,23	1,09	-3,56
SL3178	<i>bacA</i>	Undecaprenyl-diphosphatase	-1,19	-1,11	-2,21
SL3179	<i>folB</i>	Dihydroneopterin aldolase	-1,39	-1,02	-2,66

Tabla suplementaria 2

Genes afectados en las cepas mutantes *greA*, *greB* y *greAgreB* respecto a la cepa WT

ID	gene	Description	<i>greA</i> vs WT	<i>greB</i> vs WT	<i>greAgreB</i> vs WT
SL3183	<i>rpsU</i>	30S ribosomal protein S21	-1,10	1,23	-3,63
SL3184	<i>dnaG</i>	DNA primase	-1,03	1,12	-2,31
SL3189	<i>cheM</i>	methyl-accepting chemotaxis protein II	-1,38	-1,15	-3,94
SL3192	<i>fadH</i>	2,4-dienoyl-CoA reductase [NADPH]	-1,06	1,12	6,90
SL3196	<i>ygjR</i>	Uncharacterized oxidoreductase ygjR	1,34	1,05	2,00
SL3197	<i>alx</i>	Inner membrane protein alx	-1,24	-1,08	-2,21
SL3198	<i>sstT</i>	Serine/threonine transporter sstT	-1,05	1,04	2,88
SL3199	<i>yqjA</i>	Inner membrane protein yqjA	-1,37	1,17	-2,94
SL3200	<i>yqjB</i>	Uncharacterized protein yqjB	-1,21	1,17	-3,22
SL3209	<i>yhaL</i>	Hypothetical Protein yhaL	1,20	1,49	5,32
SL3211	<i>yhaO</i>	Inner membrane transport protein yhaO	1,06	1,03	2,15
SL3214	<i>tdcD</i>	Propionate kinase	1,02	1,22	-2,52
SL3216	<i>tdcB</i>	Threonine dehydratase catabolic	-1,26	1,33	-2,06
SL3217	<i>tdcA</i>	HTH-type transcriptional regulator tdcA	1,55	1,55	5,57
SL3222	<i>garL</i>	5-keto-4-deoxy-D-glucarate aldolase	1,27	1,19	2,25
SL3223	<i>garD</i>	D-galactarate dehydratase	1,28	1,27	2,13
SL3227	<i>fruK</i>	1-phosphofructokinase	-1,26	-1,39	-2,73
SL3228	<i>fruA</i>	PTS system fructose-specific EIIABC component	-1,11	-1,19	-2,11
SL3229	<i>fruB</i>	Multiphosphoryl transfer protein	-1,34	-1,41	-2,50
SL3232	<i>gatB</i>	Galactitol-specific phosphotransferase enzyme IIB component	-1,11	-1,16	2,08
SL3233	<i>gatC</i>	Galactitol permease IIC component	1,08	1,01	2,52
SL3235	<i>gatR</i>	Galactitol utilization operon repressor	1,07	-1,04	4,26
SL3249	<i>yhbW</i>	Uncharacterized protein yhbW	-1,37	-1,38	2,08
SL3252	<i>mtr</i>	Tryptophan-specific transport protein	-1,22	-1,07	-2,62
SL3253	<i>deaD</i>	Cold-shock DEAD box protein A	-1,04	-1,06	-8,59
SL3261	<i>rimP</i>	Ribosome maturation factor rimP	-1,28	-1,08	-2,79
SL3263	-	Hypothetical	-1,04	1,35	-2,48
SL3264	<i>secG</i>	Protein-export membrane protein secG	-1,16	1,05	-2,46
SL3270	<i>yhbY</i>	RNA-binding protein yhbY	2,18	1,01	1,19
SL3271	<i>greA</i>	Transcription elongation factor greA	-97,36	1,03	0,00
SL3275	<i>rpmA</i>	50S ribosomal protein L27	-1,33	-1,01	-3,03
SL3276	<i>rplU</i>	50S ribosomal protein L21	-1,20	1,03	-2,51
SL3284	<i>miaE</i>	Probable phospholipid ABC transporter permease protein miaE	-1,15	-1,10	-1,98
SL3293	<i>yhbH</i>	Probable sigma(54) modulation protein	1,24	1,43	2,78
SL3294	<i>ptsN</i>	Nitrogen regulatory protein	1,19	1,06	2,57
SL3301	<i>yhcC</i>	Uncharacterized protein yhcC	1,03	1,15	-3,69
SL3303	<i>gltD</i>	Glutamate synthase [NADPH] small chain	1,26	1,03	2,37
SL3307	<i>yhcH</i>	Uncharacterized protein yhcH	1,60	1,04	2,30
SL3308	<i>nanK</i>	N-acetylmannosamine kinase	1,30	-1,18	2,02
SL3313	<i>sspB</i>	Stringent starvation protein B	-1,27	-1,08	-2,06
SL3314	<i>sspA</i>	Stringent starvation protein A	-1,25	-1,02	-2,69
SL3318	<i>yhcM</i>	Uncharacterized protein yhcM	-1,05	-1,10	-2,14
SL3318	<i>yhcM</i>	Uncharacterized protein yhcM	-1,05	-1,10	-2,14
SL3322	<i>citG1</i>	Probable 2-(5"-triphosphoribosyl)-3'-dephosphocoenzyme-A synthase 1	1,39	1,09	2,38

Tabla suplementaria 2

Genes afectados en las cepas mutantes *greA*, *greB* y *greAgreB* respecto a la cepa WT

ID	gene	Description	greA vs WT	greB vs WT	greAgreB vs WT
SL3324	<i>oadA</i>	Oxaloacetate decarboxylase alpha chain	1,21	-1,05	2,42
SL3326	<i>ttdB</i>	L(+)-tartrate dehydratase subunit beta	1,24	-1,32	3,29
SL3327	<i>ttdA</i>	L(+)-tartrate dehydratase subunit alpha	1,12	-1,23	4,25
SL3328	<i>yfbS</i>	Uncharacterized transporter MJ0672	1,00	-1,49	3,26
SL3330	<i>pdhR</i>	GntR Family Transcriptional Regulator	-1,09	-1,03	-2,07
SL3331	<i>mdh</i>	Malate dehydrogenase	1,18	-1,00	4,77
SL3335	<i>yhcO</i>	Uncharacterized protein yhcO	1,30	1,51	5,06
SL3346	<i>mreB</i>	Rod shape-determining protein mreB	-1,11	1,01	-2,43
SL3350	<i>yedY</i>	Sulfoxide reductase catalytic subunit yedY	1,06	-1,03	2,85
SL3354	<i>yhdT</i>	Uncharacterized protein yhdT	1,09	1,17	-2,38
SL3357	<i>dusB</i>	tRNA-dihydrouridine synthase B	-1,42	-1,03	-3,85
SL3358	<i>fis</i>	DNA-binding protein fis	-1,24	-1,03	-3,28
SL3363	<i>acrE</i>	Acriflavine resistance protein E	1,26	1,10	-2,58
SL3373	<i>def</i>	Peptide deformylase	1,02	1,07	-2,19
SL3374	<i>fmt</i>	Methionyl-tRNA formyltransferase	-1,06	-1,16	-3,52
SL3375	<i>rsmB</i>	Ribosomal RNA small subunit methyltransferase B	-1,04	-1,17	-4,60
SL3376	<i>trkA</i>	Trk system potassium uptake protein trkA	1,04	-1,01	-2,57
SL3411	<i>bfd</i>	Bacterioferritin-associated ferredoxin	-1,31	1,29	-4,45
SL3419	<i>yheO</i>	Uncharacterized protein yheO	-1,04	1,03	-3,74
SL3420	<i>fkpA</i>	FKBP-type peptidyl-prolyl cis-trans isomerase fkpA	-1,28	-1,11	-2,76
SL3427	-	ABC Transporter ATPase	1,05	1,01	2,68
SL3428	<i>ydhR</i>	Putative monooxygenase ydhR	1,17	1,08	2,59
SL3437	<i>fic</i>	Probable adenosine monophosphate-protein transferase fic	1,20	1,17	2,17
SL3440	<i>tsgA</i>	Protein tsgA	-1,26	1,12	-2,99
SL3441	<i>nirB</i>	Nitrite reductase [NAD(P)H] large subunit	-1,07	1,83	-3,09
SL3442	<i>nirD</i>	Nitrite reductase [NAD(P)H] small subunit	1,11	1,18	-6,95
SL3443	<i>nirC</i>	Probable nitrite transporter	1,18	1,04	-5,91
SL3456	<i>yrfA</i>	Uncharacterized protein yrfA	-1,06	1,19	2,46
SL3468	<i>envZ</i>	Osmolarity sensor protein envZ	-1,07	-1,61	-2,23
SL3470	<i>greB</i>	Transcription elongation factor greB	1,06	-22,80	-59,94
SL3471	<i>yhgF</i>	Protein yhgF	-1,23	2,01	-1,52
SL3472	<i>feoA</i>	Ferrous iron transport protein A	-1,03	1,53	-3,17
SL3473	<i>feoB</i>	Ferrous iron transport protein B	-1,06	1,43	-3,20
SL3474	<i>feoC</i>	Ferrous iron transport protein C	-1,20	1,24	-2,73
SL3479	<i>gntT</i>	High-affinity gluconate transporter	1,06	-1,22	2,22
SL3482	<i>malT</i>	HTH-type transcriptional regulator malT	1,22	1,26	5,14
SL3484	<i>dinJ</i>	DNA-damage-inducible protein J	1,04	1,37	2,15
SL3491	<i>glpG</i>	Rhomboid protease glpG	-1,03	-1,07	-2,04
SL3497	<i>ttuB</i>	Putative tartrate transporter	1,09	1,05	2,60
SL3498	<i>ilvD</i>	Dihydroxy-acid dehydratase	1,02	1,08	3,10
SL3503	<i>glgC</i>	Glucose-1-phosphate adenyltransferase	1,25	1,15	2,20

Tabla suplementaria 2

Genes afectados en las cepas mutantes *greA*, *greB* y *greAgreB* respecto a la cepa WT

ID	gene	Description	greA vs WT	greB vs WT	greAgreB vs WT
SL3504	<i>glgX</i>	Glycogen debranching enzyme	1,17	-1,13	2,04
SL3505	<i>glgB</i>	1,4-alpha-glucan-branching enzyme	1,20	-1,03	2,35
SL3513	<i>rbsK</i>	Ribokinase	-1,18	1,03	-2,44
SL3514	-	Hypothetical	-1,08	1,27	-3,60
SL3515	-	Hypothetical	-1,08	-1,01	-2,67
SL3516	<i>php</i>	Phosphotriesterase homology protein	1,01	-1,07	-2,76
SL3518	<i>yhhA</i>	Uncharacterized protein yhhA	1,13	1,56	2,39
SL3520	<i>ugpC</i>	sn-glycerol-3-phosphate import ATP-binding protein UgpC	1,20	-1,48	4,06
SL3521	<i>ugpE</i>	sn-glycerol-3-phosphate transport system permease protein ugpE	1,12	-1,72	3,15
SL3522	<i>ugpA</i>	sn-glycerol-3-phosphate transport system permease protein ugpA	1,32	-1,43	3,48
SL3523	<i>ugpB</i>	sn-glycerol-3-phosphate-binding periplasmic protein ugpB	1,27	1,10	12,09
SL3524	<i>kil</i>	Death On Curing Protein	1,38	1,12	4,53
SL3525	<i>yhhV</i>	Uncharacterized protein yhhV	1,35	1,25	4,30
SL3532	<i>livJ</i>	Leu/Ile/Val-binding protein	-1,06	1,01	2,72
SL3536	<i>ftsY</i>	Cell division protein ftsY	1,05	1,09	-2,07
SL3541	<i>zntA</i>	Lead, cadmium, zinc and mercury-transporting ATPase	-1,06	1,04	3,05
SL3542	<i>tcp</i>	Methyl-accepting chemotaxis citrate transducer	1,12	1,11	-2,21
SL3543	<i>tusA</i>	Sulfurtransferase tusA	-1,02	-1,15	-11,47
SL3543	<i>tusA</i>	Sulfurtransferase tusA	-1,02	-1,15	-11,47
SL3544	<i>yhhQ</i>	Inner membrane protein yhhQ	-1,29	1,01	-4,91
SL3552	<i>yhil</i>	Uncharacterized protein yhil	1,18	1,31	2,20
SL3555	<i>uspB</i>	Universal stress protein B	1,18	1,24	2,84
SL3557	<i>dtpB</i>	Dipeptide and tripeptide permease B	1,53	1,11	3,02
SL3559	<i>prlC</i>	Oligopeptidase A	1,01	-1,10	-2,03
SL3561	<i>yhiR</i>	Uncharacterized protein yhiR	1,04	1,01	-2,11
SL3563	<i>ansB</i>	L-asparaginase	1,21	-1,48	32,54
SL3564	<i>dcuB</i>	Anaerobic C4-dicarboxylate transporter dcuB	1,27	-1,59	55,06
SL3565	<i>frlD</i>	Fructosamine kinase frlD	-1,09	-1,71	33,42
SL3566	<i>frlB</i>	Fructosamine deglycase frlB	1,36	-1,39	33,98
SL3566	<i>frlB</i>	Fructosamine deglycase frlB	1,36	-1,39	33,98
SL3569	-	Hypothetical	1,19	1,25	3,95
SL3571	<i>yhjB</i>	Putative HTH-type transcriptional regulator yhjB	-1,50	1,26	-3,03
SL3572	<i>yhjC</i>	Uncharacterized HTH-type transcriptional regulator yhjC	1,07	-1,06	2,24
SL3576	<i>yhjH</i>	Cyclic di-GMP phosphodiesterase YhjH	-1,44	1,20	-5,37
SL3577	<i>kdgK</i>	2-dehydro-3-deoxygluconokinase	1,12	-1,08	4,32
SL3579	<i>dctA</i>	C4-dicarboxylate transport protein	-1,06	-1,17	14,63
SL3596	<i>dppA</i>	Periplasmic dipeptide transport protein	1,12	1,02	3,36
SL3598	-	Hypothetical	-1,38	-1,04	-2,34
SL3598	-	Hypothetical	-1,38	-1,04	-2,34
SL3598	-	Hypothetical	-1,38	-1,04	-2,34

Tabla suplementaria 2

Genes afectados en las cepas mutantes *greA*, *greB* y *greAgreB* respecto a la cepa WT

ID	gene	Description	<i>greA</i> vs WT	<i>greB</i> vs WT	<i>greAgreB</i> vs WT
SL3608	<i>tag</i>	DNA-3-methyladenine glycosylase 1	1,17	-1,05	2,24
SL3609	<i>yiaC</i>	Uncharacterized N-acetyltransferase yiaC	1,15	-1,16	2,67
SL3612	<i>ghrB</i>	Glyoxylate/hydroxypyruvate reductase B	1,26	1,11	2,04
SL3615	<i>cspA</i>	Cold shock protein cspA	-1,20	-1,57	-2,91
SL3625	<i>xylB</i>	Xylulose kinase	1,11	1,10	2,26
SL3626	<i>xylA</i>	Xylose isomerase	-1,06	-1,04	2,26
SL3628	<i>bax</i>	Protein bax	-1,39	1,03	-9,21
SL3633	<i>dlgD</i>	2,3-diketo-L-gulonate reductase	1,01	-1,07	4,51
SL3635	-	Hypothetical	1,09	1,12	2,38
SL3637	<i>yiaN</i>	2,3-diketo-L-gulonate TRAP transporter large permease protein yiaN	-1,05	-1,38	2,40
SL3638	<i>yiaO</i>	2,3-diketo-L-gulonate-binding periplasmic protein yiaO	1,36	1,16	4,21
SL3639	<i>lyxK</i>	L-xylulose/3-keto-L-gulonate kinase	1,14	1,11	2,70
SL3641	<i>sgbU</i>	Putative L-ribulose-5-phosphate 3-epimerase sgbU	1,45	1,69	3,77
SL3643	<i>yisR</i>	Uncharacterized HTH-type transcriptional regulator yisR	1,24	-1,19	4,41
SL3643	<i>yisR</i>	Uncharacterized HTH-type transcriptional regulator yisR	1,24	-1,19	4,41
SL3644	-	Hypothetical	1,18	-1,02	4,20
SL3645	<i>aldB</i>	Aldehyde dehydrogenase B	1,01	1,23	2,38
SL3649	<i>yibF</i>	Uncharacterized GST-like protein yibF	1,10	1,09	2,65
SL3650	<i>mtlA</i>	PTS system mannitol-specific EIICBA component	1,02	-1,03	3,05
SL3653	<i>yibT</i>	Uncharacterized protein yibT	1,13	1,35	5,71
SL3658	<i>lldR</i>	Putative L-lactate dehydrogenase operon regulatory protein	-1,51	-1,00	2,62
SL3659	<i>lldD</i>	L-lactate dehydrogenase [cytochrome]	-1,46	-1,28	3,49
SL3662	<i>mdlA</i>	Mandelate racemase	1,18	1,01	4,34
SL3663	<i>gudP</i>	Probable glucarate transporter	1,43	1,22	4,44
SL3670	<i>gpml</i>	2,3-bisphosphoglycerate-independent phosphoglycerate mutase	-1,03	1,15	-3,23
SL3671	<i>yibP</i>	Uncharacterized protein yibP	-1,07	-1,17	-2,15
SL3674	<i>tdh</i>	L-threonine 3-dehydrogenase	1,25	-1,10	3,79
SL3675	<i>kbl</i>	Putative 8-amino-7-oxononanoate synthase/2-amino-3-ketobutyrate coenzyme A ligase	1,06	-1,25	2,94
SL3689	<i>rfaQ</i>	Lipopolysaccharide core heptosyltransferase rfaQ	-1,02	-1,01	-2,00
SL3695	<i>yicR</i>	UPF0758 protein yicR	-1,04	1,06	3,41
SL3700	<i>rph</i>	Ribonuclease PH	1,16	1,06	-2,20
SL3703	<i>ycbL</i>	Metallo-beta-lactamase L1	1,29	-1,10	2,03
SL3704	<i>yicG</i>	UPF0126 inner membrane protein yicG	1,20	1,15	-3,47
SL3711	-	Cytoplasmic Protein	1,50	-1,09	5,37
SL3712	<i>gltS</i>	Sodium/glutamate symport carrier protein	1,44	1,03	5,98
SL3714	<i>yicH</i>	Uncharacterized protein yicH	1,11	-1,08	2,92
SL3715	<i>yicI</i>	Alpha-xylosidase	1,25	1,16	1,98
SL3716	<i>yicJ</i>	Inner membrane symporter yicJ	1,23	-1,03	2,54
SL3728	<i>mgtB</i>	Magnesium-transporting ATPase, P-type 1	-1,69	1,21	-4,80
SL3729	<i>mgtC</i>	Protein mgtC	-1,98	1,06	-24,09

Tabla suplementaria 2Genes afectados en las cepas mutantes *greA*, *greB* y *greAgreB* respecto a la cepa WT

ID	gene	Description	greA vs WT	greB vs WT	greAgreB vs WT
SL3738	<i>levR</i>	Transcriptional regulatory protein levR	1,15	1,07	2,12
SL3740	<i>gmuD</i>	6-phospho-beta-glucosidase gmuD	1,31	1,12	2,95
SL3742	-		1,26	-1,01	-4,69
SL3743	-	Hypothetical	1,50	1,54	3,57
SL3744	<i>yiaG</i>	Transcriptional Regulator XRE Family	1,35	1,35	3,84
SL3750	<i>gatA</i>	PTS IIA-Like Nitrogen-Regulatory Protein PtsN	1,08	-1,01	1,99
SL3751	<i>mngR</i>	Mannosyl-D-glycerate transport/metabolism system repressor mngR	1,24	1,41	3,65
SL3756	<i>uhpA</i>	Transcriptional regulatory protein uhpA	-1,11	1,19	-2,39
SL3757	-	Hypothetical	1,24	1,05	3,49
SL3758	<i>fucP</i>	L-fucose-proton symporter	1,25	-1,02	3,39
SL3759	<i>rbsK</i>	Ribokinase	1,14	1,11	3,60
SL3760	<i>deoR</i>	Deoxyribose operon repressor	1,28	-1,00	2,51
SL3761	<i>ilvN</i>	Acetolactate synthase isozyme 1 small subunit	1,53	1,09	4,96
SL3762	<i>ilvB</i>	Acetolactate synthase isozyme 1 large subunit	1,51	1,08	5,91
SL3767	-	Hypothetical	1,23	-1,00	2,32
SL3768	<i>dsdC</i>	HTH-type transcriptional regulator dsdC	1,47	1,01	3,96
SL3769	<i>dsdX</i>	DsdX permease	1,23	1,23	2,10
SL3774	<i>yidE</i>	Putative transport protein CKO_00031	1,42	1,43	5,60
SL3776	<i>ibpA</i>	Small heat shock protein ibpA	1,29	1,47	3,13
SL3786	<i>yhjA</i>	Probable cytochrome c peroxidase	-1,07	-1,11	-2,69
SL3789	<i>torC</i>	Cytochrome c-type protein torC	1,30	-1,04	-3,23
SL3790	<i>torR</i>	TorCAD operon transcriptional regulatory protein torR	1,28	-1,04	4,44
SL3793	<i>dgoT</i>	D-galactonate transporter	1,67	1,10	2,84
SL3794	<i>dgoD1</i>	D-galactonate dehydratase 1	1,47	1,07	3,20
SL3795	<i>dgoA</i>	2-dehydro-3-deoxy-6-phosphogalactonate aldolase	1,43	1,31	2,97
SL3796	<i>dgoK</i>	2-dehydro-3-deoxygalactonokinase	1,05	-1,14	2,37
SL3797	<i>dgoR</i>	Galactonate operon transcriptional repressor	-1,02	-1,09	2,58
SL3799	<i>gudP</i>	Probable glucarate transporter	-1,03	-1,11	4,70
SL3800	<i>dgoD</i>	D-galactonate dehydratase	-1,02	1,03	3,13
SL3801	<i>ybhD</i>	Uncharacterized HTH-type transcriptional regulator ybhD	1,43	1,16	4,56
SL3805	<i>dnaA</i>	Chromosomal replication initiator protein dnaA	1,02	1,07	-2,05
SL3806	<i>rpmH</i>	50S ribosomal protein L34	-1,09	1,07	-2,20
SL3807	<i>rnpA</i>	Ribonuclease P protein component	-1,08	1,00	-2,10
SL3811	<i>intA</i>	Prophage CP4-57 integrase	-1,46	-1,21	-1,99
SL3814	<i>mdtL</i>	Multidrug resistance protein mdtL	1,00	-1,06	-3,71
SL3818	<i>purP</i>	Probable adenine permease PurP	-1,18	1,00	-2,73
SL3827	<i>sgrR</i>	HTH-type transcriptional regulator sgrR	1,01	-1,23	2,56
SL3831	<i>atpC</i>	ATP synthase epsilon chain	1,19	1,07	3,56
SL3833	<i>atpG</i>	ATP synthase gamma chain	1,01	-1,31	2,51
SL3834	<i>atpA</i>	ATP synthase subunit alpha	1,08	-1,18	2,05
SL3835	<i>atpH</i>	ATP synthase subunit delta	-1,05	-1,17	2,01
SL3842	<i>mioC</i>	Protein mioC	1,08	1,05	-2,43

Tabla suplementaria 2Genes afectados en las cepas mutantes *greA*, *greB* y *greAgreB* respecto a la cepa WT

ID	gene	Description	<i>greA</i> vs WT	<i>greB</i> vs WT	<i>greAgreB</i> vs WT
SL3848	<i>rbsD</i>	D-ribose pyranase	-2,94	-1,06	-2,87
SL3849	<i>rbsA1</i>	Ribose import ATP-binding protein RbsA 1	-3,09	-1,10	-2,95
SL3851	<i>rbsB</i>	D-ribose-binding periplasmic protein	1,20	1,08	2,16
SL3857	<i>yleP</i>	Uncharacterized HTH-type transcriptional regulator yieP	1,21	-1,02	2,53
SL3861	<i>ilvG</i>	Acetolactate synthase isozyme 2 large subunit	-1,19	1,08	3,17
SL3862	<i>ilvM</i>	Acetolactate synthase isozyme 2 small subunit	-1,01	1,08	5,19
SL3865	<i>ilvA</i>	Threonine dehydratase biosynthetic	1,35	-1,06	2,36
SL3873	<i>gppA</i>	Guanosine-5'-triphosphate,3'-diphosphate pyrophosphatase	-1,03	-1,19	-2,09
SL3874	<i>rhlB</i>	ATP-dependent RNA helicase rhlB	-1,08	-1,34	-2,45
SL3876	<i>rho</i>	Transcription termination factor rho	-1,08	1,01	-3,61
SL3894	<i>cyaA</i>	Adenylate cyclase	-1,09	1,05	-2,83
SL3903	<i>xerC</i>	Tyrosine recombinase xerC	-1,10	-1,39	-2,00
SL3906	<i>corA</i>	Magnesium transport protein corA	-1,33	1,07	-3,08
SL3935	<i>fadA</i>	3-ketoacyl-CoA thiolase	-1,12	-1,11	23,14
SL3936	<i>fadB</i>	Fatty acid oxidation complex subunit alpha	-1,07	1,23	22,96
SL3955	<i>typA</i>	GTP-binding protein TypA/BipA	1,11	1,08	-2,44
SL3961	-	Hypothetical	-1,19	-1,13	2,67
SL3962	<i>ompL</i>	Porin ompL	1,29	-1,12	3,58
SL3963	<i>yihO</i>	Uncharacterized symporter yihO	1,17	-1,02	2,27
SL3964	<i>yihP</i>	Inner membrane symporter yihP	1,33	-1,13	2,70
SL3965	<i>yihQ</i>	Alpha-glucosidase yihQ	1,27	-1,07	2,10
SL3966	<i>yihR</i>	Uncharacterized protein yihR	1,04	-1,09	2,30
SL3967	<i>yihS</i>	Uncharacterized sugar isomerase yihS	1,06	-1,19	4,13
SL3968	<i>yihT</i>	Uncharacterized aldolase yihT	-1,06	-1,69	4,63
SL3969	<i>yihU</i>	Uncharacterized oxidoreductase yihU	1,17	-1,17	6,23
SL3970	<i>yihV</i>	Uncharacterized sugar kinase yihV	1,18	1,10	3,37
SL3977	<i>ygjN</i>	Uncharacterized protein ygjN	1,03	-1,00	2,34
SL3978	<i>est</i>	Esterase	1,17	-1,01	3,87
SL3979	<i>higB-2</i>	Toxin higB-2	-1,03	-1,15	2,12
SL3980	-	Transcriptional Regulator XRE Family	1,06	-1,11	2,21
SL3986	<i>fdhD</i>	Protein fdhD	-1,04	1,08	-2,32
SL3989	-	Hypothetical	1,02	1,17	-2,15
SL3993	<i>yiaY</i>	Probable alcohol dehydrogenase	1,63	1,51	1,98
SL3995	<i>rhaA</i>	L-rhamnose isomerase	1,07	-1,37	1,98
SL3997	<i>rhaS</i>	HTH-type transcriptional activator rhaS	1,24	1,44	7,48
SL3998	<i>rhaR</i>	HTH-type transcriptional activator rhaR	1,11	1,18	3,48
SL4012	<i>sbp</i>	Sulfate-binding protein	1,43	1,13	3,15
SL4014	<i>yagG</i>	Uncharacterized symporter yagG	1,30	1,22	6,83
SL4015	<i>scrK</i>	Fructokinase	1,32	1,14	7,32
SL4016	<i>yegU</i>	Uncharacterized protein yegU	1,37	1,16	4,60
SL4018	-	Hypothetical	-1,08	1,22	-2,00
SL4019	<i>cdh</i>	CDP-diacylglycerol pyrophosphatase	1,01	1,06	2,10
SL4020	-	Conserved Hypothetical Protein	1,21	1,00	3,55
SL4021	<i>IsrK</i>	Autoinducer 2 kinase IsrK	1,15	-1,14	5,12
SL4022	<i>IsrR</i>	Transcriptional regulator IsrR	1,07	1,15	5,81

Tabla suplementaria 2

 Genes afectados en las cepas mutantes *greA*, *greB* y *greAgreB* respecto a la cepa WT

ID	gene	Description	greA vs WT	greB vs WT	greAgreB vs WT
SL4023	<i>lsrA</i>	Autoinducer 2 import ATP-binding protein lsrA	-1,19	1,31	49,79
SL4024	<i>lsrC</i>	Autoinducer 2 import system permease protein lsrC	-1,24	-1,20	18,13
SL4025	<i>lsrD</i>	Autoinducer 2 import system permease protein lsrD	-1,14	-1,11	9,85
SL4034	<i>glpX</i>	Fructose-1,6-bisphosphatase class 2	-1,05	-1,50	2,09
SL4036	<i>glpF</i>	Glycerol uptake facilitator protein	1,03	-1,01	2,43
SL4039	<i>menA</i>	1,4-dihydroxy-2-naphthoate octaprenyltransferase	1,07	-1,01	-2,24
SL4044	<i>priA</i>	Primosomal protein N'	-1,12	1,14	-1,99
SL4047	-	Arylsulfate Sulfotransferase	1,05	-1,06	2,61
SL4055	<i>metF</i>	5,10-methylenetetrahydrofolate reductase	-1,37	1,02	-3,35
SL4056	<i>katG1</i>	Catalase-peroxidase 1	1,05	1,00	-3,75
SL4057	<i>yijF</i>	Uncharacterized protein yijF	1,33	-1,25	-8,02
SL4060	<i>ptsA</i>	Multiphosphoryl transfer protein 2	1,41	1,33	2,52
SL4061	<i>frwC</i>	Fructose-like permease IIC component 2	1,36	1,35	5,71
SL4062	<i>frwB</i>	Fructose-like phosphotransferase enzyme IIB component 2	1,36	1,10	3,40
SL4075	<i>sthA</i>	Soluble pyridine nucleotide transhydrogenase	-1,05	-1,16	2,56
SL4078	<i>trmA</i>	tRNA (uracil-5-)-methyltransferase	1,06	1,07	-1,99
SL4093	<i>rpoC</i>	DNA-directed RNA polymerase subunit beta'	1,17	1,01	2,04
SL4098	<i>thiH</i>	Dehydroglycine synthase	1,23	1,13	3,47
SL4099	<i>thiG</i>	Thiazole synthase	1,42	1,35	4,86
SL4100	<i>thiS</i>	Sulfur carrier protein ThiS	1,69	1,23	3,53
SL4101	<i>thiF</i>	Sulfur carrier protein ThiS adenylyltransferase	1,43	-1,04	4,02
SL4102	<i>thiE</i>	Thiamine-phosphate pyrophosphorylase	1,31	-1,10	3,49
SL4103	<i>thiC</i>	Phosphomethylpyrimidine synthase	1,36	1,01	3,16
SL4104	<i>rsd</i>	Regulator of sigma D	-1,03	1,26	3,58
SL4111	<i>zraP</i>	Zinc resistance-associated protein	1,57	1,64	-2,57
SL4112	<i>zraS</i>	Sensor protein zraS	1,18	-1,03	2,34
SL4118	<i>aceB</i>	Malate synthase A	-1,09	-1,09	7,52
SL4119	<i>aceA</i>	Isocitrate lyase	-1,27	-1,09	4,68
SL4121	-	Hypothetical	-1,13	-1,65	2,21
SL4122	<i>iclR</i>	Acetate operon repressor	-1,08	-1,37	2,81
SL4124	<i>yjbB</i>	Uncharacterized protein yjbB	1,09	1,02	2,28
SL4131	-	Hypothetical	1,02	-1,17	-4,83
SL4134	-	Cytoplasmic Protein	-1,01	-1,23	2,11
SL4140	<i>gtrB</i>	SfII prophage-derived bactoprenol glucosyl transferase	-1,15	1,03	-2,31
SL4142	-	Phage Baseplate Assembly Protein V	1,32	1,09	3,49
SL4143	-	Late Control D Family Protein	1,23	-1,09	2,56
SL4144	-	Bacteriophage Tail Fibre Protein	1,42	1,06	2,50
SL4145	-	Hypothetical	1,19	-1,01	2,10
SL4146	-	Phage Tail Protein	1,06	-1,16	2,84
SL4147	-	Hypothetical	1,02	1,02	2,44
SL4159	<i>yjbF</i>	Uncharacterized lipoprotein yjbF	-1,15	1,05	-2,28
SL4162	<i>psiE</i>	Protein psiE	-1,22	1,16	-3,30
SL4165	-	Hypothetical Protein SL4165	-1,19	-1,46	2,30

Tabla suplementaria 2

Genes afectados en las cepas mutantes *greA*, *greB* y *greAgreB* respecto a la cepa WT

ID	gene	Description	<i>greA</i> vs WT	<i>greB</i> vs WT	<i>greAgreB</i> vs WT
SL4167	<i>malk</i>	Maltose+C3582/maltodextrin import ATP-binding protein MalK	-1,91	-2,04	1,67
SL4170	<i>ubiC</i>	Chorismate--pyruvate lyase	1,29	1,13	2,11
SL4174	<i>lexA</i>	LexA repressor	1,13	1,16	2,28
SL4180	<i>pspG</i>	Phage shock protein G	-1,04	1,32	-2,02
SL4185	<i>aphA</i>	Class B acid phosphatase	-1,19	-1,10	2,41
SL4191	-	Cytoplasmic Protein	-1,16	1,03	-2,80
SL4193	<i>siiA</i>	Hypothetical	-2,30	-1,86	-26,54
SL4194	<i>siiB</i>	Integral Membrane Protein	-2,14	-1,76	-26,23
SL4195	<i>siiC</i>	Outer membrane protein tolC	-2,10	-1,38	-22,66
SL4196	<i>siiD</i>	Proteases secretion protein prtE	-1,96	-1,42	-31,87
SL4197	<i>siiiE</i>	Hypothetical	-1,31	1,08	-18,80
SL4198	<i>siiF</i>	Leukotoxin translocation ATP-binding protein lktB	-2,25	-1,23	-46,89
SL4199	<i>yjcB</i>	Uncharacterized protein yjcB	-1,49	1,15	-9,86
SL4200	<i>yjcC</i>	Uncharacterized protein yjcC	-1,93	1,10	-3,42
SL4201	<i>soxS</i>	Regulatory protein soxS	-1,57	-1,10	-3,63
SL4207	<i>cidA</i>	Holin-like protein cidA	-1,10	-1,01	-19,38
SL4208	<i>ywbG</i>	Uncharacterized protein ywbG	-1,18	-1,29	-19,43
SL4209	<i>actP</i>	Cation/acetate symporter ActP	-1,02	-1,45	13,02
SL4210	<i>yjch</i>	Inner membrane protein yjch	1,08	-1,46	39,97
SL4211	<i>acs</i>	Acetyl-coenzyme A synthetase	-1,26	-1,40	21,68
SL4212	-	Hypothetical	-1,04	1,03	3,32
SL4213	<i>nrfA</i>	Cytochrome c-552	1,17	1,40	2,13
SL4221	<i>fdhF</i>	Formate dehydrogenase H	1,16	1,06	-2,29
SL4231	<i>adiC</i>	Arginine/agmatine antiporter	-1,10	-1,77	-4,64
SL4234	<i>melR</i>	Melibiose operon regulatory protein	1,19	1,12	6,19
SL4236	<i>melB</i>	Melibiose carrier protein	2,07	-1,79	1,46
SL4238	<i>dcuB</i>	Anaerobic C4-dicarboxylate transporter dcuB	1,02	1,56	-11,02
SL4239	-	Hypothetical	-1,18	1,39	-24,27
SL4247	<i>yjiK</i>	Uncharacterized protein yjiK	-1,74	1,10	-24,46
SL4248	-	Hypothetical	-2,43	-1,91	-28,20
SL4248	-	Hypothetical	-2,43	-1,91	-28,20
SL4249	-	Cytoplasmic Protein	-3,07	-2,48	-41,36
SL4250	<i>rtsB</i>	GerE Family Regulatory Protein	-3,14	-2,47	-60,33
SL4251	<i>rtsA</i>	Transcriptional regulator sirC	-2,64	-1,89	-47,96
SL4252	-	Hypothetical	-1,52	1,12	-5,47
SL4253	-	Hypothetical	-1,44	1,09	-2,43
SL4260	<i>dsbD</i>	Thiol:disulfide interchange protein dsbD	-1,04	-1,45	-2,77
SL4261	<i>cutA</i>	Divalent-cation tolerance protein cutA	-1,04	-1,19	-2,17
SL4266	<i>groS</i>	10 kDa chaperonin	1,19	1,04	3,79
SL4267	<i>groL</i>	60 kDa chaperonin	1,17	-1,02	2,58
SL4270	<i>yjeK</i>	Uncharacterized KamA family protein YjeK	1,08	1,01	-2,15
SL4281	<i>yjeA</i>	Uncharacterized protein YjeA	-1,18	-1,30	-2,31
SL4282	<i>yjeM</i>	Inner membrane transporter yjeM	-1,01	-1,06	-3,47
SL4310	<i>aidB</i>	Protein AidB	1,35	1,22	9,60
SL4311	<i>yjfN</i>	Uncharacterized protein yjfN	1,41	1,24	6,64
SL4312	<i>bsmA</i>	Lipoprotein BsmA	1,31	1,21	5,00
SL4313	<i>yjfP</i>	Esterase yjfP	1,04	1,03	2,55

Tabla suplementaria 2

 Genes afectados en las cepas mutantes *greA*, *greB* y *greAgreB* respecto a la cepa WT

ID	gene	Description	greA vs WT	greB vs WT	greAgreB vs WT
SL4315	<i>ulaG</i>	Probable L-ascorbate-6-phosphate lactonase ulaG	1,10	1,15	2,27
SL4316	<i>ulaA</i>	Ascorbate-specific permease IIC component ulaA	1,34	1,14	9,06
SL4317	<i>ulaB</i>	Ascorbate-specific phosphotransferase enzyme IIB component	1,29	1,06	6,92
SL4318	<i>ulaC</i>	Ascorbate-specific phosphotransferase enzyme IIA component	1,14	-1,11	5,04
SL4319	<i>ulaD</i>	3-keto-L-gulonate-6-phosphate decarboxylase ulaD	1,23	-1,49	3,02
SL4320	<i>ulaE</i>	L-ribulose-5-phosphate 3-epimerase ulaE	1,06	-1,20	2,25
SL4327	<i>rplI</i>	50S ribosomal protein L9	-1,15	1,10	-2,28
SL4329	<i>ytfB</i>	Uncharacterized protein ytfB	1,24	1,19	2,09
SL4333	<i>ytfF</i>	Inner membrane protein ytfF	1,15	1,22	2,16
SL4334	<i>qorB</i>	Quinone oxidoreductase 2	1,06	1,26	2,70
SL4336	<i>cpdB</i>	2',3'-cyclic-nucleotide 2'-phosphodiesterase/3'-nucleotidase	1,31	1,04	4,00
SL4338	<i>ytfJ</i>	Uncharacterized protein ytfJ	-1,19	1,16	2,51
SL4340	<i>ytfL</i>	UPF0053 inner membrane protein ytfL	-1,12	-1,16	-2,96
SL4341	<i>msrA</i>	Peptide methionine sulfoxide reductase msrA	-1,09	1,23	2,87
SL4350	<i>hexR</i>	Uncharacterized HTH-type transcriptional regulator HI_0143	-1,08	1,02	-2,14
SL4351	<i>xylE</i>	D-xylose-proton symporter	1,00	-1,60	7,99
SL4353	<i>iolB</i>	5-deoxy-glucuronate isomerase	1,33	1,06	3,00
SL4354	<i>iolA1</i>	Methylmalonate semialdehyde dehydrogenase [acylating] 1	1,29	1,10	3,93
SL4355	<i>ydiP</i>	Uncharacterized HTH-type transcriptional regulator ydiP	1,09	1,48	6,37
SL4359	<i>iolI</i>	Inosose isomerase	1,20	-1,01	2,12
SL4361	<i>iolC</i>	5-dehydro-2-deoxygluconokinase	1,02	-1,26	5,41
SL4362	<i>iolD1</i>	3D-(3,5/4)-trihydroxycyclohexane-1,2-dione hydrolase 1	1,04	-1,38	5,81
SL4365	-	Xylose Isomerase Domain-Containing Protein	1,03	-1,04	2,81
SL4366	<i>iolH</i>	Protein iolH	1,00	-1,15	2,02
SL4369	<i>cybC</i>	Soluble cytochrome b562	1,05	1,04	2,03
SL4371	-	Hypothetical	1,37	1,18	2,22
SL4372	-	Hypothetical	1,39	1,09	2,71
SL4373	-	Hypothetical	1,09	1,02	2,64
SL4374	-	Hypothetical	1,13	1,07	2,36
SL4375	-	Dihydroorotase	1,22	-1,08	2,21
SL4376	<i>selA</i>	Uncharacterized protein mlr3804	1,21	1,00	2,54
SL4377	-	Hypothetical	1,23	-1,01	2,59
SL4381	<i>nrdG</i>	Anaerobic ribonucleoside-triphosphate reductase-activating protein	1,27	-1,20	-2,24
SL4382	<i>nrdD</i>	Anaerobic ribonucleoside-triphosphate reductase	1,27	-1,05	-2,21
SL4384	<i>treC</i>	Trehalose-6-phosphate hydrolase	-1,16	1,06	2,06
SL4385	<i>treB</i>	PTS system trehalose-specific EIIBC component	1,06	1,34	2,48
SL4387	<i>mgtA</i>	Magnesium-transporting ATPase, P-type 1	-1,61	1,04	-2,08
SL4393	<i>argR</i>	Arginine repressor	2,49	1,35	-1,35
SL4394	<i>yfcC</i>	Uncharacterized protein HI_0594	2,59	1,62	-1,71

Tabla suplementaria 2

Genes afectados en las cepas mutantes *greA*, *greB* y *greAgreB* respecto a la cepa WT

ID	gene	Description	greA vs WT	greB vs WT	greAgreB vs WT
SL4395	<i>arcB</i>	Ornithine carbamoyltransferase, catabolic	2,46	1,57	-1,54
SL4397	<i>arcA</i>	Arginine deiminase	2,65	2,16	1,41
SL4402	<i>ytgA</i>	Uncharacterized protein ytgA	1,31	-1,20	2,30
SL4406	<i>holC</i>	DNA polymerase III subunit chi	1,13	-1,20	2,20
SL4407	<i>pepA</i>	Probable cytosol aminopeptidase	1,17	-1,08	2,78
SL4412	<i>idnT</i>	Gnt-II system L-idonate transporter	1,58	-1,02	3,38
SL4413	<i>idnO</i>	Gluconate 5-dehydrogenase	1,50	-1,24	3,80
SL4414	<i>idnD</i>	L-idonate 5-dehydrogenase	1,71	-1,04	4,59
SL4415	<i>idnK</i>	Thermosensitive gluconokinase	1,14	1,03	2,28
SL4419	-	Restriction Endonuclease	1,20	1,05	2,21
SL4429	<i>yeeN</i>	UPF0082 protein LACR_0237	1,08	-1,07	-2,10
SL4430	<i>yjhP</i>	Uncharacterized protein yjhP	1,27	1,18	2,26
SL4431	-	UPF0386 protein KPN78578_02510	1,35	1,24	2,78
SL4434	-	Hypothetical	-2,10	1,20	-4,98
SL4435	-	Hypothetical	-1,43	1,10	-2,04
SL4438	<i>trpS</i>	Tryptophanyl-tRNA synthetase	-1,02	-1,11	2,21
SL4450	<i>ssdA</i>	Succinate-semialdehyde dehydrogenase [NADP+]	1,49	1,45	2,77
SL4451	-	Hypothetical	1,32	-1,32	2,30
SL4457	<i>hsdR</i>	Type I restriction enzyme EcoKI R protein	1,09	1,02	2,34
SL4459	-	Hypothetical	1,29	1,33	2,48
SL4460	-	Hypothetical	1,26	1,49	3,02
SL4462	<i>yjiX</i>	Uncharacterized protein yjiX	-1,09	-1,08	-2,97
SL4463	<i>yjiY</i>	Inner membrane protein yjiY	1,11	1,19	-18,87
SL4464	<i>tsr</i>	Methyl-accepting chemotaxis protein I	-1,03	-1,00	-2,50
SL4465	<i>levR</i>	Transcriptional regulatory protein levR	1,19	1,17	1,99
SL4466	<i>manX</i>	PTS System Fructocific IIA Component	2,51	1,25	13,66
SL4467	<i>manX</i>	Probable phosphotransferase enzyme IIB component M6_Spy0801	1,80	-1,22	15,83
SL4468	<i>agaC</i>	N-acetylgalactosamine permease IIC component 1	2,23	-1,04	17,29
SL4469	<i>manZ</i>	Mannose permease IID component	2,24	1,09	14,20
SL4470	<i>glmS</i>	Glucosamine--fructose-6-phosphate aminotransferase [isomerizing]	3,29	1,02	23,21
SL4471	<i>frlB</i>	Fructosamine deglycase frlB	2,57	1,34	14,58
SL4484	<i>rsmC</i>	Ribosomal RNA small subunit methyltransferase C	1,03	-1,07	-2,63
SL4496	<i>deoB</i>	Phosphopentomutase	-1,09	-1,00	-2,17
SL4500	<i>yhcA</i>	Uncharacterized fimbrial chaperone yhcA	-1,65	-1,01	-1,99
SL4509	<i>slt</i>	Soluble lytic murein transglycosylase	1,26	-1,04	2,00
SL4510	<i>trpR</i>	Trp operon repressor	1,10	-1,25	2,05
SLP1_0013	<i>traQ</i>	Protein traQ	1,07	-1,04	2,12
SLP1_0022	<i>traC</i>	Protein traC	1,31	-1,11	2,12
SLP1_0025	<i>traV</i>	Protein TraV	1,03	-1,17	2,31
SLP1_0026	<i>trbD</i>	Conjugal Transfer Protein TrbD	1,16	1,24	2,84
SLP1_0039	<i>yubM</i>	Uncharacterized protein yubM	-1,01	-1,02	2,75
SLP1_0043	-	Hypothetical	1,34	1,21	2,35
SLP1_0054	<i>parB</i>	Plasmid Partition par B protein	1,09	1,12	5,19
SLP1_0055	<i>parA</i>	Plasmid partition protein A	-1,14	-1,37	5,75
SLP1_0057	-	Cytoplasmic Protein	1,14	-1,02	2,77

Tabla suplementaria 2Genes afectados en las cepas mutantes *greA*, *greB* y *greAgreB* respecto a la cepa WT

ID	gene	Description	greA vs WT	greB vs WT	greAgreB vs WT
SLP1_0058	-	Uncharacterized protein pSLT049	1,01	-1,09	2,85
SLP1_0059	-	Myosin Heavy Chain Gizzard Smooth	-1,00	1,14	2,65
SLP1_0065	-	Insertion element IS630 uncharacterized 39 kDa protein	1,15	1,14	-2,02
SLP1_0067	<i>spvA</i>	28.1 kDa virulence protein	-1,35	1,10	-6,22
SLP1_0068	<i>vsdC</i>	65 kDa virulence protein	-1,39	1,03	-12,28
SLP1_0069	<i>spvC</i>	27.5 kDa virulence protein	-1,59	-1,30	-34,55
SLP1_0070	<i>vsdE</i>	Virulence protein vsdE	-1,34	-1,34	-10,27
SLP1_0077	-	Cytoplasmic Protein	-1,01	-1,14	2,14
SLP1_0079	<i>ccdB</i>	Cytotoxic protein CcdB	-1,01	-1,01	2,35
SLP1_0080	<i>ccdA</i>	Protein CcdA	1,08	1,02	2,95
SLP1_0086	<i>papB</i>	Major pilu subunit operon regulatory protein papB	1,95	2,29	-1,65
SLP1_0087	<i>fedA</i>	F107 fimbrial protein	1,31	1,36	2,72
SLP1_0096	<i>pagC</i>	Virulence membrane protein pagC	1,40	1,04	2,84
SLP2_0003	-	Hypothetical	1,01	1,12	4,59
SLP2_0004	-	Addiction Module Antitoxin	1,09	1,15	3,55
SLP2_0005	<i>dnaQ</i>	Uncharacterized protein pSLT049	1,03	1,28	4,21
SLP2_0006	-	viria25	1,03	1,12	1,99
SLP2_0009	-	Hypothetical	-1,52	-1,18	2,29
SLP2_0011	-	Uncharacterized protein in cib 5'region	1,10	1,08	5,04
SLP2_0012	<i>cib</i>	Colicin-Ib	1,33	1,46	4,20
SLP2_0015	-	Hypothetical	-1,09	-1,09	2,04
SLP2_0016	-	Hypothetical	-1,09	-1,31	2,65
SLP2_0017	<i>resD</i>	Resolvase	-1,24	-1,45	2,37
SLP2_0020	-	Hypothetical	-1,03	-1,12	2,26
SLP2_0029	<i>yubF</i>	Uncharacterized protein yubF	1,32	1,06	2,34
SLP2_0030	-	Uncharacterized protein yubG	1,40	1,39	2,83
SLP2_0031	<i>yubH</i>	Uncharacterized protein yubH	-1,04	-1,23	2,24
SLP2_0032	<i>yubI</i>	Putative antirestriction protein YubI	1,27	1,21	3,00
SLP2_0033	<i>yubJ</i>	Uncharacterized protein yubJ	1,06	1,04	3,01
SLP2_0036	<i>yubM</i>	Uncharacterized protein yubM	1,09	1,12	2,51
SLP2_0037	<i>psiB</i>	Protein psiB	1,24	1,17	4,39
SLP2_0038	<i>psiA</i>	Protein psiA	1,23	1,09	5,34
SLP2_0039	-	Hypothetical	1,36	1,11	4,78
SLP2_0044	<i>yfcl</i>	Uncharacterized protein pSLT051	1,09	1,07	2,09
SLP2_0063	-	Hypothetical	1,03	1,08	-2,42
SLP2_0064	-	TraQ Protein	1,13	1,18	-2,04
SLP2_0078	-	Hypothetical	1,48	1,07	3,93
SLP2_0079	-	Hypothetical	1,29	1,13	3,02
SLP2_0086	-	Prepilin Peptidase	-1,08	-1,21	-3,05
SLP2_0087	<i>pbl</i>	Peptidoglycan-binding-like protein	1,09	1,03	-2,03
SLP3_0001	<i>sullI</i>	Dihydropteroate synthase type-2	1,09	1,00	-2,14
SLP3_0004	<i>repA</i>	Regulatory protein repA	1,20	1,20	2,05
SLP3_0005	-	Hypothetical Protein SLP3_0005	1,08	1,10	2,21
SLP3_0006	-	Hypothetical Protein SLP3_0006	1,15	1,23	2,23
SLP3_0007	<i>mobA</i>	Mobilization protein A	1,27	1,09	2,75
SLP3_0008	<i>mobA</i>	Mobilization protein A	1,39	1,26	2,71

Tabla suplementaria 2Genes afectados en las cepas mutantes *greA*, *greB* y *greAgreB* respecto a la cepa WT

ID	gene	Description	greA vs WT	greB vs WT	greAgreB vs WT
SLP3_0009	<i>mobB</i>	Mobilization protein B	1,30	1,14	2,64
SLP3_0011	<i>mobC</i>	Mobilization protein C	1,12	1,04	3,03

Tabla Suplementaria 5

Genes afectados en las cepas mutantes *dksA* y *greAgreB*, respecto a la cepa WT

ID	gene	Description	<i>dksA</i> vs WT	<i>greAgreB</i> vs WT
SL0036	<i>betC</i>	Choline-sulfatase	1,70	3,95
SL0043	<i>xylP</i>	Putative xylose-proton symporter	5,23	7,93
SL0044	<i>rpsT</i>	30S ribosomal protein S20	1,12	-3,04
SL0052	<i>rihC</i>	Non-specific ribonucleoside hydrolase rihC	1,74	3,12
SL0057	<i>oadG1</i>	Probable oxaloacetate decarboxylase gamma chain 1	8,83	4,14
SL0058	<i>citS</i>	Citrate-sodium symporter	9,18	3,02
SL0059	<i>citC</i>	[Citrate [pro-3S]-lyase] ligase	10,46	1,87
SL0060	<i>citD2</i>	Citrate lyase acyl carrier protein 2	3,43	1,73
SL0061	<i>citE</i>	Citrate lyase subunit beta	12,65	7,85
SL0062	<i>citF</i>	Citrate lyase alpha chain	6,04	5,71
SL0063	<i>citX</i>	Apo-citrate lyase phosphoribosyl-dephospho-CoA transferase	4,27	2,72
SL0066	-	Hypothetical	-4,07	-4,48
SL0074	<i>caiA</i>	Crotonobetainyl-CoA dehydrogenase	3,58	1,33
SL0075	<i>caiT</i>	L-carnitine/gamma-butyrobetaine antiporter	9,31	1,83
SL0076	<i>fixA</i>	Protein fixA	3,23	1,64
SL0077	<i>fixB</i>	Protein fixB	3,01	1,73
SL0102	<i>araA</i>	L-arabinose isomerase	5,26	2,50
SL0103	<i>araB</i>	Ribulokinase	7,11	3,31
SL0104	<i>araC</i>	Arabinose operon regulatory protein	9,28	10,58
SL0111	<i>leuC1</i>	3-isopropylmalate dehydratase large subunit 1	1,11	3,98
SL0112	<i>leuB</i>	3-isopropylmalate dehydrogenase	-1,13	3,10
SL0144	<i>ppdD</i>	Prepilin peptidase-dependent protein D	3,64	2,04
SL0153	<i>aceF</i>	Dihydrolipoyllysine-residue acetyltransferase component of pyruvate dehydrogenase complex	2,66	3,97
SL0159	<i>acnB</i>	Aconitate hydratase 2	1,23	3,83
SL0160	-	Restriction Endonuclease	-3,43	-2,18
SL0163	<i>ygbK</i>	Uncharacterized protein HI_1011	1,59	4,11
SL0178	<i>fimF</i>	Fimbrial subunit type 1	2,50	3,27
SL0183	<i>panB</i>	3-methyl-2-oxobutanoate hydroxymethyltransferase	4,25	-1,33
SL0186	<i>gluQ</i>	Glutamyl-Q tRNA(Asp) synthetase	-45,85	-3,74
SL0187	<i>dksA</i>	DnaK suppressor protein	-818,57	1,21
SL0196	<i>smfA</i>	Fimbria A protein	-1,80	3,38
SL0211	<i>cdaR</i>	Carbohydrate diacid regulator	5,18	4,32
SL0212	<i>yaeH</i>	UPF0325 protein ESA_03178	3,85	3,29
SL0244	<i>yaeB</i>	UPF0066 protein yaeB	-3,80	-2,27
SL0255	<i>mltD</i>	Membrane-bound lytic murein transglycosylase D	-4,66	-6,32
SL0266	<i>clpB</i>	Chaperone protein clpB	1,30	3,43
SL0267	-	Hypothetical	1,66	3,82
SL0295	-	Lipoprotein	-3,63	-1,63
SL0305	<i>fadE</i>	Acyl-coenzyme A dehydrogenase	3,82	9,79
SL0336	-	Transmembrane Regulator	-4,37	-3,98
SL0344	<i>yjel</i>	Uncharacterized protein yjel	2,68	3,73
SL0348	<i>actP</i>	Copper-transporting P-type ATPase	1,67	4,15

Tabla Suplementaria 5

Genes afectados en las cepas mutantes *dksA* y *greAgreB*, respecto a la cepa WT

ID	gene	Description	<i>dksA</i> vs WT	<i>greAgreB</i> vs WT
SL0360	<i>yahN</i>	Uncharacterized membrane protein yahN	5,41	3,45
SL0363	<i>prpB</i>	Methylisocitrate lyase	-3,95	2,74
SL0364	<i>prpC</i>	2-methylcitrate synthase	-2,42	5,33
SL0365	<i>prpD</i>	2-methylcitrate dehydratase	-1,50	6,64
SL0366	<i>prpE</i>	Propionate--CoA ligase	-1,92	4,91
SL0369	<i>yaiV</i>	Uncharacterized protein yaiV	-3,52	-1,73
SL0371	<i>sbmA</i>	Protein sbmA	-3,76	-2,98
SL0376	-	Extensin Family Protein	1,68	4,71
SL0377	<i>mdtG</i>	Multidrug resistance protein mdtG	-3,46	-2,63
SL0396	<i>malZ</i>	Maltodextrin glucosidase	4,43	-1,05
SL0407	<i>tsx</i>	Nucleoside-specific channel-forming protein tsx	3,41	1,90
SL0433	<i>cyoE</i>	Protoheme IX farnesyltransferase	4,16	11,62
SL0434	<i>cyoD</i>	Cytochrome o ubiquinol oxidase protein cyoD	5,08	13,42
SL0435	<i>cyoC</i>	Cytochrome o ubiquinol oxidase subunit 3	4,41	13,28
SL0436	<i>cyoB</i>	Ubiquinol oxidase subunit 1	2,57	5,97
SL0437	<i>cyoA</i>	Ubiquinol oxidase subunit 2	2,05	6,05
SL0446	<i>ppiD</i>	Peptidyl-prolyl cis-trans isomerase D	-3,61	-1,27
SL0450	<i>ybaE</i>	Uncharacterized protein ybaE	3,86	6,33
SL0480	<i>htpG</i>	Chaperone protein htpG	1,50	3,68
SL0482	<i>hemH</i>	Ferrocyclase	-9,75	-8,01
SL0485	<i>ybaL</i>	Inner membrane protein ybaL	-3,63	-1,70
SL0487	<i>ushA</i>	Protein ushA	5,19	4,38
SL0502	-	Outer Membrane Protein	4,41	2,30
SL0507	<i>allS</i>	HTH-type transcriptional activator AllS	1,77	7,16
SL0510	<i>gcl</i>	Glyoxylate carboligase	1,60	7,44
SL0511	<i>hyi</i>	Hydroxypyruvate isomerase	1,80	10,16
SL0512	<i>glxR</i>	2-hydroxy-3-oxopropionate reductase	1,44	5,13
SL0513	<i>yybO</i>	Uncharacterized transporter yybO	1,01	4,88
SL0515	<i>ybbW</i>	Putative allantoin permease	1,49	3,89
SL0520	<i>allC</i>	Allantoate amidohydrolase	2,19	3,13
SL0521	<i>allD</i>	Ureidoglycolate dehydrogenase	3,62	5,10
SL0522	<i>fdrA</i>	Protein fdrA	1,84	3,41
SL0523	<i>ylbE</i>	Uncharacterized protein ylbE	1,51	3,61
SL0536	<i>sfmA</i>	Fimbrial subunit type 1	-6,11	-9,56
SL0537	<i>fimI</i>	Putative fimbrin-like protein fimI	-9,92	-17,41
SL0538	<i>fimC</i>	Chaperone protein fimC	-12,54	-22,44
SL0539	<i>fimD</i>	Outer membrane usher protein fimD	-4,82	-5,31
SL0540	<i>fimH</i>	Protein fimH	-3,62	-2,74
SL0544	-	Hypothetical	-3,69	-2,09
SL0551	<i>ykgD</i>	Uncharacterized HTH-type transcriptional regulator ykgD	-1,11	3,20
SL0556	<i>pheP</i>	Phenylalanine-specific permease	3,17	-1,29
SL0559	<i>levR</i>	Transcriptional regulatory protein levR	4,63	2,64
SL0588	<i>cstA</i>	Carbon starvation protein A	4,30	9,48

Tabla Suplementaria 5

Genes afectados en las cepas mutantes *dksA* y *greAgreB*, respecto a la cepa WT

ID	gene	Description	<i>dksA</i> vs WT	<i>greAgreB</i> vs WT
SL0589	<i>ybdD</i>	Uncharacterized protein ybdD	2,74	9,97
SL0593	<i>ybdN</i>	Uncharacterized protein ybdN	-2,98	-1,24
SL0596	<i>ahpC</i>	Alkyl hydroperoxide reductase subunit C	-3,65	-2,32
SL0597	<i>ahpF</i>	Alkyl hydroperoxide reductase subunit F	-3,53	-2,42
SL0598	<i>ynfl</i>	Cytoplasmic Chaperone rD Family Protein	-2,26	-3,67
SL0606	<i>citT</i>	Citrate carrier	4,10	-1,87
SL0607	<i>citG2</i>	Probable 2-(5"-triphosphoribosyl)-3'-dephosphocoenzyme-A synthase 2	5,25	-1,25
SL0608	<i>citX</i>	Apo-citrate lyase phosphoribosyl-dephospho-CoA transferase	18,14	-1,87
SL0609	<i>citF</i>	Citrate lyase alpha chain	21,53	-1,61
SL0610	<i>citE</i>	Citrate lyase subunit beta	21,38	-2,50
SL0611	<i>citD1</i>	Citrate lyase acyl carrier protein 1	22,22	-2,36
SL0612	<i>citC</i>	[Citrate [pro-3S]-lyase] ligase	8,29	-2,47
SL0613	<i>dpiB</i>	Sensor histidine kinase DpiB	-1,36	-3,56
SL0616	<i>crcA</i>	Protein crcA	-4,69	-6,65
SL0617	<i>cspE</i>	Cold shock-like protein cspE	-3,51	-2,78
SL0632	<i>cobD</i>	Threonine-phosphate decarboxylase	3,16	1,02
SL0637	<i>uxaA</i>	SAF Domain-Containing Protein	-9,19	-7,34
SL0638	<i>uxaA</i>	Altronate hydrolase	-8,11	-5,57
SL0639	<i>kdgT2</i>	2-keto-3-deoxygluconate permease 2	-3,33	-2,50
SL0641	<i>ybeL</i>	Uncharacterized protein ybeL	2,12	4,14
SL0651	<i>gltL</i>	Glutamate/aspartate transport ATP-binding protein gltL	3,26	8,59
SL0652	<i>gltK</i>	Glutamate/aspartate transport system permease protein gltK	2,42	8,36
SL0653	<i>gltJ</i>	Glutamate/aspartate transport system permease protein gltJ	1,58	5,50
SL0654	<i>gltI</i>	Glutamate/aspartate periplasmic-binding protein	1,58	6,78
SL0669	<i>ybfM</i>	Uncharacterized protein ybfM	3,25	2,74
SL0670	<i>ybfN</i>	Uncharacterized lipoprotein ybfN	3,37	3,34
SL0672	<i>citB</i>	Citrate utilization protein B	1,07	3,82
SL0675	<i>fur</i>	Ferric uptake regulation protein	-3,29	-2,81
SL0681	-	5-Nitroimidazole Antibiotic Resistance Protein	-1,24	-5,70
SL0682	<i>potE</i>	Putrescine-ornithine antiporter	-1,11	-4,57
SL0683	<i>speF</i>	Ornithine decarboxylase, inducible	1,21	-4,29
SL0691	<i>dtpD</i>	Dipeptide permease D	-4,97	-2,14
SL0713	-	Hypothetical	2,02	3,77
SL0714	<i>sdhC</i>	Succinate dehydrogenase cytochrome b556 subunit	5,16	8,34
SL0715	<i>sdhD</i>	Succinate dehydrogenase hydrophobic membrane anchor subunit	3,84	6,00
SL0716	<i>sdhA</i>	Succinate dehydrogenase flavoprotein subunit	4,37	8,19
SL0717	<i>sdhB</i>	Succinate dehydrogenase iron-sulfur subunit	4,79	8,63
SL0720	<i>sucC</i>	Succinyl-CoA ligase [ADP-forming] subunit beta	1,40	3,54
SL0733	<i>nadA</i>	Quinolinate synthase A	-4,30	-1,61

Tabla Suplementaria 5

Genes afectados en las cepas mutantes *dksA* y *greAgreB*, respecto a la cepa WT

ID	gene	Description	<i>dksA</i> vs WT	<i>greAgreB</i> vs WT
SL0740	<i>ywbl</i>	Uncharacterized HTH-type transcriptional regulator ywbl	3,78	3,02
SL0764	<i>hutI</i>	Imidazolonepropionase	1,31	3,21
SL0765	<i>hutG</i>	Formimidoylglutamase	1,66	4,38
SL0767	<i>hutU</i>	Urocanate hydratase	23,77	21,16
SL0768	<i>hutH</i>	Histidine ammonia-lyase	16,86	18,07
SL0776	<i>slrP</i>	E3 ubiquitin-protein ligase slrP	-5,25	-6,12
SL0790	<i>ybhQ</i>	Inner membrane protein ybhQ	4,45	1,17
SL0796	<i>rhIE</i>	ATP-dependent RNA helicase rhIE	-1,21	-4,28
SL0799	<i>ybiJ</i>	Uncharacterized protein ybiJ	-5,03	-3,65
SL0805	<i>glnH</i>	Glutamine-binding periplasmic protein	1,24	3,68
SL0813	<i>ybiT</i>	Uncharacterized ABC transporter ATP-binding protein ybiT	-3,51	-2,82
SL0825	<i>gsiB</i>	Glutathione-binding protein gsiB	1,50	3,72
SL0835	<i>cysL</i>	HTH-type transcriptional regulator cysL	-6,20	-5,57
SL0836	<i>yxjC</i>	Uncharacterized transporter yxjC	-3,76	-2,37
SL0841	<i>ybjG</i>	Putative undecaprenyl-diphosphatase ybjG	-3,26	-2,77
SL0846	<i>ybjL</i>	Putative transport protein ybjL	-3,92	-2,78
SL0854	<i>potF</i>	Putrescine-binding periplasmic protein	-1,24	3,91
SL0879	<i>ybjX</i>	Uncharacterized protein ybjX	-3,90	-5,97
SL0880	<i>macA</i>	Macrolide-specific efflux protein macA	-4,80	-2,43
SL0881	<i>macB</i>	Macrolide export ATP-binding/permease protein macB	-3,32	-1,49
SL0883	<i>clpS</i>	ATP-dependent Clp protease adapter protein clpS	-4,94	-3,50
SL0909	<i>sopD2</i>	Secreted effector protein sopD2	-5,55	-3,81
SL0911	<i>focA</i>	Probable formate transporter 1	-3,08	-7,51
SL0936	<i>ompF</i>	Outer membrane protein F	3,64	7,42
SL0937	<i>asnS</i>	Asparaginyl-tRNA synthetase	-3,14	-1,25
SL0939	<i>dpaL</i>	Diaminopropionate ammonia-lyase	2,68	3,64
SL0940	<i>yfIA</i>	Uncharacterized transporter yfIA	1,65	3,99
SL0966	<i>arrD</i>	Probable lysozyme from lambdoid prophage DLP12	1,02	-3,53
SL0967	<i>rzpD</i>	Putative Rz endopeptidase from lambdoid prophage DLP12	-1,16	-4,10
SL0968	-	Hypothetical	-1,48	-3,14
SL0989	<i>ycdD</i>	Tail fiber assembly protein homolog from lambdoid prophage Fels-1	-1,34	-3,53
SL0990	-	Hypothetical	-1,53	-6,38
SL0994	-	Hypothetical	-2,56	-3,96
SL0995	-	Prophage Encoded Virulence Factor	-3,35	-1,84
SL0996	<i>msgA</i>	Virulence protein msgA	-2,83	-5,56
SL0999	<i>ycbW</i>	Uncharacterized protein ycbW	-1,73	-3,12
SL1012	<i>sxy</i>	Protein sxy	4,04	3,23
SL1020	<i>rlmI</i>	Ribosomal RNA large subunit methyltransferase I	3,16	-1,01
SL1026	-	Hypothetical	-2,23	-3,52
SL1027	<i>pipB</i>	Secreted effector protein pipB	-6,51	-16,02
SL1028	-	Inner Membrane Protein	-12,86	-47,98
SL1029	<i>sigE</i>	Chaperone protein sigE	-6,14	-8,91

Tabla Suplementaria 5

Genes afectados en las cepas mutantes *dksA* y *greAgreB*, respecto a la cepa WT

ID	gene	Description	<i>dksA</i> vs WT	<i>greAgreB</i> vs WT
SL1030	<i>sopB</i>	Inositol phosphate phosphatase <i>sopB</i>	-7,58	-10,63
SL1031	-	Hypothetical	9,42	-1,75
SL1032	-	Hypothetical	7,87	-1,49
SL1040	<i>hpaG</i>	4-hydroxyphenylacetate degradation bifunctional isomerase/decarboxylase	2,59	7,56
SL1041	<i>hpcC</i>	5-carboxymethyl-2-hydroxymuconate semialdehyde dehydrogenase	2,98	7,23
SL1042	<i>hpcB</i>	3,4-dihydroxyphenylacetate 2,3-dioxygenase	2,43	6,00
SL1043	<i>hpcD</i>	5-carboxymethyl-2-hydroxymuconate Delta-isomerase	2,36	5,31
SL1044	<i>hpcG</i>	2-oxo-hepta-3-ene-1,7-dioic acid hydratase	1,38	3,18
SL1045	<i>hpcH</i>	4-hydroxy-2-oxo-heptane-1,7-dioate aldolase	1,31	3,02
SL1046	<i>ttuB</i>	Putative tartrate transporter	1,35	3,69
SL1056	<i>agp</i>	Glucose-1-phosphatase	3,19	3,03
SL1061	-	Uncharacterized protein R02472	3,52	9,50
SL1062	<i>putA</i>	Bifunctional protein <i>putA</i>	14,32	77,71
SL1063	<i>putP</i>	Sodium/proline symporter	3,39	12,16
SL1066	<i>sglT</i>	Sodium/glucose cotransporter	-1,01	6,36
SL1067	<i>nanE1</i>	Putative N-acetylmannosamine-6-phosphate 2-epimerase 1	2,40	4,53
SL1068	<i>nanM</i>	N-acetylneuraminate epimerase	1,16	4,04
SL1069	<i>yiiY</i>	Uncharacterized protein <i>yiiY</i>	1,10	5,40
SL1077	<i>csgF</i>	Curli production assembly/transport component <i>csgF</i>	-3,23	2,00
SL1083	<i>ymdA</i>	Uncharacterized protein <i>ymdA</i>	1,64	3,20
SL1089	<i>yceK</i>	Uncharacterized protein <i>yceK</i>	4,06	2,17
SL1090	<i>msyB</i>	Acidic protein <i>msyB</i>	5,67	2,50
SL1105	<i>yceH</i>	UPF0502 protein <i>yceH</i>	2,06	3,95
SL1110	<i>flgA</i>	Flagella basal body P-ring formation protein <i>flgA</i>	4,05	3,45
SL1124	<i>yiaF</i>	Uncharacterized protein <i>yiaF</i>	6,82	-1,14
SL1129	<i>plsX</i>	Phosphate acyltransferase	-1,60	-4,72
SL1151	<i>bhsA</i>	Multiple stress resistance protein <i>BhsA</i>	-3,31	-2,12
SL1161	<i>sifA</i>	Secreted effector protein <i>sifA</i>	-2,70	-3,57
SL1176	<i>icd</i>	Isocitrate dehydrogenase [NADP]	1,65	3,29
SL1177	-	Bacteriophage Protein	-16,74	-25,20
SL1178	-	Hypothetical Protein SL1178	-6,61	-7,87
SL1181	<i>envE</i>	Probable lipoprotein <i>envE</i>	-4,06	-3,82
SL1182	<i>cspH</i>	Cold shock-like protein <i>cspH</i>	-1,12	-3,33
SL1183	<i>pagD</i>	Virulence protein <i>pagD</i>	-10,07	-6,00
SL1184	<i>pagC</i>	Virulence membrane protein <i>pagC</i>	-15,69	-11,99
SL1186	-	Hypothetical	-4,93	-4,22
SL1191	<i>xp55</i>	Protein XP55	4,29	3,96
SL1192	<i>dppB</i>	Putative peptide transport system permease protein BMEI10209	3,41	2,88
SL1204	<i>aroQ</i>	Monofunctional chorismate mutase	-1,13	-3,35
SL1218	<i>yeaJ</i>	Putative diguanylate cylase <i>YeaJ</i>	-2,57	-3,03
SL1227	<i>yeaC</i>	Uncharacterized protein <i>yeaC</i>	1,72	3,00
SL1238	<i>astC</i>	Succinylornithine transaminase	12,92	43,62

Tabla Suplementaria 5

Genes afectados en las cepas mutantes *dksA* y *greAgreB*, respecto a la cepa WT

ID	gene	Description	<i>dksA</i> vs WT	<i>greAgreB</i> vs WT
SL1239	<i>astA</i>	Arginine N-succinyltransferase	10,81	26,67
SL1240	<i>astD</i>	N-succinylglutamate 5-semialdehyde dehydrogenase	7,93	23,23
SL1241	<i>astB</i>	N-succinylarginine dihydrolase	4,94	14,27
SL1242	<i>astE</i>	Succinylglutamate desuccinylase	3,04	8,31
SL1250	<i>chbR</i>	HTH-type transcriptional regulator chbR	-5,19	-1,16
SL1251	<i>chbF</i>	6-phospho-beta-glucosidase	-2,98	1,23
SL1255	<i>ydjN</i>	Uncharacterized symporter ydjN	1,84	3,28
SL1259	<i>yniA</i>	Uncharacterized protein yniA	2,01	3,45
SL1262	<i>ydiY</i>	Uncharacterized protein ydiY	-1,20	-3,05
SL1263	-	Hypothetical	-8,24	-12,64
SL1264	-	DNA/RNA Non-Specific Endonuclease	-5,85	-7,63
SL1265	<i>nucA</i>	Nuclease	-14,89	-13,64
SL1278	<i>cdgR</i>	Cyclic di-GMP regulator cdgR	-5,00	-2,05
SL1283	<i>ppsA</i>	Phosphoenolpyruvate synthase	-1,07	4,30
SL1291	<i>ydiF</i>	Uncharacterized protein ydiF	1,13	4,23
SL1302	<i>ydjN</i>	Uncharacterized symporter ydjN	8,97	6,96
SL1303	<i>sufA</i>	Protein sufA	1,12	4,08
SL1313	<i>puuP</i>	Putrescine importer	2,88	4,25
SL1314	<i>pip</i>	Proline iminopeptidase	2,83	4,08
SL1315	-	Hypothetical	2,91	3,97
SL1316	<i>rbsK</i>	Ribokinase	8,36	8,68
SL1318	-	Tetrathionate Reductase Subunit C	-1,45	-2,98
SL1325	<i>nreC</i>	Oxygen regulatory protein nreC	-3,72	-2,58
SL1326	<i>rscC</i>	Sensor kinase protein rscC	-5,34	-2,56
SL1327	<i>spiC</i>	Salmonella pathogenicity island protein C	-9,52	-7,03
SL1328	<i>yscC</i>	Yop proteins translocation protein C	-7,91	-6,06
SL1329	-	Type-III Secretion Protein	-8,23	-7,92
SL1330	-	Secretion System Protein	-7,09	-4,88
SL1331	<i>sseA</i>	Type III secretion system chaperone sseA	-4,87	-3,08
SL1332	<i>sseB</i>	Secreted effector protein sseB	-3,85	-2,69
SL1333	-	Type III Secretion Low Calcium Response Chaperone LcrH/SycD	-3,32	-2,44
SL1337	-	Type III Secretion Chaperone	-3,87	-1,55
SL1341	-	Hypothetical	-14,03	-18,14
SL1342	-	Type III Secretion System Apparatus Protein	-15,77	-22,27
SL1343	<i>ssaJ</i>	Secretion system apparatus lipoprotein ssaJ	-15,33	-17,00
SL1344	-	Type III Secretion Apparatus	-11,84	-16,48
SL1345	<i>ssaK</i>	Secretion system apparatus protein ssaK	-9,59	-11,64
SL1346	<i>ssaL</i>	Secretion system apparatus protein ssaL	-8,72	-5,60
SL1347	<i>ssaM</i>	Secretion system apparatus protein ssaM	-12,72	-5,75
SL1348	<i>ssaV</i>	Secretion system apparatus protein ssaV	-3,70	-1,41
SL1353	<i>yscR</i>	Virulence protein yscR	-3,66	-4,01
SL1354	<i>ssaS</i>	Secretion system apparatus protein SsaS	-6,29	-6,62
SL1355	<i>ssaT</i>	Secretion system apparatus protein ssaT	-4,26	-4,28
SL1360	<i>ydhC</i>	Inner membrane transport protein ydhC	-8,66	-24,59

Tabla Suplementaria 5

Genes afectados en las cepas mutantes *dksA* y *greAgreB*, respecto a la cepa WT

ID	gene	Description	<i>dksA</i> vs WT	<i>greAgreB</i> vs WT
SL1371	<i>ydhF</i>	Oxidoreductase ydhF	3,41	1,92
SL1398	<i>fumA</i>	Fumarate hydratase class I, aerobic	2,49	5,66
SL1399	-	Hypothetical Protein SL1399	2,13	7,56
SL1400	<i>fumC</i>	Fumarate hydratase class II	1,45	4,75
SL1401	<i>tus</i>	DNA replication terminus site-binding protein	1,34	3,56
SL1405	<i>rstA</i>	Transcriptional regulatory protein rstA	-1,68	-3,50
SL1422	<i>opuCB</i>	Glycine betaine/carnitine/choline transport system permease protein opuCB	2,33	3,34
SL1423	<i>opuCC</i>	Glycine betaine/carnitine/choline-binding protein	2,35	4,59
SL1424	<i>opuCB</i>	Glycine betaine/carnitine/choline transport system permease protein opuCB	2,03	3,48
SL1434	<i>ynfA</i>	UPF0060 membrane protein ynfA	3,16	-1,97
SL1435	<i>rspA</i>	Starvation-sensing protein rspA	5,16	7,90
SL1436	<i>rspB</i>	Starvation-sensing protein rspB	4,95	8,06
SL1437	<i>ydfJ</i>	Putative inner membrane metabolite transport protein ydfJ	1,70	4,11
SL1439	<i>ydfZ</i>	Putative selenoprotein ydfZ	6,74	1,39
SL1444	<i>ydeJ</i>	Protein ydeJ	-3,51	-1,03
SL1452	<i>sotB</i>	Probable sugar efflux transporter	-7,72	-3,01
SL1467	<i>hupB</i>	Uptake hydrogenase large subunit	1,16	3,66
SL1472	<i>exuT</i>	Hexuronate transporter	1,38	3,48
SL1473	-	Hypothetical	-1,35	-3,72
SL1475	<i>yhjG</i>	Uncharacterized aromatic compound monooxygenase yhjG	2,79	3,46
SL1489	<i>treY</i>	Maltotoligosyl trehalose synthase	2,33	3,14
SL1492	<i>hdeB</i>	Protein hdeB	3,96	-1,20
SL1494	<i>bdm</i>	Protein bdm homolog	-4,75	-4,02
SL1498	<i>fdnI</i>	Formate dehydrogenase, nitrate-inducible, cytochrome b556(fdn) subunit	3,85	-1,34
SL1499	<i>fdnH</i>	Formate dehydrogenase, nitrate-inducible, iron-sulfur subunit	3,50	-1,09
SL1500	<i>fdnG</i>	Formate dehydrogenase, nitrate-inducible, major subunit	3,60	-1,19
SL1501	<i>fdnG</i>	Formate dehydrogenase, nitrate-inducible, major subunit	4,12	1,12
SL1505	<i>smvA</i>	Methyl viologen resistance protein smvA	-3,14	-2,99
SL1507	<i>narU</i>	Nitrite extrusion protein 2	1,61	11,11
SL1508	<i>narZ</i>	Respiratory nitrate reductase 2 alpha chain	3,12	6,46
SL1509	<i>narY</i>	Respiratory nitrate reductase 2 beta chain	3,24	5,04
SL1510	<i>narW</i>	Probable nitrate reductase molybdenum cofactor assembly chaperone NarW	3,00	4,15
SL1511	<i>narV</i>	Respiratory nitrate reductase 2 gamma chain	2,99	4,38
SL1525	-	Virulence Protein SrfB	1,72	4,34
SL1531	-	D-Alanyl-D-Alanine Dipeptidase	-9,15	-4,95
SL1532	<i>sifB</i>	Secreted effector protein sifB	-3,52	-3,28
SL1553	<i>pnbA</i>	Para-nitrobenzyl esterase	4,58	3,07
SL1554	<i>ydcJ</i>	Uncharacterized protein ydcJ	15,31	9,60
SL1559	<i>steB</i>	Secreted effector protein steB	-30,72	-16,75
SL1561	<i>sseJ</i>	Secreted effector protein sseJ	-4,11	-2,52
SL1578	<i>hslJ</i>	Heat shock protein hslJ	-3,39	-2,04

Tabla Suplementaria 5

Genes afectados en las cepas mutantes *dksA* y *greAgreB*, respecto a la cepa WT

ID	gene	Description	<i>dksA</i> vs WT	<i>greAgreB</i> vs WT
SL1596	-	Hypothetical	5,27	-1,06
SL1602	-	Hypothetical	-10,61	-4,92
SL1619	<i>pspB</i>	Phage shock protein B	-3,81	-2,10
SL1620	<i>pspA</i>	Phage shock protein A	-3,48	-1,75
SL1627	<i>ydiV</i>	Uncharacterized protein ydiV	3,11	1,44
SL1637	<i>osmB</i>	Osmotically-inducible lipoprotein B	-6,38	-4,73
SL1644	<i>acnA</i>	Aconitate hydratase 1	1,65	3,38
SL1649	<i>yciK</i>	Uncharacterized oxidoreductase yciK	4,55	2,60
SL1650	<i>btuR</i>	Cob(II)yrinic acid a,c-diamide adenosyltransferase	4,35	2,90
SL1659	<i>ymdF</i>	Uncharacterized protein ymdF	-1,52	-3,54
SL1660	<i>yciF</i>	Protein yciF	-1,84	-3,65
SL1661	<i>yciE</i>	Protein yciE	-1,98	-3,21
SL1677	<i>oppA</i>	Periplasmic oligopeptide-binding protein	1,43	3,54
SL1679	<i>yehE</i>	UPF0056 membrane protein yhcE	1,13	-3,72
SL1689	<i>narI</i>	Respiratory nitrate reductase 1 gamma chain	9,45	2,45
SL1690	<i>narJ</i>	Nitrate reductase molybdenum cofactor assembly chaperone NarJ	9,45	2,43
SL1691	<i>narH</i>	Respiratory nitrate reductase 1 beta chain	7,87	2,12
SL1692	<i>narG</i>	Respiratory nitrate reductase 1 alpha chain	5,16	2,24
SL1693	<i>narK</i>	Nitrite extrusion protein 1	32,48	1,66
SL1710	<i>yehH</i>	Uncharacterized protein yehH	2,43	3,18
SL1723	<i>gdhA</i>	Glutamate dehydrogenase	6,36	17,53
SL1726	<i>ycgR</i>	Flagellar brake protein YcgR	-2,06	-5,01
SL1729	<i>cvrA</i>	Cell volume regulation protein A	-3,26	-2,77
SL1730	<i>dadX</i>	Alanine racemase, catabolic	1,36	6,94
SL1731	<i>dadA</i>	D-amino acid dehydrogenase small subunit	1,82	9,25
SL1737	<i>gns</i>	Protein gns	3,14	2,78
SL1739	<i>ycgN</i>	UPF0260 protein CKO_01185	3,15	-1,74
SL1742	<i>minC</i>	Probable septum site-determining protein minC	-1,72	-4,10
SL1762	<i>yobD</i>	UPF0266 membrane protein yobD	-1,41	-5,91
SL1768	<i>yebO</i>	Uncharacterized protein yebO	-2,49	-3,12
SL1769	<i>mgrB</i>	Protein mgrB	-2,85	-3,11
SL1770	<i>yobH</i>	Uncharacterized protein yobH	-3,58	-2,58
SL1772	<i>yebQ</i>	Uncharacterized transporter yebQ	-3,40	-1,64
SL1780	<i>yebV</i>	Uncharacterized protein yebV	-5,37	-2,02
SL1782	<i>pphA</i>	Serine/threonine-protein phosphatase 1	-2,73	-4,92
SL1783	-	Hypothetical	-3,53	-8,58
SL1784	<i>sopE2</i>	Guanine nucleotide exchange factor sopE2	-5,12	-16,49
SL1785	<i>ycgX</i>	Uncharacterized protein ycgX	-4,00	-6,12
SL1793	<i>pagO</i>	Protein pagO	-4,98	-5,37
SL1794	-	Hypothetical	-8,02	-7,65
SL1795	-	Hypothetical	-6,18	-5,78
SL1798	<i>insF1</i>	Hypothetical Protein insF1	-3,08	-1,34
SL1799	-	PagK-Like Protein	-4,51	-4,28
SL1804	-	Hypothetical	1,20	-3,58
SL1810	<i>holE</i>	DNA polymerase III subunit theta	4,58	-1,04
SL1819	<i>edd</i>	Phosphogluconate dehydratase	-2,54	-5,50

Tabla Suplementaria 5

Genes afectados en las cepas mutantes *dksA* y *greAgreB*, respecto a la cepa WT

ID	gene	Description	<i>dksA</i> vs WT	<i>greAgreB</i> vs WT
SL1844	<i>argS</i>	Arginyl-tRNA synthetase	1,29	-3,31
SL1852	<i>cheB</i>	Chemotaxis response regulator protein-glutamate methyltransferase	-1,80	-3,86
SL1853	<i>cheR</i>	Chemotaxis protein methyltransferase	-2,09	-3,83
SL1857	<i>motB</i>	Motility protein B	-1,45	-2,99
SL1858	<i>motA</i>	Motility protein A	-1,72	-3,31
SL1859	<i>flhC</i>	Flagellar transcriptional activator flhC	-1,47	-3,09
SL1860	<i>flhD</i>	Transcriptional activator FlhD	-1,05	-3,17
SL1861	<i>uspC</i>	Universal stress protein C	3,43	1,74
SL1865	<i>ftnB</i>	Ferritin-like protein 2	2,31	3,10
SL1872	-	Hypothetical	-4,34	-4,52
SL1874	-	Hypothetical	-2,98	-4,78
SL1878	<i>yecF</i>	Uncharacterized protein yecF	-3,51	-8,87
SL1879	<i>sdiA</i>	Regulatory protein sdiA	-1,66	-3,85
SL1890	<i>fliS</i>	Flagellar protein fliS	1,03	-3,14
SL1891	<i>fliT</i>	Flagellar protein fliT	1,06	-3,00
SL1894	<i>yedE</i>	UPF0394 inner membrane protein yedE	17,08	3,86
SL1895	<i>yedF</i>	UPF0033 protein yedF	17,78	3,15
SL1896	-	Hypothetical A	-2,08	-3,36
SL1911	<i>rcsA</i>	Colanic acid capsular biosynthesis activation protein A	-3,43	-2,52
SL1922	<i>yedR</i>	Inner membrane protein yedR	-6,03	-4,09
SL1928	-	Cytoplasmic Protein	-3,87	-7,81
SL1950	<i>ymfN</i>	Uncharacterized protein ymfN	1,02	-3,34
SL1951	-	P27 Family Phage Terminase Small Subunit	1,03	-3,72
SL1952	-	Hypothetical	1,25	-3,08
SL1955	<i>rzpD</i>	Putative Rz endopeptidase from lambdoid prophage DLP12	1,03	-3,37
SL1956	-	Uncharacterized protein HI_1415	1,24	-3,36
SL1957	-	Phage Holin Lambda Family	1,15	-3,53
SL1968	<i>yfdP</i>	Uncharacterized protein yfdP	1,90	2,99
SL1969	<i>yfdQ</i>	Uncharacterized protein yfdQ	1,90	3,27
SL2007	<i>cbiE</i>	Probable cobalt-precorrin-6Y C(5)-methyltransferase	-1,97	-3,51
SL2010	<i>cbiB</i>	Cobalamin biosynthesis protein cbiB	-1,69	-3,16
SL2013	<i>pduF</i>	Propanediol diffusion facilitator	-1,60	-3,03
SL2014	<i>pduA</i>	Propanediol utilization protein pduA	-1,26	-22,81
SL2015	<i>pduB</i>	Propanediol utilization protein pduB	-1,93	-40,16
SL2016	<i>pduC</i>	Propanediol dehydratase large subunit	-2,41	-24,41
SL2017	<i>pduD</i>	Propanediol dehydratase medium subunit	-4,45	-38,60
SL2018	<i>pduE</i>	Propanediol dehydratase small subunit	-6,69	-66,46
SL2019	-	Glycerol Dehydratase Reactivation Factor Large Subunit	-8,05	-53,01
SL2020	-	Hypothetical	-12,58	-77,87
SL2021	<i>pduA</i>	Propanediol utilization protein pduA	-11,89	-20,95
SL2022	-	Propanediol Utilization Protein PduK	-12,06	-18,88
SL2023	-	Propanediol Utilization Protein	-14,23	-25,45
SL2024	-	Propanediol Utilization Protein	-13,88	-26,37

Tabla Suplementaria 5

Genes afectados en las cepas mutantes *dksA* y *greAgreB*, respecto a la cepa WT

ID	gene	Description	<i>dksA</i> vs WT	<i>greAgreB</i> vs WT
SL2025	<i>ccmL</i>	Carbon dioxide concentrating mechanism protein ccmL	-11,06	-20,64
SL2026	-	Cob(II)yrinic acid a,c-diamide adenosyltransferase	-10,59	-21,04
SL2027	<i>eutE</i>	Ethanolamine utilization protein eutE	-4,51	-8,20
SL2028	<i>adh1</i>	NADPH-dependent butanol dehydrogenase	-4,82	-9,36
SL2029	<i>rnfC</i>	Electron transport complex protein rnfC	-2,90	-4,59
SL2030	<i>eutM</i>	Microcompartments Protein	-2,19	-3,61
SL2031	<i>pduU</i>	Propanediol utilization protein pduU	-2,04	-4,09
SL2032	<i>pduV</i>	Propanediol utilization protein pduV	-2,07	-3,98
SL2033	<i>pduW</i>	Probable propionate kinase	-1,80	-3,31
SL2037	<i>gyrI</i>	DNA gyrase inhibitory protein homolog	2,61	4,09
SL2038	<i>dacD</i>	D-alanyl-D-alanine carboxypeptidase dacD	-1,60	-3,59
SL2043	<i>sopA</i>	E3 ubiquitin-protein ligase SopA	-16,06	-11,05
SL2049	<i>hisD</i>	Histidinol dehydrogenase	-1,50	3,14
SL2050	<i>hisC</i>	Histidinol-phosphate aminotransferase	-1,08	3,41
SL2056	<i>wzzB</i>	Chain length determinant protein	-2,36	-6,76
SL2057	<i>udg</i>	UDP-glucose 6-dehydrogenase	-8,32	-6,30
SL2077	<i>wcaL</i>	Putative colanic acid biosynthesis glycosyltransferase wcaL	1,78	3,22
SL2087	<i>wcaF</i>	Putative colanic acid biosynthesis acetyltransferase wcaF	-3,34	-1,57
SL2115	-	Hypothetical	-5,31	-2,96
SL2119	<i>yegT</i>	Putative nucleoside transporter yegT	2,44	4,25
SL2130	<i>yehE</i>	Uncharacterized protein yehE	-31,09	-15,13
SL2136	<i>yehT</i>	Uncharacterized response regulatory protein yehT	21,86	3,14
SL2137	<i>yehU</i>	Inner membrane protein yehU	10,40	1,50
SL2153	<i>maiA</i>	Probable maleylacetoacetate isomerase	1,79	3,04
SL2154	<i>ycgM</i>	Uncharacterized protein PYRAB13970	2,31	3,97
SL2155	-	Gentisate 1 2-Dioxygenase	2,58	5,13
SL2158	<i>yohJ</i>	UPF0299 membrane protein CKO_00648	-9,78	-11,34
SL2159	<i>yohK</i>	Inner membrane protein yohK	-13,53	-12,19
SL2160	<i>cdd</i>	Cytidine deaminase	-10,57	-8,24
SL2165	<i>mgIC</i>	Galactoside transport system permease protein mgIC	2,33	6,61
SL2166	<i>mgIA</i>	Galactose/methyl galactoside import ATP-binding protein MglA	2,14	11,23
SL2167	<i>mgIB</i>	D-galactose-binding periplasmic protein	3,67	10,18
SL2168	<i>galS</i>	HTH-type transcriptional regulator galS	4,52	1,68
SL2169	<i>yeiB</i>	Uncharacterized protein yeiB	-6,56	-4,93
SL2170	<i>folE</i>	GTP cyclohydrolase 1	-5,82	-3,82
SL2181	<i>fruA</i>	PTS system fructose-specific EIIBC component	-2,54	-10,61
SL2182	<i>fruK</i>	1-phosphofructokinase	-2,52	-8,46
SL2183	<i>fruB</i>	Multiphosphoryl transfer protein	-2,11	-6,16
SL2184	<i>setB</i>	Sugar efflux transporter B	-1,31	-5,41
SL2188	<i>yeiP</i>	Elongation factor P-like protein	4,21	-1,18
SL2191	<i>spr</i>	Lipoprotein spr	-1,01	-3,81
SL2214	<i>pifA</i>	KAP P-Loop Domain-Containing Protein	8,00	2,07
SL2225	<i>napC</i>	Cytochrome c-type protein napC	6,57	2,49
SL2226	<i>napB</i>	Diheme cytochrome c napB	3,46	1,77

Tabla Suplementaria 5

Genes afectados en las cepas mutantes *dksA* y *greAgreB*, respecto a la cepa WT

ID	gene	Description	<i>dksA</i> vs WT	<i>greAgreB</i> vs WT
SL2227	<i>napH</i>	Ferredoxin-type protein napH	6,95	2,21
SL2228	<i>napG</i>	Ferredoxin-type protein napG	8,39	2,65
SL2229	<i>napA</i>	Periplasmic nitrate reductase	8,88	3,48
SL2230	<i>napD</i>	Protein napD	5,81	-1,16
SL2231	<i>napF</i>	Ferredoxin-type protein napF	4,56	1,09
SL2243	<i>ttuB</i>	Putative tartrate transporter	1,01	3,31
SL2251	<i>glpQ</i>	Glycerophosphoryl diester phosphodiesterase	3,61	-1,04
SL2256	<i>sseL</i>	Deubiquitinase sseL	-2,80	-9,57
SL2265	<i>ais</i>	Lipopolysaccharide core heptose(II)-phosphate phosphatase	-1,91	-4,74
SL2266	<i>arnB</i>	UDP-4-amino-4-deoxy-L-arabinose--oxoglutarate aminotransferase	-3,45	-2,44
SL2267	<i>arnC</i>	Undecaprenyl-phosphate 4-deoxy-4-formamido-L-arabinose transferase	-3,30	-2,05
SL2283	<i>cheV</i>	Chemotaxis protein cheV	-1,51	-10,75
SL2299	<i>lrhA</i>	Probable HTH-type transcriptional regulator LrhA	-4,14	-2,65
SL2306	<i>ackA</i>	Acetate kinase	-2,28	-3,07
SL2313	<i>ulaC</i>	Ascorbate-specific phosphotransferase enzyme IIA component	2,57	3,39
SL2324	<i>argT</i>	Lysine-arginine-ornithine-binding periplasmic protein	2,23	7,89
SL2327	-	Amino Acid Racemase	3,25	2,86
SL2357	<i>fadJ</i>	Fatty acid oxidation complex subunit alpha	1,43	4,65
SL2360	<i>fadL</i>	Long-chain fatty acid transport protein	7,03	7,09
SL2362	<i>yfdC</i>	Inner membrane protein yfdC	-3,14	1,40
SL2363	<i>pgtE</i>	Outer membrane protease E	-3,07	-2,42
SL2369	<i>ddg</i>	Protein ddg	-4,29	-11,56
SL2379	<i>yfeC</i>	Uncharacterized protein yfeC	5,24	1,46
SL2380	<i>yfeD</i>	Uncharacterized protein yfeD	3,64	1,87
SL2404	<i>cysA</i>	Sulfate/thiosulfate import ATP-binding protein cysA	-1,07	12,67
SL2405	<i>cysW</i>	Sulfate transport system permease protein cysW	-1,26	6,01
SL2406	<i>cysU</i>	Sulfate transport system permease protein cysT	-1,10	8,74
SL2407	<i>cysP</i>	Thiosulfate-binding protein	1,12	13,02
SL2408	<i>ucpA</i>	Oxidoreductase ucpA	-1,10	3,08
SL2432	<i>eutP</i>	Ethanolamine utilization protein eutP	4,93	2,01
SL2433	<i>eutS</i>	Ethanolamine utilization protein eutS	4,42	1,70
SL2435	<i>maeB</i>	NADP-dependent malic enzyme	2,59	5,97
SL2451	<i>nlpB</i>	Lipoprotein 34	-3,86	-1,89
SL2467	-	Hypothetical	-1,21	-3,33
SL2468	<i>yfgG</i>	Uncharacterized protein yfgG	-1,21	-3,19
SL2472	<i>guaB</i>	Inosine-5'-monophosphate dehydrogenase	-1,30	-3,20
SL2481	<i>engA</i>	GTP-binding protein engA	-3,03	-1,82
SL2488	<i>ndk</i>	Nucleoside diphosphate kinase	5,40	6,14
SL2506	<i>iscR</i>	HTH-type transcriptional regulator iscR	-2,77	-3,23
SL2510	<i>asrA</i>	Anaerobic sulfite reductase subunit A	-1,62	-3,47
SL2511	<i>asrB</i>	Anaerobic sulfite reductase subunit B	-1,82	-3,42
SL2515	<i>csiE</i>	Stationary phase-inducible protein csiE	6,04	6,85
SL2518	<i>hmp</i>	Flavoheмоprotein	2,80	5,21

Tabla Suplementaria 5

Genes afectados en las cepas mutantes *dksA* y *greAgreB*, respecto a la cepa WT

ID	gene	Description	<i>dksA</i> vs WT	<i>greAgreB</i> vs WT
SL2521	<i>cadA</i>	Lysine decarboxylase, inducible	1,93	-4,98
SL2522	<i>yjdL</i>	Probable dipeptide and tripeptide permease YjdL	2,24	-6,76
SL2532	<i>ybbF</i>	Putative PTS system EIIBC component ybbF	2,21	3,24
SL2533	<i>murQ</i>	N-acetylmuramic acid 6-phosphate etherase	2,27	3,66
SL2537	<i>cynR</i>	HTH-type transcriptional regulator cynR	1,64	3,05
SL2548	-	Hypothetical Protein SL2548	-2,00	-3,48
SL2549	-	PagK-Like Protein	-4,06	-4,10
SL2550	<i>ycdD</i>	Tail fiber assembly protein homolog from lambdoid prophage Fels-1	-1,49	-4,98
SL2551	-	Appr-1-P Processing Domain-Containing Protein	-1,52	-4,76
SL2552	<i>stfQ</i>	Side tail fiber protein homolog from lambdoid prophage Qin	-1,38	-3,35
SL2553	-	Hocificity Protein J	-1,84	-11,08
SL2555	-	NLP/P60 Protein	-1,38	-3,95
SL2559	-	Minor Tail Protein	-1,70	-4,83
SL2560	-	Minor Tail Component Of Putative Prophage	-1,50	-5,25
SL2564	-	Phage Tail Component	-1,14	-3,00
SL2566	-	DNA Packaging-Like Protein	-1,25	-3,76
SL2567	-	P21 prophage-derived major head protein	-1,34	-4,91
SL2568	-	Head Decoration Protein	-1,25	-4,48
SL2569	<i>sppA</i>	Putative signal peptide peptidase sppA	-1,10	-10,71
SL2570	-	Lambda Family Phage Portal Protein	1,01	-6,06
SL2572	<i>tfaD</i>	Putative tail fiber assembly protein homolog from lambdoid prophage DLP12	1,39	-4,71
SL2573	<i>nohA</i>	P21 prophage-derived terminase small subunit	-1,00	-8,60
SL2575	<i>rzpD</i>	Putative Rz endopeptidase from lambdoid prophage DLP12	-1,01	-5,68
SL2576	<i>arrD</i>	Probable lysozyme from lambdoid prophage DLP12	1,01	-3,56
SL2595	-	Hypothetical	-3,18	-1,90
SL2609	<i>eamB</i>	Cysteine/O-acetylserine efflux protein	-4,44	-7,15
SL2619	-	Hypothetical	4,28	1,51
SL2673	<i>pinE</i>	DNA-invertase from lambdoid prophage e14	-3,29	-3,80
SL2674	<i>sopE</i>	Guanine nucleotide exchange factor sopE	-4,85	-27,69
SL2696	-	Hypothetical	1,92	3,87
SL2704	-	Putative uncharacterized protein ORFC-like in prophage region	1,29	-3,46
SL2710	<i>yopC</i>	SPBc2 prophage-derived uncharacterized protein yopC	2,67	3,11
SL2719	-	Hypothetical	3,48	3,69
SL2720	-	Hypothetical	3,25	3,04
SL2722	<i>traC</i>	DNA primase traC	2,56	4,29
SL2723	<i>intA</i>	Prophage CP4-57 integrase	5,32	6,56
SL2724	<i>intA</i>	Integrase	2,89	3,40
SL2728	-	Cytoplasmic Protein	3,68	1,38
SL2743	<i>sgrR</i>	HTH-type transcriptional regulator sgrR	4,48	3,19
SL2755	<i>fljA</i>	Repressor of phase 1 flagellin gene	-1,47	-15,85

Tabla Suplementaria 5

Genes afectados en las cepas mutantes *dksA* y *greAgreB*, respecto a la cepa WT

ID	gene	Description	<i>dksA</i> vs WT	<i>greAgreB</i> vs WT
SL2757	NA	NA	3,30	-1,06
SL2758	-	Hypothetical	-1,34	-5,31
SL2763	<i>pipB2</i>	Secreted effector protein pipB2	-3,40	-1,57
SL2764	<i>ybjX</i>	Uncharacterized protein ybjX	-5,61	-4,33
SL2765	-	Hypothetical	-6,91	-3,63
SL2766	-	Hypothetical	-3,68	-2,82
SL2768	<i>qseC</i>	Sensor protein qseC	3,07	7,27
SL2769	<i>tctD</i>	Transcriptional regulatory protein tctD	3,86	13,84
SL2770	<i>yfiP</i>	UPF0065 protein yfiP	34,16	3,01
SL2771	-	Hypothetical	42,49	4,00
SL2772	-	Uncharacterized 52.8 kDa protein in TAR-I ttuC' 3'region	6,58	1,94
SL2773	<i>csiD</i>	Protein csiD	1,04	11,87
SL2774	<i>ygaF</i>	Uncharacterized protein ygaF	-1,02	9,95
SL2775	<i>gabD</i>	Succinate-semialdehyde dehydrogenase [NADP+]	1,99	12,61
SL2776	<i>gabT</i>	4-aminobutyrate aminotransferase	1,68	7,78
SL2777	<i>gabP</i>	GABA permease	1,51	6,21
SL2783	<i>stpA</i>	DNA-binding protein stpA	-6,63	-10,03
SL2784	<i>ygaW</i>	Uncharacterized protein ygaW	-2,45	-3,82
SL2794	<i>proV</i>	Glycine betaine/L-proline transport ATP-binding protein proV	-3,01	-1,46
SL2823	<i>hydN</i>	Electron transport protein hydN	-4,73	-7,66
SL2831	<i>hycC</i>	Formate hydrogenlyase subunit 3	-4,84	-3,72
SL2832	<i>hycB</i>	Formate hydrogenlyase subunit 2	-4,99	-4,92
SL2833	<i>hycA</i>	Formate hydrogenlyase regulatory protein hycA	-2,89	-7,96
SL2844	<i>znuB</i>	Probable iron transport system membrane protein HI_0359	-2,82	-3,87
SL2845	<i>yopJ</i>	Effector protein yopJ	-5,19	-5,48
SL2846	-	Hypothetical	-8,00	-14,85
SL2847	<i>sirC</i>	Transcriptional regulator sirC	-5,01	-10,80
SL2848	-	Hypothetical	-10,57	-20,93
SL2849	<i>orgB</i>	Oxygen-regulated invasion protein orgB	-4,16	-9,10
SL2850	<i>orgA</i>	Oxygen-regulated invasion protein orgA	-8,93	-21,71
SL2851	<i>prgK</i>	Lipoprotein prgK	-4,18	-8,73
SL2852	<i>prgJ</i>	Protein prgJ	-3,95	-8,23
SL2853	<i>prgI</i>	Protein prgI	-2,47	-4,71
SL2854	<i>prgH</i>	Protein prgH	-6,16	-18,46
SL2855	<i>hilD</i>	Transcriptional regulator hilD	-3,33	-5,63
SL2856	<i>hilA</i>	Transcriptional regulator hilA	-8,69	-10,34
SL2857	<i>iagB</i>	Invasion protein iagB	-6,81	-7,09
SL2858	<i>sptP</i>	Secreted effector protein sptP	-5,70	-5,53
SL2859	<i>sicP</i>	Chaperone protein sicP	-6,65	-8,37
SL2860	<i>iacP</i>	Probable acyl carrier protein iacP	-10,41	-21,34
SL2861	<i>sipA</i>	Cell invasion protein sipA	-8,69	-15,35

Tabla Suplementaria 5

Genes afectados en las cepas mutantes *dksA* y *greAgreB*, respecto a la cepa WT

ID	gene	Description	<i>dksA</i> vs WT	<i>greAgreB</i> vs WT
SL2862	<i>sipD</i>	Cell invasion protein sipD	-10,28	-18,49
SL2863	<i>sipC</i>	Cell invasion protein sipC	-3,67	-6,21
SL2864	<i>sipB</i>	Cell invasion protein sipB	-4,20	-7,20
SL2865	<i>sicA</i>	Chaperone protein sicA	-5,55	-8,04
SL2866	<i>spaS</i>	Surface presentation of antigens protein spaS	-21,32	-21,68
SL2867	<i>spaR</i>	Surface presentation of antigens protein spaR	-23,99	-22,12
SL2868	<i>spaQ</i>	Surface presentation of antigens protein SpaQ	-33,25	-32,11
SL2869	<i>spaP</i>	Surface presentation of antigens protein spaP	-31,82	-29,30
SL2870	<i>spaO</i>	Surface presentation of antigens protein SpaO	-14,20	-14,14
SL2871	<i>spaN</i>	Surface presentation of antigens protein spaN	-10,53	-9,31
SL2872	<i>spaM</i>	Surface presentation of antigens protein spaM	-8,84	-10,63
SL2873	<i>spaL</i>	Probable ATP synthase spaL	-10,05	-10,53
SL2874	<i>spaK</i>	Surface presentation of antigens protein spaK	-5,56	-6,61
SL2875	<i>invA</i>	Invasion protein invA	-12,19	-12,89
SL2876	<i>invE</i>	Invasion protein invE	-18,50	-20,75
SL2877	<i>invG</i>	Protein invG	-6,34	-8,31
SL2878	<i>invF</i>	Invasion protein invF	-5,21	-8,31
SL2879	<i>invH</i>	Invasion lipoprotein invH	-5,38	-10,98
SL2881	-	Hypothetical	-1,99	-3,47
SL2884	-	Hypothetical	1,87	6,08
SL2885	-	GCN5-Related N-Acetyltransferase	1,67	5,08
SL2892	<i>ygbN</i>	Uncharacterized permease HI_1015	-1,02	3,82
SL2893	<i>rffG</i>	Uncharacterized protein HI_1014	1,08	4,43
SL2894	<i>ygbM</i>	Protein ygbM	-1,33	4,27
SL2895	<i>ygbL</i>	Putative aldolase class 2 protein ygbL	-1,08	5,99
SL2896	<i>ygbK</i>	Uncharacterized protein ygbK	-1,12	7,13
SL2897	<i>ygbJ</i>	Uncharacterized oxidoreductase ygbJ	1,01	6,18
SL2912	<i>cysC</i>	Adenylyl-sulfate kinase	-1,13	9,51
SL2913	<i>cysN</i>	Sulfate adenylyltransferase subunit 1	1,02	11,16
SL2914	<i>cysD</i>	Sulfate adenylyltransferase subunit 2	-1,47	4,76
SL2915	<i>iap</i>	Alkaline phosphatase isozyme conversion protein	-2,93	-3,91
SL2924	<i>sopD</i>	Secreted effector protein sopD	-16,87	-23,34
SL2925	<i>cysH</i>	Phosphoadenosine phosphosulfate reductase	-1,73	5,34
SL2926	<i>cysI</i>	Sulfite reductase [NADPH] hemoprotein beta-component	-2,06	6,16
SL2927	<i>cysJ</i>	Sulfite reductase [NADPH] flavoprotein alpha-component	-2,43	4,34
SL2940	<i>garK</i>	Glycerate kinase 2	3,66	1,41
SL2941	<i>gudD</i>	Glucarate dehydratase	4,39	1,87
SL2942	<i>gudX</i>	Glucarate dehydratase-related protein	6,36	3,30
SL2943	<i>gudP</i>	Probable glucarate transporter	6,47	5,33
SL2950	<i>sdaC</i>	Serine transporter	6,74	2,59

Tabla Suplementaria 5

Genes afectados en las cepas mutantes *dksA* y *greAgreB*, respecto a la cepa WT

ID	gene	Description	<i>dksA</i> vs WT	<i>greAgreB</i> vs WT
SL2951	<i>sdaB</i>	L-serine dehydratase 2	8,11	3,60
SL2953	<i>fucO</i>	Lactaldehyde reductase	1,68	3,10
SL2959	<i>fucR</i>	L-fucose operon activator	6,68	2,02
SL2962	<i>gcvA</i>	Glycine cleavage system transcriptional activator	-3,31	-2,75
SL2977	<i>ppdB</i>	Prepilin peptidase-dependent protein B	7,11	2,36
SL2978	<i>ppdA</i>	Prepilin peptidase-dependent protein A	3,67	1,23
SL2984	<i>ygdQ</i>	UPF0053 inner membrane protein ygdQ	-3,45	-4,13
SL2991	<i>lysA</i>	Diaminopimelate decarboxylase	-4,95	-1,32
SL2994	<i>araE</i>	Arabinose-proton symporter	2,27	4,71
SL2996	<i>kdul</i>	4-deoxy-L-threo-5-hexosulose-uronate ketol-isomerase	2,72	3,46
SL2997	<i>yqeF</i>	Probable acetyl-CoA acetyltransferase	3,16	4,20
SL3000	<i>yqeG</i>	Inner membrane transport protein yqeG	-1,92	-3,13
SL3029	<i>gcvP</i>	Glycine dehydrogenase [decarboxylating]	-4,23	1,01
SL3042	<i>argO</i>	Arginine exporter protein ArgO	3,40	-1,49
SL3047	<i>glmU</i>	Bifunctional protein glmU	17,73	1,59
SL3048	-	Hypothetical	11,28	3,16
SL3049	-	Permease Protein Of ABC-Type Cobalt Transporter	6,30	2,71
SL3050	<i>cbiO1</i>	Cobalt import ATP-binding protein CbiO 1	4,71	2,22
SL3051	<i>cbiO</i>	Cobalt import ATP-binding protein CbiO	4,26	2,12
SL3053	<i>yggG</i>	Uncharacterized metalloprotease yggG	-3,11	-1,48
SL3059	<i>uxuB</i>	D-mannonate oxidoreductase	1,95	3,52
SL3064	<i>yqgD</i>	Uncharacterized protein yqgD	-1,56	-4,69
SL3080	<i>yggM</i>	Uncharacterized protein yggM	9,61	2,39
SL3081	<i>ansB</i>	L-asparaginase 2	4,78	4,33
SL3108	<i>exuT</i>	Hexuronate transporter	5,32	4,36
SL3109	<i>uxuA</i>	Mannonate dehydratase	2,97	3,06
SL3109	<i>uxuA</i>	Mannonate dehydratase	2,97	3,06
SL3112	<i>bdIA</i>	Biofilm dispersion protein BdIA	-3,42	-3,40
SL3125	<i>yghW</i>	Uncharacterized protein yghW	-1,23	-6,35
SL3126	<i>tse</i>	Methyl-accepting chemotaxis serine transducer	-1,18	-8,28
SL3129	-	Hypothetical	-2,96	-5,12
SL3130	-	Hypothetical	-3,85	-7,27
SL3134	<i>b3007</i> ;	Hypothetical	4,98	1,27
SL3143	<i>yiiZ</i>	Uncharacterized protein yiiZ	3,36	7,98
SL3144	-	C4-Dicarboxylate Transport System Permease Small Protein	2,47	6,19
SL3145	<i>ygiK</i>	Uncharacterized protein ygiK	1,15	3,14
SL3163	<i>ygiD</i>	Uncharacterized protein ygiD	-6,71	-9,28
SL3165	-	Arylsulfotransferase	1,45	3,35
SL3166	<i>dsbA</i>	Thiol:disulfide interchange protein dsbA	1,18	3,06
SL3167	<i>dsbB</i>	Putative protein-disulfide oxidoreductase	1,04	3,38
SL3176	<i>ygiM</i>	Uncharacterized protein ygiM	-1,46	-3,56
SL3183	<i>rpsU</i>	30S ribosomal protein S21	-1,52	-3,63

Tabla Suplementaria 5

Genes afectados en las cepas mutantes *dksA* y *greAgreB*, respecto a la cepa WT

ID	gene	Description	<i>dksA</i> vs WT	<i>greAgreB</i> vs WT
SL3189	<i>tse</i>	Methyl-accepting chemotaxis serine transducer	-1,05	-3,94
SL3192	<i>fadH</i>	2,4-dienoyl-CoA reductase [NADPH]	4,94	6,90
SL3200	<i>yqjB</i>	Uncharacterized protein yqjB	-1,66	-3,22
SL3209	<i>yhaL</i>	Hypothetical Protein yhaL	5,71	5,32
SL3211	<i>yhaO</i>	Inner membrane transport protein yhaO	3,93	2,15
SL3216	<i>tdcB</i>	Threonine dehydratase catabolic	4,61	-2,06
SL3217	<i>tdcA</i>	HTH-type transcriptional regulator tdcA	32,27	5,57
SL3235	<i>gatR</i>	Galactitol utilization operon repressor	3,15	4,26
SL3253	<i>deaD</i>	Cold-shock DEAD box protein A	-7,63	-8,59
SL3262	<i>argG</i>	Argininosuccinate synthase	-4,12	1,18
SL3271	<i>greA</i>	Transcription elongation factor greA	-2,91	-320,40
SL3275	<i>rpmA</i>	50S ribosomal protein L27	1,01	-3,03
SL3301	<i>yhcC</i>	Uncharacterized protein yhcC	2,46	-3,69
SL3304	<i>yhcG</i>	Uncharacterized protein yhcG	6,91	1,35
SL3305	<i>codB</i>	Cytosine permease	3,48	-1,80
SL3306	<i>codA</i>	Cytosine deaminase	3,61	-1,13
SL3326	<i>ttdB</i>	L(+)-tartrate dehydratase subunit beta	1,98	3,29
SL3327	<i>ttdA</i>	L(+)-tartrate dehydratase subunit alpha	2,64	4,25
SL3328	<i>yfbS</i>	Uncharacterized transporter MJ0672	2,26	3,26
SL3331	<i>mdh</i>	Malate dehydrogenase	5,89	4,77
SL3335	<i>yhcO</i>	Uncharacterized protein yhcO	2,41	5,06
SL3357	<i>dusB</i>	tRNA-dihydrouridine synthase B	-1,57	-3,85
SL3358	<i>fis</i>	DNA-binding protein fis	-1,78	-3,28
SL3360	<i>yhdU</i>	Uncharacterized protein yhdU	2,98	1,74
SL3372	<i>smf</i>	Protein smf	3,26	1,60
SL3374	<i>fmt</i>	Methionyl-tRNA formyltransferase	-4,23	-3,52
SL3375	<i>rsmB</i>	Ribosomal RNA small subunit methyltransferase B	-4,63	-4,60
SL3376	<i>trkA</i>	Trk system potassium uptake protein trkA	-3,78	-2,57
SL3411	<i>bfd</i>	Bacterioferritin-associated ferredoxin	-4,61	-4,45
SL3419	<i>yheO</i>	Uncharacterized protein yheO	-1,67	-3,74
SL3440	<i>tsgA</i>	Protein tsgA	-3,97	-2,99
SL3441	<i>nirB</i>	Nitrite reductase [NAD(P)H] large subunit	4,39	-3,09
SL3442	<i>nirD</i>	Nitrite reductase [NAD(P)H] small subunit	3,43	-6,95
SL3443	<i>nirC</i>	Probable nitrite transporter	2,27	-5,91
SL3470	<i>greB</i>	Transcription elongation factor greB	-2,08	-59,94
SL3472	<i>feoA</i>	Ferrous iron transport protein A	-1,31	-3,17
SL3473	<i>feoB</i>	Ferrous iron transport protein B	-1,62	-3,20
SL3482	<i>malT</i>	HTH-type transcriptional regulator malT	5,98	5,14
SL3490	<i>glpR</i>	Glycerol-3-phosphate regulon repressor	-3,00	-1,84
SL3498	<i>ilvD</i>	Dihydroxy-acid dehydratase	2,01	3,10
SL3514	-	Hypothetical	-1,47	-3,60
SL3520	<i>ugpC</i>	sn-glycerol-3-phosphate import ATP-binding protein UgpC	1,88	4,06
SL3521	<i>ugpE</i>	sn-glycerol-3-phosphate transport system permease protein UgpE	1,31	3,15

Tabla Suplementaria 5

Genes afectados en las cepas mutantes *dksA* y *greAgreB*, respecto a la cepa WT

ID	gene	Description	<i>dksA</i> vs WT	<i>greAgreB</i> vs WT
SL3522	<i>ugpA</i>	sn-glycerol-3-phosphate transport system permease protein <i>ugpA</i>	1,19	3,48
SL3523	<i>ugpB</i>	sn-glycerol-3-phosphate-binding periplasmic protein <i>ugpB</i>	3,38	12,09
SL3524	-	Death On Curing Protein	1,71	4,53
SL3525	<i>yhhV</i>	Uncharacterized protein <i>yhhV</i>	1,68	4,30
SL3540	<i>yhhN</i>	Uncharacterized membrane protein <i>yhhN</i>	-3,96	-1,05
SL3541	<i>zntA</i>	Lead, cadmium, zinc and mercury-transporting ATPase	-1,05	3,05
SL3543	<i>tusA</i>	Sulfurtransferase <i>tusA</i>	-6,94	-11,47
SL3544	<i>yhhQ</i>	Inner membrane protein <i>yhhQ</i>	-1,17	-4,91
SL3557	<i>dtpB</i>	Dipeptide and tripeptide permease B	2,86	3,02
SL3559	<i>prlC</i>	Oligopeptidase A	-3,84	-2,03
SL3563	<i>ansB</i>	L-asparaginase	12,37	32,54
SL3564	<i>dcuB</i>	Anaerobic C4-dicarboxylate transporter <i>dcuB</i>	25,68	55,06
SL3565	<i>frlD</i>	Fructosamine kinase <i>frlD</i>	24,98	33,42
SL3566	<i>frlB</i>	Fructosamine deglycase <i>frlB</i>	25,25	33,98
SL3569	-	Hypothetical	2,47	3,95
SL3571	<i>yhjB</i>	Putative HTH-type transcriptional regulator <i>yhjB</i>	-4,61	-3,03
SL3576	<i>yhjH</i>	Cyclic di-GMP phosphodiesterase <i>YhjH</i>	1,16	-5,37
SL3577	<i>kdgK</i>	2-dehydro-3-deoxygluconokinase	4,44	4,32
SL3579	<i>dctA</i>	C4-dicarboxylate transport protein	8,22	14,63
SL3590	-	Hypothetical Protein SL3590	-3,58	-1,82
SL3592	<i>dppF</i>	Dipeptide transport ATP-binding protein <i>dppF</i>	-3,99	1,31
SL3593	<i>dppD</i>	Dipeptide transport ATP-binding protein <i>dppD</i>	-4,77	1,11
SL3594	<i>dppC</i>	Dipeptide transport system permease protein <i>dppC</i>	-6,99	-1,14
SL3595	<i>dppB</i>	Dipeptide transport system permease protein <i>dppB</i>	-7,97	-1,12
SL3596	<i>dppA</i>	Periplasmic dipeptide transport protein	-2,14	3,36
SL3614	<i>yiaG</i>	Uncharacterized HTH-type transcriptional regulator <i>yiaG</i>	3,52	1,04
SL3628	<i>bax</i>	Protein <i>bax</i>	-2,16	-9,21
SL3633	<i>dlgD</i>	2,3-diketo-L-gulonate reductase	3,90	4,51
SL3638	<i>yiaO</i>	2,3-diketo-L-gulonate-binding periplasmic protein <i>yiaO</i>	1,64	4,21
SL3641	<i>sgbU</i>	Putative L-ribulose-5-phosphate 3-epimerase <i>sgbU</i>	2,13	3,77
SL3643	<i>yisR</i>	Uncharacterized HTH-type transcriptional regulator <i>yisR</i>	2,76	4,41
SL3644	-	Hypothetical	2,01	4,20
SL3645	<i>aldB</i>	Aldehyde dehydrogenase B	3,84	2,38
SL3650	<i>mtlA</i>	PTS system mannitol-specific EIICBA component	2,62	3,05
SL3653	<i>yibT</i>	Uncharacterized protein <i>yibT</i>	1,96	5,71
SL3659	<i>lldD</i>	L-lactate dehydrogenase [cytochrome]	2,43	3,49
SL3660	<i>yibK</i>	Uncharacterized tRNA/rRNA methyltransferase <i>yibK</i>	3,68	-1,22
SL3662	<i>mdlA</i>	Mandelate racemase	2,01	4,34
SL3663	<i>gudP</i>	Probable glucarate transporter	2,07	4,44

Tabla Suplementaria 5

Genes afectados en las cepas mutantes *dksA* y *greAgreB*, respecto a la cepa WT

ID	gene	Description	<i>dksA</i> vs WT	<i>greAgreB</i> vs WT
SL3670	<i>gpml</i>	2,3-bisphosphoglycerate-independent phosphoglycerate mutase	-1,28	-3,23
SL3674	<i>tdh</i>	L-threonine 3-dehydrogenase	4,44	3,79
SL3675	<i>kbl</i>	Putative 8-amino-7-oxononanoate synthase/2-amino-3-ketobutyrate coenzyme A ligase	6,06	2,94
SL3690	<i>waaA</i>	3-deoxy-D-manno-octulosonic-acid transferase	3,06	-1,20
SL3695	<i>yicR</i>	UPF0758 protein yicR	15,77	3,41
SL3704	<i>yicG</i>	UPF0126 inner membrane protein yicG	-1,74	-3,47
SL3705	<i>ligB</i>	DNA ligase B	10,68	1,50
SL3711	-	Cytoplasmic Protein	1,98	5,37
SL3712	<i>gltS</i>	Sodium/glutamate symport carrier protein	3,17	5,98
SL3713	<i>xanP</i>	Xanthine permease XanP	3,94	1,11
SL3728	<i>mgtB</i>	Magnesium-transporting ATPase, P-type 1	-7,14	-4,80
SL3729	<i>mgtC</i>	Protein mgtC	-44,71	-24,09
SL3740	<i>gmuD</i>	6-phospho-beta-glucosidase gmuD	3,39	2,95
SL3742	<i>nepl</i>	Purine ribonucleoside efflux pump nepl	-3,40	-4,69
SL3743	-	Hypothetical	2,38	3,57
SL3744	<i>yiaG</i>	Transcriptional Regulator XRE Family	2,32	3,84
SL3750	<i>gatA</i>	PTS IIA-Like Nitrogen-Regulatory Protein PtsN	2,98	1,99
SL3751	<i>mngR</i>	Mannosyl-D-glycerate transport/metabolism system repressor mngR	5,24	3,65
SL3752	<i>yicN</i>	Uncharacterized protein yicN	3,22	1,11
SL3753	<i>uhpT</i>	Hexose phosphate transport protein	3,98	1,42
SL3757	-	Hypothetical	1,17	3,49
SL3758	<i>fucP</i>	L-fucose-proton symporter	1,27	3,39
SL3759	<i>rbsK</i>	Ribokinase	1,43	3,60
SL3761	<i>ilvN</i>	Acetolactate synthase isozyme 1 small subunit	2,70	4,96
SL3762	<i>ilvB</i>	Acetolactate synthase isozyme 1 large subunit	3,33	5,91
SL3768	<i>dsdC</i>	HTH-type transcriptional regulator dsdC	3,74	3,96
SL3774	<i>yidE</i>	Putative transport protein CKO_00031	3,18	5,60
SL3776	<i>ibpA</i>	Small heat shock protein ibpA	-1,03	3,13
SL3786	<i>yhjA</i>	Probable cytochrome c peroxidase	-3,11	-2,69
SL3789	<i>torC</i>	Cytochrome c-type protein torC	-1,90	-3,23
SL3790	<i>torR</i>	TorCAD operon transcriptional regulatory protein torR	2,32	4,44
SL3794	<i>dgoD1</i>	D-galactonate dehydratase 1	-1,03	3,20
SL3799	<i>gudP</i>	Probable glucarate transporter	1,54	4,70
SL3800	<i>dgoD</i>	D-galactonate dehydratase	1,33	3,13
SL3801	<i>ybhD</i>	Uncharacterized HTH-type transcriptional regulator ybhD	2,82	4,56
SL3814	<i>mdtL</i>	Multidrug resistance protein mdtL	-1,22	-3,71
SL3831	<i>atpC</i>	ATP synthase epsilon chain	1,81	3,56

Tabla Suplementaria 5

Genes afectados en las cepas mutantes *dksA* y *greAgreB*, respecto a la cepa WT

ID	gene	Description	<i>dksA</i> vs WT	<i>greAgreB</i> vs WT
SL3848	<i>rbsD</i>	D-ribose pyranase	-4,44	-2,87
SL3849	<i>rbsA1</i>	Ribose import ATP-binding protein RbsA 1	-4,19	-2,95
SL3859	<i>yifE</i>	UPF0438 protein yifE	7,01	1,55
SL3861	<i>ilvG</i>	Acetolactate synthase isozyme 2 large subunit	1,88	3,17
SL3862	<i>ilvM</i>	Acetolactate synthase isozyme 2 small subunit	2,57	5,19
SL3871	-	Inner Membrane Protein	3,48	1,45
SL3876	<i>rho</i>	Transcription termination factor rho	-2,45	-3,61
SL3889	<i>yifK</i>	Probable transport protein yifK	3,81	1,60
SL3894	<i>cyaA</i>	Adenylate cyclase	-3,10	-2,83
SL3906	<i>corA</i>	Magnesium transport protein corA	-1,38	-3,08
SL3935	<i>fadA</i>	3-ketoacyl-CoA thiolase	5,63	23,14
SL3936	<i>fadB</i>	Fatty acid oxidation complex subunit alpha	5,93	22,96
SL3954	<i>glnA</i>	Glutamine synthetase	-3,78	-1,77
SL3962	<i>ompL</i>	Porin ompL	2,21	3,58
SL3967	<i>yihS</i>	Uncharacterized sugar isomerase yihS	1,59	4,13
SL3968	<i>yihT</i>	Uncharacterized aldolase yihT	1,89	4,63
SL3969	<i>yihU</i>	Uncharacterized oxidoreductase yihU	1,52	6,23
SL3970	<i>yihV</i>	Uncharacterized sugar kinase yihV	3,53	3,37
SL3978	<i>est</i>	Esterase	3,79	3,87
SL3989	-	Hypothetical	-3,77	-2,15
SL3997	<i>rhaS</i>	HTH-type transcriptional activator rhaS	5,18	7,48
SL3998	<i>rhaR</i>	HTH-type transcriptional activator rhaR	5,45	3,48
SL4009	<i>cpxP</i>	Periplasmic protein cpxP	-2,98	-1,82
SL4012	<i>sbp</i>	Sulfate-binding protein	1,01	3,15
SL4014	<i>yagG</i>	Uncharacterized symporter yagG	2,24	6,83
SL4015	<i>scrK</i>	Fructokinase	2,56	7,32
SL4016	<i>yegU</i>	Uncharacterized protein yegU	1,69	4,60
SL4020	-	Conserved Hypothetical Protein	1,41	3,55
SL4021	<i>lsrK</i>	Autoinducer 2 kinase lsrK	1,54	5,12
SL4022	<i>lsrR</i>	Transcriptional regulator lsrR	3,64	5,81
SL4023	<i>lsrA</i>	Autoinducer 2 import ATP-binding protein lsrA	22,29	49,79
SL4024	<i>lsrC</i>	Autoinducer 2 import system permease protein lsrC	5,57	18,13
SL4025	<i>lsrD</i>	Autoinducer 2 import system permease protein lsrD	2,42	9,85
SL4053	-	Hypothetical	3,84	1,48
SL4054	<i>yfkN</i>	Trifunctional nucleotide phosphoesterase protein yfkN	3,68	1,50
SL4055	<i>metF</i>	5,10-methylenetetrahydrofolate reductase	1,08	-3,35
SL4056	<i>katG1</i>	Catalase-peroxidase 1	-2,70	-3,75
SL4057	<i>yijF</i>	Uncharacterized protein yijF	-5,09	-8,02
SL4061	<i>frwC</i>	Fructose-like permease IIC component 2	17,80	5,71
SL4062	<i>frwB</i>	Fructose-like phosphotransferase enzyme IIB component 2	7,78	3,40
SL4069	<i>ppc</i>	Phosphoenolpyruvate carboxylase	-4,32	-1,26
SL4071	<i>argC</i>	N-acetyl-gamma-glutamyl-phosphate reductase	-2,98	1,02

Tabla Suplementaria 5

Genes afectados en las cepas mutantes *dksA* y *greAgreB*, respecto a la cepa WT

ID	gene	Description	<i>dksA</i> vs WT	<i>greAgreB</i> vs WT
SL4098	<i>thiH</i>	Dehydroglycine synthase	1,93	3,47
SL4099	<i>thiG</i>	Thiazole synthase	2,29	4,86
SL4100	<i>thiS</i>	Sulfur carrier protein ThiS	2,18	3,53
SL4101	<i>thiF</i>	Sulfur carrier protein ThiS adenyltransferase	2,18	4,02
SL4102	<i>thiE</i>	Thiamine-phosphate pyrophosphorylase	1,73	3,49
SL4103	<i>thiC</i>	Phosphomethylpyrimidine synthase	1,64	3,16
SL4104	<i>rsd</i>	Regulator of sigma D	2,95	3,58
SL4118	<i>aceB</i>	Malate synthase A	1,65	7,52
SL4119	<i>aceA</i>	Isocitrate lyase	1,95	4,68
SL4131	-	Hypothetical	-1,33	-4,83
SL4142	-	Phage Baseplate Assembly Protein V	2,41	3,49
SL4159	<i>yjbF</i>	Uncharacterized lipoprotein yjbF	-3,86	-2,28
SL4160	<i>yjbG</i>	Uncharacterized protein yjbG	-3,95	-1,70
SL4162	<i>psiE</i>	Protein psiE	-4,25	-3,30
SL4164	<i>malF</i>	Maltose transport system permease protein malF	4,45	1,14
SL4165	-	Hypothetical Protein SL4165	11,67	2,30
SL4166	<i>malE</i>	Maltose-binding periplasmic protein	3,45	1,50
SL4167	<i>malK</i>	Maltose/maltodextrin import ATP-binding protein MalK	12,13	1,67
SL4180	<i>pspG</i>	Phage shock protein G	-3,56	-2,02
SL4185	<i>aphA</i>	Class B acid phosphatase	5,38	2,41
SL4193	-	Hypothetical	-8,63	-26,54
SL4194	-	Integral Membrane Protein	-8,57	-26,23
SL4195	<i>tolC</i>	Outer membrane protein tolC	-7,84	-22,66
SL4196	<i>prtE</i>	Proteases secretion protein prtE	-7,15	-31,87
SL4197	-	Hypothetical	-8,49	-18,80
SL4198	<i>lktB</i>	Leukotoxin translocation ATP-binding protein lktB	-17,32	-46,89
SL4199	<i>yjcB</i>	Uncharacterized protein yjcB	-20,52	-9,86
SL4200	<i>yjcC</i>	Uncharacterized protein yjcC	-6,40	-3,42
SL4201	<i>soxS</i>	Regulatory protein soxS	-2,53	-3,63
SL4207	<i>cidA</i>	Holin-like protein cidA	-9,77	-19,38
SL4208	<i>ywbG</i>	Uncharacterized protein ywbG	-15,23	-19,43
SL4209	<i>actP</i>	Cation/acetate symporter ActP	2,48	13,02
SL4210	<i>yjcH</i>	Inner membrane protein yjcH	5,66	39,97
SL4211	<i>acs</i>	Acetyl-coenzyme A synthetase	4,90	21,68
SL4212	-	Hypothetical	2,23	3,32
SL4213	<i>nrfA</i>	Cytochrome c-552	5,15	2,13
SL4214	<i>nrfB</i>	Cytochrome c-type protein nrfB	3,64	-1,02
SL4230	<i>eptA</i>	Phosphoethanolamine transferase eptA	-4,20	-1,50
SL4231	<i>adiC</i>	Arginine/agmatine antiporter	1,36	-4,64
SL4234	<i>melR</i>	Melibiose operon regulatory protein	5,38	6,19
SL4238	<i>dcuB</i>	Anaerobic C4-dicarboxylate transporter dcuB	-9,28	-11,02
SL4239	-	Hypothetical	-39,41	-24,27
SL4247	<i>yjiK</i>	Uncharacterized protein yjiK	-15,24	-24,46

Tabla Suplementaria 5

Genes afectados en las cepas mutantes *dksA* y *greAgreB*, respecto a la cepa WT

ID	gene	Description	<i>dksA</i> vs WT	<i>greAgreB</i> vs WT
SL4248	-	Hypothetical	-8,48	-28,20
SL4249	-	Cytoplasmic Protein	-9,33	-41,36
SL4250	<i>yjiQ</i>	GerE Family Regulatory Protein	-9,42	-60,33
SL4251	<i>sirC</i>	Transcriptional regulator sirC	-8,74	-47,96
SL4252	-	Hypothetical	-6,03	-5,47
SL4253	-	Hypothetical	-3,33	-2,43
SL4266	<i>groS</i>	10 kDa chaperonin	1,75	3,79
SL4282	<i>yjeM</i>	Inner membrane transporter yjeM	-2,23	-3,47
SL4310	<i>aidB</i>	Protein AidB	7,60	9,60
SL4311	<i>yjfN</i>	Uncharacterized protein yjfN	9,48	6,64
SL4312	<i>bsmA</i>	Lipoprotein BsmA	8,24	5,00
SL4316	<i>ulaA</i>	Ascorbate-specific permease IIC component ulaA	3,66	9,06
SL4317	<i>ulaB</i>	Ascorbate-specific phosphotransferase enzyme IIB component	2,92	6,92
SL4318	<i>ulaC</i>	Ascorbate-specific phosphotransferase enzyme IIA component	2,55	5,04
SL4319	<i>ulaD</i>	3-keto-L-gulonate-6-phosphate decarboxylase ulaD	1,74	3,02
SL4336	<i>cpdB</i>	2',3'-cyclic-nucleotide 2'-phosphodiesterase/3'-nucleotidase	4,02	4,00
SL4351	<i>xylE</i>	D-xylose-proton symporter	1,22	7,99
SL4353	<i>iolB</i>	5-deoxy-glucuronate isomerase	1,78	3,00
SL4354	<i>iolA1</i>	Methylmalonate semialdehyde dehydrogenase [acylating] 1	1,66	3,93
SL4355	<i>ydiP</i>	Uncharacterized HTH-type transcriptional regulator ydiP	4,58	6,37
SL4361	<i>iolC</i>	5-dehydro-2-deoxygluconokinase	2,80	5,41
SL4362	<i>iolD1</i>	3D-(3,5/4)-trihydroxycyclohexane-1,2-dione hydrolase 1	2,17	5,81
SL4383	-	Hypothetical	5,18	-1,04
SL4384	<i>treC</i>	Trehalose-6-phosphate hydrolase	10,59	2,06
SL4385	<i>treB</i>	PTS system trehalose-specific EIIBC component	37,70	2,48
SL4390	<i>pyrI</i>	Aspartate carbamoyltransferase regulatory chain	4,61	1,05
SL4391	<i>pyrB</i>	Aspartate carbamoyltransferase	3,84	-1,15
SL4392	<i>pyrL</i>	PyrBI operon leader peptide	3,07	-1,50
SL4397	<i>arcA</i>	Arginine deiminase	3,40	1,41
SL4412	<i>idnT</i>	Gnt-II system L-idonate transporter	1,46	3,38
SL4413	<i>idnO</i>	Gluconate 5-dehydrogenase	1,86	3,80
SL4414	<i>idnD</i>	L-idonate 5-dehydrogenase	2,80	4,59
SL4431	-	UPF0386 protein KPN78578_02510	5,45	2,78
SL4432	-	Hypothetical	4,12	1,88
SL4434	-	Hypothetical	-5,31	-4,98
SL4460	-	Hypothetical	2,69	3,02
SL4463	<i>yjiY</i>	Inner membrane protein yjiY	-3,30	-18,87
SL4466	<i>manX</i>	PTS System Fructocific IIA Component	5,24	13,66
SL4467	<i>manX</i>	Probable phosphotransferase enzyme IIB component M6_Spy0801	4,12	15,83

Tabla Suplementaria 5Genes afectados en las cepas mutantes *dksA* y *greAgreB*, respecto a la cepa WT

ID	gene	Description	<i>dksA</i> vs WT	<i>greAgreB</i> vs WT
SL4468	<i>agaC</i>	N-acetylgalactosamine permease IIC component 1	3,49	17,29
SL4469	<i>manZ</i>	Mannose permease IID component	2,92	14,20
SL4470	<i>glmS</i>	Glucosamine--fructose-6-phosphate aminotransferase [isomerizing]	2,82	23,21
SL4471	<i>friB</i>	Fructosamine deglycase friB	1,19	14,58
SL4492	<i>yjjW</i>	Uncharacterized protein yjjW	6,32	1,57
SL4493	<i>yjjI</i>	Uncharacterized protein yjjI	6,45	1,64
SLP1_0030	<i>traE</i>	Protein traE	-3,15	-1,55
SLP1_0031	<i>traL</i>	Protein traL	-3,38	-1,36
SLP1_0054	<i>parB</i>	Plasmid Partition par B protein	3,01	5,19
SLP1_0055	<i>parA</i>	Plasmid partition protein A	3,75	5,75
SLP1_0067	<i>spvA</i>	28.1 kDa virulence protein	1,16	-6,22
SLP1_0068	<i>spvB</i>	65 kDa virulence protein	1,35	-12,28
SLP1_0069	<i>spvC</i>	27.5 kDa virulence protein	-1,61	-34,55
SLP1_0070	<i>spvD</i>	Virulence protein vsdE	-2,05	-10,27
SLP1_0080	<i>ccdA</i>	Protein CcdA	2,99	2,95
SLP2_0003	-	Hypothetical	3,16	4,59
SLP2_0004	-	Addiction Module Antitoxin	2,74	3,55
SLP2_0005	<i>dnaQ</i>	Uncharacterized protein pSLT049	5,21	4,21
SLP2_0012	<i>cib</i>	Colicin-Ib	1,63	4,20
SLP2_0032	<i>yubl</i>	Putative antirestriction protein Yubl	3,23	3,00
SLP2_0033	<i>yubJ</i>	Uncharacterized protein yubJ	2,54	3,01
SLP2_0037	<i>psiB</i>	Protein psiB	2,79	4,39
SLP2_0038	<i>psiA</i>	Protein psiA	3,67	5,34
SLP2_0039	-	Hypothetical	3,30	4,78
SLP2_0078	-	Hypothetical	1,11	3,93
SLP2_0079	-	Hypothetical	1,63	3,02
SLP2_0086	-	Prepilin Peptidase	1,25	-3,05
SLP3_0011	<i>mobC</i>	Mobilization protein C	1,44	3,03