UNIVERSITAT DE BARCELONA

Facultat de Biologia

Departament de Microbiologia

Les famílies de proteïnes Hha/YmoA i H-NS: regulació global de l'expressió gènica a *Escherichia coli* i paper en la conjugació plasmídica.

Núria Forns Fradera

Tesi Doctoral

Barcelona, abril 2006

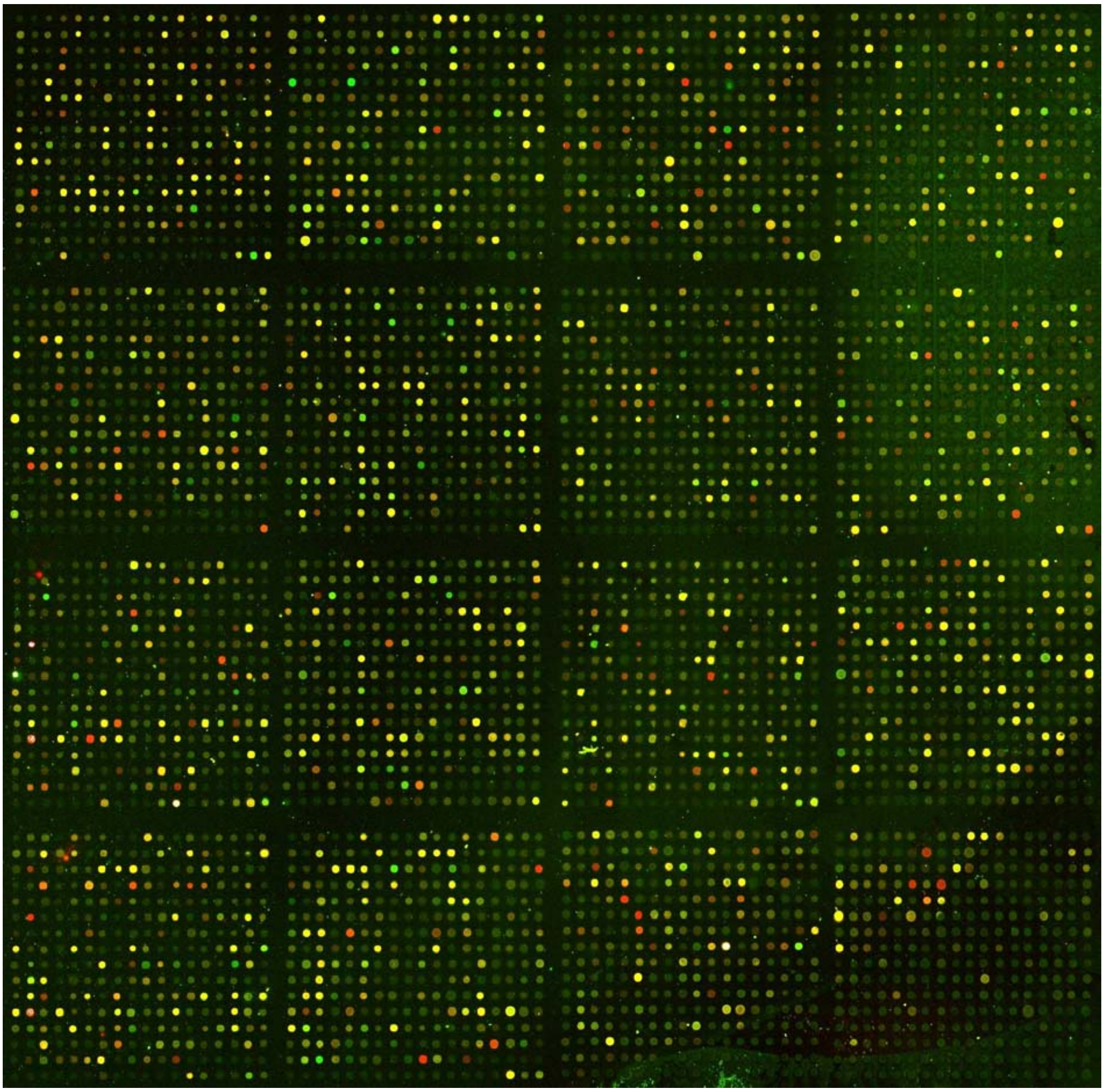
ANNEX 2

En aquest annex i podrem trobar totes les imatges, gràfiques i taules derivades de l'estudi de la transcripció dels gens d'*Escherichia coli* mitjançant microxips (apartat 3.3). Per tal de simplificar-ho, a cada microxip li hem donat un nom per identificar els tipus de mostres que s'hi han hibridat, com estaven marcades i el dia en què es va fer la hibridació. A la següent taula s'especifiquen les característiques de cada microxip, on Cy3 i Cy5 són les dues mostres hibridades en cada xip marcades en Cy3 i Cy5, respectivament:

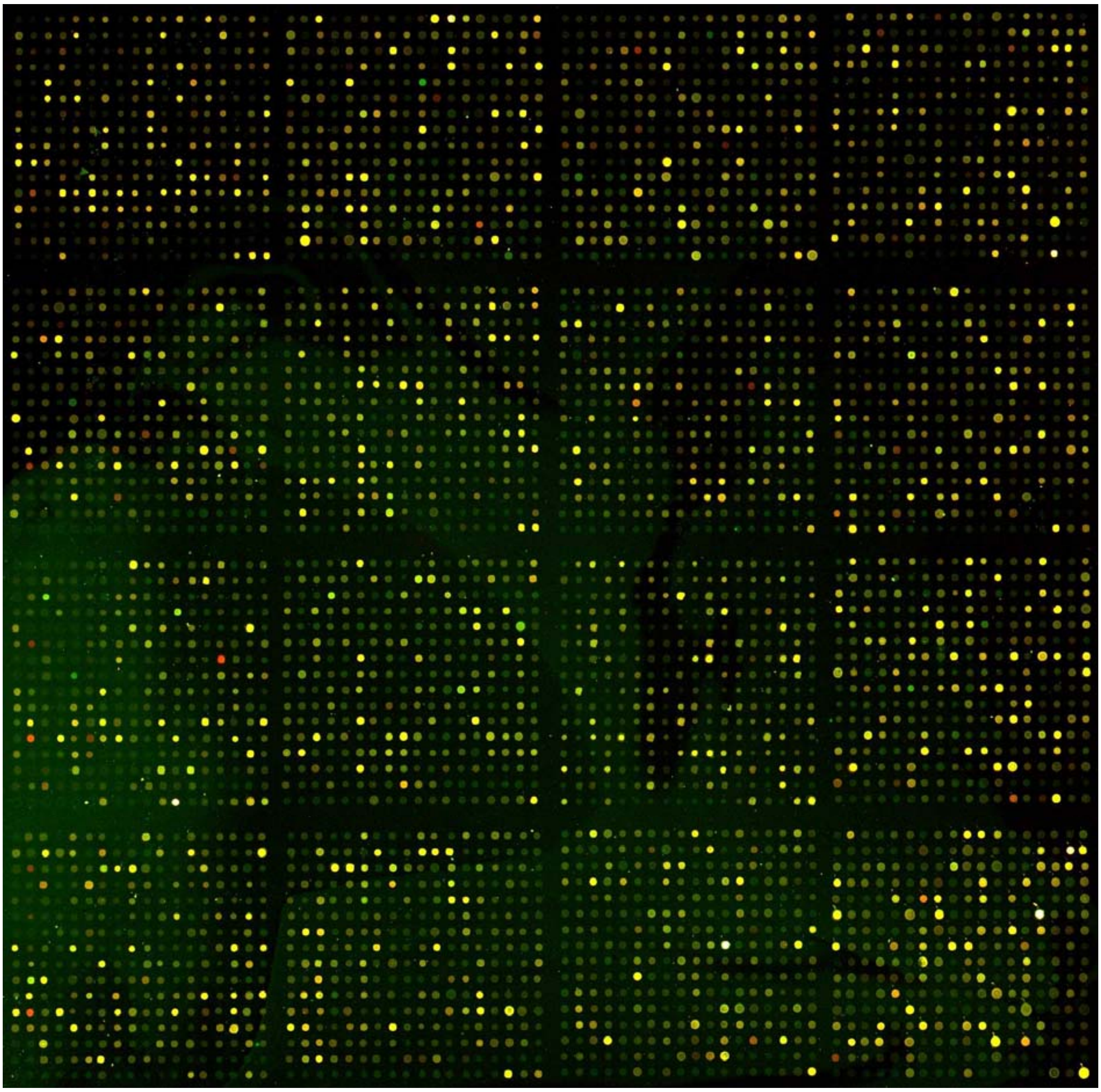
Nom	**Dia**	**Cy3**	**Cy5**
1-W-M1	1	BSN26	BSN27
2-W-M2	1	BSN26	BSN26HY
3-M2-M1	1	BSN26HY	BSN27
4-M1-W	2	BSN27	BSN26
5-M2-W	2	BSN26HY	BSN26
6-M1-M2	2	BSN27	BSN26HY
7-W-M1	3	BSN26	BSN27
8-W-M2	3	BSN26	BSN26HY
9-M2-M1	3	BSN26HY	BSN27
10-M1-W	4	BSN27	BSN26
11-M2-W	4	BSN26HY	BSN26
12-M1-M2	4	BSN27	BSN26HY

A. IMATGES SELECCIONADES PER CADASCUN DELS MICROXIPS

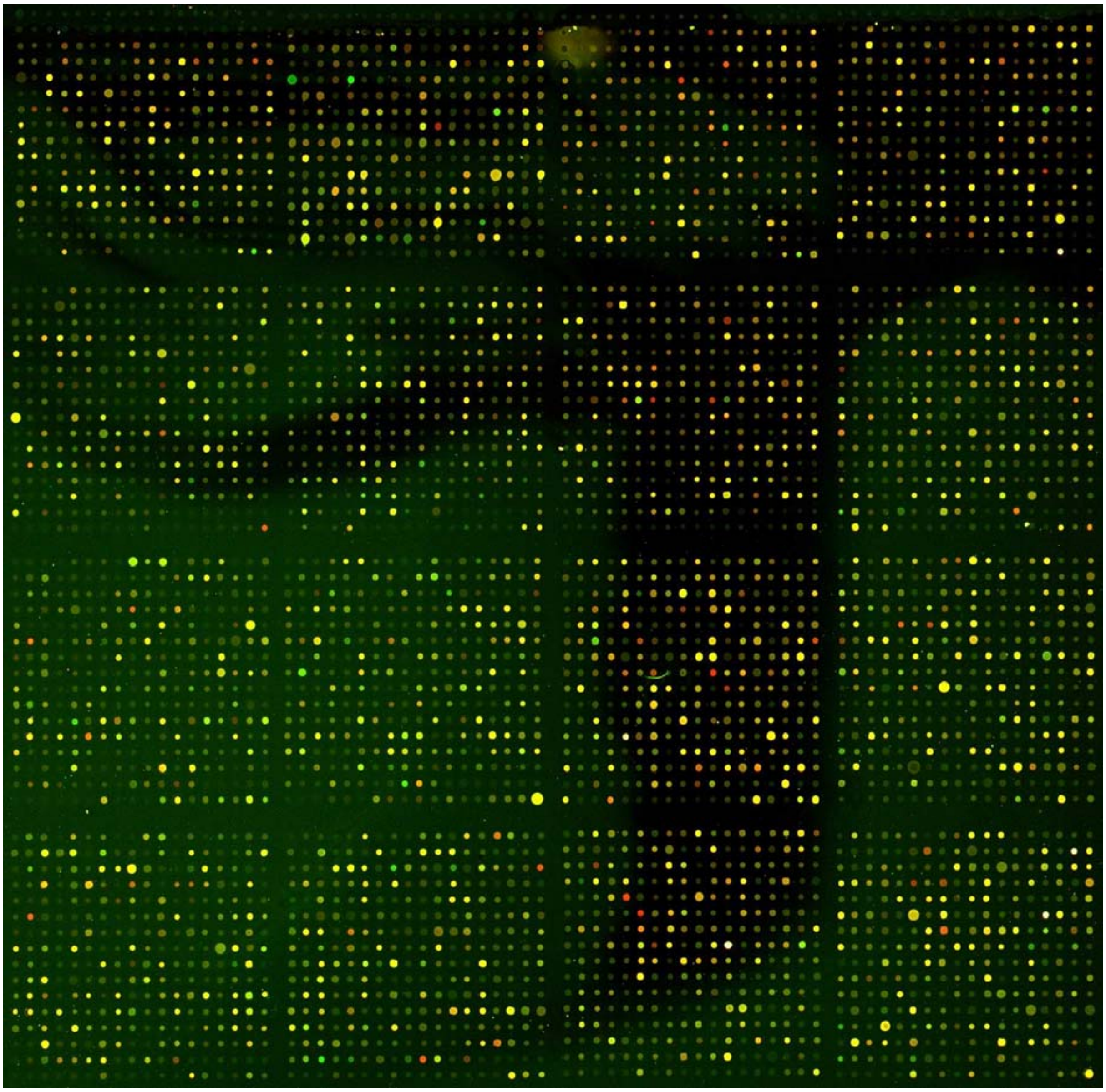
1-W-M1



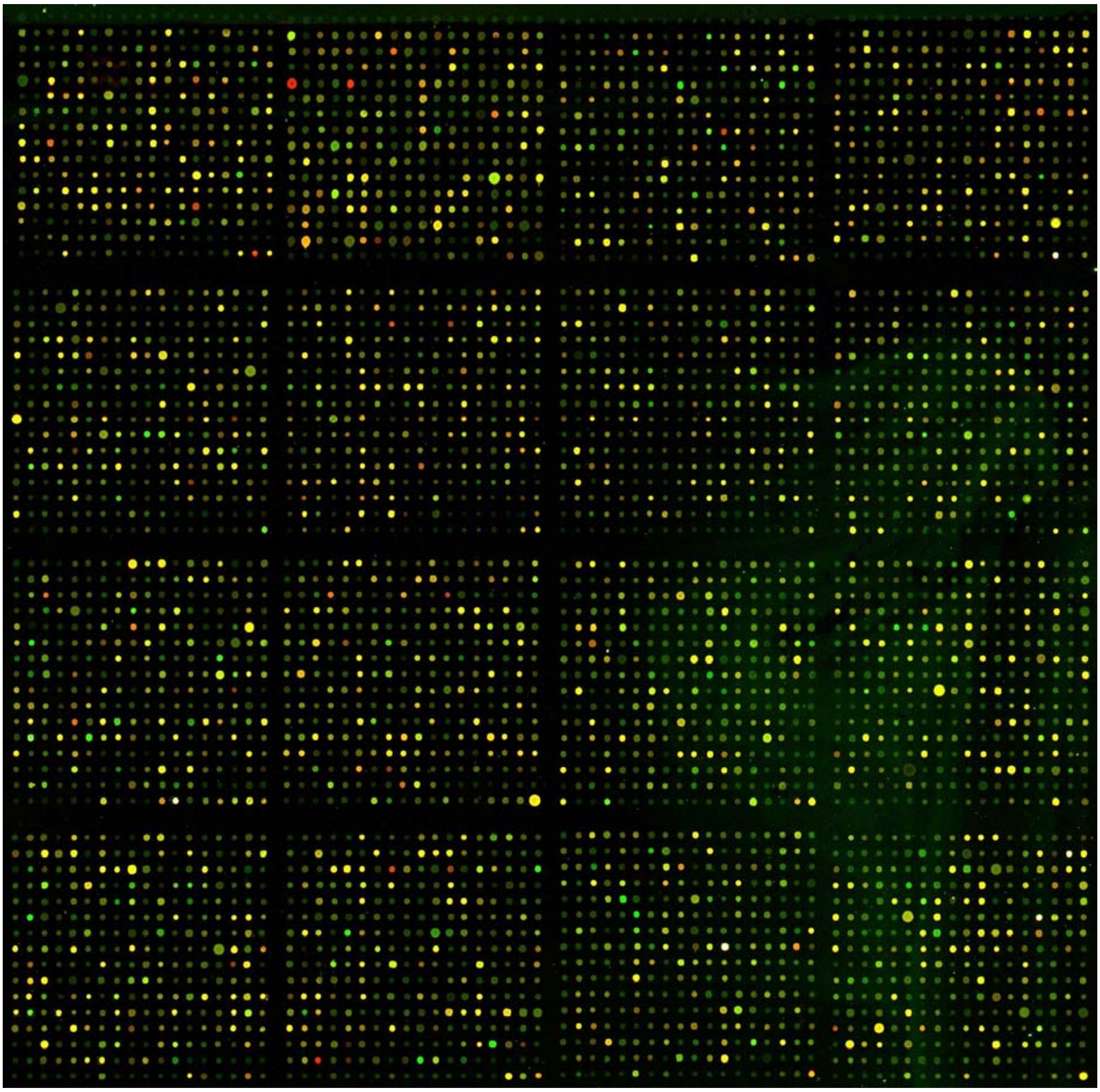
2-W-M2



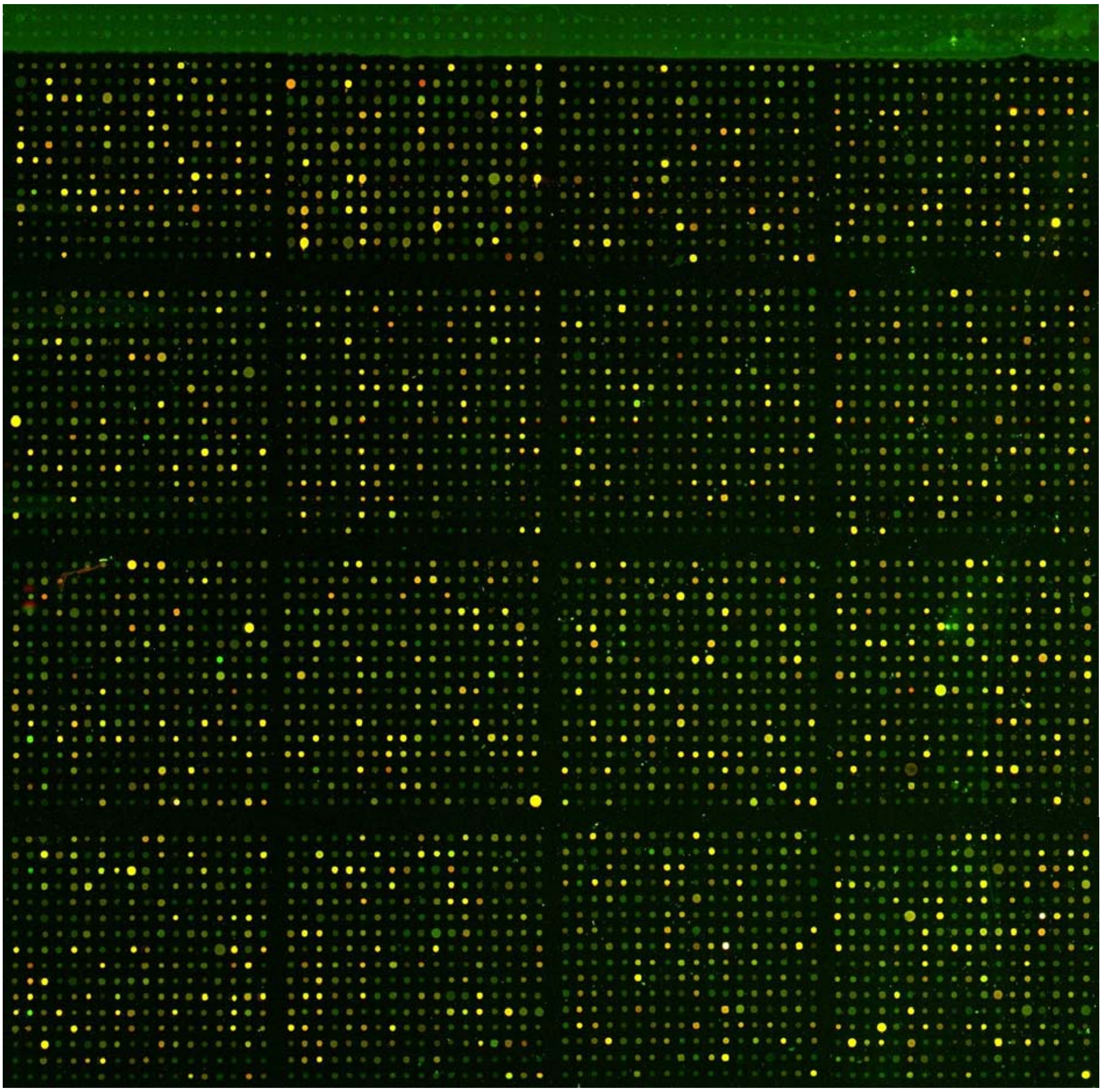
3-M2-M1



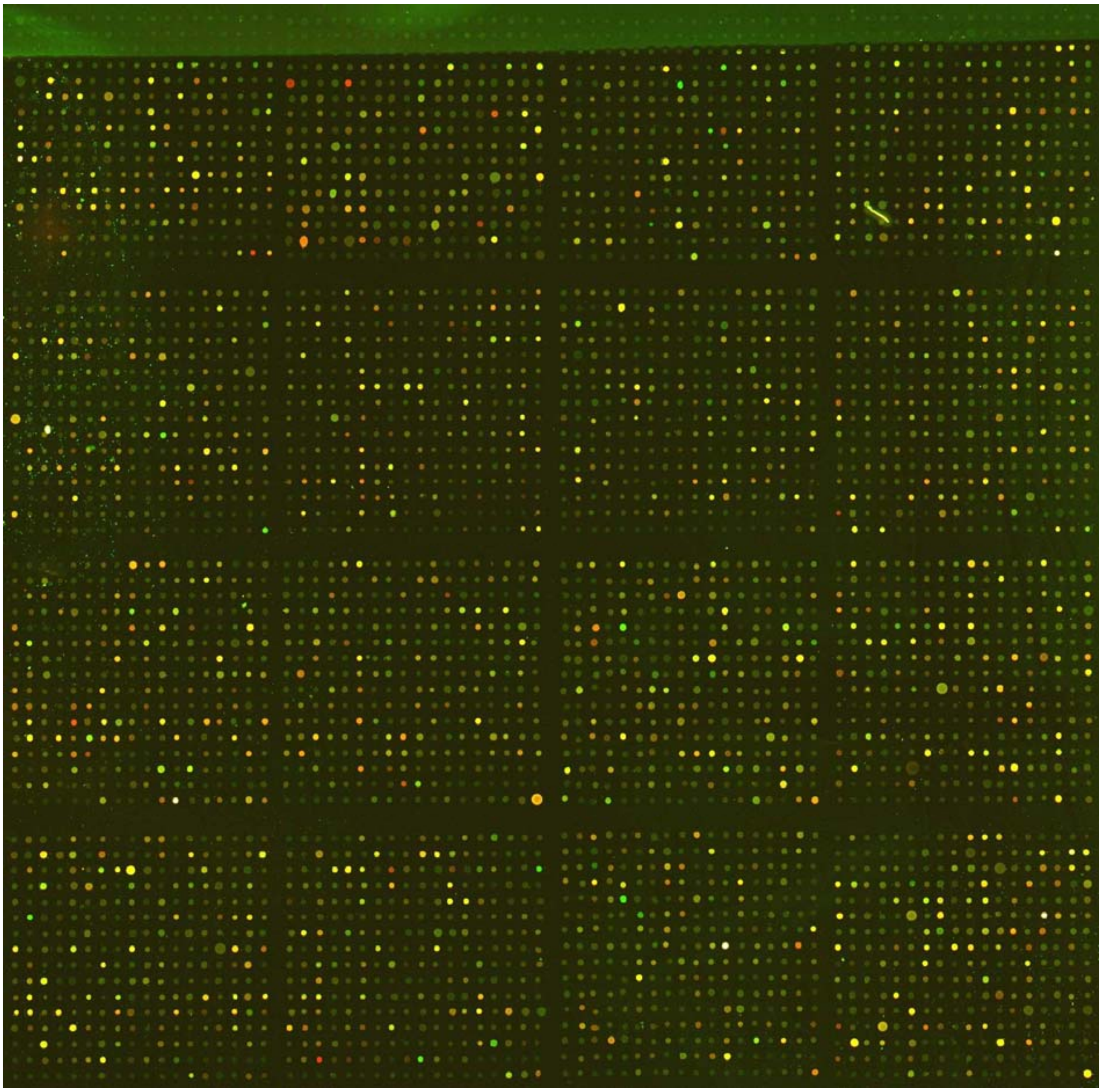
4-M1-W



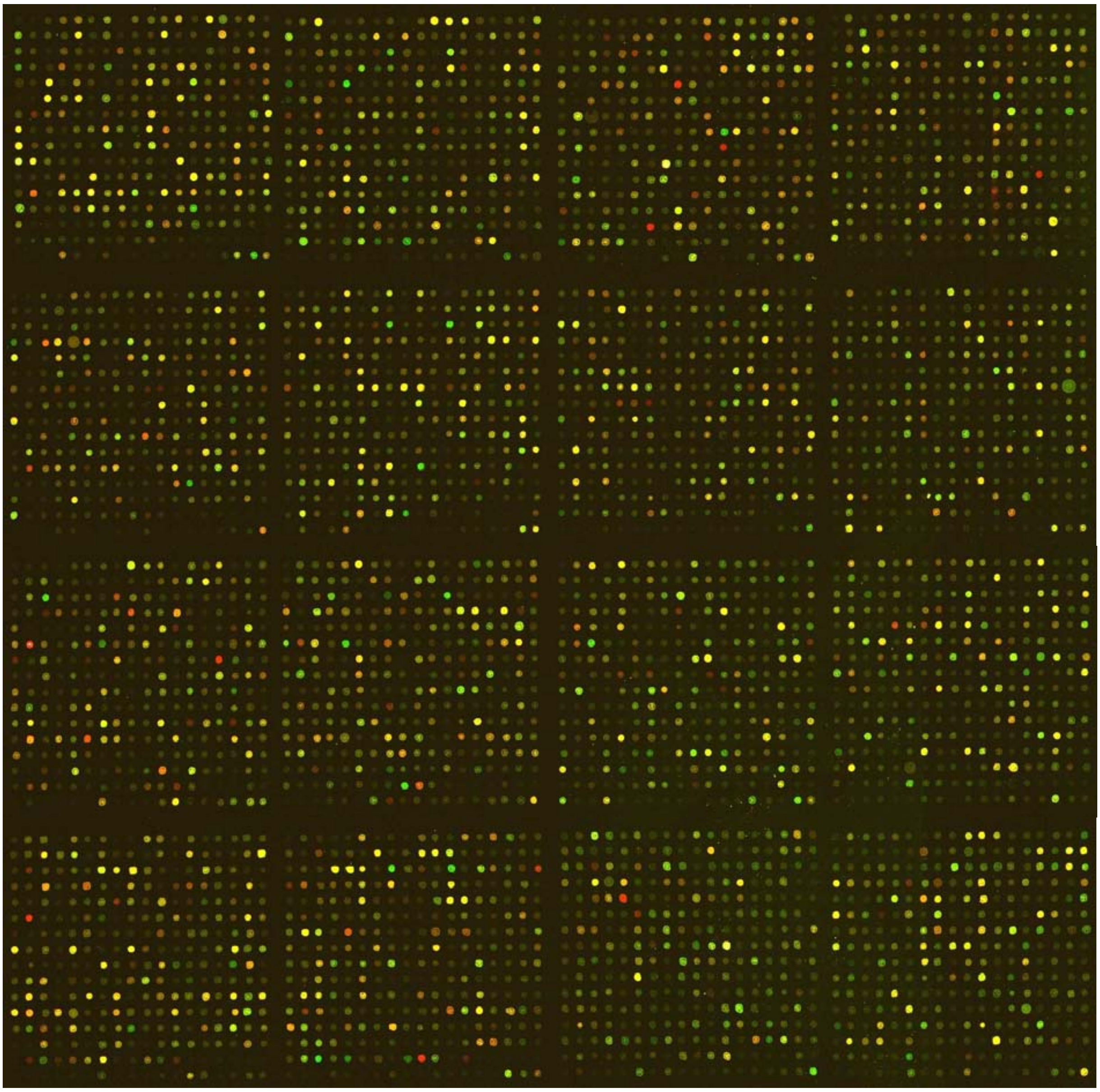
5-M2-W



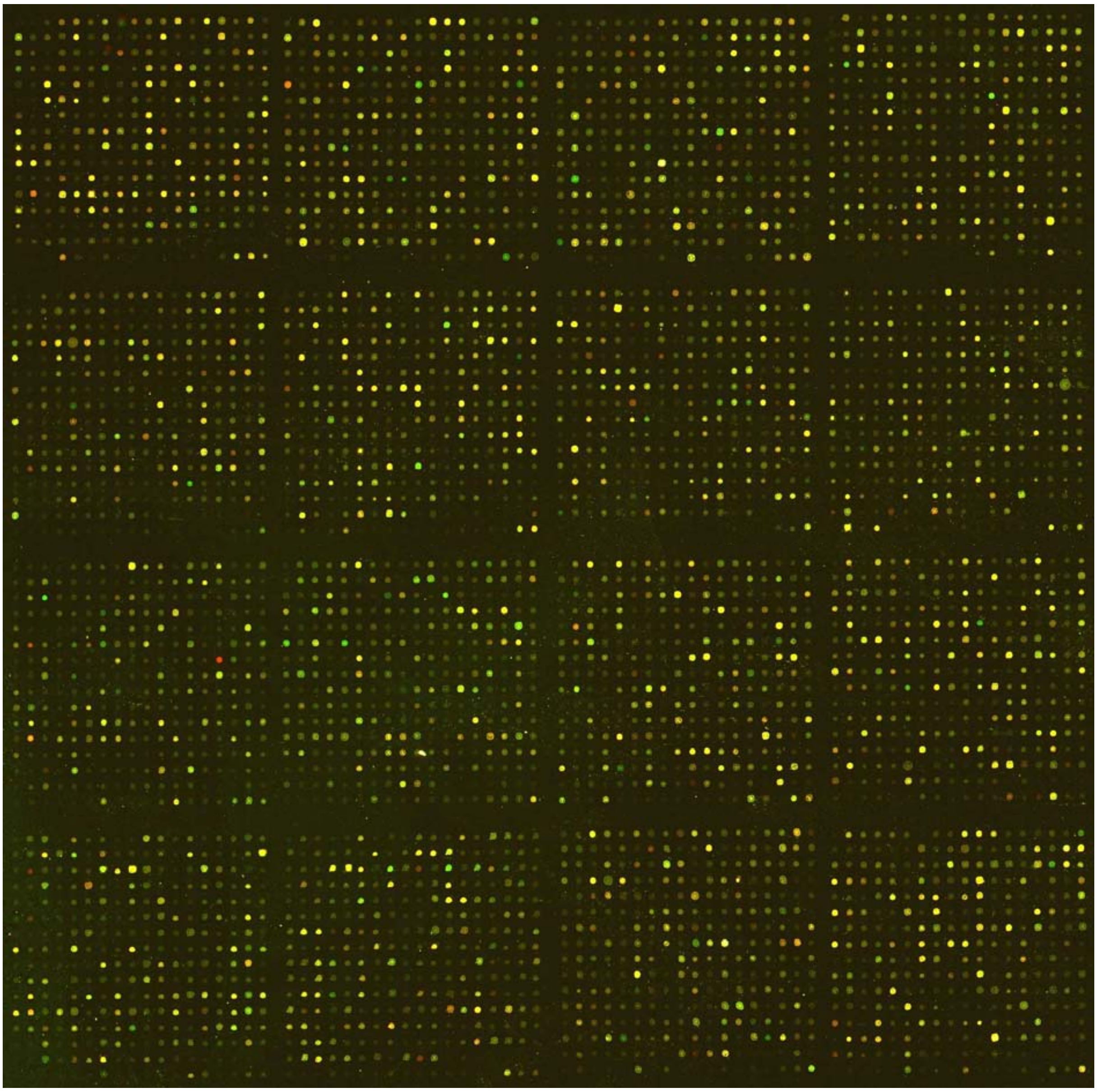
6-M1-M2



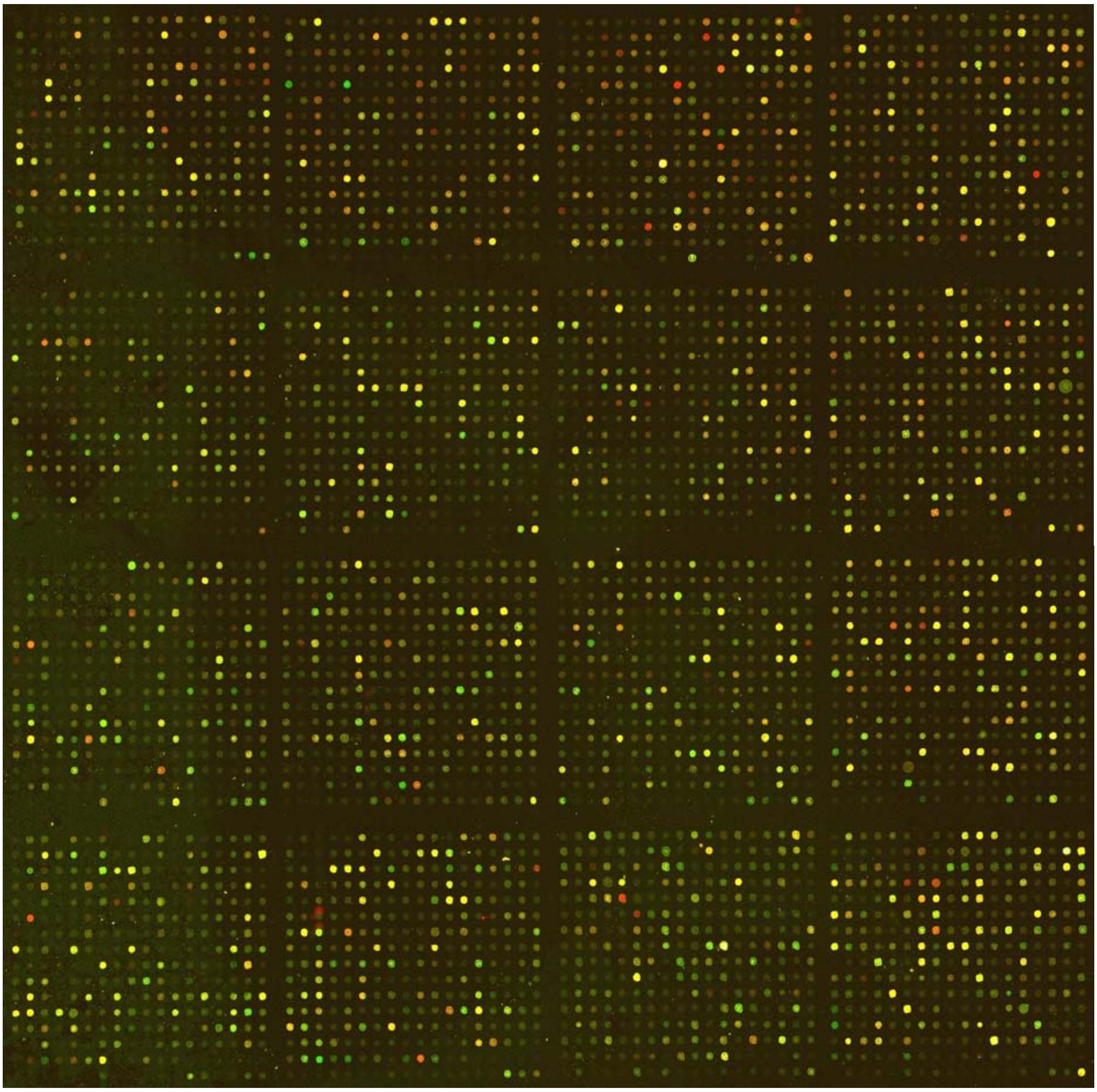
7-W-M1



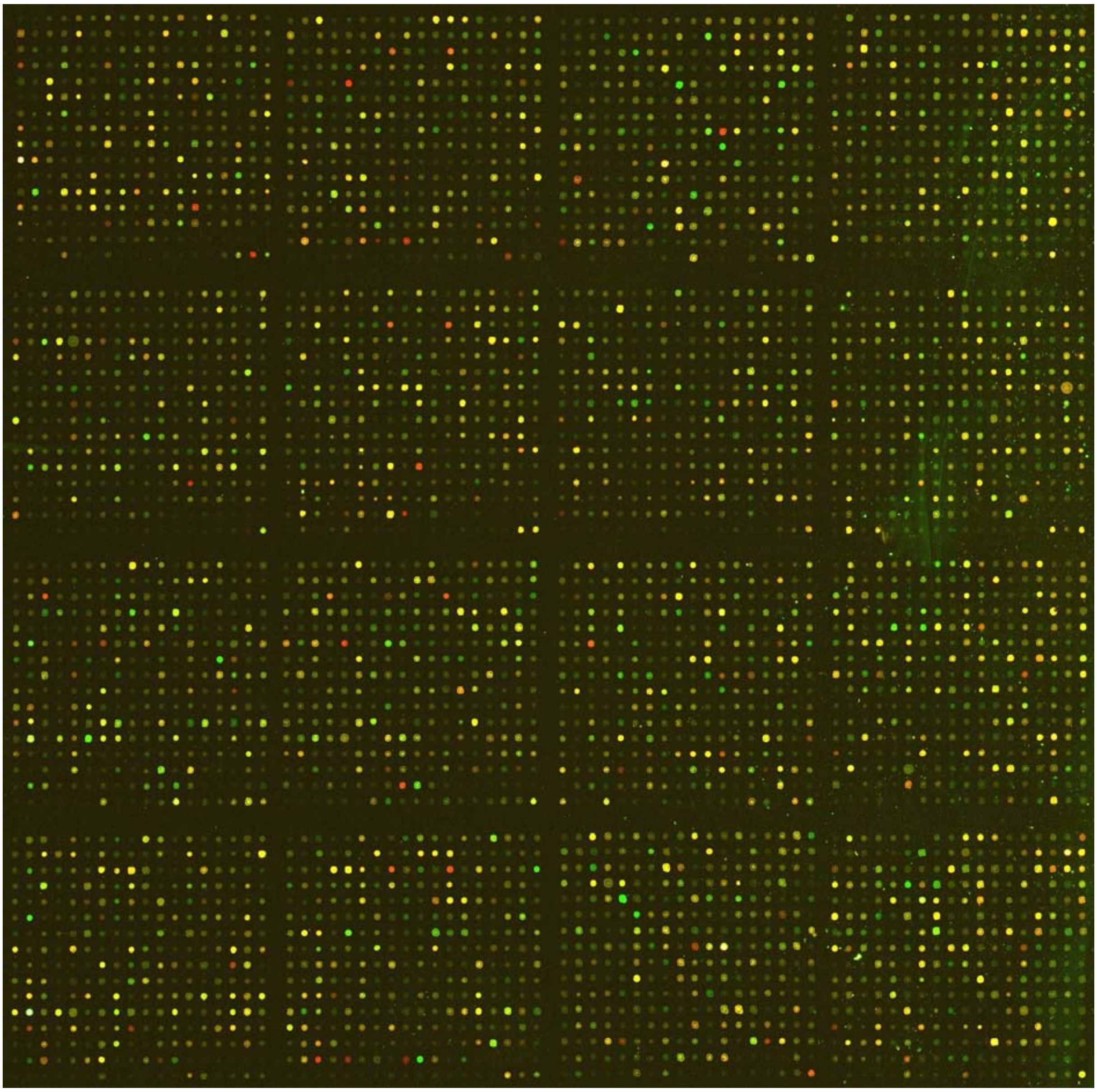
8-W-M2



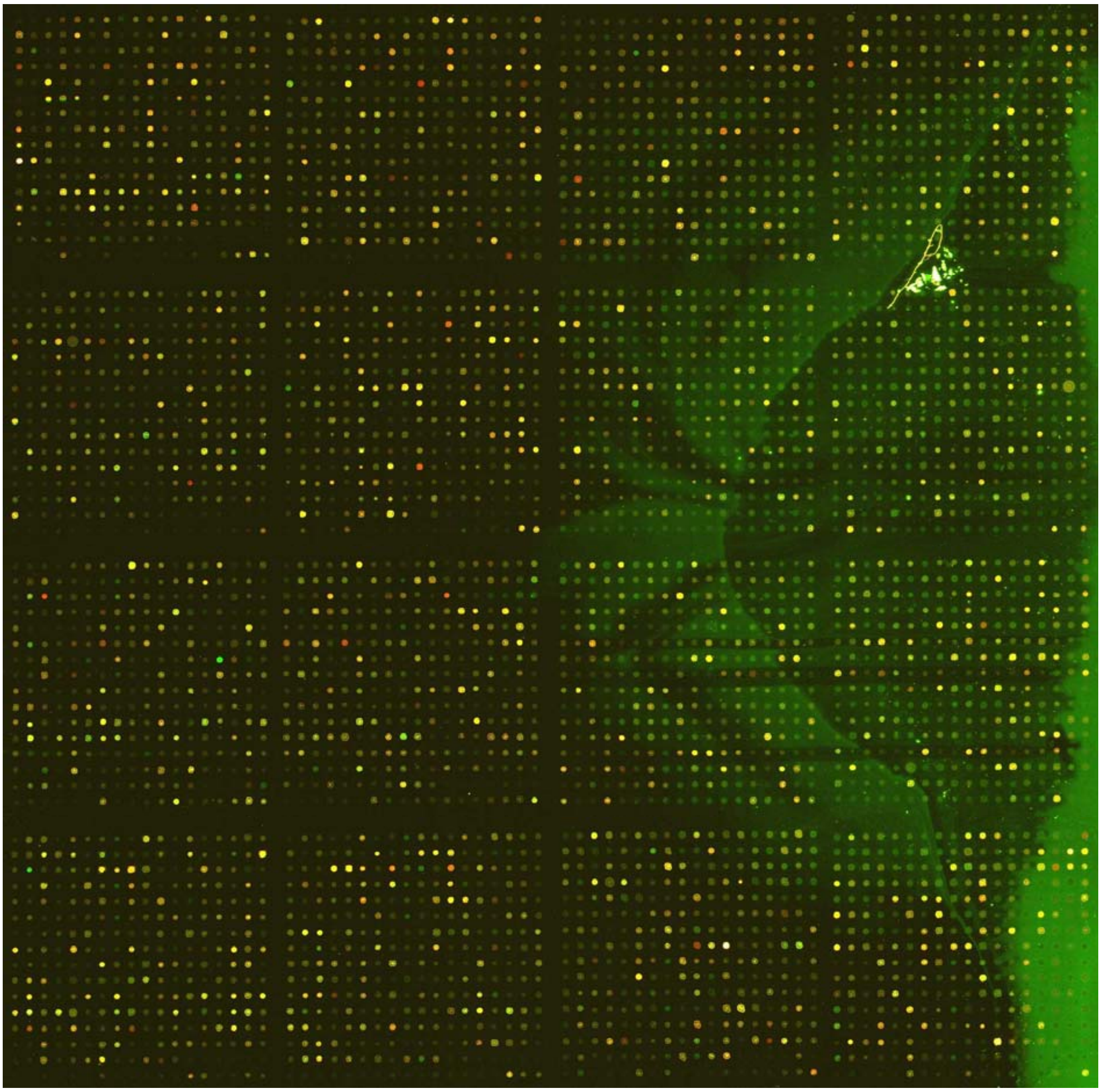
9-M2-M1



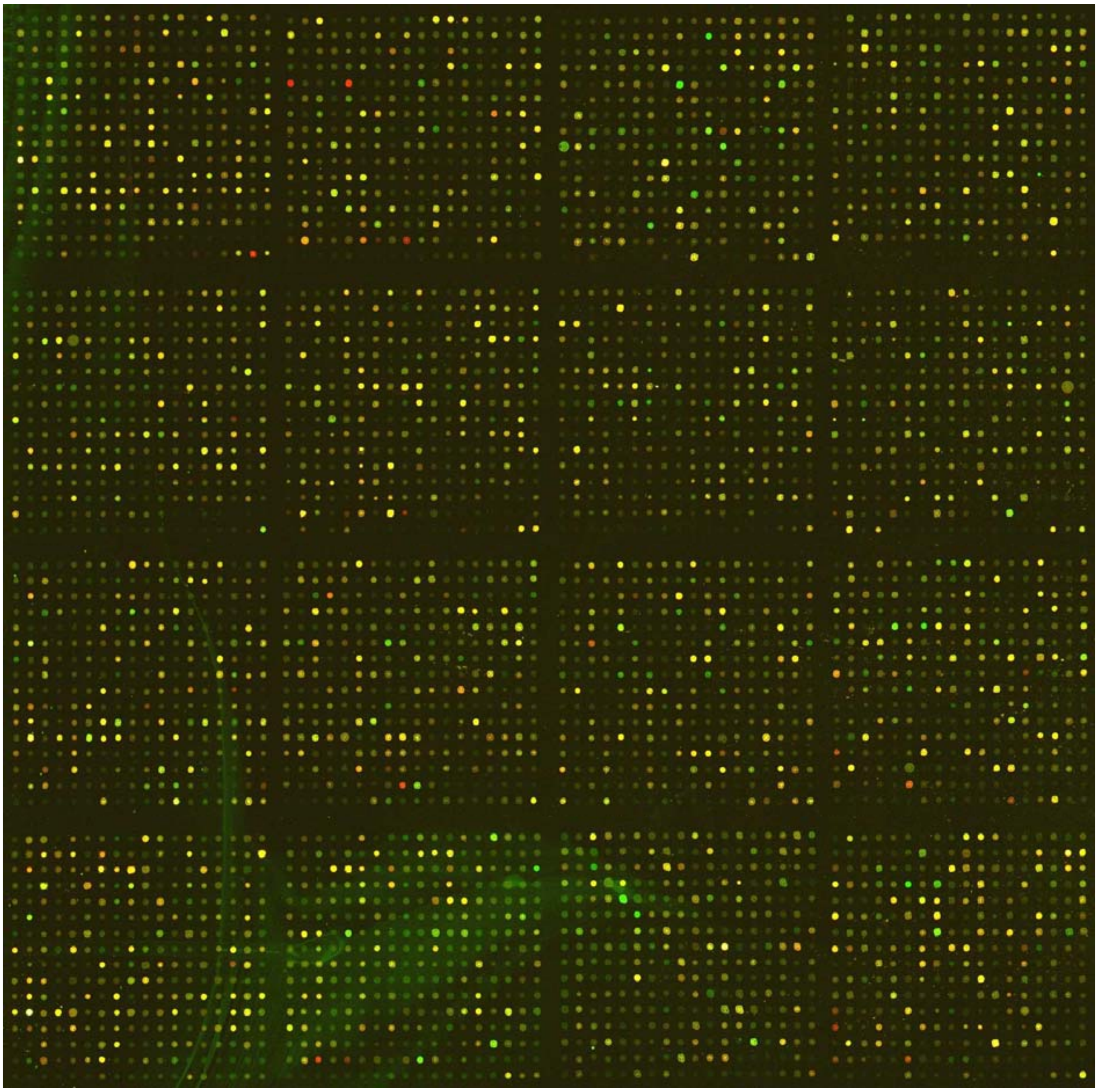
10-M1-W



11-M2-W



12-M1-M2

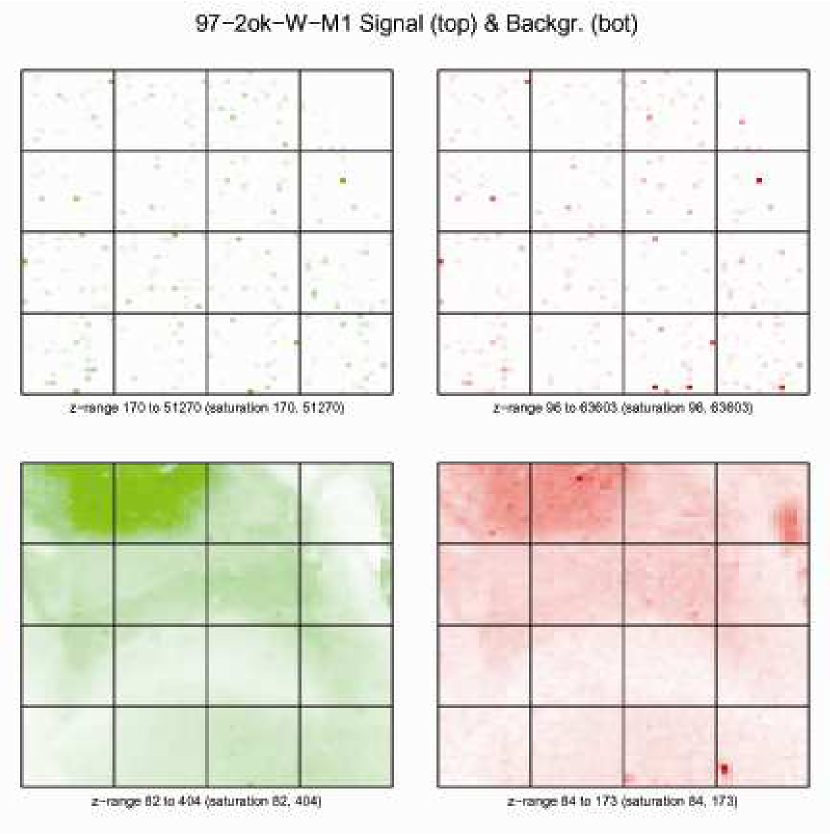


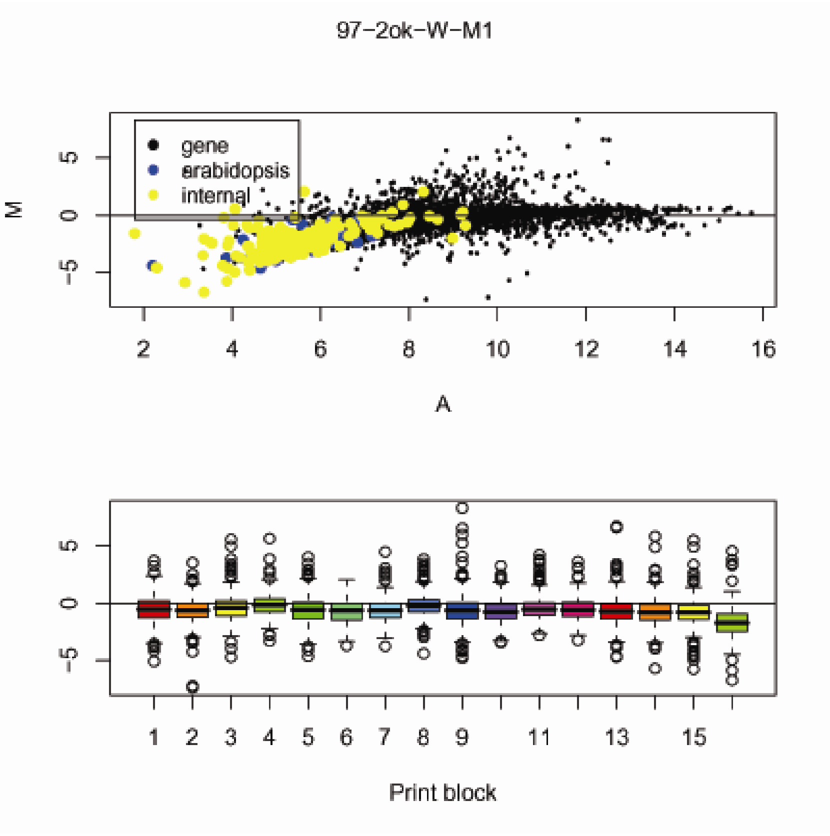
B. DIAGNÒSTICS INICIALS

Imatges utilitzades pel diagnòstic de les dades inicials sense corregir. Per cadascun dels microxips podem veure:

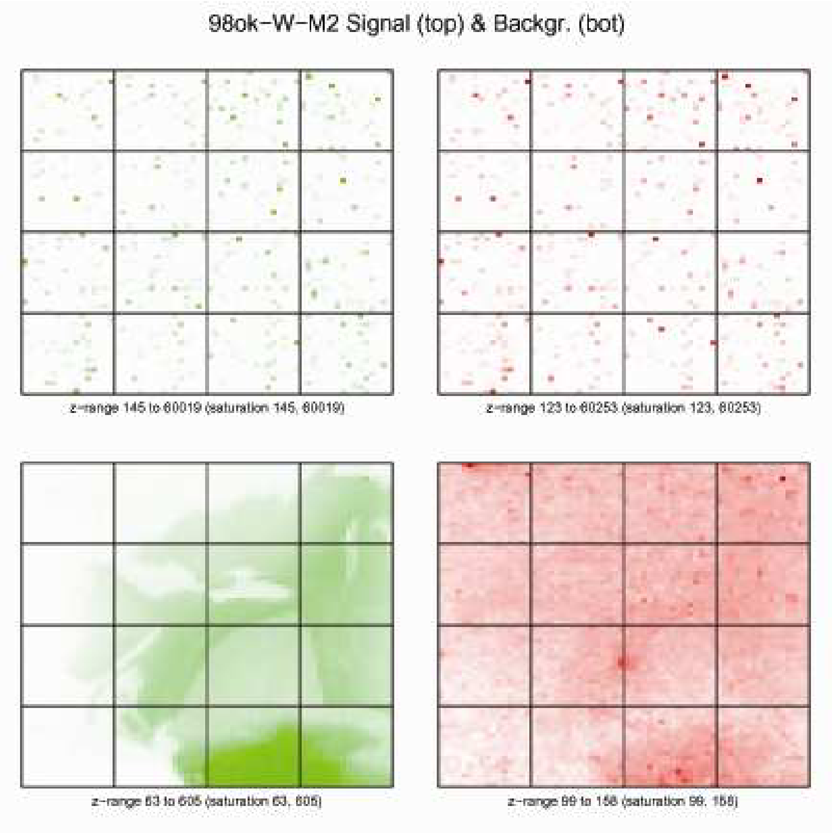
5. "Image plots" de la senyal pels dos canals (verd i vermell) en els dos requadres superiors;
6. per sota podem veure els "Image plots" del soroll de fons pels dos canals;
7. "M-A plots" on es representa la intensitat de cada punt en funció del valor relatiu de l'expressió pels gens (punts negres), pels controls (punts grocs), i pels controls d'*Arabidopsis thaliana* (punts blaus);
8. a la part inferior, "Boxplots" que mostren la distribució dels punts de cada sector del microxip.

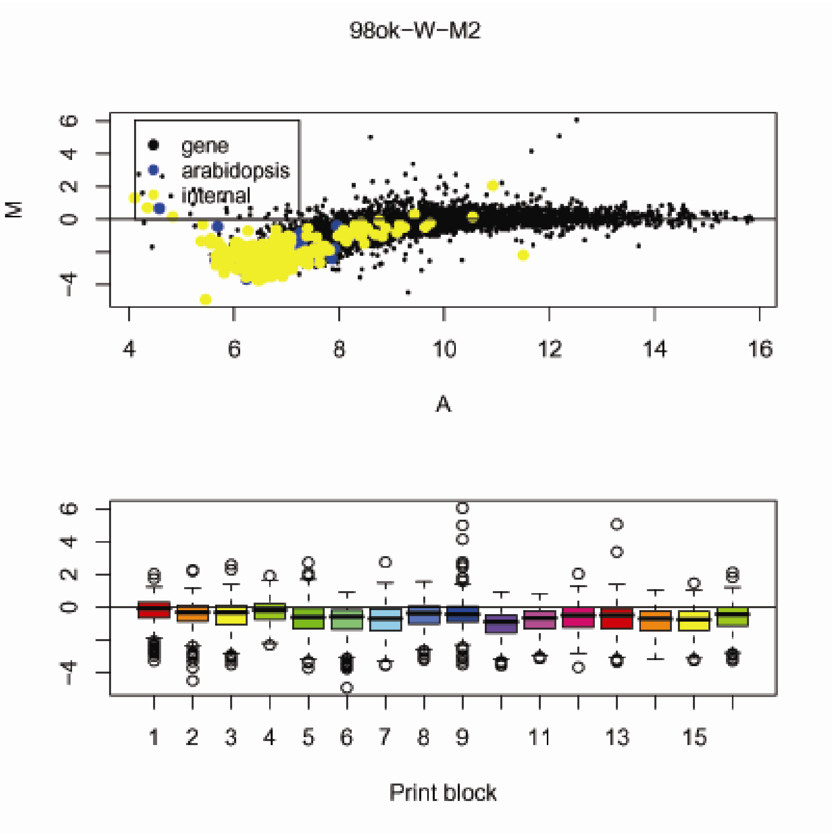
1-W-M1


97−2ok−W−M1 Signal (top) & Backgr. (bot)
z−range 170 to 51270 (saturation 170, 51270)
z−range 96 to 63603 (saturation 96, 63603)
z−range 82 to 404 (saturation 82, 404)
z−range 84 to 173 (saturation 84, 173)


97−2ok−W−M1
gene
arabidopsis
internal
M
5
0
−5
2
4
6
8
10
12
14
16
A
5
0
−5
1
2
3
4
5
6
7
8
9
11
13
15
Print block

2-W-M2


98ok−W−M2 Signal (top) & Backgr. (bot)
z−range 145 to 60019 (saturation 145, 60019)
z−range 123 to 60253 (saturation 123, 60253)
z−range 63 to 605 (saturation 63, 605)
z−range 99 to 158 (saturation 99, 158)


98ok−W−M2
gene
arabidopsis
internal
M
−4
0
2
4
6
4
6
8
10
12
14
16
A
−4
0
2
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6
1
2
3
4
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6
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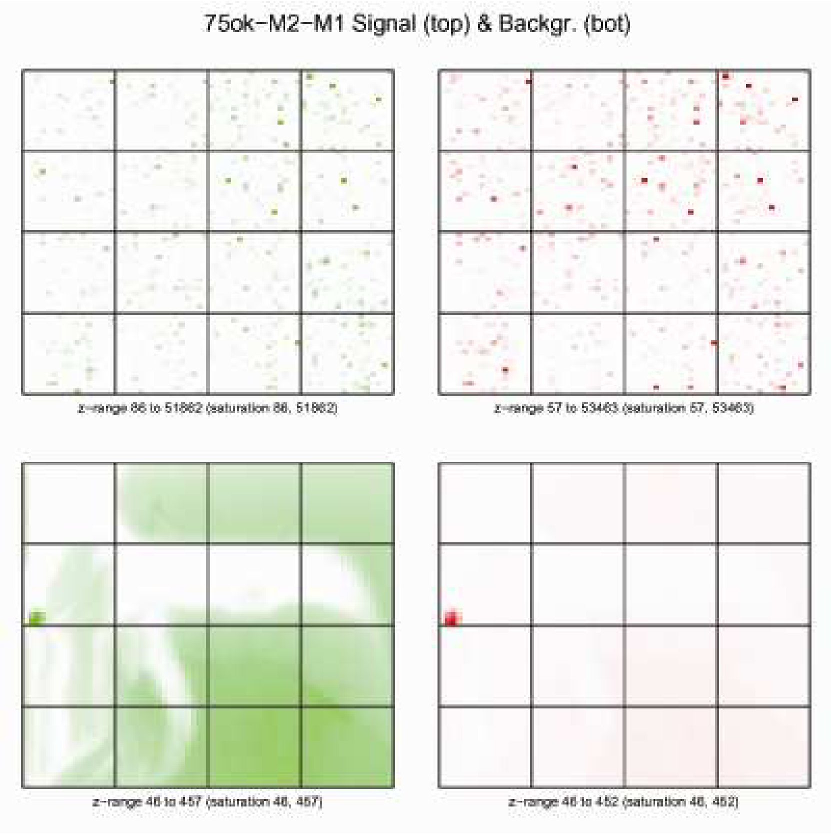
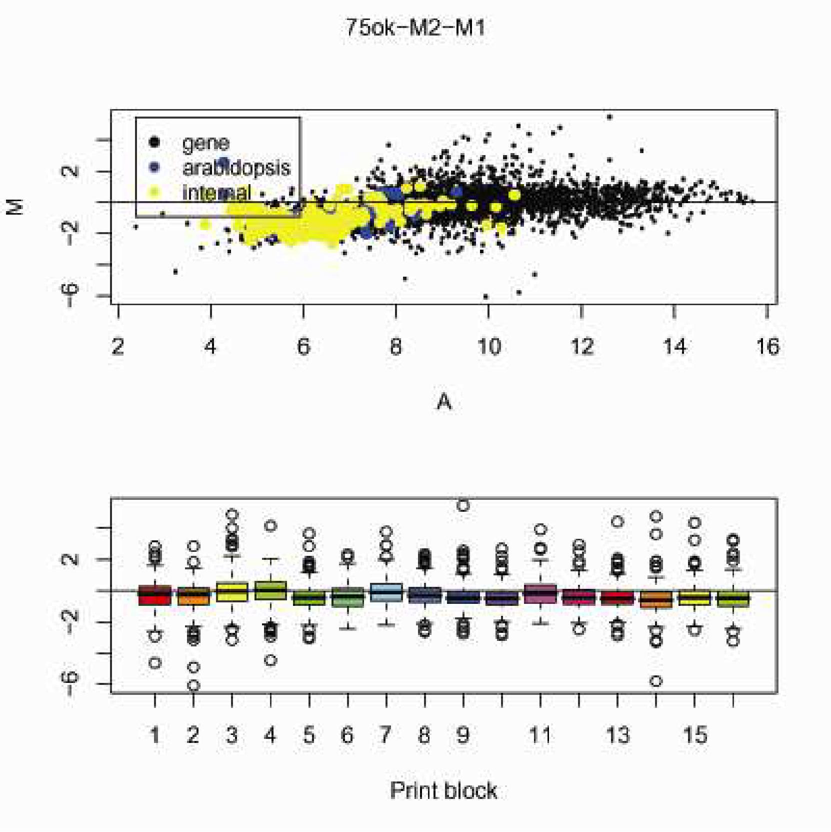
8
9
11
13
15
Print block

3-M2-M1


75ok−M2−M1 Signal (top) & Backgr. (bot)
z−range 86 to 51862 (saturation 86, 51862)
z−range 57 to 53463 (saturation 57, 53463)
z−range 46 to 457 (saturation 46, 457)
z−range 46 to 452 (saturation 46, 452)


75ok−M2−M1
gene
arabidopsis
internal
M
2
−2
−6
2
4
6
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12
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16
A
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6
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11
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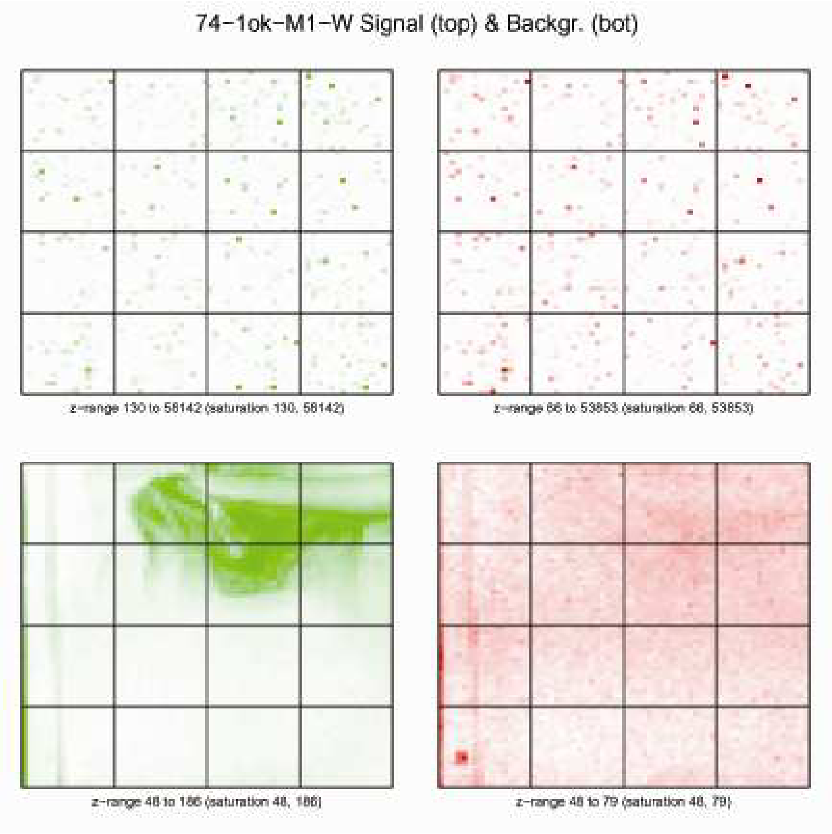
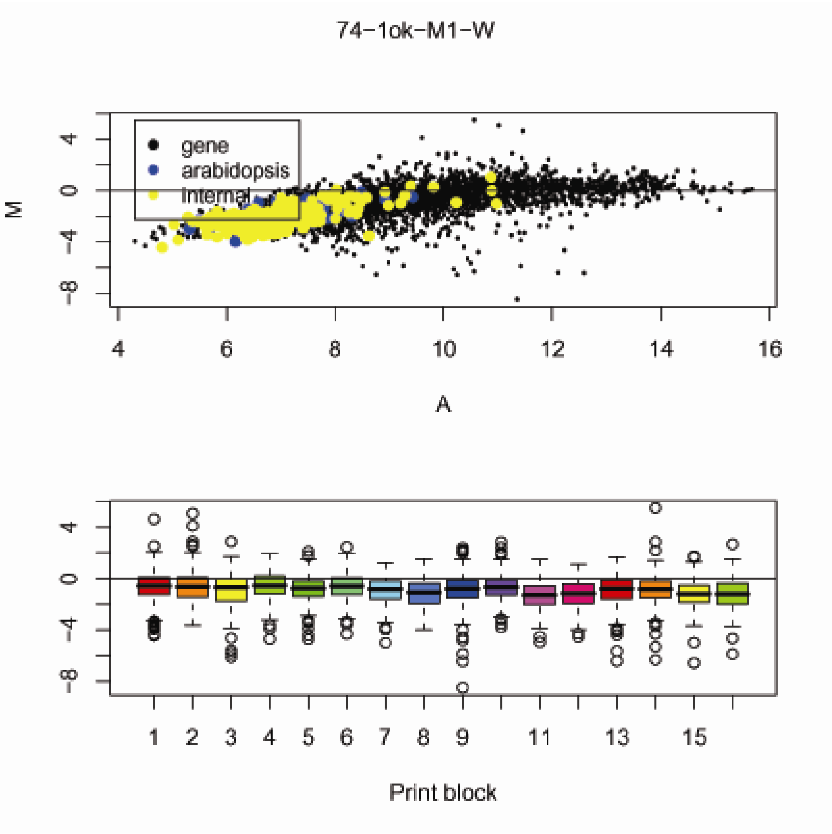
15
Print block

4M1-W


74−1ok−M1−W Signal (top) & Backgr. (bot)
z−range 130 to 58142 (saturation 130, 58142)
z−range 66 to 53853 (saturation 66, 53853)
z−range 48 to 186 (saturation 48, 186)
z−range 48 to 79 (saturation 48, 79)


74−1ok−M1−W
gene
arabidopsis
internal
M
4
0
−4
−8
A
4
6
8
10
12
14
16
4
0
−4
−8
1
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7
8
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11
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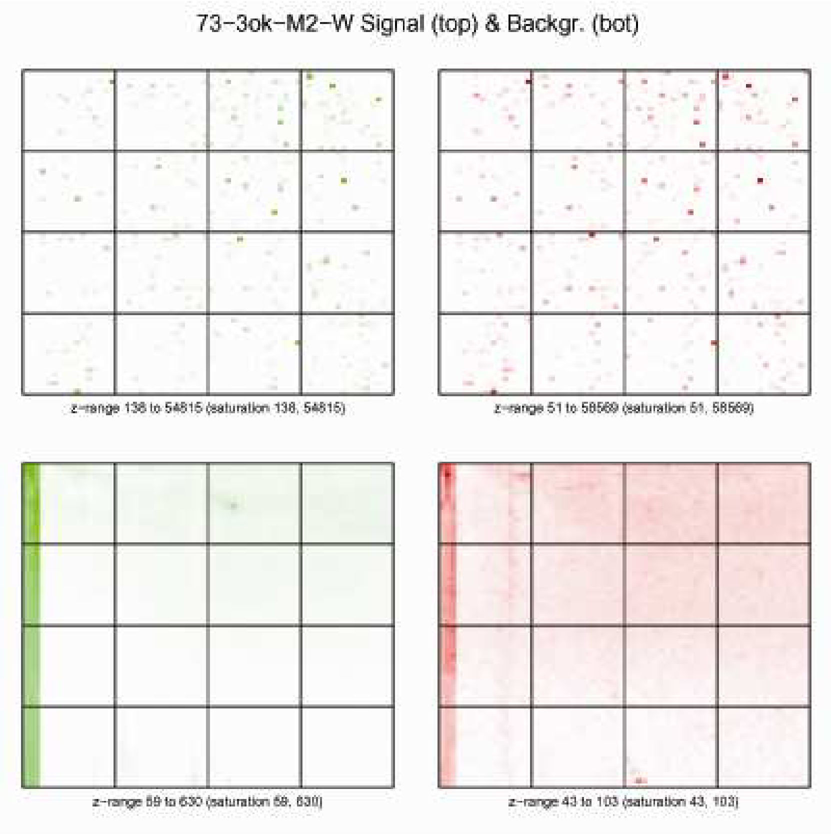
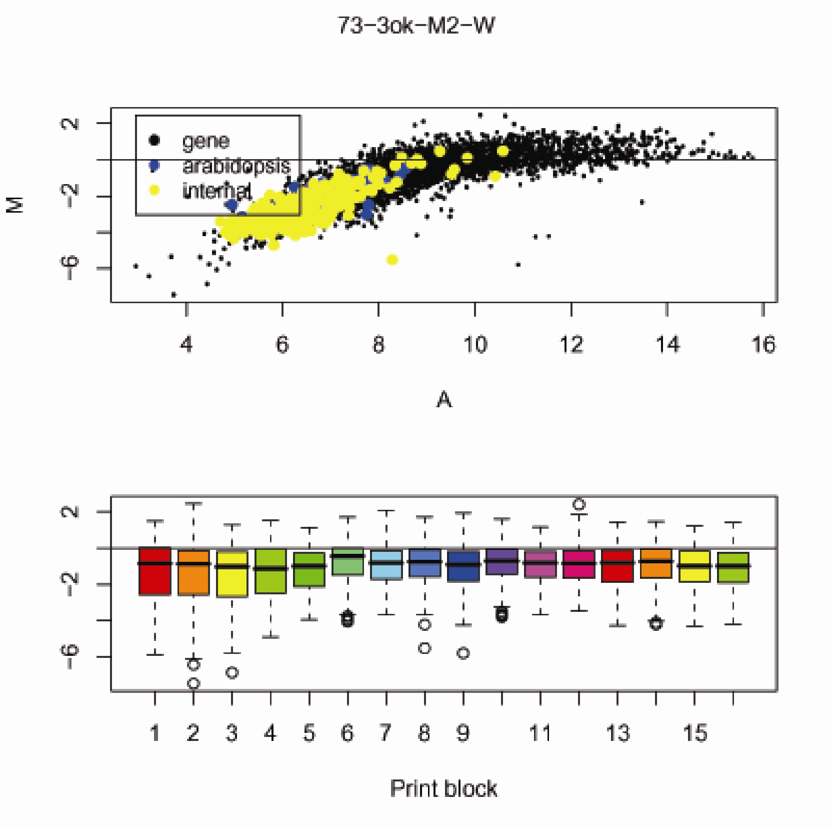
15
Print block

5-M1-W


73−3ok−M2−W Signal (top) & Backgr. (bot)
z−range 138 to 54815 (saturation 138, 54815)
z−range 51 to 58569 (saturation 51, 58569)
z−range 59 to 630 (saturation 59, 630)
z−range 43 to 103 (saturation 43, 103)


73−3ok−M2−W
gene
arabidopsis
internal
M
2
−2
−6
4
6
8
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12
14
16
A
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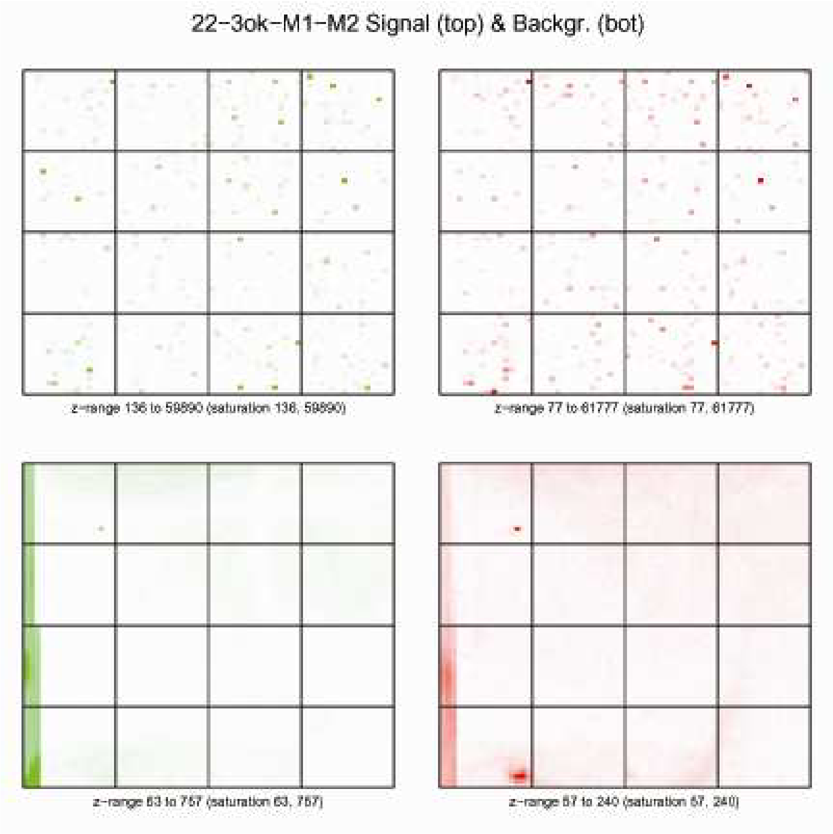
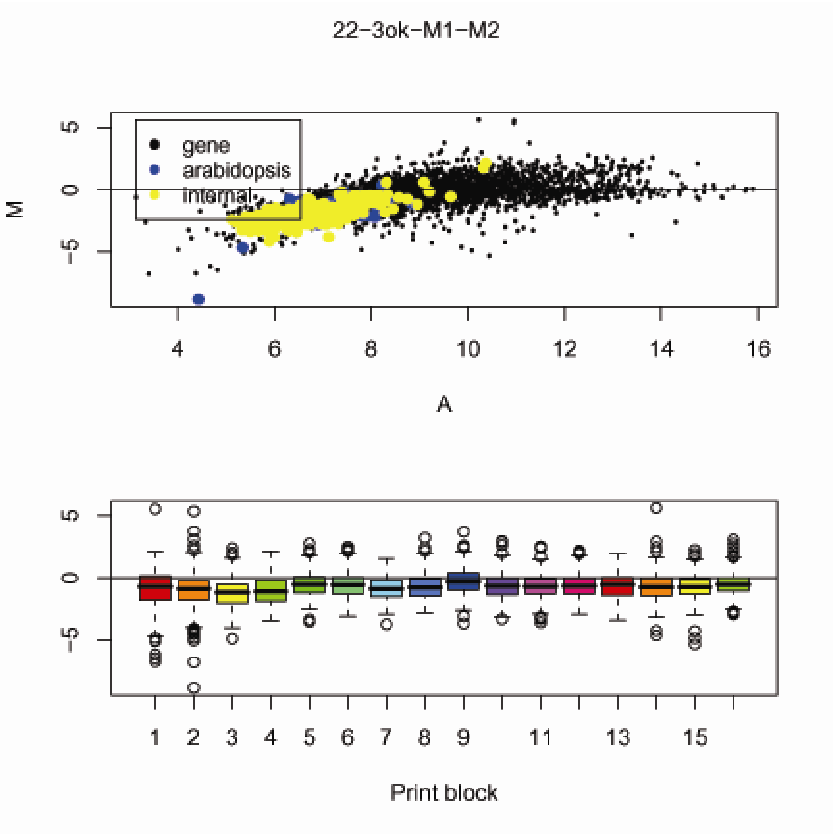
Print block

6-M1-M2


22−3ok−M1−M2 Signal (top) & Backgr. (bot)
z−range 136 to 59890 (saturation 136, 59890)
z−range 77 to 61777 (saturation 77, 61777)
z−range 63 to 757 (saturation 63, 757)
z−range 57 to 240 (saturation 57, 240)


22−3ok−M1−M2
gene
arabidopsis
internal
M
5
0
−5
4
6
8
10
12
14
16
A
5
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−5
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6
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11
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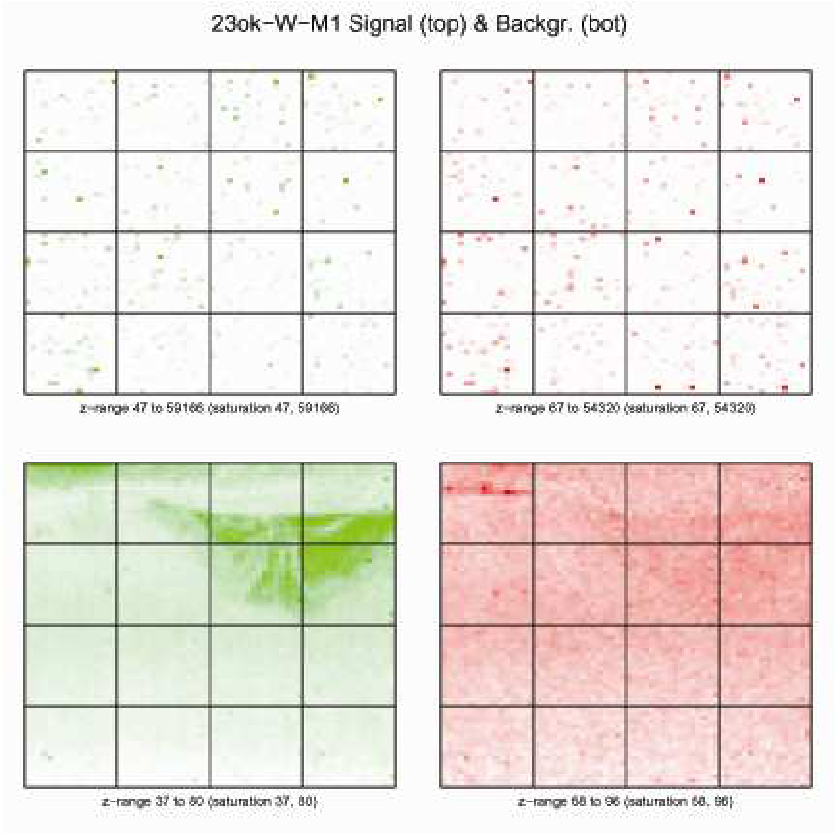
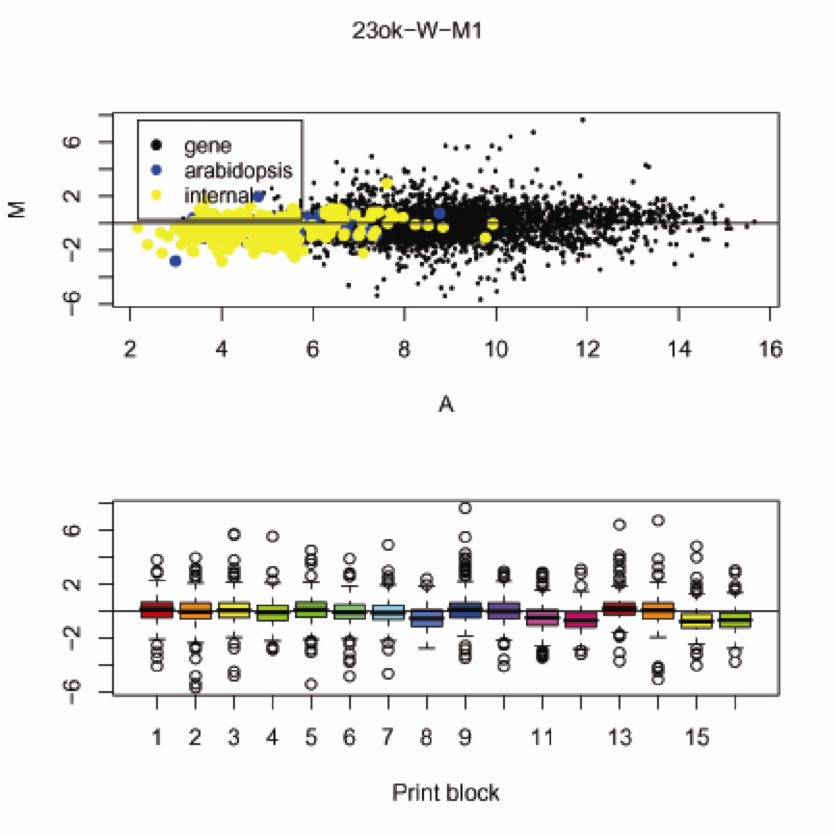
15
Print block

7-W-M1


23ok−W−M1 Signal (top) & Backgr. (bot)
z−range 47 to 59166 (saturation 47, 59166)
z−range 67 to 54320 (saturation 67, 54320)
z−range 37 to 80 (saturation 37, 80)
z−range 58 to 96 (saturation 58, 96)


23ok−W−M1
gene
arabidopsis
internal
M
−6
−2
2
6
2
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6
8
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14
16
A
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11
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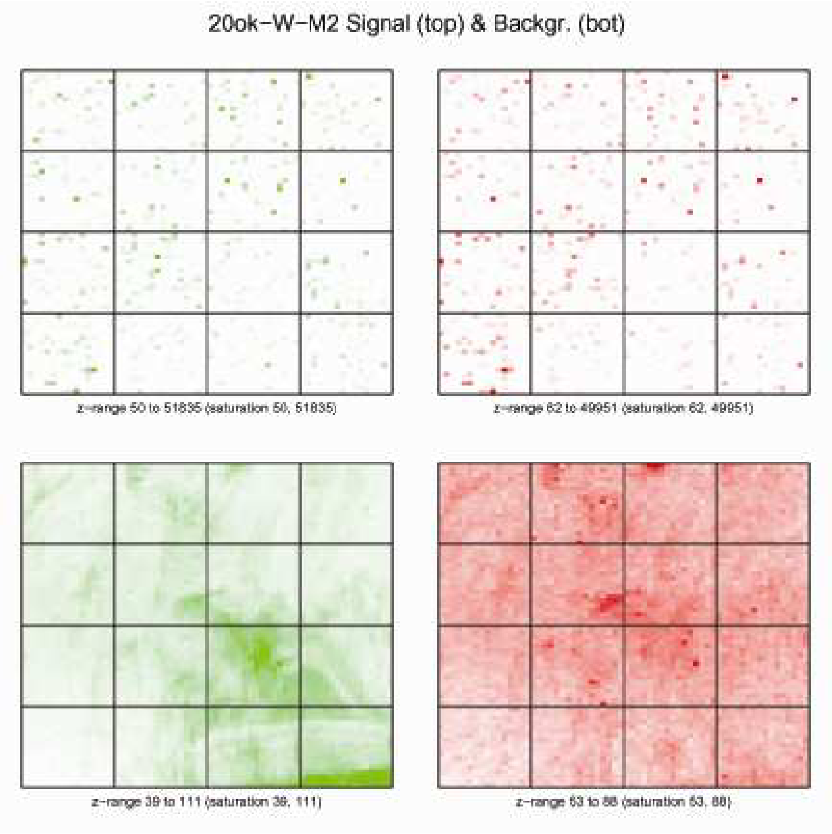
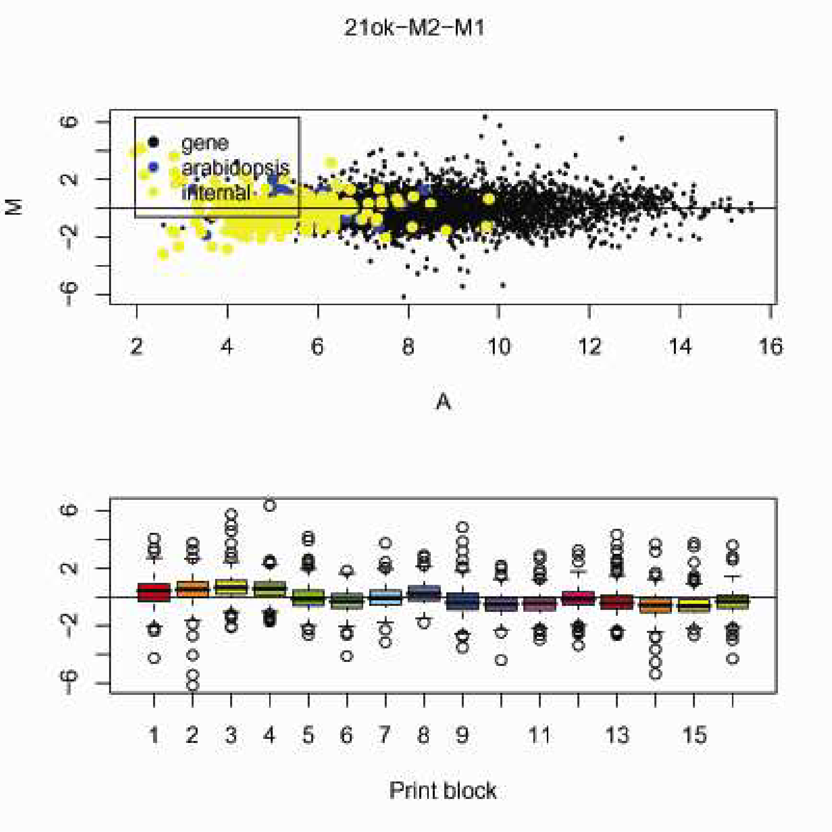
15
Print block

8-W-M2


20ok−W−M2 Signal (top) & Backgr. (bot)
z−range 50 to 51835 (saturation 50, 51835)
z−range 62 to 49951 (saturation 62, 49951)
z−range 39 to 111 (saturation 39, 111)
z−range 53 to 88 (saturation 53, 88)


21ok−M2−M1
gene
arabidopsis
internal
M
6
2
−2
−6
2
4
6
8
10
12
14
16
A
6
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−2
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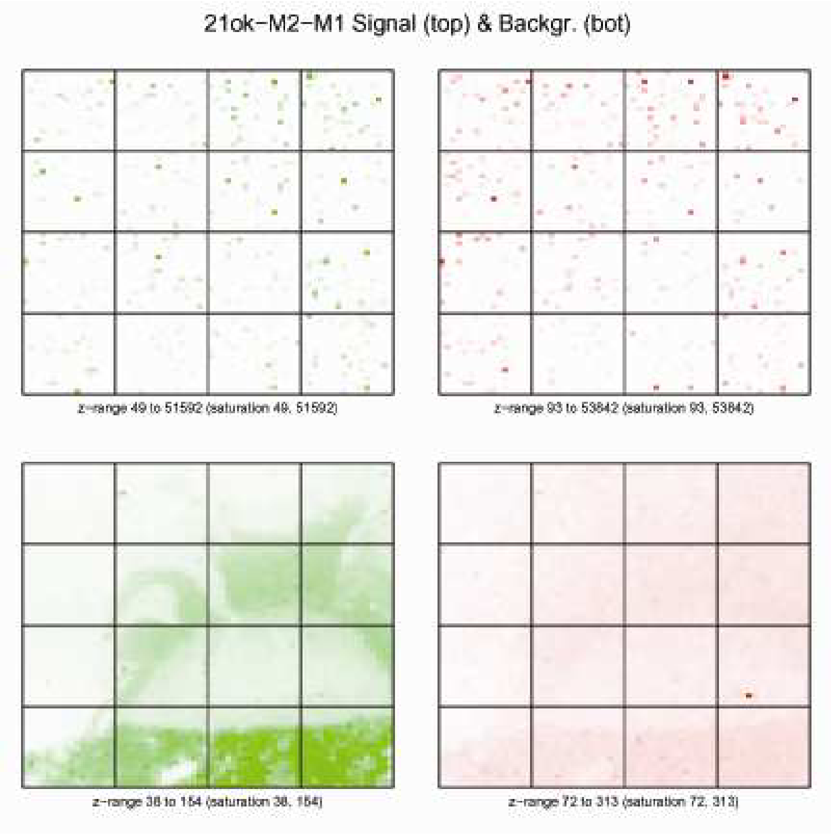
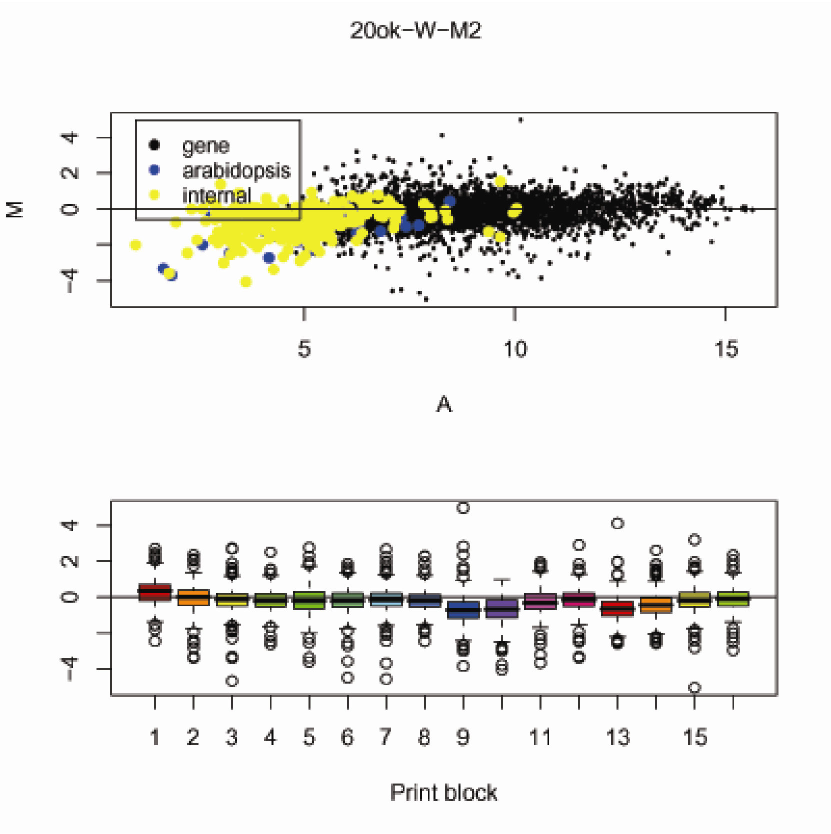
11
13
15
Print block

9-M2-M1


21ok−M2−M1 Signal (top) & Backgr. (bot)
z−range 49 to 51592 (saturation 49, 51592)
z−range 93 to 53842 (saturation 93, 53842)
z−range 38 to 154 (saturation 38, 154)
z−range 72 to 313 (saturation 72, 313)


20ok−W−M2
gene
arabidopsis
internal
M
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−4
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10
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A
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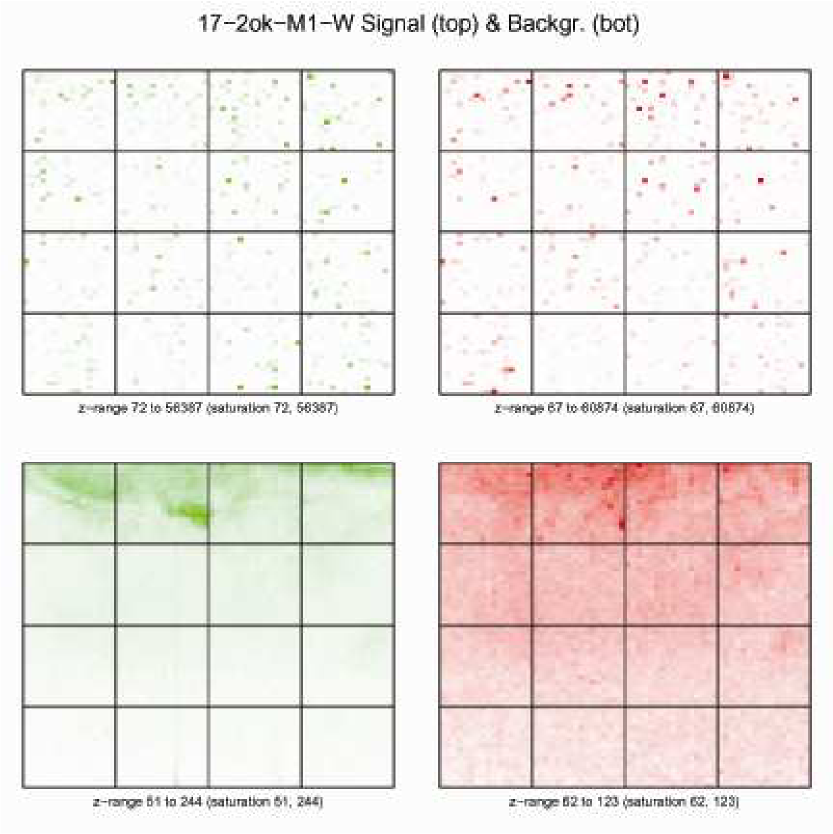
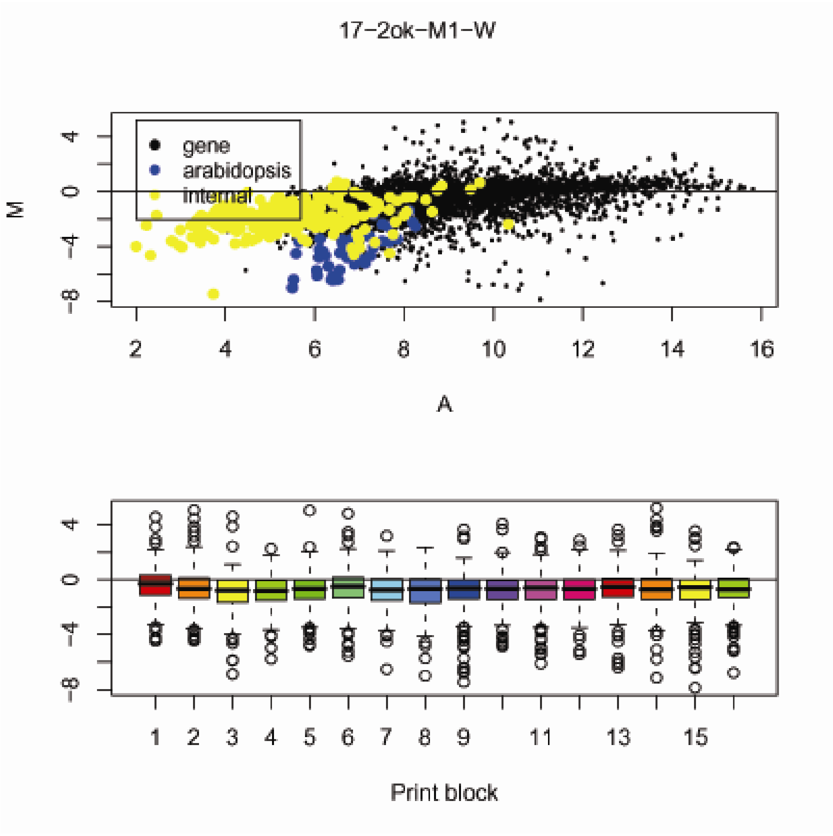
15
Print block

10-M1-W


17−2ok−M1−W Signal (top) & Backgr. (bot)
z−range 72 to 56387 (saturation 72, 56387)
z−range 67 to 60874 (saturation 67, 60874)
z−range 51 to 244 (saturation 51, 244)
z−range 62 to 123 (saturation 62, 123)


17−2ok−M1−W
gene
arabidopsis
internal
M
4
0
−4
−8
2
4
6
8
10
12
14
16
A
4
0
−4
−8
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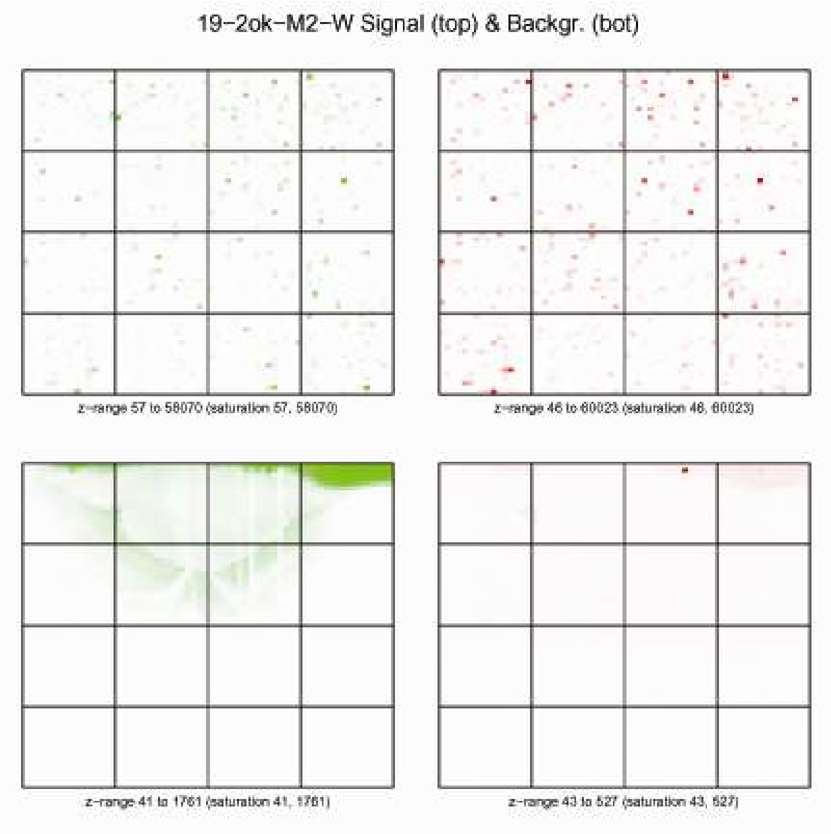
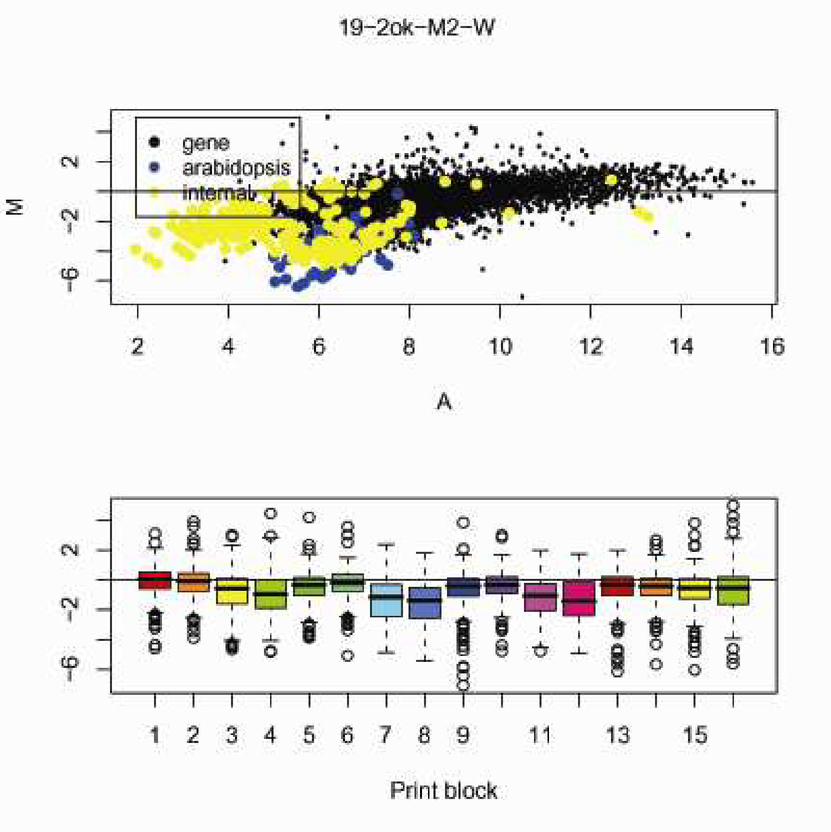
15
Print block

11-M2-W


19−2ok−M2−W Signal (top) & Backgr. (bot)
z−range 57 to 58070 (saturation 57, 58070)
z−range 46 to 60023 (saturation 46, 60023)
z−range 41 to 1761 (saturation 41, 1761)
z−range 43 to 527 (saturation 43, 527)


19−2ok−M2−W
gene
arabidopsis
internal
M
2
−2
−6
2
4
6
8
10
12
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16
A
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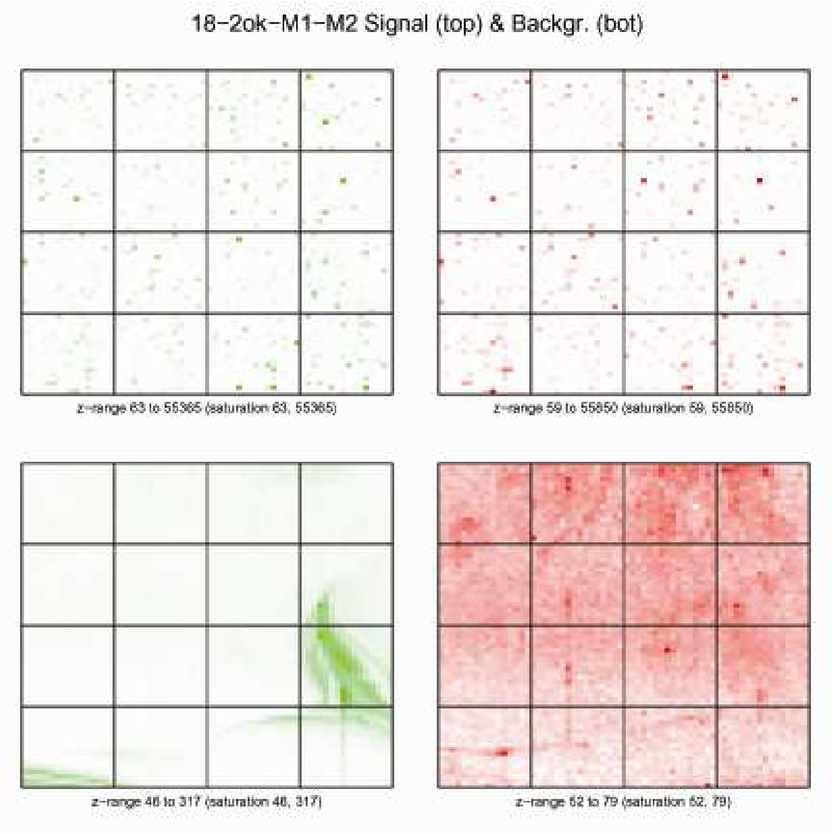
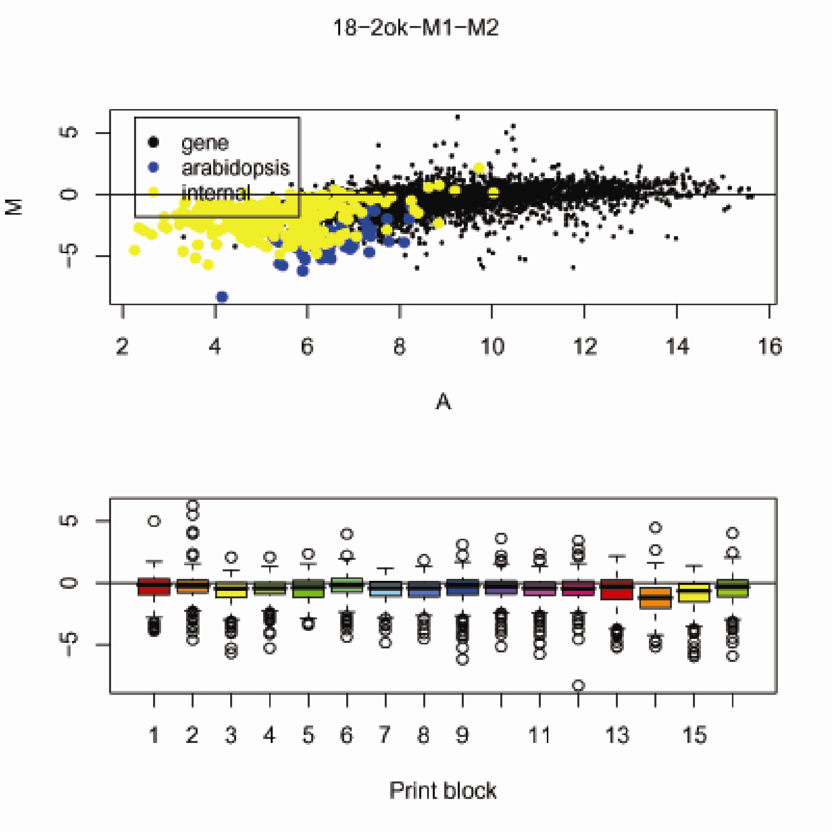
Print block

12-M1-M2

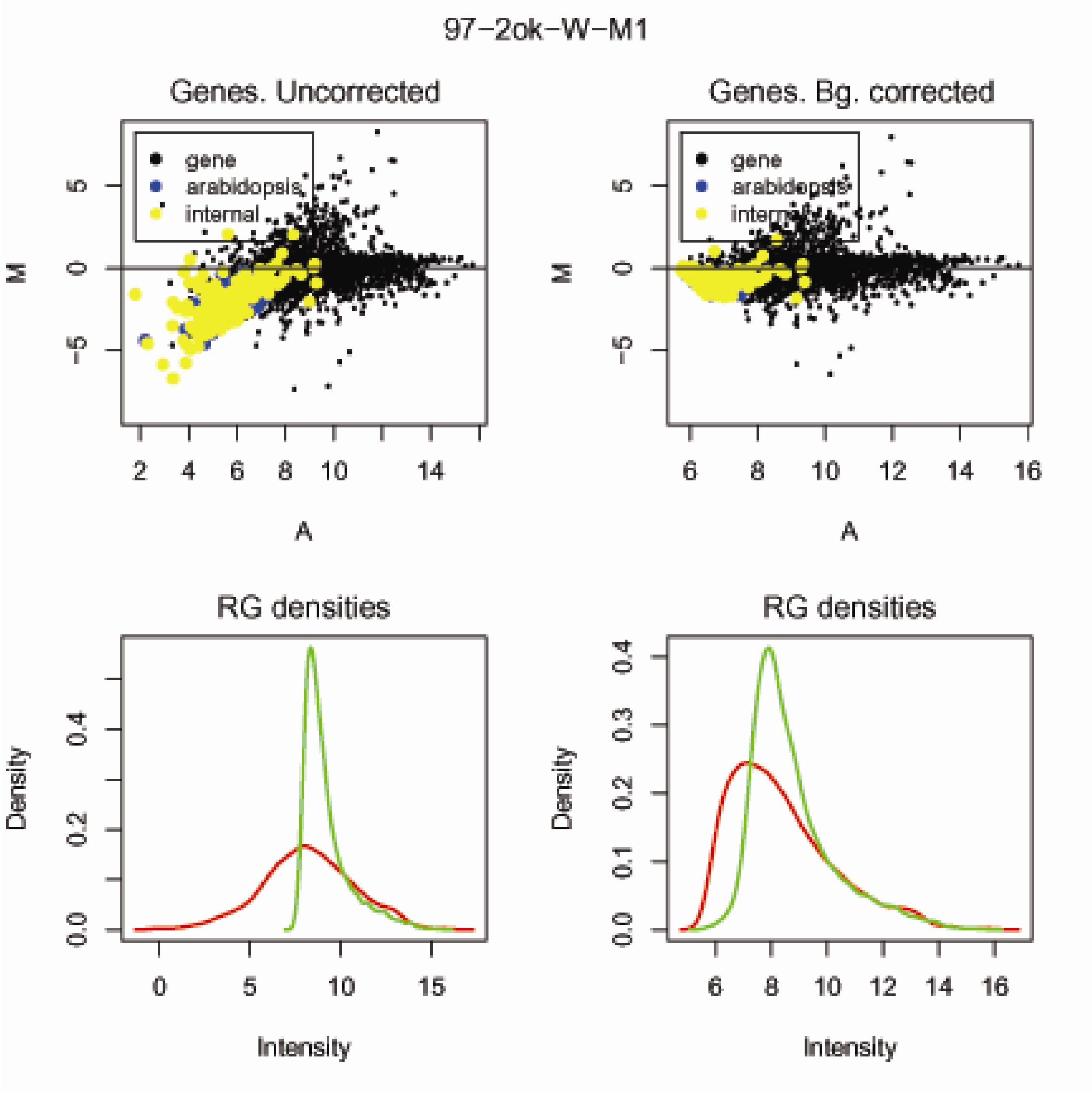

18−2ok−M1−M2 Signal (top) & Backgr. (bot)
z−range 63 to 55365 (saturation 63, 55365)
z−range 59 to 55850 (saturation 59, 55850)
z−range 46 to 317 (saturation 46, 317)
z−range 52 to 79 (saturation 52, 79)


18−2ok−M1−M2
● gene
● arabidopsis
● internal
M
5
0
−5
2
4
6
8
10
12
14
16
A
1
2
3
4
5
6
7
8
9
11
13
15
Print block

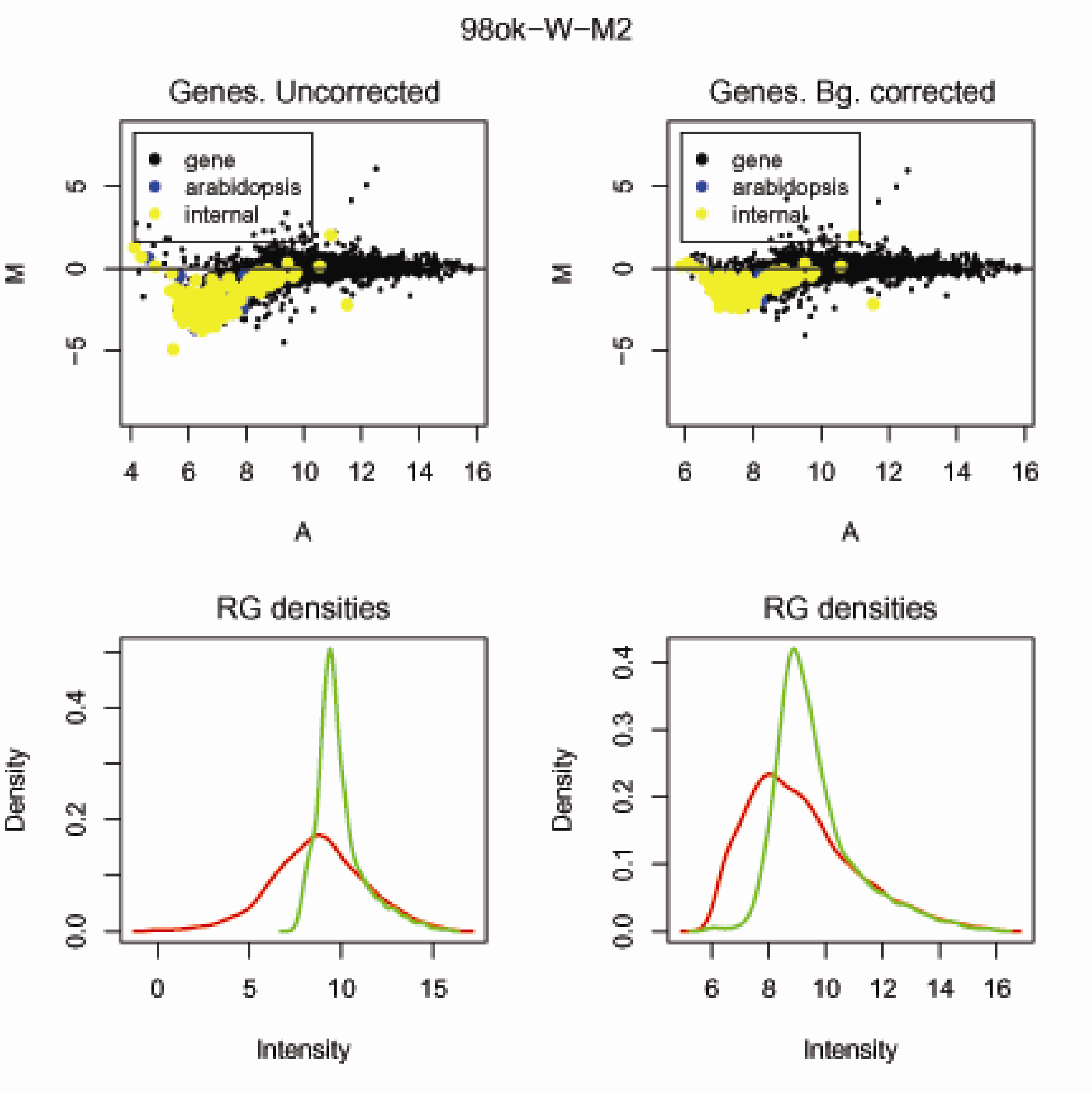
C. RESULTATS DE L'ELIMINACIÓ DEL SOROLL DE FONS

En aquestes gràfiques podem veure el resultat de l'eliminació del soroll de fons per cadascun dels microxips. Es tracta de "M-A plots" (part superior) dels gens abans (esquerra) i després (dreta) de l'eliminació del soroll de fons; els punts negres corresponen als gens, els grocs als controls interns i els blaus als controls d'Arabidopsis thaliana. A la part inferior hi trobem gràfiques de la distribució dels punts en funció de la intensitat per cada canal , abans (esquerra) i després (dreta) de l'eliminació del soroll de fons.

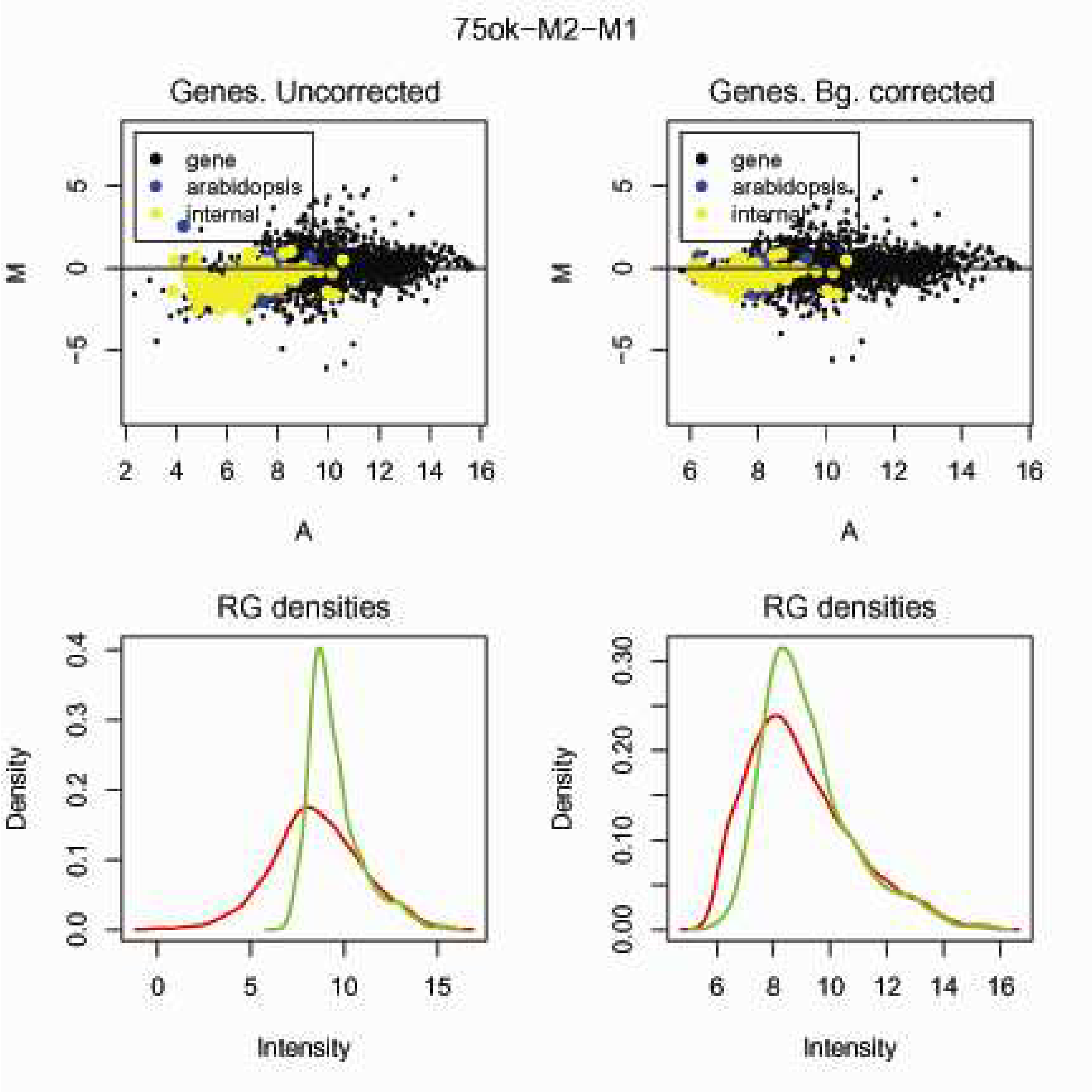
1-W-M1



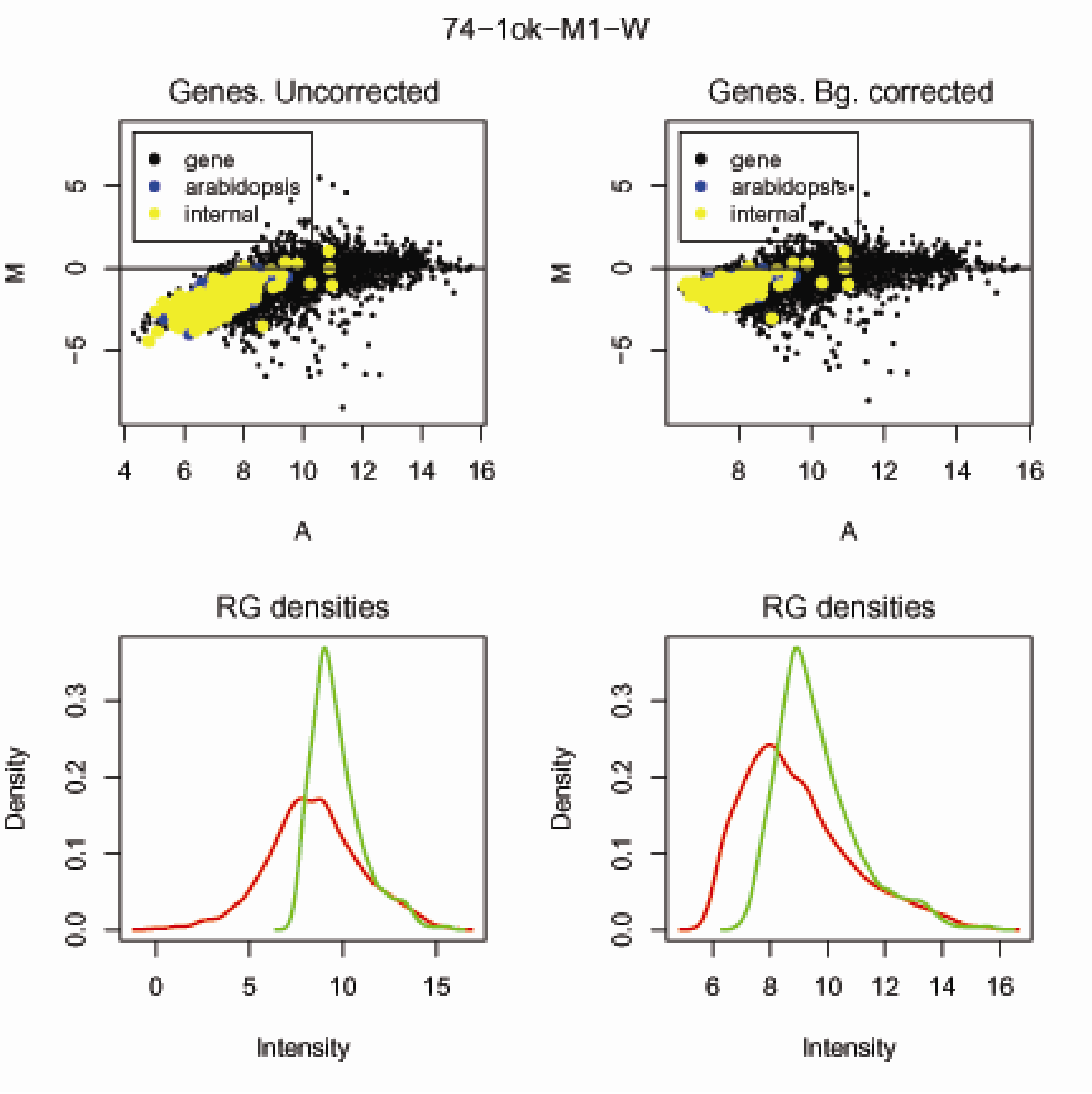
2-W-M2


98ok−W−M2
Genes. Uncorrected
Genes. Bg. corrected
gene
arabidopsis
internal
M
A
5
0
−5
4
6
8
10
12
14
16
RG densities
Density
Intensity
0.0
0.2
0.4
0.1
0.3
0
5
10
15

3-M2-M1


75ok-M2-M1
Genes. Uncorrected
Genes. Bg. corrected
gene
arabidopsis
internal
M
A
5
0
-5
2
4
6
8
10
12
14
16
RG densities
Density
Intensity
0.0
0.1
0.2
0.3
0.4
0.00
0.10
0.20
0.30
0
5
10
15

4-M1-W


74−1ok−M1−W
Genes. Uncorrected
Genes. Bg. corrected
gene
arabidopsis
internal
M
A
5
0
−5
4
6
8
10
12
14
16
RG densities
Density
Intensity
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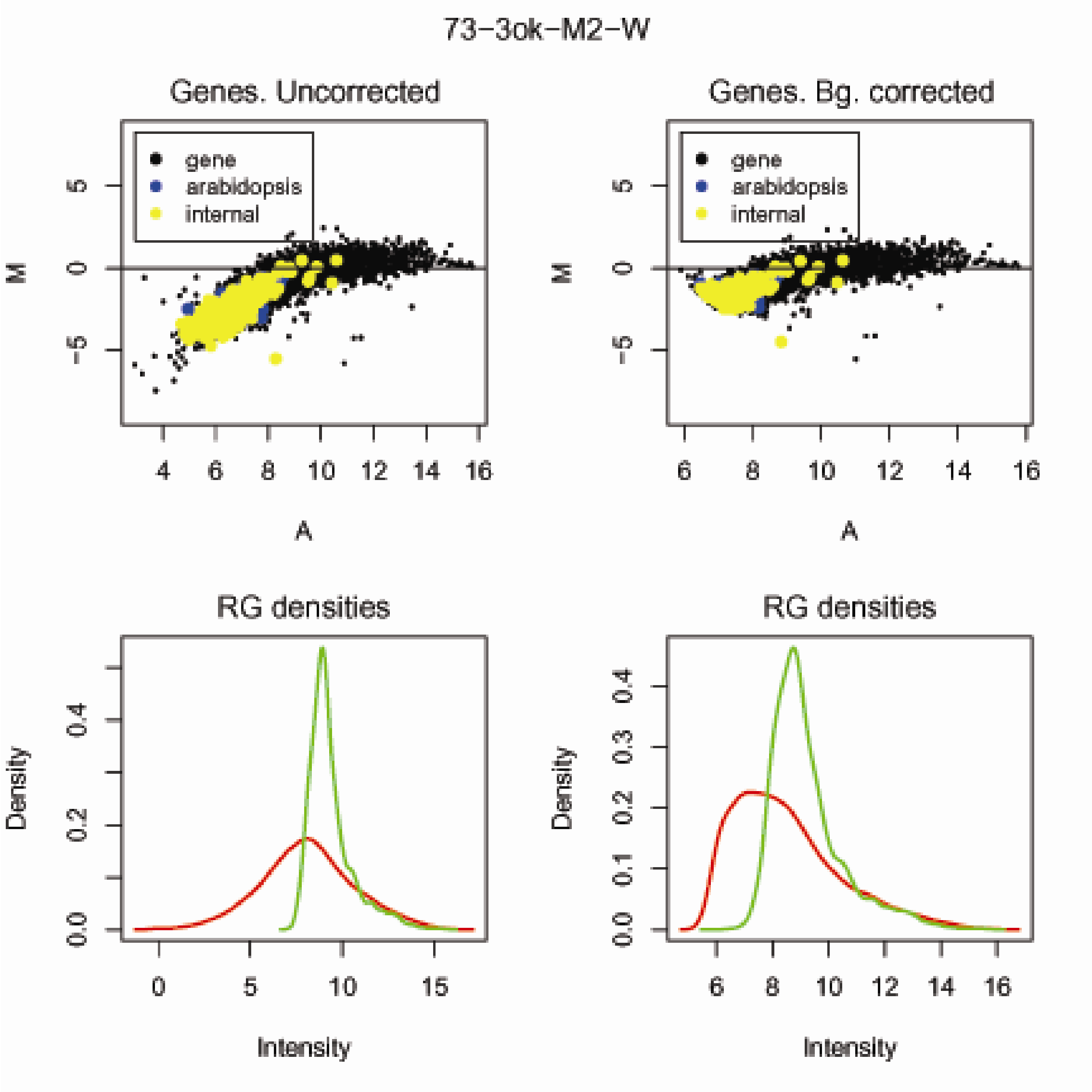
0.1
0.2
0.3
0
5
10
15
6
8
10
12
14
16

5-M2-W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Genes. Uncorrected
Genes. Bg. corrected
● gene
● arabidopsis
● internal
M
A
−5
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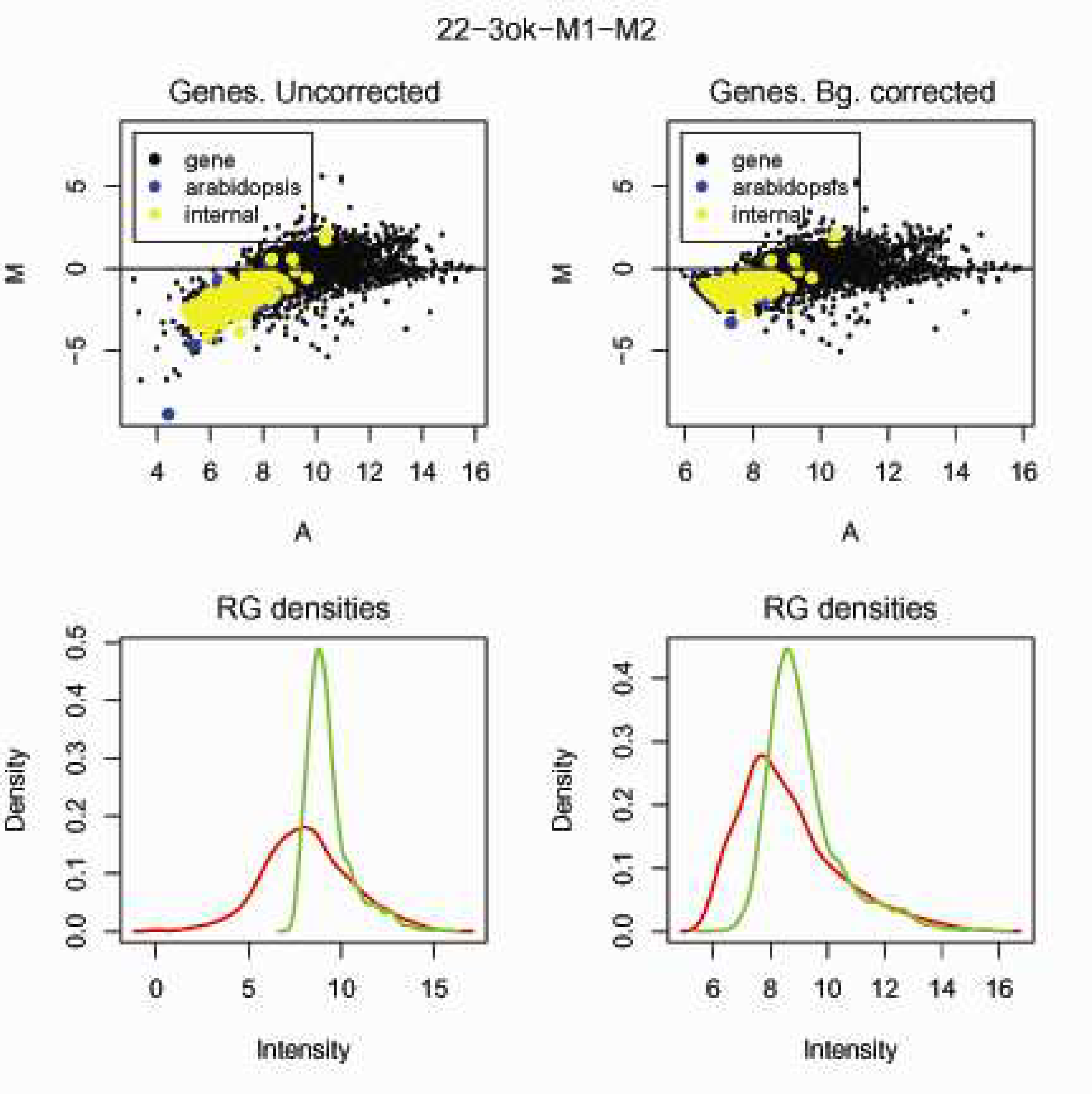
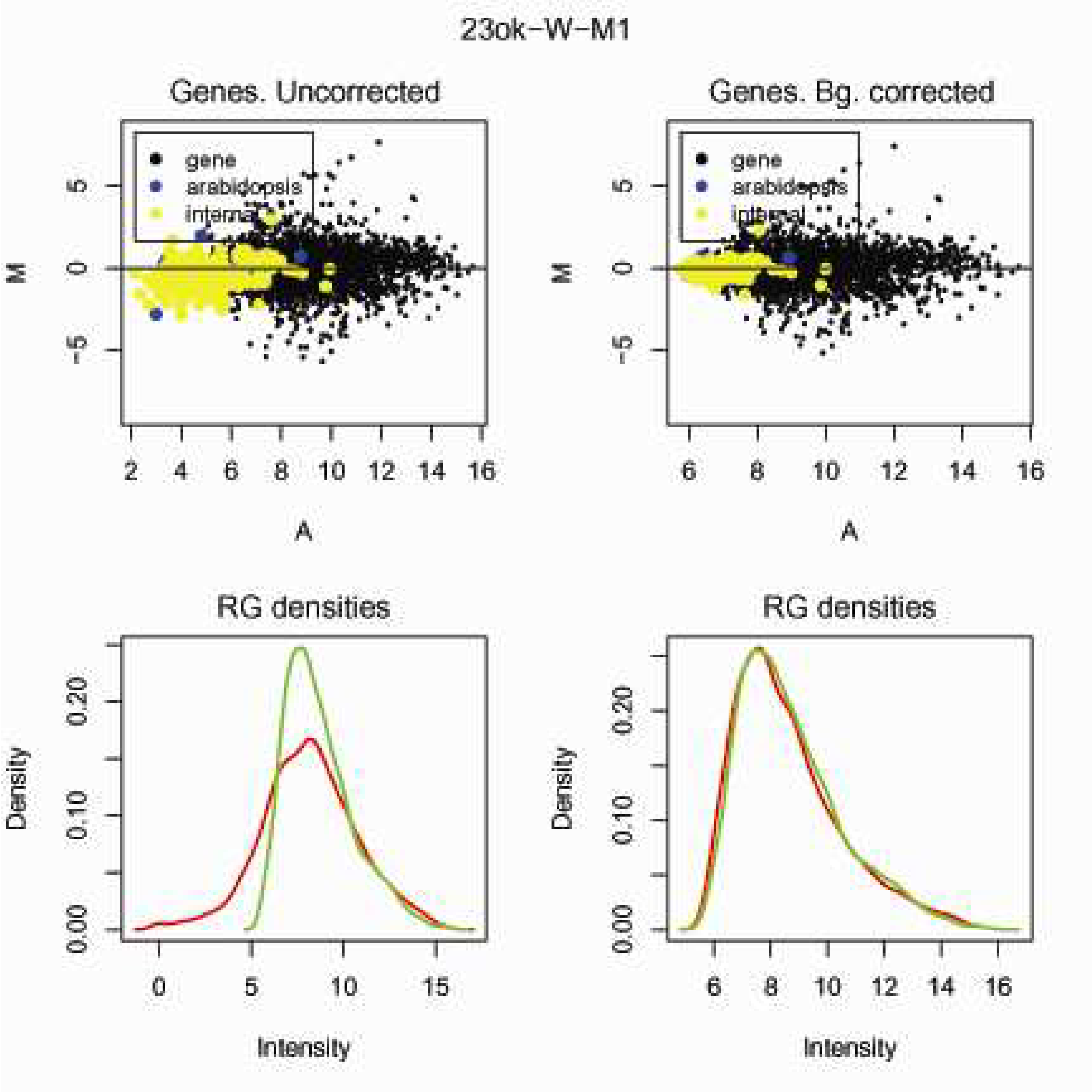
4
6
8
10
12
14
16
RG densities
Density
Intensity
0.0
0.2
0.4
0.1
0.3
0
5
10
15

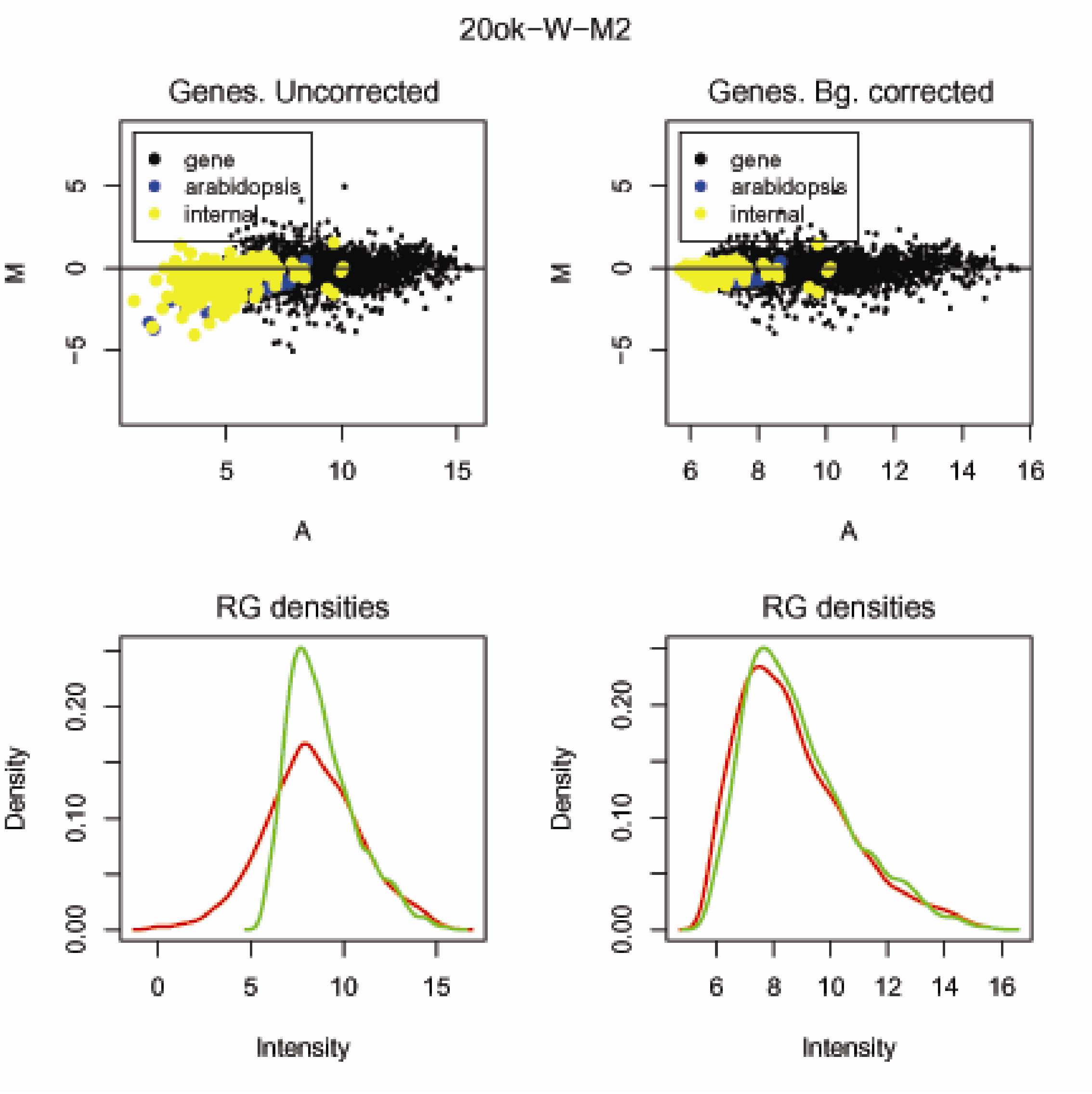
6-M1-M2


22-3ok-M1-M2
Genes. Uncorrected
Genes. Bg. corrected
gene
arabidopsis
internal
M
A
5
0
-5
4
6
8
10
12
14
16
RG densities
Density
Intensity
0.0
0.1
0.2
0.3
0.4
0.5
0
5
10
15

7-W-M1


23ok-W-M1
Genes. Uncorrected
Genes. Bg. corrected
● gene
● arabidopsis
● internal
M
A
5
0
-5
2
4
6
8
10
12
14
16
RG densities
Density
Intensity
0.00
0.10
0.20
0
5
10
15

8-W-M2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Genes. Bg. corrected
● gene
● arabidopsis
● internal
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−5
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10
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6
8
10
12
14
16
RG densities
Density
Intensity
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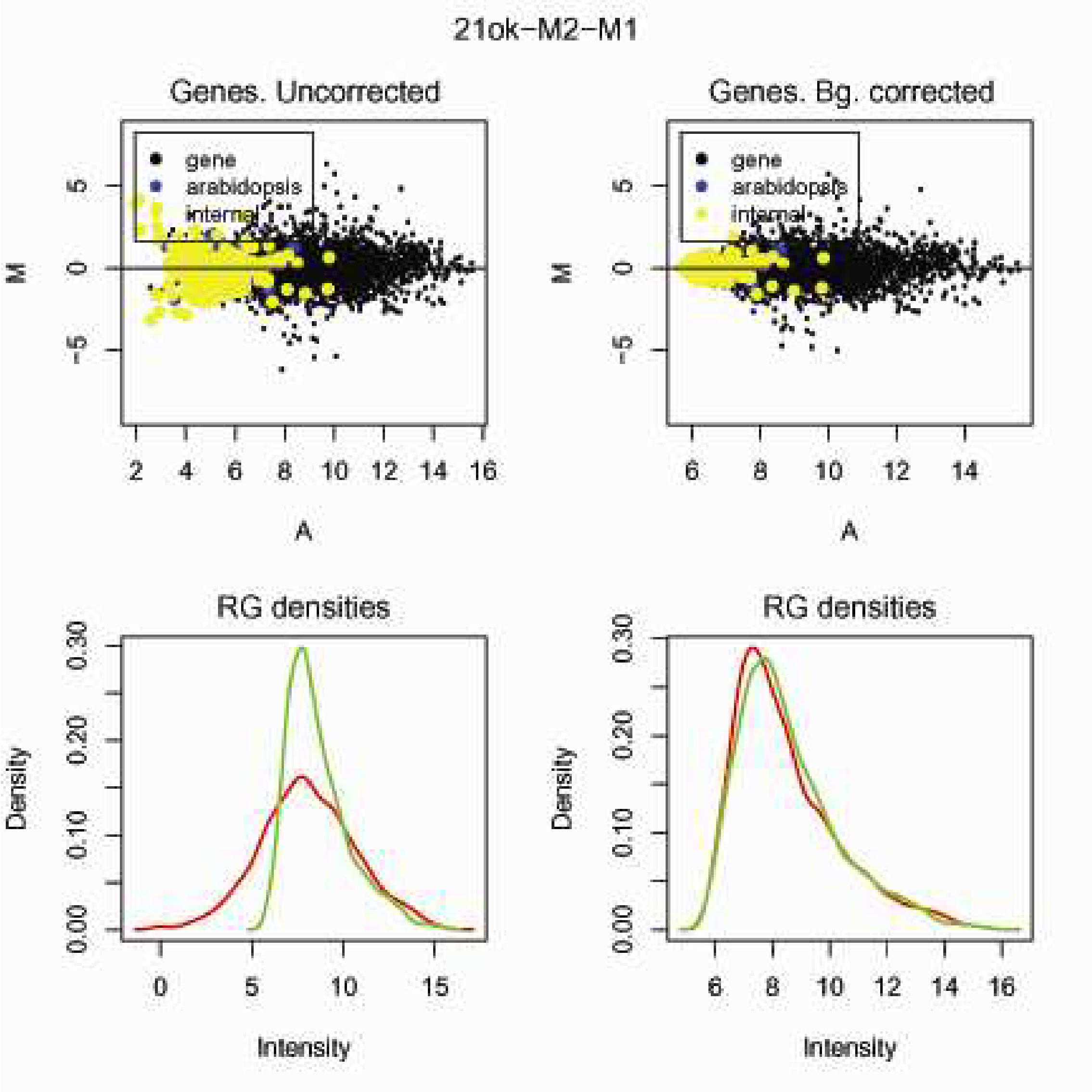
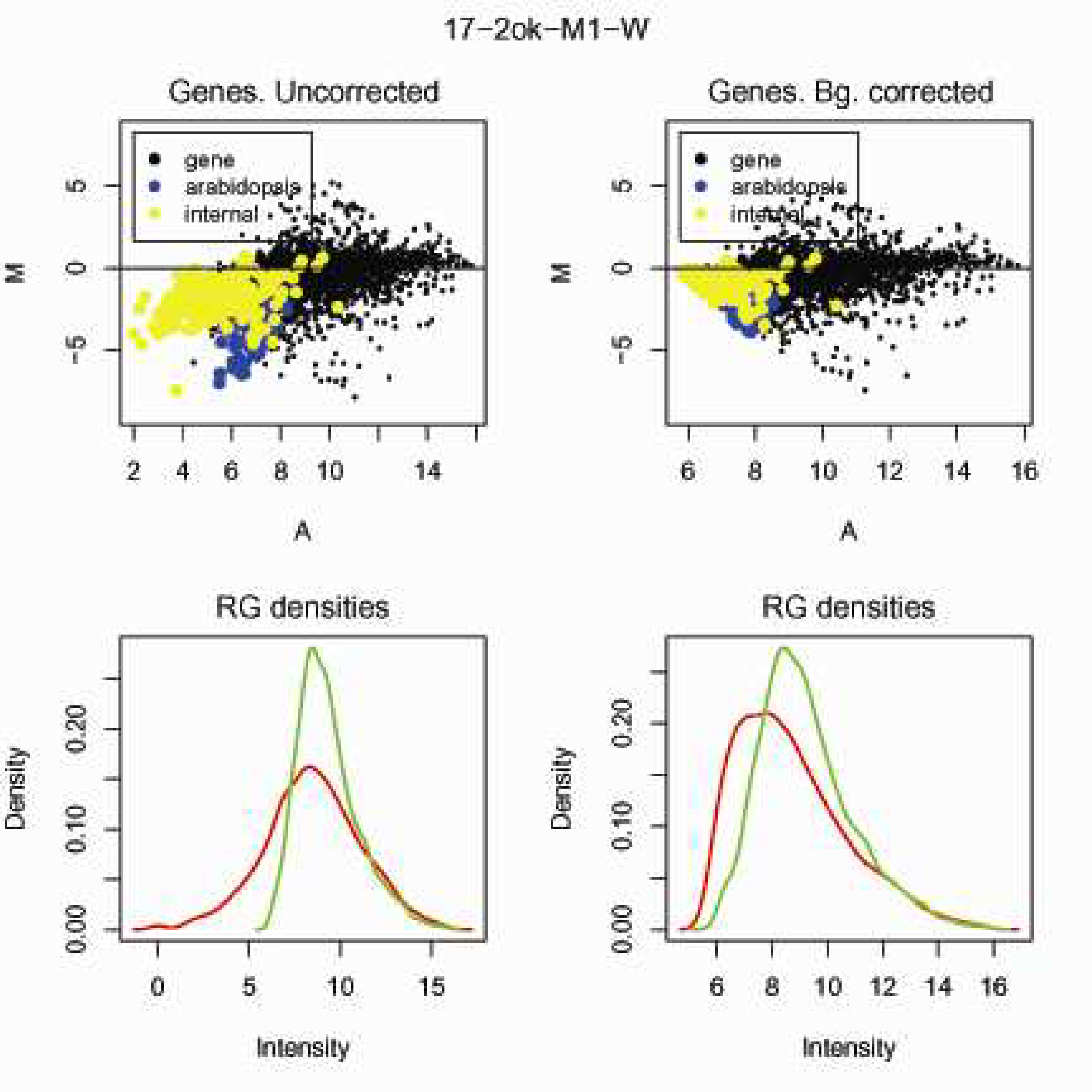
0.10
0.20
0
5
10
15
6
8
10
12
14
16

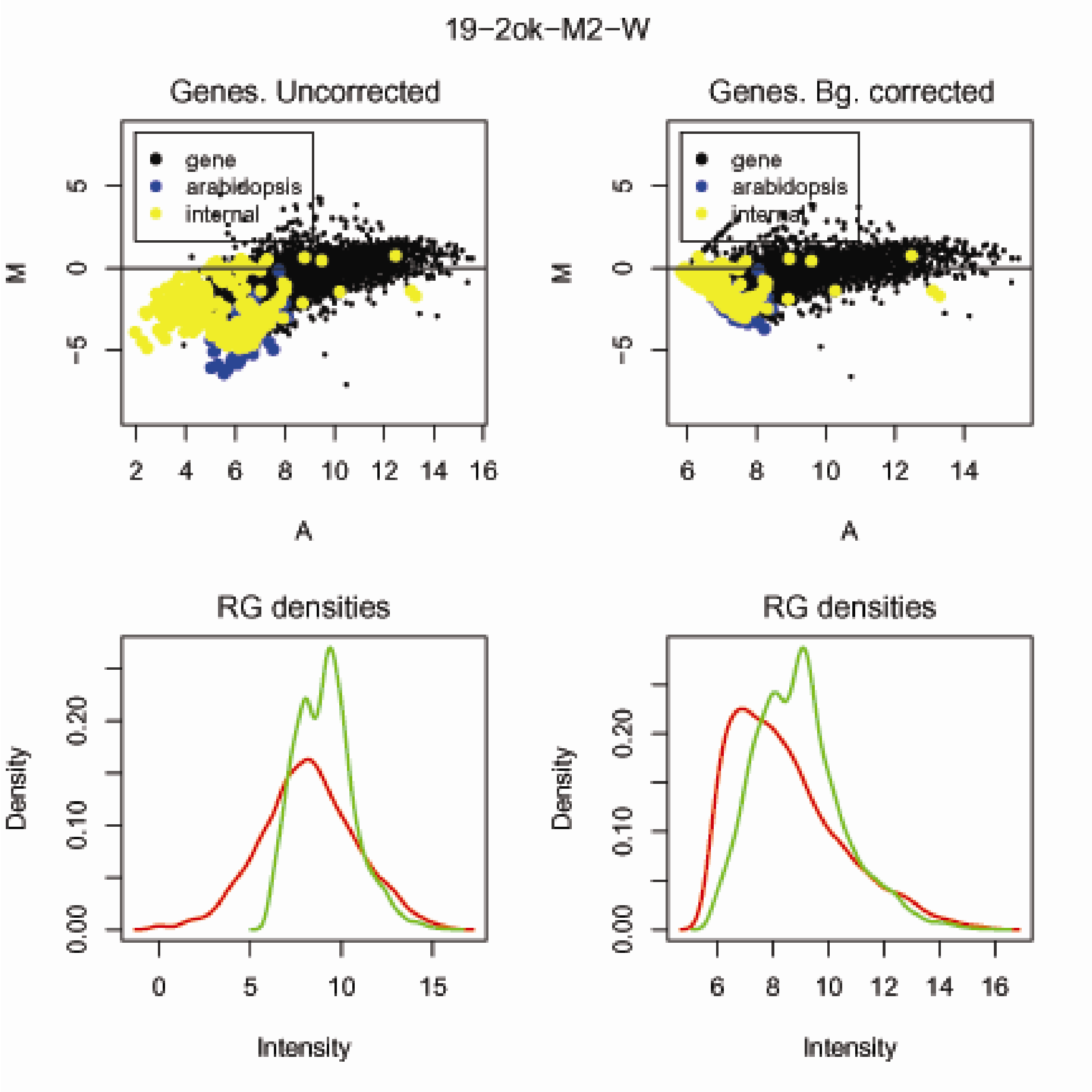
9-M2-M1


21ok-M2-M1
Genes. Uncorrected
Genes. Bg. corrected
gene
arabidopsis
internal
M
-5
0
5
A
2
4
6
8
10
12
14
16
RG densities
Density
0.00
0.10
0.20
0.30
Intensity
0
5
10
15

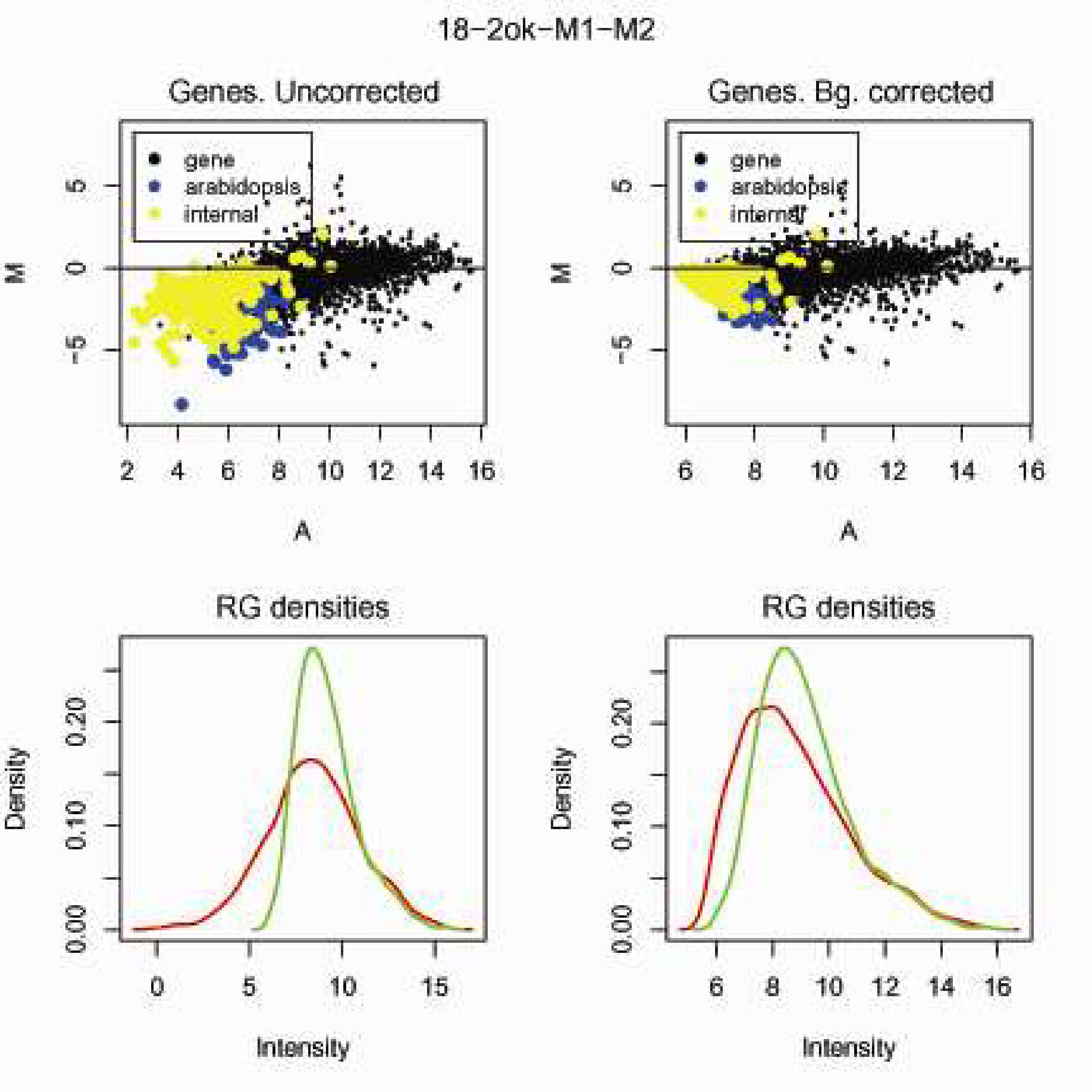
10-M1-W


17−2ok−M1−W
Genes. Uncorrected
Genes. Bg. corrected
gene
arabidopsis
internal
M
A
5
0
−5
2
4
6
8
10
14
12
16
RG densities
Density
Intensity
0.00
0.10
0.20
15

11-M2-W


19−2ok−M2−W
Genes. Uncorrected
Genes. Bg. corrected
gene
arabidopsis
internal
M
A
5
0
−5
2
4
6
8
10
12
14
16
RG densities
Density
Intensity
0.00
0.10
0.20
0
5
10
15

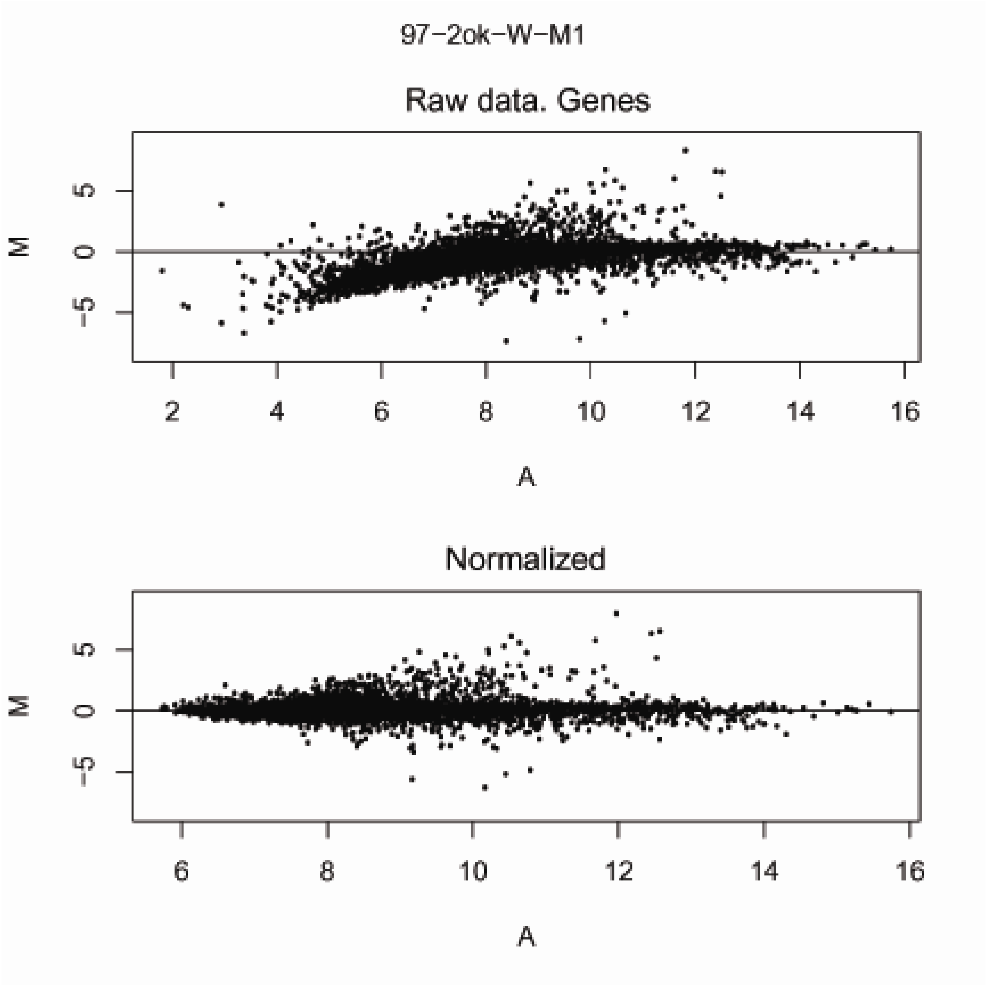
12-M1-M2

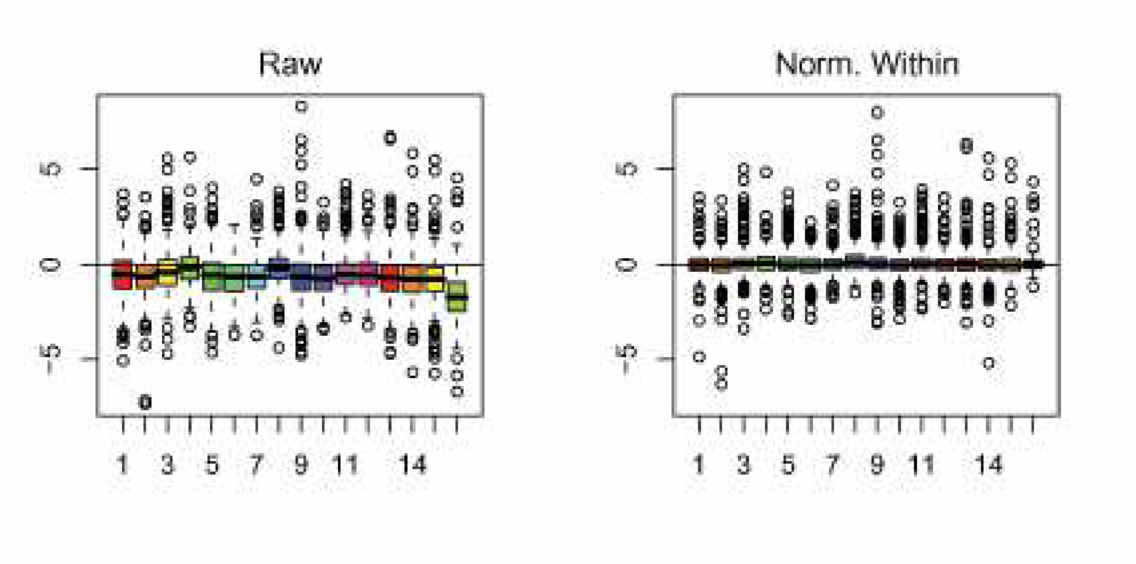

18−2ok−M1−M2
Genes. Uncorrected
Genes. Bg. corrected
gene
arabidopsis
internal
M
A
5
0
−5
2
4
6
8
10
12
14
16
RG densities
Density
Intensity
0.00
0.10
0.20
0
5
10
15

D. RESULTATS DE LA NORMALITZACIÓ

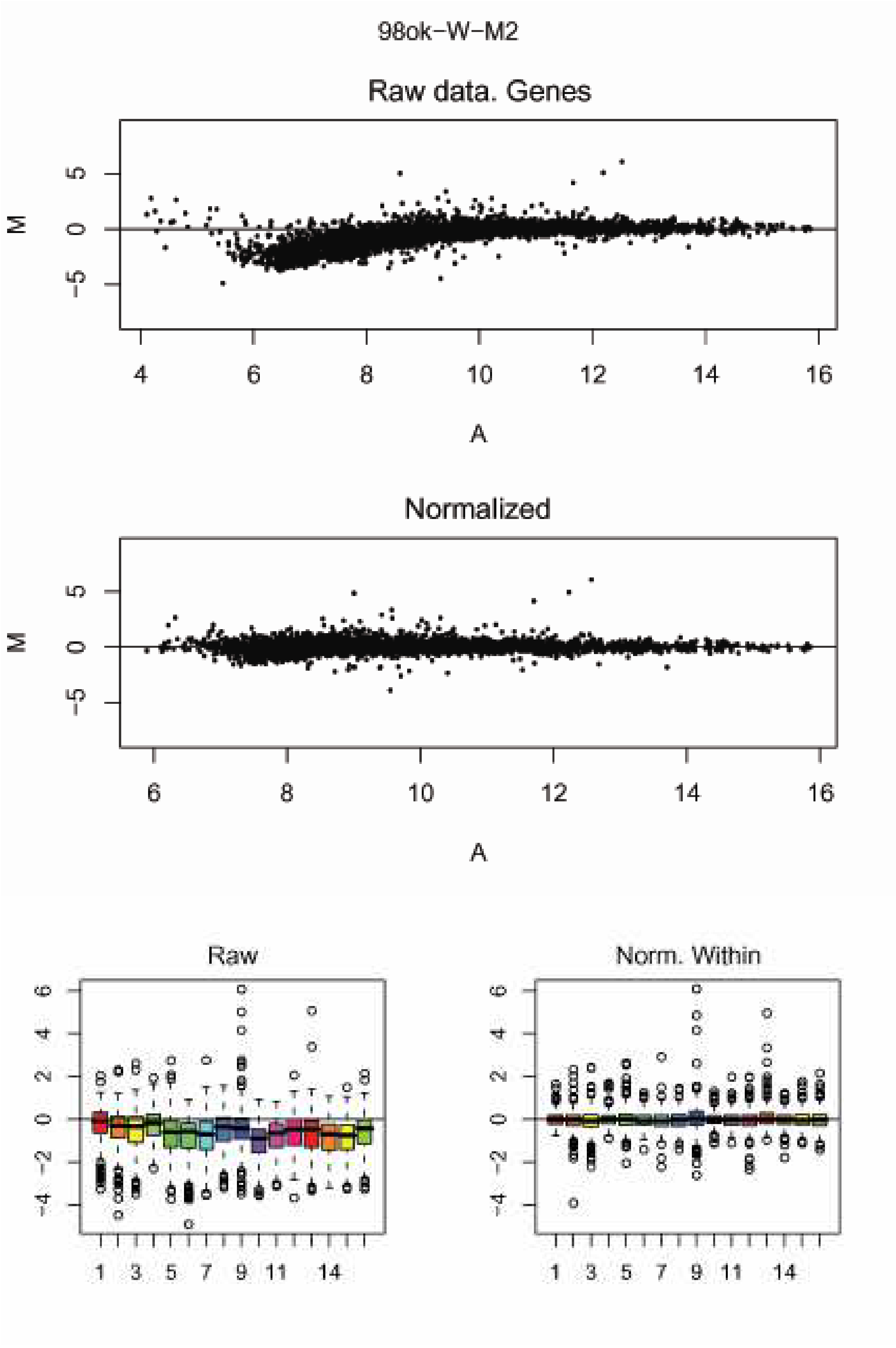
Comparació dels gens abans i després de normalitzar. “M-A plots” dels gen sense normalitzar a la part superior, i normalitzats per sota d’aquests. A la part inferior, “Boxplots” de cada sector del microxip abans (esquerra) i després de normalitzar (dreta).

1-W-M1


97−2ok−W−M1
Raw data. Genes
M
5
0
−5
2
4
6
8
10
12
14
16
A
Normalized
M
5
0
−5
6
8
10
12
14
16
A


Raw
5
0
−5
1
3
5
7
9
11
14
Norm. Within
5
0
−5
1
3
5
7
9
11
14

2-W-M2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−5
4
6
8
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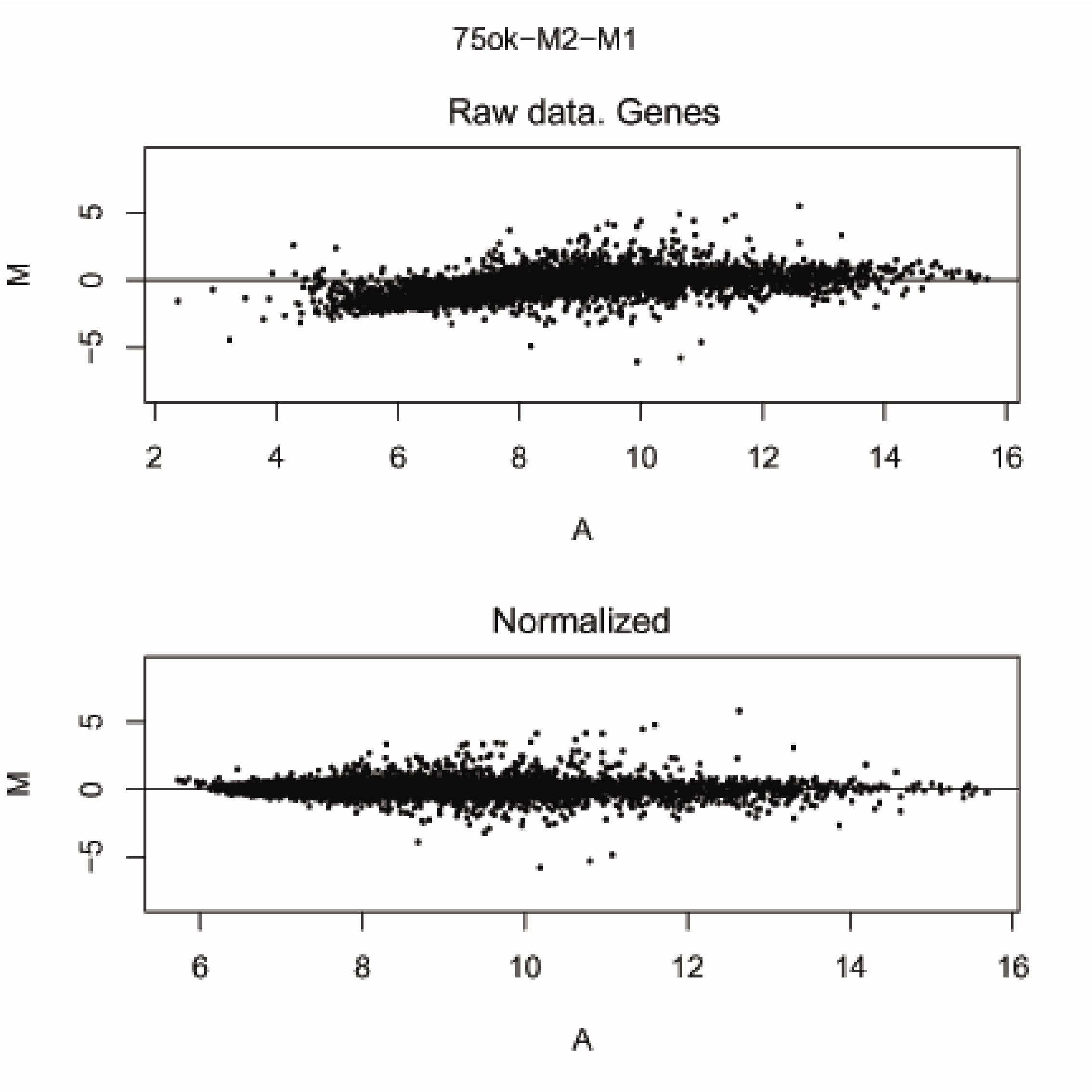
14
16
A
Normalized
M
5
0
−5
6
8
10
12
14
16
A
Raw
6
4
2
0
−2
−4
1
3
5
7
9
11
14
Norm. Within
6
4
2
0
−2
−4
1
3
5
7
9
11
14

3-M2-M1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Normalized
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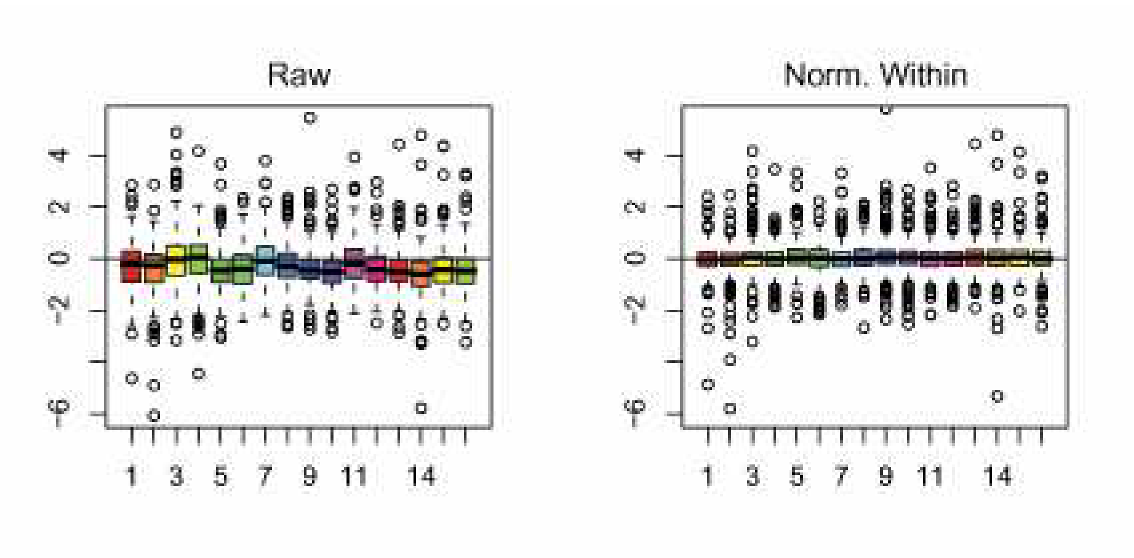
12
14
16
A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-6
1
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5
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11
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Norm. Within
4
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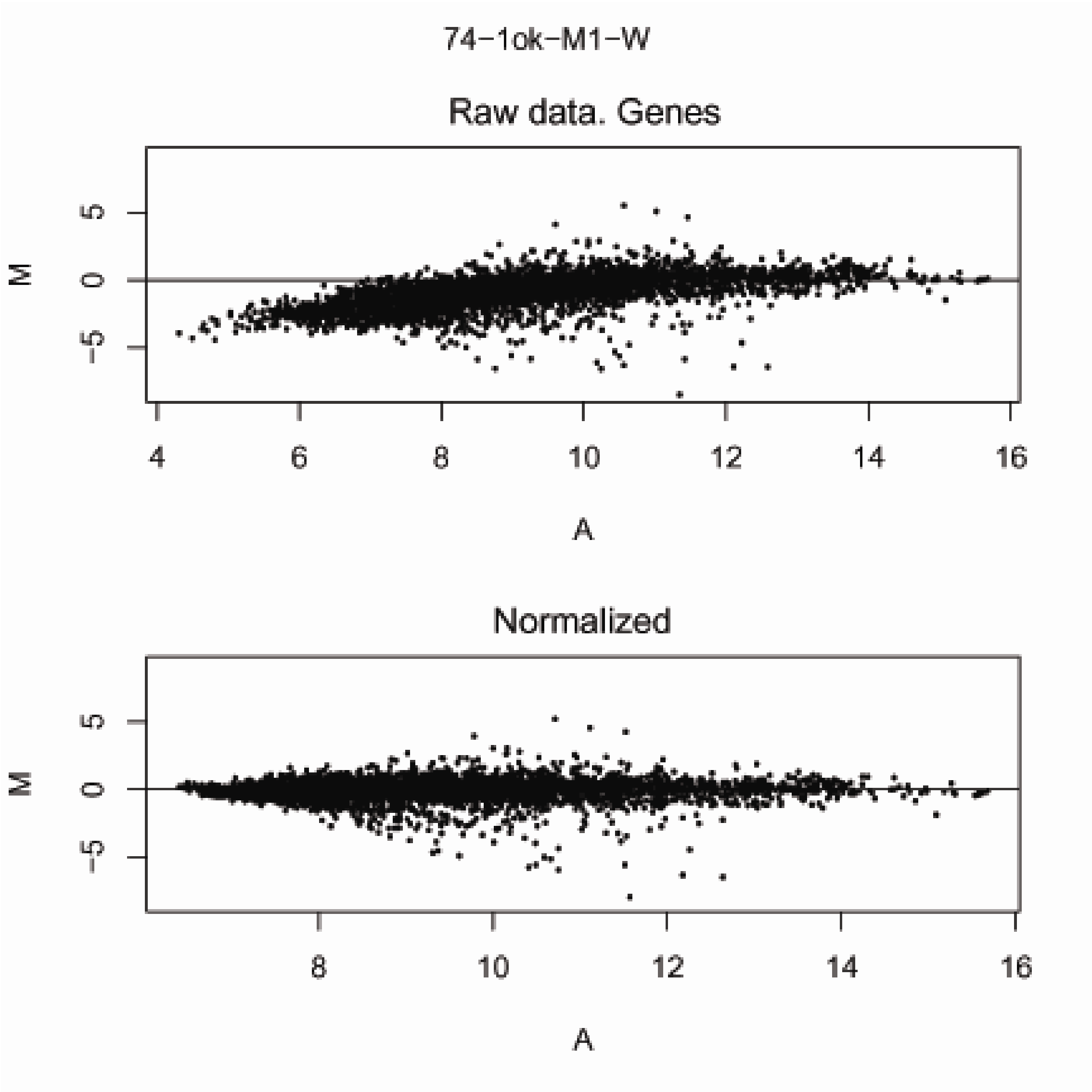
-2
-6
1
3
5
7
9
11
14

4-M1-W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12
14
16
A
Normalized
M
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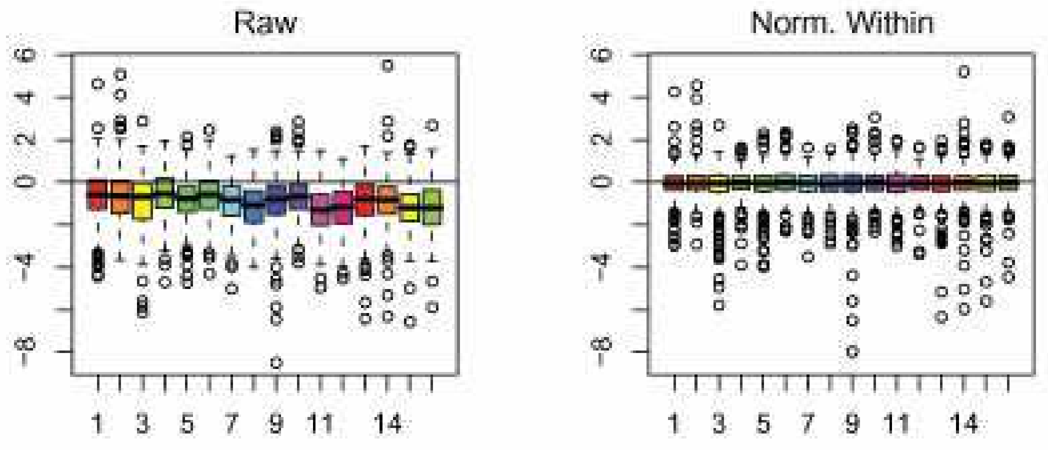
0
−5
8
10
12
14
16
A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2
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−4
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1
3
5
7
9
11
14
Norm. Within
6
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−4
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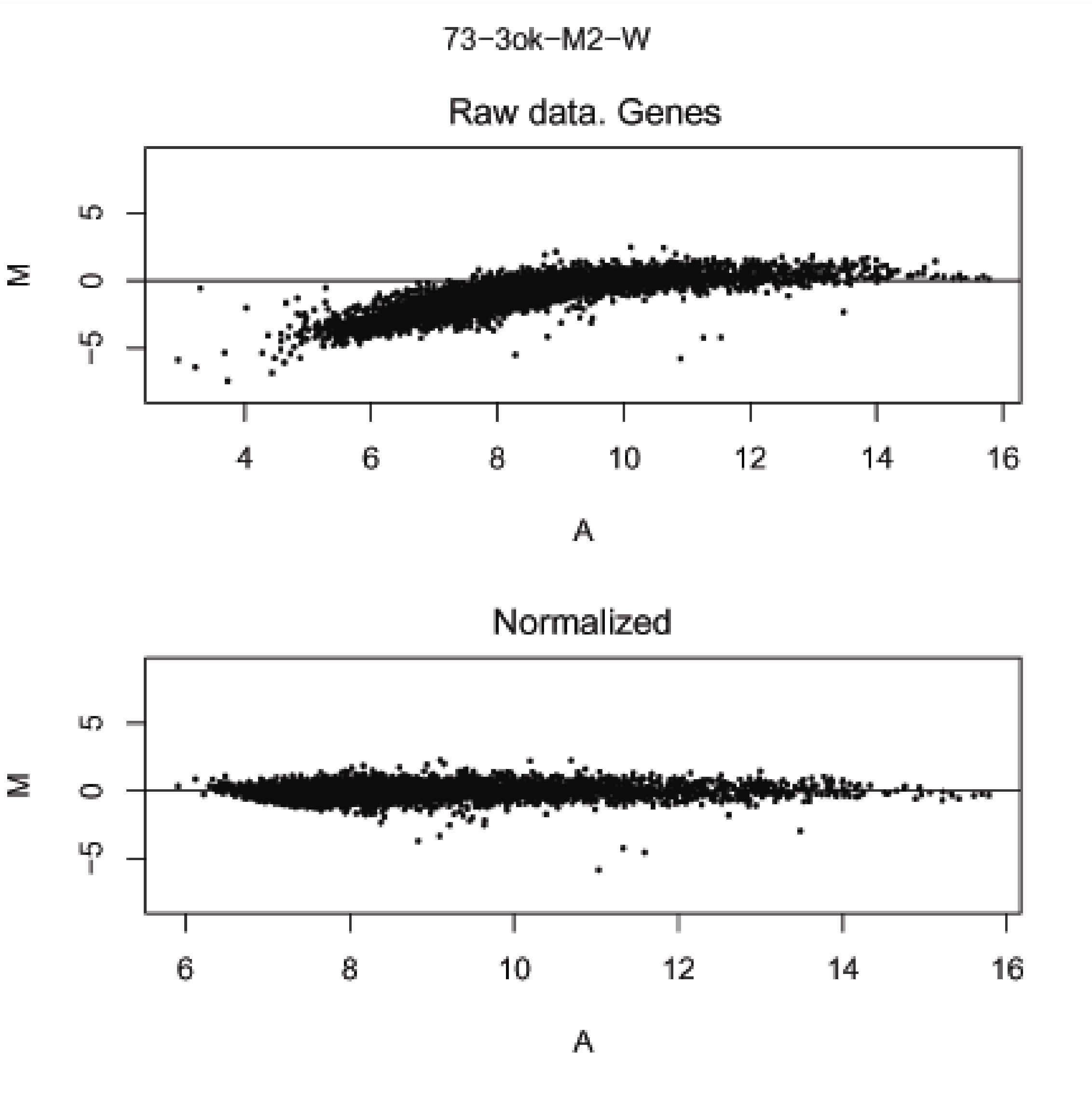
1
3
5
7
9
11
14

5-M2-W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14
16
A
Normalized
M
5
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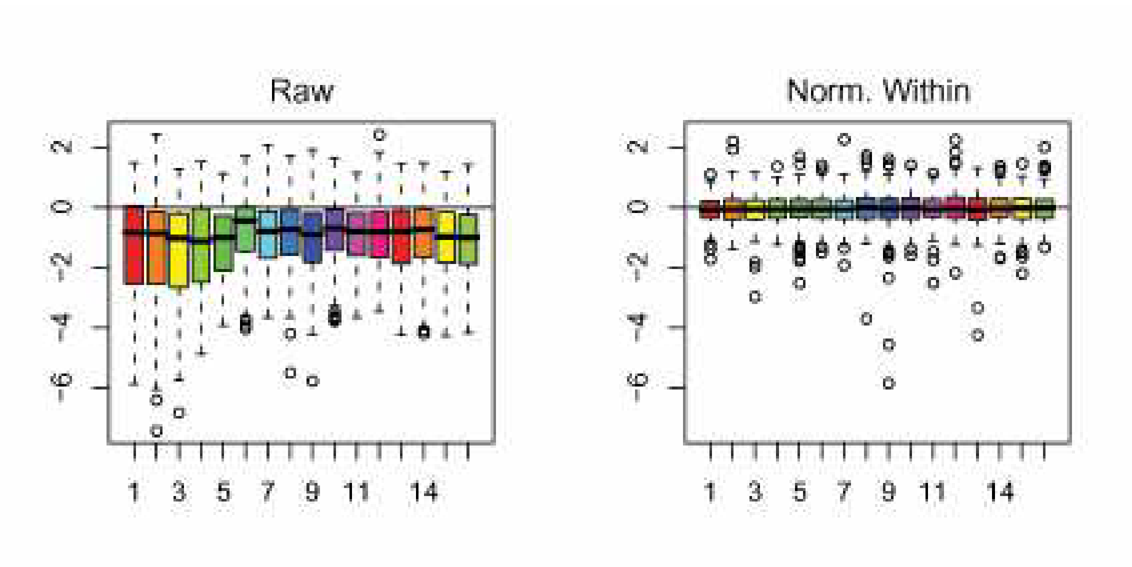
-5
6
8
10
12
14
16
A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Norm. Within
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-6
1
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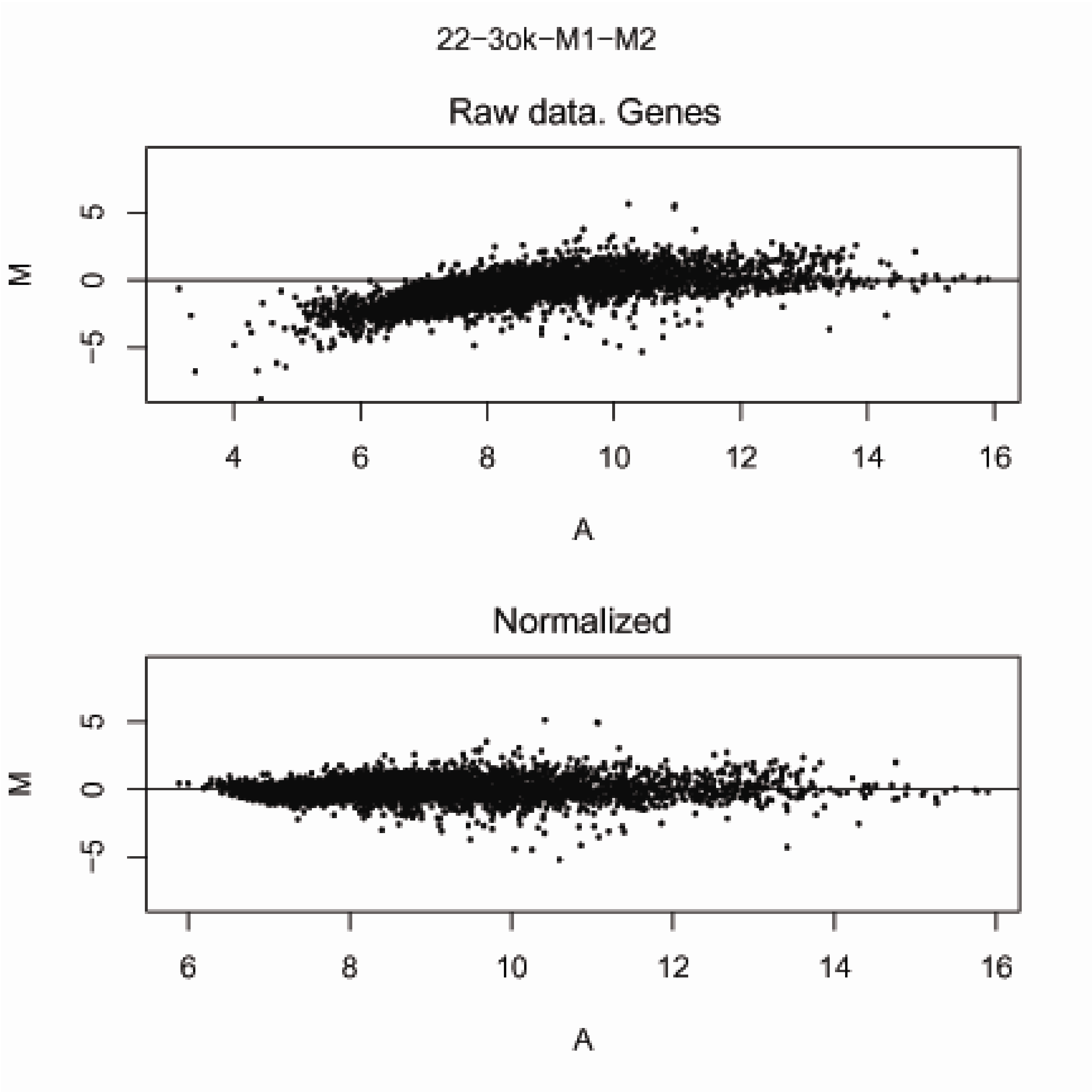
5
7
9
11
14

6-M1-M2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A
Normalized
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6
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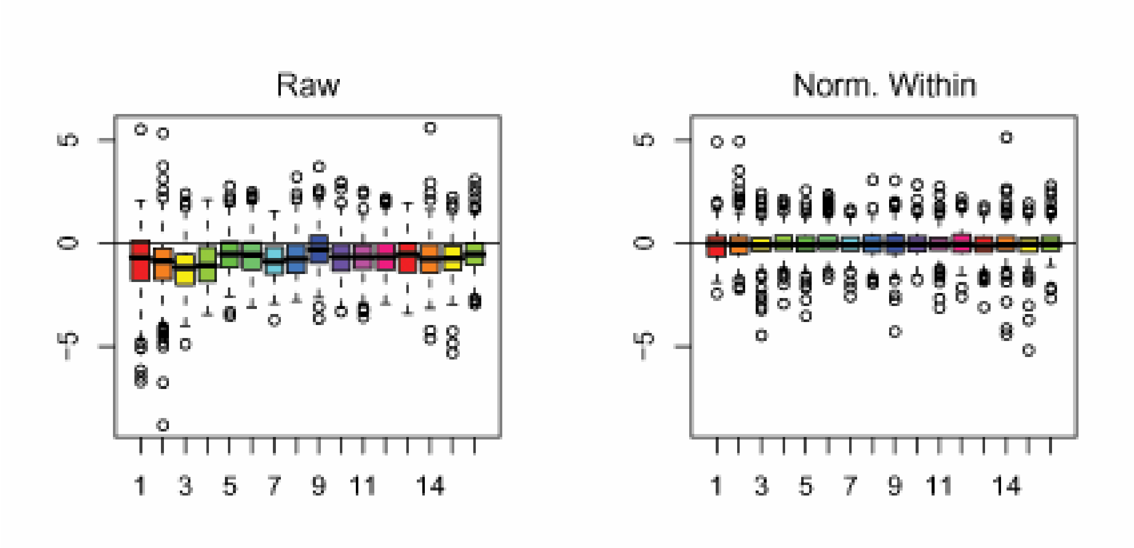
14
16
A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Norm. Within
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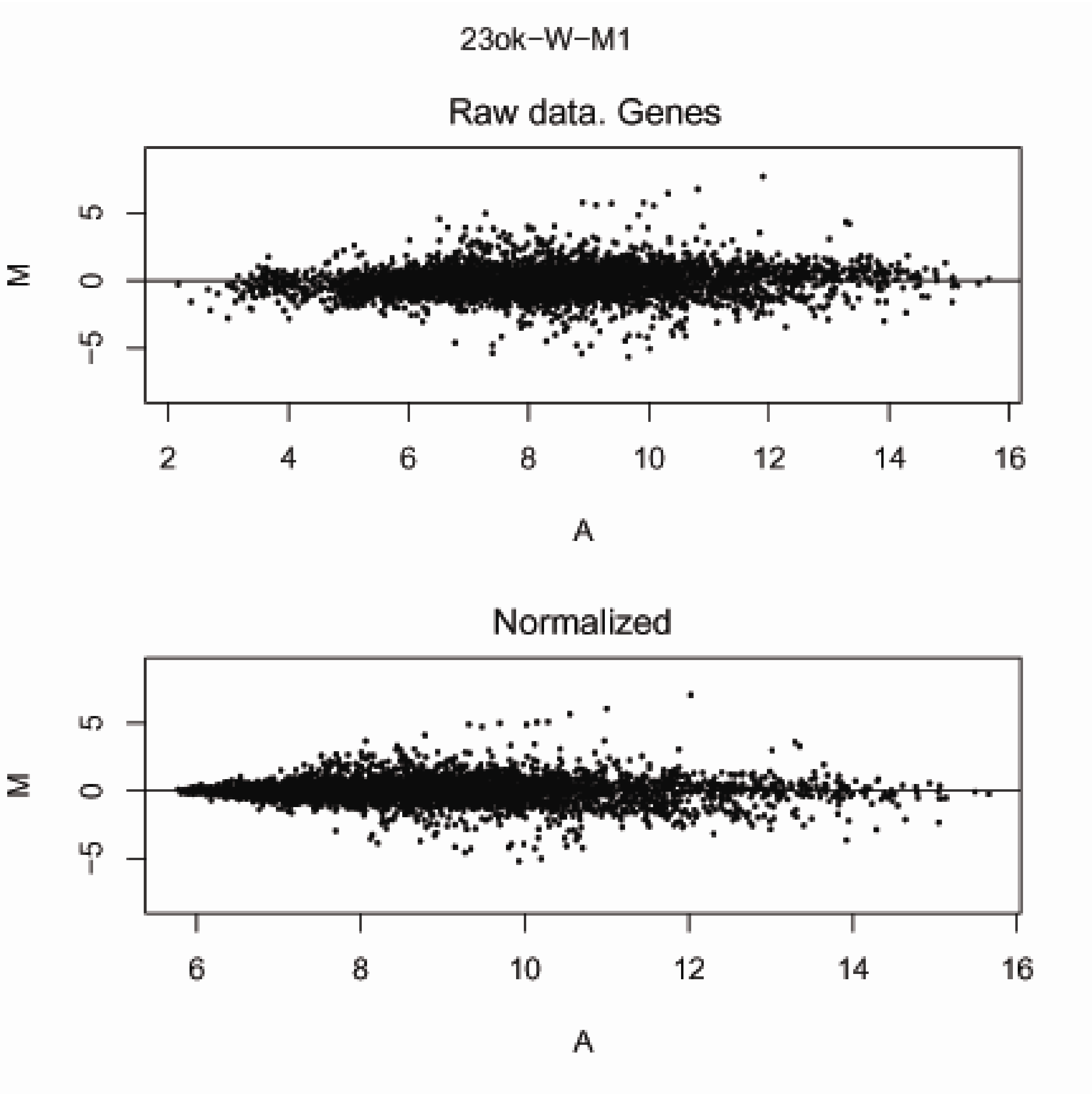
14

7-W-M1


23ok-W-M1
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-5
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16
A
Normalized
M
5
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-5
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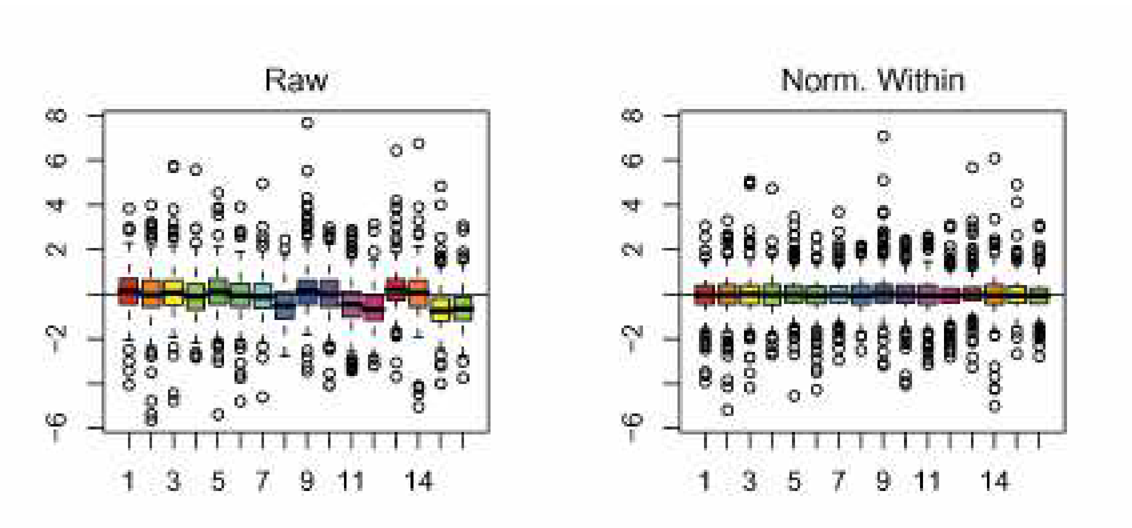
12
14
16
A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-2
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Norm. Within
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-2
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3
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7
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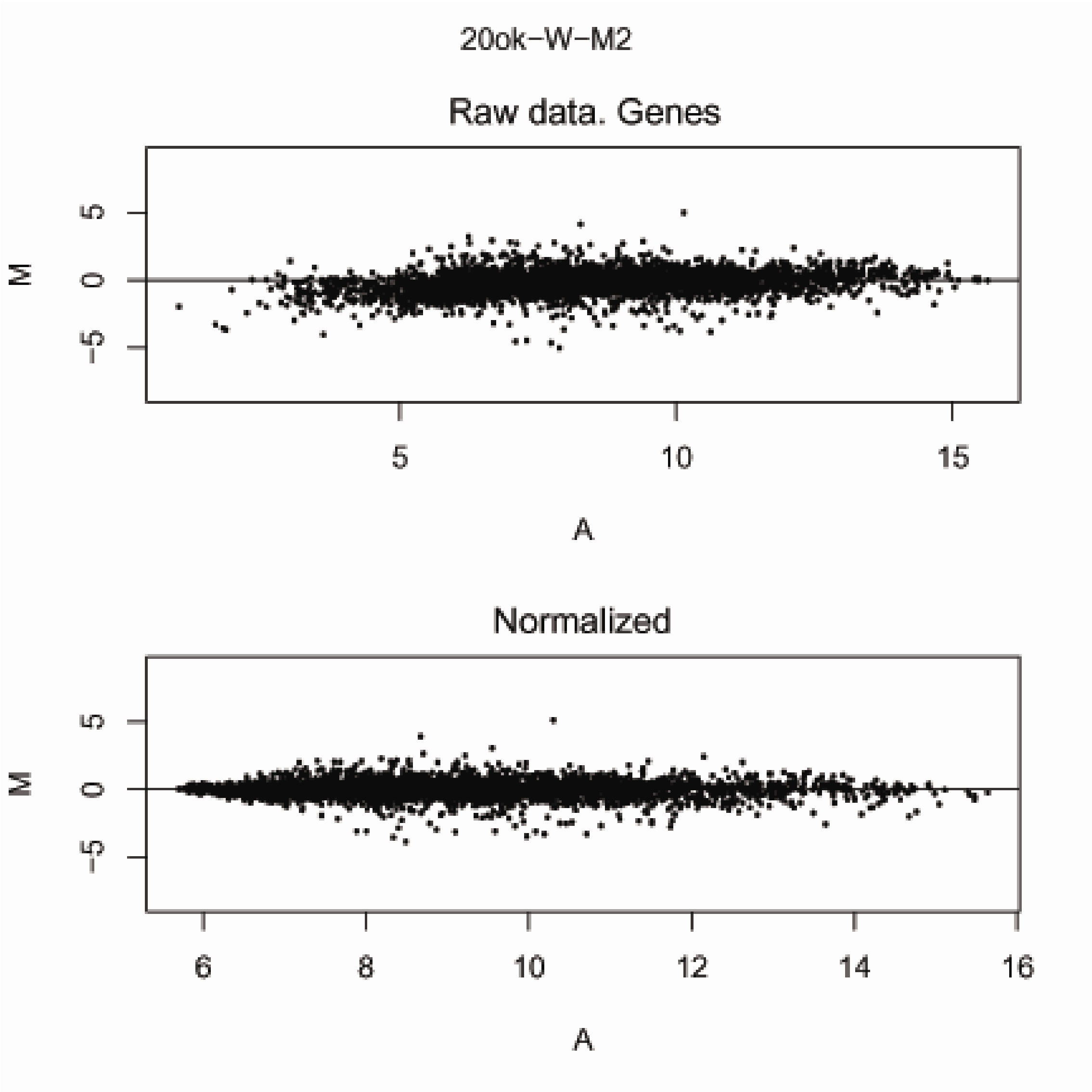
11
14

8-W-M2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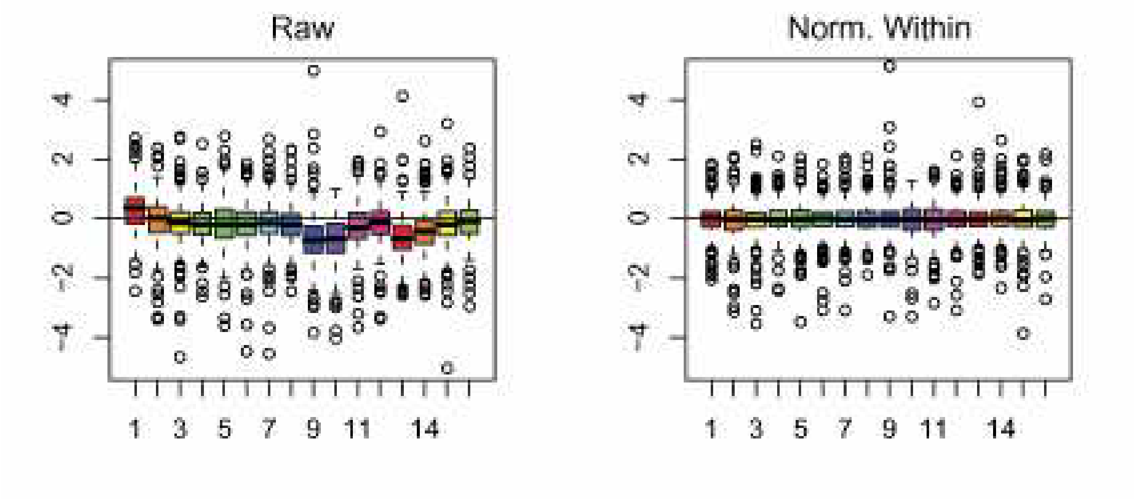
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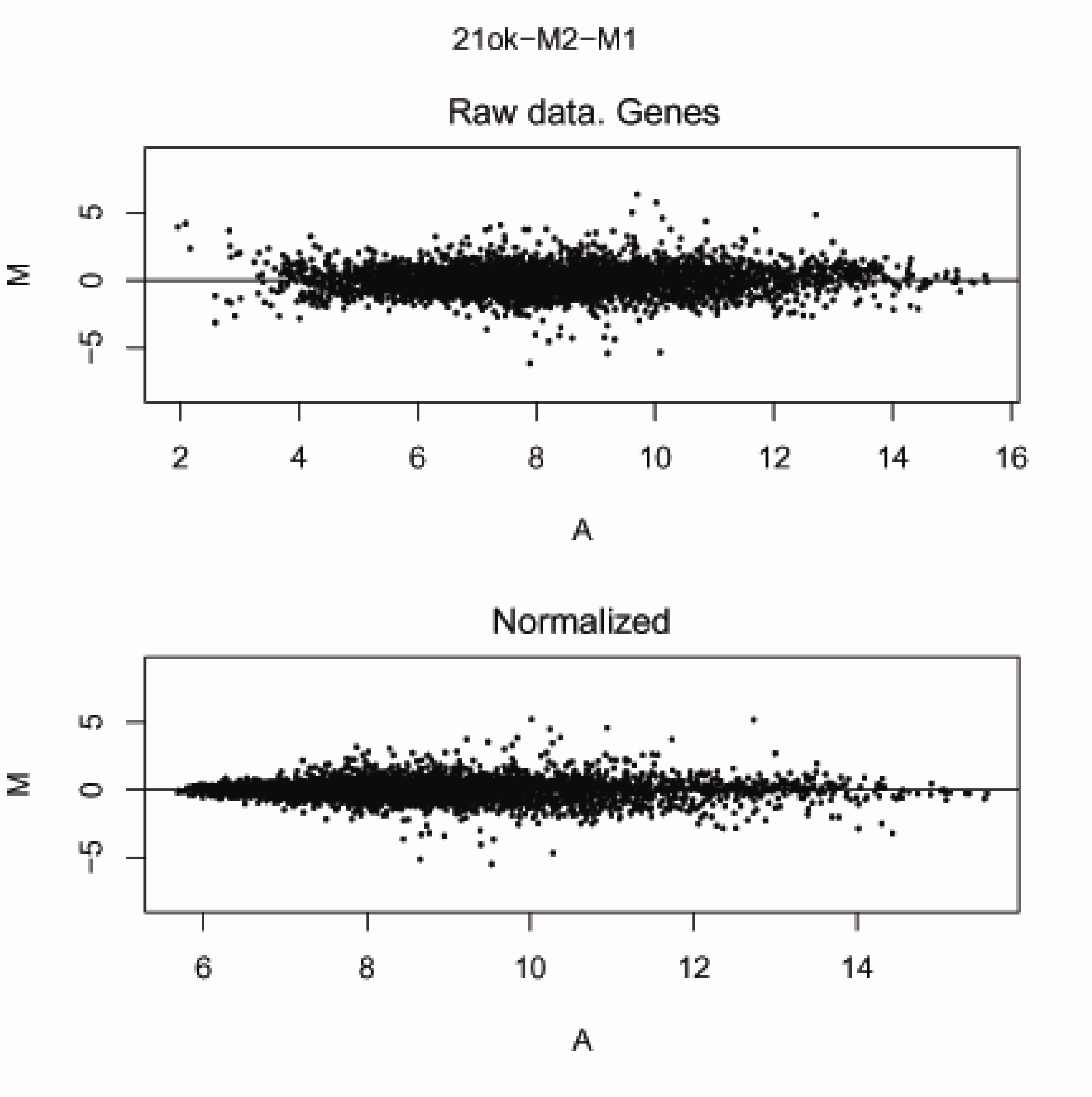
9-M2-M1


21ok-M2-M1
Raw data. Genes
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14
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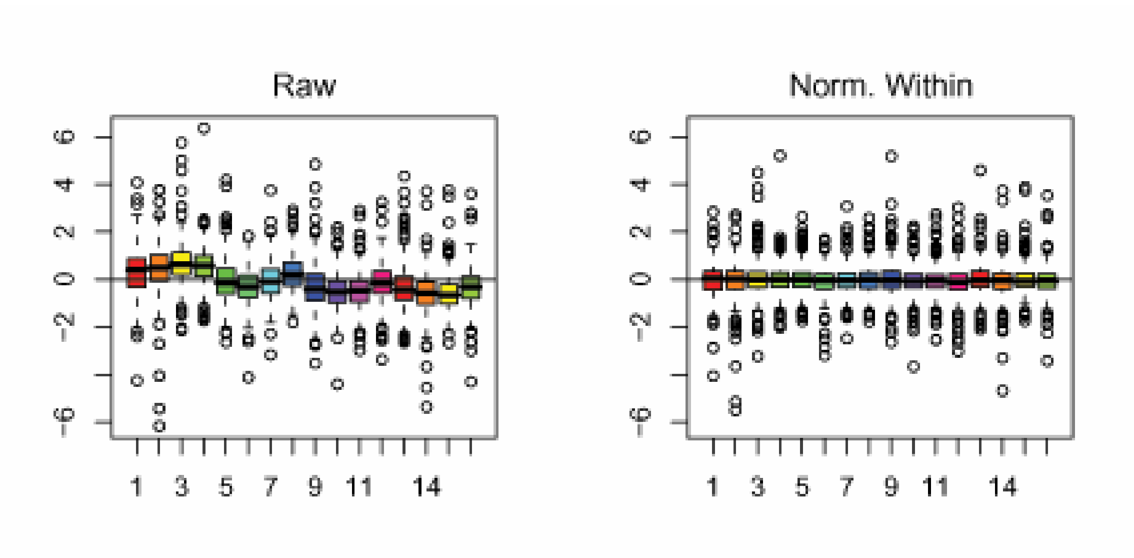
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9
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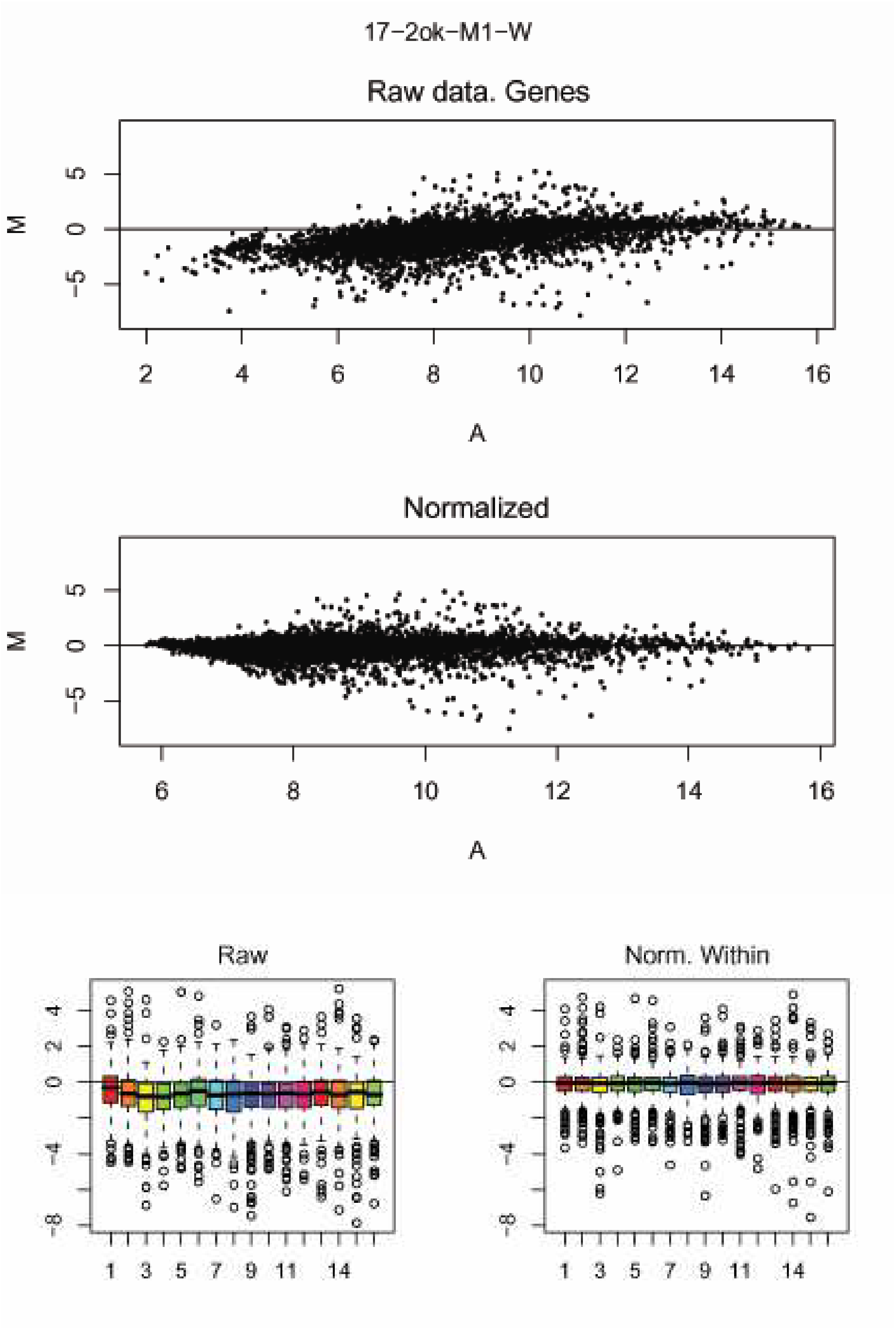
14

10-M1-W


17-2ok-M1-W
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Normalized
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5
0
-5
6
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10
12
14
16
A
Raw
4
2
0
-4
-8
1
3
5
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-4
-8
1
3
5
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9
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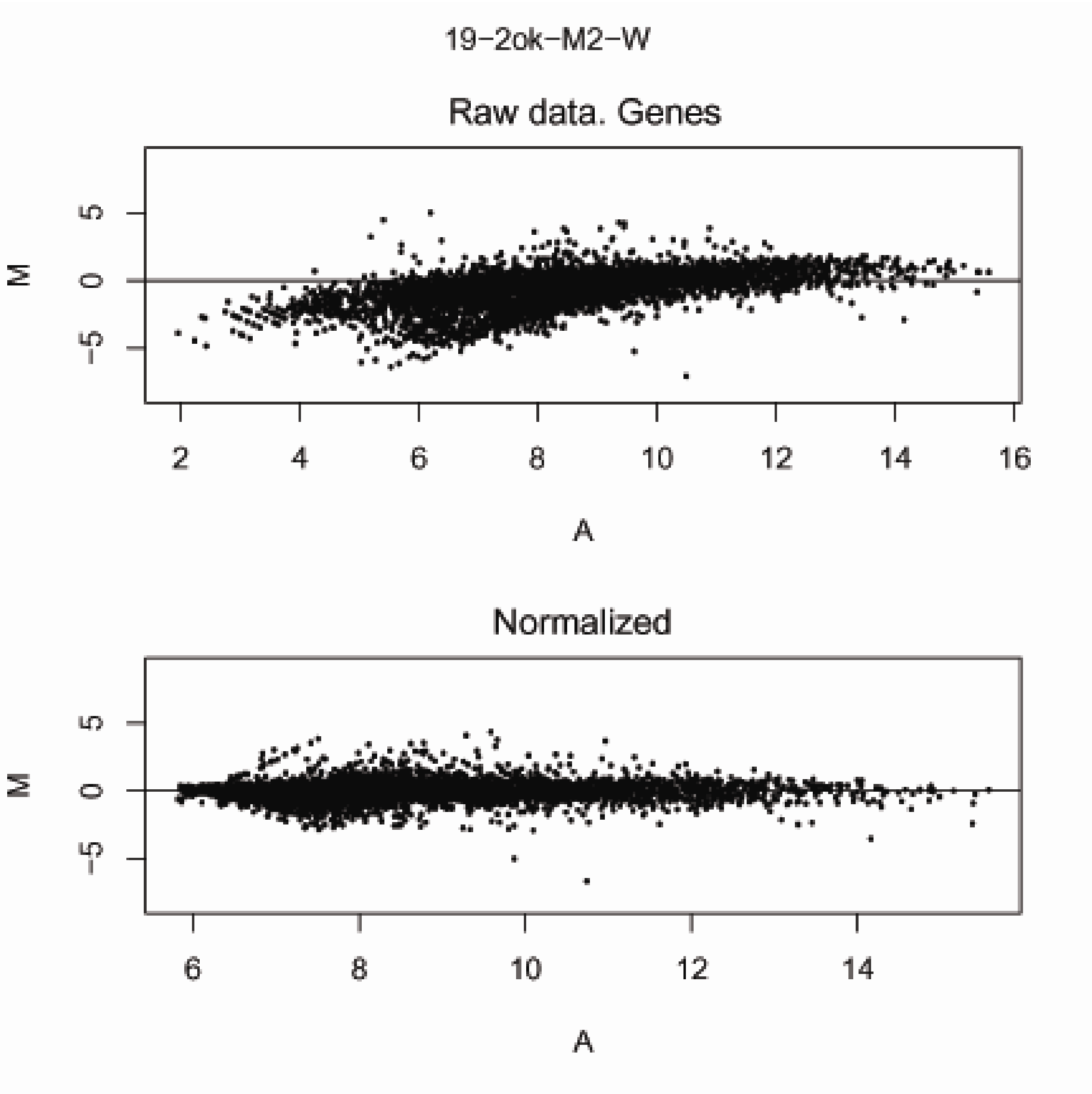
14

11-M2-W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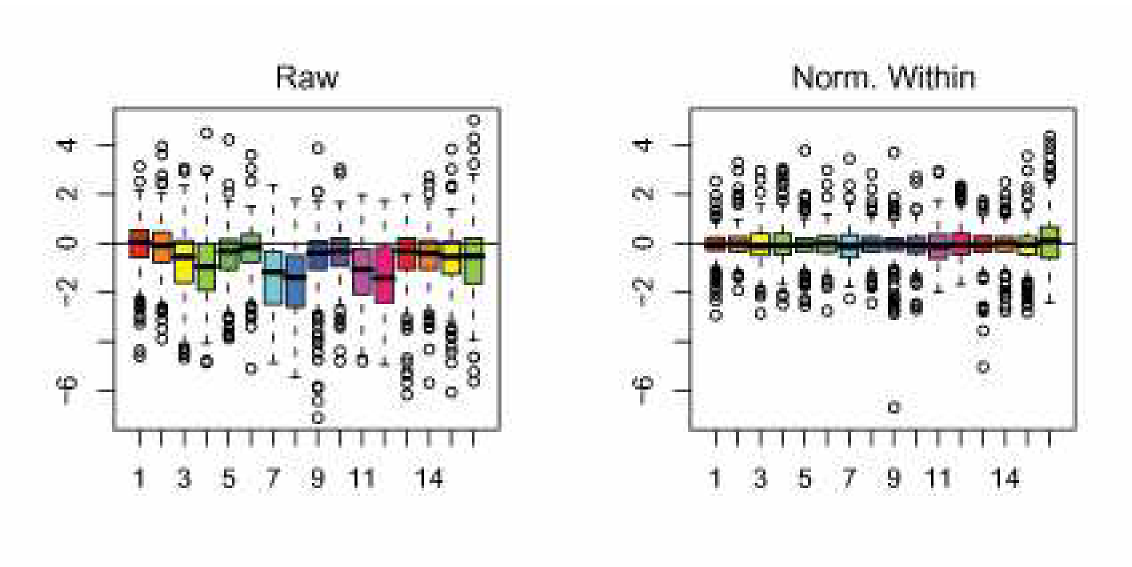
A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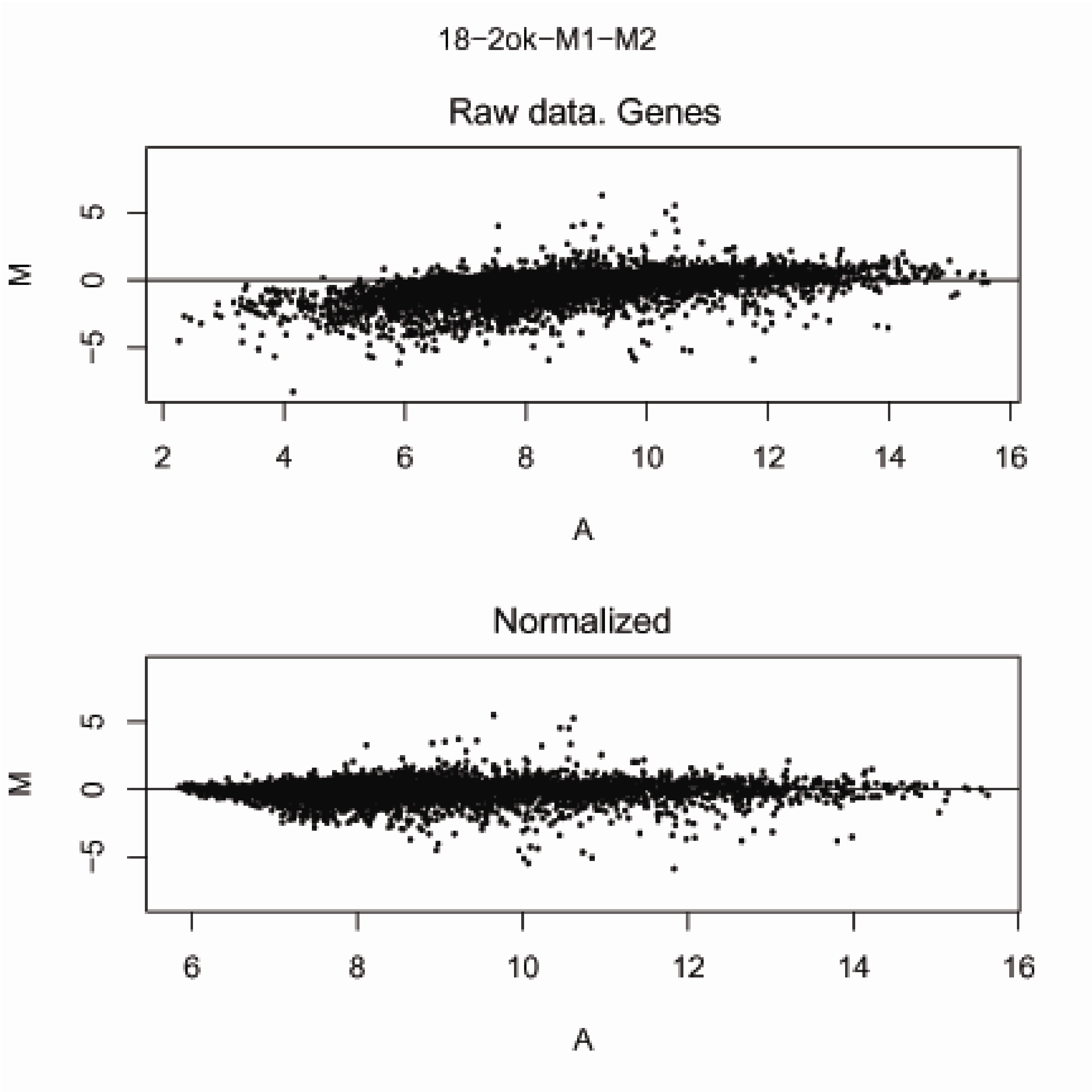
14

12-M1-M2


18−2ok−M1−M2
Raw data. Genes
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2
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16
A
Normalized
M
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−5
6
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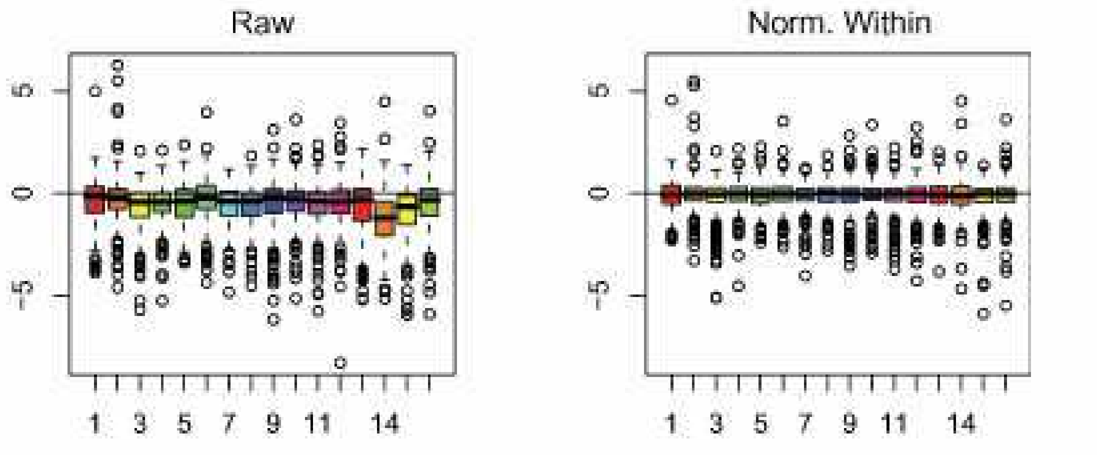
12
14
16
A


Raw
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0
−5
1
3
5
7
9
11
14
Norm. Within
5
0
−5
1
3
5
7
9
11
14

E. GENS EXPRESSATS DIFERENCIALMENT

En aquest apartat tenim les taules corresponents a l'anàlisi de l'expressió dels gens estudiats amb cadascun dels estadístics fets per determinar quins gens estan diferencialment expressats significativament. A l'apartat 2.7.4.5.4 hi trobem la descripció de a què correspon cada columna.

Taula 1 Gens expressats diferencialment entre la soca BSN27 (*hns*$^-$) respecte la soca salvatge BSN26.

	Row	Column	ID	Name	Status	M	A	t	P.Value	B
9	6	2	mwgecov2#1414	glutamate decarboxylase isozyme; gada	gene	6.51	11.47	11.38	5.66E-07	9.97
15	5	5	mwgecov2#1185	putative structural proteins; ycif	gene	5.47	9.81	24.32	2.19E-10	20.43
14	15	10	mwgecov2#3901	lysine decarboxylase 1; cada	gene	5.35	10.27	14.14	5.87E-08	12.93
3	5	9	mwgecov2#1184	orf, hypothetical protein; ycie	gene	5.16	9.58	32.03	1.00E-11	24.07
13	6	2	mwgecov2#1413	acid sensitivity protein, putative transporter; xasa	gene	5.12	10.31	17.63	7.02E-09	16.00
15	6	6	mwgecov2#1455	orf, hypothetical protein; ydei	gene	4.47	8.85	31.26	1.14E-11	23.75
4	11	15	mwgecov2#3306	orf, hypothetical protein; yhim	gene	4.45	9.08	22.01	5.72E-10	19.07
14	3	18	mwgecov2#0877	putative fimbrial-like protein; ycbq	gene	4.41	9.60	25.42	1.52E-10	21.03
3	9	12	mwgecov2#2612	orf, hypothetical protein; ygck	gene	4.15	9.54	11.83	3.89E-07	10.49
3	14	7	mwgecov2#3854	putative enzyme; yjcp	gene	4.05	9.05	16.80	1.14E-08	15.33
16	4	6	mwgecov2#1111	hemolysin e; hlye	gene	4.03	8.87	15.86	1.87E-08	14.53
9	12	6	mwgecov2#3320	outer membrane protein induced after carbon starvation; slp	gene	3.84	10.84	13.97	6.75E-08	12.77
7	8	7	mwgecov2#1941	putative colanic acid polymerase; wcad	gene	3.77	8.19	27.78	5.05E-11	22.21
16	5	7	mwgecov2#1401	30s ribosomal subunit protein s22; rpsv	gene	3.61	12.62	20.06	1.72E-09	17.79
12	5	5	mwgecov2#1210	osmotically inducible lipoprotein; osmb	gene	3.36	10.21	24.50	2.19E-10	20.53
12	5	7	mwgecov2#1402	orf, hypothetical protein; b1481	gene	3.33	9.24	17.17	9.38E-09	15.63
11	8	11	mwgecov2#1936	gdp-mannose mannosyl hydrolase; wcah	gene	3.29	8.42	22.87	3.90E-10	19.60
15	3	3	mwgecov2#0607	putative alpha helical protein; ybel	gene	3.27	8.16	18.57	4.29E-09	16.72
9	4	9	mwgecov2#0942	orf, hypothetical protein; ycdf	gene	2.97	10.32	20.79	1.11E-09	18.29
11	6	18	mwgecov2#1848	positive regulator for ctr capsule biosynthesis, positive transcription factor; rcsa	gene	2.94	8.94	21.52	7.31E-10	18.76
2	8	11	mwgecov2#1914	udp-glucose 6-dehydrogenase; ugd	gene	2.88	8.51	23.33	3.53E-10	19.87
3	2	11	mwgecov2#0430	haemolysin expression modulating protein; hha	gene	2.74	9.31	5.19	1.06E-03	0.51
8	3	13	mwgecov2#0837	orf, hypothetical protein; ycac	gene	2.73	10.62	16.02	1.76E-08	14.67
11	9	12	mwgecov2#2610	orf, hypothetical protein; b2757	gene	2.70	8.49	11.57	4.75E-07	10.19
5	12	2	mwgecov2#3325	orf, hypothetical protein; hded	gene	2.65	10.38	7.91	2.54E-05	5.25
9	15	12	mwgecov2#4070	orf, hypothetical protein; yjha	gene	2.58	8.70	14.93	3.54E-08	13.69
11	5	5	mwgecov2#1186	orf, hypothetical protein; ycig	gene	2.57	11.69	10.04	2.30E-06	8.29
16	4	8	mwgecov2#0917	probable third cytochrome oxidase, subunit ii; appb	gene	2.56	9.15	13.70	8.37E-08	12.50

14	7	5	mwgecov2#1531	nad-dependent 7alpha-hydroxysteroid dehydrogenase, dehydroxylation of bile acids; hdha	gene	2.55	10.40	17.79	6.68E-09	16.12
3	12	10	mwgecov2#3366	orf, hypothetical protein; yiag	gene	2.55	9.26	18.22	5.15E-09	16.46
5	16	18	mwgecov2#0892-r	ribosome modulation factor; rmf	gene	2.54	10.80	9.84	2.87E-06	8.03
1	4	17	mwgecov2#0936	orf, hypothetical protein; yccd	gene	2.54	9.74	16.17	1.65E-08	14.80
13	5	8	mwgecov2#1425	putative fimbrial-like protein; b1504	gene	2.53	8.46	16.31	1.51E-08	14.92
3	4	12	mwgecov2#0892	ribosome modulation factor; rmf	gene	2.51	11.24	12.20	2.83E-07	10.91
7	3	12	mwgecov2#0697	putative homeobox protein; b0753	gene	2.46	8.80	17.75	6.68E-09	16.09
3	8	11	mwgecov2#1938	gdp-d-mannose dehydratase; gmd	gene	2.44	11.00	11.96	3.49E-07	10.64
7	8	11	mwgecov2#1937	putative nucleotide di-p-sugar epimerase or dehydratase; wcag	gene	2.44	8.49	22.94	3.90E-10	19.64
14	14	15	mwgecov2#3819	orf, hypothetical protein; yjbj	gene	2.43	10.41	9.79	3.02E-06	7.97
10	15	10	mwgecov2#3902	transport of lysine/cadaverine; cadb	gene	2.39	10.99	19.16	2.91E-09	17.16
3	2	4	mwgecov2#0129	putative fimbrial protein; yadk	gene	2.39	7.86	9.27	5.25E-06	7.25
5	4	3	mwgecov2#0757	outer membrane protein x; ompx	gene	2.38	11.62	12.02	3.38E-07	10.71
8	15	13	mwgecov2#4867	orf, hypothetical protein; yeaq	gene	2.37	10.62	14.89	3.54E-08	13.66
5	7	11	mwgecov2#1695	orf, hypothetical protein; yeai	gene	2.37	7.51	12.01	3.38E-07	10.70
1	12	2	mwgecov2#3326	orf, hypothetical protein; yhie	gene	2.37	11.45	8.25	1.69E-05	5.76
7	8	5	mwgecov2#2133	putative sugar transferase; b2254	gene	2.35	9.24	11.80	3.97E-07	10.46
2	4	13	mwgecov2#0964	orf, hypothetical protein; ycdu	gene	2.30	8.14	11.00	8.41E-07	9.52
11	8	7	mwgecov2#1940	putative colanic acid biosynthesis glycosyl transferase; wcae	gene	2.30	8.69	14.19	5.64E-08	12.99
6	13	14	mwgecov2#3531	positive regulation of bgl operon; bglg	gene	2.30	7.63	14.44	4.78E-08	13.23
1	7	2	mwgecov2#1610	orf, hypothetical protein; ydit	gene	2.30	8.18	14.89	3.54E-08	13.66
16	7	8	mwgecov2#1863	orf, hypothetical protein; yedu	gene	2.29	10.30	7.53	4.11E-05	4.64
4	8	3	mwgecov2#1970	orf, hypothetical protein; b2085	gene	2.27	8.25	13.68	8.37E-08	12.48
9	7	1	mwgecov2#1512	possible chaperone; b1600	gene	2.23	8.00	11.78	3.99E-07	10.44
5	10	11	mwgecov2#2661	orf, hypothetical protein; b2809	gene	2.22	9.83	13.30	1.15E-07	12.10
13	4	13	mwgecov2#0937	curved dna-binding protein; functions closely related to dnaj; cbpa	gene	2.21	9.69	13.73	8.31E-08	12.53
10	7	13	mwgecov2#1928	orf, hypothetical protein; wcam	gene	2.19	8.04	14.65	4.08E-08	13.43
3	13	1	mwgecov2#3474	probable adenine deaminase (synthesis xanthine); yicp	gene	2.18	8.48	16.73	1.16E-08	15.27
3	3	6	mwgecov2#0512	putative arac-type regulatory protein; ybcm	gene	2.18	9.54	5.31	8.72E-04	0.73
6	3	18	mwgecov2#0879	putative outer membrane protein; ycbs	gene	2.17	7.94	13.28	1.16E-07	12.07
11	4	9	mwgecov2#0988	putative cytochrome; b1057	gene	2.16	8.81	15.78	1.95E-08	14.46

10	6	8	mwgecov2#1642	catalase; hydroperoxidase hpii(iii); kate	gene	2.14	10.02	19.26	2.88E-09	17.23
10	3	18	mwgecov2#0878	putative chaperone; ycbr	gene	2.10	8.31	8.79	9.04E-06	6.57
13	15	12	mwgecov2#4069	orf, hypothetical protein; yjht	gene	2.09	8.23	13.24	1.16E-07	12.03
8	5	7	mwgecov2#1403	osmotically inducible protein; osmc	gene	2.09	10.54	14.81	3.75E-08	13.58
5	10	10	mwgecov2#2949	anaerobically inducible l-threonine, l-serine permease; tdcc	gene	2.08	10.80	5.93	3.46E-04	1.90
3	5	16	mwgecov2#1466	orf, hypothetical protein; b1550	gene	2.08	9.83	9.33	5.03E-06	7.33
1	5	16	mwgecov2#1420	putative arac-type regulatory protein; b1499	gene	2.07	7.53	14.74	3.90E-08	13.52
16	2	7	mwgecov2#0455	putative glutaminase; ybas	gene	2.05	9.42	13.41	1.06E-07	12.21
9	5	12	mwgecov2#1422	putative oxidoreductase, major subunit; b1501	gene	2.05	8.06	10.30	1.72E-06	8.63
11	8	5	mwgecov2#2132	putative enzyme; b2253	gene	2.05	9.24	9.46	4.44E-06	7.51
9	11	16	mwgecov2#3328	putative transport system permease protein; yhiv	gene	2.05	8.05	15.18	2.89E-08	13.92
15	1	18	mwgecov2#0130	putative fimbrial protein; yadl	gene	2.04	8.62	7.12	6.63E-05	3.98
13	5	13	mwgecov2#1131	putative adhesion and penetration protein; b1202	gene	2.03	7.68	15.98	1.78E-08	14.63
15	8	7	mwgecov2#1939	putative transferase; wcaf	gene	2.02	8.08	16.61	1.21E-08	15.17
9	11	13	mwgecov2#3044	regulator of gltbdf operon, induction of ntr enzymes; gltf	gene	2.00	8.47	11.98	3.47E-07	10.66
7	6	7	mwgecov2#1573	cyclopropane fatty acyl phospholipid synthase; cfa	gene	2.00	9.98	17.06	9.84E-09	15.55
5	7	10	mwgecov2#1601	putative amino acid/amine transport protein; b1691	gene	1.99	7.69	10.67	1.19E-06	9.11
5	7	4	mwgecov2#1797	trehalose-6-phosphate synthase; otsa	gene	1.98	8.64	11.17	7.07E-07	9.72
9	4	3	mwgecov2#0756	putative transmembrane subunit; ybif	gene	1.95	7.98	12.90	1.50E-07	11.67
13	4	3	mwgecov2#0755	global regulator, starvation conditions; dps	gene	1.92	11.64	7.88	2.63E-05	5.20
11	6	6	mwgecov2#1456	orf, hypothetical protein; ydej	gene	1.89	8.67	11.63	4.56E-07	10.26
8	6	1	mwgecov2#1391	nitrite extrusion protein 2; naru	gene	1.88	8.01	11.54	4.85E-07	10.16
2	3	18	mwgecov2#0880	homolog of salmonella fimh protein; b0941	gene	1.87	7.68	7.42	4.75E-05	4.46
12	1	9	mwgecov2#0072	probable transcriptional activator for leuabcd operon; leuo	gene	1.86	9.65	13.25	1.16E-07	12.04
13	15	2	mwgecov2#3885	putative amino acid/amine transport protein, cryptic; yjde	gene	1.85	7.59	9.84	2.87E-06	8.03
8	5	14	mwgecov2#1299	orf, hypothetical protein; ynae	gene	1.84	9.43	8.85	8.46E-06	6.66
9	5	16	mwgecov2#1418	putative enzyme; b1497	gene	1.84	8.25	17.31	8.66E-09	15.75
14	15	13	mwgecov2#4576	curlin major subunit, coiled surface structures; cryptic; csga	gene	1.82	8.05	8.37	1.46E-05	5.94
4	14	9	mwgecov2#4068	orf, hypothetical protein; yjhs	gene	1.81	7.77	11.91	3.65E-07	10.58
5	7	18	mwgecov2#1995	orf, hypothetical protein; yehe	gene	1.79	8.87	13.16	1.20E-07	11.95
13	9	9	mwgecov2#2275	regulator for xapa; xapr	gene	1.79	8.08	15.40	2.48E-08	14.13
7	7	14	mwgecov2#2047	putative kinase; yeic	gene	1.77	9.06	5.36	7.95E-04	0.84

6	7	1	mwgecov2#1537	orf, hypothetical protein; b1625	gene	1.77	9.81	5.69	4.93E-04	1.45
7	7	16	mwgecov2#2237	orf, hypothetical protein; b2359	gene	1.76	8.83	14.40	4.87E-08	13.19
16	6	4	mwgecov2#1289	orf, hypothetical protein; b1365	gene	1.75	8.06	8.77	9.26E-06	6.53
15	14	14	mwgecov2#4131	hyperosmotically inducible periplasmic protein; osmy	gene	1.74	10.77	6.18	2.42E-04	2.35
8	8	17	mwgecov2#2145	orf, hypothetical protein; elab	gene	1.74	10.17	8.00	2.29E-05	5.38
9	8	16	mwgecov2#1980	orf, hypothetical protein; b2097	gene	1.74	9.56	13.17	1.20E-07	11.96
8	8	3	mwgecov2#1969	orf, hypothetical protein; b2084	gene	1.73	7.87	9.96	2.51E-06	8.19
8	10	7	mwgecov2#2737	protein disulfide isomerase ii; dsbc	gene	1.73	10.30	7.45	4.59E-05	4.51
12	1	8	mwgecov2#0356	orf, hypothetical protein; yaib	gene	1.73	9.57	13.04	1.34E-07	11.82
10	6	2	mwgecov2#1436	putative transport system permease protein; ydez	gene	1.70	8.86	11.65	4.50E-07	10.29
15	11	11	mwgecov2#2881	putative fimbrial-like protein; ygil	gene	1.69	7.99	10.10	2.15E-06	8.38
5	7	5	mwgecov2#1509	acid shock protein; asr	gene	1.68	8.02	12.86	1.52E-07	11.64
1	7	4	mwgecov2#1798	trehalose-6-phosphate phophatase, biosynthetic; otsb	gene	1.68	9.75	13.23	1.16E-07	12.02
3	8	15	mwgecov2#1934	mannose-1-phosphate guanyltransferase; cpsb	gene	1.67	8.65	10.36	1.61E-06	8.72
14	1	15	mwgecov2#0205	orf, hypothetical protein; ykfe	gene	1.67	10.54	15.35	2.54E-08	14.08
14	12	2	mwgecov2#3347	orf, hypothetical protein; yhjr	gene	1.66	9.39	6.05	2.89E-04	2.12
15	5	11	mwgecov2#1373	orf, hypothetical protein; b1450	gene	1.65	9.33	13.67	8.37E-08	12.47
9	7	6	mwgecov2#1604	putative enzyme; ydif	gene	1.61	8.09	6.08	2.80E-04	2.16
10	10	8	mwgecov2#2784	methionine adenosyltransferase 1 (adomet synthetase); methyl and propylamine donor, corepressor of met genes; metk	gene	1.60	9.07	8.05	2.16E-05	5.46
13	4	9	mwgecov2#0941	trp repressor binding protein; affects association of trp repressor and operator; wrba	gene	1.57	10.57	5.17	1.08E-03	0.48
3	8	5	mwgecov2#2134	putative transformylase; b2255	gene	1.56	9.15	15.63	2.17E-08	14.33
13	7	11	mwgecov2#1693	orf, hypothetical protein; yeag	gene	1.55	9.20	10.32	1.69E-06	8.66
3	9	1	mwgecov2#2334	transaldolase a; tala	gene	1.54	9.37	8.79	9.04E-06	6.56
10	3	14	mwgecov2#0882	putative fimbrial-like protein; b0943	gene	1.54	7.76	12.50	2.13E-07	11.25
6	4	17	mwgecov2#0959	orf, hypothetical protein; ycdq	gene	1.53	8.63	11.08	7.79E-07	9.61
9	14	11	mwgecov2#3800	orf, hypothetical protein; yjbe	gene	1.52	11.46	11.76	4.07E-07	10.41
3	8	16	mwgecov2#2028	putative oxidoreductase; b2146	gene	1.52	10.29	11.53	4.87E-07	10.14
10	3	3	mwgecov2#0586	orf, hypothetical protein; crca	gene	1.52	8.35	6.94	8.43E-05	3.67
9	14	8	mwgecov2#3898	orf, hypothetical protein; yjdk	gene	1.52	8.27	8.96	7.62E-06	6.81
5	15	10	mwgecov2#3879	putative vimentin; yjda	gene	1.51	8.07	9.53	4.06E-06	7.62

2	4	5	mwgecov2#0970	curli production assembly/transport component, 2nd curli operon; csgg	gene	1.51	7.97	7.53	4.09E-05	4.65
12	4	8	mwgecov2#0918	phosphoanhydride phosphorylase; ph 2.5 acid phosphatase; periplasmic; appa	gene	1.51	9.17	12.44	2.25E-07	11.18
4	15	10	mwgecov2#3952	putative acyl coenzyme a dehydrogenase; aidb	gene	1.47	9.75	13.32	1.15E-07	12.11
14	4	1	mwgecov2#0971	curli production assembly/transport component, 2nd curli operon; csgf	gene	1.47	8.78	5.81	4.11E-04	1.67
14	7	11	mwgecov2#1717	orf, hypothetical protein; b1810	gene	1.47	9.55	10.07	2.22E-06	8.34
4	4	12	mwgecov2#0916	probable third cytochrome oxidase, subunit i; appc	gene	1.46	10.01	7.02	7.57E-05	3.81
3	9	16	mwgecov2#2608	orf, hypothetical protein; b2755	gene	1.44	9.11	8.98	7.46E-06	6.85
1	4	13	mwgecov2#0940	orf, hypothetical protein; yccj	gene	1.44	10.07	5.75	4.49E-04	1.56
11	3	13	mwgecov2#0812	pyruvate oxidase; poxb	gene	1.44	8.95	11.33	5.97E-07	9.91
13	7	1	mwgecov2#1511	possible chaperone; b1599	gene	1.43	7.22	7.99	2.29E-05	5.37
10	4	17	mwgecov2#0958	orf, hypothetical protein; ycdp	gene	1.43	8.01	6.76	1.06E-04	3.37
4	10	5	mwgecov2#2528	dna-binding protein; h-ns-like protein; chaperone activity; rna splicing?; stpa	gene	1.42	8.77	9.60	3.77E-06	7.71
8	3	12	mwgecov2#0721	biotin biosynthesis; reaction prior to pimeloyl coa; bioc	gene	1.42	8.17	13.02	1.34E-07	11.80
2	12	4	mwgecov2#3158	bacterioferrin, an iron storage homoprotein; bfr	gene	1.41	11.23	7.22	5.87E-05	4.14
2	7	13	mwgecov2#1930	putative galactokinase (ec 2.7.1.6).; wcak	gene	1.41	7.70	10.16	2.01E-06	8.46
9	11	8	mwgecov2#2932	orf, hypothetical protein; yqjd	gene	1.41	10.29	7.30	5.46E-05	4.27
8	5	5	mwgecov2#1211	putative deor-type transcriptional regulator; b1284	gene	1.39	8.72	8.65	1.05E-05	6.37
11	14	14	mwgecov2#4132	orf, hypothetical protein; yjju	gene	1.39	10.15	10.69	1.17E-06	9.13
2	6	5	mwgecov2#1340	glyceraldehyde-3-phosphate dehydrogenase; gapc	gene	1.39	9.05	7.06	7.20E-05	3.87
3	9	3	mwgecov2#2524	orf, hypothetical protein; ygau	gene	1.39	9.37	6.14	2.57E-04	2.28
4	4	7	mwgecov2#0826	atp-binding component of cytochrome-related transport; cydc	gene	1.39	8.95	9.31	5.03E-06	7.31
12	14	17	mwgecov2#4058	putative regulator; yjhi	gene	1.38	9.14	5.65	5.17E-04	1.38
5	12	6	mwgecov2#3321	orf, hypothetical protein; yhif	gene	1.38	7.97	12.73	1.72E-07	11.49
11	5	12	mwgecov2#1468	cold shock-like protein; cspi	gene	1.37	9.77	9.70	3.35E-06	7.85
15	7	6	mwgecov2#1649	activator of ntrl gene; osme	gene	1.36	10.55	7.25	5.72E-05	4.18
10	4	9	mwgecov2#0965	putative ribosomal protein; ycdv	gene	1.35	8.22	13.17	1.20E-07	11.95
2	7	1	mwgecov2#1538	orf, hypothetical protein; b1626	gene	1.35	8.77	5.16	1.11E-03	0.44
2	3	7	mwgecov2#0584	sequence similarity to shigella regulator; citb	gene	1.35	7.76	8.13	1.96E-05	5.58
13	11	3	mwgecov2#2841	putative oxidoreductase; ygha	gene	1.33	9.07	7.29	5.49E-05	4.25
15	4	5	mwgecov2#0991	orf, hypothetical protein; ycep	gene	1.32	12.07	8.48	1.29E-05	6.11
5	11	8	mwgecov2#2933	orf, hypothetical protein; yqje	gene	1.31	9.28	7.71	3.29E-05	4.93
8	15	3	mwgecov2#4055	putative transport system permease; yjhf	gene	1.30	7.90	5.43	7.16E-04	0.96

7	14	14	mwgecov2#4133	mg-dependent dnase; yjjv	gene	1.30	8.33	8.31	1.56E-05	5.86
11	16	4	mwgecov2#5125	glycogen biosynthesis, rpos dependent; glgs	gene	1.30	11.12	5.02	1.37E-03	0.19
5	7	6	mwgecov2#1605	putative oxidoreductase; b1695	gene	1.30	7.97	6.19	2.39E-04	2.37
6	9	15	mwgecov2#2487	orf, hypothetical protein; yfjj	gene	1.29	8.30	14.66	4.08E-08	13.44
12	8	3	mwgecov2#1968	orf, hypothetical protein; b2083	gene	1.29	8.07	7.25	5.72E-05	4.19
9	7	11	mwgecov2#1694	orf, hypothetical protein; yeah	gene	1.28	8.13	8.12	1.97E-05	5.57
10	14	3	mwgecov2#3428	involved in lipopolysaccharide biosynthesis; htrl	gene	1.28	9.08	6.61	1.31E-04	3.11
12	9	3	mwgecov2#2546	orf, hypothetical protein; ygag	gene	1.27	10.32	8.93	7.90E-06	6.77
11	15	10	mwgecov2#3926	orf, hypothetical protein; yjen	gene	1.27	8.10	5.45	6.85E-04	1.01
5	9	6	mwgecov2#2375	putative outer membrane lipoprotein; b2505	gene	1.27	7.84	12.50	2.13E-07	11.24
1	4	4	mwgecov2#0852	integration host factor (ihf), beta subunit; site-specific recombination; himd	gene	1.27	10.17	13.75	8.20E-08	12.56
8	10	1	mwgecov2#2531	orf, hypothetical protein; ygam	gene	1.26	10.05	7.68	3.41E-05	4.88
7	8	3	mwgecov2#1945	orf, hypothetical protein; b2060	gene	1.26	8.14	6.83	9.76E-05	3.48
2	2	18	mwgecov2#0686	orf, hypothetical protein; ybge	gene	1.26	9.19	7.26	5.62E-05	4.21
2	5	4	mwgecov2#1454	orf, hypothetical protein; ydeh	gene	1.24	8.29	8.06	2.12E-05	5.48
12	6	1	mwgecov2#1390	cryptic nitrate reductase 2, alpha subunit; narz	gene	1.23	8.54	7.50	4.30E-05	4.59
16	14	17	mwgecov2#4057	putative lyase/synthase; yjhh	gene	1.22	8.50	5.17	1.08E-03	0.48
12	2	9	mwgecov2#0644	orf, hypothetical protein; ybfg	gene	1.21	8.21	11.85	3.85E-07	10.52
15	5	13	mwgecov2#1177	putative potassium channel protein; kch	gene	1.21	10.33	6.85	9.43E-05	3.52
8	6	11	mwgecov2#1593	orf, hypothetical protein; ynhe	gene	1.21	8.42	9.78	3.04E-06	7.95
1	7	11	mwgecov2#1696	orf, hypothetical protein; yeaj	gene	1.21	7.90	10.64	1.23E-06	9.06
6	2	18	mwgecov2#0685	cytochrome d terminal oxidase polypeptide subunit ii; cydb	gene	1.20	11.93	7.41	4.79E-05	4.44
6	7	12	mwgecov2#1813	orf, hypothetical protein; yecf	gene	1.19	8.58	8.96	7.61E-06	6.82
4	4	18	mwgecov2#1102	orf, hypothetical protein; b1172	gene	1.18	9.10	7.70	3.33E-05	4.91
11	14	10	mwgecov2#4136	thymidine phosphorylase; deoa	gene	1.18	9.80	8.30	1.56E-05	5.85
16	10	3	mwgecov2#2335	transketolase 2 isozyme; tktb	gene	1.18	8.13	5.89	3.65E-04	1.82
6	5	10	mwgecov2#1255	orf, hypothetical protein; b1330	gene	1.17	8.90	7.26	5.62E-05	4.21
3	15	16	mwgecov2#6109	orf, hypothetical protein; yiis	gene	1.17	9.63	7.74	3.16E-05	4.98
10	11	7	mwgecov2#2862	orf, hypothetical protein; ygiw	gene	1.16	10.60	7.27	5.62E-05	4.21
6	4	1	mwgecov2#0973	putative 2-component transcriptional regulator for 2nd curli operon; csgd	gene	1.16	7.90	5.08	1.26E-03	0.30
8	9	3	mwgecov2#2547	gamma-glutamate-cysteine ligase; gsha	gene	1.16	10.68	11.03	8.21E-07	9.55
2	14	7	mwgecov2#3830	orf, hypothetical protein; yjbq	gene	1.15	9.61	8.82	8.70E-06	6.62

9	2	12	mwgecov2#0476	putative regulator; ybbu	gene	1.13	9.94	11.68	4.40E-07	10.32
4	8	10	mwgecov2#2250	putative receptor protein; b2372	gene	1.12	7.79	8.74	9.48E-06	6.50
15	7	2	mwgecov2#1653	periplasmic protein related to spheroblast formation; spy	gene	1.12	10.04	8.56	1.17E-05	6.23
12	6	11	mwgecov2#1592	putative atp-binding component of a transport system; ynhd	gene	1.11	8.42	7.87	2.69E-05	5.17
15	7	17	mwgecov2#1947	putative polysaccharide export protein; wza	gene	1.10	7.83	8.90	8.10E-06	6.72
6	3	7	mwgecov2#0583	putative sensor-type protein; cita	gene	1.10	7.95	6.73	1.11E-04	3.31
13	11	8	mwgecov2#2931	orf, hypothetical protein; yqjc	gene	1.09	12.06	4.96	1.52E-03	0.06
5	14	11	mwgecov2#3801	orf, hypothetical protein; yjbf	gene	1.09	7.33	9.04	6.92E-06	6.93
4	2	4	mwgecov2#0153	periplasmic serine protease do; heat shock protein htra; htra	gene	1.08	8.76	5.98	3.21E-04	1.98
7	5	3	mwgecov2#1383	orf, hypothetical protein; ydce	gene	1.08	9.01	5.50	6.36E-04	1.10
8	8	14	mwgecov2#2245	multidrug resistance protein y; emry	gene	1.06	7.38	7.22	5.87E-05	4.14
8	8	10	mwgecov2#2249	putative enzyme; yfde	gene	1.05	7.98	7.24	5.76E-05	4.17
12	14	14	mwgecov2#4156	orf, hypothetical protein; yjjy	gene	1.05	9.14	8.79	9.04E-06	6.56
14	8	7	mwgecov2#1915	gluconate-6-phosphate dehydrogenase, decarboxylating; gnd	gene	1.04	12.05	8.10	2.03E-05	5.53
10	2	18	mwgecov2#0684	cytochrome d terminal oxidase, polypeptide subunit i; cyda	gene	1.04	11.06	5.75	4.50E-04	1.56
16	15	10	mwgecov2#3949	orf, hypothetical protein; yjfl	gene	1.03	7.98	5.67	5.07E-04	1.41
2	12	16	mwgecov2#3146	putative general secretion pathway for protein export (gsp); yhee	gene	1.03	7.73	6.24	2.23E-04	2.46
11	8	3	mwgecov2#1944	putative regulator; wcaa	gene	1.03	8.23	7.66	3.46E-05	4.85
2	1	5	mwgecov2#0038	probable flavoprotein subunit, carnitine metabolism; fixa	gene	1.03	7.28	7.18	6.15E-05	4.07
11	9	8	mwgecov2#2613	orf, hypothetical protein; b2760	gene	1.02	11.95	8.45	1.33E-05	6.07
2	4	1	mwgecov2#0974	minor curlin subunit precursor, similar ro csga; csgb	gene	1.01	7.53	7.22	5.87E-05	4.13
1	3	4	mwgecov2#0658	orf, hypothetical protein; ybga	gene	1.01	8.67	7.36	5.07E-05	4.37
3	10	7	mwgecov2#2714	putative carbamoyl transferase; ygew	gene	1.01	7.64	6.00	3.10E-04	2.02
12	8	16	mwgecov2#2050	pts system, fructose-specific iia/fpr component; frub	gene	1.00	8.19	6.90	8.91E-05	3.60
8	8	7	mwgecov2#1965	orf, hypothetical protein; b2080	gene	1.00	10.54	8.64	1.06E-05	6.35
7	9	16	mwgecov2#2607	orf, hypothetical protein; ygbf	gene	1.00	9.51	7.67	3.43E-05	4.87
12	8	15	mwgecov2#1956	orf, hypothetical protein; b2071	gene	1.00	8.05	7.99	2.29E-05	5.36
11	15	3	mwgecov2#4030	l-idonate dehydrogenase; idnd	gene	1.00	8.49	5.46	6.83E-04	1.01
6	6	18	mwgecov2#1825	cytoplasmic alpha-amylase; amya	gene	1.00	9.40	9.50	4.25E-06	7.56
9	4	12	mwgecov2#0844	probable formate transporter (formate channel 1); foca	gene	1.00	11.93	5.71	4.77E-04	1.49
16	7	3	mwgecov2#1771	orf, hypothetical protein; yecd	gene	0.99	8.63	7.23	5.87E-05	4.14
12	7	8	mwgecov2#1864	putative 2-component sensor protein; yedv	gene	0.99	8.25	5.07	1.28E-03	0.28

4	8	9	mwgecov2#2154	orf, hypothetical protein; b2275	gene	0.98	7.77	7.35	5.17E-05	4.34
3	5	15	mwgecov2#1372	putative oxidoreductase; yncb	gene	0.98	8.36	8.73	9.54E-06	6.48
2	7	3	mwgecov2#1728	orf, hypothetical protein; b1821	gene	0.98	9.33	7.04	7.44E-05	3.83
10	11	13	mwgecov2#3068	orf, hypothetical protein; yhco	gene	0.98	8.93	6.71	1.14E-04	3.28
15	4	9	mwgecov2#0987	orf, hypothetical protein; ycei	gene	0.97	9.79	6.51	1.52E-04	2.93
8	4	16	mwgecov2#0911	hydrogenase-1 large subunit; hyab	gene	0.97	7.69	8.43	1.37E-05	6.03
7	9	12	mwgecov2#2611	orf, hypothetical protein; b2758	gene	0.97	10.76	7.27	5.62E-05	4.21
4	9	15	mwgecov2#2536	atp-binding component of transport system for glycine, betaine and proline; prov	gene	0.97	9.77	10.72	1.16E-06	9.17
5	6	17	mwgecov2#1707	putative tartrate dehydrogenase; yeau	gene	0.96	10.50	5.04	1.34E-03	0.21
15	8	15	mwgecov2#1931	probable export protein; wzxc	gene	0.96	8.78	7.58	3.88E-05	4.71
5	6	6	mwgecov2#1411	orf, hypothetical protein; b1490	gene	0.96	9.61	6.61	1.31E-04	3.10
4	6	15	mwgecov2#1590	orf, hypothetical protein; b1680	gene	0.96	7.87	7.62	3.63E-05	4.79
9	15	10	mwgecov2#3878	orf, hypothetical protein; phna	gene	0.95	9.50	6.09	2.74E-04	2.19
3	9	18	mwgecov2#2412	orf, hypothetical protein; ypha	gene	0.95	8.56	7.55	4.00E-05	4.68
3	4	6	mwgecov2#1090	orf, hypothetical protein; ycgw	gene	0.94	7.71	5.89	3.65E-04	1.82
14	7	12	mwgecov2#1811	excinuclease abc, subunit c; repair of uv damage to dna; uvrc	gene	0.94	8.75	9.40	4.66E-06	7.44
4	6	17	mwgecov2#1778	copper homeostasis protein; cutc	gene	0.93	9.57	8.97	7.59E-06	6.82
3	7	18	mwgecov2#2044	putative transcriptional regulator; yeil	gene	0.92	7.60	8.32	1.54E-05	5.87
6	4	3	mwgecov2#0781	d-alanyl-d-alanine carboxypeptidase; penicillin-binding protein 6; dacc	gene	0.92	9.06	8.90	8.07E-06	6.73
7	2	14	mwgecov2#0713	orf, hypothetical protein; ybhh	gene	0.91	8.01	9.36	4.90E-06	7.37
3	11	9	mwgecov2#2694	orf, hypothetical protein; yqeh	gene	0.91	7.71	7.29	5.49E-05	4.25
6	15	3	mwgecov2#4007	mg2+ transport atpase, p-type 1; mgta	gene	0.91	9.27	6.97	8.20E-05	3.71
6	7	13	mwgecov2#1929	putative colanic acid biosynthesis glycosyl transferase; wcal	gene	0.91	8.93	6.49	1.56E-04	2.90
1	2	13	mwgecov2#0572	putative oxidoreductase; ybdr	gene	0.91	8.06	6.20	2.36E-04	2.38
5	5	12	mwgecov2#1423	putative adhesin; similar to fimh protein; b1502	gene	0.91	8.37	5.82	4.04E-04	1.69
14	7	13	mwgecov2#1927	homolog of salmonella utp--glucose-1-p uridyltransferase, probably a udp-gal transferase; galf	gene	0.90	10.14	5.67	5.02E-04	1.42
8	4	12	mwgecov2#0915	nickel incorporation into hydrogenase-1 proteins; hyaf	gene	0.90	8.76	5.81	4.13E-04	1.67
10	6	17	mwgecov2#1730	orf, hypothetical protein; b1824	gene	0.90	14.70	9.26	5.29E-06	7.24
11	8	1	mwgecov2#2136	orf, hypothetical protein; b2257	gene	0.90	8.29	5.50	6.44E-04	1.09
8	12	16	mwgecov2#3191	orf, hypothetical protein; yhfl	gene	0.90	8.19	6.81	9.99E-05	3.45

13	4	14	mwgecov2#1031	pts system, glucose-specific iibc component; ptsg	gene	0.90	9.98	5.87	3.74E-04	1.79
15	15	4	mwgecov2#4123	putative regulator; yjjq	gene	0.88	7.83	8.23	1.72E-05	5.74
13	5	12	mwgecov2#1139	enzyme in alternate path of synthesis of 5-aminolevulinate; hema	gene	0.86	7.25	6.50	1.54E-04	2.92
12	9	16	mwgecov2#2628	putative transport protein; yqce	gene	0.86	8.35	8.21	1.76E-05	5.71
10	6	11	mwgecov2#1544	orf, hypothetical protein; ydgq	gene	0.86	8.03	7.21	5.93E-05	4.12
8	6	4	mwgecov2#1291	orf, hypothetical protein; b1367	gene	0.85	7.54	6.80	1.00E-04	3.44
16	4	4	mwgecov2#0921	putative function in exopolysaccharide production; yccz	gene	0.85	9.26	8.92	7.94E-06	6.75
5	15	3	mwgecov2#3983	putative transport protein; ytfl	gene	0.84	7.84	6.10	2.73E-04	2.20
12	8	6	mwgecov2#2252	putative enzyme; b2374	gene	0.83	8.52	5.29	9.02E-04	0.69
3	8	7	mwgecov2#1942	putative glycosyl transferase; wcac	gene	0.83	7.94	6.64	1.26E-04	3.15
3	15	3	mwgecov2#4032	putative oxidoreductase; yjgb	gene	0.82	9.58	7.97	2.36E-05	5.33
5	8	4	mwgecov2#1991	putative type-1 fimbrial protein; yeha	gene	0.82	7.56	6.22	2.32E-04	2.41
16	3	4	mwgecov2#0727	molybdopterin biosynthesis, protein c; moac	gene	0.82	9.99	6.44	1.68E-04	2.80
5	12	3	mwgecov2#3037	orf, hypothetical protein; yrbl	gene	0.81	10.13	7.77	3.06E-05	5.02
15	2	14	mwgecov2#0711	putative isomerase; ybhe	gene	0.81	9.46	7.19	6.09E-05	4.09
5	6	8	mwgecov2#1620	vitamin b12 transport; btue	gene	0.81	8.79	5.53	6.18E-04	1.15
6	6	17	mwgecov2#1731	orf, hypothetical protein; b1825	gene	0.81	9.62	7.86	2.70E-05	5.16
7	6	14	mwgecov2#1853	orf, hypothetical protein; b1957	gene	0.80	10.93	6.38	1.82E-04	2.70
9	15	11	mwgecov2#3974	orf, hypothetical protein; ytfe	gene	0.79	8.40	6.69	1.17E-04	3.25
13	4	12	mwgecov2#0843	formate acetyltransferase 1; pflb	gene	0.79	9.32	6.31	2.02E-04	2.57
3	8	3	mwgecov2#1946	probable protein-tyrosine-phosphatase; wzb	gene	0.79	8.93	5.52	6.26E-04	1.13
5	13	4	mwgecov2#3711	putative regulator; yiit	gene	0.78	8.79	7.16	6.34E-05	4.03
9	8	18	mwgecov2#2168	nadh dehydrogenase transcriptional regulator, lysr family; lrha	gene	0.78	10.18	5.31	8.70E-04	0.74
11	4	3	mwgecov2#0804	arginine 3rd transport system periplasmic binding protein; arti	gene	0.78	10.18	6.21	2.34E-04	2.39
1	7	3	mwgecov2#1704	orf, hypothetical protein; year	gene	0.77	8.98	8.83	8.64E-06	6.63
4	3	4	mwgecov2#0730	orf, hypothetical protein; ybhm	gene	0.76	8.06	6.00	3.09E-04	2.02
14	6	11	mwgecov2#1543	orf, hypothetical protein; b1631	gene	0.76	8.06	7.43	4.68E-05	4.48
4	6	16	mwgecov2#1684	putative oxidoreductase; ydjj	gene	0.75	8.65	7.66	3.46E-05	4.86
16	7	4	mwgecov2#1867	putative reductase; b1971	gene	0.75	8.18	7.18	6.15E-05	4.07
15	15	9	mwgecov2#3831	orf, hypothetical protein; yjbr	gene	0.75	9.74	7.30	5.45E-05	4.27
6	15	10	mwgecov2#3903	transcriptional activator of cad operon; cadc	gene	0.74	6.85	5.96	3.28E-04	1.95
2	2	12	mwgecov2#0500	putative fimbrial-like protein; sfma	gene	0.74	7.60	4.96	1.51E-03	0.07

15	4	16	mwgecov2#0885	orf, hypothetical protein; ycbw	gene	0.74	9.91	8.34	1.51E-05	5.90
7	4	3	mwgecov2#0805	atp-binding component of 3rd arginine transport system; artp	gene	0.73	10.50	7.38	4.92E-05	4.41
3	9	9	mwgecov2#2326	detox protein; cchb	gene	0.73	8.42	6.33	1.96E-04	2.61
10	4	7	mwgecov2#0776	orf, hypothetical protein; b0834	gene	0.73	8.01	5.02	1.37E-03	0.18
7	15	3	mwgecov2#4031	gluconate kinase, thermosensitive glucokinase; idnk	gene	0.73	8.10	4.93	1.59E-03	0.00
3	7	5	mwgecov2#1558	superoxide dismutase precursor (cu-zn); sodc	gene	0.73	8.12	6.72	1.13E-04	3.29
1	5	1	mwgecov2#1146	cation transport regulator; chab	gene	0.72	7.73	7.79	2.96E-05	5.06
4	7	9	mwgecov2#1578	orf, hypothetical protein; b1668	gene	0.72	7.84	6.46	1.63E-04	2.84
9	4	13	mwgecov2#0938	orf, hypothetical protein; ycce	gene	0.72	7.96	4.96	1.50E-03	0.07
5	1	5	mwgecov2#0019	na+/h antiporter, ph dependent; nhaa	gene	0.72	9.99	6.87	9.30E-05	3.54
10	3	15	mwgecov2#0976	orf, hypothetical protein; b1044	gene	0.72	7.32	5.00	1.42E-03	0.14
2	6	15	mwgecov2#1542	orf, hypothetical protein; ydgo	gene	0.72	9.09	6.49	1.56E-04	2.90
15	2	3	mwgecov2#0039	probable flavoprotein subunit, carnitine metabolism; fixb	gene	0.71	7.64	5.19	1.06E-03	0.50
14	6	3	mwgecov2#1147	cation transport regulator; chac	gene	0.71	8.16	6.16	2.49E-04	2.31
7	8	9	mwgecov2#2129	orf, hypothetical protein; b2250	gene	0.71	7.45	6.08	2.79E-04	2.17
10	5	5	mwgecov2#1162	hnr protein; hnr	gene	0.70	8.54	5.69	4.92E-04	1.45
9	6	11	mwgecov2#1520	response transcriptional regulatory protein (rstb sensor); rsta	gene	0.70	7.78	5.56	5.87E-04	1.21
5	8	13	mwgecov2#2079	heme exporter protein b, cytochrome c-type biogenesis protein; ccmb	gene	0.70	8.50	9.15	6.06E-06	7.08
10	6	16	mwgecov2#1634	orf, hypothetical protein; b1724	gene	0.70	10.85	6.92	8.66E-05	3.64
4	7	16	mwgecov2#2262	orf, hypothetical protein; b2384	gene	0.69	8.00	7.65	3.53E-05	4.83
4	8	11	mwgecov2#1962	putative transport protein; yegb	gene	0.69	7.46	6.27	2.13E-04	2.51
12	4	4	mwgecov2#0922	orf, hypothetical protein; ymca	gene	0.69	8.97	7.33	5.27E-05	4.31
10	12	12	mwgecov2#3148	putative general secretion pathway for protein export (gsp) (type ii traffic warden atpase); yheg	gene	0.68	7.59	5.24	9.74E-04	0.60
13	6	14	mwgecov2#1803	ferritin-like protein; yeci	gene	0.68	8.96	5.05	1.32E-03	0.24
7	10	13	mwgecov2#2899	putative o-sialoglycoprotein endopeptidase; ygjd	gene	0.68	8.69	5.23	9.91E-04	0.58
6	3	15	mwgecov2#0977	putative polyprotein; b1045	gene	0.67	8.50	7.62	3.64E-05	4.78
12	12	2	mwgecov2#3396	putative transcriptional regulator lysr-type; yiau	gene	0.67	8.06	5.41	7.38E-04	0.92
7	2	4	mwgecov2#0128	putative fimbrial-like protein; yadc	gene	0.67	8.58	6.02	3.03E-04	2.05
8	6	15	mwgecov2#1589	orf, hypothetical protein; ynha	gene	0.66	8.04	5.88	3.68E-04	1.81
12	12	10	mwgecov2#3388	orf, hypothetical protein; yiam	gene	0.65	7.71	7.06	7.21E-05	3.87
11	5	14	mwgecov2#1274	exonuclease viii, ds dna exonuclease, 5' --> 3' specific; rece	gene	0.65	9.22	5.52	6.26E-04	1.13

2	15	10	mwgecov2#3904	orf, hypothetical protein; yjdc	gene	0.65	9.08	6.93	8.63E-05	3.64
2	1	14	mwgecov2#0113	s-adenosylmethionine decarboxylase; sped	gene	0.65	7.89	5.45	6.92E-04	1.00
9	10	13	mwgecov2#2850	orf, hypothetical protein; yqhe	gene	0.65	8.17	6.96	8.30E-05	3.70
3	7	11	mwgecov2#1742	orf, hypothetical protein; -	gene	0.65	10.47	5.18	1.08E-03	0.48
16	6	7	mwgecov2#1595	orf, hypothetical protein; b1685	gene	0.64	8.09	5.60	5.56E-04	1.28
14	4	4	mwgecov2#0873	putative atp-binding component of a transport system; ycbe	gene	0.64	8.70	5.58	5.67E-04	1.25
15	4	1	mwgecov2#0995	glutaredoxin 2; grxb	gene	0.64	10.40	4.97	1.50E-03	0.08
8	7	5	mwgecov2#1581	putative oxidoreductase, fe-s subunit; b1671	gene	0.64	8.08	6.27	2.13E-04	2.51
8	6	16	mwgecov2#1683	putative aldolase; b1773	gene	0.63	9.43	7.16	6.34E-05	4.03
14	11	6	mwgecov2#2767	putative transport protein; yggb	gene	0.63	11.72	6.70	1.16E-04	3.25
8	2	11	mwgecov2#0453	orf, hypothetical protein; ybaq	gene	0.63	9.34	5.67	5.03E-04	1.42
14	8	4	mwgecov2#2013	putative transport system permease protein; yehz	gene	0.62	8.22	5.51	6.31E-04	1.11
3	8	9	mwgecov2#2130	orf, hypothetical protein; yfao	gene	0.62	8.63	5.85	3.86E-04	1.74
3	6	14	mwgecov2#1854	orf, hypothetical protein; yedi	gene	0.62	8.02	5.24	9.66E-04	0.61
3	13	11	mwgecov2#3656	orf, hypothetical protein; yihi	gene	0.61	10.42	5.65	5.17E-04	1.37
2	8	8	mwgecov2#2012	putative transport system permease protein; yehy	gene	0.60	7.44	5.22	1.01E-03	0.56
7	10	16	mwgecov2#2801	orf, hypothetical protein; yggh	gene	0.60	9.46	5.56	5.87E-04	1.21
15	8	1	mwgecov2#2135	orf, hypothetical protein; b2256	gene	0.60	7.76	4.98	1.46E-03	0.11
14	10	10	mwgecov2#2971	pts system n-acetylgalactosamine-specific iic component 1; agac	gene	0.59	7.00	5.86	3.83E-04	1.76
14	7	9	mwgecov2#1527	membrane-associated protein; uidc	gene	0.59	7.45	6.26	2.17E-04	2.49
6	1	13	mwgecov2#0031	transcriptional regulator of cai operon; caif	gene	0.59	8.32	6.95	8.30E-05	3.69
4	7	10	mwgecov2#1672	orf, hypothetical protein; b1762	gene	0.59	8.11	5.87	3.77E-04	1.78
8	2	7	mwgecov2#0457	putative transcriptional regulator; ybbi	gene	0.58	9.47	5.93	3.47E-04	1.89
8	10	11	mwgecov2#2733	putative enzyme; b2889	gene	0.58	9.68	5.12	1.17E-03	0.38
13	7	7	mwgecov2#1697	orf, hypothetical protein; yeak	gene	0.58	8.02	5.38	7.78E-04	0.86
3	4	13	mwgecov2#0986	orf, hypothetical protein; ycea	gene	0.58	8.03	6.06	2.86E-04	2.13
15	8	2	mwgecov2#2231	orf, hypothetical protein; b2353	gene	0.58	7.96	5.60	5.56E-04	1.28
11	13	5	mwgecov2#3468	two-module transport protein; yick	gene	0.57	7.15	5.78	4.33E-04	1.61
1	14	8	mwgecov2#3900	putative peptide transporter; yjdl	gene	0.56	8.72	5.23	9.90E-04	0.58
10	15	12	mwgecov2#4094	orf, hypothetical protein; yjim	gene	0.56	6.95	6.47	1.60E-04	2.86
14	5	17	mwgecov2#1151	nitrate/nitrate sensor, histidine protein kinase acts on narl regulator; narx	gene	0.56	8.90	5.74	4.52E-04	1.55
4	4	14	mwgecov2#1106	orf, hypothetical protein; ycgj	gene	0.55	9.87	5.92	3.50E-04	1.87

10	14	16	mwgecov2#3914	orf, hypothetical protein; yjej	gene	0.54	8.02	5.47	6.72E-04	1.03
6	8	8	mwgecov2#2011	putative atp-binding component of a transport system; yehx	gene	0.54	7.47	6.23	2.26E-04	2.44
5	14	7	mwgecov2#3805	xylose-proton symport; xyle	gene	0.54	7.47	7.10	6.87E-05	3.93
1	4	16	mwgecov2#0842	pyruvate formate lyase activating enzyme 1; pfla	gene	0.54	9.31	6.15	2.53E-04	2.29
2	6	3	mwgecov2#1150	pleiotrophic regulation of anaerobic respiration: response regulator for nar, frd, dms and tor genes; narl	gene	0.54	9.90	5.49	6.47E-04	1.08
6	11	10	mwgecov2#2765	putative actin; ygge	gene	0.51	9.86	5.27	9.24E-04	0.66
6	3	10	mwgecov2#0483	putative transport; ybby	gene	0.51	7.74	6.57	1.40E-04	3.03
1	5	2	mwgecov2#1240	putative oxidoreductase; ycjq	gene	0.50	7.53	5.02	1.38E-03	0.18
9	16	12	mwgecov2#4871	cold shock protein; cspc	gene	0.49	14.74	5.26	9.46E-04	0.63
6	7	10	mwgecov2#1623	phenylalanine trna synthetase, beta-subunit; phet	gene	0.47	12.56	5.27	9.28E-04	0.66
7	3	14	mwgecov2#0907	orf, hypothetical protein; b0968	gene	0.46	9.44	5.08	1.27E-03	0.29
10	7	2	mwgecov2#1630	ankyrin repeat protein; -	gene	0.44	8.06	5.03	1.35E-03	0.20
6	6	3	mwgecov2#1149	putative factor; ychp	gene	0.43	7.99	5.37	7.84E-04	0.85
5	10	16	mwgecov2#2753	orf, hypothetical protein; ygfb	gene	-0.44	11.38	-5.04	1.34E-03	0.21
3	4	1	mwgecov2#0998	orf, hypothetical protein; yceh	gene	-0.44	9.31	-5.60	5.56E-04	1.29
4	5	17	mwgecov2#1200	orf, hypothetical protein; ycin	gene	-0.46	10.53	-5.00	1.41E-03	0.15
1	8	9	mwgecov2#2084	ferredoxin-type protein: electron transfer; napg	gene	-0.47	7.76	-4.97	1.50E-03	0.07
10	13	11	mwgecov2#3630	orf, hypothetical protein; yigp	gene	-0.48	9.43	-5.15	1.13E-03	0.42
2	5	3	mwgecov2#1360	orf, hypothetical protein; -	gene	-0.48	7.53	-4.99	1.45E-03	0.12
14	14	7	mwgecov2#3827	alanine racemase 1; alr	gene	-0.49	7.66	-5.90	3.59E-04	1.84
2	8	4	mwgecov2#2016	penicillin-binding protein 7; pbpg	gene	-0.51	7.51	-5.57	5.81E-04	1.22
2	5	13	mwgecov2#1158	a protaminelike protein; tpr	gene	-0.51	8.71	-5.29	9.02E-04	0.69
14	13	7	mwgecov2#3633	putative histone; b3837	gene	-0.52	8.39	-5.65	5.17E-04	1.38
12	14	4	mwgecov2#3570	branched-chain amino-acid aminotransferase; ilve	gene	-0.53	8.91	-6.05	2.90E-04	2.11
14	10	1	mwgecov2#2481	orf, hypothetical protein; b2619	gene	-0.54	8.90	-5.58	5.68E-04	1.25
6	16	2	mwgecov2#5954	l-isoaspartate protein carboxylmethyltransferase type ii; pcm	gene	-0.54	9.05	-6.65	1.23E-04	3.18
5	11	10	mwgecov2#2741	orf, hypothetical protein; ygfy	gene	-0.55	8.45	-6.60	1.33E-04	3.09
7	13	7	mwgecov2#3659	histidine protein kinase sensor for glng regulator (nitrogen regulator ii, nrii); glnl	gene	-0.55	7.99	-5.57	5.78E-04	1.23
2	12	11	mwgecov2#3054	n-acetylneuraminate lyase (aldolase); catabolism of sialic acid; not k12?; nana	gene	-0.55	8.81	-5.05	1.32E-03	0.24
7	14	2	mwgecov2#3743	phosphoenolpyruvate carboxylase; ppc	gene	-0.56	9.91	-6.36	1.85E-04	2.67

14	12	10	mwgecov2#3339	ketodeoxygluconokinase; kdgk	gene	-0.56	8.17	-6.91	8.86E-05	3.61
13	13	15	mwgecov2#3601	porphobilinogen deaminase = hydroxymethylbilane synthase; hemc	gene	-0.56	10.02	-5.07	1.29E-03	0.27
8	14	18	mwgecov2#4153	catabolite repression sensor kinase for phob; alternative sensor for pho regulon; crec	gene	-0.57	7.85	-5.75	4.47E-04	1.57
3	10	6	mwgecov2#2600	orf, hypothetical protein; ygbp	gene	-0.57	10.03	-6.41	1.75E-04	2.75
16	13	13	mwgecov2#3483	putative transcriptional regulator; yidf	gene	-0.58	8.21	-5.14	1.13E-03	0.42
5	12	14	mwgecov2#3313	oligopeptidase a; prlc	gene	-0.59	8.96	-5.43	7.09E-04	0.97
2	15	3	mwgecov2#4008	orf, hypothetical protein; yjgf	gene	-0.59	8.66	-6.03	2.97E-04	2.08
2	5	7	mwgecov2#1356	putative membrane transport protein; b1433	gene	-0.59	7.59	-6.51	1.52E-04	2.93
9	11	10	mwgecov2#2740	orf, hypothetical protein; b2896	gene	-0.60	8.51	-5.49	6.47E-04	1.08
16	12	11	mwgecov2#3099	putative transport system permease protein; yhdy	gene	-0.60	7.68	-5.17	1.08E-03	0.48
14	13	11	mwgecov2#3629	2-octaprenyl-6-methoxy-1,4-benzoquinone --> 2-octaprenyl-3-methyl-6-methoxy-1,4-benzoquinone; ubie	gene	-0.60	8.89	-5.17	1.09E-03	0.46
13	7	4	mwgecov2#1795	regulator of flagellar biosynthesis, acting on class 2 operons; transcriptional initiation factor; flhd	gene	-0.60	8.28	-5.70	4.88E-04	1.46
6	13	11	mwgecov2#3631	orf, hypothetical protein; yigr	gene	-0.61	8.44	-6.82	9.84E-05	3.47
1	10	2	mwgecov2#2556	pts system, glucitol/sorbitol-specific iic component, one of two; srla	gene	-0.61	12.51	-5.15	1.12E-03	0.44
1	10	9	mwgecov2#2856	1-acyl-sn-glycerol-3-phosphate acyltransferase; plsc	gene	-0.61	8.27	-6.34	1.92E-04	2.63
6	6	13	mwgecov2#1735	heat shock protein, integral membrane protein; htpx	gene	-0.62	10.22	-5.77	4.34E-04	1.60
2	14	6	mwgecov2#3716	orf, hypothetical protein; yiiu	gene	-0.62	10.04	-5.80	4.19E-04	1.65
8	7	6	mwgecov2#1675	orf, hypothetical protein; ydja	gene	-0.63	10.05	-5.34	8.24E-04	0.80
3	15	6	mwgecov2#3932	orf, hypothetical protein; yjes	gene	-0.63	7.97	-5.59	5.66E-04	1.26
16	13	12	mwgecov2#3771	thiamin biosynthesis, thiazole moiety; thie	gene	-0.63	8.48	-5.06	1.30E-03	0.26
8	15	12	mwgecov2#4141	orf, hypothetical protein; smp	gene	-0.64	8.34	-6.02	3.03E-04	2.05
5	8	18	mwgecov2#2169	putative aminotransferase; b2290	gene	-0.64	7.99	-5.71	4.79E-04	1.49
14	10	17	mwgecov2#2869	orf, hypothetical protein; yqia	gene	-0.65	8.72	-5.90	3.59E-04	1.84
9	5	17	mwgecov2#1128	putative dihydroxyacetone kinase (ec 2.7.1.2); b1199	gene	-0.65	12.87	-5.68	5.00E-04	1.43
3	7	10	mwgecov2#1648	pep-dependent phosphotransferase enzyme iv for cellobiose, arbutin, and salicin; cela	gene	-0.65	8.63	-5.01	1.39E-03	0.17
6	12	11	mwgecov2#3053	sialic acid transporter; nant	gene	-0.66	8.09	-4.97	1.50E-03	0.08
12	4	11	mwgecov2#0820	putative atp-binding component of a transport system; ybjz	gene	-0.66	8.53	-5.34	8.24E-04	0.80
7	15	2	mwgecov2#3935	n-acetylmuramoyl-l-alanine amidase ii; a murein hydrolase; amib	gene	-0.67	8.44	-5.63	5.32E-04	1.34
7	4	1	mwgecov2#0997	acetylation of n-terminal alanine of 30s ribosomal subunit protein s5; rimj	gene	-0.67	9.72	-6.21	2.32E-04	2.41

12	9	7	mwgecov2#2542	orf, hypothetical protein; ygah	gene	-0.67	8.28	-5.59	5.61E-04	1.27
6	13	17	mwgecov2#3433	probably hexose transferase; lipopolysaccharide core biosynthesis; rfak	gene	-0.68	8.33	-6.08	2.80E-04	2.16
3	14	12	mwgecov2#3944	orf, hypothetical protein; yjeb	gene	-0.68	9.19	-5.39	7.57E-04	0.89
11	14	3	mwgecov2#3452	orotate phosphoribosyltransferase; pyre	gene	-0.68	7.95	-5.92	3.50E-04	1.87
7	3	5	mwgecov2#0417	orf, hypothetical protein; ybae	gene	-0.68	8.11	-6.31	2.01E-04	2.58
3	13	8	mwgecov2#3754	glutamate racemase, required for biosynthesis of d-glutamate and peptidoglycan; muri	gene	-0.69	8.40	-5.76	4.40E-04	1.59
9	15	7	mwgecov2#3978	2':3'-cyclic-nucleotide 2'-phosphodiesterase; cpdb	gene	-0.69	8.17	-6.40	1.76E-04	2.74
3	6	1	mwgecov2#1368	orf, hypothetical protein; b1445	gene	-0.69	8.72	-6.03	3.00E-04	2.07
16	12	13	mwgecov2#3289	orf, hypothetical protein; b3472	gene	-0.69	9.42	-6.89	8.97E-05	3.58
2	4	8	mwgecov2#0872	aminopeptidase n; pepn	gene	-0.69	9.88	-5.77	4.33E-04	1.61
7	12	4	mwgecov2#3179	cyclic amp receptor protein; crp	gene	-0.69	10.04	-7.55	4.00E-05	4.67
11	11	10	mwgecov2#2788	glutathione synthetase; gshb	gene	-0.70	8.50	-5.63	5.31E-04	1.34
4	9	8	mwgecov2#2638	putative enzyme; ygca	gene	-0.70	8.95	-7.38	4.92E-05	4.41
4	13	8	mwgecov2#3778	dna-binding protein hu-alpha (hu-2); hupa	gene	-0.70	12.87	-6.15	2.53E-04	2.29
1	11	7	mwgecov2#2840	orf, hypothetical protein; yqha	gene	-0.71	7.98	-5.47	6.67E-04	1.04
13	5	6	mwgecov2#1233	phage shock protein: activates phage shock-protein expression; pspc	gene	-0.71	8.26	-5.04	1.34E-03	0.21
13	10	2	mwgecov2#2553	dna strand exchange and renaturation, dna-dependent atpase, dna- and atp-dependent coprotease; reca	gene	-0.72	11.28	-4.97	1.49E-03	0.09
15	10	9	mwgecov2#2901	dna biosynthesis; dna primase; dnag	gene	-0.72	9.76	-7.34	5.19E-05	4.33
16	10	13	mwgecov2#2921	orf, hypothetical protein; ygjr	gene	-0.72	9.30	-6.22	2.30E-04	2.42
5	10	15	mwgecov2#2657	positive regulator of the fuc operon; fucr	gene	-0.72	8.55	-6.55	1.43E-04	3.00
8	13	4	mwgecov2#3781	sensor kinase for hydg, hydrogenase 3 activity; hydh	gene	-0.72	7.66	-8.54	1.19E-05	6.20
5	11	7	mwgecov2#2839	putative reductase; b3001	gene	-0.72	9.07	-6.48	1.58E-04	2.88
13	10	13	mwgecov2#2849	putative oxidoreductase; yqhd	gene	-0.73	8.74	-6.76	1.07E-04	3.36
8	1	5	mwgecov2#0077	orf, hypothetical protein; yabb	gene	-0.74	9.67	-6.46	1.63E-04	2.84
8	13	15	mwgecov2#3675	putative phosphatase; yihx	gene	-0.74	10.32	-5.45	6.89E-04	1.00
6	14	7	mwgecov2#3829	diadenosine tetraphosphatase; apha	gene	-0.74	10.58	-5.59	5.62E-04	1.27
15	13	17	mwgecov2#3455	dna-damage-inducible protein; dind	gene	-0.74	7.62	-6.04	2.94E-04	2.09
5	11	2	mwgecov2#2749	aminomethyltransferase (t protein; tetrahydrofolate-dependent) of glycine cleavage system; gcvt	gene	-0.74	12.16	-7.15	6.39E-05	4.02
8	8	5	mwgecov2#2157	nadh dehydrogenase i chain l; nuol	gene	-0.75	10.66	-6.37	1.85E-04	2.68

12	16	16	mwgecov2#1689-r	glyceraldehyde-3-phosphate dehydrogenase a; gapa	gene	-0.76	12.56	-5.75	4.50E-04	1.55
6	14	8	mwgecov2#3923	fumarate reductase, anaerobic, flavoprotein subunit; frda	gene	-0.76	11.43	-5.52	6.22E-04	1.14
6	10	5	mwgecov2#2479	small membrane protein a; smpa	gene	-0.76	10.09	-5.00	1.43E-03	0.13
11	12	4	mwgecov2#3178	orf, hypothetical protein; yhfa	gene	-0.76	9.21	-7.45	4.59E-05	4.51
14	14	3	mwgecov2#3427	2-amino-3-ketobutyrate coa ligase (glycine acetyltransferase); kbl	gene	-0.76	10.90	-5.53	6.15E-04	1.16
7	11	6	mwgecov2#2793	putative resistance protein; yggt	gene	-0.77	8.83	-5.18	1.07E-03	0.50
6	9	6	mwgecov2#2399	putative aminotransferase; yfho	gene	-0.78	10.64	-5.05	1.33E-03	0.23
11	3	9	mwgecov2#0412	dna-binding protein hu-beta, ns1 (hu-1); hupb	gene	-0.78	12.55	-6.84	9.69E-05	3.49
13	9	12	mwgecov2#2561	regulator for gut (srl), glucitol operon; srlr	gene	-0.78	9.09	-6.44	1.68E-04	2.80
7	14	5	mwgecov2#3643	proline dipeptidase; pepq	gene	-0.78	9.41	-7.28	5.57E-05	4.23
1	15	2	mwgecov2#3888	regulator of melibiose operon; melr	gene	-0.79	8.03	-6.04	2.94E-04	2.09
15	14	7	mwgecov2#3851	glutamate-aspartate symport protein; gltp	gene	-0.79	8.50	-6.45	1.65E-04	2.82
1	12	18	mwgecov2#3310	universal stress protein; broad regulatory function?; uspa	gene	-0.79	11.28	-6.40	1.75E-04	2.74
9	14	12	mwgecov2#3894	putative 2-component transcriptional regulator; yjdg	gene	-0.80	7.71	-7.71	3.29E-05	4.93
9	11	15	mwgecov2#3234	orf, hypothetical protein; yhgi	gene	-0.81	10.50	-6.67	1.20E-04	3.21
4	11	17	mwgecov2#3114	putative transcriptional regulator; yhdm	gene	-0.81	8.53	-5.05	1.31E-03	0.25
8	9	2	mwgecov2#2451	orf, hypothetical protein; yfiq	gene	-0.81	9.07	-5.32	8.58E-04	0.75
12	6	8	mwgecov2#1690	orf, hypothetical protein; yead	gene	-0.81	10.01	-7.42	4.70E-05	4.47
15	13	8	mwgecov2#3753	outer membrane receptor for transport of vitamin b12, e colicins, and bacteriophage bf23; btub	gene	-0.82	8.88	-8.73	9.54E-06	6.48
1	7	14	mwgecov2#2000	putative regulator; yehi	gene	-0.82	8.92	-7.08	6.95E-05	3.91
12	14	9	mwgecov2#4066	orf, hypothetical protein; yjhq	gene	-0.82	8.22	-9.31	5.06E-06	7.30
10	11	6	mwgecov2#2768	fructose-bisphosphate aldolase, class ii; fba	gene	-0.82	11.81	-6.41	1.75E-04	2.75
7	13	10	mwgecov2#3559	ribokinase; rbsk	gene	-0.82	11.24	-6.10	2.72E-04	2.20
3	3	8	mwgecov2#0702	galactose-1-phosphate uridylyltransferase; galt	gene	-0.82	9.13	-6.13	2.61E-04	2.26
2	13	1	mwgecov2#3450	deoxyuridinetriphosphatase; dut	gene	-0.83	9.42	-5.62	5.37E-04	1.33
6	15	7	mwgecov2#4003	anaerobic ribonucleoside-triphosphate reductase; nrdd	gene	-0.83	7.47	-8.11	2.01E-05	5.55
2	12	3	mwgecov2#3062	orf, hypothetical protein; yhcb	gene	-0.84	9.60	-8.68	1.02E-05	6.40
6	16	17	mwgecov2#0412-r	dna-binding protein hu-beta, ns1 (hu-1); hupb	gene	-0.84	12.28	-6.41	1.74E-04	2.76
16	11	13	mwgecov2#3115	orf, hypothetical protein; yhdn	gene	-0.84	9.96	-4.96	1.52E-03	0.06
9	7	16	mwgecov2#2188	histidine-binding periplasmic protein of high-affinity histidine transport system; hisj	gene	-0.84	8.85	-5.65	5.16E-04	1.39

7	13	6	mwgecov2#3563	transcription regulator; yifda	gene	-0.85	7.54	-8.89	8.11E-06	6.71
7	3	13	mwgecov2#0813	putative enzyme; b0872	gene	-0.85	8.73	-5.30	8.89E-04	0.71
1	14	14	mwgecov2#4088	orf, hypothetical protein; yjig	gene	-0.86	8.45	-6.68	1.19E-04	3.22
5	9	13	mwgecov2#2273	orf, hypothetical protein; yfed	gene	-0.86	9.04	-4.94	1.56E-03	0.02
6	13	3	mwgecov2#3639	putative oxidoreductase; yigc	gene	-0.87	10.25	-9.21	5.59E-06	7.17
2	15	1	mwgecov2#3818	dna-damage-inducible protein f; dinf	gene	-0.87	7.85	-9.41	4.66E-06	7.44
5	14	12	mwgecov2#3895	putative 2-component sensor protein; yjdh	gene	-0.87	8.32	-6.92	8.63E-05	3.64
10	13	2	mwgecov2#3542	membrane-bound atp synthase, f1 sector, alpha-subunit; atpa	gene	-0.87	11.50	-5.65	5.17E-04	1.38
6	2	13	mwgecov2#0595	orf, hypothetical protein; ybed	gene	-0.87	9.50	-6.56	1.42E-04	3.02
9	16	18	mwgecov2#3555-r	d-ribose high-affinity transport system; membrane-associated protein; rbsd	gene	-0.88	10.86	-7.11	6.74E-05	3.96
8	2	13	mwgecov2#0641	negative modulator of initiation of replication; seqa	gene	-0.88	9.95	-6.46	1.62E-04	2.85
6	10	16	mwgecov2#2777	transketolase 1 isozyme; tkta	gene	-0.89	11.05	-6.99	7.87E-05	3.76
2	14	12	mwgecov2#3920	fumarate reductase, anaerobic, membrane anchor polypeptide; frdd	gene	-0.90	8.51	-9.41	4.66E-06	7.45
1	14	7	mwgecov2#3806	part of maltose permease, inner membrane; malg	gene	-0.90	8.57	-5.11	1.19E-03	0.36
7	13	18	mwgecov2#3551	asparagine synthetase a; asna	gene	-0.91	7.95	-4.95	1.54E-03	0.04
9	11	2	mwgecov2#2748	in glycine cleavage complex, carrier of aminomethyl moiety via covalently bound lipoyl cofactor; gcvh	gene	-0.92	13.37	-5.62	5.42E-04	1.32
14	14	5	mwgecov2#3617	outer membrane phospholipase a; plda	gene	-0.93	7.82	-5.52	6.24E-04	1.13
1	9	3	mwgecov2#2476	phage lambda replication; host dna synthesis; heat shock protein; protein repair; grpe	gene	-0.93	10.17	-5.93	3.47E-04	1.89
8	3	17	mwgecov2#0833	serine trna synthetase; also charges selenocystein trna with serine; sers	gene	-0.94	11.59	-7.22	5.87E-05	4.14
2	14	2	mwgecov2#3720	heat shock protein hslvu, proteasome-related peptidase subunit; hslv	gene	-0.95	11.11	-6.89	8.97E-05	3.59
7	13	14	mwgecov2#3555	d-ribose high-affinity transport system; membrane-associated protein; rbsd	gene	-0.95	11.11	-6.07	2.82E-04	2.15
8	13	17	mwgecov2#3481	ilvb operon leader peptide; ivbl	gene	-0.95	9.53	-6.11	2.69E-04	2.22
14	13	2	mwgecov2#3541	membrane-bound atp synthase, f1 sector, gamma-subunit; atpg	gene	-0.96	11.27	-8.13	1.96E-05	5.58
6	15	1	mwgecov2#3817	regulator for sos(lexa) regulon; lexa	gene	-0.97	7.94	-8.35	1.48E-05	5.92
14	5	11	mwgecov2#1349	orf, hypothetical protein; ydch	gene	-0.98	9.68	-6.86	9.32E-05	3.54
11	3	8	mwgecov2#0700	galactose-1-epimerase (mutarotase); galm	gene	-0.98	10.33	-7.35	5.13E-05	4.35
4	8	1	mwgecov2#2162	nadh dehydrogenase i chain g; nuog	gene	-1.00	10.93	-7.99	2.29E-05	5.37
13	15	3	mwgecov2#3981	orf, hypothetical protein; ytfj	gene	-1.01	9.25	-6.12	2.67E-04	2.23
5	5	16	mwgecov2#1419	putative sulfatase; b1498	gene	-1.02	8.29	-6.01	3.08E-04	2.03
14	13	6	mwgecov2#3537	l-glutamine:d-fructose-6-phosphate aminotransferase; glms	gene	-1.02	10.28	-8.62	1.08E-05	6.33

16	7	15	mwgecov2#2163	nadh dehydrogenase i chain f; nuof	gene	-1.06	10.54	-6.08	2.79E-04	2.17
5	11	5	mwgecov2#2649	l-serine dehydratase (deaminase), l-sd2; sdab	gene	-1.07	8.40	-5.48	6.58E-04	1.06
10	8	2	mwgecov2#2208	chorismate synthase; aroc	gene	-1.08	10.43	-5.92	3.50E-04	1.87
1	5	13	mwgecov2#1134	orf, hypothetical protein; ychh	gene	-1.12	11.45	-7.86	2.70E-05	5.16
8	7	13	mwgecov2#1977	galactitol-specific enzyme iia of phosphotransferase system; gata	gene	-1.12	13.49	-8.38	1.44E-05	5.97
13	8	18	mwgecov2#2167	nadh dehydrogenase i chain a; nuoa	gene	-1.13	11.19	-5.60	5.56E-04	1.28
6	14	6	mwgecov2#3715	facilitated diffusion of glycerol; glpf	gene	-1.13	10.30	-8.00	2.29E-05	5.38
13	6	7	mwgecov2#1523	fumarase c= fumarate hydratase class ii; isozyme; fumc	gene	-1.14	8.35	-5.96	3.28E-04	1.96
15	3	9	mwgecov2#0411	dna-binding, atp-dependent protease la; heat shock k-protein; lon	gene	-1.14	10.68	-9.61	3.76E-06	7.72
3	13	6	mwgecov2#3564	transcription regulator; yifda	gene	-1.15	8.69	-7.88	2.63E-05	5.20
12	8	1	mwgecov2#2160	nadh dehydrogenase i chain i; nuoi	gene	-1.16	10.93	-8.62	1.08E-05	6.32
10	3	8	mwgecov2#0676	orf, hypothetical protein; b0725	gene	-1.16	8.01	-5.51	6.31E-04	1.12
2	14	18	mwgecov2#4108	host restriction; endonuclease r; hsdr	gene	-1.18	8.83	-10.69	1.17E-06	9.13
3	16	17	mwgecov2#0328-r	2-keto-4-pentenoate hydratase; mhpd	gene	-1.18	10.92	-9.06	6.79E-06	6.96
6	15	5	mwgecov2#3813	chorismate lyase; ubic	gene	-1.20	8.23	-9.33	5.01E-06	7.34
5	5	6	mwgecov2#1235	phage shock protein; pspe	gene	-1.20	9.54	-8.54	1.20E-05	6.20
16	3	1	mwgecov2#0443	chaperone hsp90, heat shock protein c 62.5; htpg	gene	-1.21	9.16	-9.39	4.71E-06	7.42
9	10	2	mwgecov2#2554	orf, hypothetical protein; ygad	gene	-1.24	9.93	-9.35	4.94E-06	7.36
3	13	7	mwgecov2#3660	glutamine synthetase; glna	gene	-1.24	9.61	-9.97	2.50E-06	8.20
4	7	13	mwgecov2#1978	putative tagatose 6-phosphate kinase 1; gatz	gene	-1.25	13.81	-5.85	3.85E-04	1.75
7	9	1	mwgecov2#2333	putative multimodular enzyme; b2463	gene	-1.25	9.58	-8.38	1.44E-05	5.97
2	13	6	mwgecov2#3540	membrane-bound atp synthase, f1 sector, beta-subunit; atpd	gene	-1.25	11.88	-11.60	4.63E-07	10.23
16	13	7	mwgecov2#3681	formate dehydrogenase, cytochrome b556 (fdo) subunit; fdoi	gene	-1.26	11.05	-6.18	2.42E-04	2.35
6	13	6	mwgecov2#3539	membrane-bound atp synthase, f1 sector, epsilon-subunit; atpc	gene	-1.26	11.67	-6.75	1.09E-04	3.34
6	14	14	mwgecov2#4111	orf, hypothetical protein; yjix	gene	-1.27	9.35	-7.44	4.61E-05	4.50
5	10	5	mwgecov2#2455	heat shock protein; clpb	gene	-1.27	10.21	-8.49	1.26E-05	6.13
14	5	1	mwgecov2#1165	thymidine kinase; tdk	gene	-1.28	7.91	-8.38	1.44E-05	5.97
8	8	1	mwgecov2#2161	nadh dehydrogenase i chain h; nuoh	gene	-1.29	10.98	-12.35	2.45E-07	11.08
12	7	15	mwgecov2#2164	nadh dehydrogenase i chain e; nuoe	gene	-1.29	11.02	-8.02	2.25E-05	5.41
10	14	17	mwgecov2#4010	aspartate carbamoyltransferase, catalytic subunit; pyrb	gene	-1.32	8.41	-7.85	2.72E-05	5.15
14	14	8	mwgecov2#3921	fumarate reductase, anaerobic, membrane anchor polypeptide; frdc	gene	-1.33	8.40	-15.88	1.87E-08	14.55
4	7	15	mwgecov2#2166	nadh dehydrogenase i chain b; nuob	gene	-1.33	10.73	-6.74	1.10E-04	3.33

6	1	17	mwgecov2#0027	orf, hypothetical protein; yaaf	gene	-1.34	8.86	-10.46	1.46E-06	8.84
13	13	2	mwgecov2#3517	low affinity tryptophan permease; tnab	gene	-1.35	9.72	-6.37	1.85E-04	2.68
9	9	13	mwgecov2#2272	orf, hypothetical protein; yfec	gene	-1.36	10.31	-10.41	1.54E-06	8.77
7	3	8	mwgecov2#0701	galactokinase; galk	gene	-1.38	9.53	-10.69	1.17E-06	9.13
6	14	2	mwgecov2#3719	heat shock protein hslvu, atpase subunit, homologous to chaperones; hslu	gene	-1.39	9.22	-12.85	1.52E-07	11.62
10	1	14	mwgecov2#0111	aconitate hydrase b; acnb	gene	-1.40	9.07	-7.40	4.84E-05	4.43
6	11	17	mwgecov2#3065	malate dehydrogenase; mdh	gene	-1.41	11.52	-7.00	7.87E-05	3.76
11	13	7	mwgecov2#3658	response regulator for gln (sensor glnl) (nitrogen regulator i, nri); glng	gene	-1.41	9.10	-6.90	8.87E-05	3.60
14	14	17	mwgecov2#4009	aspartate carbamoyltransferase, regulatory subunit; pyri	gene	-1.41	8.51	-8.61	1.10E-05	6.30
16	7	13	mwgecov2#1975	pts system galactitol-specific enzyme iic; gatc	gene	-1.43	12.64	-9.28	5.19E-06	7.27
11	16	17	mwgecov2#3065-r	malate dehydrogenase; mdh	gene	-1.44	11.53	-7.64	3.58E-05	4.81
8	13	7	mwgecov2#3683	formate dehydrogenase-o, major subunit; fdog	gene	-1.46	12.14	-11.52	4.87E-07	10.14
2	3	12	mwgecov2#0674	succinate dehydrogenase, flavoprotein subunit; sdha	gene	-1.46	10.69	-5.07	1.28E-03	0.28
10	9	13	mwgecov2#2296	putative oxidoreductase; ucpa	gene	-1.48	11.44	-7.15	6.37E-05	4.02
9	11	5	mwgecov2#2648	probable serine transporter; sdac	gene	-1.49	10.24	-5.15	1.12E-03	0.43
4	6	12	mwgecov2#1688	orf, hypothetical protein; yeaa	gene	-1.52	10.60	-5.49	6.47E-04	1.08
1	12	9	mwgecov2#3224	phosphoenolpyruvate carboxykinase; pcka	gene	-1.53	11.36	-10.61	1.26E-06	9.03
12	15	6	mwgecov2#3954	orf, hypothetical protein; yjfo	gene	-1.53	10.89	-5.70	4.88E-04	1.46
4	7	17	mwgecov2#1974	galactitol-1-phosphate dehydrogenase; gatd	gene	-1.54	11.14	-10.49	1.42E-06	8.87
10	14	6	mwgecov2#3714	glycerol kinase; glpk	gene	-1.54	12.01	-7.32	5.33E-05	4.30
2	15	2	mwgecov2#3912	groel, chaperone hsp60, peptide-dependent atpase, heat shock protein; mopa	gene	-1.55	12.04	-9.59	3.80E-06	7.69
16	8	14	mwgecov2#2243	transport system permease (serine?); dsdx	gene	-1.56	9.43	-7.02	7.59E-05	3.80
1	10	1	mwgecov2#2460	putative yhbh sigma 54 modulator; yfia	gene	-1.60	14.85	-8.74	9.48E-06	6.50
9	6	7	mwgecov2#1524	fumarase a = fumarate hydratase class i; aerobic isozyme; fuma	gene	-1.63	9.00	-6.17	2.46E-04	2.33
12	7	13	mwgecov2#1976	galactitol-specific enzyme iib of phosphotransferase system; gatb	gene	-1.63	13.78	-10.59	1.28E-06	9.00
16	15	6	mwgecov2#3953	orf, hypothetical protein; yjfn	gene	-1.68	9.52	-6.78	1.04E-04	3.40
2	15	6	mwgecov2#3908	aspartate ammonia-lyase (aspartase); aspa	gene	-1.68	11.59	-15.56	2.27E-08	14.26
9	1	9	mwgecov2#0014	chaperone hsp70; dna biosynthesis; autoregulated heat shock proteins; dnak	gene	-1.70	12.81	-16.88	1.10E-08	15.40
15	16	18	mwgecov2#0674-r	succinate dehydrogenase, flavoprotein subunit; sdha	gene	-1.71	11.02	-5.30	8.84E-04	0.72
2	7	15	mwgecov2#2118	glycerophosphodiester phosphodiesterase, periplasmic; glpq	gene	-1.78	11.28	-7.09	6.94E-05	3.91
6	15	2	mwgecov2#3911	groes, 10 kd chaperone binds to hsp60 in pres. mg-atp, suppressing its atpase activity; mopb	gene	-1.81	13.68	-10.21	1.91E-06	8.52

2	3	8	mwgecov2#0678	2-oxoglutarate dehydrogenase (dihydrolipoyltranssuccinase e2 component); sucb	gene	-1.82	10.35	-8.01	2.26E-05	5.40
11	13	12	mwgecov2#3750	orf, hypothetical protein; yijc	gene	-1.83	10.37	-14.52	4.53E-08	13.30
12	8	14	mwgecov2#2244	d-serine dehydratase (deaminase); dsda	gene	-1.83	9.82	-7.88	2.65E-05	5.19
1	13	6	mwgecov2#3516	tryptophanase; tnaa	gene	-1.85	13.72	-7.45	4.61E-05	4.50
14	15	9	mwgecov2#3807	part of maltose permease, periplasmic; malf	gene	-1.91	8.54	-6.76	1.07E-04	3.36
10	14	8	mwgecov2#3922	fumarate reductase, anaerobic, iron-sulfur protein subunit; frdb	gene	-1.99	9.16	-14.35	4.97E-08	13.14
13	13	9	mwgecov2#3415	l-lactate dehydrogenase; lldd	gene	-2.01	9.17	-7.30	5.46E-05	4.26
10	3	4	mwgecov2#0680	succinyl-coa synthetase, alpha subunit; sucd	gene	-2.02	11.11	-16.69	1.16E-08	15.24
5	9	16	mwgecov2#2559	glucitol (sorbitol)-6-phosphate dehydrogenase; srld	gene	-2.10	8.85	-18.20	5.15E-09	16.44
6	12	10	mwgecov2#3341	uptake of c4-dicarboxylic acids; dcta	gene	-2.23	10.32	-6.02	3.03E-04	2.05
6	3	8	mwgecov2#0677	2-oxoglutarate dehydrogenase (decarboxylase component); suca	gene	-2.24	10.63	-12.89	1.50E-07	11.67
6	3	12	mwgecov2#0673	succinate dehydrogenase, hydrophobic subunit; sdhd	gene	-2.25	10.21	-5.85	3.84E-04	1.75
12	13	1	mwgecov2#3496	heat shock protein; ibpa	gene	-2.26	9.94	-10.56	1.31E-06	8.96
11	13	10	mwgecov2#3558	d-ribose periplasmic binding protein; rbsb	gene	-2.29	13.37	-14.34	4.97E-08	13.14
13	9	16	mwgecov2#2557	pts system, glucitol/sorbitol-specific iib component and second of two iic components; srle	gene	-2.36	9.64	-11.84	3.85E-07	10.51
16	13	1	mwgecov2#3495	heat shock protein; ibpb	gene	-2.37	9.45	-7.10	6.87E-05	3.93
10	6	5	mwgecov2#1338	aldehyde dehydrogenase, nad-linked; alda	gene	-2.47	9.67	-5.68	4.94E-04	1.44
11	6	3	mwgecov2#1170	oligopeptide transport; periplasmic binding protein; oppa	gene	-2.54	10.73	-15.51	2.31E-08	14.22
14	3	12	mwgecov2#0671	citrate synthase; glta	gene	-2.59	10.20	-8.19	1.80E-05	5.68
1	13	13	mwgecov2#3414	transcriptional regulator; lldr	gene	-2.62	10.05	-9.32	5.03E-06	7.32
10	3	12	mwgecov2#0672	succinate dehydrogenase, cytochrome b556; sdhc	gene	-2.66	10.38	-6.26	2.16E-04	2.50
9	9	16	mwgecov2#2558	pts system, glucitol/sorbitol-specific enzyme iia component; srlb	gene	-2.69	9.45	-16.04	1.76E-08	14.69
14	15	5	mwgecov2#3811	periplasmic protein of mal regulon; malm	gene	-2.84	8.99	-10.59	1.28E-06	9.00
6	15	9	mwgecov2#3809	atp-binding component of transport system for maltose; malk	gene	-2.84	9.20	-8.38	1.45E-05	5.95
2	15	7	mwgecov2#4004	trehalase 6-p hydrolase; trec	gene	-2.88	8.94	-22.22	5.41E-10	19.20
2	15	9	mwgecov2#3810	phage lambda receptor protein; maltose high-affinity receptor; lamb	gene	-2.88	9.44	-8.87	8.34E-06	6.68
10	15	9	mwgecov2#3808	periplasmic maltose-binding protein; substrate recognition for transport and chemotaxis; male	gene	-2.99	10.95	-12.13	3.02E-07	10.84
5	13	13	mwgecov2#3413	l-lactate permease; lldp	gene	-3.00	9.19	-5.85	3.85E-04	1.75
14	3	8	mwgecov2#0675	succinate dehydrogenase, iron sulfur protein; sdhb	gene	-3.05	10.88	-9.81	2.98E-06	7.99

3	8	12	mwgecov2#2032	galactose-binding transport protein; receptor for galactose taxis; mglb	gene	-3.16	10.20	-10.78	1.09E-06	9.24
2	5	1	mwgecov2#1168	coa-linked acetaldehyde dehydrogenase and iron-dependent alcohol dehydrogenase; pyruvate-formate-lyase deactivase; adhe	gene	-4.29	9.89	-11.62	4.56E-07	10.25
1	16	17	mwgecov2#1164-r	dna-binding protein hlp-ii (hu, bh2, hd, ns); pleiotropic regulator; hns	gene	-4.39	11.27	-32.48	1.00E-11	24.24
14	15	3	mwgecov2#4005	pts system enzyme ii, trehalose specific; treb	gene	-4.97	11.25	-34.04	1.00E-11	24.84
2	5	5	mwgecov2#1164	dna-binding protein hlp-ii (hu, bh2, hd, ns); pleiotropic regulator; hns	gene	-5.21	11.34	-32.61	1.00E-11	24.29

Taula 2 Gens expressats diferencialment entre la soca BSN26HY (*hha*$^{-}$ *ydgt*$^{-}$) respecte la soca BSN26 (*wt*).

Block	Row	Column	ID	Name	Status	M	A	t	P.Value	B
9	7	15	mwgecov2#2094	outer membrane protein 1b (ib;c); ompc	gene	4.26	11.95	4.59	9.06E-02	0.29
7	7	14	mwgecov2#2047	putative kinase; yeic	gene	1.70	9.06	5.01	9.06E-02	0.98
7	8	6	mwgecov2#2229	putative glycan biosynthesis enzyme; b2351	gene	1.64	10.34	5.02	9.06E-02	0.99
3	9	12	mwgecov2#2612	orf, hypothetical protein; ygck	gene	1.62	9.54	4.49	9.06E-02	0.10
1	12	2	mwgecov2#3326	orf, hypothetical protein; yhie	gene	1.32	11.45	4.46	9.06E-02	0.06
16	15	1	mwgecov2#3861	putative atp-binding component of a transport system; yjcw	gene	1.31	8.80	5.00	9.06E-02	0.97
3	8	6	mwgecov2#2230	putative ligase; b2352	gene	1.19	8.59	4.99	9.06E-02	0.95
5	3	8	mwgecov2#0653	rhsc protein in rhs element; rhsc	gene	1.12	8.29	4.51	9.06E-02	0.14
2	6	11	mwgecov2#1546	putative transport protein; ydgr	gene	1.05	8.03	4.75	9.06E-02	0.55
11	7	14	mwgecov2#2046	orf, hypothetical protein; yein	gene	1.00	8.52	4.86	9.06E-02	0.74
7	5	3	mwgecov2#1383	orf, hypothetical protein; ydce	gene	0.92	9.01	4.56	9.06E-02	0.23
10	14	3	mwgecov2#3428	involved in lipopolysaccharide biosynthesis; htrl	gene	0.92	9.08	4.62	9.06E-02	0.33
11	5	12	mwgecov2#1468	cold shock-like protein; cspi	gene	0.74	9.77	5.13	9.06E-02	1.17
6	4	17	mwgecov2#0959	orf, hypothetical protein; ycdq	gene	0.68	8.63	4.76	9.06E-02	0.56
4	9	14	mwgecov2#2440	sigma-e factor, negative regulatory protein; rsea	gene	0.59	11.29	5.08	9.06E-02	1.09
4	6	17	mwgecov2#1778	copper homeostasis protein; cutc	gene	0.58	9.57	5.43	9.06E-02	1.66
16	9	10	mwgecov2#2441	rna polymerase, sigma-e factor; heat shock and oxidative stress; rpoe	gene	0.52	10.16	4.89	9.06E-02	0.78
10	6	17	mwgecov2#1730	orf, hypothetical protein; b1824	gene	0.52	14.70	5.19	9.06E-02	1.27
10	3	4	mwgecov2#0680	succinyl-coa synthetase, alpha subunit; sucd	gene	-0.56	11.11	-4.52	9.06E-02	0.16
5	11	11	mwgecov2#2835	putative hydrogenase subunit; b2997	gene	-0.65	7.82	-4.68	9.06E-02	0.43
13	5	6	mwgecov2#1233	phage shock protein: activates phage shock-protein expression; pspc	gene	-0.66	8.26	-4.54	9.06E-02	0.20
5	5	16	mwgecov2#1419	putative sulfatase; b1498	gene	-0.83	8.29	-4.75	9.06E-02	0.55

Taula 3 Gens expressats diferencialment entre la soca BSN26HY (*hha*$^-$ *ydgt*$^-$) respecte la soca BSN27 (*hns*$^-$).

Block	Row	Column	ID	Name	Status	M	A	t	P.Value	B
2	5	5	mwgecov2#1164	dna-binding protein hlp-ii (hu, bh2, hd, ns); pleiotropic regulator; hns	gene	5.52	11.34	27.95	1.10E-10	21.83
14	15	3	mwgecov2#4005	pts system enzyme ii, trehalose specific; treb	gene	5.06	11.25	28.04	1.10E-10	21.87
1	16	17	mwgecov2#1164-r	dna-binding protein hlp-ii (hu, bh2, hd, ns); pleiotropic regulator; hns	gene	4.61	11.27	27.62	1.10E-10	21.69
2	5	1	mwgecov2#1168	coa-linked acetaldehyde dehydrogenase and iron-dependent alcohol dehydrogenase; pyruvate-formate-lyase deactivase; adhe	gene	4.52	9.89	9.90	6.24E-06	8.31
10	15	9	mwgecov2#3808	periplasmic maltose-binding protein; substrate recognition for transport and chemotaxis; male	gene	2.99	10.95	9.82	6.86E-06	8.20
16	13	1	mwgecov2#3495	heat shock protein; ibpb	gene	2.85	9.45	6.92	2.01E-04	3.88
14	15	5	mwgecov2#3811	periplasmic protein of mal regulon; malm	gene	2.76	8.99	8.34	3.23E-05	6.13
2	15	9	mwgecov2#3810	phage lambda receptor protein; maltose high-affinity receptor; lamb	gene	2.53	9.44	6.30	4.43E-04	2.83
2	15	7	mwgecov2#4004	trehalase 6-p hydrolase; trec	gene	2.52	8.94	15.75	5.90E-08	14.47
3	8	12	mwgecov2#2032	galactose-binding transport protein; receptor for galactose taxis; mglb	gene	2.50	10.20	6.88	2.11E-04	3.82
12	13	1	mwgecov2#3496	heat shock protein; ibpa	gene	2.43	9.94	9.19	1.18E-05	7.35
6	15	9	mwgecov2#3809	atp-binding component of transport system for maltose; malk	gene	2.35	9.20	5.61	1.18E-03	1.58
8	15	1	mwgecov2#3863	transcriptional repressor of rpib expression; rpir	gene	2.22	9.11	6.97	1.91E-04	3.97
9	9	16	mwgecov2#2558	pts system, glucitol/sorbitol-specific enzyme iia component; srlb	gene	2.20	9.45	10.63	3.01E-06	9.23
11	13	10	mwgecov2#3558	d-ribose periplasmic binding protein; rbsb	gene	2.16	13.37	10.94	2.36E-06	9.61
14	3	8	mwgecov2#0675	succinate dehydrogenase, iron sulfur protein; sdhb	gene	2.15	10.88	5.59	1.20E-03	1.53
11	6	3	mwgecov2#1170	oligopeptide transport; periplasmic binding protein; oppa	gene	2.08	10.73	10.27	4.59E-06	8.78
9	11	5	mwgecov2#2648	probable serine transporter; sdac	gene	2.00	10.24	5.60	1.18E-03	1.56
10	14	6	mwgecov2#3714	glycerol kinase; glpk	gene	1.99	12.01	7.63	7.63E-05	5.04
2	7	15	mwgecov2#2118	glycerophosphodiester phosphodiesterase, periplasmic; glpq	gene	1.98	11.28	6.38	3.96E-04	2.96
1	10	1	mwgecov2#2460	putative yhbh sigma 54 modulator; yfia	gene	1.97	14.85	8.69	2.13E-05	6.64
16	15	1	mwgecov2#3861	putative atp-binding component of a transport system; yjcw	gene	1.92	8.80	6.10	5.95E-04	2.46
14	15	9	mwgecov2#3807	part of maltose permease, periplasmic; malf	gene	1.85	8.54	5.30	1.75E-03	1.00
13	9	16	mwgecov2#2557	pts system, glucitol/sorbitol-specific iib component and second of two iic components; srle	gene	1.80	9.64	7.33	1.15E-04	4.56
3	16	17	mwgecov2#0328-r	2-keto-4-pentenoate hydratase; mhpd	gene	1.78	10.92	11.00	2.29E-06	9.68
15	8	17	mwgecov2#2119	sn-glycerol-3-phosphate permease; glpt	gene	1.75	11.46	5.31	1.73E-03	1.02
6	3	8	mwgecov2#0677	2-oxoglutarate dehydrogenase (decarboxylase component); suca	gene	1.73	10.63	8.06	4.56E-05	5.70

6	15	2	mwgecov2#3911	groes, 10 kd chaperone binds to hsp60 in pres. mg-atp, suppressing its atpase activity; mopb	gene	1.71	13.68	7.79	6.35E-05	5.30
1	13	13	mwgecov2#3414	transcriptional regulator; lldr	gene	1.69	10.05	4.87	3.33E-03	0.17
12	7	13	mwgecov2#1976	galactitol-specific enzyme iib of phosphotransferase system; gatb	gene	1.61	13.78	8.42	2.95E-05	6.25
2	15	6	mwgecov2#3908	aspartate ammonia-lyase (aspartase); aspa	gene	1.60	11.59	12.03	1.10E-06	10.86
2	15	2	mwgecov2#3912	groel, chaperone hsp60, peptide-dependent atpase, heat shock protein; mopa	gene	1.60	12.04	8.02	4.78E-05	5.64
10	14	8	mwgecov2#3922	fumarate reductase, anaerobic, iron-sulfur protein subunit; frdb	gene	1.59	9.16	9.26	1.12E-05	7.45
5	9	16	mwgecov2#2559	glucitol (sorbitol)-6-phosphate dehydrogenase; srld	gene	1.58	8.85	11.05	2.27E-06	9.74
1	13	6	mwgecov2#3516	tryptophanase; tnaa	gene	1.57	13.72	5.13	2.30E-03	0.67
16	15	6	mwgecov2#3953	orf, hypothetical protein; yjfn	gene	1.55	9.52	5.06	2.50E-03	0.54
6	14	6	mwgecov2#3715	facilitated diffusion of glycerol; glpf	gene	1.51	10.30	8.65	2.21E-05	6.58
12	8	14	mwgecov2#2244	d-serine dehydratase (deaminase); dsda	gene	1.50	9.82	5.22	1.97E-03	0.85
4	7	17	mwgecov2#1974	galactitol-1-phosphate dehydrogenase; gatd	gene	1.49	11.14	8.21	3.77E-05	5.94
16	7	13	mwgecov2#1975	pts system galactitol-specific enzyme iic; gatc	gene	1.48	12.64	7.78	6.42E-05	5.27
11	13	12	mwgecov2#3750	orf, hypothetical protein; yijc	gene	1.47	10.37	9.43	9.83E-06	7.67
16	8	14	mwgecov2#2243	transport system permease (serine?); dsdx	gene	1.46	9.43	5.32	1.71E-03	1.03
10	3	4	mwgecov2#0680	succinyl-coa synthetase, alpha subunit; sucd	gene	1.46	11.11	9.75	7.27E-06	8.11
14	5	1	mwgecov2#1165	thymidine kinase; tdk	gene	1.45	7.91	7.71	6.81E-05	5.17
8	8	1	mwgecov2#2161	nadh dehydrogenase i chain h; nuoh	gene	1.43	10.98	11.09	2.23E-06	9.79
9	9	13	mwgecov2#2272	orf, hypothetical protein; yfec	gene	1.39	10.31	8.60	2.32E-05	6.51
6	13	6	mwgecov2#3539	membrane-bound atp synthase, f1 sector, epsilon-subunit; atpc	gene	1.38	11.67	5.96	7.00E-04	2.22
9	1	9	mwgecov2#0014	chaperone hsp70; dna biosynthesis; autoregulated heat shock proteins; dnak	gene	1.37	12.81	11.01	2.29E-06	9.69
6	14	14	mwgecov2#4111	orf, hypothetical protein; yjix	gene	1.37	9.35	6.50	3.48E-04	3.18
2	3	8	mwgecov2#0678	2-oxoglutarate dehydrogenase (dihydrolipoyltranssuccinase e2 component); sucb	gene	1.34	10.35	4.79	3.78E-03	0.01
5	11	5	mwgecov2#2649	l-serine dehydratase (deaminase), l-sd2; sdab	gene	1.32	8.40	5.43	1.48E-03	1.23
4	7	15	mwgecov2#2166	nadh dehydrogenase i chain b; nuob	gene	1.28	10.73	5.26	1.85E-03	0.92
6	14	2	mwgecov2#3719	heat shock protein hslvu, atpase subunit, homologous to chaperones; hslu	gene	1.28	9.22	9.58	8.55E-06	7.88
2	13	6	mwgecov2#3540	membrane-bound atp synthase, f1 sector, beta-subunit; atpd	gene	1.28	11.88	9.58	8.55E-06	7.88
4	7	13	mwgecov2#1978	putative tagatose 6-phosphate kinase 1; gatz	gene	1.27	13.81	4.82	3.58E-03	0.07
1	12	9	mwgecov2#3224	phosphoenolpyruvate carboxykinase; pcka	gene	1.23	11.36	6.94	1.99E-04	3.92
3	13	7	mwgecov2#3660	glutamine synthetase; glna	gene	1.22	9.61	7.90	5.58E-05	5.47
15	3	9	mwgecov2#0411	dna-binding, atp-dependent protease la; heat shock k-protein; lon	gene	1.20	10.68	8.20	3.79E-05	5.92

5	9	13	mwgecov2#2273	orf, hypothetical protein; yfed	gene	1.20	9.04	5.56	1.22E-03	1.49
12	7	15	mwgecov2#2164	nadh dehydrogenase i chain e; nuoe	gene	1.15	11.02	5.80	8.75E-04	1.93
12	8	1	mwgecov2#2160	nadh dehydrogenase i chain i; nuoi	gene	1.15	10.93	6.92	2.01E-04	3.88
8	13	7	mwgecov2#3683	formate dehydrogenase-o, major subunit; fdog	gene	1.14	12.14	7.29	1.21E-04	4.50
1	5	13	mwgecov2#1134	orf, hypothetical protein; ychh	gene	1.14	11.45	6.44	3.70E-04	3.07
14	13	6	mwgecov2#3537	l-glutamine:d-fructose-6-phosphate aminotransferase; glms	gene	1.13	10.28	7.76	6.45E-05	5.25
8	7	13	mwgecov2#1977	galactitol-specific enzyme iia of phosphotransferase system; gata	gene	1.13	13.49	6.82	2.24E-04	3.73
6	14	7	mwgecov2#3829	diadenosine tetraphosphatase; apha	gene	1.13	10.58	6.90	2.05E-04	3.85
13	12	14	mwgecov2#3311	putative transport protein; yhip	gene	1.11	8.39	6.54	3.28E-04	3.25
1	15	2	mwgecov2#3888	regulator of melibiose operon; melr	gene	1.11	8.03	6.87	2.12E-04	3.80
14	13	2	mwgecov2#3541	membrane-bound atp synthase, f1 sector, gamma-subunit; atpg	gene	1.09	11.27	7.47	9.44E-05	4.78
9	10	2	mwgecov2#2554	orf, hypothetical protein; ygad	gene	1.09	9.93	6.65	2.80E-04	3.43
2	13	1	mwgecov2#3450	deoxyuridinetriphosphatase; dut	gene	1.08	9.42	5.94	7.21E-04	2.19
5	5	6	mwgecov2#1235	phage shock protein; pspe	gene	1.06	9.54	6.09	5.99E-04	2.45
6	10	5	mwgecov2#2479	small membrane protein a; smpa	gene	1.04	10.09	5.54	1.25E-03	1.45
4	8	1	mwgecov2#2162	nadh dehydrogenase i chain g; nuog	gene	1.03	10.93	6.66	2.78E-04	3.44
16	3	1	mwgecov2#0443	chaperone hsp90, heat shock protein c 62.5; htpg	gene	1.00	9.16	6.28	4.58E-04	2.78
2	12	3	mwgecov2#3062	orf, hypothetical protein; yhcb	gene	1.00	9.60	8.34	3.23E-05	6.13
12	8	5	mwgecov2#2156	nadh dehydrogenase i chain m; nuom	gene	0.98	10.54	4.94	3.00E-03	0.30
10	11	6	mwgecov2#2768	fructose-bisphosphate aldolase, class ii; fba	gene	0.98	11.81	6.18	5.34E-04	2.60
3	13	6	mwgecov2#3564	transcription regulator; yifda	gene	0.98	8.69	5.42	1.48E-03	1.23
14	14	8	mwgecov2#3921	fumarate reductase, anaerobic, membrane anchor polypeptide; frdc	gene	0.97	8.40	9.38	1.03E-05	7.61
6	1	17	mwgecov2#0027	orf, hypothetical protein; yaaf	gene	0.95	8.86	6.03	6.46E-04	2.34
4	13	8	mwgecov2#3778	dna-binding protein hu-alpha (hu-2); hupa	gene	0.95	12.87	6.70	2.68E-04	3.51
8	8	5	mwgecov2#2157	nadh dehydrogenase i chain l; nuol	gene	0.94	10.66	6.46	3.60E-04	3.11
7	13	14	mwgecov2#3555	d-ribose high-affinity transport system; membrane-associated protein; rbsd	gene	0.93	11.11	4.80	3.70E-03	0.03
3	7	10	mwgecov2#1648	pep-dependent phosphotransferase enzyme iv for cellobiose, arbutin, and salicin; cela	gene	0.93	8.63	5.79	8.80E-04	1.91
2	14	2	mwgecov2#3720	heat shock protein hslvu, proteasome-related peptidase subunit; hslv	gene	0.91	11.11	5.38	1.54E-03	1.15
5	10	5	mwgecov2#2455	heat shock protein; clpb	gene	0.91	10.21	4.96	2.91E-03	0.34
11	3	8	mwgecov2#0700	galactose-1-epimerase (mutarotase); galm	gene	0.90	10.33	5.47	1.40E-03	1.31
7	9	1	mwgecov2#2333	putative multimodular enzyme; b2463	gene	0.90	9.58	4.86	3.38E-03	0.15
1	14	14	mwgecov2#4088	orf, hypothetical protein; yjig	gene	0.89	8.45	5.60	1.18E-03	1.55

6	13	17	mwgecov2#3433	probably hexose transferase; lipopolysaccharide core biosynthesis; rfak	gene	0.87	8.33	6.30	4.46E-04	2.82
6	10	16	mwgecov2#2777	transketolase 1 isozyme; tkta	gene	0.85	11.05	5.44	1.45E-03	1.26
7	3	8	mwgecov2#0701	galactokinase; galk	gene	0.84	9.53	5.30	1.74E-03	1.00
6	2	13	mwgecov2#0595	orf, hypothetical protein; ybed	gene	0.83	9.50	5.03	2.64E-03	0.47
6	13	3	mwgecov2#3639	putative oxidoreductase; yigc	gene	0.82	10.25	7.10	1.60E-04	4.19
9	11	15	mwgecov2#3234	orf, hypothetical protein; yhgi	gene	0.82	10.50	5.50	1.33E-03	1.37
5	14	12	mwgecov2#3895	putative 2-component sensor protein; yjdh	gene	0.80	8.32	5.19	2.11E-03	0.78
12	16	16	mwgecov2#1689-r	glyceraldehyde-3-phosphate dehydrogenase a; gapa	gene	0.80	12.56	4.92	3.10E-03	0.26
16	12	13	mwgecov2#3289	orf, hypothetical protein; b3472	gene	0.80	9.42	6.46	3.60E-04	3.10
12	9	7	mwgecov2#2542	orf, hypothetical protein; ygah	gene	0.80	8.28	5.43	1.47E-03	1.24
15	13	8	mwgecov2#3753	outer membrane receptor for transport of vitamin b12, e colicins, and bacteriophage bf23; btub	gene	0.80	8.88	6.87	2.12E-04	3.80
6	15	5	mwgecov2#3813	chorismate lyase; ubic	gene	0.80	8.23	5.00	2.73E-03	0.42
9	16	18	mwgecov2#3555-r	d-ribose high-affinity transport system; membrane-associated protein; rbsd	gene	0.78	10.86	5.09	2.41E-03	0.60
2	14	12	mwgecov2#3920	fumarate reductase, anaerobic, membrane anchor polypeptide; frdd	gene	0.76	8.51	6.43	3.71E-04	3.04
11	12	4	mwgecov2#3178	orf, hypothetical protein; yhfa	gene	0.74	9.21	5.90	7.63E-04	2.10
2	14	18	mwgecov2#4108	host restriction; endonuclease r; hsdr	gene	0.74	8.83	5.46	1.42E-03	1.29
13	10	13	mwgecov2#2849	putative oxidoreductase; yqhd	gene	0.74	8.74	5.57	1.22E-03	1.49
5	11	2	mwgecov2#2749	aminomethyltransferase (t protein; tetrahydrofolate-dependent) of glycine cleavage system; gcvt	gene	0.74	12.16	5.80	8.79E-04	1.92
2	14	6	mwgecov2#3716	orf, hypothetical protein; yiiu	gene	0.74	10.04	5.56	1.22E-03	1.48
15	15	11	mwgecov2#4021	valine trna synthetase; vals	gene	0.73	10.07	5.08	2.43E-03	0.58
7	13	6	mwgecov2#3563	transcription regulator; yifda	gene	0.73	7.54	6.20	5.11E-04	2.65
11	3	9	mwgecov2#0412	dna-binding protein hu-beta, ns1 (hu-1); hupb	gene	0.72	12.55	5.11	2.35E-03	0.63
4	9	8	mwgecov2#2638	putative enzyme; ygca	gene	0.72	8.95	6.12	5.75E-04	2.51
15	10	9	mwgecov2#2901	dna biosynthesis; dna primase; dnag	gene	0.71	9.76	5.87	8.01E-04	2.05
9	14	12	mwgecov2#3894	putative 2-component transcriptional regulator; yjdg	gene	0.69	7.71	5.39	1.54E-03	1.16
12	6	8	mwgecov2#1690	orf, hypothetical protein; yead	gene	0.68	10.01	5.08	2.43E-03	0.57
3	6	1	mwgecov2#1368	orf, hypothetical protein; b1445	gene	0.68	8.72	4.84	3.50E-03	0.11
2	15	3	mwgecov2#4008	orf, hypothetical protein; yjgf	gene	0.66	8.66	5.45	1.44E-03	1.27
2	15	1	mwgecov2#3818	dna-damage-inducible protein f; dinf	gene	0.66	7.85	5.76	9.19E-04	1.85
3	14	2	mwgecov2#3744	acetylornithine deacetylase; arge	gene	0.65	9.05	5.55	1.25E-03	1.45

9	15	7	mwgecov2#3978	2':3'-cyclic-nucleotide 2'-phosphodiesterase; cpdb	gene	0.65	8.17	4.88	3.27E-03	0.19
2	5	7	mwgecov2#1356	putative membrane transport protein; b1433	gene	0.65	7.59	5.74	9.55E-04	1.81
6	15	7	mwgecov2#4003	anaerobic ribonucleoside-triphosphate reductase; nrdd	gene	0.64	7.47	5.06	2.50E-03	0.54
3	10	6	mwgecov2#2600	orf, hypothetical protein; ygbp	gene	0.62	10.03	5.61	1.18E-03	1.58
7	12	4	mwgecov2#3179	cyclic amp receptor protein; crp	gene	0.57	10.04	5.06	2.51E-03	0.53
7	14	2	mwgecov2#3743	phosphoenolpyruvate carboxylase; ppc	gene	0.57	9.91	5.26	1.85E-03	0.92
12	14	9	mwgecov2#4066	orf, hypothetical protein; yjhq	gene	0.56	8.22	5.12	2.31E-03	0.65
4	5	17	mwgecov2#1200	orf, hypothetical protein; ycin	gene	0.55	10.53	4.87	3.33E-03	0.17
2	9	14	mwgecov2#2392	putative peptidase; pepb	gene	0.55	8.71	4.96	2.91E-03	0.34
14	4	10	mwgecov2#1059	sensor protein phoq; phoq	gene	-0.46	8.47	-4.90	3.19E-03	0.22
5	14	7	mwgecov2#3805	xylose-proton symport; xyle	gene	-0.51	7.47	-5.42	1.48E-03	1.23
15	4	16	mwgecov2#0885	orf, hypothetical protein; ycbw	gene	-0.55	9.91	-5.05	2.54E-03	0.51
6	3	15	mwgecov2#0977	putative polyprotein; b1045	gene	-0.56	8.50	-5.14	2.27E-03	0.69
3	4	13	mwgecov2#0986	orf, hypothetical protein; ycea	gene	-0.57	8.03	-4.83	3.54E-03	0.09
1	5	1	mwgecov2#1146	cation transport regulator; chab	gene	-0.57	7.73	-4.95	2.93E-03	0.33
1	4	16	mwgecov2#0842	pyruvate formate lyase activating enzyme 1; pfla	gene	-0.57	9.31	-5.33	1.69E-03	1.05
10	15	12	mwgecov2#4094	orf, hypothetical protein; yjim	gene	-0.60	6.95	-5.56	1.22E-03	1.48
10	6	16	mwgecov2#1634	orf, hypothetical protein; b1724	gene	-0.62	10.85	-4.97	2.84E-03	0.37
5	12	3	mwgecov2#3037	orf, hypothetical protein; yrbl	gene	-0.62	10.13	-4.82	3.58E-03	0.07
12	4	4	mwgecov2#0922	orf, hypothetical protein; ymca	gene	-0.63	8.97	-5.39	1.54E-03	1.16
6	1	13	mwgecov2#0031	transcriptional regulator of cai operon; caif	gene	-0.64	8.32	-6.12	5.75E-04	2.50
6	4	3	mwgecov2#0781	d-alanyl-d-alanine carboxypeptidase; penicillin-binding protein 6; dacc	gene	-0.65	9.06	-5.12	2.30E-03	0.66
1	7	3	mwgecov2#1704	orf, hypothetical protein; year	gene	-0.65	8.98	-6.02	6.46E-04	2.33
5	13	4	mwgecov2#3711	putative regulator; yiit	gene	-0.67	8.79	-4.98	2.81E-03	0.39
4	7	16	mwgecov2#2262	orf, hypothetical protein; b2384	gene	-0.68	8.00	-6.03	6.46E-04	2.34
1	4	9	mwgecov2#0944	orf, hypothetical protein; b1007	gene	-0.69	8.63	-5.25	1.88E-03	0.90
3	7	5	mwgecov2#1558	superoxide dismutase precursor (cu-zn); sodc	gene	-0.71	8.12	-5.29	1.79E-03	0.97
14	4	4	mwgecov2#0873	putative atp-binding component of a transport system; ycbe	gene	-0.71	8.70	-5.00	2.73E-03	0.42
6	6	18	mwgecov2#1825	cytoplasmic alpha-amylase; amya	gene	-0.71	9.40	-5.49	1.35E-03	1.35
16	4	4	mwgecov2#0921	putative function in exopolysaccharide production; yccz	gene	-0.72	9.26	-6.13	5.72E-04	2.52
14	8	4	mwgecov2#2013	putative transport system permease protein; yehz	gene	-0.73	8.22	-5.22	2.00E-03	0.83
5	8	13	mwgecov2#2079	heme exporter protein b, cytochrome c-type biogenesis protein; ccmb	gene	-0.74	8.50	-7.84	6.04E-05	5.37

14	7	12	mwgecov2#1811	excinuclease abc, subunit c; repair of uv damage to dna; uvrc	gene	-0.74	8.75	-6.00	6.63E-04	2.28
14	11	6	mwgecov2#2767	putative transport protein; yggb	gene	-0.75	11.72	-6.42	3.71E-04	3.04
13	4	12	mwgecov2#0843	formate acetyltransferase 1; pflb	gene	-0.75	9.32	-4.84	3.50E-03	0.11
12	8	15	mwgecov2#1956	orf, hypothetical protein; b2071	gene	-0.75	8.05	-4.83	3.51E-03	0.10
4	9	15	mwgecov2#2536	atp-binding component of transport system for glycine, betaine and proline; prov	gene	-0.75	9.77	-6.72	2.62E-04	3.55
7	2	14	mwgecov2#0713	orf, hypothetical protein; ybhh	gene	-0.76	8.01	-6.28	4.58E-04	2.78
15	15	9	mwgecov2#3831	orf, hypothetical protein; yjbr	gene	-0.76	9.74	-6.00	6.63E-04	2.29
3	5	15	mwgecov2#1372	putative oxidoreductase; yncb	gene	-0.78	8.36	-5.61	1.18E-03	1.57
7	6	14	mwgecov2#1853	orf, hypothetical protein; b1957	gene	-0.79	10.93	-5.09	2.42E-03	0.59
8	4	16	mwgecov2#0911	hydrogenase-1 large subunit; hyab	gene	-0.80	7.69	-5.61	1.18E-03	1.57
5	7	9	mwgecov2#1505	orf, hypothetical protein; b1593	gene	-0.80	8.34	-5.39	1.54E-03	1.17
15	15	4	mwgecov2#4123	putative regulator; yjjq	gene	-0.80	7.83	-6.07	6.10E-04	2.42
9	15	11	mwgecov2#3974	orf, hypothetical protein; ytfe	gene	-0.81	8.40	-5.50	1.33E-03	1.38
3	9	18	mwgecov2#2412	orf, hypothetical protein; ypha	gene	-0.82	8.56	-5.26	1.85E-03	0.92
8	8	7	mwgecov2#1965	orf, hypothetical protein; b2080	gene	-0.84	10.54	-5.82	8.53E-04	1.97
5	15	3	mwgecov2#3983	putative transport protein; ytfl	gene	-0.84	7.84	-4.92	3.10E-03	0.26
6	4	17	mwgecov2#0959	orf, hypothetical protein; ycdq	gene	-0.86	8.63	-5.02	2.68E-03	0.45
11	14	10	mwgecov2#4136	thymidine phosphorylase; deoa	gene	-0.86	9.80	-4.92	3.09E-03	0.27
12	14	14	mwgecov2#4156	orf, hypothetical protein; yjjy	gene	-0.87	9.14	-5.85	8.21E-04	2.02
12	6	11	mwgecov2#1592	putative atp-binding component of a transport system; ynhd	gene	-0.90	8.42	-5.14	2.27E-03	0.69
15	7	2	mwgecov2#1653	periplasmic protein related to spheroblast formation; spy	gene	-0.90	10.04	-5.58	1.21E-03	1.52
6	7	12	mwgecov2#1813	orf, hypothetical protein; yecf	gene	-0.96	8.58	-5.82	8.57E-04	1.96
2	14	7	mwgecov2#3830	orf, hypothetical protein; yjbq	gene	-0.96	9.61	-5.93	7.34E-04	2.16
10	11	13	mwgecov2#3068	orf, hypothetical protein; yhco	gene	-0.97	8.93	-5.37	1.58E-03	1.12
15	8	15	mwgecov2#1931	probable export protein; wzxc	gene	-0.97	8.78	-6.16	5.48E-04	2.57
15	7	17	mwgecov2#1947	putative polysaccharide export protein; wza	gene	-0.98	7.83	-6.36	4.03E-04	2.93
5	9	6	mwgecov2#2375	putative outer membrane lipoprotein; b2505	gene	-0.98	7.84	-7.80	6.35E-05	5.31
6	9	15	mwgecov2#2487	orf, hypothetical protein; yfjj	gene	-0.98	8.30	-8.97	1.55E-05	7.05
6	5	10	mwgecov2#1255	orf, hypothetical protein; b1330	gene	-0.98	8.90	-4.92	3.09E-03	0.27
1	7	11	mwgecov2#1696	orf, hypothetical protein; yeaj	gene	-0.99	7.90	-7.04	1.74E-04	4.08
4	10	5	mwgecov2#2528	dna-binding protein; h-ns-like protein; chaperone activity; rna splicing?; stpa	gene	-0.99	8.77	-5.39	1.54E-03	1.17
10	11	7	mwgecov2#2862	orf, hypothetical protein; ygiw	gene	-0.99	10.60	-5.00	2.72E-03	0.43

9	2	12	mwgecov2#0476	putative regulator; ybbu	gene	-0.99	9.94	-8.29	3.39E-05	6.06
5	15	10	mwgecov2#3879	putative vimentin; yjda	gene	-1.00	8.07	-5.09	2.42E-03	0.59
8	9	3	mwgecov2#2547	gamma-glutamate-cysteine ligase; gsha	gene	-1.00	10.68	-7.73	6.70E-05	5.20
16	3	4	mwgecov2#0727	molybdopterin biosynthesis, protein c; moac	gene	-1.00	9.99	-6.41	3.81E-04	3.01
7	9	16	mwgecov2#2607	orf, hypothetical protein; ygbf	gene	-1.00	9.51	-6.21	5.11E-04	2.66
11	8	1	mwgecov2#2136	orf, hypothetical protein; b2257	gene	-1.04	8.29	-5.12	2.30E-03	0.66
3	15	16	mwgecov2#6109	orf, hypothetical protein; yiis	gene	-1.04	9.63	-5.57	1.22E-03	1.49
8	10	1	mwgecov2#2531	orf, hypothetical protein; ygam	gene	-1.05	10.05	-5.15	2.24E-03	0.71
7	14	14	mwgecov2#4133	mg-dependent dnase; yjjv	gene	-1.05	8.33	-5.40	1.52E-03	1.19
5	12	6	mwgecov2#3321	orf, hypothetical protein; yhif	gene	-1.05	7.97	-7.86	5.86E-05	5.41
5	14	11	mwgecov2#3801	orf, hypothetical protein; yjbf	gene	-1.05	7.33	-7.09	1.62E-04	4.17
8	6	11	mwgecov2#1593	orf, hypothetical protein; ynhe	gene	-1.07	8.42	-7.00	1.83E-04	4.01
9	14	8	mwgecov2#3898	orf, hypothetical protein; yjdk	gene	-1.07	8.27	-5.11	2.33E-03	0.64
11	8	3	mwgecov2#1944	putative regulator; wcaa	gene	-1.10	8.23	-6.61	2.97E-04	3.36
8	5	5	mwgecov2#1211	putative deor-type transcriptional regulator; b1284	gene	-1.11	8.72	-5.57	1.21E-03	1.51
12	2	9	mwgecov2#0644	orf, hypothetical protein; ybfg	gene	-1.11	8.21	-8.79	1.90E-05	6.78
15	11	11	mwgecov2#2881	putative fimbrial-like protein; ygil	gene	-1.12	7.99	-5.43	1.48E-03	1.24
7	10	7	mwgecov2#2713	putative transcriptional regulator; ygev	gene	-1.12	8.98	-6.49	3.54E-04	3.16
11	3	13	mwgecov2#0812	pyruvate oxidase; poxb	gene	-1.13	8.95	-7.18	1.41E-04	4.33
3	8	16	mwgecov2#2028	putative oxidoreductase; b2146	gene	-1.15	10.29	-7.03	1.76E-04	4.06
10	3	14	mwgecov2#0882	putative fimbrial-like protein; b0943	gene	-1.15	7.76	-7.56	8.19E-05	4.94
14	7	11	mwgecov2#1717	orf, hypothetical protein; b1810	gene	-1.16	9.55	-6.43	3.71E-04	3.05
3	9	16	mwgecov2#2608	orf, hypothetical protein; b2755	gene	-1.18	9.11	-5.93	7.34E-04	2.16
3	8	15	mwgecov2#1934	mannose-1-phosphate guanyltransferase; cpsb	gene	-1.18	8.65	-5.91	7.53E-04	2.12
15	7	6	mwgecov2#1649	activator of ntrl gene; osme	gene	-1.19	10.55	-5.14	2.27E-03	0.69
9	7	11	mwgecov2#1694	orf, hypothetical protein; yeah	gene	-1.20	8.13	-6.17	5.40E-04	2.59
9	4	12	mwgecov2#0844	probable formate transporter (formate channel 1); foca	gene	-1.20	11.93	-5.58	1.21E-03	1.52
4	14	9	mwgecov2#4068	orf, hypothetical protein; yjhs	gene	-1.21	7.77	-6.46	3.60E-04	3.10
1	4	4	mwgecov2#0852	integration host factor (ihf), beta subunit; site-specific recombination; himd	gene	-1.21	10.17	-10.66	2.97E-06	9.27
11	14	14	mwgecov2#4132	orf, hypothetical protein; yjju	gene	-1.22	10.15	-7.57	8.19E-05	4.94
12	6	1	mwgecov2#1390	cryptic nitrate reductase 2, alpha subunit; narz	gene	-1.22	8.54	-6.02	6.46E-04	2.33
2	12	4	mwgecov2#3158	bacterioferrin, an iron storage homoprotein; bfr	gene	-1.22	11.23	-5.07	2.48E-03	0.55

4	4	7	mwgecov2#0826	atp-binding component of cytochrome-related transport; cydc	gene	-1.23	8.95	-6.67	2.73E-04	3.47
8	4	12	mwgecov2#0915	nickel incorporation into hydrogenase-1 proteins; hyaf	gene	-1.24	8.76	-6.43	3.71E-04	3.04
2	7	13	mwgecov2#1930	putative galactokinase (ec 2.7.1.6).; wcak	gene	-1.25	7.70	-7.28	1.21E-04	4.49
13	7	11	mwgecov2#1693	orf, hypothetical protein; yeag	gene	-1.25	9.20	-6.76	2.47E-04	3.62
3	9	1	mwgecov2#2334	transaldolase a; tala	gene	-1.26	9.37	-5.81	8.72E-04	1.93
10	4	9	mwgecov2#0965	putative ribosomal protein; ycdv	gene	-1.26	8.22	-9.94	6.03E-06	8.36
4	4	18	mwgecov2#1102	orf, hypothetical protein; b1172	gene	-1.27	9.10	-6.68	2.72E-04	3.48
12	8	3	mwgecov2#1968	orf, hypothetical protein; b2083	gene	-1.27	8.07	-5.76	9.19E-04	1.85
8	8	3	mwgecov2#1969	orf, hypothetical protein; b2084	gene	-1.30	7.87	-6.04	6.42E-04	2.36
5	7	5	mwgecov2#1509	acid shock protein; asr	gene	-1.31	8.02	-8.10	4.35E-05	5.77
12	1	8	mwgecov2#0356	orf, hypothetical protein; yaib	gene	-1.31	9.57	-8.00	4.88E-05	5.61
12	4	8	mwgecov2#0918	phosphoanhydride phosphorylase; ph 2.5 acid phosphatase; periplasmic; appa	gene	-1.32	9.17	-8.82	1.85E-05	6.83
13	11	3	mwgecov2#2841	putative oxidoreductase; ygha	gene	-1.33	9.07	-5.91	7.50E-04	2.13
3	5	16	mwgecov2#1466	orf, hypothetical protein; b1550	gene	-1.35	9.83	-4.89	3.22E-03	0.21
3	8	5	mwgecov2#2134	putative transformylase; b2255	gene	-1.35	9.15	-10.96	2.36E-06	9.63
8	6	1	mwgecov2#1391	nitrite extrusion protein 2; naru	gene	-1.37	8.01	-6.80	2.32E-04	3.68
15	5	11	mwgecov2#1373	orf, hypothetical protein; b1450	gene	-1.38	9.33	-9.27	1.12E-05	7.46
5	7	10	mwgecov2#1601	putative amino acid/amine transport protein; b1691	gene	-1.39	7.69	-6.01	6.55E-04	2.31
4	4	12	mwgecov2#0916	probable third cytochrome oxidase, subunit i; appc	gene	-1.39	10.01	-5.40	1.52E-03	1.18
5	7	18	mwgecov2#1995	orf, hypothetical protein; yehe	gene	-1.40	8.87	-8.30	3.39E-05	6.07
1	7	4	mwgecov2#1798	trehalose-6-phosphate phophatase, biosynthetic; otsb	gene	-1.40	9.75	-8.93	1.63E-05	6.98
7	7	16	mwgecov2#2237	orf, hypothetical protein; b2359	gene	-1.41	8.83	-9.33	1.08E-05	7.55
9	11	13	mwgecov2#3044	regulator of gltbdf operon, induction of ntr enzymes; gltf	gene	-1.43	8.47	-6.92	2.01E-04	3.89
9	8	16	mwgecov2#1980	orf, hypothetical protein; b2097	gene	-1.44	9.56	-8.81	1.87E-05	6.81
4	15	10	mwgecov2#3952	putative acyl coenzyme a dehydrogenase; aidb	gene	-1.46	9.75	-10.66	2.97E-06	9.27
8	3	12	mwgecov2#0721	biotin biosynthesis; reaction prior to pimeloyl coa; bioc	gene	-1.49	8.17	-11.10	2.23E-06	9.80
13	15	2	mwgecov2#3885	putative amino acid/amine transport protein, cryptic; yjde	gene	-1.50	7.59	-6.49	3.54E-04	3.15
16	2	7	mwgecov2#0455	putative glutaminase; ybas	gene	-1.53	9.42	-8.09	4.37E-05	5.76
10	6	2	mwgecov2#1436	putative transport system permease protein; ydez	gene	-1.56	8.86	-8.65	2.21E-05	6.59
9	14	11	mwgecov2#3800	orf, hypothetical protein; yjbe	gene	-1.56	11.46	-9.75	7.27E-06	8.10
1	5	18	mwgecov2#1224	putative glutamine synthetase (ec 6.3.1.2); b1297	gene	-1.58	8.79	-4.80	3.69E-03	0.04
9	5	12	mwgecov2#1422	putative oxidoreductase, major subunit; b1501	gene	-1.59	8.06	-6.47	3.60E-04	3.12

13	4	3	mwgecov2#0755	global regulator, starvation conditions; dps	gene	-1.60	11.64	-5.31	1.74E-03	1.01
1	5	16	mwgecov2#1420	putative arac-type regulatory protein; b1499	gene	-1.61	7.53	-9.30	1.11E-05	7.50
5	4	3	mwgecov2#0757	outer membrane protein x; ompx	gene	-1.62	11.62	-6.60	3.00E-04	3.35
8	8	17	mwgecov2#2145	orf, hypothetical protein; elab	gene	-1.63	10.17	-6.05	6.29E-04	2.38
13	15	12	mwgecov2#4069	orf, hypothetical protein; yjht	gene	-1.63	8.23	-8.39	3.08E-05	6.20
13	9	9	mwgecov2#2275	regulator for xapa; xapr	gene	-1.63	8.08	-11.39	1.85E-06	10.14
10	3	18	mwgecov2#0878	putative chaperone; ycbr	gene	-1.65	8.31	-5.61	1.18E-03	1.58
13	5	13	mwgecov2#1131	putative adhesion and penetration protein; b1202	gene	-1.68	7.68	-10.68	2.97E-06	9.30
9	11	16	mwgecov2#3328	putative transport system permease protein; yhiv	gene	-1.68	8.05	-10.03	5.56E-06	8.48
5	7	4	mwgecov2#1797	trehalose-6-phosphate synthase; otsa	gene	-1.68	8.64	-7.69	6.94E-05	5.14
7	6	7	mwgecov2#1573	cyclopropane fatty acyl phospholipid synthase; cfa	gene	-1.69	9.98	-11.70	1.40E-06	10.50
11	4	9	mwgecov2#0988	putative cytochrome; b1057	gene	-1.69	8.81	-10.04	5.56E-06	8.48
11	8	5	mwgecov2#2132	putative enzyme; b2253	gene	-1.72	9.24	-6.40	3.84E-04	2.99
1	4	13	mwgecov2#0940	orf, hypothetical protein; yccj	gene	-1.73	10.07	-5.60	1.18E-03	1.56
9	4	3	mwgecov2#0756	putative transmembrane subunit; ybif	gene	-1.74	7.98	-9.29	1.11E-05	7.49
8	5	7	mwgecov2#1403	osmotically inducible protein; osmc	gene	-1.77	10.54	-10.16	5.06E-06	8.65
2	4	13	mwgecov2#0964	orf, hypothetical protein; ycdu	gene	-1.77	8.14	-6.84	2.21E-04	3.75
12	1	9	mwgecov2#0072	probable transcriptional activator for leuabcd operon; leuo	gene	-1.78	9.65	-10.26	4.59E-06	8.76
6	3	18	mwgecov2#0879	putative outer membrane protein; ycbs	gene	-1.78	7.94	-8.83	1.84E-05	6.85
14	1	15	mwgecov2#0205	orf, hypothetical protein; ykfe	gene	-1.82	10.54	-13.57	2.81E-07	12.47
3	11	14	mwgecov2#3188	nitrite reductase (nad(p)h) subunit; nird	gene	-1.83	8.54	-5.01	2.69E-03	0.44
11	6	6	mwgecov2#1456	orf, hypothetical protein; ydej	gene	-1.86	8.67	-9.25	1.12E-05	7.43
10	7	13	mwgecov2#1928	orf, hypothetical protein; wcam	gene	-1.86	8.04	-10.05	5.56E-06	8.51
15	8	7	mwgecov2#1939	putative transferase; wcaf	gene	-1.87	8.08	-12.47	7.68E-07	11.34
7	8	5	mwgecov2#2133	putative sugar transferase; b2254	gene	-1.87	9.24	-7.60	7.86E-05	5.00
4	8	3	mwgecov2#1970	orf, hypothetical protein; b2085	gene	-1.88	8.25	-9.18	1.18E-05	7.34
10	6	8	mwgecov2#1642	catalase; hydroperoxidase hpii(iii); kate	gene	-1.88	10.02	-13.72	2.68E-07	12.62
6	13	14	mwgecov2#3531	positive regulation of bgl operon; bglg	gene	-1.89	7.63	-9.62	8.28E-06	7.94
13	4	13	mwgecov2#0937	curved dna-binding protein; functions closely related to dnaj; cbpa	gene	-1.90	9.69	-9.51	9.00E-06	7.79
11	8	7	mwgecov2#1940	putative colanic acid biosynthesis glycosyl transferase; wcae	gene	-1.91	8.69	-9.54	8.77E-06	7.84
11	9	12	mwgecov2#2610	orf, hypothetical protein; b2757	gene	-1.92	8.49	-6.68	2.72E-04	3.48
16	4	8	mwgecov2#0917	probable third cytochrome oxidase, subunit ii; appb	gene	-1.99	9.15	-8.62	2.27E-05	6.54

10	3	3	mwgecov2#0586	orf, hypothetical protein; crca	gene	-1.99	8.35	-7.37	1.09E-04	4.62
9	5	16	mwgecov2#1418	putative enzyme; b1497	gene	-2.01	8.25	-15.28	7.81E-08	14.06
9	15	12	mwgecov2#4070	orf, hypothetical protein; yjha	gene	-2.02	8.70	-9.47	9.35E-06	7.74
3	13	1	mwgecov2#3474	probable adenine deaminase (synthesis xanthine); yicp	gene	-2.02	8.48	-12.54	7.39E-07	11.42
3	12	10	mwgecov2#3366	orf, hypothetical protein; yiag	gene	-2.02	9.26	-11.69	1.40E-06	10.49
9	7	1	mwgecov2#1512	possible chaperone; b1600	gene	-2.04	8.00	-8.75	1.98E-05	6.73
1	7	2	mwgecov2#1610	orf, hypothetical protein; ydit	gene	-2.05	8.18	-10.75	2.90E-06	9.38
14	14	15	mwgecov2#3819	orf, hypothetical protein; yjbj	gene	-2.05	10.41	-6.70	2.68E-04	3.51
10	15	10	mwgecov2#3902	transport of lysine/cadaverine; cadb	gene	-2.12	10.99	-13.74	2.68E-07	12.64
14	7	5	mwgecov2#1531	nad-dependent 7alpha-hydroxysteroid dehydrogenase, dehydroxylation of bile acids; hdha	gene	-2.15	10.40	-12.12	1.03E-06	10.96
13	5	8	mwgecov2#1425	putative fimbrial-like protein; b1504	gene	-2.16	8.46	-11.24	2.02E-06	9.97
16	7	8	mwgecov2#1863	orf, hypothetical protein; yedu	gene	-2.18	10.30	-5.79	8.84E-04	1.90
8	15	13	mwgecov2#4867	orf, hypothetical protein; yeaq	gene	-2.18	10.62	-11.10	2.23E-06	9.81
5	10	11	mwgecov2#2661	orf, hypothetical protein; b2809	gene	-2.21	9.83	-10.67	2.97E-06	9.28
7	8	11	mwgecov2#1937	putative nucleotide di-p-sugar epimerase or dehydratase; wcag	gene	-2.22	8.49	-16.88	2.91E-08	15.39
1	4	17	mwgecov2#0936	orf, hypothetical protein; yccd	gene	-2.28	9.74	-11.74	1.40E-06	10.54
7	3	12	mwgecov2#0697	putative homeobox protein; b0753	gene	-2.33	8.80	-13.60	2.81E-07	12.50
8	3	13	mwgecov2#0837	orf, hypothetical protein; ycac	gene	-2.36	10.62	-11.24	2.02E-06	9.97
5	7	11	mwgecov2#1695	orf, hypothetical protein; yeai	gene	-2.44	7.51	-10.00	5.72E-06	8.43
3	8	11	mwgecov2#1938	gdp-d-mannose dehydratase; gmd	gene	-2.45	11.00	-9.70	7.55E-06	8.05
11	5	5	mwgecov2#1186	orf, hypothetical protein; ycig	gene	-2.46	11.69	-7.77	6.42E-05	5.27
3	9	12	mwgecov2#2612	orf, hypothetical protein; ygck	gene	-2.53	9.54	-5.84	8.32E-04	2.00
9	4	9	mwgecov2#0942	orf, hypothetical protein; ycdf	gene	-2.56	10.32	-14.48	1.52E-07	13.34
3	4	12	mwgecov2#0892	ribosome modulation factor; rmf	gene	-2.58	11.24	-10.12	5.23E-06	8.60
2	8	11	mwgecov2#1914	udp-glucose 6-dehydrogenase; ugd	gene	-2.58	8.51	-16.93	2.91E-08	15.43
9	12	6	mwgecov2#3320	outer membrane protein induced after carbon starvation; slp	gene	-2.63	10.84	-7.75	6.51E-05	5.24
11	6	18	mwgecov2#1848	positive regulator for ctr capsule biosynthesis, positive transcription factor; rcsa	gene	-2.69	8.94	-15.92	5.50E-08	14.61
12	5	5	mwgecov2#1210	osmotically inducible lipoprotein; osmb	gene	-2.76	10.21	-16.31	4.24E-08	14.94
16	5	7	mwgecov2#1401	30s ribosomal subunit protein s22; rpsv	gene	-2.80	12.62	-12.62	7.10E-07	11.50
5	16	18	mwgecov2#0892-r	ribosome modulation factor; rmf	gene	-2.95	10.80	-9.25	1.12E-05	7.43
12	5	7	mwgecov2#1402	orf, hypothetical protein; b1481	gene	-2.96	9.24	-12.32	8.63E-07	11.18

11	8	11	mwgecov2#1936	gdp-mannose mannosyl hydrolase; wcah	gene	-3.09	8.42	-17.36	2.71E-08	15.77
15	3	3	mwgecov2#0607	putative alpha helical protein; ybel	gene	-3.14	8.16	-14.41	1.54E-07	13.27
7	8	7	mwgecov2#1941	putative colanic acid polymerase; wcad	gene	-3.18	8.19	-18.99	8.99E-09	16.95
3	14	7	mwgecov2#3854	putative enzyme; yjcp	gene	-3.56	9.05	-11.94	1.16E-06	10.77
16	4	6	mwgecov2#1111	hemolysin e; hlye	gene	-3.59	8.87	-11.41	1.85E-06	10.16
4	11	15	mwgecov2#3306	orf, hypothetical protein; yhim	gene	-3.88	9.08	-15.54	6.60E-08	14.29
15	6	6	mwgecov2#1455	orf, hypothetical protein; ydei	gene	-4.04	8.85	-22.84	9.52E-10	19.34
13	6	2	mwgecov2#1413	acid sensitivity protein, putative transporter; xasa	gene	-4.07	10.31	-11.32	1.94E-06	10.06
14	3	18	mwgecov2#0877	putative fimbrial-like protein; ycbq	gene	-4.14	9.60	-19.32	8.23E-09	17.18
14	15	10	mwgecov2#3901	lysine decarboxylase 1; cada	gene	-4.31	10.27	-9.22	1.16E-05	7.39
9	6	2	mwgecov2#1414	glutamate decarboxylase isozyme; gada	gene	-4.57	11.47	-6.46	3.60E-04	3.11
3	5	9	mwgecov2#1184	orf, hypothetical protein; ycie	gene	-4.67	9.58	-23.48	8.11E-10	19.69
15	5	5	mwgecov2#1185	putative structural proteins; ycif	gene	-4.79	9.81	-17.21	2.71E-08	15.65

Taula 4 Gens expressats diferencialment entre la soca BSN27 respecte la BSN26 (valor relatiu de l'expressió a la segona columna), que coincideixen amb gens expressats diferencialment entre la soca BSN27 respecte la BSN26HY (valor relatiu de l'expressió a la tercera columna).

Descripció i gen	Raó d'expressió M1W	Raó d'expressió M1M2
2':3'-cyclic-nucleotide 2'-phosphodiesterase; cpdb	0.62	0.64
2-keto-4-pentenoate hydratase; mhpd	0.44	0.29
2-oxoglutarate dehydrogenase (decarboxylase component); suca	0.21	0.30
2-oxoglutarate dehydrogenase (dihydrolipoyltranssuccinase e2 component); sucb	0.28	0.39
30s ribosomal subunit protein s22; rpsv	12.17	6.98
acid sensitivity protein, putative transporter; xasa	34.85	16.76
acid shock protein; asr	3.20	2.47
activator of ntrl gene; osme	2.57	2.28
aminomethyltransferase (t protein; tetrahydrofolate-dependent) of glycine cleavage system; gcvt	0.60	0.60
anaerobic ribonucleoside-triphosphate reductase; nrdd	0.56	0.64
aspartate ammonia-lyase (aspartase); aspa	0.31	0.33
atp-binding component of cytochrome-related transport; cydc	2.62	2.34
atp-binding component of transport system for glycine, betaine and proline; prov	1.96	1.68
atp-binding component of transport system for maltose; malk	0.14	0.20
bacterioferrin, an iron storage homoprotein; bfr	2.66	2.33
biotin biosynthesis; reaction prior to pimeloyl coa; bioc	2.67	2.82
catalase; hydroperoxidase hpii(iii); kate	4.40	3.69
cation transport regulator; chab	1.65	1.48
chaperone hsp70; dna biosynthesis; autoregulated heat shock proteins; dnak	0.31	0.39
chaperone hsp90, heat shock protein c 62.5; htpg	0.43	0.50
chorismate lyase; ubic	0.43	0.58
coa-linked acetaldehyde dehydrogenase and iron-dependent alcohol dehydrogenase; pyruvate-formate-lyase deactivase; adhe	0.05	0.04
cryptic nitrate reductase 2, alpha subunit; narz	2.35	2.33
curved dna-binding protein; functions closely related to dnaj; cbpa	4.64	3.72
cyclic amp receptor protein; crp	0.62	0.67
cyclopropane fatty acyl phospholipid synthase; cfa	4.00	3.23
cytoplasmic alpha-amylase; amya	2.00	1.64
d-alanyl-d-alanine carboxypeptidase; penicillin-binding protein 6; dacc	1.89	1.57
deoxyuridinetriphosphatase; dut	0.56	0.47
diadenosine tetraphosphatase; apha	0.60	0.46
dna biosynthesis; dna primase; dnag	0.61	0.61
dna-binding protein hlp-ii (hu, bh2, hd, ns); pleiotropic regulator; hns	0.05	0.02
dna-binding protein hlp-ii (hu, bh2, hd, ns); pleiotropic regulator; hns	0.03	0.04
dna-binding protein hu-alpha (hu-2); hupa	0.61	0.52
dna-binding protein hu-beta, ns1 (hu-1); hupb	0.58	0.61
dna-binding protein; h-ns-like protein; chaperone activity; rna splicing?; stpa	2.68	1.98

dna-binding, atp-dependent protease la; heat shock k-protein; lon	0.45	0.43
dna-damage-inducible protein f; dinf	0.55	0.63
d-ribose high-affinity transport system; membrane-associated protein; rbsd	0.54	0.52
d-ribose high-affinity transport system; membrane-associated protein; rbsd	0.52	0.58
d-ribose periplasmic binding protein; rbsb	0.20	0.22
d-serine dehydratase (deaminase); dsda	0.28	0.35
excinuclease abc, subunit c; repair of uv damage to dna; uvrc	1.92	1.67
facilitated diffusion of glycerol; glpf	0.46	0.35
formate acetyltransferase 1; pflb	1.73	1.68
formate dehydrogenase-o, major subunit; fdog	0.36	0.45
fructose-bisphosphate aldolase, class ii; fba	0.57	0.51
fumarate reductase, anaerobic, iron-sulfur protein subunit; frdb	0.25	0.33
fumarate reductase, anaerobic, membrane anchor polypeptide; frdc	0.40	0.51
fumarate reductase, anaerobic, membrane anchor polypeptide; frdd	0.54	0.59
galactitol-1-phosphate dehydrogenase; gatd	0.34	0.36
galactitol-specific enzyme iia of phosphotransferase system; gata	0.46	0.46
galactitol-specific enzyme iib of phosphotransferase system; gatb	0.32	0.33
galactokinase; galk	0.39	0.56
galactose-1-epimerase (mutarotase); galm	0.51	0.54
galactose-binding transport protein; receptor for galactose taxis; mglb	0.11	0.18
gamma-glutamate-cysteine ligase; gsha	2.23	2.00
gdp-d-mannose dehydratase; gmd	5.44	5.46
gdp-mannose mannosyl hydrolase; wcah	9.80	8.51
global regulator, starvation conditions; dps	3.78	3.03
glucitol (sorbitol)-6-phosphate dehydrogenase; srld	0.23	0.34
glutamate decarboxylase isozyme; gada	91.20	23.74
glutamine synthetase; glna	0.42	0.43
glyceraldehyde-3-phosphate dehydrogenase a; gapa	0.59	0.57
glycerol kinase; glpk	0.34	0.25
glycerophosphodiester phosphodiesterase, periplasmic; glpq	0.29	0.25
groel, chaperone hsp60, peptide-dependent atpase, heat shock protein; mopa	0.34	0.33
groes, 10 kd chaperone binds to hsp60 in pres. mg-atp, suppressing its atpase activity; mopb	0.28	0.31
heat shock protein hslvu, atpase subunit, homologous to chaperones; hslu	0.38	0.41
heat shock protein hslvu, proteasome-related peptidase subunit; hslv	0.52	0.53
heat shock protein; clpb	0.42	0.53
heat shock protein; ibpa	0.21	0.19
heat shock protein; ibpb	0.19	0.14
heme exporter protein b, cytochrome c-type biogenesis protein; ccmb	1.62	1.67
hemolysin e; hlye	16.38	12.01
host restriction; endonuclease r; hsdr	0.44	0.60
hydrogenase-1 large subunit; hyab	1.96	1.74
integration host factor (ihf), beta subunit; site-specific recombination; himd	2.40	2.32
l-glutamine:d-fructose-6-phosphate aminotransferase; glms	0.49	0.46

l-serine dehydratase (deaminase), l-sd2; sdab	0.47	0.40
lysine decarboxylase 1; cada	40.76	19.84
mannose-1-phosphate guanyltransferase; cpsb	3.19	2.26
membrane-bound atp synthase, f1 sector, beta-subunit; atpd	0.42	0.41
membrane-bound atp synthase, f1 sector, epsilon-subunit; atpc	0.42	0.38
membrane-bound atp synthase, f1 sector, gamma-subunit; atpg	0.51	0.47
mg-dependent dnase; yjjv	2.47	2.07
molybdopterin biosynthesis, protein c; moac	1.76	2.00
nad-dependent 7alpha-hydroxysteroid dehydrogenase, dehydroxylation of bile acids; hdha	5.87	4.44
nadh dehydrogenase i chain b; nuob	0.40	0.41
nadh dehydrogenase i chain e; nuoe	0.41	0.45
nadh dehydrogenase i chain g; nuog	0.50	0.49
nadh dehydrogenase i chain h; nuoh	0.41	0.37
nadh dehydrogenase i chain i; nuoi	0.45	0.45
nadh dehydrogenase i chain l; nuol	0.59	0.52
nickel incorporation into hydrogenase-1 proteins; hyaf	1.87	2.35
nitrite extrusion protein 2; naru	3.68	2.58
oligopeptide transport; periplasmic binding protein; oppa	0.17	0.24
orf, hypothetical protein; b1172	2.27	2.41
orf, hypothetical protein; b1330	2.26	1.98
orf, hypothetical protein; b1445	0.62	0.62
orf, hypothetical protein; b1450	3.14	2.61
orf, hypothetical protein; b1481	10.09	7.77
orf, hypothetical protein; b1550	4.22	2.54
orf, hypothetical protein; b1724	1.62	1.54
orf, hypothetical protein; b1810	2.76	2.23
orf, hypothetical protein; b1957	1.75	1.73
orf, hypothetical protein; b2071	2.00	1.68
orf, hypothetical protein; b2080	2.00	1.78
orf, hypothetical protein; b2083	2.45	2.41
orf, hypothetical protein; b2084	3.33	2.46
orf, hypothetical protein; b2085	4.82	3.69
orf, hypothetical protein; b2097	3.33	2.70
orf, hypothetical protein; b2257	1.86	2.05
orf, hypothetical protein; b2359	3.40	2.66
orf, hypothetical protein; b2384	1.62	1.60
orf, hypothetical protein; b2755	2.72	2.26
orf, hypothetical protein; b2757	6.48	3.80
orf, hypothetical protein; b2809	4.67	4.61
orf, hypothetical protein; b3472	0.62	0.57
orf, hypothetical protein; crca	2.87	3.98
orf, hypothetical protein; elab	3.35	3.09
orf, hypothetical protein; wcam	4.57	3.63

orf, hypothetical protein; yaaf	0.40	0.52
orf, hypothetical protein; yaib	3.31	2.48
orf, hypothetical protein; ybed	0.55	0.56
orf, hypothetical protein; ybfg	2.31	2.16
orf, hypothetical protein; ybhh	1.88	1.69
orf, hypothetical protein; ycac	6.62	5.15
orf, hypothetical protein; ycbw	1.67	1.47
orf, hypothetical protein; yccd	5.81	4.85
orf, hypothetical protein; yccj	2.71	3.33
orf, hypothetical protein; ycdf	7.83	5.88
orf, hypothetical protein; ycdq	2.90	1.81
orf, hypothetical protein; ycdu	4.94	3.41
orf, hypothetical protein; ycea	1.49	1.48
orf, hypothetical protein; ychh	0.46	0.45
orf, hypothetical protein; ycie	35.75	25.53
orf, hypothetical protein; ycig	5.93	5.50
orf, hypothetical protein; ycin	0.73	0.68
orf, hypothetical protein; ydei	22.22	16.46
orf, hypothetical protein; ydej	3.70	3.62
orf, hypothetical protein; ydit	4.91	4.14
orf, hypothetical protein; yead	0.57	0.62
orf, hypothetical protein; yeag	2.92	2.38
orf, hypothetical protein; yeah	2.43	2.30
orf, hypothetical protein; yeai	5.17	5.42
orf, hypothetical protein; yeaj	2.31	1.98
orf, hypothetical protein; yeaq	5.17	4.54
orf, hypothetical protein; year	1.71	1.57
orf, hypothetical protein; yecf	2.29	1.94
orf, hypothetical protein; yedu	4.90	4.53
orf, hypothetical protein; yehe	3.47	2.63
orf, hypothetical protein; yfec	0.39	0.38
orf, hypothetical protein; yfed	0.55	0.44
orf, hypothetical protein; yfjj	2.45	1.97
orf, hypothetical protein; ygad	0.42	0.47
orf, hypothetical protein; ygah	0.63	0.57
orf, hypothetical protein; ygam	2.40	2.06
orf, hypothetical protein; ygbf	2.00	2.00
orf, hypothetical protein; ygbp	0.67	0.65
orf, hypothetical protein; ygck	17.79	5.79
orf, hypothetical protein; ygiw	2.24	1.98
orf, hypothetical protein; yhcb	0.56	0.50
orf, hypothetical protein; yhco	1.97	1.95
orf, hypothetical protein; yhfa	0.59	0.60

orf, hypothetical protein; yhgi	0.57	0.57
orf, hypothetical protein; yhif	2.60	2.08
orf, hypothetical protein; yhim	21.89	14.77
orf, hypothetical protein; yiag	5.86	4.06
orf, hypothetical protein; yiis	2.26	2.06
orf, hypothetical protein; yiiu	0.65	0.60
orf, hypothetical protein; yijc	0.28	0.36
orf, hypothetical protein; yjbe	2.87	2.95
orf, hypothetical protein; yjbf	2.13	2.08
orf, hypothetical protein; yjbj	5.39	4.15
orf, hypothetical protein; yjbq	2.22	1.94
orf, hypothetical protein; yjbr	1.68	1.69
orf, hypothetical protein; yjdk	2.86	2.10
orf, hypothetical protein; yjfn	0.31	0.34
orf, hypothetical protein; yjgf	0.66	0.63
orf, hypothetical protein; yjha	5.97	4.06
orf, hypothetical protein; yjhq	0.57	0.68
orf, hypothetical protein; yjhs	3.50	2.32
orf, hypothetical protein; yjht	4.25	3.10
orf, hypothetical protein; yjig	0.55	0.54
orf, hypothetical protein; yjim	1.48	1.51
orf, hypothetical protein; yjix	0.42	0.39
orf, hypothetical protein; yjju	2.62	2.33
orf, hypothetical protein; yjjy	2.07	1.82
orf, hypothetical protein; ykfe	3.18	3.54
orf, hypothetical protein; ymca	1.61	1.54
orf, hypothetical protein; ynhe	2.31	2.10
orf, hypothetical protein; ypha	1.93	1.76
orf, hypothetical protein; yrbl	1.76	1.54
orf, hypothetical protein; ytfe	1.73	1.75
osmotically inducible lipoprotein; osmb	10.23	6.78
osmotically inducible protein; osmc	4.24	3.41
outer membrane protein induced after carbon starvation; slp	14.31	6.20
outer membrane protein x; ompx	5.21	3.07
outer membrane receptor for transport of vitamin b12, e colicins, and bacteriophage bf23; btub	0.57	0.58
part of maltose permease, periplasmic; malf	0.27	0.28
periplasmic maltose-binding protein; substrate recognition for transport and chemotaxis; male	0.13	0.13
periplasmic protein of mal regulon; malm	0.14	0.15
periplasmic protein related to spheroblast formation; spy	2.17	1.87
phage lambda receptor protein; maltose high-affinity receptor; lamb	0.14	0.17
phage shock protein; pspe	0.43	0.48
phosphoanhydride phosphorylase; ph 2.5 acid phosphatase; periplasmic; appa	2.84	2.50

phosphoenolpyruvate carboxykinase; pcka	0.35	0.43
phosphoenolpyruvate carboxylase; ppc	0.68	0.67
positive regulation of bgl operon; bglg	4.93	3.72
positive regulator for ctr capsule biosynthesis, positive transcription factor; rcsa	7.68	6.44
possible chaperone; b1600	4.68	4.12
probable adenine deaminase (synthesis xanthine); yicp	4.54	4.06
probable export protein; wzxc	1.95	1.95
probable formate transporter (formate channel 1); foca	2.00	2.30
probable serine transporter; sdac	0.36	0.25
probable third cytochrome oxidase, subunit i; appc	2.75	2.62
probable third cytochrome oxidase, subunit ii; appb	5.89	3.97
probable transcriptional activator for leuabcd operon; leuo	3.63	3.43
probably hexose transferase; lipopolysaccharide core biosynthesis; rfak	0.62	0.55
pts system enzyme ii, trehalose specific; treb	0.03	0.03
pts system galactitol-specific enzyme iic; gatc	0.37	0.36
pts system, glucitol/sorbitol-specific enzyme iia component; srlb	0.16	0.22
pts system, glucitol/sorbitol-specific iib component and second of two iic components; srle	0.19	0.29
putative 2-component sensor protein; yjdh	0.55	0.57
putative 2-component transcriptional regulator; yjdg	0.58	0.62
putative acyl coenzyme a dehydrogenase; aidb	2.77	2.74
putative adhesion and penetration protein; b1202	4.08	3.19
putative alpha helical protein; ybel	9.66	8.80
putative amino acid/amine transport protein, cryptic; yjde	3.60	2.84
putative amino acid/amine transport protein; b1691	3.98	2.61
putative arac-type regulatory protein; b1499	4.19	3.06
putative atp-binding component of a transport system; ycbe	1.56	1.63
putative atp-binding component of a transport system; ynhd	2.16	1.86
putative chaperone; ycbr	4.27	3.15
putative colanic acid biosynthesis glycosyl transferase; wcae	4.93	3.77
putative colanic acid polymerase; wcad	13.61	9.07
putative cytochrome; b1057	4.46	3.24
putative deor-type transcriptional regulator; b1284	2.63	2.16
putative enzyme; b1497	3.58	4.02
putative enzyme; b2253	4.15	3.28
putative enzyme; ygca	0.62	0.61
putative enzyme; yjcp	16.51	11.76
putative fimbrial-like protein; b0943	2.90	2.22
putative fimbrial-like protein; b1504	5.78	4.46
putative fimbrial-like protein; ycbq	21.27	17.67
putative function in exopolysaccharide production; yccz	1.80	1.65
putative galactokinase (ec 2.7.1.6).; wcak	2.66	2.37
putative glutaminase; ybas	4.15	2.89
putative homeobox protein; b0753	5.51	5.03

putative membrane transport protein; b1433	0.66	0.64
putative multimodular enzyme; b2463	0.42	0.54
putative nucleotide di-p-sugar epimerase or dehydratase; wcag	5.44	4.66
putative outer membrane lipoprotein; b2505	2.41	1.97
putative outer membrane protein; ycbs	4.50	3.45
putative oxidoreductase, major subunit; b1501	4.15	3.02
putative oxidoreductase; b2146	2.87	2.21
putative oxidoreductase; ygha	2.51	2.52
putative oxidoreductase; yigc	0.55	0.56
putative oxidoreductase; yncb	1.97	1.71
putative oxidoreductase; yqhd	0.60	0.60
putative polyprotein; b1045	1.59	1.47
putative polysaccharide export protein; wza	2.15	1.97
putative regulator; wcaa	2.04	2.14
putative regulator; ybbu	2.18	1.99
putative regulator; yiit	1.72	1.59
putative regulator; yjjq	1.84	1.74
putative ribosomal protein; ycdv	2.56	2.40
putative structural proteins; ycif	44.43	27.63
putative sugar transferase; b2254	5.10	3.66
putative tagatose 6-phosphate kinase 1; gatz	0.42	0.41
putative transferase; wcaf	4.04	3.66
putative transformylase; b2255	2.96	2.56
putative transmembrane subunit; ybif	3.86	3.33
putative transport protein; yegb	1.62	1.68
putative transport protein; yggb	1.55	0.46
putative transport protein; ytfl	1.80	1.79
putative transport system permease protein; ydez	3.24	2.94
putative transport system permease protein; yehz	1.54	1.66
putative transport system permease protein; yhiv	4.15	3.19
putative vimentin; yjda	2.85	1.99
putative yhbh sigma 54 modulator; yfia	0.33	0.26
pyruvate formate lyase activating enzyme 1; pfla	1.45	1.49
pyruvate oxidase; poxb	2.71	2.18
regulator for xapa; xapr	3.46	3.10
regulator of gltbdf operon, induction of ntr enzymes; gltf	4.00	2.69
regulator of melibiose operon; melr	0.58	0.46
ribosome modulation factor; rmf	5.82	5.97
ribosome modulation factor; rmf	5.71	7.74
small membrane protein a; smpa	0.59	0.49
succinate dehydrogenase, hydrophobic subunit; sdhd	0.21	0.23
succinyl-coa synthetase, alpha subunit; sucd	0.25	0.36
superoxide dismutase precursor (cu-zn); sodc	1.65	1.63

thymidine kinase; tdk	0.41	0.37
thymidine phosphorylase; deoa	2.27	1.82
transaldolase a; tala	2.91	2.39
transcription regulator; yifda	0.56	0.51
transcription regulator; yifda	0.45	0.60
transcriptional regulator of cai operon; caif	1.51	1.56
transcriptional regulator; lldr	0.16	0.31
transketolase 1 isozyme; tkta	0.54	0.55
transport of lysine/cadaverine; cadb	5.26	4.35
transport system permease (serine?); dsdx	0.34	0.36
trehalase 6-p hydrolase; trec	0.14	0.17
trehalose-6-phosphate phophatase, biosynthetic; otsb	3.20	2.64
trehalose-6-phosphate synthase; otsa	3.93	3.21
tryptophanase; tnaa	0.28	0.34
udp-glucose 6-dehydrogenase; ugd	7.37	6.00
xylose-proton symport; xyle	1.46	1.43

Taula 5 Gens diferencialment expressats en la comparació de les soques BSN27 i salvatge, pels que no es detecten diferències en la comparació BSN26HY/BSN27.

Funció i gens	**Raó d'expressió**	**B**
Traducció		
phenylalanine trna synthetase, beta-subunit; phet	1.38	0.66
acetylation of n-terminal alanine of 30s ribosomal subunit protein s5; rimj	0.63	2.41
serine trna synthetase; also charges selenocystein trna with serine; sers	0.52	4.14
Transport i metabolisme dels aminoàcids		
anaerobically inducible l-threonine, l-serine permease; tdcc	4.24	1.90
methionine adenosyltransferase 1 (adomet synthetase); methyl and propylamine donor, corepressor of met genes; metk	3.02	5.46
arginine 3rd transport system periplasmic binding protein; arti	1.71	2.39
atp-binding component of 3rd arginine transport system; artp	1.66	4.41
s-adenosylmethionine decarboxylase; sped	1.57	1.00
alanine racemase 1; alr	0.71	1.84
branched-chain amino-acid aminotransferase; ilve	0.69	2.11
putative transport system permease protein; yhdy	0.66	0.48
aminopeptidase n; pepn	0.62	1.61
glutathione synthetase; gshb	0.62	1.34
2-amino-3-ketobutyrate coa ligase (glycine acetyltransferase); kbl	0.59	1.16
proline dipeptidase; pepq	0.58	4.23
glutamate-aspartate symport protein; gltp	0.58	2.82
histidine-binding periplasmic protein of high-affinity histidine transport system; hisj	0.56	1.39

asparagine synthetase a; asna	0.53	0.04
in glycine cleavage complex, carrier of aminomethyl moiety via covalently bound lipoyl cofactor; gcvh	0.53	1.32
ilvb operon leader peptide; ivbl	0.52	2.22
putative sulfatase; b1498	0.49	2.03
chorismate synthase; aroc	0.47	1.87
aspartate carbamoyltransferase, catalytic subunit; pyrb	0.40	5.15
low affinity tryptophan permease; tnab	0.39	2.68
aspartate carbamoyltransferase, regulatory subunit; pyri	0.38	6.30
Transport i metabolisme dels sucres		
putative kinase; yeic	3.42	0.84
glyceraldehyde-3-phosphate dehydrogenase; gapc	2.62	3.87
putative transport system permease; yjhf	2.47	0.96
glycogen biosynthesis, rpos dependent; glgs	2.46	0.19
transketolase 2 isozyme; tktb	2.26	1.82
gluconate-6-phosphate dehydrogenase, decarboxylating; gnd	2.06	5.53
pts system, fructose-specific iia/fpr component; frub	2.01	3.60
l-idonate dehydrogenase; idnd	2.00	1.01
pts system, glucose-specific iibc component; ptsg	1.86	1.79
putative transport protein; yqce	1.82	5.71
putative isomerase; ybhe	1.75	4.09
gluconate kinase, thermosensitive glucokinase; idnk	1.65	0.00
putative transport protein; yegb	1.62	2.51
putative aldolase; b1773	1.55	4.03
pts system n-acetylgalactosamine-specific iic component 1; agac	1.51	1.76
ketodeoxygluconokinase; kdgk	0.68	3.61
pts system, glucitol/sorbitol-specific iic component, one of two; srla	0.65	0.44
galactose-1-phosphate uridylyltransferase; galt	0.57	2.26
ribokinase; rbsk	0.57	2.20
part of maltose permease, inner membrane; malg	0.54	0.36
uptake of c4-dicarboxylic acids; dcta	0.21	2.05
Reguladors		
haemolysin expression modulating protein; hha	6.67	0.51
putative arac-type regulatory protein; ybcm	4.52	0.73
trp repressor binding protein; affects association of trp repressor and operator; wrba	2.97	0.48
putative regulator; yjhi	2.60	1.38
sequence similarity to shigella regulator; citb	2.54	5.58
putative 2-component transcriptional regulator for 2nd curli operon; csgd	2.23	0.30
putative sensor-type protein; cita	2.15	3.31
putative 2-component sensor protein; yedv	1.99	0.28
putative transcriptional regulator; yeil	1.89	5.87
nadh dehydrogenase transcriptional regulator, lysr family; lrha	1.72	0.74
transcriptional activator of cad operon; cadc	1.67	1.95
cation transport regulator; chac	1.64	2.31
hnr protein; hnr	1.62	1.45
response transcriptional regulatory protein (rstb sensor); rsta	1.62	1.21

putative transcriptional regulator lysr-type; yiau	1.59	0.92
nitrate/nitrate sensor, histidine protein kinase acts on narl regulator; narx	1.47	1.55
pleiotrophic regulation of anaerobic respiration: response regulator for nar, frd, dms and tor genes; narl	1.45	1.08
cold shock protein; cspc	1.40	0.63
histidine protein kinase sensor for glng regulator (nitrogen regulator ii, nrii); glnl	0.68	1.23
catabolite repression sensor kinase for phob; alternative sensor for pho regulon; crec	0.67	1.57
putative transcriptional regulator; yidf	0.67	0.42
regulator of flagellar biosynthesis, acting on class 2 operons; transcriptional initiation factor; flhd	0.66	1.46
phage shock protein: activates phage shock-protein expression; pspc	0.61	0.21
positive regulator of the fuc operon; fucr	0.61	3.00
sensor kinase for hydg, hydrogenase 3 activity; hydh	0.61	6.20
regulator for gut (srl), glucitol operon; srlr	0.58	2.80
universal stress protein; broad regulatory function?; uspa	0.58	2.74
regulator for sos(lexa) regulon; lexa	0.51	5.92
response regulator for gln (sensor glnl) (nitrogen regulator i, nri); glng	0.38	3.60
Síntesi de membranes, paret i altres estructures extracel·lulars		
curlin major subunit, coiled surface structures; cryptic; csga	3.53	5.94
curli production assembly/transport component, 2nd curli operon; csgg	2.85	4.65
curli production assembly/transport component, 2nd curli operon; csgf	2.77	1.67
involved in lipopolysaccharide biosynthesis; htrl	2.42	3.11
minor curlin subunit precursor, similar ro csga; csgb	2.02	4.13
putative glycosyl transferase; wcac	1.77	3.15
probable protein-tyrosine-phosphatase; wzb	1.73	1.13
penicillin-binding protein 7; pbpg	0.70	1.22
n-acetylneuraminate lyase (aldolase); catabolism of sialic acid; not k12?; nana	0.68	0.24
1-acyl-sn-glycerol-3-phosphate acyltransferase; plsc	0.65	2.63
sialic acid transporter; nant	0.63	0.08
n-acetylmuramoyl-l-alanine amidase ii; a murein hydrolase; amib	0.63	1.34
glutamate racemase, required for biosynthesis of d-glutamate and peptidoglycan; muri	0.62	1.59
outer membrane phospholipase a; plda	0.53	1.13
Motilitat		
putative fimbrial protein; yadk	5.24	7.25
putative fimbrial protein; yadl	4.12	3.98
homolog of salmonella fimh protein; b0941	3.65	4.46
putative adhesin; similar to fimh protein; b1502	1.87	1.69
putative type-1 fimbrial protein; yeha	1.76	2.41
putative fimbrial-like protein; sfma	1.67	0.07
putative fimbrial-like protein; yadc	1.59	2.05
Proteases, xaperones i modificadors post-traduccionals		
protein disulfide isomerase ii; dsbc	3.32	4.51
possible chaperone; b1599; ydge	2.70	5.37

periplasmic serine protease do; heat shock protein htra; htra	2.12	1.98
putative o-sialoglycoprotein endopeptidase; ygjd	1.60	0.58
glutaredoxin 2; grxb	1.55	0.08
l-isoaspartate protein carboxylmethyltransferase type ii; pcm	0.69	3.18
heat shock protein, integral membrane protein; htpx	0.65	1.60
phage lambda replication; host dna synthesis; heat shock protein; protein repair; grpe	0.53	1.89
groes, 10 kd chaperone binds to hsp60 in pres. mg-atp, suppressing its atpase activity; mopb	0.28	8.52
Producció i conversió d'energia		
cytochrome d terminal oxidase polypeptide subunit ii; cydb	2.30	4.44
putative enzyme; yfde	2.07	4.17
cytochrome d terminal oxidase, polypeptide subunit i; cyda	2.06	1.56
probable flavoprotein subunit, carnitine metabolism; fixa	2.04	4.07
putative tartrate dehydrogenase; yeau	1.95	0.21
putative oxidoreductase; ybdr	1.88	2.38
putative oxidoreductase; yjgb	1.76	5.33
putative oxidoreductase; ydjj	1.68	4.86
probable flavoprotein subunit, carnitine metabolism; fixb	1.64	0.50
putative oxidoreductase, fe-s subunit; b1671	1.55	2.51
putative oxidoreductase; ycjq	1.42	0.18
ferredoxin-type protein: electron transfer; napg	0.72	0.07
putative reductase; b3001	0.61	2.88
fumarate reductase, anaerobic, flavoprotein subunit; frda	0.59	1.14
putative enzyme; b0872	0.56	0.71
membrane-bound atp synthase, f1 sector, alpha-subunit; atpa	0.55	1.38
nadh dehydrogenase i chain f; nuof	0.48	2.17
nadh dehydrogenase i chain a; nuoa	0.46	1.28
fumarase c= fumarate hydratase class ii; isozyme; fumc	0.46	1.96
formate dehydrogenase, cytochrome b556 (fdo) subunit; fdoi	0.42	2.35
aconitate hydrase b; acnb	0.38	4.43
malate dehydrogenase; mdh	0.37	4.81
succinate dehydrogenase, flavoprotein subunit; sdha	0.36	0.72
fumarase a = fumarate hydratase class i; aerobic isozyme; fuma	0.32	2.33
l-lactate dehydrogenase; lldd	0.25	4.26
succinate dehydrogenase, hydrophobic subunit; sdhd	0.21	1.75
aldehyde dehydrogenase, nad-linked; alda	0.18	1.44
citrate synthase; glta	0.17	5.68
succinate dehydrogenase, cytochrome b556; sdhc	0.16	2.50
l-lactate permease; lldp	0.12	1.75
Transport i metabolisme dels nucleòtids		
homolog of salmonella utp--glucose-1-p uridyltransferase, probably a udp-gal transferase; galf	1.87	1.42
thiamin biosynthesis, thiazole moiety; thie	0.64	0.26
orotate phosphoribosyltransferase; pyre	0.62	1.87
Replicació, recombinació i reparació del DNA		
exonuclease viii, ds dna exonuclease, 5' --> 3' specific; rece	1.57	1.13

dna strand exchange and renaturation, dna-dependent atpase, dna- and atp-dependent coprotease; reca	0.61	0.09
dna-damage-inducible protein; dind	0.60	2.09
negative modulator of initiation of replication; seqa	0.54	2.85
Metabolisme i transport de lípids		
putative enzyme; ydif	3.04	2.16
putative oxidoreductase; b1695	2.46	2.37
putative enzyme; b2889	1.49	0.38
2-octaprenyl-6-methoxy-1,4-benzoquinone --> 2-octaprenyl-3-methyl-6-methoxy-1,4-benzoquinone; ubie	0.66	0.46
putative dihydroxyacetone kinase (ec 2.7.1.2); b1199	0.64	1.43
putative oxidoreductase; ucpa	0.36	4.02
Metabolisme i transport de compostos inorgànics		
putative potassium channel protein; kch	2.31	3.52
copper homeostasis protein; cutc	1.91	6.82
mg2+ transport atpase, p-type 1; mgta	1.88	3.71
na+/h antiporter, ph dependent; nhaa	1.64	3.54
ferritin-like protein; yeci	1.60	0.24
Síntesi, transport i metabolisme de metabòlits secundaris i toxines		
multidrug resistance protein y; emry	2.08	4.14
enzyme in alternate path of synthesis of 5-aminolevulinate; hema	1.82	2.92
vitamin b12 transport; btue	1.75	1.15
detox protein; cchb	1.66	2.61
porphobilinogen deaminase = hydroxymethylbilane synthase; hemc	0.68	0.27
Gens de funció desconeguda i proteïnes hipotètiques		
orf, hypothetical protein; hded	6.26	5.25
orf, hypothetical protein; yhie	5.16	5.76
orf, hypothetical protein; ynae	3.59	6.66
orf, hypothetical protein; b1625	3.40	1.45
orf, hypothetical protein; b1365	3.36	6.53
hyperosmotically inducible periplasmic protein; osmy	3.35	2.35
orf, hypothetical protein; yhjr	3.16	2.12
orf, hypothetical protein; ycdp	2.69	3.37
orf, hypothetical protein; yqjd	2.65	4.27
orf, hypothetical protein; ygau	2.62	2.28
cold shock-like protein; cspi	2.59	7.85
orf, hypothetical protein; b1626	2.55	0.44
orf, hypothetical protein; ycep	2.49	6.11
orf, hypothetical protein; yqje	2.49	4.93
orf, hypothetical protein; ygag	2.42	6.77
orf, hypothetical protein; yjen	2.41	1.01
orf, hypothetical protein; b2060	2.40	3.48
orf, hypothetical protein; ybge	2.39	4.21
orf, hypothetical protein; ydeh	2.37	5.48
putative lyase/synthase; yjhh	2.33	0.48
putative receptor protein; b2372	2.17	6.50
orf, hypothetical protein; yqjc	2.13	0.06
orf, hypothetical protein; ydce	2.11	1.10

orf, hypothetical protein; yjfl	2.04	1.41
putative general secretion pathway for protein export (gsp); yhee	2.04	2.46
orf, hypothetical protein; b2760	2.02	6.07
orf, hypothetical protein; ybga	2.01	4.37
orf, hypothetical protein; yecd	1.99	4.14
orf, hypothetical protein; b2275	1.97	4.34
orf, hypothetical protein; b1821	1.97	3.83
orf, hypothetical protein; ycei	1.96	2.93
orf, hypothetical protein; b2758	1.96	4.21
orf, hypothetical protein; b1490	1.94	3.10
orf, hypothetical protein; b1680	1.94	4.79
orf, hypothetical protein; phna	1.94	2.19
orf, hypothetical protein; ycgw	1.92	1.82
orf, hypothetical protein; yqeh	1.88	4.25
orf, hypothetical protein; b1824	1.87	7.24
orf, hypothetical protein; yhfl	1.86	3.45
orf, hypothetical protein; ydgq	1.81	4.12
orf, hypothetical protein; b1367	1.81	3.44
putative enzyme; b2374	1.77	0.69
orf, hypothetical protein; b1825	1.75	5.16
orf, hypothetical protein; ybhm	1.70	2.02
orf, hypothetical protein; b1631	1.69	4.48
putative reductase; b1971	1.68	4.07
orf, hypothetical protein; b0834	1.66	0.18
orf, hypothetical protein; b1668	1.65	2.84
orf, hypothetical protein; ycce	1.65	0.07
orf, hypothetical protein; b1044	1.64	0.14
orf, hypothetical protein; ydgo	1.64	2.90
orf, hypothetical protein; b2250	1.63	2.17
putative general secretion pathway for protein export (gsp) (type ii traffic warden atpase); yheg	1.61	0.60
orf, hypothetical protein; ynha	1.58	1.81
orf, hypothetical protein; yiam	1.57	3.87
orf, hypothetical protein; yjdc	1.57	3.64
orf, hypothetical protein; yqhe	1.57	3.70
orf, hypothetical protein; -	1.56	0.48
orf, hypothetical protein; b1685	1.56	1.28
orf, hypothetical protein; ybaq	1.54	1.42
orf, hypothetical protein; yfao	1.54	1.74
orf, hypothetical protein; yedi	1.53	0.61
orf, hypothetical protein; yihi	1.53	1.37
putative transport system permease protein; yehy	1.52	0.56
orf, hypothetical protein; yggh	1.51	1.21
orf, hypothetical protein; b2256	1.51	0.11
membrane-associated protein; uidc	1.51	2.49
orf, hypothetical protein; b1762	1.50	1.78
putative transcriptional regulator; ybbi	1.49	1.89
orf, hypothetical protein; yeak	1.49	0.86

orf, hypothetical protein; b2353	1.49	1.28
two-module transport protein; yick	1.49	1.61
putative peptide transporter; yjdl	1.48	0.58
orf, hypothetical protein; ycgj	1.46	1.87
orf, hypothetical protein; yjej	1.46	1.03
putative atp-binding component of a transport system; yehx	1.46	2.44
putative actin; ygge	1.43	0.66
putative transport; ybby	1.42	3.03
orf, hypothetical protein; b0968	1.38	0.29
putative factor; ychp	1.34	0.85
orf, hypothetical protein; ygfb	0.74	0.21
orf, hypothetical protein; yceh	0.74	1.29
orf, hypothetical protein; yigp	0.72	0.42
orf, hypothetical protein; -	0.72	0.12
a protaminelike protein; tpr	0.70	0.69
putative histone; b3837	0.70	1.38
orf, hypothetical protein; b2619	0.69	1.25
orf, hypothetical protein; ygfy	0.68	3.09
oligopeptidase a; prlc	0.67	0.97
orf, hypothetical protein; b2896	0.66	1.08
orf, hypothetical protein; yigr	0.65	3.47
orf, hypothetical protein; ydja	0.65	0.80
orf, hypothetical protein; yjes	0.65	1.26
orf, hypothetical protein; smp	0.64	2.05
putative aminotransferase; b2290	0.64	1.49
orf, hypothetical protein; yqia	0.64	1.84
putative atp-binding component of a transport system; ybjz	0.63	0.80
orf, hypothetical protein; yjeb	0.62	0.89
orf, hypothetical protein; ybae	0.62	2.58
orf, hypothetical protein; yqha	0.61	1.04
orf, hypothetical protein; ygjr	0.61	2.42
orf, hypothetical protein; yabb	0.60	2.84
putative phosphatase; yihx	0.60	1.00
putative resistance protein; yggt	0.59	0.50
putative aminotransferase; yfho	0.58	0.23
putative transcriptional regulator; yhdm	0.57	0.25
orf, hypothetical protein; yfiq	0.57	0.75
putative regulator; yehi	0.57	3.91
orf, hypothetical protein; yhdn	0.56	0.06
orf, hypothetical protein; ydch	0.51	3.54
orf, hypothetical protein; ytfj	0.50	2.23
orf, hypothetical protein; b0725	0.45	1.12
orf, hypothetical protein; yeaa	0.35	1.08
orf, hypothetical protein; yjfo	0.35	1.46