Supplementary Table 1. Clinical observations summary during GAS soft-tissue infection for expression microarray profiling.

RMLChip	Cage Code	Strain	Pre- Weight (g)	Post- Weight (g)	Mean Weight Change (g)	Percent Original Weight (%)	Approx. Excised Tissue (g)	Estimated Time to Lesion (hr)*	Measured Lesion Width (cm) †	Measured Lesion Length (cm) †	Estimated Lesion Area (cm^2)	Estimated Lesion Volume (cm^3)	Measured Erythema Width (cm) †	Measured Erythema Length (cm) †	Estimated Erythema Area (cm^2)	Estimated Erythema Volume (cm^3)
Mse-01	A	WT	27.3	24.9	-2.4	91.2	1.5	46	0.5	0.8	0.3	0.2	1	1.5	1.2	1.2
Mse-02	H	Mutant	24.4	21.3	-3.1	87.3	1.7	28	0.9	1.8	1.3	1.5	0.9	2.3	1.6	2.5
Mse-03	B	WT	27.9	24.9	-3	89.2	1.6	46	0.6	0.7	0.3	0.2	1.1	1.9	1.6	2.1
Mse-04	I	Mutant	23.9	21.1	-2.8	88.3	2.1	28	1	1.8	1.4	1.7	1.4	1.8	2.0	2.4
Mse-06	J	Mutant	26.7	19.7	-7	73.8	1	22	2	6.6	10.4	45.6	0	0	0.0	0.0
Mse-07	D	WT	28	24.7	-3.3	88.2	1.6	N/A	0	0	0.0	0.0	0.9	2	1.4	1.9
Mse-08	K	Mutant	25	20.4	-4.6	81.6	0.9	22	0.7	3	1.8	4.0	0.8	3.6	2.3	5.4
Mse-09	E	WT	28	25.4	-2.6	90.7	2.2	N/A	0	0	0.0	0.0	1.1	2.3	2.0	3.0
Mse-10	L	Mutant	20.5	17.5	-3	85.4	0.7	22	1	3.4	2.7	6.1	1.1	3.5	3.0	7.1
Mse-11	F	WT	22.2	17.7	-4.5	79.7	0.9	N/A	0	0	0.0	0.0	1.8	5.3	7.5	26.5
Mse-12	M	Mutant	24.6	19.2	-5.4	78	1.1	22	2.5	2.8	5.5	10.3	0.4	1	0.3	0.2
Mse-13	G	WT	26.2	24.6	-1.6	93.9	1.4	46	0.2	0.3	0.0	0.0	0.6	1.2	0.6	0.5
Mse-14	N	Mutant	26.7	23.6	-3.1	88.4	1.9	46	0.7	2.4	1.3	2.1	0.5	3	1.2	2.4
Mse-15	A	WT	26.2	23.4	-2.8	89.3	1.1	N/A	0	0	0.0	0.0	1	2.1	1.6	2.3
Mse-16	H	Mutant	25.1	21.4	-3.7	85.3	1.3	22	1.8	6	8.5	33.9	0	0	0.0	0.0
Mse-17	B	WT	25.2	21.3	-3.9	84.5	1.8	N/A	0	0	0.0	0.0	2.8	4	8.8	23.5
Mse-18	I	Mutant	24.8	21.5	-3.3	86.7	1.4	22	2.6	3.6	7.4	17.6	2.7	3.7	7.8	19.4
Mse-19	C	WT	22.1	19.9	-2.2	90	0.9	46	0.5	1	0.4	0.3	0.9	1.4	1.0	0.9
Mse-20	J	Mutant	26.8	22.1	-4.7	82.5	1.3	22	0.8	3.1	1.9	4.0	1.2	3.6	3.4	8.1
Mse-21	D	WT	25.3	20	-5.3	79.1	1.3	N/A	0	0	0.0	0.0	2	2.5	3.9	6.5
Mse-22	K	Mutant	22.8	19.8	-3	86.8	1.3	22	1.4	5.7	6.3	23.8	2	5.7	6.7	25.5
Mse-23	E	WT	26.3	21.4	-4.9	81.4	1.3	N/A	0	0	0.0	0.0	1.3	2.1	2.1	3.0
Mse-24	L	Mutant	26	22.3	-3.7	85.8	0.5	22	2.4	4.5	8.5	25.4	2.5	4.5	8.8	26.5
Mse-25	F	WT	26.3	26.4	0.1	100.4	0.8	N/A	0	0	0.0	0.0	0.5	0.7	0.3	0.1

RMLChip	Cage Code	Strain	Pre- Weight (g)	Post-Weight (g)	Mean Weight Change (g)	Percent Original Weight (%)	Approx. Excised Tissue (g)	Estimated Time to Lesion (hr)*	Measured Lesion Width (cm) †	Measured Lesion Length (cm) †	Estimated Lesion Area (cm^2)	Estimated Lesion Volume (cm^3)	Measured Erythema Width (cm) †	Measured Erythema Length (cm) †	Estimated Erythema Area (cm^2)	Estimated Erythema Volume (cm^3)
Mse-26	M	Mutant	24.7	24.1	-0.6	97.6	1.3	22	2.4	2.5	4.7	7.9	2.4	3.7	7.0	17.2
Mse-27	G	WT	25.7	24.4	-1.3	94.9	1.9	N/A	0	0	0.0	0.0	0.7	1.2	0.7	0.5
Mse-28	N	Mutant	25.7	22.4	-3.3	87.2	1.3	10.5	0.5	1.4	0.5	0.5	1.1	3.6	3.1	7.5
Mse-30	H	Mutant	27.2	23.1	-4.1	84.9	2.4	22	1.7	2.7	3.6	6.5	1.7	2.9	3.9	7.5
Mse-31	B	WT	25.7	24	-1.7	93.4	0.6	46	0.3	0.3	0.1	0.0	0.6	0.9	0.4	0.3
Mse-32	I	Mutant	21.7	17.9	-3.8	82.5	0.9	22	1.5	1.9	2.2	2.8	1.9	2.3	3.4	5.3
Mse-33	C	WT	25.2	19.3	-5.9	76.6	1.3	32	1	1.2	0.9	0.8	3	5	11.8	39.3
Mse-34	J	Mutant	26.6	23.2	-3.4	87.2	1.1	22	0.45	1	0.4	0.2	0.5	1.3	0.5	0.4
Mse-35	D	WT	27.4	22	-5.4	80.3	1.5	N/A	0	0	0.0	0.0	1.3	2.5	2.6	4.3
Mse-36	K	Mutant	26.3	22.3	-4	84.8	1.4	32	1.3	3	3.1	6.1	1.7	3	4.0	8.0
Mse-37	E	WT	21.2	17.8	-3.4	84	1.8	N/A	0	0	0.0	0.0	1.6	1.6	2.0	2.1
Mse-40	M	Mutant	20	16.6	-3.4	83	1	22	1	3.8	3.0	7.6	0.5	0.9	0.4	0.2
Mse-41	G	WT	25.9	22.8	-3.1	88	0.9	N/A	0	0	0.0	0.0	0.5	1.5	0.6	0.6
Mse-42	N	Mutant	27.2	23.7	-3.5	87.1	2.5	32	0.9	4.9	3.5	11.3	1	1.5	1.2	1.2
Mse-44	H	Mutant	25.4	22.6	-2.8	89	1.7	22	1.2	3.4	3.2	7.3	1.4	3.6	4.0	9.5
Mse-45	B	WT	25.6	22.6	-3	88.3	1.1	48	0.1	0.1	0.0	0.0	0.7	2	1.1	1.5
Mse-46	I	Mutant	24.8	17	-7.8	68.5	1.8	22	3.2	3.4	8.5	19.4	3.2	3.5	8.8	20.5
Mse-47	C	WT	27.1	24.3	-2.8	89.7	0.9	N/A	0	0	0.0	0.0	0.5	1.5	0.6	0.6
Mse-48	J	Mutant	27	23.3	-3.7	86.3	1.7	22	2.5	4	7.9	20.9	2.6	4.4	9.0	26.4
Mse-49	D	WT	25.8	23.6	-2.2	91.5	0.5	N/A	0	0	0.0	0.0	1.2	1.7	1.6	1.8
Mse-50	K	Mutant	24.7	22.9	-1.8	92.7	1.7	22	0.5	2.1	0.8	1.2	1.1	2.5	2.2	3.6
Mse-51	E	WT	26.1	20.6	-5.5	78.9	1.6	46	0.4	0.8	0.3	0.1	2	3.5	5.5	12.8
Mse-52	L	Mutant	22.7	22	-0.7	96.9	1.3	22	1.4	4	4.4	11.7	1.5	4	4.7	12.6
Mse-53	F	WT	27.9	23	-4.9	82.4	0.9	N/A	0	0	0.0	0.0	3	5	11.8	39.3
Mse-54	M	Mutant	24.7	22.6	-2.1	91.5	1.1	22	0.9	1.1	0.8	0.6	1.8	2	2.8	3.8

*Estimated time to lesion substantially higher than specfied, as 15 of 27 WT-infected animals failed to develop necrotic lesions.

†Measured length (L) and width (W) values used to calculate lesion and erythema area [A = π(L/2) x (W/2)] and volume [V = 4/3π(L/2)2 x (W/2)].

Supplementary Table 2. Statistical assessment of clinical measurements during Group A *Streptococcus* soft-tissue infection for microarray expression profiling.

Variable	Adjusted *P*-value (Strain) *	Mean Ratio (Mutant / WT)	Fold Change (Mutant : WT)	Rank Sum (Mutant)	Rank Sum (WT)	Strain MGAS5005	Strain JRS950 (Δ*covR*)
Measured lesion length (cm)	**2.1 x 10^{-9}**	**14.3**	**14.3**	**947**	**279**	**0.2 ± 0.4** (Range: N/A - 1.2)	**3.2 ± 1.5** (Range: 1.0 - 6.6)
Estimated lesion volume (cm^3) †	**2.6 x 10^{-9}**	**0.5**	**-1.9**	**945**	**280**	**0.1 ± 0.2** (Range: N/A - 0.8)	**10.8 ± 11.4** (Range: 0.2 - 45.6)
Estimated lesion area (cm^2) †	**2.9 x 10^{-9}**	**9.2**	**9.2**	**944**	**281**	**0.1 ± 0.4** (Range: N/A - 0.9)	**4.0 ± 0.3** (Range: 0.4 - 10.4)
Measured lesion width (cm)	**1.2 x 10^{-8}**	**38.8**	**38.8**	**932**	**294**	**0.2 ± 0.3** (Range: N/A - 1)	**1.4 ± 0.8** (Range: 0.5 - 3.2)
Estimated time to lesion development (hr) †	**< 6.0 x 10^{-6}**	**< 0.5**	**> 1.9**	**356**	**239**	**44.5 ± 5.1** (Range: 32 - N/A)	**23.7 ± 6.0** (Range: 10.5 - 46)
Measured erythema length (cm)	0.1459	1.2	1.2	723	503	2.3 ± 1.3 (Range: 0.7 - 5.3)	2.8 ± 1.4 (Range: 0 - 5.7)
Estimated erythema volume (cm^3) †	0.1963	1.1	1.1	715	511	7.6 ± 12.2 (Range: 0.1 - 39.3)	8.6 ± 8.7 (Range: 0 - 26.5)
Estimated erythema area (cm^2) †	0.2748	1.0	-1.0	705	521	3.1 ± 3.5 (Range: 0.3 - 11.8)	3.5 ± 2.9 (Range: 0 - 9.0)
Measured percent of original weight, %	0.3567	1.1	1.1	604	621	-12.8 ± 6.1 (Range: 87.2 - 100.4)	-14.3 ± 6.1 (Range: 68.5 - 98.5)
Measured mean weight change (g)	0.4283	1.2	1.2	611	615	-3.3 ± 1.5 (Range: -5.9 to +0.1)	-3.4 ± 1.5 (Range: -7.8 to -0.6)
Approximate amount of tissue excised (g) ‡	0.4320	1.1	1.1	689	536	1.3 ± 0.4 (Range: 0.5 - 2.2)	1.4 ± 0.5 (Range: 0.5 - 2.5)
Measured erythema width (cm)	0.6955	1.1	1.1	670	556	1.3 ± 0.8 (Range: 0.5 - 3.0)	1.4 ± 0.8 (Range: 0 - 3.2)

*Mann-Whitney rank sum statistic.

†Measured length (L) and width (W) values used to calculate lesion and erythema area [A = π(L/2) x (W/2)] and volume [V = 4/3π(L/2)2 x (W/2)].

‡Estimates for time to cutaneous lesion development are substantial, as 15 of 27 WT-infected animals failed to develop necrotic lesions.

Supplementary Table 3. GAS RMLChip microarray *in vivo* transcriptome summary.

M5005_gene	RML Probeset	Gene	Description	Function	Predicted Cellular Localization *	Synonym †	Normalized Expression (WT) ‡	Transcript Rank (WT) §	Normalized Expression (Mutant) ‡	Transcript Rank (Mutant) §	Fold Change (Mutant : WT) **	*P* -value (Strain)	*Q* -value (Strain)††	Strain Significance (FDR=0.05)
M5005_Spy0001	SpM1_ChORF0002_s_at	*dnaA*	Chromosomal replication initiator protein	Cellular processing	Cytoplasmic	SPy0002	279	370	252	427	0.81	0.1709	0.3817	
M5005_Spy0002	SpM1_ChORF0003_s_at	*dnaN*	DNA polymerase III, beta chain (EC 2.7.7.7)	Cellular processing	Cytoplasmic	SPy0003	168	668	154	778	0.83	0.8276	0.6539	
M5005_Spy0003	SpM1_ChORF0004_s_at	-	Hypothetical cytosolic protein	Unknown	Unknown	SPy0004	53	1805	55	1562	1.10	0.7569	0.6368	
M5005_Spy0004	SpM1_ChORF0006_s_at	-	GTP-binding protein	Unknown	Cytoplasmic	SPy0006	204	568	175	635	0.74	0.8635	0.6616	
M5005_Spy0005	SpM1_ChORF0007_s_at	*pth*	Peptidyl-tRNA hydrolase (EC 3.1.1.29)	Protein synthesis	Unknown	SPy0007	73	1394	73	1364	1.00	0.1055	0.3149	
M5005_Spy0006	SpM1_ChORF0008_s_at	*trcF*	Transcription-repair coupling factor	Cellular processing	Cytoplasmic	SPy0008	77	1375	77	1289	1.01	0.2490	0.4321	
M5005_Spy0008	SpM1_ChORF0009_s_at	*divIC*	Cell division protein	Cellular processing	Unknown	SPy0009	51	1635	48	1606	0.89	0.4504	0.5295	
M5005_Spy0008	SpM1_ChORF0010_s_at	*divIC*	Cell division protein	Cellular processing	Unknown	SPy0010	26	2155	29	2044	1.25	0.7083	0.6201	
M5005_Spy0010	SpM12_ChORF239-12_s_at	-	Predicted open reading frame	Unknown	Unknown		71	1332	73	1394	1.03	0.0118	0.1377	
M5005_Spy0011	SpM1_ChORF0013_s_at	-	Cell cycle protein MesJ	Cellular processing	Cytoplasmic	SPy0013	27	1831	22	2019	0.62	0.3925	0.5061	
M5005_Spy0012	SpM18_ChORF0013_s_at	*hpt*	Hypoxanthine-guanine phosphoribosyltransferase (EC 2.4.2.8)	Nucleotide metabolism	Cytoplasmic	spyM18_0013	184	623	161	796	0.77	0.6929	0.6184	
M5005_Spy0013	SpM1_ChORF0015_s_at	*ftsH*	Cell division protein ftsH (EC 3.4.24.-)	Cellular processing	Cytoplasmic Membrane	SPy0015	585	128	545	189	0.87	0.1012	0.3109	
M5005_Spy0014	SpM1_ChORF0016_s_at	-	Amino acid permease	Membrane transport	Cytoplasmic Membrane	SPy0016	63	1577	64	1419	1.01	0.1589	0.3719	
M5005_Spy0015	M12_0138_s_at	-	Hypothetical protein	Unknown	Unknown		10	2654	12	2587	1.48	0.2324	0.4227	
M5005_Spy0015	SpM5_ChORF223b-1_s_at	-	Hypothetical protein	Unknown	Unknown		24	2193	30	1887	1.55	0.6303	0.6000	
M5005_Spy0016	M12_0555_s_at	-	Hypothetical protein	Unknown	Unknown		2182	18	1979	27	0.82	0.4892	0.5453	
M5005_Spy0017	SpM1_ChORF0019_s_at	*sibA*	Secreted protein	Cellular processing	Extracellular	SPy0019	508	135	377	317	0.55	0.0603	0.2682	
M5005_Spy0018	SpM1_ChORF0020_s_at	*prsA.2*	Ribose-phosphate pyrophosphokinase (EC 2.7.6.1)	Carbohydrate metabolism	Cytoplasmic	SPy0020	157	806	171	623	1.19	0.8568	0.6602	

M5005_gene	RML Probeset	Gene	Description	Function	Predicted Cellular Localization *	Synonym †	Normalized Expression (WT) ‡	Transcript Rank (WT) §	Normalized Expression (Mutant) ‡	Transcript Rank (Mutant) §	Fold Change (Mutant : WT) **	*P* -value (Strain)	*Q* -value (Strain)††	Strain Significance (FDR=0.05)
M5005_Spy0019	SpM1_ChORF0021_s_at	-	DNA repair protein recO	Cellular processing	Cytoplasmic	SPy0021	31	2160	49	1504	2.61	0.3934	0.5064	
M5005_Spy0020	SpM1_ChORF0022_s_at	*plsX*	Fatty acid/phospholipid synthesis protein plsX	Cellular processing	Unknown	SPy0022	216	517	267	461	1.52	0.0894	0.3002	
M5005_Spy0021	SpM1_ChORF0023_s_at	*acpP.2*	Acyl carrier protein	Cellular processing	Cytoplasmic	SPy0023	62	1541	73	1282	1.38	0.2748	0.4463	
M5005_Spy0022	SpM5_ChORF275f-5_s_at	-	Phosphoribosylamino-imidazole-succinocarboxamide synthase (EC 6.3.2.6)	Cellular processing	Cytoplasmic		101	1152	81	1226	0.64	0.0521	0.2541	
M5005_Spy0023	SpM49_ChORF8094-13_s_at	-	Phosphoribosylformylglycinamidine synthase (EC 6.3.5.3)	Cellular processing	Cytoplasmic		26	2230	13	2478	0.26	0.0133	0.1481	
M5005_Spy0024	SpM1_ChORF0026_s_at	*purF*	Amidophosphoribosyltransferase (EC 2.4.2.14)	Nucleotide metabolism	Cytoplasmic	SPy0026	85	1303	153	859	3.19	0.6454	0.6041	
M5005_Spy0025	SpM1_ChORF0027_s_at	*purM*	Phosphoribosylformyl-glycinamidine cyclo-ligase (EC 6.3.3.1)	Nucleotide metabolism	Cytoplasmic	SPy0027	78	1262	95	1064	1.49	0.6704	0.6108	
M5005_Spy0026	SpM1_ChORF0028_s_at	*purN*	Phosphoribosylglycinamide formyltransferase (EC 2.1.2.2)	Nucleotide metabolism	Cytoplasmic	SPy0028	45	1639	70	1395	2.41	0.3299	0.4776	
M5005_Spy0027	SpM18_ChORF0030_s_at	-	Phosphoribosylaminoimidazolecarboxamide formyltransferase (EC 2.1.2.3) / IMP cyclohydrolase (EC 3.5.4.10)	Nucleotide metabolism	Cytoplasmic	spyM18_0030	78	1165	90	1138	1.32	0.6331	0.6008	
M5005_Spy0028	SpM1_ChORF0031_s_at	-	Autolysin (EC 3.5.1.28)	Cellular processing	Unknown	SPy0031	34	2025	27	1997	0.65	0.4893	0.5453	
M5005_Spy0029	SpM1_ChORF0032_s_at	*purD*	Phosphoribosylamine--glycine ligase (EC 6.3.4.13)	Nucleotide metabolism	Cytoplasmic	SPy0032	170	631	185	669	1.19	0.4106	0.5151	
M5005_Spy0030	SpM1_ChORF0033_s_at	*purE*	Phosphoribosylaminoimidazole carboxylase catalytic subunit (EC 4.1.1.21)	Nucleotide metabolism	Cytoplasmic Membrane	SPy0033	51	1602	37	1847	0.51	0.6996	0.6184	
M5005_Spy0031	SpM1_ChORF0034_at	*purK*	Phosphoribosylaminoimidazole carboxylase ATPase subunit (EC 4.1.1.21)	Nucleotide metabolism	Cytoplasmic	SPy0034	58	1438	61	1400	1.11	0.0264	0.1949	

M5005_gene	RML Probeset	Gene	Description	Function	Predicted Cellular Localization *	Synonym †	Normalized Expression (WT) ‡	Transcript Rank (WT) §	Normalized Expression (Mutant) ‡	Transcript Rank (Mutant) §	Fold Change (Mutant : WT) **	*P* -value (Strain)	*Q* -value (Strain)††	Strain Significance (FDR=0.05)
M5005_Spy0033	SpM1_ChORF0036_s_at	*purB*	Adenylosuccinate lyase (EC 4.3.2.2)	Nucleotide metabolism	Cytoplasmic	SPy0036	185	564	208	626	1.25	0.8105	0.6512	
M5005_Spy0034	SpM49_ChORF8094-24_s_at	-	Transcriptional regulator	Information processing	Cytoplasmic		102	1102	88	1276	0.74	0.5107	0.5539	
M5005_Spy0035	SpM1_ChORF0038_s_at	*ruvB*	Holliday junction DNA helicase	Cellular processing	Cytoplasmic	SPy0038	771	91	667	131	0.75	0.0162	0.1619	
M5005_Spy0035	SpM12_ChORF296-2_s_at	-	Holliday junction DNA helicase	Cellular processing	Cytoplasmic		27	1982	25	2010	0.89	0.4373	0.5231	
M5005_Spy0036	SpM1_ChORF0039_s_at	-	Protein tyrosine phosphatase (EC 3.1.3.48)	Cellular processing	Cytoplasmic	SPy0039	128	887	100	1148	0.62	0.3710	0.4929	
M5005_Spy0037	SpM1_ChORF0040_s_at	-	Hypothetical membrane associated protein	Unknown	Unknown	SPy0040	411	255	343	313	0.70	0.4041	0.5120	
M5005_Spy0037	SpM12_ChORF296-1_s_at	-	Hypothetical membrane associated protein	Unknown	Unknown		36	1931	19	2146	0.29	0.2774	0.4482	
M5005_Spy0038	SpM1_ChORF0041_s_at	-	Acyltransferase family	Unknown	Cytoplasmic Membrane	SPy0041	295	438	335	376	1.29	0.2118	0.4110	
M5005_Spy0039	SpM18_ChORF0043_s_at	*purK*	Alcohol dehydrogenase (EC 1.1.1.1) / Acetaldehyde dehydrogenase [acetylating] (EC 1.2.1.10)	Nucleotide metabolism	Cytoplasmic	spyM18_0043	105	1016	182	646	3.00	0.6163	0.5962	
M5005_Spy0040	SpM1_ChORF0044_s_at	*adhA*	Alcohol dehydrogenase (EC 1.1.1.1)	Carbohydrate metabolism	Cytoplasmic	SPy0044	424	218	506	197	1.42	0.1936	0.3989	
M5005_Spy0041	SpM1_ChORF0045_s_at	-	Na+ driven multidrug efflux pump	Membrane transport	Cytoplasmic Membrane	SPy0045	55	1471	71	1438	1.67	0.3210	0.4751	
M5005_Spy0043	SpM1_ChORF0047_s_at	*rpsJ*	SSU ribosomal protein S10P	Protein synthesis	Unknown	SPy0047	215	549	202	580	0.88	0.5732	0.5804	
M5005_Spy0043	SpM5_ChORF275f-245_at	*rpsJ*	SSU ribosomal protein S10P	Protein synthesis	Unknown		20	2379	18	2247	0.79	0.2492	0.4321	
M5005_Spy0044	SpM1_ChORF0049_s_at	*rplC*	LSU ribosomal protein L3P	Protein synthesis	Cytoplasmic	SPy0049	386	264	297	374	0.59	0.4538	0.5310	
M5005_Spy0045	SpM1_ChORF0050_s_at	*rplD*	LSU ribosomal protein L1E (= L4P)	Protein synthesis	Unknown	SPy0050	332	307	304	397	0.84	0.3772	0.4968	
M5005_Spy0046	SpM1_ChORF0051_s_at	*rplW*	LSU ribosomal protein L23P	Protein synthesis	Unknown	SPy0051	282	432	282	383	1.00	0.7810	0.6442	
M5005_Spy0047	SpM1_ChORF0052_s_at	*rplB*	LSU ribosomal protein L2P	Protein synthesis	Unknown	SPy0052	476	213	410	245	0.74	0.9002	0.6700	

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M5005_Spy0048	SpM1_ChORF0053_x_at	*rpsS*	SSU ribosomal protein S19P	Protein synthesis	Unknown	SPy0053	321	294	328	354	1.04	0.1757	0.3859	
M5005_Spy0049	SpM1_ChORF0055_s_at	*rplV*	LSU ribosomal protein L22P	Protein synthesis	Unknown	SPy0055	240	569	204	642	0.72	0.0076	0.1081	
M5005_Spy0050	SpM1_ChORF0056_s_at	*rpsC*	SSU ribosomal protein S3P	Protein synthesis	Cytoplasmic	SPy0056	563	161	510	181	0.82	0.0780	0.2917	
M5005_Spy0051	SpM1_ChORF0057_s_at	*rplP*	LSU ribosomal protein L16P	Protein synthesis	Cytoplasmic	SPy0057	802	89	765	100	0.91	0.2182	0.4166	
M5005_Spy0052	SpM1_ChORF0059_s_at	*rpmC*	LSU ribosomal protein L29P	Protein synthesis	Cytoplasmic	SPy0059	251	436	235	485	0.88	0.5777	0.5829	
M5005_Spy0053	SpM1_ChORF0060_s_at	*rpsQ*	SSU ribosomal protein S17P	Protein synthesis	Cytoplasmic	SPy0060	419	224	369	297	0.78	0.2218	0.4184	
M5005_Spy0054	SpM1_ChORF0061_s_at	*rplN*	LSU ribosomal protein L14P	Protein synthesis	Unknown	SPy0061	575	167	492	202	0.73	0.1652	0.3758	
M5005_Spy0055	SpM1_ChORF0062_s_at	*rplX*	LSU ribosomal protein L24P	Protein synthesis	Unknown	SPy0062	489	186	473	194	0.94	0.1097	0.3154	
M5005_Spy0056	SpM1_ChORF0063_s_at	*rplE*	LSU ribosomal protein L5P	Protein synthesis	Cytoplasmic	SPy0063	380	235	369	252	0.94	0.2128	0.4110	
M5005_Spy0057	SpM1_ChORF0064_s_at	*rpsN*	SSU ribosomal protein S14P	Protein synthesis	Cytoplasmic	SPy0064	551	170	500	208	0.83	0.3347	0.4792	
M5005_Spy0058	SpM1_ChORF0065_s_at	*rpsH*	SSU ribosomal protein S8P	Protein synthesis	Cytoplasmic	SPy0065	286	317	206	480	0.52	0.0257	0.1923	
M5005_Spy0059	SpM1_ChORF0066_s_at	*rplF*	LSU ribosomal protein L6P	Protein synthesis	Cytoplasmic	SPy0066	257	398	205	597	0.64	0.0306	0.2057	
M5005_Spy0060	SpM1_ChORF0067_s_at	*rplR*	LSU ribosomal protein L18P	Protein synthesis	Unknown	SPy0067	1141	48	993	57	0.76	0.7102	0.6201	
M5005_Spy0061	SpM1_ChORF0069_s_at	*rpsE*	SSU ribosomal protein S5P	Protein synthesis	Cytoplasmic	SPy0069	290	352	297	426	1.05	0.7102	0.6201	
M5005_Spy0062	SpM1_ChORF0071_s_at	*rpmD*	LSU ribosomal protein L30P	Protein synthesis	Unknown	SPy0071	352	284	412	248	1.37	0.4975	0.5504	
M5005_Spy0063	SpM1_ChORF0072_s_at	*rplO*	LSU ribosomal protein L15P	Protein synthesis	Unknown	SPy0072	994	69	838	84	0.71	0.0848	0.2979	
M5005_Spy0064	SpM1_ChORF0073_s_at	*secY*	Protein translocase subunit secY	Secretion	Cytoplasmic Membrane	SPy0073	528	171	396	278	0.56	0.0242	0.1908	
M5005_Spy0065	SpM1_ChORF0074_s_at	*adk*	Adenylate kinase (EC 2.7.4.3)	Cellular processing	Cytoplasmic	SPy0074	123	869	115	990	0.87	0.3855	0.5006	
M5005_Spy0066	SpM1_ChORF0075_s_at	*infA*	Bacterial Protein Translation Initiation Factor 1 (IF-1)	Cellular processing	Cytoplasmic	SPy0075	871	62	874	61	1.01	0.5429	0.5695	
M5005_Spy0067	SpM1_ChORF0076_x_at	*rpmJ*	LSU ribosomal protein L36P	Protein synthesis	Extracellular	SPy0076	439	202	488	186	1.24	0.3344	0.4792	

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M5005_Spy0068	SpM1_ChORF0077_s_at	*rpsM*	SSU ribosomal protein S13P	Protein synthesis	Cytoplasmic	SPy0077	332	323	373	269	1.26	0.5968	0.5891	
M5005_Spy0069	SpM1_ChORF0078_s_at	*rpsK*	SSU ribosomal protein S11P	Protein synthesis	Unknown	SPy0078	738	104	716	116	0.94	0.7323	0.6294	
M5005_Spy0070	SpM1_ChORF0080_s_at	*rpoA*	DNA-directed RNA polymerase alpha chain (EC 2.7.7.6)	Cellular processing	Cytoplasmic	SPy0080	868	66	937	60	1.17	0.7848	0.6463	
M5005_Spy0071	SpM1_ChORF0080a_s_at	*rplQ*	LSU ribosomal protein L17P	Protein synthesis	Cytoplasmic	SPy0080a	290	396	320	391	1.22	0.3264	0.4776	
M5005_Spy0073	SpM18_ChORF0084_s_at	-	Hypothetical protein	Unknown	Unknown	spyM18_0084	6731	3	7437	4	1.22	0.0062	0.0976	
M5005_Spy0073	SpM5_ChORF270b-605_s_at	-	Hypothetical protein	Unknown	Unknown		118	729	166	686	1.96	0.2907	0.4558	
M5005_Spy0074	SpM12_ChORF300-26_s_at	-	4-diphosphocytidyl-2-C-methyl-D-erythritol kinase (EC 2.7.1.148)	Unknown	Extracellular		212	516	222	601	1.09	0.7208	0.6254	
M5005_Spy0076	M12_1023_s_at	-	4-diphosphocytidyl-2-C-methyl-D-erythritol kinase (EC 2.7.1.148)	Lipid metabolism	Cytoplasmic		341	330	341	316	1.00	0.0740	0.2853	
M5005_Spy0077	SpM1_ChORF0092_s_at	*adcR*	Transcriptional regulator, MarR family	Information processing	Unknown	SPy0092	806	86	726	102	0.81	0.4542	0.5310	
M5005_Spy0078	SpM1_ChORF0093_s_at	*adcC*	High-affinity zinc uptake system ATP-binding protein znuC	Membrane transport	Cytoplasmic Membrane	SPy0093	542	156	409	247	0.57	0.0893	0.3002	
M5005_Spy0079	SpM1_ChORF0094_s_at	*adcB*	High-affinity zinc uptake system membrane protein znuB	Membrane transport	Cytoplasmic Membrane	SPy0094	396	241	312	395	0.62	0.3625	0.4888	
M5005_Spy0080	SpM1_ChORF0095_s_at	-	Bis(5'-nucleosyl)-tetraphosphatase (asymmetrical) (EC 3.6.1.17)	Virulence	Cytoplasmic	SPy0095	30	1867	32	1876	1.09	0.9851	0.6910	
M5005_Spy0081	SpM1_ChORF0096_s_at	*tyrS*	Tyrosyl-tRNA synthetase (EC 6.1.1.1)	Protein synthesis	Cytoplasmic	SPy0096	35	1854	46	1687	1.72	0.9193	0.6743	
M5005_Spy0082	SpM1_ChORF0097_s_at	*pbp1b*	Multimodular transpeptidase-transglycosylase PBP 1B	Cell wall metabolism	Cytoplasmic Membrane	SPy0097	288	394	323	337	1.26	0.2620	0.4400	

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M5005_Spy0083	SpM1_ChORF0098_s_at	*rpoB*	DNA-directed RNA polymerase beta chain (EC 2.7.7.6)	Cellular processing	Cytoplasmic	SPy0098	523	179	486	195	0.87	0.7436	0.6328	
M5005_Spy0084	SpM1_ChORF0099_s_at	*rpoC*	DNA-directed RNA polymerase beta' chain (EC 2.7.7.6)	Cellular processing	Cytoplasmic	SPy0099	868	68	791	75	0.83	0.9946	0.6928	
M5005_Spy0085	SpM1_ChORF0100_s_at	-	Putative DNA binding protein	Unknown	Unknown	SPy0100	412	254	341	318	0.68	0.0980	0.3076	
M5005_Spy0086	SpM1_ChORF0101_s_at	*comYA*	ComG operon protein 1	Membrane transport	Cytoplasmic	SPy0101	44	1744	40	1796	0.82	0.1501	0.3618	
M5005_Spy0087	SpM1_ChORF0102_s_at	*comYB*	ComG operon protein 2	Membrane transport	Cytoplasmic Membrane	SPy0102	26	2110	29	1941	1.19	0.4735	0.5400	
M5005_Spy0088	SpM1_ChORF0103_s_at	*comYC*	ComG operon protein 3	Membrane transport	Unknown	SPy0103	22	2327	22	2328	1.00	0.8944	0.6690	
M5005_Spy0089	SpM1_ChORF0104_s_at	-	ComG operon protein 4	Membrane transport	Unknown	SPy0104	34	1866	45	1580	1.75	0.3573	0.4884	
M5005_Spy0090	SpM1_ChORF0105_s_at	-	Hypothetical protein	Unknown	Unknown	SPy0105	32	1811	13	2531	0.16	0.2610	0.4394	
M5005_Spy0091	SpM1_ChORF0106_s_at	*comYD*	ComG operon protein 6	Membrane transport	Unknown	SPy0106	21	2435	20	2284	0.96	0.3615	0.4888	
M5005_Spy0092	SpM1_ChORF0107_s_at	-	ComG operon protein 6	Unknown	Unknown	SPy0107	19	2428	35	1832	3.20	0.2512	0.4334	
M5005_Spy0093	SpM1_ChORF0108_s_at	-	Adenine-specific methyltransferase (EC 2.1.1.72)	Cellular processing	Cytoplasmic	SPy0108	272	483	218	518	0.64	0.0923	0.3002	
M5005_Spy0094	SpM1_ChORF0109_s_at	*ackA*	Acetate kinase (EC 2.7.2.1)	Carbohydrate metabolism	Cytoplasmic	SPy0109	210	553	178	716	0.72	0.0732	0.2853	
M5005_Spy0095	SpM1_ChORF0110_s_at	-	Hypothetical protein	Unknown	Unknown	SPy0110	80	1334	80	1222	1.01	0.0208	0.1798	
M5005_Spy0096	SpM1_ChORF0112_s_at	*proC*	Pyrroline-5-carboxylate reductase (EC 1.5.1.2)	Amino acid metabolism	Cytoplasmic	SPy0112	298	347	235	490	0.62	0.3743	0.4941	
M5005_Spy0097	SpM1_ChORF0115_s_at	*pepA*	Glutamyl aminopeptidase (EC 3.4.11.7)	Amino acid metabolism	Unknown	SPy0115	332	280	276	401	0.69	0.4706	0.5388	
M5005_Spy0098	SpM1_ChORF0116_at	-	Hypothetical protein	Unknown	Unknown	SPy0116	656	138	639	121	0.95	0.4954	0.5494	
M5005_Spy0099	SpM1_ChORF0117_s_at	-	Hypothetical membrane associated protein	Unknown	Unknown	SPy0117	64	1380	56	1512	0.76	0.7857	0.6463	
M5005_Spy0101	SpM18_ChORF0118_s_at	*adhE*	tRNA binding domain protein	Protein synthesis	Cytoplasmic	spyM18_0118	93	1083	114	989	1.49	0.9157	0.6743	

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M5005_Spy0101	SpM18_ChORF0119_s_at	*adhE*	tRNA binding domain protein	Protein synthesis	Cytoplasmic	spyM18_0119	99	1314	99	1135	1.00	0.0060	0.0952	
M5005_Spy0102	SpM18_ChORF0120_s_at	-	Single-strand DNA binding protein	Phage	Cytoplasmic	spyM18_0120	27	2137	36	1913	1.68	0.8415	0.6564	
M5005_Spy0103	SpM1_ChORF0121_s_at	-	Deoxyadenosine kinase (EC 2.7.1.76) / Deoxyguanosine kinase (EC 2.7.1.113)	Nucleotide metabolism	Unknown	SPy0121	143	853	141	846	0.98	0.8973	0.6690	
M5005_Spy0104	SpM1_ChORF0122_s_at	-	tRNA-dihydrouridine synthase	Protein synthesis	Cytoplasmic	SPy0122	228	476	261	499	1.31	0.2995	0.4612	
M5005_Spy0104	SpM1_ChORF0123_s_at	-	tRNA-dihydrouridine synthase	Protein synthesis	Cytoplasmic	SPy0123	185	661	147	730	0.63	0.2355	0.4227	
M5005_Spy0106	SpM1_ChORF0124_s_at	*rofA*	Transcriptional regulator	Information processing	Unknown	SPy0124	1389	30	1420	32	1.05	0.6065	0.5923	
M5005_Spy0108	SpM1_ChORF0127_at	-	Signal peptidase I (EC 3.4.21.89)	Secretion	Unknown	SPy0127	65	1434	77	1302	1.40	0.0293	0.2028	
M5005_Spy0109	SpM1_ChORF0128_at	-	Fibronectin-binding protein	Virulence	Unknown	SPy0128	137	685	136	912	0.99	0.6613	0.6081	
M5005_Spy0110	SpM1_ChORF0129_at	*eftLSL.B*	Hypothetical Exported Protein	Unknown	Unknown (This protein may have multiple localization sites.)	SPy0129	118	856	95	1164	0.64	0.0503	0.2538	
M5005_Spy0111	SpM1_ChORF0130_at	-	Hypothetical protein	Unknown	Cell Wall	SPy0130	61	1345	78	1299	1.67	0.8963	0.6690	
M5005_Spy0112	SpM1_ChORF0131_at	-	Transposase	Mobile genetic element	Cytoplasmic Membrane	SPy0131	141	812	105	1111	0.56	0.5875	0.5871	
M5005_Spy0113	SpM1_ChORF0133_at	-	Transposase	Mobile genetic element	Unknown	SPy0133	38	1781	74	1520	3.91	0.9205	0.6743	
M5005_Spy0114	SpM1_ChORF0135_at	-	Sortase	Cell wall metabolism	Unknown	SPy0135	19	2272	42	1662	5.10	0.6932	0.6184	
M5005_Spy0114	SpM1_ChORF0135_s_at	-	Sortase	Cell wall metabolism	Unknown	SPy0135	19	2346	20	2262	1.12	0.3824	0.4990	
M5005_Spy0114	SpM12_ChORF300-50_s_at	-	Sortase	Cell wall metabolism	Unknown		33	1886	63	1450	3.59	0.7317	0.6294	
M5005_Spy0115	SpM1_ChORF0136_s_at	-	Hypothetical protein	Unknown	Unknown	SPy0136	86	1302	311	410	13.20	2.4E-12	**6.6E-10**	**Significant**
M5005_Spy0116	SpM1_ChORF0137_s_at	*atoE*	Short-chain fatty acids transporter	Membrane transport	Cytoplasmic Membrane	SPy0137	82	1246	56	1428	0.46	0.8078	0.6512	

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M5005_Spy0117	SpM18_ChORF0135_s_at	-	Transcriptional regulators, LysR family	Information processing	Unknown	spyM18_0135	135	784	109	1095	0.65	0.2090	0.4110	
M5005_Spy0119	SpM1_ChORF0140_s_at	-	Acetyl-CoA acetyltransferase (EC 2.3.1.9)	Cell wall metabolism	Cytoplasmic	SPy0140	68	1447	79	1330	1.34	0.4222	0.5176	
M5005_Spy0120	SpM1_ChORF0141_s_at	*atoD.2*	Acetate CoA-transferase alpha subunit (EC 2.8.3.8)	Carbohydrate metabolism	Cytoplasmic	SPy0141	59	1388	78	1362	1.77	0.0407	0.2321	
M5005_Spy0121	M12_0965_at	-	Acetyl-CoA:acetoacetyl-CoA transferase beta subunit (EC 2.8.3.-)	Carbohydrate metabolism	Cytoplasmic		19	2349	21	2172	1.30	0.9878	0.6915	
M5005_Spy0121	SpM1_ChORF0142_s_at	-	Acetyl-CoA:acetoacetyl-CoA transferase beta subunit (EC 2.8.3.-)	Carbohydrate metabolism	Cytoplasmic	SPy0142	33	1893	26	2102	0.60	0.4771	0.5418	
M5005_Spy0122	SpM1_ChORF0144_s_at	-	Putative DNA-binding protein	Information processing	Cytoplasmic	SPy0144	64	1605	82	1343	1.65	0.2096	0.4110	
M5005_Spy0123	SpM1_ChORF0145_s_at	-	Translation initiation inhibitor	Cellular processing	Cytoplasmic	SPy0145	29	2037	35	1716	1.50	0.7965	0.6489	
M5005_Spy0124	SpM1_ChORF0146_s_at	*sloR*	Transcriptional regulator	Information processing	Cytoplasmic Membrane	SPy0146	87	1197	117	1005	1.82	0.0218	0.1830	
M5005_Spy0125	SpM1_ChORF0147_s_at	-	Hypothetical protein	Unknown	Cytoplasmic	SPy0147	39	1846	21	2259	0.28	0.8086	0.6512	
M5005_Spy0126	SpM1_ChORF0148_s_at	*ntpI*	V-type sodium ATP synthase subunit I (EC 3.6.3.15)	Membrane transport	Cytoplasmic Membrane	SPy0148	98	953	141	856	2.05	0.3331	0.4779	
M5005_Spy0126	SpM12_ChORF175-2_s_at	*ntpI*	V-type sodium ATP synthase subunit I (EC 3.6.3.15)	Membrane transport	Cytoplasmic Membrane		48	1524	95	1043	4.03	0.0150	0.1577	
M5005_Spy0127	SpM1_ChORF0149_s_at	*ntpK*	V-type sodium ATP synthase subunit K (EC 3.6.3.15)	Membrane transport	Cytoplasmic Membrane	SPy0149	35	1952	83	1298	5.61	0.0591	0.2676	
M5005_Spy0128	SpM1_ChORF0150_s_at	*ntpE*	V-type sodium ATP synthase subunit E (EC 3.6.3.14)	Membrane transport	Cytoplasmic	SPy0150	69	1295	101	1050	2.11	0.0060	0.0952	
M5005_Spy0129	SpM1_ChORF0151_s_at	*ntpC*	V-type ATP synthase subunit C (EC 3.6.3.14)	Membrane transport	Cytoplasmic	SPy0151	98	890	182	663	3.45	0.0269	0.1976	
M5005_Spy0130	SpM18_ChORF0148_s_at	*msmRL*	V-type ATP synthase subunit F (EC 3.6.3.14)	Carbohydrate metabolism	Cytoplasmic	spyM18_0148	58	1496	76	1352	1.71	0.2686	0.4436	

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M5005_Spy0131	SpM1_ChORF0154_s_at	*ntpA*	V-type sodium ATP synthase subunit A (EC 3.6.3.15)	Membrane transport	Cytoplasmic	SPy0154	79	1105	156	750	3.88	0.0716	0.2838	
M5005_Spy0132	SpM1_ChORF0155_s_at	*ntpB*	V-type sodium ATP synthase subunit B (EC 3.6.3.15)	Membrane transport	Cytoplasmic	SPy0155	123	957	241	509	3.85	0.0145	0.1538	
M5005_Spy0133	SpM1_ChORF0157_s_at	*ntpD*	V-type sodium ATP synthase subunit D (EC 3.6.3.15)	Membrane transport	Cytoplasmic	SPy0157	55	1539	74	1253	1.82	0.8675	0.6623	
M5005_Spy0134	SpM1_ChORF0158_s_at	-	Tellurite resistance protein	Unknown	Unknown	SPy0158	249	490	279	440	1.26	0.5081	0.5532	
M5005_Spy0135	SpM1_ChORF0159_s_at	-	Hypothetical membrane associated protein	Unknown	Cytoplasmic	SPy0159	256	458	244	483	0.91	0.4905	0.5463	
M5005_Spy0136	SpM1_ChORF0160_s_at	*purA*	Adenylosuccinate synthetase (EC 6.3.4.4)	Nucleotide metabolism	Cytoplasmic	SPy0160	206	541	251	472	1.48	0.7816	0.6442	
M5005_Spy0137	SpM1_ChORF0163_s_at	-	Nucleoside-binding protein	Unknown	Unknown	SPy0163	143	845	133	938	0.87	0.9124	0.6743	
M5005_Spy0138	SpM1_ChORF0164_s_at	*nusG*	Transcription antitermination protein nusG	Information processing	Cytoplasmic	SPy0164	94	1061	109	978	1.34	0.6684	0.6104	
M5005_Spy0139	SpM1_ChORF0165_s_at	*nga*	NAD glycohydrolase; NADase (EC 3.2.2.5)	Virulence	Unknown	SPy0165	144	780	158	819	1.21	0.0483	0.2502	
M5005_Spy0140	SpM1_ChORF0166_s_at	-	Hypothetical protein	Unknown	Cytoplasmic	SPy0166	105	1079	101	1047	0.93	0.0056	0.0949	
M5005_Spy0141	SpM1_ChORF0167_s_at	*slo*	Streptolysin O	Virulence	Unknown	SPy0167	391	268	485	193	1.54	0.1712	0.3817	
M5005_Spy0146	SpM1_ChORF0172_s_at	*metB*	Cystathionine beta-lyase (EC 4.4.1.8)	Amino acid metabolism	Cytoplasmic	SPy0172	36	1960	155	906	18.91	0.0405	0.2314	
M5005_Spy0147	SpM1_ChORF0173_s_at	*leuS*	Leucyl-tRNA synthetase (EC 6.1.1.4)	Protein synthesis	Cytoplasmic	SPy0173	212	615	195	567	0.84	0.4257	0.5176	
M5005_Spy0147	SpM12_ChORF286-3_s_at	*leuS*	Leucyl-tRNA synthetase (EC 6.1.1.4)	Protein synthesis	Cytoplasmic		111	867	111	1061	1.00	0.5115	0.5540	
M5005_Spy0148	SpM1_ChORF0174_s_at	-	PTS system, 3-keto-L-gulonate specific IIC component (EC 2.7.1.69)	Membrane transport	Cytoplasmic Membrane	SPy0174	70	1247	111	982	2.57	0.8673	0.6623	

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M5005_Spy0149	SpM1_ChORF0175_s_at	-	PTS system, 3-keto-L-gulonate specific IIB component (EC 2.7.1.69)	Carbohydrate metabolism	Cytoplasmic	SPy0175	113	1108	120	904	1.12	0.8673	0.6623	
M5005_Spy0150	SpM1_ChORF0176_s_at	-	PTS system, 3-keto-L-gulonate specific IIA component (EC 2.7.1.69)	Membrane transport	Unknown	SPy0176	75	1259	99	1100	1.74	1.1E-05	**0.0006**	**Significant**
M5005_Spy0151	SpM1_ChORF0177_s_at	-	3-keto-L-gulonate-6-phosphate decarboxylase (EC 4.1.1.-)	Carbohydrate metabolism	Cytoplasmic	SPy0177	114	914	211	629	3.46	0.4277	0.5178	
M5005_Spy0152	SpM1_ChORF0178_s_at	-	L-xylulose 5-phosphate 3-epimerase (EC 5.3.1.-)	Carbohydrate metabolism	Cytoplasmic	SPy0178	116	1093	170	619	2.14	0.0012	**0.0315**	**Significant**
M5005_Spy0152	SpM12_ChORF286-31_s_at	-	L-xylulose 5-phosphate 3-epimerase (EC 5.3.1.-)	Carbohydrate metabolism	Cytoplasmic		29	2035	24	2073	0.64	0.8949	0.6690	
M5005_Spy0153	SpM1_ChORF0179_s_at	*araD*	L-ribulose-5-phosphate 4-epimerase (EC 5.1.3.4)	Carbohydrate metabolism	Cytoplasmic	SPy0179	240	511	322	301	1.80	0.0002	**0.0087**	**Significant**
M5005_Spy0154	SpM1_ChORF0180_s_at	-	Hypothetical protein	Unknown	Unknown	SPy0180	51	1507	76	1344	2.20	0.7961	0.6488	
M5005_Spy0155	SpM1_ChORF0181_s_at	-	Transcription antiterminator, BglG family	Cellular processing	Cytoplasmic Membrane	SPy0181	91	1213	89	1210	0.96	0.8346	0.6555	
M5005_Spy0156	SpM1_ChORF0182_s_at	-	Metal-dependent hydrolase (EC 3.-.-.-)	Cellular processing	Cytoplasmic	SPy0182	416	287	339	302	0.66	0.3841	0.4999	
M5005_Spy0157	SpM1_ChORF0183_s_at	*opuAA*	Glycine betaine transport ATP-binding protein	Membrane transport	Cytoplasmic Membrane	SPy0183	493	184	365	315	0.55	0.0050	0.0897	
M5005_Spy0158	SpM1_ChORF0184_s_at	*opuABC*	Glycine betaine-binding protein / Glycine betaine transport system permease protein	Membrane transport	Cytoplasmic Membrane	SPy0184	463	134	297	435	0.41	0.0045	0.0846	
M5005_Spy0160	SpM1_ChORF0186_s_at	-	CoA binding protein	Unknown	Cytoplasmic	SPy0186	456	250	477	212	1.10	0.1021	0.3116	

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M5005_Spy0161	SpM1_ChORF0187_s_at	*perR*	Ferric transport regulator protein/Ferric uptake regulation protein	Information processing	Cytoplasmic	SPy0187	632	130	741	101	1.37	0.0132	0.1479	
M5005_Spy0162	SpM1_ChORF0188_s_at	*vlg*	Trans-acting positive regulator Mry	Information processing	Unknown	SPy0188	478	212	553	169	1.33	0.3124	0.4706	
M5005_Spy0163	SpM1_ChORF0189_s_at	-	3'-phosphoadenosine 5'-phosphosulfate sulfotransferase (PAPS reductase)	Unknown	Cytoplasmic	SPy0189	360	298	438	238	1.48	0.0233	0.1901	
M5005_Spy0164	SpM1_ChORF0190_s_at	-	ParB-like nuclease	Unknown	Cytoplasmic	SPy0190	342	318	403	260	1.39	0.0003	**0.0105**	**Significant**
M5005_Spy0165	SpM1_ChORF0191_at	-	Transposase	Mobile genetic element	Extracellular	SPy0191	45	1585	42	1713	0.89	0.8121	0.6512	
M5005_Spy0167	SpM12_ChORF286-28_s_at	-	Transposase	Mobile genetic element	Cytoplasmic		34	2057	30	1920	0.76	0.8520	0.6586	
M5005_Spy0167	SpM3_ChORF1054_s_at	-	Transposase	Mobile genetic element	Cytoplasmic	spyM3_1054	232	427	228	493	0.97	0.1147	0.3225	
M5005_Spy0168	SpM5_ChORF270b-541_x_at	-	Transposase	Mobile genetic element	Unknown		107	903	118	976	1.23	0.0217	0.1827	
M5005_Spy0169	SpM1_ChORF0196_s_at	-	Malonate permease	Membrane transport	Cytoplasmic Membrane	SPy0196	20	2179	29	1926	2.18	0.1777	0.3875	
M5005_Spy0170	SpM1_ChORF0197_s_at	*nadC*	Nicotinate-nucleotide pyrophosphorylase [carboxylating] (EC 2.4.2.19)	Coenzyme and cofactor metabolism	Cytoplasmic	SPy0197	27	2010	19	2242	0.48	0.6999	0.6184	
M5005_Spy0171	SpM1_ChORF0198_s_at	-	Transposase	Mobile genetic element	Unknown	SPy0198	18	2518	19	2375	1.04	0.1165	0.3229	
M5005_Spy0172	SpM1_ChORF0199_s_at	-	Transposase	Mobile genetic element	Cytoplasmic	SPy0199	70	1428	30	1888	0.19	0.9725	0.6874	
M5005_Spy0173	SpM1_ChORF0201_s_at	-	Integral membrane protein	Unknown	Cytoplasmic Membrane	SPy0201	124	965	137	852	1.22	0.9385	0.6780	
M5005_Spy0175	M12_0671_s_at	*tgt*	Queuine tRNA-ribosyltransferase (EC 2.4.2.29)	Protein synthesis	Cytoplasmic		24	2216	43	1674	3.20	0.2128	0.4110	
M5005_Spy0175	SpM1_ChORF0203_s_at	*tgt*	Queuine tRNA-ribosyltransferase (EC 2.4.2.29)	Protein synthesis	Cytoplasmic	SPy0203	53	1281	94	1228	3.12	0.6324	0.6007	
M5005_Spy0176	SpM1_ChORF0205_s_at	-	Zinc finger protein	Unknown	Unknown	SPy0205	69	1538	46	1703	0.45	0.6171	0.5962	

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M5005_Spy0177	SpM1_ChORF0207_s_at	-	BioY protein	Unknown	Cytoplasmic Membrane	SPy0207	41	1814	40	1879	0.97	0.3711	0.4929	
M5005_Spy0178	SpM1_ChORF0208_s_at	-	Metal-dependent hydrolase (EC 3.-.-.-)	Unknown	Cytoplasmic	SPy0208	89	1179	81	1323	0.84	0.6296	0.6000	
M5005_Spy0179	SpM18_ChORF0196_s_at	-	tRNA-specific adenosine deaminase	Unknown	Cytoplasmic	spyM18_0196	270	413	262	478	0.94	0.7228	0.6262	
M5005_Spy0180	SpM1_ChORF0210_s_at	-	Putative murein endopeptidase	Unknown	Unknown	SPy0210	52	1703	57	1644	1.18	0.0494	0.2521	
M5005_Spy0182	SpM1_ChORF0212_s_at	*speG*	Exotoxin type G precursor	Virulence	Extracellular	SPy0212	37	1969	32	2099	0.74	0.9022	0.6705	
M5005_Spy0183	SpM18_ChORF0202_s_at	-	Hypothetical membrane associated protein	Unknown	Extracellular	spyM18_0202	93	1089	65	1404	0.49	0.2663	0.4436	
M5005_Spy0185	SpM1_ChORF0215_s_at	*pgi*	Glucose-6-phosphate isomerase (EC 5.3.1.9)	Carbohydrate metabolism	Cytoplasmic	SPy0215	122	929	141	905	1.33	0.2835	0.4537	
M5005_Spy0186	SpM1_ChORF0216_s_at	-	Transcriptional regulator	Information processing	Unknown	SPy0216	70	1227	86	1234	1.49	0.1157	0.3228	
M5005_Spy0186	SpM3_ChORF0158_s_at	-	Transcriptional regulator	Information processing	Unknown	spyM3_0158	39	1572	53	1496	1.83	0.5515	0.5708	
M5005_Spy0187	SpM12_ChORF197-4_s_at	-	Transposase	Mobile genetic element	Cytoplasmic		155	740	161	711	1.08	0.0678	0.2770	
M5005_Spy0189	SpM1_ChORF0219_x_at	-	Hypothetical protein	Unknown	Extracellular	SPy0219	317	324	367	246	1.34	0.3507	0.4854	
M5005_Spy0191	SpM12_ChORF279-21_s_at	-	Integral membrane protein (Rhomboid family)	Unknown	Cytoplasmic Membrane		39	1779	55	1501	2.00	0.5086	0.5532	
M5005_Spy0192	SpM1_ChORF0224_s_at	*hasC.2*	UTP--glucose-1-phosphate uridylyltransferase (EC 2.7.7.9)	Carbohydrate metabolism	Cytoplasmic	SPy0224	331	332	432	251	1.70	0.0895	0.3002	
M5005_Spy0194	SpM1_ChORF0226_s_at	*gpsA*	Glycerol-3-phosphate dehydrogenase [NAD(P)+] (EC 1.1.1.94)	Cellular processing	Unknown	SPy0226	415	173	566	173	1.86	0.0872	0.3002	
M5005_Spy0195	SpM1_ChORF0227_s_at	-	Transcriptional regulator, MarR family	Information processing	Cytoplasmic	SPy0227	69	1271	60	1476	0.78	0.1897	0.3986	
M5005_Spy0195	SpM1_ChORF0228_s_at	-	Transcriptional regulator, MarR family	Information processing	Cytoplasmic	SPy0228	75	1320	82	1336	1.21	0.6161	0.5962	

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M5005_Spy0196	SpM1_ChORF0229_s_at	-	Multidrug resistance ABC transporter ATP-binding and permease protein	Membrane transport	Cytoplasmic Membrane	SPy0229	146	749	170	696	1.36	0.0063	0.0991	
M5005_Spy0197	SpM1_ChORF0230_s_at	-	Multidrug resistance ABC transporter ATP-binding and permease protein	Membrane transport	Cytoplasmic Membrane	SPy0230	38	1789	50	1489	1.69	0.3985	0.5106	
M5005_Spy0198	SpM1_ChORF0233_s_at	-	Hypothetical cytosolic protein	Unknown	Cytoplasmic	SPy0233	21	2182	46	1641	4.63	0.0249	0.1913	
M5005_Spy0199	SpM1_ChORF0235_s_at	-	Deoxyuridine 5'-triphosphate nucleotidohydrolase (EC 3.6.1.23)	Nucleotide metabolism	Unknown	SPy0235	124	955	111	963	0.80	0.2729	0.4451	
M5005_Spy0200	SpM1_ChORF0236_s_at	*sms*	DNA repair protein RadA	Stress adaptation	Cytoplasmic	SPy0236	149	781	110	1028	0.54	0.2439	0.4278	
M5005_Spy0201	SpM1_ChORF0237_s_at	-	Carbonic anhydrase (EC 4.2.1.1)	Unknown	Cytoplasmic	SPy0237	102	1239	78	1215	0.59	0.5130	0.5550	
M5005_Spy0202	SpM1_ChORF0238_s_at	-	Hypothetical protein	Unknown	Unknown	SPy0238	78	1244	84	1223	1.14	0.3165	0.4736	
M5005_Spy0203	SpM1_ChORF0239_s_at	*gltX*	Glutamyl-tRNA synthetase (EC 6.1.1.17)	Protein synthesis	Cytoplasmic	SPy0239	146	763	125	922	0.74	0.1775	0.3875	
M5005_Spy0204	SpM1_ChORF0242_s_at	*fasB*	Sensory transduction protein kinase FasB (EC 2.7.3.-)	Signal transduction	Cytoplasmic Membrane	SPy0242	39	1749	17	2269	0.20	0.4351	0.5221	
M5005_Spy0205	SpM5_ChORF275f-139_s_at	*fasC*	Sensory transduction protein kinase FasC (EC 2.7.3.-)	Signal transduction	Cytoplasmic Membrane		16	2552	29	1955	3.46	0.9318	0.6750	
M5005_Spy0206	SpM1_ChORF0245_s_at	*fasA*	Sensory transduction response regulator FasA	Signal transduction	Cytoplasmic	SPy0245	39	1734	51	1770	1.68	0.3681	0.4914	
M5005_Spy0207	SpM1_ChORF0246_s_at	*fasX*	Sensory transduction, Ribonuclease P protein component (EC 3.1.26.5)	Signal transduction	Cytoplasmic	SPy0246	215	551	168	689	0.61	0.1682	0.3801	
M5005_Spy0208	SpM1_ChORF0247_s_at	-	60 kDa inner membrane protein YIDC	Cellular processing	Cytoplasmic Membrane	SPy0247	229	585	259	546	1.28	0.3713	0.4929	
M5005_Spy0209	SpM1_ChORF0248_s_at	-	Jag protein	Cellular processing	Cytoplasmic	SPy0248	235	537	176	664	0.56	0.3256	0.4776	

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M5005_Spy0211	SpM1_ChORF0250_x_at	*rpmH*	LSU ribosomal protein L34P	Protein synthesis	Extracellular	SPy0250	77	1401	73	1277	0.89	0.4189	0.5169	
M5005_Spy0212	SpM1_ChORF0251_s_at	-	N-acetylmannosamine-6-phosphate 2-epimerase (EC 5.1.3.9)	Carbohydrate metabolism	Cytoplasmic	SPy0251	201	550	210	534	1.09	0.4630	0.5348	
M5005_Spy0213	SpM1_ChORF0252_s_at	-	N-acetylneuraminate-binding protein	Membrane transport	Unknown	SPy0252	132	798	214	573	2.64	0.2627	0.4400	
M5005_Spy0213	SpM12_ChORF295-17_s_at	-	N-acetylneuraminate-binding protein	Membrane transport	Unknown		33	2060	28	1979	0.73	0.4976	0.5504	
M5005_Spy0213	SpM3_ChORF0181_s_at	-	N-acetylneuraminate-binding protein	Membrane transport	Unknown	spyM3_0181	92	1087	179	662	3.84	0.0582	0.2665	
M5005_Spy0214	SpM1_ChORF0254_s_at	-	N-acetylneuraminate transport system permease protein	Membrane transport	Cytoplasmic Membrane	SPy0254	85	1189	116	972	1.86	0.3847	0.4999	
M5005_Spy0215	SpM12_ChORF295-23_s_at	-	N-acetylneuraminate transport system permease protein	Membrane transport	Cytoplasmic Membrane		96	1172	87	1207	0.81	0.2469	0.4310	
M5005_Spy0216	SpM1_ChORF0256_s_at	-	Hypothetical membrane spanning protein	Unknown	Cytoplasmic Membrane	SPy0256	102	964	139	825	1.86	0.2403	0.4266	
M5005_Spy0217	SpM1_ChORF0257_s_at	*nanH*	N-acetylneuraminate lyase (EC 4.1.3.3)	Cell wall metabolism	Unknown (This protein may have multiple localization sites.)	SPy0257	203	608	204	572	1.01	0.9337	0.6759	
M5005_Spy0218	SpM1_ChORF0258_s_at	-	N-acetylmannosamine kinase (EC 2.7.1.60)	Carbohydrate metabolism	Cytoplasmic	SPy0258	55	1551	120	992	4.71	0.0257	0.1923	
M5005_Spy0219	SpM1_ChORF0259_s_at	-	Transcriptional regulator, RpiR family	Information processing	Cytoplasmic	SPy0259	87	1103	84	1296	0.92	0.5844	0.5864	
M5005_Spy0220	SpM1_ChORF0260_s_at	-	Sec-independent protein translocase protein tatD (EC 3.1.21.-)	Secretion	Cytoplasmic	SPy0260	220	575	261	462	1.41	0.6001	0.5893	
M5005_Spy0221	SpM1_ChORF0261_s_at	-	Ribonuclease M5 (EC 3.1.26.8)	Cellular processing	Cytoplasmic	SPy0261	199	619	213	612	1.15	0.1295	0.3379	
M5005_Spy0222	SpM1_ChORF0262_s_at	*ksgA*	Dimethyladenosine transferase (EC 2.1.1.-)	Cellular processing	Cytoplasmic	SPy0262	195	629	199	691	1.04	0.3592	0.4888	
M5005_Spy0223	SpM1_ChORF0263_s_at	-	GTPase (EC 3.6.1.-)	Unknown	Cytoplasmic	SPy0263	440	215	387	287	0.77	0.1612	0.3722	

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M5005_Spy0224	SpM1_ChORF0264_s_at	*rpe*	Ribulose-phosphate 3-epimerase (EC 5.1.3.1)	Carbohydrate metabolism	Cytoplasmic	SPy0264	264	402	244	533	0.86	0.1331	0.3410	
M5005_Spy0225	SpM1_ChORF0265_s_at	-	Thiamin pyrophosphokinase (EC 2.7.6.2)	Coenzyme and cofactor metabolism	Unknown	SPy0265	325	361	273	420	0.71	0.4263	0.5176	
M5005_Spy0226	SpM1_ChORF0266_s_at	-	RmuC family protein	Unknown	Unknown	SPy0266	705	120	648	148	0.84	0.2116	0.4110	
M5005_Spy0227	SpM1_ChORF0267_s_at	*cbf*	CMP-binding factor	Virulence	Cytoplasmic	SPy0267	382	256	395	275	1.07	0.5392	0.5674	
M5005_Spy0228	SpM1_ChORF0268_s_at	*purR*	Pur operon repressor	Information processing	Unknown	SPy0268	407	249	404	290	0.99	0.7263	0.6276	
M5005_Spy0229	SpM1_ChORF0269_s_at	*prgA*	Surface exclusion protein	Virulence	Cell Wall	SPy0269	1280	36	1126	37	0.77	0.5802	0.5838	
M5005_Spy0230	SpM1_ChORF0271_s_at	*rpsL*	SSU ribosomal protein S12P	Protein synthesis	Unknown	SPy0271	365	319	315	418	0.74	0.6608	0.6081	
M5005_Spy0231	SpM1_ChORF0272_s_at	*rpsG*	SSU ribosomal protein S7P	Protein synthesis	Unknown	SPy0272	816	100	684	103	0.70	0.2741	0.4460	
M5005_Spy0232	SpM1_ChORF0273_s_at	*fus*	Protein Translation Elongation Factor G (EF-G)	Cellular processing	Cytoplasmic	SPy0273	884	83	856	65	0.94	0.9570	0.6842	
M5005_Spy0233	SpM1_ChORF0274_s_at	*plr, gap, NAPlr*	Glyceraldehyde 3-phosphate dehydrogenase (EC 1.2.1.12); plasmin receptor	Carbohydrate metabolism	Cytoplasmic	SPy0274	854	71	812	81	0.90	0.8978	0.6691	
M5005_Spy0234	SpM18_ChORF0262_at	-	Hypothetical protein	Unknown	Extracellular	spyM18_0262	64	1456	74	1354	1.32	0.6619	0.6081	
M5005_Spy0236	SpM1_ChORF0276_s_at	-	ABC transporter amino acid-binding protein / Amino acid ABC transporter permease protein	Membrane transport	Cytoplasmic Membrane	SPy0276	95	1157	93	1265	0.96	0.0141	0.1511	
M5005_Spy0236	SpM1_ChORF0277_s_at	-	ABC transporter amino acid-binding protein / Amino acid ABC transporter permease protein	Membrane transport	Cytoplasmic Membrane	SPy0277	85	1166	83	1141	0.96	0.5273	0.5626	
M5005_Spy0237	SpM1_ChORF0278_s_at	-	Hypothetical membrane spanning protein	Unknown	Cytoplasmic	SPy0278	131	1017	137	884	1.09	0.9017	0.6704	

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M5005_Spy0238	SpM1_ChORF0280_s_at	*bacA*	Putative undecaprenol kinase (EC 2.7.1.66)	Lipid metabolism	Cytoplasmic Membrane	SPy0280	100	1145	98	1162	0.96	0.6194	0.5962	
M5005_Spy0239	SpM1_ChORF0281_s_at	*mecA*	Negative regulator of genetic competence mecA	Information processing	Cytoplasmic	SPy0281	165	663	138	835	0.70	0.1935	0.3989	
M5005_Spy0241	SpM1_ChORF0282_s_at	*rgpG*	Hypothetical cytosolic protein	Cellular processing	Unknown	SPy0282	161	778	176	666	1.19	0.5624	0.5763	
M5005_Spy0242	SpM1_ChORF0285_s_at	-	ABC transporter ATP-binding protein	Membrane transport	Cytoplasmic Membrane	SPy0285	127	1037	149	805	1.37	0.7660	0.6382	
M5005_Spy0243	SpM1_ChORF0287_s_at	-	ABC transporter-associated protein	Membrane transport	Cytoplasmic	SPy0287	234	503	238	537	1.04	0.8807	0.6649	
M5005_Spy0244	SpM1_ChORF0288_s_at	*nifS, csd*	Cysteine desulfhydrase (EC 4.4.1.-) / Selenocysteine lyase (EC 4.4.1.16)	Amino acid metabolism	Cytoplasmic	SPy0288	208	610	193	600	0.85	0.6081	0.5926	
M5005_Spy0245	SpM1_ChORF0289_s_at	*nifU, yurV*	IscU protein	Coenzyme and cofactor metabolism	Unknown	SPy0289	202	593	227	464	1.26	0.8446	0.6565	
M5005_Spy0246	SpM1_ChORF0290_s_at	-	ABC transporter-associated protein	Membrane transport	Unknown	SPy0290	110	928	150	879	1.86	0.6798	0.6139	
M5005_Spy0247	SpM18_ChORF0279_s_at	-	D-alanyl-D-alanine carboxypeptidase (EC 3.4.16.4)	Cell wall metabolism	Unknown	spyM18_0279	139	881	149	808	1.15	0.7764	0.6419	
M5005_Spy0248	SpM1_ChORF0292_s_at	*dacA*	D-alanyl-D-alanine carboxypeptidase (EC 3.4.16.4)	Cell wall metabolism	Unknown	SPy0292	136	893	107	1070	0.62	0.1062	0.3149	
M5005_Spy0249	SpM18_ChORF0281_s_at	*oppA*	Oligopeptide-binding protein oppA	Membrane transport	Unknown	spyM18_0281	464	242	521	175	1.26	0.1547	0.3672	
M5005_Spy0250	SpM1_ChORF0294_s_at	*oppB*	Oligopeptide transport system permease protein oppB	Membrane transport	Cytoplasmic Membrane	SPy0294	98	1076	126	881	1.65	0.1151	0.3225	
M5005_Spy0251	SpM1_ChORF0295_s_at	*oppC*	Oligopeptide transport system permease protein oppC	Membrane transport	Cytoplasmic Membrane	SPy0295	182	696	201	661	1.22	0.0027	0.0566	
M5005_Spy0252	SpM1_ChORF0296_s_at	*oppD*	Oligopeptide transport ATP-binding protein oppD	Membrane transport	Cytoplasmic Membrane	SPy0296	240	417	254	414	1.12	0.8224	0.6525	
M5005_Spy0253	SpM1_ChORF0297_s_at	*oppF*	Oligopeptide transport ATP-binding protein oppF	Membrane transport	Cytoplasmic Membrane	SPy0297	247	471	269	475	1.19	0.5482	0.5698	

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M5005_Spy0254	M12_0466_at	-	Transposase	Mobile genetic element	Extracellular		8	2645	9	2626	1.43	0.5700	0.5800	
M5005_Spy0256	SpM1_ChORF0300_s_at	*comX1.1*	Competence-specific sigma factor ComX	Membrane transport	Cytoplasmic	SPy0300	72	1307	66	1402	0.83	0.4056	0.5120	
M5005_Spy0259	SpM1_ChORF1806_s_at	-	Hypothetical protein	Unknown	Extracellular	SPy1806	87	1199	84	1065	0.92	0.7932	0.6481	
M5005_Spy0260	SpM1_ChORF0305_s_at	-	Putative lipase	Unknown	Cytoplasmic	SPy0305	399	251	384	289	0.93	0.1973	0.4010	
M5005_Spy0261	SpM1_ChORF0306_s_at	-	GTP-binding protein	Cellular processing	Cytoplasmic	SPy0306	120	848	123	951	1.04	0.8173	0.6517	
M5005_Spy0262	SpM1_ChORF0307_s_at	-	Hypothetical RNA binding protein	Unknown	Cytoplasmic	SPy0307	78	1326	107	1062	1.89	0.8871	0.6667	
M5005_Spy0263	SpM1_ChORF0308_s_at	*nadD*	Nicotinate-nucleotide adenylyltransferase (EC 2.7.7.18)	Coenzyme and cofactor metabolism	Cytoplasmic	SPy0308	200	620	198	593	0.98	0.6322	0.6007	
M5005_Spy0263	SpM5_ChORFJ7578C-5_s_at	*nadD*	Nicotinate-nucleotide adenylyltransferase (EC 2.7.7.18)	Coenzyme and cofactor metabolism	Cytoplasmic		330	320	329	282	0.99	0.7210	0.6254	
M5005_Spy0264	SpM1_ChORF0309_s_at	-	Hydrolase (HAD superfamily)	Unknown	Cytoplasmic	SPy0309	144	846	168	740	1.36	0.5311	0.5653	
M5005_Spy0265	SpM1_ChORF0310_s_at	-	iojap protein family	Unknown	Unknown	SPy0310	174	644	170	795	0.96	0.5485	0.5698	
M5005_Spy0266	SpM1_ChORF0312_s_at	-	Methyltransferase (EC 2.1.1.-)	Unknown	Cytoplasmic	SPy0312	127	991	122	1188	0.93	0.3846	0.4999	
M5005_Spy0268	SpM1_ChORF0315_s_at	-	Hypothetical protein	Unknown	Unknown	SPy0315	50	1249	66	1444	1.77	0.6495	0.6051	
M5005_Spy0269	SpM1_ChORF0316_s_at	-	Hypothetical cytosolic protein	Unknown	Cytoplasmic	SPy0316	202	603	231	529	1.31	0.5485	0.5698	
M5005_Spy0270	SpM1_ChORF0317_s_at	-	ABC transporter substrate-binding protein	Membrane transport	Unknown	SPy0317	589	142	856	94	2.11	0.6691	0.6106	
M5005_Spy0271	M12_0652_at	-	ABC transporter substrate-binding protein	Membrane transport	Unknown		25	2111	13	2545	0.28	0.8051	0.6509	
M5005_Spy0271	SpM1_ChORF0319_s_at	*atmB*	ABC transporter substrate-binding protein	Membrane transport	Unknown	SPy0319	278	366	335	425	1.45	0.7871	0.6466	
M5005_Spy0272	SpM1_ChORF0320_s_at	-	ABC transporter ATP-binding protein	Membrane transport	Cytoplasmic Membrane	SPy0320	433	243	355	347	0.67	0.0653	0.2754	
M5005_Spy0273	SpM1_ChORF0321_s_at	-	ABC transporter permease protein	Membrane transport	Cytoplasmic Membrane	SPy0321	119	863	85	1197	0.51	0.0567	0.2634	

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M5005_Spy0274	SpM1_ChORF0323_s_at	*braB*	Branched-chain amino acid transport system carrier protein	Membrane transport	Cytoplasmic Membrane	SPy0323	72	1357	69	1379	0.91	0.0430	0.2393	
M5005_Spy0274	SpM5_ChORFJ7578C-342_s_at	*braB*	Branched-chain amino acid transport system carrier protein	Membrane transport	Cytoplasmic Membrane		85	1342	69	1418	0.66	0.7456	0.6339	
M5005_Spy0275	SpM1_ChORF0324_s_at	-	Serine/threonine sodium symporter	Membrane transport	Cytoplasmic Membrane	SPy0324	121	909	142	926	1.40	0.0073	0.1081	
M5005_Spy0276	SpM1_ChORF0326_s_at	-	Potassium uptake protein ktrA	Membrane transport	Cytoplasmic	SPy0326	101	1160	145	813	2.05	0.3231	0.4765	
M5005_Spy0277	SpM1_ChORF0327_s_at	*ntpJ*	Potassium uptake protein ktrB	Membrane transport	Cytoplasmic Membrane	SPy0327	233	494	235	504	1.02	0.5888	0.5874	
M5005_Spy0278	SpM1_ChORF0329_s_at	*gidB*	Glucose inhibited division protein B	Cellular processing	Cytoplasmic	SPy0329	65	1513	55	1475	0.72	0.0207	0.1793	
M5005_Spy0279	SpM1_ChORF0330_s_at	*lemA*	Hypothetical protein LemA	Unknown	Unknown	SPy0330	491	168	621	128	1.60	0.0369	0.2229	
M5005_Spy0280	SpM12_ChORF273-5_s_at	-	Heat shock protein HtpX	Stress adaptation	Cytoplasmic Membrane		274	420	296	367	1.17	0.2252	0.4208	
M5005_Spy0281	SpM1_ChORF0334_s_at	-	Hypothetical cytosolic protein	Unknown	Cytoplasmic	SPy0334	235	501	324	346	1.91	1.8E-05	**0.0008**	**Significant**
M5005_Spy0282	SpM18_ChORF0328_s_at	*covR*	Two-component response regulator CovR (CsrR)	Signal transduction	Cytoplasmic	spyM18_0328	368	269	195	541	0.28	1.7E-07	**1.3E-05**	**Significant**
M5005_Spy0283	SpM1_ChORF0337_s_at	*covS*	Two-component histidine sensor kinase CovS (CsrS)	Signal transduction	Cytoplasmic Membrane	SPy0337	151	755	336	324	4.98	3.0E-09	**5.6E-07**	**Significant**
M5005_Spy0284	SpM1_ChORF0338_s_at	-	Putative regulatory protein	Unknown	Cytoplasmic	SPy0338	113	1204	147	831	1.72	0.8419	0.6564	
M5005_Spy0285	SpM1_ChORF0339_s_at	*dnaB*	Replicative DNA helicase (EC 3.6.1.-)	Unknown	Unknown	SPy0339	428	266	466	211	1.19	0.7348	0.6294	
M5005_Spy0286	SpM1_ChORF0340_s_at	*dnaI*	Primosomal protein dnaI	Information processing	Cytoplasmic	SPy0340	488	214	529	180	1.18	0.5022	0.5512	
M5005_Spy0287	SpM1_ChORF0341_s_at	*pgdA*	GTP-binding protein	Unknown	Cytoplasmic	SPy0341	303	340	400	225	1.75	0.2012	0.4048	
M5005_Spy0288	SpM1_ChORF0342_s_at	*snf*	SWF/SNF family helicase	Information processing	Cytoplasmic	SPy0342	278	391	190	620	0.47	0.0854	0.2979	
M5005_Spy0289	SpM1_ChORF0343_s_at	-	Hypothetical cytosolic protein	Unknown	Cytoplasmic	SPy0343	377	338	319	353	0.71	0.6446	0.6041	

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M5005_Spy0290	SpM1_ChORF0345_s_at	*murC*	UDP-N-acetylmuramate--alanine ligase (EC 6.3.2.8)	Cell wall metabolism	Cytoplasmic	SPy0345	537	151	521	179	0.94	0.7091	0.6201	
M5005_Spy0291	SpM1_ChORF0346_s_at	-	Acetyltransferase (GNAT) family	Unknown	Unknown	SPy0346	213	556	227	568	1.14	0.3373	0.4798	
M5005_Spy0292	SpM1_ChORF0348_s_at	-	Aminodeoxychorismate lyase family	Unknown	Cytoplasmic	SPy0348	618	148	620	134	1.01	0.3199	0.4745	
M5005_Spy0293	SpM1_ChORF0349_s_at	*greA*	Transcription elongation factor greA	Information processing	Cytoplasmic	SPy0349	200	607	186	607	0.87	0.4154	0.5169	
M5005_Spy0295	SpM1_ChORF0351_s_at	-	60 kDa inner membrane protein YIDC	Cellular processing	Cytoplasmic Membrane	SPy0351	441	206	338	342	0.59	0.4257	0.5176	
M5005_Spy0296	SpM1_ChORF0352_s_at	-	Acylphosphatase (EC 3.6.1.7)	Unknown	Cytoplasmic	SPy0352	171	707	151	722	0.78	0.5911	0.5875	
M5005_Spy0299	SpM1_ChORF0356_s_at	-	23S rRNA methyltransferase (EC 2.1.1.-)	Information processing	Cytoplasmic	SPy0356	153	718	124	961	0.65	0.4002	0.5107	
M5005_Spy0300	SpM1_ChORF0357_s_at	-	Hydrolase (HAD superfamily)	Unknown	Unknown	SPy0357	243	422	212	577	0.77	0.0289	0.2024	
M5005_Spy0301	SpM1_ChORF0358_s_at	-	Integral membrane protein	Unknown	Cytoplasmic Membrane	SPy0358	258	424	203	519	0.62	0.0036	0.0713	
M5005_Spy0302	SpM1_ChORF0359_s_at	-	Hypothetical exported protein	Unknown	Unknown	SPy0359	221	523	185	630	0.70	0.3207	0.4751	
M5005_Spy0303	SpM1_ChORF0361_s_at	*glr*	Glutamate racemase (EC 5.1.1.3)	Cellular processing	Unknown	SPy0361	186	595	130	932	0.49	0.0919	0.3002	
M5005_Spy0304	SpM1_ChORF0362_s_at	-	Xanthosine triphosphate pyrophosphatase (EC 3.6.1.-)	Unknown	Cytoplasmic	SPy0362	146	858	132	842	0.81	0.4230	0.5176	
M5005_Spy0305	SpM1_ChORF0363_s_at	-	Putative phosphoesterase	Unknown	Cytoplasmic	SPy0363	162	735	151	718	0.87	0.0599	0.2677	
M5005_Spy0306	SpM1_ChORF0364_s_at	-	CBS domain containing protein	Unknown	Unknown	SPy0364	120	927	79	1263	0.43	0.0205	0.1787	
M5005_Spy0307	SpM1_ChORF0365_s_at	-	DNA integration/recombination/invertion protein	Phage	Unknown	SPy0365	29	2213	47	1872	2.58	0.0027	0.0566	
M5005_Spy0308	SpM1_ChORF0366_s_at	-	Hypothetical cytosolic protein	Unknown	Cytoplasmic	SPy0366	109	971	92	1174	0.71	0.5447	0.5696	
M5005_Spy0309	SpM1_ChORF0367_s_at	-	Hypothetical cytosolic protein	Unknown	Cytoplasmic	SPy0367	84	1147	85	1169	1.02	0.2610	0.4394	

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M5005_Spy0310	SpM1_ChORF0369_s_at	-	Ribosomal large subunit pseudouridine synthase B (EC 4.2.1.70)	Protein synthesis	Cytoplasmic	SPy0369	133	939	105	1168	0.62	0.0619	0.2713	
M5005_Spy0311	SpM1_ChORF0370_s_at	-	Hypothetical cytosolic protein	Unknown	Unknown	SPy0370	34	1983	28	2081	0.69	0.2846	0.4541	
M5005_Spy0312	SpM1_ChORF0371_s_at	-	23S rRNA methyltransferase (EC 2.1.1.-)	Information processing	Cytoplasmic	SPy0371	96	1000	103	1126	1.17	0.4056	0.5120	
M5005_Spy0313	SpM1_ChORF0373_s_at	-	Riboflavin transporter	Membrane transport	Cytoplasmic Membrane	SPy0373	18	2434	37	1833	4.18	0.9962	0.6930	
M5005_Spy0314	SpM1_ChORF0374_s_at	-	Phosphatidylglycerophosphatase B homolog	Unknown	Cytoplasmic Membrane	SPy0374	115	906	138	790	1.46	0.2992	0.4612	
M5005_Spy0315	SpM1_ChORF0376_s_at	-	Fe-S Oxidoreductase (1.8.-.-)	Unknown	Cytoplasmic	SPy0376	244	572	212	581	0.75	0.1812	0.3887	
M5005_Spy0316	SpM1_ChORF0377_s_at	-	SAM-dependent methyltransferase (EC 2.1.-.-)	Unknown	Unknown	SPy0377	154	771	151	764	0.96	0.2667	0.4436	
M5005_Spy0317	SpM1_ChORF0378_s_at	*hlyX*	Putative hemolysin	Virulence	Cytoplasmic Membrane	SPy0378	443	223	387	268	0.76	0.3196	0.4745	
M5005_Spy0318	SpM1_ChORF0379_s_at	*pflC*	Pyruvate formate-lyase activating enzyme (EC 1.97.1.4)	Carbohydrate metabolism	Cytoplasmic	SPy0379	283	390	235	476	0.69	0.0849	0.2979	
M5005_Spy0319	SpM1_ChORF0380_s_at	*ppaC*	Manganese-dependent inorganic pyrophosphatase (EC 3.6.1.1)	Cellular processing	Cytoplasmic	SPy0380	364	305	382	314	1.10	0.4734	0.5400	
M5005_Spy0320	SpM1_ChORF0382_s_at	-	Hypothetical cytosolic protein	Unknown	Cytoplasmic	SPy0382	272	409	288	447	1.12	0.9622	0.6850	
M5005_Spy0321	SpM1_ChORF0384_s_at	*ftsA*	Ferrichrome transport system permease protein fhuB	Membrane transport	Cytoplasmic Membrane	SPy0383	53	1487	25	1987	0.22	0.7812	0.6442	
M5005_Spy0322	SpM1_ChORF0383_s_at	*ftsB*	Ferrichrome transport system permease protein fhuB	Membrane transport	Cytoplasmic Membrane	SPy0384	26	2211	42	1828	2.67	0.7044	0.6200	
M5005_Spy0323	SpM1_ChORF0385_s_at	*ftsC*	Ferrichrome-binding protein	Membrane transport	Unknown	SPy0385	32	1945	16	2252	0.24	0.2044	0.4077	
M5005_Spy0324	SpM1_ChORF0386_s_at	*ftsD*	Ferrichrome transport ATP-binding protein fhuC	Membrane transport	Cytoplasmic Membrane	SPy0386	29	2159	17	2400	0.34	0.2392	0.4255	

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M5005_Spy0325	SpM1_ChORF0388_s_at	*murE*	UDP-N-acetylmuramoyl-L-alanyl-D-glutamate--lysine ligase (EC 6.3.2.7)	Cellular processing	Cytoplasmic	SPy0388	223	528	235	521	1.10	0.0173	0.1656	
M5005_Spy0326	SpM1_ChORF0390_s_at	-	Export protein for polysaccharides and teichoic acids	Unknown	Cytoplasmic Membrane	SPy0390	217	613	189	673	0.76	0.4220	0.5176	
M5005_Spy0327	SpM1_ChORF0392_s_at	*upp*	Uracil phosphoribosyltransferase (EC 2.4.2.9)	Nucleotide metabolism	Cytoplasmic	SPy0392	110	1041	136	867	1.53	0.5245	0.5615	
M5005_Spy0327	SpM1_ChORF0393_x_at	*upp*	Uracil phosphoribosyltransferase (EC 2.4.2.9)	Nucleotide metabolism	Cytoplasmic	SPy0393	53	1630	38	1776	0.52	0.0986	0.3081	
M5005_Spy0327	SpM18_ChORF0444_x_at	*upp*	Uracil phosphoribosyltransferase (EC 2.4.2.9)	Nucleotide metabolism	Cytoplasmic	spyM18_0444	53	1609	34	1882	0.42	0.2123	0.4110	
M5005_Spy0328	SpM1_ChORF0395_s_at	*clpP*	ATP-dependent Clp protease proteolytic subunit (EC 3.4.21.92)	Information processing	Cytoplasmic	SPy0395	1223	46	955	56	0.61	0.1857	0.3933	
M5005_Spy0329	SpM1_ChORF0397_s_at	-	Hypothetical cytosolic protein	Unknown	Unknown	SPy0397	184	628	234	500	1.62	0.7686	0.6388	
M5005_Spy0330	SpM1_ChORF0399_s_at	*tmk*	Thymidylate kinase (EC 2.7.4.9)	Nucleotide metabolism	Cytoplasmic	SPy0399	130	986	168	736	1.67	0.1995	0.4022	
M5005_Spy0331	SpM1_ChORF0400_s_at	*dnaX*	DNA polymerase III, delta' subunit (EC 2.7.7.7)	Information processing	Cytoplasmic	SPy0400	140	885	196	668	1.96	0.0436	0.2408	
M5005_Spy0332	SpM1_ChORF0401_s_at	-	Tpl protein	Unknown	Unknown	SPy0401	90	1194	125	1099	1.95	0.0739	0.2853	
M5005_Spy0333	SpM18_ChORF0453_at	-	Hypothetical signal peptidase-like protein	Unknown	Unknown	spyM18_0453	32	2034	20	2302	0.40	0.7662	0.6382	
M5005_Spy0334	SpM1_ChORF0405_s_at	-	Hypothetical protein	Unknown	Cytoplasmic	SPy0405	140	923	138	860	0.97	0.6534	0.6061	
M5005_Spy0335	SpM1_ChORF0406_s_at	-	Corrin/porphyrin methyltransferase (EC 2.1.1.-)	Unknown	Cytoplasmic	SPy0406	468	180	635	141	1.84	0.1543	0.3672	
M5005_Spy0336	SpM1_ChORF0407_s_at	-	Hypothetical membrane associated protein	Unknown	Cytoplasmic Membrane	SPy0407	128	912	163	731	1.60	0.1116	0.3181	
M5005_Spy0337	SpM12_ChORF270-2_s_at	*cutC*	Copper homeostasis protein cutC	Unknown	Cytoplasmic		103	1032	117	1115	1.31	0.3529	0.4869	

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M5005_Spy0338	SpM1_ChORF0410_s_at	-	Arsenate reductase family protein	Unknown	Unknown	SPy0410	61	1536	69	1337	1.30	0.0872	0.3002	
M5005_Spy0339	SpM1_ChORF0412_s_at	*exoA*	Exodeoxyribonuclease III (EC 3.1.11.2)	Information processing	Cytoplasmic	SPy0412	216	586	202	814	0.87	0.1845	0.3917	
M5005_Spy0340	SpM1_ChORF0414_s_at	*lctO*	L-lactate oxidase (EC 1.13.12.4)	Carbohydrate metabolism	Cytoplasmic	SPy0414	850	63	579	176	0.46	0.0197	0.1745	
M5005_Spy0341	SpM5_ChORFJ7578C-323_s_at	*prtS*	Lactocepin (EC 3.4.21.96)	Unknown	Cell Wall		22	2342	33	1873	2.28	0.9067	0.6727	
M5005_Spy0342	SpM1_ChORF0416_s_at	*prtS*	Lactocepin (EC 3.4.21.96)	Amino acid metabolism	Unknown	SPy0416	787	97	728	129	0.86	0.3174	0.4745	
M5005_Spy0344	SpM1_ChORF0421_s_at	-	Permease	Unknown	Cytoplasmic Membrane	SPy0421	33	1892	19	2216	0.31	0.5950	0.5886	
M5005_Spy0345	SpM1_ChORF0422_s_at	*metS*	Methionyl-tRNA synthetase (EC 6.1.1.10)	Protein synthesis	Cytoplasmic	SPy0422	139	973	139	812	1.00	0.3315	0.4779	
M5005_Spy0346	M12_0056_at	-	Hypothetical protein	Unknown	Unknown		165	737	158	827	0.91	0.2913	0.4558	
M5005_Spy0347	SpM1_ChORF0425_s_at	*nrdF.1*	Ribonucleoside-diphosphate reductase beta chain (EC 1.17.4.1)	Unknown	Cytoplasmic	SPy0425	176	612	181	702	1.06	0.6272	0.5995	
M5005_Spy0348	SpM1_ChORF0426_s_at	*nrdI*	NrdI protein	Nucleotide metabolism	Unknown	SPy0426	129	900	135	959	1.10	0.0994	0.3083	
M5005_Spy0349	SpM1_ChORF0427_s_at	*nrdE.1*	Ribonucleoside-diphosphate reductase alpha chain (EC 1.17.4.1)	Unknown	Cytoplasmic	SPy0427	449	225	486	204	1.17	0.0788	0.2918	
M5005_Spy0351	SpM1_ChORF0428_s_at	*spyA*	C3 family ADP-ribosyltransferase (EC 2.4.2.-)	Virulence	Extracellular	SPy0428	485	211	647	125	1.78	0.0108	0.1351	
M5005_Spy0352	SpM1_ChORF0430_at	-	Hypothetical membrane associated protein	Unknown	Unknown (This protein may have multiple localization sites.)	SPy0430	125	956	385	226	9.45	4.7E-06	**0.0003**	**Significant**
M5005_Spy0353	SpM1_ChORF0431_at	-	Hypothetical membrane spanning protein	Unknown	Cytoplasmic Membrane	SPy0431	48	1497	58	1358	1.43	0.2414	0.4269	
M5005_Spy0353	SpM1_ChORF0432_x_at	-	Hypothetical membrane spanning protein	Unknown	Cytoplasmic Membrane	SPy0432	122	940	103	1161	0.71	0.7217	0.6257	

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M5005_Spy0354	SpM1_ChORF0433_at	-	Hypothetical protein	Unknown	Unknown	SPy0433	64	1565	83	1333	1.68	0.2101	0.4110	
M5005_Spy0355	SpM1_ChORF0435_at	-	Hypothetical protein	Unknown	Unknown	SPy0435	26	2052	24	2248	0.85	0.4854	0.5443	
M5005_Spy0356	SpM1_ChORF0436_at	*speJ*	Pyrogenic toxin superantigen exotoxin type J precursor	Virulence	Extracellular	SPy0436	16	2514	44	1717	7.87	0.8240	0.6525	
M5005_Spy0357	SpM1_ChORF0437_at	-	Hypothetical protein	Unknown	Unknown	SPy0437	42	1575	58	1468	1.89	0.6213	0.5966	
M5005_Spy0358	SpM1_ChORF0439_s_at	-	Hypothetical protein	Unknown	Cytoplasmic	SPy0439	102	1052	114	1023	1.25	0.9939	0.6928	
M5005_Spy0358	SpM12_ChORF212-2_s_at	-	Hypothetical protein	Unknown	Cytoplasmic		86	1085	97	1116	1.27	0.7347	0.6294	
M5005_Spy0360	SpM1_ChORF0441_s_at	-	NAD-dependent oxidoreductase	Unknown	Cytoplasmic	SPy0441	86	1272	79	1240	0.85	0.7975	0.6493	
M5005_Spy0361	SpM1_ChORF0442_s_at	-	Phosphoglycerate transporter protein	Membrane transport	Cytoplasmic Membrane	SPy0442	306	345	320	360	1.09	0.7036	0.6200	
M5005_Spy0362	SpM1_ChORF0443_s_at	*gcaD*	Glucosamine-1-phosphate acetyltransferase (EC 2.3.1.-) / UDP-N-acetylglucosamine pyrophosphorylase (EC 2.7.7.23)	Cellular processing	Cytoplasmic	SPy0443	268	382	257	507	0.92	0.8116	0.6512	
M5005_Spy0363	SpM1_ChORF0444_s_at	-	Phosphohydrolase (MutT/nudix family protein)	Unknown	Cytoplasmic	SPy0444	280	423	281	428	1.01	0.6826	0.6146	
M5005_Spy0364	SpM1_ChORF0446_s_at	-	Hypothetical membrane associated protein	Unknown	Cytoplasmic	SPy0446	326	333	344	322	1.12	0.3034	0.4653	
M5005_Spy0365	SpM1_ChORF0447_s_at	*pfs*	5'-methylthioadenosine nucleosidase (EC 3.2.2.16) / S-adenosylhomocysteine nucleosidase (EC 3.2.2.9)	Carbohydrate metabolism	Cytoplasmic	SPy0447	359	316	391	270	1.19	0.1534	0.3665	
M5005_Spy0366	SpM5_ChORFJ7578C-81_s_at	-	Hypothetical protein	Unknown	Unknown		231	495	258	495	1.25	0.5499	0.5698	
M5005_Spy0367	SpM1_ChORF0450_s_at	*scaR*	Iron-dependent repressor	Information processing	Cytoplasmic	SPy0450	295	381	277	421	0.88	0.3998	0.5106	

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M5005_Spy0368	SpM1_ChORF0453_s_at	*mtsA*	Manganese-binding protein	Membrane transport	Unknown	SPy0453	742	88	690	111	0.87	0.1226	0.3296	
M5005_Spy0369	SpM1_ChORF0454_s_at	*mtsB*	Manganese transport system ATP-binding protein mntA	Membrane transport	Cytoplasmic Membrane	SPy0454	239	534	265	436	1.22	0.8259	0.6532	
M5005_Spy0370	SpM1_ChORF0456_s_at	*mtsC*	Manganese transport system membrane protein mntB	Membrane transport	Cytoplasmic Membrane	SPy0456	105	919	113	1091	1.16	0.4722	0.5394	
M5005_Spy0371	SpM1_ChORF0457_s_at	-	Peptidyl-prolyl cis-trans isomerase (EC 5.2.1.8)	Unknown	Unknown	SPy0457	224	682	203	516	0.82	0.3775	0.4968	
M5005_Spy0372	SpM1_ChORF0458_s_at	*ftsK*	Cell division protein ftsK	Unknown	Cytoplasmic Membrane	SPy0458	111	1019	112	1036	1.02	0.1386	0.3492	
M5005_Spy0373	SpM1_ChORF0459_s_at	-	Integral membrane protein	Unknown	Cytoplasmic Membrane	SPy0459	118	1030	104	1072	0.78	0.1152	0.3225	
M5005_Spy0374	SpM1_ChORF0460_s_at	*rplK*	LSU ribosomal protein L11P	Protein synthesis	Unknown	SPy0460	232	527	215	594	0.86	0.7087	0.6201	
M5005_Spy0375	SpM1_ChORF0461_s_at	*rplA*	LSU ribosomal protein L1P	Protein synthesis	Unknown	SPy0461	114	888	125	979	1.19	0.7430	0.6328	
M5005_Spy0378	SpM1_ChORF0462_s_at	*pyrH*	Uridylate kinase (EC 2.7.4.-)	Cellular processing	Unknown	SPy0462	271	429	278	403	1.05	0.0392	0.2297	
M5005_Spy0380	SpM1_ChORF0463_s_at	*rrf*	Ribosome Recycling Factor (RRF)	Cellular processing	Cytoplasmic	SPy0463	172	733	162	802	0.89	0.0845	0.2979	
M5005_Spy0381	SpM1_ChORF0464_s_at	-	S1 RNA binding domain	Cellular processing	Cytoplasmic	SPy0464	73	1287	53	1568	0.52	0.5851	0.5864	
M5005_Spy0382	SpM1_ChORF0466_s_at	*msrA.2*	Peptide methionine sulfoxide reductase msrA (EC 1.8.4.6)	Cellular processing	Cytoplasmic	SPy0466	85	1200	78	1285	0.83	0.2609	0.4394	
M5005_Spy0383	SpM1_ChORF0467_s_at	-	D-alanyl-D-alanine carboxypeptidase (EC 3.4.16.4)	Cell wall metabolism	Cytoplasmic	SPy0467	101	988	115	962	1.28	0.5134	0.5551	
M5005_Spy0384	SpM1_ChORF0469_s_at	-	Surface antigen	Virulence	Cell Wall	SPy0469	218	452	233	530	1.13	0.5954	0.5886	
M5005_Spy0385	SpM1_ChORF0470_s_at	-	67 kDa Myosin-crossreactive streptococcal antigen	Virulence	Cytoplasmic Membrane	SPy0470	638	125	958	76	2.26	0.0009	**0.0239**	**Significant**
M5005_Spy0386	SpM1_ChORF0471_s_at	*phoH*	PhoH protein	Unknown	Cytoplasmic	SPy0471	83	1217	120	1026	2.10	0.0131	0.1479	
M5005_Spy0387	SpM1_ChORF0472_s_at	-	Uracil DNA glycosylase superfamily protein	Information processing	Cytoplasmic	SPy0472	87	1218	115	966	1.75	0.2058	0.4088	

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M5005_Spy0388	SpM1_ChORF0473_s_at	*dgk*	Hypothetical Metal-Binding Protein	Unknown	Cytoplasmic	SPy0473	193	648	203	590	1.11	0.0215	0.1827	
M5005_Spy0389	SpM1_ChORF0475_s_at	*dgk*	Diacylglycerol kinase (EC 2.7.1.107)	Lipid metabolism	Cytoplasmic Membrane	SPy0475	123	910	139	870	1.27	0.0189	0.1707	
M5005_Spy0390	SpM1_ChORF0476_s_at	*era*	GTP-binding protein era homolog	Unknown	Cytoplasmic	SPy0476	271	448	273	465	1.02	0.6565	0.6068	
M5005_Spy0391	SpM1_ChORF0477_s_at	-	Phosphohydrolase (MutT/nudix family protein)	Unknown	Cytoplasmic	SPy0477	98	1170	117	991	1.44	0.9857	0.6910	
M5005_Spy0392	SpM1_ChORF0478_s_at	-	Hypothetical protein	Unknown	Cytoplasmic	SPy0478	17	2535	19	2264	1.28	0.0186	0.1707	
M5005_Spy0393	SpM1_ChORF0479_at	-	Hypothetical protein	Unknown	Unknown	SPy0479	66	1343	70	1238	1.14	0.4600	0.5330	
M5005_Spy0394	SpM1_ChORF0480_at	-	Hypothetical protein	Unknown	Unknown	SPy0480	128	872	103	988	0.64	0.0195	0.1736	
M5005_Spy0396	SpM12_ChORF282-20_s_at	-	Transposase	Mobile genetic element	Unknown		72	1420	43	1706	0.36	0.2790	0.4502	
M5005_Spy0398	SpM18_ChORF0544_s_at	-	Bacteriocin	Virulence	Cytoplasmic	spyM18_0544	115	983	101	1180	0.76	0.3516	0.4859	
M5005_Spy0399	SpM1_ChORF0484_s_at	-	Hypothetical membrane associated protein	Unknown	Unknown	SPy0484	128	933	109	919	0.73	0.0507	0.2541	
M5005_Spy0400	SpM18_ChORF0547_s_at	*silD*	Hypothetical protein	Virulence	Unknown	spyM18_0547	42	1731	32	1901	0.58	0.2673	0.4436	
M5005_Spy0400	SpM3_ChORF0341_s_at	*silD*	Hypothetical protein	Virulence	Unknown	spyM3_0341	48	1684	57	1609	1.38	0.0772	0.2905	
M5005_Spy0401	SpM1_ChORF0486_s_at	-	Hypothetical protein	Virulence	Unknown	SPy0486	1051	60	809	79	0.59	0.7063	0.6200	
M5005_Spy0402	SpM1_ChORF0488_s_at	-	Hypothetical protein	Unknown	Cytoplasmic	SPy0488	57	1583	66	1503	1.31	0.6289	0.5999	
M5005_Spy0403	SpM1_ChORF0489_s_at	-	Hypothetical protein	Unknown	Unknown	SPy0489	61	1499	27	1825	0.20	0.8374	0.6562	
M5005_Spy0404	M12_0889_at	-	Hypothetical protein	Unknown	Unknown		103	1120	69	1341	0.45	0.0728	0.2853	
M5005_Spy0405	SpM18_ChORF0551_s_at	*silE*	Hypothetical protein	Virulence	Unknown	spyM18_0551	10	2611	21	2120	4.20	0.4141	0.5164	
M5005_Spy0407	SpM1_ChORF0496_s_at	*mutR*	Transcriptional regulator	Information processing	Unknown	SPy0496	32	2101	34	1910	1.08	0.1584	0.3712	
M5005_Spy0408	SpM1_ChORF0497_s_at	*fpg*	Formamidopyrimidine-DNA glycosylase (EC 3.2.2.23)	Information processing	Cytoplasmic	SPy0497	54	1274	63	1470	1.38	0.8468	0.6565	

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M5005_Spy0409	SpM1_ChORF0498_s_at	-	Dephospho-CoA kinase (EC 2.7.1.24)	Coenzyme and cofactor metabolism	Cytoplasmic	SPy0498	86	1214	99	1045	1.34	0.1436	0.3546	
M5005_Spy0410	SpM1_ChORF0500_s_at	-	ATPase	Unknown	Cytoplasmic	SPy0500	276	374	344	345	1.56	0.2443	0.4280	
M5005_Spy0411	SpM1_ChORF0501_s_at	-	Multidrug resistance protein B	Membrane transport	Cytoplasmic Membrane	SPy0501	253	477	219	560	0.75	0.2904	0.4558	
M5005_Spy0413	SpM1_ChORF0502_s_at	*secG*	Protein translocase subunit secG	Secretion	Unknown	SPy0502	311	322	294	375	0.89	0.9760	0.6879	
M5005_Spy0414	SpM1_ChORF0503_s_at	-	Exoribonuclease II (EC 3.1.13.1)	Information processing	Cytoplasmic	SPy0503	598	154	580	149	0.94	0.3624	0.4888	
M5005_Spy0415	SpM1_ChORF0504_s_at	-	SsrA-binding protein	Information processing	Cytoplasmic	SPy0504	607	144	664	114	1.20	0.0972	0.3072	
M5005_Spy0416	SpM1_ChORF0505_s_at	-	Glutaminyl-peptide cyclotransferase (EC 2.3.2.5)	Unknown	Cytoplasmic	SPy0505	196	571	191	717	0.95	0.4755	0.5410	
M5005_Spy0417	SpM1_ChORF0506_s_at	*pcp*	Pyrrolidone-carboxylate peptidase (EC 3.4.19.3)	Amino acid metabolism	Cytoplasmic	SPy0506	175	630	200	615	1.31	0.6004	0.5893	
M5005_Spy0418	SpM1_ChORF0507_s_at	-	Permease	Unknown	Cytoplasmic Membrane	SPy0507	151	679	197	644	1.70	0.2066	0.4088	
M5005_Spy0419	SpM1_ChORF0508_s_at	-	Permease	Unknown	Cytoplasmic Membrane	SPy0508	122	864	164	725	1.81	0.5188	0.5590	
M5005_Spy0420	SpM1_ChORF0510_s_at	-	Glucosyltransferase (EC 2.4.1.-)	Carbohydrate metabolism	Cytoplasmic Membrane	SPy0510	70	1176	83	1288	1.39	0.4051	0.5120	
M5005_Spy0421	SpM1_ChORF0511_s_at	*gloA*	Lactoylglutathione lyase (EC 4.4.1.5)	Carbohydrate metabolism	Cytoplasmic	SPy0511	88	1167	99	1112	1.26	0.8680	0.6623	
M5005_Spy0422	SpM1_ChORF0512_s_at	-	NAD(P)H-dependent quinone reductase (EC 1.-.-.-)	Unknown	Cytoplasmic	SPy0512	175	748	208	547	1.41	0.2304	0.4227	
M5005_Spy0423	SpM1_ChORF0513_s_at	*pepQ*	Xaa-Pro dipeptidase (EC 3.4.13.9)	Amino acid metabolism	Cytoplasmic	SPy0513	139	777	165	771	1.41	0.0015	**0.0381**	**Significant**
M5005_Spy0424	SpM1_ChORF0514_s_at	*ccpA*	Catabolite control protein A	Information processing	Cytoplasmic	SPy0514	343	342	428	223	1.55	0.0922	0.3002	
M5005_Spy0425	SpM1_ChORF0515_s_at	-	Glycosyltransferase (EC 2.4.1.-)	Carbohydrate metabolism	Cytoplasmic	SPy0515	940	57	912	73	0.94	0.3183	0.4745	
M5005_Spy0426	SpM1_ChORF0516_s_at	-	1,2-diacylglycerol 3-glucosyltransferase (EC 2.4.1.157)	Cell wall metabolism	Cytoplasmic	SPy0516	815	110	582	139	0.51	0.3474	0.4838	

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M5005_Spy0427	SpM1_ChORF0517_s_at	*thrS*	Threonyl-tRNA synthetase (EC 6.1.1.3)	Protein synthesis	Cytoplasmic	SPy0517	135	768	219	527	2.64	0.1070	0.3149	
M5005_Spy0428	SpM1_ChORF0518_s_at	-	Daunorubicin resistance ATP-binding protein drrA	Membrane transport	Cytoplasmic Membrane	SPy0518	25	2195	59	1449	5.81	0.0829	0.2979	
M5005_Spy0429	SpM1_ChORF0519_s_at	-	Daunorubicin resistance transmembrane protein	Membrane transport	Cytoplasmic Membrane	SPy0519	22	2264	24	2188	1.20	0.6808	0.6145	
M5005_Spy0430	SpM1_ChORF0521_s_at	-	ABC transporter permease protein	Membrane transport	Cytoplasmic Membrane	SPy0521	21	2449	19	2260	0.80	0.8748	0.6641	
M5005_Spy0432	SpM1_ChORF0524_s_at	-	Acetyl-CoA acetyltransferase (EC 2.3.1.9)	Lipid metabolism	Cytoplasmic	SPy0524	42	1722	30	1985	0.51	0.7050	0.6200	
M5005_Spy0433	SpM1_ChORF0526_s_at	-	Long-chain-fatty-acid--CoA ligase (EC 6.2.1.3)	Lipid metabolism	Unknown	SPy0526	25	2256	29	1927	1.40	0.1827	0.3892	
M5005_Spy0434	SpM1_ChORF0527_s_at	-	Hypothetical cytosolic protein	Unknown	Cytoplasmic	SPy0527	40	1729	53	1525	1.77	0.1454	0.3573	
M5005_Spy0435	SpM1_ChORF0528_s_at	*vicR*	Two-component response regulator VicR	Signal transduction	Cytoplasmic	SPy0528	254	444	228	535	0.81	0.1047	0.3149	
M5005_Spy0436	SpM1_ChORF0529_s_at	*vicK*	Two-component sensor histidine kinase VicK	Signal transduction	Cytoplasmic Membrane	SPy0529	226	636	202	613	0.79	0.3124	0.4706	
M5005_Spy0437	SpM1_ChORF0530_s_at	*vicX*	Zn-dependent hydrolase (beta-lactamase superfamily)	Unknown	Cytoplasmic	SPy0530	104	987	139	780	1.76	0.4231	0.5176	
M5005_Spy0438	SpM1_ChORF0531_s_at	*acpA*	Ribonuclease III (EC 3.1.26.3)	Information processing	Cytoplasmic	SPy0531	24	2270	20	2204	0.65	0.3625	0.4888	
M5005_Spy0439	SpM1_ChORF0532_s_at	*smc*	Chromosome partition protein smc	Information processing	Cytoplasmic	SPy0532	106	989	165	862	2.42	0.1885	0.3977	
M5005_Spy0440	SpM1_ChORF0533_s_at	-	Transcriptional regulator	Information processing	Cytoplasmic	SPy0533	11	2623	14	2498	1.52	0.6650	0.6091	
M5005_Spy0441	SpM1_ChORF0534_s_at	*aroE.2*	Shikimate 5-dehydrogenase (EC 1.1.1.25)	Amino acid metabolism	Cytoplasmic	SPy0534	37	1974	40	1760	1.12	0.1290	0.3379	
M5005_Spy0442	SpM1_ChORF0535_s_at	-	Hypothetical cytosolic protein	Unknown	Cytoplasmic	SPy0535	18	2339	13	2527	0.53	0.3634	0.4889	
M5005_Spy0443	SpM1_ChORF0536_s_at	-	Hypothetical protein	Unknown	Cytoplasmic	SPy0536	81	1240	74	1316	0.83	0.6794	0.6139	

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M5005_Spy0444	SpM12_ChORF277-20_s_at	-	Hypothetical protein	Unknown	Cytoplasmic		54	1714	49	1508	0.80	0.7245	0.6270	
M5005_Spy0445	SpM1_ChORF0538_s_at	*metK*	S-adenosylmethionine synthetase (EC 2.5.1.6)	Cellular processing	Cytoplasmic	SPy0538	21	2269	14	2451	0.43	0.1073	0.3149	
M5005_Spy0446	SpM1_ChORF0539_s_at	-	Hypothetical membrane associated protein	Unknown	Cytoplasmic Membrane	SPy0539	57	1439	45	1647	0.61	0.5604	0.5750	
M5005_Spy0447	SpM1_ChORF0540_s_at	-	Glycosyltransferase involved in cell wall biogenesis (EC 2.4.-.-)	Cell wall metabolism	Unknown	SPy0540	24	2240	26	2096	1.12	0.0117	0.1377	
M5005_Spy0447	SpM5_ChORFJ7578C-298_at	-	Glycosyltransferase involved in cell wall biogenesis (EC 2.4.-.-)	Cell wall metabolism	Unknown		29	2176	20	2253	0.47	0.9359	0.6772	
M5005_Spy0448	SpM18_ChORF0607_s_at	-	Hypothetical protein	Unknown	Extracellular	spyM18_0607	40	1932	40	1769	1.01	0.8770	0.6641	
M5005_Spy0448	SpM5_ChORFJ7578C-142_s_at	-	Hypothetical protein	Unknown	Extracellular		18	2314	10	2591	0.29	0.1630	0.3740	
M5005_Spy0449	SpM1_ChORF0542_s_at	-	UDP-glucose 6-dehydrogenase (EC 1.1.1.22)	Carbohydrate metabolism	Cytoplasmic	SPy0542	42	1581	50	1566	1.41	0.3486	0.4848	
M5005_Spy0450	SpM1_ChORF0543_s_at	*mefE*	Macrolide-efflux protein	Membrane transport	Cytoplasmic Membrane	SPy0543	49	1523	53	1592	1.18	0.7258	0.6276	
M5005_Spy0452	SpM1_ChORF0544_s_at	-	Chromosome segregation ATPases	Cellular processing	Unknown	SPy0544	30	1973	67	1412	5.09	0.3114	0.4706	
M5005_Spy0452	SpM3_ChORF0388_s_at	-	Chromosome segregation ATPases	Cellular processing	Unknown	spyM3_0388	15	2584	19	2347	1.71	0.7962	0.6488	
M5005_Spy0454	SpM1_ChORF0546_s_at	-	Hypothetical protein	Unknown	Cytoplasmic	SPy0546	37	1682	44	1759	1.44	0.9991	0.6933	
M5005_Spy0454	SpM1_ChORF0547_s_at	-	Hypothetical protein	Unknown	Cytoplasmic	SPy0547	15	2523	18	2433	1.50	0.2901	0.4558	
M5005_Spy0455	SpM1_ChORF0549_s_at	-	Hypothetical protein	Unknown	Unknown	SPy0549	11	2562	28	1956	6.16	0.8982	0.6691	
M5005_Spy0455	SpM3_ChORF0391_at	-	Hypothetical protein	Unknown	Unknown	spyM3_0391	110	920	141	806	1.64	0.5212	0.5596	
M5005_Spy0456	SpM1_ChORF0550_s_at	-	Plasmid stabilization system antitoxin protein	Unknown	Cytoplasmic	SPy0550	34	1827	44	1665	1.64	0.8111	0.6512	
M5005_Spy0457	SpM1_ChORF0552_s_at	-	Plasmid stabilization system protein (putative toxin)	Unknown	Unknown	SPy0552	51	1607	46	1463	0.81	0.2674	0.4436	

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M5005_Spy0458	SpM18_ChORF0618_s_at	-	Hypothetical cytosolic protein	Unknown	Cytoplasmic	spyM18_0618	20	2418	25	2076	1.55	0.4864	0.5443	
M5005_Spy0459	SpM1_ChORF0555_s_at	-	Portal protein	Phage	Cytoplasmic	SPy0555	31	2061	36	1822	1.41	0.3578	0.4885	
M5005_Spy0460	SpM1_ChORF0556_s_at	-	Hypothetical protein	Unknown	Unknown	SPy0556	59	1473	37	1725	0.39	0.0291	0.2024	
M5005_Spy0461	SpM1_ChORF0558_s_at	-	Hypothetical cytosolic protein	Unknown	Unknown	SPy0558	59	1431	57	1597	0.94	0.3161	0.4734	
M5005_Spy0462	SpM1_ChORF0559_s_at	-	Hypothetical protein	Unknown	Cytoplasmic	SPy0559	116	1006	135	837	1.35	0.2791	0.4502	
M5005_Spy0462	SpM18_ChORF0626_s_at	-	Hypothetical protein	Unknown	Cytoplasmic	spyM18_0626	103	1149	79	1309	0.58	0.8961	0.6690	
M5005_Spy0463	SpM18_ChORF0630_s_at	-	Hypothetical cytosolic protein	Phage	Unknown	spyM18_0630	171	647	159	727	0.86	0.2487	0.4321	
M5005_Spy0463	SpM5_ChORFJ7578C-152_s_at	-	Hypothetical cytosolic protein	Phage	Unknown		121	876	126	833	1.09	0.2766	0.4473	
M5005_Spy0465	SpM18_ChORF0631_s_at	-	Hypothetical protein	Unknown	Unknown	spyM18_0631	174	677	138	850	0.63	0.6920	0.6184	
M5005_Spy0466	SpM18_ChORF0632_s_at	-	Hypothetical phage protein	Phage	Cytoplasmic	spyM18_0632	257	468	255	470	0.99	0.1135	0.3210	
M5005_Spy0466	SpM18_ChORF0633_s_at	-	Hypothetical phage protein	Phage	Cytoplasmic	spyM18_0633	43	1806	36	1874	0.70	0.6198	0.5962	
M5005_Spy0468	SpM1_ChORF0565_s_at	*tnpA*	Transposase	Mobile genetic element	Unknown	SPy0565	34	2132	11	2567	0.11	0.5319	0.5655	
M5005_Spy0468	SpM18_ChORF0635_s_at	-	Transposase	Mobile genetic element	Unknown	spyM18_0635	23	2001	33	1996	2.04	0.6054	0.5923	
M5005_Spy0470	SpM1_ChORF0567_s_at	-	Hydrolase (HAD superfamily)	Unknown	Cytoplasmic	SPy0567	110	1007	106	1117	0.94	0.0644	0.2748	
M5005_Spy0471	SpM1_ChORF0568_s_at	-	Hydrolase (HAD superfamily)	Unknown	Unknown	SPy0568	93	1141	83	1230	0.80	0.1923	0.3989	
M5005_Spy0472	SpM1_ChORF0569_s_at	*ftsY*	Cell division protein ftsY	Cellular processing	Unknown	SPy0569	257	457	335	352	1.70	0.0469	0.2467	
M5005_Spy0473	SpM1_ChORF0570_s_at	-	Multidrug resistance protein B	Membrane transport	Cytoplasmic Membrane	SPy0570	121	981	159	765	1.71	0.5464	0.5698	
M5005_Spy0474	SpM1_ChORF0571_s_at	*licT*	Transcription antiterminator, BglG family	Information processing	Cytoplasmic	SPy0571	54	1705	25	1989	0.22	0.6460	0.6041	
M5005_Spy0475	SpM1_ChORF0572_s_at	-	PTS system, beta-glucoside-specific IIABC component (EC 2.7.1.69)	Carbohydrate metabolism	Cytoplasmic Membrane	SPy0572	119	808	117	941	0.96	0.1172	0.3234	

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M5005_Spy0476	SpM1_ChORF0574_s_at	*bglA*	6-phospho-beta-glucosidase (EC 3.2.1.86)	Carbohydrate metabolism	Cytoplasmic	SPy0574	75	1133	79	1320	1.12	0.8016	0.6499	
M5005_Spy0477	SpM1_ChORF0575_s_at	-	Hypothetical membrane spanning protein	Unknown	Unknown	SPy0575	133	1001	154	817	1.34	0.3602	0.4888	
M5005_Spy0478	SpM1_ChORF0576_s_at	-	Hypothetical membrane spanning protein	Unknown	Cytoplasmic Membrane	SPy0576	100	1146	100	1120	1.01	0.2203	0.4177	
M5005_Spy0479	SpM1_ChORF0577_at	-	Hypothetical membrane spanning protein	Unknown	Unknown	SPy0577	220	577	186	617	0.72	0.9141	0.6743	
M5005_Spy0479	SpM1_ChORF0578_s_at	-	Hypothetical membrane spanning protein	Unknown	Unknown	SPy0578	21	2325	15	2348	0.55	0.8301	0.6540	
M5005_Spy0480	SpM12_ChORF220-1_s_at	-	Transcription accessory protein (S1 RNA binding domain)	Cellular processing	Cytoplasmic		29	1984	25	1973	0.78	0.2875	0.4544	
M5005_Spy0480	SpM12_ChORF266-14_s_at	-	Transcription accessory protein (S1 RNA binding domain)	Cellular processing	Cytoplasmic		85	1161	90	1201	1.12	0.4235	0.5176	
M5005_Spy0482	SpM1_ChORF0581_s_at	-	Zinc metalloprotease (EC 3.4.24.-)	Unknown	Cytoplasmic	SPy0581	49	1621	60	1563	1.50	0.9673	0.6854	
M5005_Spy0483	SpM1_ChORF0583_s_at	-	Stress-responsive transcriptional regulator PspC	Stress adaptation	Unknown	SPy0583	660	107	585	174	0.79	0.5270	0.5626	
M5005_Spy0484	SpM1_ChORF0584_s_at	*ptsK, hprK*	Hpr(ser) kinase (EC 2.7.1.-) / Phosphatase (EC 3.1.3.-)	Cellular processing	Cytoplasmic	SPy0584	284	376	264	496	0.86	0.6415	0.6035	
M5005_Spy0485	SpM1_ChORF0585_s_at	*lgt*	Prolipoprotein diacylglyceryl transferase (EC 2.4.99.-)	Information processing	Cytoplasmic Membrane	SPy0585	359	293	257	439	0.51	0.0305	0.2054	
M5005_Spy0486	SpM1_ChORF0587_s_at	-	Hypothetical protein	Unknown	Unknown	SPy0587	140	711	156	767	1.23	0.3609	0.4888	
M5005_Spy0487	SpM1_ChORF0588_s_at	-	Hypothetical exported protein	Unknown	Unknown	SPy0588	329	350	296	364	0.81	0.7540	0.6364	
M5005_Spy0488	SpM1_ChORF0589_s_at	-	Hypothetical protein	Unknown	Unknown	SPy0589	111	935	109	1073	0.96	0.6975	0.6184	
M5005_Spy0490	SpM1_ChORF0590_s_at	-	Peptidase family U32	Unknown	Cytoplasmic	SPy0590	99	959	84	1355	0.72	0.3099	0.4702	

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M5005_Spy0491	SpM1_ChORF0591_s_at	-	Peptidase family U32	Information processing	Cytoplasmic	SPy0591	166	736	133	869	0.64	0.9824	0.6906	
M5005_Spy0493	SpM1_ChORF0593_s_at	-	Hypothetical cytosolic protein	Unknown	Cytoplasmic	SPy0593	193	691	218	558	1.27	0.0893	0.3002	
M5005_Spy0495	SpM1_ChORF0595_s_at	*lysS*	Lysyl-tRNA synthetase (EC 6.1.1.6)	Protein synthesis	Cytoplasmic	SPy0595	475	204	414	258	0.76	0.1003	0.3098	
M5005_Spy0496	SpM1_ChORF0596_s_at	-	Hydrolase (HAD superfamily)	Unknown	Cytoplasmic	SPy0596	148	639	161	756	1.19	0.5787	0.5830	
M5005_Spy0497	SpM1_ChORF0598_s_at	-	Phosphoglycerate mutase (EC 5.4.2.1)	Carbohydrate metabolism	Cytoplasmic	SPy0598	115	1084	112	1002	0.95	0.8994	0.6697	
M5005_Spy0498	SpM1_ChORF0599_s_at	-	Transcriptional regulator	Information processing	Unknown	SPy0599	106	960	153	729	2.08	0.3145	0.4728	
M5005_Spy0499	SpM1_ChORF0600_s_at	-	Thiamine transporter	Membrane transport	Cytoplasmic Membrane	SPy0600	66	1362	114	1025	2.96	0.5588	0.5745	
M5005_Spy0500	SpM1_ChORF0601_s_at	-	N-acetylmuramoyl-L-alanine amidase (EC 3.5.1.28)	Cell wall metabolism	Unknown	SPy0601	276	405	377	250	1.87	0.0001	**0.0043**	**Significant**
M5005_Spy0501	SpM1_ChORF0603_s_at	-	Hypothetical integral membrane protein	Unknown	Cytoplasmic Membrane	SPy0603	250	419	167	634	0.44	0.0009	**0.0253**	**Significant**
M5005_Spy0502	SpM1_ChORF0604_s_at	-	Hypothetical exported protein	Unknown	Unknown	SPy0604	350	285	308	362	0.77	0.0374	0.2246	
M5005_Spy0503	SpM18_ChORF0672_s_at	*gpoA*	Glutathione peroxidase (EC 1.11.1.9)	Stress adaptation	Unknown	spyM18_0672	82	1183	78	1329	0.90	0.7904	0.6470	
M5005_Spy0504	SpM1_ChORF0606_s_at	*pepF*	Oligoendopeptidase F (EC 3.4.24.-)	Amino acid metabolism	Cytoplasmic	SPy0606	108	1013	134	882	1.54	0.2558	0.4345	
M5005_Spy0505	SpM1_ChORF0608_s_at	*ppc*	Phosphoenolpyruvate carboxylase (EC 4.1.1.31)	Carbohydrate metabolism	Cytoplasmic	SPy0608	201	617	171	719	0.73	0.6704	0.6108	
M5005_Spy0506	SpM1_ChORF0609_s_at	*ftsW*	Cell division protein ftsW	Cellular processing	Cytoplasmic Membrane	SPy0609	132	905	118	933	0.80	0.3802	0.4981	
M5005_Spy0507	SpM18_ChORF0677_x_at	-	Hypothetical cytosolic protein	Unknown	Unknown	spyM18_0677	47	1707	44	1660	0.89	0.8757	0.6641	
M5005_Spy0508	SpM1_ChORF0611_s_at	*tufA*	Protein Translation Elongation Factor Tu (EF-TU)	Cellular processing	Cytoplasmic	SPy0611	3061	13	3069	14	1.01	0.9286	0.6750	
M5005_Spy0509	SpM1_ChORF0613_s_at	*tpi*	Triosephosphate isomerase (EC 5.3.1.1)	Carbohydrate metabolism	Cytoplasmic	SPy0613	273	393	276	438	1.02	0.3900	0.5057	

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M5005_Spy0511	SpM1_ChORF0615_s_at	*murM*	UDP-N-acetylmuramoylpentapeptide-lysine N(6)-alanyltransferase (EC 2.3.2.10)	Cell wall metabolism	Unknown	SPy0615	150	786	179	658	1.43	0.9016	0.6704	
M5005_Spy0511	SpM1_ChORF0616_s_at	*murM*	UDP-N-acetylmuramoylpentapeptide-lysine N(6)-alanyltransferase (EC 2.3.2.10)	Cell wall metabolism	Unknown	SPy0616	141	829	152	878	1.16	0.1678	0.3797	
M5005_Spy0512	SpM1_ChORF0617_s_at	-	Hydrolase (HAD superfamily)	Unknown	Cytoplasmic	SPy0617	246	502	259	445	1.11	0.6821	0.6146	
M5005_Spy0513	SpM1_ChORF0619_s_at	-	Hypothetical cytosolic protein	Unknown	Unknown	SPy0619	111	779	78	1322	0.49	0.1078	0.3150	
M5005_Spy0514	SpM1_ChORF0621_s_at	-	dGTP triphosphohydrolase	Unknown	Cytoplasmic	SPy0621	64	1378	64	1368	0.98	0.7389	0.6305	
M5005_Spy0515	SpM1_ChORF0622_s_at	-	Hypothetical cytosolic protein	Unknown	Unknown	SPy0622	38	1822	78	1366	4.22	0.6778	0.6136	
M5005_Spy0516	SpM1_ChORF0623_s_at	*pacL*	Calcium-transporting ATPase (EC 3.6.3.8)	Membrane transport	Cytoplasmic Membrane	SPy0623	409	265	427	236	1.09	0.8306	0.6541	
M5005_Spy0516	SpM12_ChORF280-10_s_at	*pacL*	Calcium-transporting ATPase (EC 3.6.3.8)	Membrane transport	Cytoplasmic Membrane		35	2164	25	2164	0.51	0.4466	0.5280	
M5005_Spy0517	SpM1_ChORF0627_at	*regR*	Transcriptional regulator, LacI family	Information processing	Cytoplasmic	SPy0627	66	1396	79	1324	1.46	0.7369	0.6295	
M5005_Spy0517	SpM1_ChORF0627_s_at	*regR*	Transcriptional regulator, LacI family	Information processing	Cytoplasmic	SPy0627	91	1153	80	1311	0.77	0.0510	0.2541	
M5005_Spy0518	SpM1_ChORF0628_at	-	Oligohyaluronate lyase (EC 4.2.2.-)	Unknown	Cytoplasmic	SPy0628	26	1888	29	2030	1.19	0.1591	0.3719	
M5005_Spy0518	SpM1_ChORF0628_s_at	-	Oligohyaluronate lyase (EC 4.2.2.-)	Unknown	Cytoplasmic	SPy0628	29	2202	30	1986	1.11	0.9478	0.6811	
M5005_Spy0519	SpM1_ChORF0629_s_at	*agaD*	PTS system, N-acetylgalactosamine-specific IID component (EC 2.7.1.69)	Carbohydrate metabolism	Cytoplasmic Membrane	SPy0629	25	2095	66	1417	6.99	0.0611	0.2713	
M5005_Spy0519	SpM1_ChORF0630_s_at	*agaD*	PTS system, N-acetylgalactosamine-specific IID component (EC 2.7.1.69)	Carbohydrate metabolism	Cytoplasmic Membrane	SPy0630	33	1928	102	1001	9.58	0.5194	0.5590	

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M5005_Spy0521	SpM1_ChORF0631_s_at	*agaV*	PTS system, N-acetylgalactosamine-specific IIB component (EC 2.7.1.69)	Carbohydrate metabolism	Cytoplasmic	SPy0631	54	1579	91	1187	2.83	0.0017	**0.0421**	**Significant**
M5005_Spy0522	SpM5_ChORFJ7578C-260_s_at	-	Unsaturated glucuronyl hydrolase (EC 3.2.1.-)	Unknown	Unknown		52	1590	124	981	5.58	0.0198	0.1745	
M5005_Spy0523	SpM1_ChORF0634_s_at	-	Hypothetical protein	Membrane transport	Unknown	SPy0634	29	2093	43	1653	2.29	0.1864	0.3938	
M5005_Spy0523	SpM12_ChORF280-25_s_at	-	Hypothetical protein	Unknown	Unknown		33	2028	21	2255	0.43	0.6009	0.5893	
M5005_Spy0524	SpM1_ChORF0636_s_at	*idnO*	Gluconate 5-dehydrogenase (EC 1.1.1.69) Reaction: D-gluconate + NAD(P)+ = 5-dehydro-D-gluconate + NAD(P)H + H+	Carbohydrate metabolism	Cytoplasmic	SPy0636	101	877	323	378	10.24	0.0001	**0.0048**	**Significant**
M5005_Spy0525	SpM1_ChORF0637_s_at	-	Galactose-6-phosphate isomerase LacB subunit (EC 5.3.1.26)	Carbohydrate metabolism	Cytoplasmic	SPy0637	42	1706	171	829	16.57	3.4E-07	**2.3E-05**	**Significant**
M5005_Spy0526	SpM18_ChORF0701_s_at	-	2-dehydro-3-deoxygluconokinase (EC 2.7.1.45) Reaction: ATP + 2-dehydro-3-deoxy-D-gluconate = ADP + 6-phospho-2-dehydro-3-deoxy-D-gluconate	Carbohydrate metabolism	Cytoplasmic	spyM18_0701	73	1070	275	379	13.99	4.7E-05	**0.0019**	**Significant**
M5005_Spy0527	SpM1_ChORF0639_s_at	*kgdA*	4-Hydroxy-2-oxoglutarate aldolase (EC 4.1.3.16) / 2-dehydro-3-deoxyphosphogluconate aldolase (EC 4.1.2.14) Reaction: 2-dehydro-3-deoxy-D-gluconate 6-phosphate = pyruvate + D-glyceraldehyde 3-phosphate	Carbohydrate metabolism	Cytoplasmic	SPy0639	83	1436	178	698	4.66	0.0047	0.0859	

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M5005_Spy0528	SpM1_ChORF0640_s_at	-	Beta-phosphoglucomutase (EC 5.4.2.6) / Glucose-1-phosphate phosphodismutase (EC 2.7.1.41)	Unknown	Cytoplasmic	SPy0640	41	1769	54	1588	1.77	0.0832	0.2979	
M5005_Spy0529	SpM1_ChORF0642_s_at	-	Conserved hypothetical protein	Unknown	Cytoplasmic	SPy0642	110	1059	198	595	3.25	0.0006	**0.0179**	**Significant**
M5005_Spy0530	SpM1_ChORF0643_s_at	*prfB*	Bacterial Peptide Chain Release Factor 2 (RF-2)	Information processing	Cytoplasmic	SPy0643	248	440	284	385	1.31	0.0430	0.2393	
M5005_Spy0531	SpM1_ChORF0644_s_at	*ftsE*	Cell division ATP-binding protein ftsE	Cellular processing	Cytoplasmic Membrane	SPy0644	420	219	606	143	2.08	0.0004	**0.0132**	**Significant**
M5005_Spy0531	SpM1_ChORF0645_s_at	*ftsE*	Cell division ATP-binding protein ftsE	Cellular processing	Cytoplasmic Membrane	SPy0645	251	467	345	321	1.89	0.0018	**0.0442**	**Significant**
M5005_Spy0533	SpM1_ChORF0646_s_at	-	Hydroxyacylglutathione hydrolase (EC 3.1.2.6)	Amino acid metabolism	Unknown	SPy0646	115	990	122	924	1.13	0.7096	0.6201	
M5005_Spy0534	SpM18_ChORF0709_s_at	*bsaA*	Acetoin(diacetyl) reductase (EC 1.1.1.5)	Carbohydrate metabolism	Cytoplasmic	spyM18_0709	157	734	172	723	1.21	0.8403	0.6563	
M5005_Spy0536	SpM1_ChORF0649_s_at	*dinG*	ATP-dependent helicase, DinG family	Cellular processing	Cytoplasmic	SPy0649	123	891	150	888	1.49	0.1803	0.3887	
M5005_Spy0537	SpM1_ChORF0650_s_at	*aspC*	Aspartate aminotransferase (EC 2.6.1.1)	Amino acid metabolism	Cytoplasmic	SPy0650	399	258	459	219	1.32	0.7535	0.6363	
M5005_Spy0538	SpM12_ChORF263-13_s_at	*asnS*	Asparaginyl-tRNA synthetase (EC 6.1.1.22)	Protein synthesis	Cytoplasmic		109	1080	146	836	1.79	0.3711	0.4929	
M5005_Spy0539	SpM1_ChORF0652_s_at	-	ATP-binding protein (contains P-loop)	Membrane transport	Cytoplasmic	SPy0652	364	306	403	265	1.23	0.0797	0.2939	
M5005_Spy0540	SpM1_ChORF0653_s_at	-	Transporter	Membrane transport	Unknown	SPy0653	316	301	431	259	1.86	0.0016	**0.0395**	**Significant**
M5005_Spy0541	SpM1_ChORF0654_s_at	-	Hypothetical cytosolic protein	Phage	Cytoplasmic	SPy0654	205	496	323	370	2.49	0.2211	0.4181	
M5005_Spy0542	SpM1_ChORF0713_s_at	*pepD*	Dipeptidase (EC 3.4.-.-)	Amino acid metabolism	Unknown	SPy0713	93	930	139	798	2.21	0.0855	0.2979	
M5005_Spy0543	SpM1_ChORF0714_s_at	*adcA*	High-affinity zinc uptake system protein znuA precursor	Membrane transport	Unknown	SPy0714	830	92	555	159	0.45	0.2540	0.4334	
M5005_Spy0544	SpM1_ChORF0715_at	-	Transcriptional regulator, GntR family	Information processing	Cytoplasmic	SPy0715	207	489	269	443	1.70	0.2915	0.4558	

M5005_gene	RML Probeset	Gene	Description	Function	Predicted Cellular Localization *	Synonym †	Normalized Expression (WT) ‡	Transcript Rank (WT) §	Normalized Expression (Mutant) ‡	Transcript Rank (Mutant) §	Fold Change (Mutant : WT) **	*P* -value (Strain)	*Q* -value (Strain)††	Strain Significance (FDR=0.05)
M5005_Spy0544	SpM12_ChORF293-41_s_at	-	Transcriptional regulator, GntR family	Information processing	Cytoplasmic		16	2581	16	2494	1.00	0.1956	0.3995	
M5005_Spy0545	SpM1_ChORF0716_s_at	*agaS*	Galactosamine-6-phosphate deaminase (isomerizing) (EC 3.5.99.-)	Carbohydrate metabolism	Unknown	SPy0716	99	1053	205	632	4.29	6.2E-08	**6.4E-06**	**Significant**
M5005_Spy0546	SpM1_ChORF0717_s_at	*rpmE*	LSU ribosomal protein L31P	Protein synthesis	Unknown	SPy0717	650	122	716	132	1.22	0.3985	0.5106	
M5005_Spy0547	SpM1_ChORF0720_s_at	-	Phosphoesterase, DHH family protein	Unknown	Cytoplasmic	SPy0720	284	371	276	432	0.94	0.8815	0.6650	
M5005_Spy0548	SpM1_ChORF0721_s_at	-	Flavodoxin	Carbohydrate metabolism	Unknown	SPy0721	228	611	180	709	0.62	0.3329	0.4779	
M5005_Spy0549	SpM1_ChORF0722_s_at	-	Chorismate mutase (EC 5.4.99.5)	Amino acid metabolism	Cytoplasmic	SPy0722	61	1550	31	1898	0.26	0.2764	0.4473	
M5005_Spy0550	SpM1_ChORF0723_at	-	Chloride channel protein	Membrane transport	Cytoplasmic Membrane	SPy0723	40	1847	48	1546	1.43	0.8901	0.6676	
M5005_Spy0550	SpM1_ChORF0723_s_at	-	Chloride channel protein	Membrane transport	Cytoplasmic Membrane	SPy0723	39	1809	60	1515	2.29	0.8301	0.6540	
M5005_Spy0551	SpM1_ChORF0724_s_at	*rplS*	LSU ribosomal protein L19P	Protein synthesis	Cytoplasmic	SPy0724	194	633	183	687	0.89	0.5082	0.5532	
M5005_Spy0552	SpM1_ChORF0726_s_at	-	DNA gyrase related protein (probably a hydrolase/phosphatase)	Unknown	Unknown	SPy0726	310	400	276	510	0.79	0.4392	0.5231	
M5005_Spy0552	SpM12_ChORF224-2_at	-	DNA gyrase related protein (probably a hydrolase/phosphatase)	Unknown	Unknown		39	1762	30	1935	0.59	0.1812	0.3887	
M5005_Spy0553	SpM1_ChORF0727_s_at	*gyrB*	DNA gyrase subunit B (EC 5.99.1.3)	Cellular processing	Cytoplasmic	SPy0727	546	160	522	183	0.91	0.2513	0.4334	
M5005_Spy0554	SpM1_ChORF0728_s_at	-	Septation ring formation regulator	Information processing	Cytoplasmic	SPy0728	699	124	629	151	0.81	0.4099	0.5148	
M5005_Spy0555	SpM1_ChORF0729_s_at	-	Hypothetical cytosolic protein	Unknown	Unknown	SPy0729	32	1885	48	1686	2.35	0.7343	0.6294	
M5005_Spy0556	SpM1_ChORF0731_s_at	*eno*	Enolase (EC 4.2.1.11)	Carbohydrate metabolism	Cytoplasmic	SPy0731	672	117	740	91	1.21	0.1694	0.3814	
M5005_Spy0557	SpM1_ChORF0732_at	-	Transposase	Mobile genetic element	Cytoplasmic	SPy0732	16	2304	70	1411	19.55	0.0157	0.1619	
M5005_Spy0558	SpM1_ChORF0733_at	-	Transposase	Mobile genetic element	Unknown	SPy0733	16	2259	84	1274	29.51	0.0093	0.1209	

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M5005_Spy0559	SpM12_ChORF262-5_s_at	-	Transcriptional regulator	Unknown	Cytoplasmic Membrane		44	1618	109	1089	6.05	2.4E-08	**2.9E-06**	**Significant**
M5005_Spy0561	SpM1_ChORF0737_at	*epf*	Putative extracellular matrix binding protein	Virulence	Cell Wall	SPy0737	47	1633	89	1304	3.54	0.4782	0.5421	
M5005_Spy0561	SpM12_ChORF262-1_s_at	*epf*	Putative extracellular matrix binding protein	Virulence	Cell Wall		18	2237	14	2492	0.57	0.0741	0.2853	
M5005_Spy0561	SpM12_ChORF262-3_s_at	*epf*	Putative extracellular matrix binding protein	Virulence	Cell Wall		17	2531	12	2543	0.53	0.8407	0.6563	
M5005_Spy0561	SpM12_ChORF262-4_s_at	*epf*	Putative extracellular matrix binding protein	Virulence	Cell Wall		23	2027	23	2196	1.01	0.8555	0.6602	
M5005_Spy0562	SpM1_ChORF0738_at	*sagA, pel*	Streptolysin S precursor; pleiotropic effector locus	Virulence	Extracellular	SPy0738	1372	28	5858	8	18.24	8.7E-07	**5.5E-05**	**Significant**
M5005_Spy0563	SpM1_ChORF0739_s_at	*sagB*	Streptolysin S biosynthesis protein SagB	Protein synthesis	Unknown	SPy0739	258	487	392	261	2.30	8.9E-07	**5.5E-05**	**Significant**
M5005_Spy0564	SpM1_ChORF0740_s_at	*sagC*	Streptolysin S biosynthesis protein SagC	Protein synthesis	Cytoplasmic	SPy0740	276	312	644	123	5.43	1.4E-07	**1.2E-05**	**Significant**
M5005_Spy0565	SpM1_ChORF0741_s_at	*sagD*	Streptolysin S biosynthesis protein SagD	Protein synthesis	Cytoplasmic	SPy0741	303	404	593	126	3.83	5.2E-07	**3.5E-05**	**Significant**
M5005_Spy0566	SpM1_ChORF0742_s_at	*sagE*	Streptolysin S putative self-immunity protein SagE	Protein synthesis	Cytoplasmic Membrane	SPy0742	70	1561	159	745	5.26	1.3E-05	**0.0006**	**Significant**
M5005_Spy0567	SpM1_ChORF0743_s_at	*sagF*	Streptolysin S biosynthesis protein SagF	Protein synthesis	Cytoplasmic Membrane	SPy0743	142	841	346	340	5.95	2.6E-07	**1.9E-05**	**Significant**
M5005_Spy0568	SpM1_ChORF0744_s_at	*sagG*	Streptolysin S export ATP-binding protein SagG	Membrane transport	Cytoplasmic Membrane	SPy0744	276	379	478	185	2.99	8.7E-08	**8.0E-06**	**Significant**
M5005_Spy0568	SpM12_ChORF262-15_s_at	*sagG*	Streptolysin S export ATP-binding protein SagG	Membrane transport	Cytoplasmic Membrane		115	862	282	392	5.99	5.0E-06	**0.0003**	**Significant**
M5005_Spy0569	SpM1_ChORF0745_s_at	*sagH*	Streptolysin S export transmembrane protein SagH	Membrane transport	Cytoplasmic Membrane	SPy0745	175	681	261	419	2.23	6.9E-08	**6.7E-06**	**Significant**
M5005_Spy0570	SpM12_ChORF205-1_s_at	*sagI*	Streptolysin S export transmembrane protein SagI	Membrane transport	Cytoplasmic Membrane		207	547	393	237	3.61	1.5E-07	**1.3E-05**	**Significant**

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M5005_Spy0571	SpM1_ChORF0747_s_at	-	Endonuclease/Exonuclease/phosphatase family protein	Unknown	Cell Wall	SPy0747	586	153	890	72	2.31	0.0081	0.1126	
M5005_Spy0572	SpM1_ChORF0749_s_at	-	Hypothetical membrane spanning protein	Unknown	Cytoplasmic Membrane	SPy0749	214	539	226	531	1.12	0.0581	0.2665	
M5005_Spy0573	SpM1_ChORF0751_s_at	*lig*	NAD-dependent DNA ligase (EC 6.5.1.2)	Cellular processing	Cytoplasmic	SPy0751	99	985	110	1179	1.25	0.5643	0.5766	
M5005_Spy0574	SpM1_ChORF0752_s_at	-	Diacylglycerol kinase family	Cellular processing	Cytoplasmic	SPy0752	63	1530	101	1155	2.57	0.0457	0.2439	
M5005_Spy0575	SpM1_ChORF0754_s_at	*atpE*	ATP synthase C chain (EC 3.6.3.14)	Carbohydrate metabolism	Unknown	SPy0754	72	1284	53	1637	0.54	0.8454	0.6565	
M5005_Spy0575	SpM3_ChORF0493_s_at	*atpE*	ATP synthase C chain (EC 3.6.3.14)	Carbohydrate metabolism	Unknown	spyM3_0493	59	1555	43	1671	0.52	0.4269	0.5178	
M5005_Spy0576	SpM1_ChORF0755_s_at	*atpB*	ATP synthase A chain (EC 3.6.3.14)	Carbohydrate metabolism	Cytoplasmic Membrane	SPy0755	123	1008	125	957	1.03	0.9076	0.6729	
M5005_Spy0577	SpM1_ChORF0756_s_at	*atpF*	ATP synthase B chain (EC 3.6.3.14)	Carbohydrate metabolism	Cytoplasmic	SPy0756	94	1254	114	1031	1.48	0.4259	0.5176	
M5005_Spy0578	SpM1_ChORF0757_s_at	*atpH*	ATP synthase delta chain (EC 3.6.3.14)	Carbohydrate metabolism	Unknown	SPy0757	102	1009	107	1022	1.09	0.2086	0.4107	
M5005_Spy0579	SpM1_ChORF0758_s_at	*atpA*	ATP synthase alpha chain (EC 3.6.3.14)	Carbohydrate metabolism	Cytoplasmic	SPy0758	171	666	169	720	0.98	0.9131	0.6743	
M5005_Spy0580	SpM1_ChORF0759_s_at	*atpG*	ATP synthase gamma chain (EC 3.6.3.14)	Carbohydrate metabolism	Unknown	SPy0759	82	1181	115	1000	1.95	0.7903	0.6470	
M5005_Spy0581	SpM1_ChORF0760_s_at	*atpD*	ATPase, beta subunit	Carbohydrate metabolism	Cytoplasmic	SPy0760	161	670	201	665	1.57	0.6528	0.6061	
M5005_Spy0581	SpM12_ChORF269-12_s_at	*atpD*	ATPase, beta subunit	Carbohydrate metabolism	Cytoplasmic		87	1078	107	1166	1.53	0.4123	0.5159	
M5005_Spy0582	SpM1_ChORF0761_s_at	*atpC*	ATP synthase epsilon chain (EC 3.6.3.14)	Carbohydrate metabolism	Cytoplasmic	SPy0761	254	504	236	657	0.87	0.6411	0.6034	
M5005_Spy0583	M12_0158_at	-	Hypothetical membrane associated protein	Unknown	Unknown		9	2655	11	2561	1.74	0.2356	0.4227	
M5005_Spy0583	SpM1_ChORF0762_s_at	-	Hypothetical membrane associated protein	Unknown	Unknown	SPy0762	127	969	150	713	1.40	0.1294	0.3379	
M5005_Spy0584	SpM1_ChORF0763_s_at	*murA*	UDP-N-acetylglucosamine 1-carboxyvinyltransferase (EC 2.5.1.7)	Cellular processing	Cytoplasmic	SPy0763	378	297	339	328	0.80	0.7580	0.6368	

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M5005_Spy0585	SpM1_ChORF0764_s_at	*epuA*	EpuA protein	Virulence	Cytoplasmic Membrane	SPy0764	208	482	160	690	0.59	0.1743	0.3851	
M5005_Spy0585	SpM18_ChORF0822_s_at	*epuA*	EpuA protein	Virulence	Cytoplasmic Membrane	spyM18_0822	181	565	177	667	0.96	0.0474	0.2480	
M5005_Spy0585	SpM3_ChORF0503_s_at	*epuA*	EpuA protein	Virulence	Cytoplasmic Membrane	spyM3_0503	131	758	148	751	1.29	0.1057	0.3149	
M5005_Spy0586	SpM1_ChORF0766_s_at	*endA*	DNA-entry nuclease (EC 3.1.30.-)	Virulence	Unknown	SPy0766	50	1407	61	1431	1.45	0.5544	0.5726	
M5005_Spy0587	SpM1_ChORF0768_s_at	*pheS*	Phenylalanyl-tRNA synthetase alpha chain (EC 6.1.1.20)	Protein synthesis	Cytoplasmic	SPy0768	86	1159	80	1295	0.86	0.0867	0.3002	
M5005_Spy0588	SpM1_ChORF0769_s_at	*pheT*	Phenylalanyl-tRNA synthetase beta chain (EC 6.1.1.20)	Protein synthesis	Cytoplasmic	SPy0769	95	1131	92	1192	0.95	0.4174	0.5169	
M5005_Spy0589	SpM1_ChORF0770_s_at	-	Salt-stress induced protein	Unknown	Cytoplasmic	SPy0770	36	1889	57	1497	2.53	0.2897	0.4558	
M5005_Spy0590	SpM1_ChORF0771_s_at	-	Hypothetical protein	Unknown	Unknown	SPy0771	91	1168	102	1048	1.27	0.2687	0.4436	
M5005_Spy0591	SpM1_ChORF0772_s_at	-	ABC transporter permease protein	Membrane transport	Cytoplasmic Membrane	SPy0772	266	375	215	587	0.66	0.8683	0.6623	
M5005_Spy0592	SpM1_ChORF0773_s_at	-	ABC transporter ATP-binding protein	Membrane transport	Cytoplasmic Membrane	SPy0773	151	738	113	956	0.56	0.1164	0.3229	
M5005_Spy0593	SpM1_ChORF0775_s_at	-	Neutral zinc metallopeptidase family	Unknown	Unknown	SPy0775	78	1257	89	1242	1.32	0.2197	0.4175	
M5005_Spy0594	SpM1_ChORF0776_s_at	*rexB*	ATP-dependent nuclease subunit B	Cellular processing	Cytoplasmic	SPy0776	133	913	112	1044	0.72	0.4298	0.5198	
M5005_Spy0595	SpM1_ChORF0777_s_at	*rexA*	ATP-dependent nuclease subunit A	Information processing	Cytoplasmic	SPy0777	133	949	211	585	2.54	0.0388	0.2287	
M5005_Spy0596	SpM1_ChORF0778_s_at	-	Arginine-binding protein	Membrane transport	Unknown	SPy0778	133	785	150	766	1.28	0.5495	0.5698	
M5005_Spy0597	SpM18_ChORF0838_x_at	*rplU*	SSU ribosomal protein S21P	Protein synthesis	Cytoplasmic	spyM18_0838	221	530	239	552	1.17	0.6941	0.6184	
M5005_Spy0598	SpM1_ChORF0780_s_at	*mscL*	Large-conductance mechanosensitive channel	Membrane transport	Cytoplasmic Membrane	SPy0780	220	532	273	486	1.55	0.3297	0.4776	
M5005_Spy0599	SpM1_ChORF0781_s_at	*dnaG*	DNA primase (EC 2.7.7.-)	Cellular processing	Cytoplasmic	SPy0781	306	329	300	368	0.96	0.2724	0.4449	
M5005_Spy0600	SpM1_ChORF0782_s_at	*rpoD*	RNA polymerase sigma factor rpoD	Information processing	Cytoplasmic	SPy0782	228	466	238	471	1.09	0.2948	0.4579	
M5005_Spy0601	SpM1_ChORF0783_s_at	-	Hypothetical cytosolic protein	Unknown	Cytoplasmic	SPy0783	79	1138	107	930	1.85	0.4262	0.5176	

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M5005_Spy0602	SpM1_ChORF0784_s_at	*rmlD*	dTDP-4-dehydrorhamnose reductase (EC 1.1.1.133)	Cell wall metabolism	Unknown	SPy0784	159	828	204	575	1.66	0.0355	0.2190	
M5005_Spy0602	SpM5_ChORF4P31a-86_s_at	*rmlD*	dTDP-4-dehydrorhamnose reductase (EC 1.1.1.133)	Cell wall metabolism	Unknown		43	1629	34	1859	0.63	0.9201	0.6743	
M5005_Spy0603	SpM1_ChORF0786_s_at	*rgpAc*	Alpha-(1,2)-rhamnosyltransferase (EC 2.4.1.-)	Cell wall metabolism	Cytoplasmic	SPy0786	307	372	317	338	1.07	0.3809	0.4981	
M5005_Spy0604	SpM1_ChORF0787_s_at	*rgpBc*	alpha-L-Rha alpha-1,3-L-rhamnosyltransferase (EC 2.4.1.-)	Cell wall metabolism	Unknown	SPy0787	246	508	257	416	1.09	0.1102	0.3154	
M5005_Spy0605	SpM1_ChORF0789_s_at	*rgpCc*	Polysaccharide export ABC transporter permease protein	Cell wall metabolism	Cytoplasmic Membrane	SPy0789	81	1113	140	880	2.97	0.5430	0.5695	
M5005_Spy0606	SpM1_ChORF0790_s_at	*rgpDc*	Polysaccharide export ATP-binding protein	Cell wall metabolism	Cytoplasmic Membrane	SPy0790	252	486	262	473	1.08	0.9257	0.6750	
M5005_Spy0607	SpM1_ChORF0791_s_at	*rgpEc*	Glycosyltransferase (EC 2.4.1.-)	Cell wall metabolism	Cytoplasmic	SPy0791	214	543	192	520	0.81	0.5089	0.5532	
M5005_Spy0608	SpM1_ChORF0792_s_at	*rgpFc*	alpha-L-Rha alpha-1,2-L-rhamnosyltransferase (EC 2.4.1.-) / alpha-L-Rha alpha-1,3-L-rhamnosyltransferase (EC 2.4.1.-)	Cell wall metabolism	Cytoplasmic	SPy0792	205	594	225	549	1.20	0.2020	0.4059	
M5005_Spy0609	SpM1_ChORF0793_s_at	-	Phosphoglycerol transferase	Unknown	Cytoplasmic Membrane	SPy0793	191	653	252	466	1.74	0.0076	0.1081	
M5005_Spy0610	SpM1_ChORF0794_s_at	-	Glycosyltransferase involved in cell wall biogenesis (EC 2.4.-.-)	Unknown	Cytoplasmic	SPy0794	111	970	88	1198	0.63	0.1253	0.3349	
M5005_Spy0611	SpM1_ChORF0796_s_at	-	Hypothetical protein	Unknown	Cytoplasmic Membrane	SPy0796	80	1169	75	1184	0.88	0.1731	0.3845	
M5005_Spy0612	SpM1_ChORF0797_s_at	*amrA*	Transcriptional activator amrA	Information processing	Cytoplasmic Membrane	SPy0797	145	861	148	776	1.05	0.0188	0.1707	
M5005_Spy0613	SpM1_ChORF0798_s_at	-	Hypothetical membrane spanning protein	Unknown	Cytoplasmic Membrane	SPy0798	78	1191	83	1219	1.13	0.5400	0.5678	
M5005_Spy0614	SpM1_ChORF0799_s_at	*pepT*	Peptidase T (EC 3.4.11.14)	Amino acid metabolism	Cytoplasmic	SPy0799	458	232	597	146	1.69	0.0005	**0.0139**	**Significant**

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M5005_Spy0615	SpM1_ChORF0800_s_at	*ebsA*	Hypothetical pore-forming peptide	Unknown	Cytoplasmic Membrane	SPy0800	302	410	394	281	1.71	0.0006	**0.0175**	**Significant**
M5005_Spy0615	SpM1_ChORF0801_s_at	*ebsA*	Pore forming protein ebsA	Unknown	Cytoplasmic Membrane	SPy0801	14	2453	15	2358	1.18	0.4581	0.5317	
M5005_Spy0617	SpM12_ChORF246-9_s_at	-	Hypothetical membrane associated protein	Unknown	Unknown		221	497	302	348	1.86	0.0074	0.1081	
M5005_Spy0618	SpM1_ChORF0803_s_at	*cmk*	Cytidylate kinase (EC 2.7.4.14)	Nucleotide metabolism	Cytoplasmic	SPy0803	556	155	897	63	2.60	0.0002	**0.0060**	**Significant**
M5005_Spy0619	SpM1_ChORF0804_s_at	*infC*	Bacterial Protein Translation Initiation Factor 3 (IF-3)	Information processing	Cytoplasmic	SPy0804	349	299	340	305	0.95	0.5223	0.5602	
M5005_Spy0620	SpM1_ChORF0805_s_at	*rpl36*	LSU ribosomal protein L35P	Protein synthesis	Unknown	SPy0805	416	260	390	274	0.88	0.3440	0.4828	
M5005_Spy0620	SpM18_ChORF0867_s_at	*rpl35*	LSU ribosomal protein L35P	Protein synthesis	Unknown	spyM18_0867	404	261	338	343	0.70	0.0178	0.1674	
M5005_Spy0621	SpM1_ChORF0806_s_at	*rplT*	LSU ribosomal protein L20P	Protein synthesis	Unknown	SPy0806	44	1746	13	2569	0.09	0.0624	0.2717	
M5005_Spy0622	SpM1_ChORF0807_s_at	-	Phosphoglycerol transferase	Unknown	Cytoplasmic Membrane	SPy0807	312	355	283	424	0.83	0.3417	0.4809	
M5005_Spy0623	SpM1_ChORF0808_s_at	-	Methyltransferase (EC 2.1.1.-)	Unknown	Cytoplasmic	SPy0808	263	415	257	508	0.96	0.0655	0.2754	
M5005_Spy0624	SpM1_ChORF0809_s_at	*aroD*	3-dehydroquinate dehydratase (EC 4.2.1.10)	Carbohydrate metabolism	Cytoplasmic	SPy0809	163	686	200	606	1.50	0.3657	0.4894	
M5005_Spy0625	SpM1_ChORF0810_s_at	*aroF*	Chorismate synthase (EC 4.2.3.5)	Amino acid metabolism	Cytoplasmic	SPy0810	166	600	220	561	1.76	0.3802	0.4981	
M5005_Spy0626	SpM1_ChORF0811_s_at	-	Hypothetical cytosolic protein	Unknown	Cytoplasmic	SPy0811	185	576	224	545	1.47	0.4443	0.5263	
M5005_Spy0627	SpM1_ChORF0813_at	*gor, gshR*	Glutathione reductase (EC 1.8.1.7)	Stress adaptation	Cytoplasmic	SPy0813	121	954	156	783	1.68	0.0016	**0.0405**	**Significant**
M5005_Spy0628	SpM1_ChORF0814_s_at	*folC.2*	Folylpolyglutamate synthase (EC 6.3.2.17) / Dihydrofolate synthase (EC 6.3.2.12)	Coenzyme and cofactor metabolism	Cytoplasmic	SPy0814	125	911	148	910	1.40	0.2723	0.4449	
M5005_Spy0629	SpM1_ChORF0815_s_at	-	Hypothetical protein	Unknown	Unknown	SPy0815	50	1772	41	1827	0.67	0.8470	0.6565	

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M5005_Spy0630	SpM1_ChORF0816_s_at	*nifS, yrvO*	Cysteine desulfhydrase (EC 4.4.1.-) / Selenocysteine lyase (EC 4.4.1.16)	Amino acid metabolism	Cytoplasmic	SPy0816	100	1117	98	1123	0.96	0.9830	0.6906	
M5005_Spy0631	SpM1_ChORF0817_s_at	*thiI*	Thiamine biosynthesis protein thiI	Coenzyme and cofactor metabolism	Cytoplasmic	SPy0817	149	672	156	746	1.11	0.0684	0.2779	
M5005_Spy0632	SpM1_ChORF0818_s_at	*capA*	Capsule biosynthesis protein capA	Unknown	Cytoplasmic	SPy0818	146	917	152	803	1.08	0.2627	0.4400	
M5005_Spy0633	SpM1_ChORF0819_s_at	*rplU*	LSU ribosomal protein L21P	Protein synthesis	Unknown	SPy0819	385	247	414	242	1.15	0.0753	0.2867	
M5005_Spy0634	SpM1_ChORF0821_s_at	-	hypothetical ribosome-associated protein	Unknown	Unknown	SPy0821	326	335	349	312	1.15	0.8024	0.6501	
M5005_Spy0635	SpM1_ChORF0822_s_at	*rpmA*	LSU ribosomal protein L27P	Protein synthesis	Unknown	SPy0822	307	359	304	335	0.98	0.1154	0.3225	
M5005_Spy0636	SpM1_ChORF0824_s_at	*epuA*	Transcriptional regulators, LysR family	Information processing	Cytoplasmic	SPy0824	147	827	89	1254	0.37	0.0157	0.1619	
M5005_Spy0636	SpM18_ChORF0886_s_at	*epuA*	Transcriptional regulators, LysR family	Information processing	Cytoplasmic	spyM18_0886	25	2311	12	2431	0.25	0.5922	0.5877	
M5005_Spy0637	SpM1_ChORF0826_s_at	*lsp*	Lipoprotein signal peptidase (EC 3.4.23.36)	Secretion	Cytoplasmic Membrane	SPy0826	68	1374	70	1357	1.05	0.0909	0.3002	
M5005_Spy0638	SpM1_ChORF0827_s_at	-	Ribosomal large subunit pseudouridine synthase D (EC 4.2.1.70)	Protein synthesis	Cytoplasmic	SPy0827	196	664	158	759	0.65	0.7897	0.6470	
M5005_Spy0639	SpM5_ChORF4P31a-118_s_at	*pyrR*	PyrR bifunctional protein	Membrane transport	Cytoplasmic		145	837	143	822	0.96	0.7416	0.6322	
M5005_Spy0640	SpM1_ChORF0831_s_at	*pyrP*	Uracil permease	Membrane transport	Cytoplasmic Membrane	SPy0831	92	1094	112	1109	1.50	0.6598	0.6081	
M5005_Spy0641	SpM1_ChORF0832_s_at	*pyrB*	Aspartate carbamoyltransferase (EC 2.1.3.2)	Cellular processing	Cytoplasmic	SPy0832	101	1003	135	900	1.80	0.1404	0.3524	
M5005_Spy0642	SpM1_ChORF0833_s_at	*carA*	Carbamoyl-phosphate synthase small chain (EC 6.3.5.5)	Nucleotide metabolism	Cytoplasmic	SPy0833	153	773	146	848	0.91	0.2521	0.4334	
M5005_Spy0643	SpM1_ChORF0835_s_at	*carB*	Carbamoyl-phosphate synthase large chain (EC 6.3.5.5)	Nucleotide metabolism	Cytoplasmic	SPy0835	135	926	134	1101	1.00	0.6648	0.6091	
M5005_Spy0645	SpM1_ChORF0836_s_at	-	ABC transporter ATP-binding protein	Membrane transport	Cytoplasmic Membrane	SPy0836	167	756	163	753	0.95	0.9283	0.6750	

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M5005_Spy0645	SpM1_ChORF0837_s_at	-	ABC transporter ATP-binding protein	Membrane transport	Cytoplasmic Membrane	SPy0837	61	1504	67	1413	1.20	0.8233	0.6525	
M5005_Spy0646	SpM1_ChORF0838_s_at	-	ABC transporter permease protein	Membrane transport	Cytoplasmic Membrane	SPy0838	70	1409	74	1294	1.11	0.7062	0.6200	
M5005_Spy0648	SpM1_ChORF0840_s_at	*rpsP*	SSU ribosomal protein S16P	Protein synthesis	Cytoplasmic	SPy0840	233	462	219	532	0.89	0.7517	0.6359	
M5005_Spy0649	SpM1_ChORF0841_s_at	-	RNA binding protein	Unknown	Cytoplasmic	SPy0841	116	999	91	1237	0.62	0.9628	0.6850	
M5005_Spy0651	SpM1_ChORF0843_s_at	-	Cell surface protein	Unknown	Unknown	SPy0843	47	1597	44	1657	0.85	0.8530	0.6588	
M5005_Spy0651	SpM12_ChORF291-7_s_at	-	Cell surface protein	Unknown	Unknown		83	1311	95	1175	1.32	0.0599	0.2677	
M5005_Spy0652	SpM1_ChORF0844_s_at	-	Hypothetical cytosolic protein	Unknown	Cytoplasmic	SPy0844	111	974	80	1292	0.52	0.0058	0.0952	
M5005_Spy0653	SpM1_ChORF0845_s_at	*czcD*	Cobalt-zinc-cadmium resistance protein czcD	Membrane transport	Cytoplasmic Membrane	SPy0845	52	1402	43	1679	0.66	0.8928	0.6690	
M5005_Spy0654	SpM1_ChORF0846_s_at	-	Transcriptional regulator, TetR family	Information processing	Cytoplasmic	SPy0846	26	2181	27	2095	1.08	0.5368	0.5672	
M5005_Spy0655	SpM1_ChORF0847_s_at	-	16S rRNA processing protein rimM	Cellular processing	Unknown	SPy0847	27	1858	48	1595	3.08	0.3462	0.4836	
M5005_Spy0656	SpM1_ChORF0849_s_at	*trmD*	tRNA (Guanine-N(1)-)-methyltransferase (EC 2.1.1.31)	Protein synthesis	Cytoplasmic	SPy0849	116	976	114	1034	0.97	0.7889	0.6469	
M5005_Spy0657	SpM1_ChORF0850_s_at	*trxB, yumC*	Thioredoxin reductase (EC 1.8.1.9)	Amino acid metabolism	Cytoplasmic	SPy0850	86	1088	94	1158	1.20	0.4870	0.5443	
M5005_Spy0658	SpM1_ChORF0851_s_at	-	Regulatory protein (pfoS/R)	Information processing	Cytoplasmic Membrane	SPy0851	239	425	242	498	1.02	0.0148	0.1557	
M5005_Spy0659	SpM1_ChORF0852_s_at	*apbA*	2-dehydropantoate 2-reductase (EC 1.1.1.169)	Unknown	Cytoplasmic	SPy0852	96	1027	90	1078	0.89	0.4451	0.5269	
M5005_Spy0660	SpM1_ChORF0853_s_at	*fruR*	Fructose repressor	Information processing	Cytoplasmic	SPy0853	208	536	282	412	1.84	0.0564	0.2629	
M5005_Spy0661	SpM1_ChORF0854_s_at	*fruB*	1-phosphofructokinase (EC 2.7.1.56)	Carbohydrate metabolism	Unknown	SPy0854	356	295	462	216	1.68	0.0784	0.2918	
M5005_Spy0662	SpM1_ChORF0855_s_at	*fruA*	PTS system, fructose-specific IIABC component (EC 2.7.1.69)	Carbohydrate metabolism	Cytoplasmic Membrane	SPy0855	290	363	333	365	1.32	0.2258	0.4208	

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M5005_Spy0662	SpM5_ChORF4P31a-19_s_at	*fruA*	PTS system, fructose-specific IIABC component (EC 2.7.1.69)	Carbohydrate metabolism	Cytoplasmic Membrane		16	2387	19	2382	1.46	0.0318	0.2095	
M5005_Spy0663	SpM1_ChORF0856_s_at	*mur1.1*	Autolysin (EC 3.5.1.28)	Cell wall metabolism	Extracellular	SPy0856	90	1192	113	1017	1.58	0.0744	0.2853	
M5005_Spy0664	SpM1_ChORF0857_s_at	*mur1.2*	Autolysin (EC 3.5.1.28)	Cell wall metabolism	Extracellular	SPy0857	464	205	293	437	0.40	0.0295	0.2028	
M5005_Spy0665	M12_1091_at	-	Transposase	Mobile genetic element	Unknown		11	2608	16	2497	1.88	0.2474	0.4310	
M5005_Spy0666	SpM12_ChORF291-52_s_at	-	Hypothetical protein	Unknown	Extracellular		28	2078	84	1224	9.17	0.8773	0.6641	
M5005_Spy0668	SpM1_ChORF0861_s_at	*ideS, mac*	IgG-degrading protease of GAS	Virulence	Unknown	SPy0861	49	1780	57	1602	1.37	0.0587	0.2676	
M5005_Spy0670	SpM3_ChORF0584_s_at	*rpsU*	Nucleoside diphosphate kinase (EC 2.7.4.6)	Cellular processing	Unknown	spyM3_0584	99	1195	125	921	1.60	0.6199	0.5962	
M5005_Spy0671	SpM1_ChORF0864_s_at	-	Transposase	Mobile genetic element	Cytoplasmic	SPy0864	194	584	205	627	1.11	0.5006	0.5512	
M5005_Spy0672	SpM1_ChORF0865_s_at	-	DegV family protein	Unknown	Unknown	SPy0865	223	546	272	373	1.50	0.1220	0.3283	
M5005_Spy0673	SpM1_ChORF0866_s_at	*papS*	Poly(A) polymerase (EC 2.7.7.19) / tRNA nucleotidyltransferase (EC 2.7.7.25)	Protein synthesis	Cytoplasmic	SPy0866	173	726	214	579	1.54	0.2055	0.4088	
M5005_Spy0674	SpM1_ChORF0867_s_at	-	ABC transporter ATP-binding protein uup	Membrane transport	Cytoplasmic Membrane	SPy0867	269	426	298	381	1.23	0.1782	0.3880	
M5005_Spy0676	SpM18_ChORF0930_s_at	-	Hypothetical protein	Unknown	Unknown	spyM18_0930	77	1370	49	1656	0.40	0.6993	0.6184	
M5005_Spy0676	SpM3_ChORF0589_s_at	-	Hypothetical protein	Unknown	Unknown	spyM3_0589	27	1873	55	1549	4.32	0.0309	0.2057	
M5005_Spy0677	SpM1_ChORF0870_s_at	*fms*	Peptide deformylase (EC 3.5.1.88)	Information processing	Cytoplasmic	SPy0870	70	1171	74	1335	1.12	0.1737	0.3845	
M5005_Spy0678	SpM1_ChORF0872_s_at	-	5'-nucleotidase (EC 3.1.3.5)	Unknown	Cell Wall	SPy0872	95	1158	91	1232	0.91	0.0703	0.2815	
M5005_Spy0679	SpM1_ChORF0873_s_at	-	GTP pyrophosphokinase (EC 2.7.6.5)	Stress adaptation	Cytoplasmic	SPy0873	127	942	119	1012	0.89	0.0495	0.2521	
M5005_Spy0680	SpM1_ChORF0874_s_at	*sptR*	Two-component response regulator	Signal transduction	Cytoplasmic	SPy0874	164	706	166	679	1.02	0.8248	0.6526	

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M5005_Spy0681	SpM1_ChORF0875_s_at	*sptS*	Two-component system histidine kinase	Signal transduction	Cytoplasmic Membrane	SPy0875	218	590	232	488	1.13	0.6372	0.6022	
M5005_Spy0682	SpM1_ChORF0876_s_at	*mvaK1*	Mevalonate kinase (EC 2.7.1.36)	Lipid metabolism	Cytoplasmic Membrane	SPy0876	114	972	129	851	1.28	0.5109	0.5539	
M5005_Spy0683	SpM1_ChORF0877_s_at	*mvaD*	Diphosphomevalonate decarboxylase (EC 4.1.1.33)	Lipid metabolism	Unknown	SPy0877	140	874	136	844	0.94	0.1620	0.3727	
M5005_Spy0684	SpM1_ChORF0878_s_at	*mvaK2*	Phosphomevalonate kinase (EC 2.7.4.2)	Lipid metabolism	Unknown	SPy0878	116	896	112	928	0.93	0.0745	0.2853	
M5005_Spy0685	SpM1_ChORF0879_s_at	-	Isopentenyl-diphosphate delta-isomerase (EC 5.3.3.2)	Lipid metabolism	Cytoplasmic	SPy0879	280	349	340	344	1.48	0.0213	0.1827	
M5005_Spy0687	SpM1_ChORF0880_s_at	*mvaS.1*	Hydroxymethylglutaryl-CoA synthase (EC 4.1.3.5)	Lipid metabolism	Unknown	SPy0880	128	915	195	659	2.32	0.8963	0.6690	
M5005_Spy0687	SpM1_ChORF0881_s_at	*mvaS.1*	Hydroxymethylglutaryl-CoA synthase (EC 4.1.3.5)	Lipid metabolism	Unknown	SPy0881	64	1549	70	1439	1.23	0.8774	0.6641	
M5005_Spy0688	SpM1_ChORF0882_s_at	*thyA*	Thymidylate synthase (EC 2.1.1.45)	Unknown	Cytoplasmic	SPy0882	128	817	147	794	1.32	0.0904	0.3002	
M5005_Spy0689	SpM1_ChORF0883_s_at	*dyr*	Dihydrofolate reductase (EC 1.5.1.3)	Coenzyme and cofactor metabolism	Cytoplasmic	SPy0883	66	1206	85	1268	1.69	0.8570	0.6602	
M5005_Spy0690	SpM1_ChORF0884_s_at	-	Hypothetical membrane associated protein	Unknown	Unknown	SPy0884	91	1225	88	1183	0.93	0.0659	0.2756	
M5005_Spy0690	SpM18_ChORF0945_s_at	-	Hypothetical membrane associated protein	Unknown	Unknown	spyM18_0945	70	1300	64	1350	0.85	0.1747	0.3853	
M5005_Spy0691	SpM1_ChORF0885_s_at	*clpX*	ATP-dependent clp protease ATP-binding subunit clpX	Stress adaptation	Cytoplasmic	SPy0885	200	622	224	592	1.25	0.3122	0.4706	
M5005_Spy0692	SpM1_ChORF0886_s_at	-	GTP-binding protein	Unknown	Unknown	SPy0886	158	723	162	779	1.05	0.7357	0.6294	
M5005_Spy0693	SpM1_ChORF0887_s_at	-	Hypothetical protein	Unknown	Cytoplasmic	SPy0887	245	542	224	574	0.83	0.2638	0.4404	
M5005_Spy0694	SpM1_ChORF0888_s_at	*clpL*	ATP-dependent protease ATP-binding subunit clpL	Stress adaptation	Cytoplasmic	SPy0888	1304	32	674	136	0.27	8.0E-06	**0.0004**	**Significant**

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M5005_Spy0695	SpM1_ChORF0889_s_at	*rpiA*	Ribose 5-phosphate isomerase (EC 5.3.1.6)	Carbohydrate metabolism	Cytoplasmic	SPy0889	523	195	500	198	0.91	0.9199	0.6743	
M5005_Spy0696	SpM1_ChORF0890_s_at	*deoB*	Phosphopentomutase (EC 5.4.2.7)	Carbohydrate metabolism	Cytoplasmic	SPy0890	683	98	823	90	1.45	0.1838	0.3906	
M5005_Spy0697	SpM1_ChORF0891_s_at	*arsC*	Arsenate reductase family protein	Membrane transport	Cytoplasmic	SPy0891	371	262	380	271	1.05	0.8770	0.6641	
M5005_Spy0698	SpM1_ChORF0892_s_at	*punA*	Purine nucleoside phosphorylase (EC 2.4.2.1)	Nucleotide metabolism	Cytoplasmic	SPy0892	520	159	613	147	1.39	0.8161	0.6512	
M5005_Spy0699	SpM1_ChORF0894_s_at	*deoD2*	Purine nucleoside phosphorylase (EC 2.4.2.1)	Nucleotide metabolism	Cytoplasmic	SPy0894	671	96	711	106	1.12	0.9602	0.6844	
M5005_Spy0700	SpM1_ChORF0895_s_at	*cpsX*	Attenuator of transcription, LytR family regulator	Information processing	Cytoplasmic	SPy0895	289	327	273	460	0.89	0.3218	0.4755	
M5005_Spy0701	SpM1_ChORF0898_s_at	*cpsY*	Transcriptional regulators, LysR family	Information processing	Cytoplasmic	SPy0898	49	1711	73	1437	2.28	0.6961	0.6184	
M5005_Spy0702	SpM1_ChORF0899_s_at	-	Hypothetical protein	Unknown	Cytoplasmic	SPy0899	137	830	165	747	1.44	0.0239	0.1908	
M5005_Spy0703	SpM1_ChORF0900_s_at	*pyrF*	Orotidine 5'-phosphate decarboxylase (EC 4.1.1.23)	Nucleotide metabolism	Cytoplasmic	SPy0900	82	1291	45	1649	0.30	0.0501	0.2538	
M5005_Spy0704	SpM1_ChORF0901_s_at	*pyrE*	Orotate phosphoribosyltransferase (EC 2.4.2.10)	Nucleotide metabolism	Unknown	SPy0901	96	1148	108	1211	1.27	0.0051	0.0898	
M5005_Spy0705	SpM1_ChORF0902_s_at	*amiC*	Amidase family protein	Unknown	Unknown	SPy0902	80	1328	94	1266	1.38	0.3953	0.5080	
M5005_Spy0706	SpM1_ChORF0903_s_at	-	Cystine-binding protein	Membrane transport	Unknown	SPy0903	108	1090	105	1086	0.95	0.6196	0.5962	
M5005_Spy0707	SpM1_ChORF0904_s_at	-	Cystine transport system permease protein	Membrane transport	Cytoplasmic Membrane	SPy0904	44	1859	60	1459	1.82	0.2874	0.4544	
M5005_Spy0708	SpM1_ChORF0905_s_at	*ung*	Uracil-DNA glycosylase (EC 3.2.2.-)	Information processing	Cytoplasmic	SPy0905	94	1154	88	1173	0.87	0.6825	0.6146	
M5005_Spy0709	SpM1_ChORF0907_s_at	*pyrC*	Dihydroorotase (EC 3.5.2.3)	Nucleotide metabolism	Cytoplasmic	SPy0907	87	1182	96	1151	1.22	0.1018	0.3116	
M5005_Spy0710	SpM1_ChORF0908_s_at	-	Hypothetical membrane spanning protein	Unknown	Cytoplasmic Membrane	SPy0908	95	1142	119	946	1.57	0.4393	0.5231	

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M5005_Spy0711	SpM1_ChORF0909_s_at	*parE*	Topoisomerase IV subunit B (EC 5.99.1.-)	Information processing	Cytoplasmic	SPy0909	86	1299	108	1003	1.60	0.4950	0.5494	
M5005_Spy0712	SpM1_ChORF0910_s_at	*parC*	Topoisomerase IV subunit A (EC 5.99.1.-)	Information processing	Unknown	SPy0910	104	1208	116	1080	1.26	0.6228	0.5977	
M5005_Spy0712	SpM5_ChORF4P31a-8_s_at	*parC*	Topoisomerase IV subunit A (EC 5.99.1.-)	Information processing	Unknown		25	1687	37	1943	2.18	0.3625	0.4888	
M5005_Spy0713	SpM1_ChORF0911_s_at	*bcaT*	Branched-chain amino acid aminotransferase (EC 2.6.1.42)	Carbohydrate metabolism	Unknown	SPy0911	50	1594	50	1681	0.99	0.9139	0.6743	
M5005_Spy0714	SpM1_ChORF0912_s_at	-	Hypothetical cytosolic protein	Unknown	Cytoplasmic	SPy0912	53	1492	26	2112	0.25	0.3595	0.4888	
M5005_Spy0715	SpM1_ChORF0913_s_at	-	SSU ribosomal protein S1P	Protein synthesis	Cytoplasmic	SPy0913	871	73	932	54	1.14	0.4690	0.5376	
M5005_Spy0716	SpM1_ChORF0914_s_at	-	Hypothetical protein	Unknown	Cytoplasmic	SPy0914	117	838	120	845	1.06	0.9912	0.6918	
M5005_Spy0717	SpM1_ChORF0915_s_at	-	Rhodanese-related sulfurtransferases	Unknown	Cytoplasmic	SPy0915	222	499	179	682	0.65	0.0921	0.3002	
M5005_Spy0718	SpM1_ChORF0916_s_at	-	Hypothetical protein	Unknown	Cytoplasmic	SPy0916	113	1058	90	1250	0.63	0.9602	0.6844	
M5005_Spy0719	SpM1_ChORF0917_s_at	-	Glutathione S-transferase (EC 2.5.1.18)	Unknown	Cytoplasmic	SPy0917	51	1489	44	1620	0.75	0.5260	0.5624	
M5005_Spy0719	SpM5_ChORF4P31a-181_x_at	-	Glutathione S-transferase (EC 2.5.1.18)	Unknown	Cytoplasmic		41	2063	40	1688	0.95	0.2376	0.4248	
M5005_Spy0720	SpM1_ChORF0918_s_at	-	Putative exfoliative toxin	Virulence	Cytoplasmic Membrane	SPy0918	53	1430	86	1287	2.58	0.0678	0.2770	
M5005_Spy0720	SpM12_ChORF248-9_s_at	-	Putative exfoliative toxin	Virulence	Cytoplasmic Membrane		70	1385	76	1313	1.18	0.2416	0.4269	
M5005_Spy0721	SpM1_ChORF0919_at	-	Hypothetical protein	Unknown	Unknown	SPy0919	715	105	795	86	1.24	0.0989	0.3083	
M5005_Spy0722	SpM1_ChORF0921_s_at	*miaA*	tRNA delta(2)-isopentenylpyrophosphate transferase (EC 2.5.1.8)	Protein synthesis	Unknown (This protein may have multiple localization sites.)	SPy0921	59	1476	57	1386	0.92	0.4877	0.5445	
M5005_Spy0723	SpM1_ChORF0922_s_at	-	GTP-binding protein hflX	Information processing	Cytoplasmic	SPy0922	243	455	206	588	0.72	0.3269	0.4776	

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M5005_Spy0724	SpM1_ChORF0923_s_at	-	Cystathionine beta-lyase (EC 4.4.1.8) / Cystathionine gamma-lyase (EC 4.4.1.1)	Amino acid metabolism	Unknown	SPy0923	136	884	128	964	0.88	0.1989	0.4020	
M5005_Spy0725	SpM1_ChORF0924_s_at	*elaC*	Metal-dependent hydrolase (EC 3.-.-.-)	Unknown	Cytoplasmic	SPy0924	433	231	439	231	1.03	0.1930	0.3989	
M5005_Spy0726	SpM1_ChORF0925_s_at	-	Short chain dehydrogenase	Unknown	Cytoplasmic	SPy0925	121	952	128	997	1.12	0.0798	0.2939	
M5005_Spy0727	SpM1_ChORF0926_s_at	*recJ*	Single-stranded-DNA-specific exonuclease recJ (EC 3.1.-.-)	Information processing	Cytoplasmic	SPy0926	219	583	210	583	0.92	0.4613	0.5335	
M5005_Spy0728	SpM1_ChORF0927_s_at	*apt*	Adenine phosphoribosyltransferase (EC 2.4.2.7)	Cellular processing	Cytoplasmic	SPy0927	94	1280	88	1165	0.89	0.4469	0.5280	
M5005_Spy0729	SpM1_ChORF0928_s_at	*dnaD*	DNA replication protein dnaD	Information processing	Cytoplasmic	SPy0928	190	674	174	726	0.84	0.4759	0.5411	
M5005_Spy0730	SpM1_ChORF0929_s_at	*nth*	Endonuclease III (EC 4.2.99.18)	Information processing	Cytoplasmic	SPy0929	116	941	127	958	1.19	0.9206	0.6743	
M5005_Spy0732	SpM1_ChORF0930_s_at	-	NIF3-related protein	Information processing	Cytoplasmic	SPy0930	74	1263	67	1273	0.81	0.3282	0.4776	
M5005_Spy0732	SpM1_ChORF0931_s_at	-	NIF3-related protein	Information processing	Cytoplasmic	SPy0931	95	1252	100	1130	1.09	0.7657	0.6382	
M5005_Spy0733	SpM1_ChORF0932_s_at	-	Glycine/D-amino acid oxidases family	Carbohydrate metabolism	Unknown	SPy0932	77	1352	72	1249	0.88	0.0440	0.2408	
M5005_Spy0734	SpM1_ChORF0933_s_at	*cpsFO*	Glucose-1-phosphate thymidylyltransferase (EC 2.7.7.24)	Carbohydrate metabolism	Cytoplasmic	SPy0933	254	478	264	450	1.08	0.2541	0.4334	
M5005_Spy0735	SpM1_ChORF0935_s_at	*cpsFP*	dTDP-4-dehydrorhamnose 3,5-epimerase (EC 5.1.3.13)	Carbohydrate metabolism	Unknown	SPy0935	173	715	203	618	1.38	0.0686	0.2779	
M5005_Spy0736	SpM1_ChORF0936_s_at	*cpsFQ*	dTDP-glucose 4,6-dehydratase (EC 4.2.1.46)	Carbohydrate metabolism	Cytoplasmic	SPy0936	124	857	151	873	1.49	0.8837	0.6655	
M5005_Spy0737	SpM1_ChORF1010_s_at	*mutX*	Mutator mutT protein (7,8-dihydro-8-oxoguanine-triphosphatase) (EC 3.6.1.-)	Information processing	Cytoplasmic	SPy1010	83	1273	85	1255	1.04	0.1595	0.3721	

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M5005_Spy0738	SpM1_ChORF1011_s_at	-	Hypothetical membrane spanning protein	Unknown	Cytoplasmic Membrane	SPy1011	69	1235	101	1052	2.18	0.0275	0.1982	
M5005_Spy0739	SpM1_ChORF1012_s_at	-	Tetratricopeptide repeat family protein	Unknown	Cytoplasmic	SPy1012	85	1231	154	923	3.31	0.3012	0.4632	
M5005_Spy0740	SpM1_ChORF1013_s_at	*fbp*	Fibronectin-binding protein / Fibrinogen-binding protein	Virulence	Cytoplasmic	SPy1013	101	1096	111	1042	1.21	0.3628	0.4888	
M5005_Spy0743	SpM1_ChORF1016_s_at	-	ABC transporter substrate-binding protein	Membrane transport	Unknown	SPy1016	31	1878	24	2094	0.59	0.5007	0.5512	
M5005_Spy0744	SpM1_ChORF1017_x_at	-	Hypothetical protein	Unknown	Unknown	SPy1017	38	1993	31	1936	0.68	0.0344	0.2168	
M5005_Spy0745	SpM1_ChORF1018_s_at	-	ABC transporter permease protein	Membrane transport	Cytoplasmic Membrane	SPy1018	28	1971	34	1886	1.51	0.2313	0.4227	
M5005_Spy0746	SpM1_ChORF1019_s_at	-	ABC transporter ATP-binding protein	Membrane transport	Cytoplasmic Membrane	SPy1019	21	2250	19	2355	0.79	0.5902	0.5874	
M5005_Spy0747	SpM1_ChORF1020_s_at	-	Zn-dependent hydrolase (EC 3.-.-.-)	Unknown	Cytoplasmic	SPy1020	514	197	456	209	0.79	0.6542	0.6061	
M5005_Spy0748	SpM1_ChORF1022_s_at	*estA*	Acetyl esterase (EC 3.1.1.-)	Unknown	Cytoplasmic	SPy1022	183	694	163	714	0.79	0.0510	0.2541	
M5005_Spy0749	SpM1_ChORF1024_s_at	-	Hypothetical protein	Unknown	Cytoplasmic Membrane	SPy1024	70	1467	50	1494	0.51	0.3182	0.4745	
M5005_Spy0750	SpM1_ChORF1025_at	-	ABC transporter ATP-binding protein	Membrane transport	Cytoplasmic Membrane	SPy1025	134	924	156	877	1.35	0.6241	0.5981	
M5005_Spy0751	SpM1_ChORF1026_s_at	*acoA*	Pyruvate dehydrogenase E1 component alpha subunit (EC 1.2.4.1)	Carbohydrate metabolism	Unknown	SPy1026	803	109	743	88	0.86	0.5486	0.5698	
M5005_Spy0752	SpM1_ChORF1028_s_at	*acoB*	Pyruvate dehydrogenase E1 component beta subunit (EC 1.2.4.1)	Carbohydrate metabolism	Cytoplasmic Membrane	SPy1028	923	56	975	80	1.12	0.3071	0.4687	
M5005_Spy0753	SpM1_ChORF1029_s_at	*acoC*	Dihydrolipoamide acetyltransferase component of pyruvate dehydrogenase complex (EC 2.3.1.12)	Information processing	Cytoplasmic	SPy1029	796	70	980	77	1.52	0.6946	0.6184	

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M5005_Spy0753	SpM12_ChORF281-7_s_at	*acoC*	Dihydrolipoamide acetyltransferase component of pyruvate dehydrogenase complex (EC 2.3.1.12)	Information processing	Cytoplasmic		27	2225	27	2070	1.00	0.0416	0.2332	
M5005_Spy0754	SpM5_ChORF270b-343_at	-	Hypothetical protein	Unknown	Unknown		19	2419	14	2488	0.57	0.9487	0.6811	
M5005_Spy0755	SpM1_ChORF1031_s_at	*acoL, pdhD*	Dihydrolipoamide dehydrogenase (EC 1.8.1.4)	Carbohydrate metabolism	Cytoplasmic	SPy1031	522	163	493	232	0.89	0.4518	0.5301	
M5005_Spy0757	SpM1_ChORF1032_s_at	*hylA*	Hyaluronate lyase precursor (EC 4.2.2.1)	Carbohydrate metabolism	Extracellular	SPy1032	39	1777	54	1672	1.90	0.5700	0.5800	
M5005_Spy0758	SpM1_ChORF1033_s_at	*lplB*	Lipoate-protein ligase A (EC 6.-.-.-)	Coenzyme and cofactor metabolism	Cytoplasmic	SPy1033	121	961	117	899	0.94	0.3319	0.4779	
M5005_Spy0759	SpM1_ChORF1034_s_at	-	Hypothetical membrane associated protein	Unknown	Unknown	SPy1034	37	1965	33	1765	0.80	0.7175	0.6236	
M5005_Spy0760	SpM12_ChORF281-1_s_at	-	UDP-N-acetylmuramoylalanyl-D-glutamate--2,6-diaminopimelate ligase (EC 6.3.2.13)	Cell wall metabolism	Unknown		52	1528	52	1491	0.98	0.2437	0.4278	
M5005_Spy0761	SpM1_ChORF1036_s_at	-	Hypothetical membrane spanning protein	Unknown	Cytoplasmic Membrane	SPy1036	84	1139	77	1346	0.84	0.1701	0.3817	
M5005_Spy0762	SpM1_ChORF1037_s_at	-	Hypothetical membrane associated protein	Unknown	Unknown	SPy1037	112	1077	97	1204	0.76	0.7869	0.6466	
M5005_Spy0763	SpM1_ChORF1038_s_at	*femD*	Phosphoglucosamine mutase (EC 5.4.2.10)	Cell wall metabolism	Cytoplasmic	SPy1038	172	665	161	732	0.88	0.0112	0.1377	
M5005_Spy0764	SpM1_ChORF1039_s_at	-	Hypothetical protein	Unknown	Cytoplasmic	SPy1039	41	1865	16	2495	0.16	0.0253	0.1923	
M5005_Spy0765	SpM1_ChORF1040_s_at	*hemN, hemC*	Coproporphyrinogen oxidase, anaerobic (EC 1.-.-.-)	Coenzyme and cofactor metabolism	Cytoplasmic	SPy1040	39	1791	65	1458	2.74	0.3569	0.4883	
M5005_Spy0766	SpM1_ChORF1042_s_at	-	ACYL-ACYL CARRIER PROTEIN THIOESTERASE (EC 3.1.2.14)	Cell wall metabolism	Cytoplasmic	SPy1042	105	810	140	773	1.80	0.8792	0.6643	

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M5005_Spy0767	SpM1_ChORF1043_s_at	-	4-nitrophenylphosphatase (EC 3.1.3.41)	Unknown	Unknown	SPy1043	129	847	115	897	0.79	0.1067	0.3149	
M5005_Spy0768	SpM1_ChORF1044_s_at	-	Hypothetical membrane spanning protein	Unknown	Cytoplasmic Membrane	SPy1044	65	1427	72	1318	1.24	0.2035	0.4066	
M5005_Spy0769	SpM1_ChORF1046_s_at	-	Hypothetical cytosolic protein	Unknown	Cytoplasmic	SPy1046	99	1188	101	1132	1.04	0.1546	0.3672	
M5005_Spy0770	SpM1_ChORF1047_s_at	-	Hypothetical cytosolic protein	Unknown	Unknown	SPy1047	21	2401	15	2406	0.50	0.8428	0.6565	
M5005_Spy0771	SpM1_ChORF1048_s_at	-	Hypothetical cytosolic protein	Unknown	Unknown	SPy1048	142	875	189	693	1.77	0.2033	0.4066	
M5005_Spy0772	SpM1_ChORF1049_s_at	-	Hypothetical protein	Unknown	Cytoplasmic	SPy1049	42	1842	35	1803	0.71	0.1612	0.3722	
M5005_Spy0776	SpM1_ChORF1053_s_at	*lepA*	GTP-binding protein lepA	Information processing	Cytoplasmic	SPy1053	315	311	336	326	1.14	0.5194	0.5590	
M5005_Spy0777	SpM1_ChORF1054_at		Collagen-like surface protein	Virulence	Cell Wall	SPy1054	104	1056	138	737	1.75	0.0231	0.1901	
M5005_Spy0778	SpM1_ChORF1055_s_at	*csrA*	Peptide methionine sulfoxide reductase msrB (EC 1.8.4.6)	Unknown	Unknown	SPy1055	122	918	128	854	1.10	0.2825	0.4537	
M5005_Spy0779	SpM1_ChORF1056_s_at	-	Hypothetical membrane spanning protein	Unknown	Cytoplasmic Membrane	SPy1056	73	1293	38	1691	0.27	0.3043	0.4656	
M5005_Spy0780	SpM1_ChORF1057_s_at	-	PTS system, mannose/fructose family IIA component	Unknown	Unknown	SPy1057	327	291	286	393	0.76	0.4422	0.5248	
M5005_Spy0781	SpM1_ChORF1058_s_at	*ptsB*	PTS system, mannose/fructose family IIB component	Carbohydrate metabolism	Cytoplasmic	SPy1058	796	106	630	142	0.63	0.4384	0.5231	
M5005_Spy0782	SpM1_ChORF1059_s_at	*ptsC*	PTS system, mannose/fructose family IIC component	Carbohydrate metabolism	Cytoplasmic Membrane	SPy1059	392	309	300	363	0.58	0.0818	0.2979	
M5005_Spy0783	SpM1_ChORF1060_s_at	*ptsD*	PTS system, mannose/fructose family IID component	Carbohydrate metabolism	Cytoplasmic Membrane	SPy1060	475	248	398	257	0.70	0.2167	0.4151	
M5005_Spy0784	SpM12_ChORF284-30_s_at	*yesM*	Two-component sensor kinase yesM	Signal transduction	Cytoplasmic Membrane		52	1521	64	1422	1.47	0.6962	0.6184	
M5005_Spy0785	SpM1_ChORF1062_s_at	*yesN*	Two-component response regulator yesN	Signal transduction	Cytoplasmic	SPy1062	107	1025	86	1271	0.64	0.9880	0.6915	

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M5005_Spy0786	SpM1_ChORF1063_at	-	Iron(III)-binding protein	Membrane transport	Cytoplasmic Membrane	SPy1063	107	1042	104	1147	0.95	0.1624	0.3730	
M5005_Spy0787	SpM1_ChORF1064_at	-	Hypothetical protein	Unknown	Cytoplasmic	SPy1064	31	2053	24	2114	0.59	0.5188	0.5590	
M5005_Spy0788	SpM1_ChORF1065_at	-	Acetyltransferase (EC 2.3.1.-)	Cellular processing	Cytoplasmic	SPy1065	107	1129	75	1270	0.49	0.8225	0.6525	
M5005_Spy0789	SpM1_ChORF1066_at	-	Hydrolase (HAD superfamily)	Unknown	Unknown	SPy1066	90	1301	103	1139	1.32	0.6465	0.6041	
M5005_Spy0790	SpM1_ChORF1067_s_at	*gabD*	Succinate-semialdehyde dehydrogenase [NADP+] (EC 1.2.1.16)	Carbohydrate metabolism	Cytoplasmic	SPy1067	233	485	227	551	0.95	0.8761	0.6641	
M5005_Spy0791	SpM1_ChORF1068_s_at	*uvrC*	Excinuclease ABC subunit C	Information processing	Cytoplasmic	SPy1068	522	176	478	203	0.84	0.1195	0.3266	
M5005_Spy0791	SpM5_ChORF270b-333_s_at	*uvrC*	Excinuclease ABC subunit C	Information processing	Cytoplasmic		52	1643	57	1416	1.23	0.0043	0.0826	
M5005_Spy0792	SpM1_ChORF1069_s_at	-	NAD(P)H-dependent quinone reductase (EC 1.-.-.-)	Carbohydrate metabolism	Cytoplasmic	SPy1069	420	217	412	234	0.96	0.7572	0.6368	
M5005_Spy0793	SpM1_ChORF1070_s_at	-	Xaa-His dipeptidase (EC 3.4.13.3)	Amino acid metabolism	Cytoplasmic	SPy1070	547	198	527	166	0.93	0.6974	0.6184	
M5005_Spy0794	SpM1_ChORF1071_s_at	*thdF*	tRNA (5-carboxymethylaminomethyl-2-thiouridylate) synthase	Protein synthesis	Cytoplasmic	SPy1071	118	968	89	1214	0.57	0.2761	0.4473	
M5005_Spy0795	SpM1_ChORF1072_s_at	*rplJ*	LSU ribosomal protein L10P	Protein synthesis	Cytoplasmic	SPy1072	198	580	218	524	1.21	0.4040	0.5120	
M5005_Spy0796	SpM1_ChORF1073_s_at	*rplL*	LSU ribosomal protein L12P (L7/L12)	Protein synthesis	Cytoplasmic	SPy1073	112	966	119	953	1.12	0.3841	0.4999	
M5005_Spy0798	SpM1_ChORF1075_at	-	IFN-response binding factor 1	Unknown	Cytoplasmic	SPy1075	38	1793	26	2027	0.46	0.3098	0.4702	
M5005_Spy0800	SpM1_ChORF1077_s_at	-	DNA-cytosine methyltransferase (EC 2.1.1.73)	Cellular processing	Cytoplasmic	SPy1077	28	2109	21	2125	0.58	0.0829	0.2979	
M5005_Spy0801	M12_1863_s_at	-	Relaxase	Information processing	Extracellular		15	2477	14	2455	0.83	0.2538	0.4334	
M5005_Spy0802	M12_1862_s_at	-	Relaxase	Information processing	Cytoplasmic		22	2381	19	2309	0.74	0.6194	0.5962	
M5005_Spy0803	SpM1_ChORF1080_s_at	*srtI*	Protein involved in lantibiotic (srt) production	Virulence	Cytoplasmic	SPy1080	35	1807	25	2206	0.51	0.0907	0.3002	

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M5005_Spy0803	SpM12_ChORF284-43_s_at	*srtI*	Protein involved in lantibiotic (srt) production	Virulence	Cytoplasmic		71	1387	48	1638	0.45	0.5245	0.5615	
M5005_Spy0804	SpM1_ChORF1081_at	*srtR*	Nisin biosynthesis two-component response regulator nisR	Signal transduction	Cytoplasmic	SPy1081	12	2610	27	2075	4.73	0.1108	0.3167	
M5005_Spy0805	SpM1_ChORF1082_at	*srtK*	Two-component nisin biosynthesis histidine sensor kinase nisK	Signal transduction	Cytoplasmic Membrane	SPy1082	67	1333	96	1104	2.06	0.2440	0.4278	
M5005_Spy0806	SpM1_ChORF1083_at	*srtA*	Lantibiotic srtA precursor	Virulence	Extracellular	SPy1083	70	1382	50	1611	0.52	0.6531	0.6061	
M5005_Spy0807	SpM1_ChORF1084_at	*srtT*	ABC transporter (ATP binding)-lantibiotic associated	Membrane transport	Cytoplasmic Membrane	SPy1084	33	1940	39	1821	1.45	0.7110	0.6205	
M5005_Spy0808	SpM1_ChORF1085_at	*srtF*	Lantibiotic transport ATP-binding protein	Membrane transport	Cytoplasmic Membrane	SPy1085	39	1792	62	1538	2.51	0.9389	0.6781	
M5005_Spy0809	SpM1_ChORF1086_s_at	*srtE*	Lantibiotic transport permease protein	Membrane transport	Cytoplasmic Membrane	SPy1086	26	2058	32	1945	1.55	0.0885	0.3002	
M5005_Spy0810	SpM1_ChORF1087_s_at	*srtG*	Lantibiotic transport permease protein	Membrane transport	Cytoplasmic Membrane	SPy1087	33	1990	31	2001	0.86	0.0879	0.3002	
M5005_Spy0811	SpM1_ChORF1088_at	-	Transcriptional regulator, Cro/CI family	Phage	Unknown	SPy1088	18	2267	31	1958	2.77	0.5947	0.5886	
M5005_Spy0812	SpM12_ChORF267-18_at	-	Hypothetical protein	Unknown	Unknown		34	1916	57	1490	2.88	0.0623	0.2717	
M5005_Spy0814	M12_0090_s_at	-	DNA integration/recombination /invertion protein	Information processing	Unknown		103	1098	89	1160	0.75	0.8420	0.6564	
M5005_Spy0815	M12_0089_s_at	-	DNA integration/recombination /invertion protein	Information processing	Unknown		45	1673	65	1403	2.12	0.2229	0.4192	
M5005_Spy0816	SpM12_ChORF267-3_s_at	-	DNA integration/recombination /invertion protein	Information processing	Cytoplasmic		109	1075	117	994	1.16	0.2061	0.4088	
M5005_Spy0817	SpM1_ChORF1093_s_at	*dacA*	D-alanyl-D-alanine carboxypeptidase (EC 3.4.16.4)	Cell wall metabolism	Cytoplasmic	SPy1093	51	1451	33	1789	0.43	0.9575	0.6843	
M5005_Spy0818	SpM1_ChORF1094_s_at	-	Polysaccharide deacetylase	Carbohydrate metabolism	Unknown	SPy1094	167	690	151	832	0.82	0.1937	0.3989	
M5005_Spy0819	SpM3_ChORF0757_s_at	-	Hypothetical protein	Unknown	Unknown	spyM3_0757	28	2081	31	1834	1.23	0.2354	0.4227	

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M5005_Spy0820	SpM1_ChORF1096_s_at	*folC.1*	Folylpolyglutamate synthase (EC 6.3.2.17) / dihydrofolate synthase (EC 6.3.2.12)	Coenzyme and cofactor metabolism	Cytoplasmic	SPy1096	311	344	330	327	1.13	0.1022	0.3116	
M5005_Spy0821	SpM1_ChORF1097_s_at	*folE*	GTP cyclohydrolase I (EC 3.5.4.16)	Coenzyme and cofactor metabolism	Cytoplasmic	SPy1097	317	384	329	332	1.08	0.2720	0.4449	
M5005_Spy0822	SpM1_ChORF1098_s_at	*folP*	Dihydropteroate synthase (EC 2.5.1.15)	Coenzyme and cofactor metabolism	Unknown	SPy1098	441	234	456	218	1.07	0.5098	0.5538	
M5005_Spy0823	SpM1_ChORF1099_s_at	*folQ*	Dihydroneopterin aldolase (EC 4.1.2.25)	Coenzyme and cofactor metabolism	Cytoplasmic	SPy1099	163	676	205	602	1.58	0.0523	0.2541	
M5005_Spy0824	SpM1_ChORF1100_s_at	*folK*	2-amino-4-hydroxy-6-hydroxymethyldihydropteridine pyrophosphokinase (EC 2.7.6.3)	Coenzyme and cofactor metabolism	Cytoplasmic	SPy1100	185	660	194	637	1.10	0.8900	0.6676	
M5005_Spy0825	SpM1_ChORF1101_s_at	*murB*	UDP-N-acetylenolpyruvoylglucosamine reductase (EC 1.1.1.158)	Carbohydrate metabolism	Cytoplasmic	SPy1101	73	1277	79	1260	1.20	0.3742	0.4941	
M5005_Spy0826	SpM1_ChORF1102_s_at	*potA*	Spermidine/putrescine transport ATP-binding protein potA	Membrane transport	Cytoplasmic Membrane	SPy1102	123	868	160	883	1.68	0.0142	0.1512	
M5005_Spy0827	SpM1_ChORF1103_s_at	*potB*	Spermidine/putrescine transport system permease protein potB	Membrane transport	Cytoplasmic Membrane	SPy1103	90	1046	76	1246	0.71	0.4189	0.5169	
M5005_Spy0828	SpM1_ChORF1104_s_at	*potC*	Spermidine/putrescine transport system permease protein potC	Membrane transport	Cytoplasmic Membrane	SPy1104	50	1525	63	1446	1.56	0.2340	0.4227	
M5005_Spy0828	SpM5_ChORF270b-433_s_at	*potC*	Spermidine/putrescine transport system permease protein potC	Membrane transport	Cytoplasmic Membrane		117	1005	121	984	1.08	0.1479	0.3590	
M5005_Spy0830	SpM1_ChORF1106_s_at	-	Transcriptional regulatory protein dpiA	Information processing	Cytoplasmic	SPy1106	55	1503	87	1106	2.50	0.0138	0.1497	
M5005_Spy0830	SpM1_ChORF1107_s_at	-	Transcriptional regulatory protein dpiA	Information processing	Cytoplasmic	SPy1107	80	1344	121	987	2.31	0.2267	0.4208	
M5005_Spy0832	SpM1_ChORF1109_s_at	*malP*	Malate-sodium symport	Membrane transport	Cytoplasmic Membrane	SPy1109	199	662	436	233	4.80	2.3E-05	**0.0010**	**Significant**

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M5005_Spy0833	SpM1_ChORF1110_s_at	-	NAD-dependent malic enzyme (EC 1.1.1.38)	Carbohydrate metabolism	Cytoplasmic Membrane	SPy1110	293	365	535	168	3.32	0.0025	0.0539	
M5005_Spy0834	SpM1_ChORF1111_s_at	-	Zn-dependent alcohol dehydrogenases and related dehydrogenases	Unknown	Cytoplasmic	SPy1111	51	1505	66	1426	1.66	0.3427	0.4819	
M5005_Spy0836	SpM1_ChORF1113_s_at	-	Class B acid phosphatase (EC 3.1.3.2)	Cellular processing	Cytoplasmic	SPy1113	237	435	299	384	1.60	0.1799	0.3887	
M5005_Spy0837	SpM1_ChORF1114_s_at	-	Chloride channel protein	Membrane transport	Cytoplasmic Membrane	SPy1114	91	1121	121	1088	1.77	0.3048	0.4656	
M5005_Spy0838	SpM1_ChORF1115_s_at	-	Lipase/Acylhydrolase family protein	Unknown	Cytoplasmic	SPy1115	98	1069	77	1326	0.62	0.5326	0.5659	
M5005_Spy0839	SpM18_ChORF1077_s_at	-	Hypothetical membrane spanning protein	Unknown	Cytoplasmic Membrane	spyM18_1077	43	1778	34	1991	0.63	0.8864	0.6665	
M5005_Spy0840	SpM1_ChORF1118_s_at	*radC*	DNA repair protein radC	Information processing	Cytoplasmic	SPy1118	29	2204	30	2071	1.04	0.8094	0.6512	
M5005_Spy0841	SpM1_ChORF1119_s_at	-	Glutamine amidotransferase, class I	Unknown	Cytoplasmic	SPy1119	84	1228	101	1157	1.46	0.2824	0.4537	
M5005_Spy0842	SpM1_ChORF1120_s_at	-	Redox-sensitive transcriptional regulator Rex	Unknown	Cytoplasmic	SPy1120	182	635	197	598	1.18	0.0413	0.2330	
M5005_Spy0844	SpM1_ChORF1121_s_at	*nifS, yrvO*	Cysteine desulfhydrase (EC 4.4.1.-) / Selenocysteine lyase (EC 4.4.1.16)	Coenzyme and cofactor metabolism	Cytoplasmic	SPy1121	61	1518	67	1327	1.23	0.3411	0.4806	
M5005_Spy0844	SpM1_ChORF1122_s_at	*nifS, yrvO*	Cysteine desulfhydrase (EC 4.4.1.-) / Selenocysteine lyase (EC 4.4.1.16)	Coenzyme and cofactor metabolism	Cytoplasmic	SPy1122	497	201	454	184	0.83	0.9374	0.6775	
M5005_Spy0844	SpM1_ChORF1123_s_at	*nifS, yrvO*	Cysteine desulfhydrase (EC 4.4.1.-) / Selenocysteine lyase (EC 4.4.1.16)	Coenzyme and cofactor metabolism	Cytoplasmic	SPy1123	257	401	269	446	1.10	0.9214	0.6743	
M5005_Spy0846	SpM1_ChORF1124_s_at	-	Putative adenylate cyclase family	Unknown	Cytoplasmic	SPy1124	27	2118	24	1965	0.78	0.1887	0.3978	
M5005_Spy0847	SpM1_ChORF1125_s_at	-	GTP pyrophosphokinase (EC 2.7.6.5)	Stress adaptation	Cytoplasmic	SPy1125	166	638	139	925	0.70	0.1472	0.3578	

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M5005_Spy0848	SpM1_ChORF1126_s_at	-	ATP-NAD kinase (EC 2.7.1.23)	Cellular processing	Cytoplasmic	SPy1126	193	574	196	660	1.03	0.2417	0.4269	
M5005_Spy0849	SpM1_ChORF1127_s_at	-	Ribosomal large subunit pseudouridine synthase D (EC 4.2.1.70)	Protein synthesis	Cytoplasmic	SPy1127	80	1365	80	1291	1.01	0.0118	0.1377	
M5005_Spy0850	SpM1_ChORF1128_s_at	*pta*	Putative phosphotransacetylase	Cellular processing	Cytoplasmic	SPy1128	691	102	581	156	0.71	0.2316	0.4227	
M5005_Spy0852	SpM3_ChORF0788_s_at	-	Short chain dehydrogenase	Unknown	Cytoplasmic	spyM3_0788	176	626	148	818	0.71	0.0184	0.1707	
M5005_Spy0854	SpM1_ChORF1131_s_at	-	Na+ driven multidrug efflux pump	Membrane transport	Unknown	SPy1131	83	1260	84	1196	1.03	0.0568	0.2634	
M5005_Spy0855	SpM1_ChORF1133_s_at	*proV*	Glycine betaine transport ATP-binding protein	Membrane transport	Cytoplasmic Membrane	SPy1133	66	1322	121	968	3.40	0.3910	0.5061	
M5005_Spy0855	SpM1_ChORF1134_s_at	*proV*	Glycine betaine transport ATP-binding protein	Membrane transport	Cytoplasmic Membrane	SPy1134	230	439	252	422	1.20	0.5907	0.5874	
M5005_Spy0857	SpM1_ChORF1135_s_at	*guaC*	GMP reductase (EC 1.7.1.7)	Unknown	Cytoplasmic	SPy1135	110	951	112	1046	1.04	0.2216	0.4184	
M5005_Spy0858	SpM1_ChORF1136_s_at	*xpt*	Xanthine phosphoribosyltransferase (EC 2.4.2.-)	Unknown	Cytoplasmic	SPy1136	60	1557	69	1374	1.32	0.6100	0.5932	
M5005_Spy0858	SpM12_ChORF256-17_at	*xpt*	Xanthine phosphoribosyltransferase (EC 2.4.2.-)	Unknown	Cytoplasmic		13	2384	8	2605	0.40	0.0982	0.3078	
M5005_Spy0859	SpM1_ChORF1137_s_at	-	Xanthine permease	Membrane transport	Cytoplasmic Membrane	SPy1137	29	2066	28	2186	0.93	0.9131	0.6743	
M5005_Spy0860	SpM1_ChORF1138_s_at	-	Thiamine biosynthesis lipoprotein apbE	Unknown	Cytoplasmic	SPy1138	63	1270	60	1448	0.89	0.3282	0.4776	
M5005_Spy0861	SpM1_ChORF1139_at	-	4-oxalocrotonate tautomerase (EC 5.3.2.-)	Unknown	Cytoplasmic	SPy1139	60	1616	88	1163	2.13	0.5078	0.5532	
M5005_Spy0862	SpM1_ChORF1140_s_at	*tdk2*	Thymidine kinase (EC 2.7.1.21)	Unknown	Cytoplasmic	SPy1140	148	731	133	917	0.80	0.0048	0.0870	
M5005_Spy0863	SpM1_ChORF1141_s_at	*prfA*	Bacterial Peptide Chain Release Factor 1 (RF-1)	Cellular processing	Cytoplasmic	SPy1141	105	977	118	1019	1.28	0.2548	0.4337	

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M5005_Spy0864	SpM1_ChORF1142_s_at	*hemK*	Peptide release factor-glutamine N5-methyltransferase (EC 2.1.1.-)	Information processing	Cytoplasmic	SPy1142	127	916	120	936	0.89	0.2964	0.4589	
M5005_Spy0865	SpM1_ChORF1143_s_at	-	SUA5 protein	Information processing	Unknown	SPy1143	188	667	162	743	0.75	0.1955	0.3995	
M5005_Spy0866	SpM1_ChORF1144_s_at	-	Phosphinothricin N-acetyltransferase (EC 2.3.1.-)	Unknown	Cytoplasmic	SPy1144	128	1106	97	1134	0.58	0.8767	0.6641	
M5005_Spy0867	SpM1_ChORF1145_s_at	*glyA*	Serine hydroxymethyltransferase (EC 2.1.2.1)	Cellular processing	Cytoplasmic	SPy1145	295	328	298	456	1.02	0.1053	0.3149	
M5005_Spy0868	SpM1_ChORF1146_s_at	-	Hypothetical protein	Unknown	Unknown	SPy1146	235	475	236	512	1.01	0.5438	0.5695	
M5005_Spy0869	SpM1_ChORF1147_s_at	-	Antigen	Unknown	Unknown	SPy1147	204	558	215	550	1.11	0.2298	0.4227	
M5005_Spy0870	SpM1_ChORF1148_s_at	-	Multidrug resistance ABC transporter ATP-binding and permease protein	Membrane transport	Cytoplasmic Membrane	SPy1148	261	421	262	468	1.01	0.6597	0.6081	
M5005_Spy0871	SpM1_ChORF1149_s_at	-	Multidrug resistance ABC transporter ATP-binding and permease protein	Membrane transport	Cytoplasmic Membrane	SPy1149	223	566	203	656	0.83	0.5031	0.5512	
M5005_Spy0872	SpM1_ChORF1150_s_at	*nox*	NADH oxidase H2O-forming (EC 1.6.-.-)	Stress adaptation	Cytoplasmic	SPy1150	644	129	694	109	1.16	0.7552	0.6366	
M5005_Spy0873	SpM1_ChORF1151_s_at	*ldh*	L-lactate dehydrogenase (EC 1.1.1.27)	Carbohydrate metabolism	Cytoplasmic	SPy1151	214	552	230	513	1.15	0.2873	0.4544	
M5005_Spy0874	SpM1_ChORF1152_s_at	*gyrA*	DNA gyrase subunit A (EC 5.99.1.3)	Information processing	Cytoplasmic	SPy1152	906	74	861	78	0.90	0.5899	0.5874	
M5005_Spy0875	SpM1_ChORF1154_s_at	*srtA*	Sortase	Cell wall metabolism	Unknown	SPy1154	618	131	605	178	0.96	0.8349	0.6555	
M5005_Spy0876	SpM1_ChORF1155_s_at	-	Lactoylglutathione lyase (EC 4.4.1.5)	Carbohydrate metabolism	Cytoplasmic	SPy1155	74	1290	64	1435	0.75	0.1139	0.3217	
M5005_Spy0877	SpM1_ChORF1156_s_at	-	Hypothetical protein	Unknown	Extracellular	SPy1156	1116	40	687	130	0.38	0.0096	0.1231	
M5005_Spy0878	SpM1_ChORF1157_s_at	-	Hypothetical protein	Unknown	Unknown	SPy1157	5494	6	3226	16	0.34	0.0834	0.2979	
M5005_Spy0879	SpM1_ChORF1158_s_at	-	Hypothetical protein	Unknown	Unknown	SPy1158	450	237	311	371	0.48	0.9370	0.6775	

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M5005_Spy0881	SpM1_ChORF1159_s_at	-	Hypothetical cytosolic protein	Virulence	Unknown	SPy1159	307	331	180	622	0.34	0.5739	0.5807	
M5005_Spy0881	SpM1_ChORF1160_s_at	-	Hypothetical cytosolic protein	Unknown	Unknown	SPy1160	109	907	84	1247	0.59	0.1091	0.3154	
M5005_Spy0882	SpM1_ChORF1161_at	-	GTP-binding protein	Unknown	Cytoplasmic	SPy1161	40	1852	45	1636	1.27	0.0341	0.2166	
M5005_Spy0882	SpM1_ChORF1161_s_at	-	GTP-binding protein	Unknown	Cytoplasmic	SPy1161	39	1519	29	1893	0.53	0.1500	0.3618	
M5005_Spy0883	SpM18_ChORF1122_s_at	-	Ribonuclease HII (EC 3.1.26.4)	Cellular processing	Cytoplasmic	spyM18_1122	57	1574	57	1469	0.99	0.9511	0.6822	
M5005_Spy0884	SpM1_ChORF1163_s_at	*smf*	Smf protein	Cellular processing	Cytoplasmic	SPy1163	30	2004	47	1574	2.43	0.3388	0.4798	
M5005_Spy0885	SpM3_ChORF0820_s_at	-	DNA topoisomerase I (EC 5.99.1.2)	Cellular processing	Cytoplasmic	spyM3_0820	159	687	133	911	0.71	0.4515	0.5301	
M5005_Spy0886	SpM12_ChORF288-15_at	-	Transcriptional regulators, LysR family	Information processing	Cytoplasmic		23	2233	20	2147	0.76	0.5470	0.5698	
M5005_Spy0889	SpM1_ChORF1169_s_at	-	Regulatory protein (pfoS/R)	Unknown	Cytoplasmic Membrane	SPy1169	22	2282	9	2578	0.16	0.3495	0.4854	
M5005_Spy0890	SpM1_ChORF1170_s_at	*ddh*	D-lactate dehydrogenase (EC 1.1.1.28)	Carbohydrate metabolism	Cytoplasmic	SPy1170	18	2416	27	1883	2.29	0.0238	0.1908	
M5005_Spy0891	SpM1_ChORF1171_s_at	*satD*	Hypothetical protein	Unknown	Cytoplasmic	SPy1171	44	1726	45	1724	1.09	0.9481	0.6811	
M5005_Spy0892	SpM1_ChORF1172_s_at	*satE*	Hypothetical protein	Unknown	Cytoplasmic Membrane	SPy1172	154	799	116	1008	0.56	0.1915	0.3986	
M5005_Spy0893	SpM1_ChORF1173_s_at	*gid*	Glucose inhibited division protein A	Cellular processing	Cytoplasmic	SPy1173	152	745	149	792	0.97	0.0174	0.1659	
M5005_Spy0894	SpM1_ChORF1174_s_at	*oadA*	Oxaloacetate decarboxylase alpha chain (EC 4.1.1.3)	Carbohydrate metabolism	Cytoplasmic	SPy1174	33	1903	43	1576	1.71	0.4381	0.5231	
M5005_Spy0895	SpM1_ChORF1175_s_at	-	Hypothetical membrane associated protein	Unknown	Cytoplasmic	SPy1175	51	1666	46	1639	0.83	0.6521	0.6061	
M5005_Spy0896	SpM1_ChORF1176_s_at	-	Biotin carboxyl carrier protein of oxaloacetate decarboxylase (EC 4.1.1.3)	Carbohydrate metabolism	Unknown	SPy1176	41	1736	39	1785	0.88	0.6731	0.6123	
M5005_Spy0897	SpM1_ChORF1177_s_at	-	Oxaloacetate decarboxylase beta chain (EC 4.1.1.3)	Carbohydrate metabolism	Cytoplasmic Membrane	SPy1177	145	722	121	931	0.69	0.7058	0.6200	

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M5005_Spy0899	SpM1_ChORF1178_s_at	*citG*	Transcriptional regulator, GntR family	Information processing	Cytoplasmic Membrane	SPy1178	54	1421	45	1617	0.69	0.1459	0.3573	
M5005_Spy0899	SpM1_ChORF1179_s_at	*citG*	Transcriptional regulator, GntR family	Information processing	Cytoplasmic Membrane	SPy1179	47	1668	65	1388	1.86	0.0096	0.1231	
M5005_Spy0900	SpM1_ChORF1180_s_at	-	Mg2+/citrate complex secondary transporter	Membrane transport	Cytoplasmic Membrane	SPy1180	48	1468	70	1360	2.13	0.4251	0.5176	
M5005_Spy0901	SpM1_ChORF1181_s_at	-	Hypothetical protein	Unknown	Unknown	SPy1181	15	2464	33	1924	4.75	0.6734	0.6123	
M5005_Spy0901	SpM18_ChORF1133_s_at	-	Hypothetical protein	Unknown	Unknown	spyM18_1133	19	2439	14	2443	0.53	0.5208	0.5595	
M5005_Spy0902	SpM1_ChORF1183_s_at	-	Biotin carboxyl carrier protein of oxaloacetate decarboxylase (EC 4.1.1.3)	Carbohydrate metabolism	Unknown	SPy1183	88	1123	76	1170	0.75	0.0660	0.2756	
M5005_Spy0903	SpM1_ChORF1184_s_at	*oadB*	Oxaloacetate decarboxylase beta chain (EC 4.1.1.3)	Carbohydrate metabolism	Cytoplasmic Membrane	SPy1184	99	1099	83	1221	0.70	0.8471	0.6565	
M5005_Spy0904	SpM18_ChORF1136_s_at	-	Hypothetical protein	Unknown	Unknown	spyM18_1136	15	2577	33	2031	4.63	0.9976	0.6931	
M5005_Spy0905	SpM1_ChORF1186_s_at	*citD*	Citrate lyase acyl carrier protein	Carbohydrate metabolism	Cytoplasmic	SPy1186	19	2372	16	2346	0.65	0.2131	0.4110	
M5005_Spy0906	SpM1_ChORF1188_s_at	*citE*	Citrate lyase beta chain (EC 4.1.3.6) / Citryl-CoA lyase subunit (EC 4.1.3.34)	Carbohydrate metabolism	Cytoplasmic	SPy1188	43	1790	52	1541	1.43	0.1060	0.3149	
M5005_Spy0907	SpM1_ChORF1189_s_at	*citF*	Citrate lyase alpha chain (EC 4.1.3.6) / Citrate CoA-transferase (EC 2.8.3.10)	Carbohydrate metabolism	Cytoplasmic	SPy1189	42	1717	34	1870	0.65	0.3466	0.4836	
M5005_Spy0908	SpM1_ChORF1190_s_at	*citX*	Apo-citrate lyase phosphoribosyl-dephospho-CoA transferase (EC 2.7.7.-)	Carbohydrate metabolism	Cytoplasmic	SPy1190	42	1699	66	1481	2.52	0.8948	0.6690	
M5005_Spy0909	SpM1_ChORF1191_s_at	*oadA*	Oxaloacetate decarboxylase alpha chain (EC 4.1.1.3)	Carbohydrate metabolism	Cytoplasmic	SPy1191	27	2277	34	1897	1.57	0.0520	0.2541	
M5005_Spy0910	SpM1_ChORF1192_s_at	*citC*	[Citrate [pro-3S]-lyase] ligase (EC 6.2.1.22)	Carbohydrate metabolism	Cytoplasmic	SPy1192	231	521	198	653	0.74	0.5362	0.5672	
M5005_Spy0911	SpM1_ChORF1193_s_at	-	Hypothetical protein	Unknown	Cytoplasmic	SPy1193	174	702	128	952	0.55	0.0048	0.0871	

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M5005_Spy0911	SpM12_ChORF288-43_s_at	-	Hypothetical protein	Unknown	Cytoplasmic		21	2338	9	2568	0.19	0.5378	0.5672	
M5005_Spy0913	SpM1_ChORF1196_s_at	-	Integrase/recombinase xerD	Phage	Cytoplasmic	SPy1196	180	678	143	840	0.63	0.0345	0.2168	
M5005_Spy0914	SpM1_ChORF1198_s_at	-	Phage transcriptional repressor	Phage	Unknown	SPy1198	50	1733	41	1772	0.66	0.1638	0.3752	
M5005_Spy0915	SpM1_ChORF1200_s_at	*ffh*	Signal recognition particle, subunit FFH/SRP54	Secretion	Cytoplasmic	SPy1200	170	712	193	591	1.30	0.5555	0.5728	
M5005_Spy0916	SpM1_ChORF1201_s_at	*ylxM*	Signal recognition particle associated protein	Secretion	Cytoplasmic	SPy1201	73	1348	101	1097	1.88	0.4435	0.5257	
M5005_Spy0917	SpM1_ChORF1202_s_at	-	Transcriptional regulator, GntR family	Information processing	Cytoplasmic	SPy1202	77	1379	74	1359	0.93	0.4978	0.5504	
M5005_Spy0918	SpM1_ChORF1203_s_at	-	Hypothetical protein	Unknown	Cytoplasmic	SPy1203	86	1324	84	1189	0.96	0.9222	0.6743	
M5005_Spy0919	SpM1_ChORF1204_s_at	*guaA*	GMP synthase [glutamine-hydrolyzing] (EC 6.3.5.2)	Nucleotide metabolism	Cytoplasmic	SPy1204	214	518	207	544	0.93	0.5716	0.5801	
M5005_Spy0920	SpM1_ChORF1205_s_at	-	UDP-N-acetylmuramoylpentapeptide-lysine N(6)-alanyltransferase (EC 2.3.2.10) / UDP-N-acetylmuramoylpentapeptide-lysine N(6)-seryltransferase (EC 2.3.2.-)	Cell wall metabolism	Cytoplasmic	SPy1205	15	2590	27	2012	3.37	0.6752	0.6129	
M5005_Spy0921	SpM1_ChORF1206_s_at	-	ABC transporter ATP-binding protein	Membrane transport	Cytoplasmic Membrane	SPy1206	35	1783	23	2079	0.44	0.4380	0.5231	
M5005_Spy0922	SpM1_ChORF1208_s_at	*pdxK*	Hypothetical membrane spanning protein	Unknown	Cytoplasmic Membrane	SPy1208	18	2406	31	1813	3.00	0.1386	0.3492	
M5005_Spy0922	SpM1_ChORF1209_s_at	*pdxK*	Hypothetical membrane spanning protein	Unknown	Cytoplasmic Membrane	SPy1209	48	1606	35	2087	0.51	0.1378	0.3489	
M5005_Spy0922	SpM18_ChORF1158_s_at	*pdxK*	Hypothetical membrane spanning protein	Unknown	Cytoplasmic Membrane	spyM18_1158	36	1997	14	2423	0.15	0.1285	0.3379	
M5005_Spy0924	SpM1_ChORF1210_s_at	-	Transcriptional regulator, GntR family	Information processing	Cytoplasmic	SPy1210	24	2201	37	1783	2.42	0.6208	0.5965	

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M5005_Spy0925	SpM1_ChORF1211_s_at	*rnhB*	Anaerobic ribonucleoside-triphosphate reductase (EC 1.17.4.2)	Unknown	Cytoplasmic	SPy1211	592	143	525	160	0.78	0.3365	0.4798	
M5005_Spy0925	SpM18_ChORF1162_s_at	*rnhB*	Anaerobic ribonucleoside-triphosphate reductase (EC 1.17.4.2)	Unknown	Cytoplasmic	spyM18_1162	49	1509	59	1506	1.41	0.9643	0.6850	
M5005_Spy0926	SpM1_ChORF1212_s_at	-	Cardiolipin synthetase (EC 2.7.8.-)	Lipid metabolism	Cytoplasmic Membrane	SPy1212	639	119	718	127	1.26	0.9137	0.6743	
M5005_Spy0927	SpM1_ChORF1213_s_at	*fhs.1*	Formate--tetrahydrofolate ligase (EC 6.3.4.3)	Carbohydrate metabolism	Cytoplasmic	SPy1213	833	72	829	93	0.99	0.7608	0.6372	
M5005_Spy0928	SpM1_ChORF1214_s_at	*lplA*	Lipoate-protein ligase A (EC 6.-.-.-)	Coenzyme and cofactor metabolism	Cytoplasmic	SPy1214	789	94	859	89	1.19	0.9285	0.6750	
M5005_Spy0929	SpM1_ChORF1215_s_at	-	SIR2 family protein	Information processing	Unknown	SPy1215	927	58	1045	59	1.27	0.9406	0.6790	
M5005_Spy0930	SpM1_ChORF1216_s_at	-	ATPase associated with chromosome architecture/replication	Unknown	Cytoplasmic	SPy1216	775	108	693	120	0.80	0.8409	0.6563	
M5005_Spy0930	SpM1_ChORF1217_s_at	-	ATPase associated with chromosome architecture/replication	Unknown	Cytoplasmic	SPy1217	779	78	949	85	1.48	0.9296	0.6750	
M5005_Spy0932	SpM1_ChORF1219_s_at	-	Luciferase-like monooxygenase (EC 1.14.-.-)	Unknown	Cytoplasmic	SPy1219	526	187	607	196	1.33	0.6899	0.6175	
M5005_Spy0933	SpM1_ChORF1218_s_at	-	Probable NADH-dependent flavin oxidoreductase yqiG (EC 1.-.-.-)	Unknown	Cytoplasmic	SPy1218	851	77	1148	55	1.82	0.6009	0.5893	
M5005_Spy0933	SpM1_ChORF1220_s_at	-	Probable NADH-dependent flavin oxidoreductase yqiG (EC 1.-.-.-)	Unknown	Cytoplasmic	SPy1220	426	277	427	240	1.00	0.9519	0.6824	
M5005_Spy0935	SpM1_ChORF1221_s_at	*dpfB*	Phosphopantothenate--cysteine ligase (EC 6.3.2.5)	Unknown	Unknown	SPy1221	28	1957	37	1906	1.74	0.0302	0.2051	
M5005_Spy0936	SpM1_ChORF1222_s_at	*dfp*	Phosphopantothenoylcysteine decarboxylase (EC 4.1.1.36)	Coenzyme and cofactor metabolism	Unknown	SPy1222	169	820	135	908	0.64	0.4036	0.5120	

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M5005_Spy0937	SpM1_ChORF1223_s_at	-	Transporter	Unknown	Cytoplasmic Membrane	SPy1223	64	1477	53	1513	0.67	0.1265	0.3361	
M5005_Spy0938	SpM1_ChORF1224_s_at	*pgmA*	Phosphoglucomutase (EC 5.4.2.2) / Phosphomannomutase (EC 5.4.2.8)	Carbohydrate metabolism	Cytoplasmic	SPy1224	229	469	255	482	1.24	0.9288	0.6750	
M5005_Spy0939	SpM1_ChORF1225_s_at	-	Nucleoside transport system permease protein	Membrane transport	Cytoplasmic Membrane	SPy1225	273	463	243	536	0.80	0.7991	0.6495	
M5005_Spy0941	SpM1_ChORF1226_s_at	-	Nucleoside transport ATP-binding protein	Membrane transport	Cytoplasmic Membrane	SPy1226	396	275	341	319	0.74	0.0753	0.2867	
M5005_Spy0941	SpM1_ChORF1227_s_at	-	Nucleoside transport ATP-binding protein	Membrane transport	Cytoplasmic Membrane	SPy1227	385	245	368	239	0.91	0.4671	0.5364	
M5005_Spy0942	SpM1_ChORF1228_s_at	-	Nucleoside-binding protein	Unknown	Unknown	SPy1228	621	189	554	150	0.80	0.2724	0.4449	
M5005_Spy0942	SpM12_ChORF290-9_s_at	-	Nucleoside-binding protein	Unknown	Unknown		14	2543	24	2312	2.84	0.8852	0.6662	
M5005_Spy0943	SpM1_ChORF1230_s_at	*cdd*	Cytidine deaminase (EC 3.5.4.5)	Nucleotide metabolism	Unknown	SPy1230	422	253	410	241	0.94	0.8484	0.6572	
M5005_Spy0944	SpM1_ChORF1232_s_at	-	16S rRNA m(2)G 1207 methyltransferase (EC 2.1.1.52)	Information processing	Cytoplasmic	SPy1232	172	770	129	876	0.56	0.2846	0.4541	
M5005_Spy0945	SpM1_ChORF1233_s_at	*coaA*	Pantothenate kinase (EC 2.7.1.33)	Coenzyme and cofactor metabolism	Cytoplasmic	SPy1233	28	2020	52	1586	3.52	0.3279	0.4776	
M5005_Spy0946	SpM1_ChORF1234_s_at	*rpsT*	SSU ribosomal protein S20P	Protein synthesis	Unknown	SPy1234	185	599	158	738	0.73	0.2544	0.4334	
M5005_Spy0947	SpM1_ChORF1236_s_at	*ciaH*	Two-component histidine sensor kinase ciaH	Signal transduction	Cytoplasmic Membrane	SPy1236	261	456	228	491	0.76	0.0847	0.2979	
M5005_Spy0948	SpM1_ChORF1237_s_at	*ciaR*	Two-component response regulator ciaR	Signal transduction	Cytoplasmic	SPy1237	122	948	124	975	1.02	0.3563	0.4882	
M5005_Spy0949	SpM1_ChORF1239_s_at	*pepN*	Lysyl aminopeptidase (EC 3.4.11.15) / alanine aminopeptidase (EC 3.4.11.2)	Amino acid metabolism	Cytoplasmic	SPy1239	488	183	590	137	1.46	0.0720	0.2840	
M5005_Spy0950	SpM1_ChORF1240_s_at	*phoU*	Phosphate transport system protein phoU	Membrane transport	Cytoplasmic	SPy1240	288	392	373	279	1.67	0.0468	0.2467	

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M5005_Spy0951	SpM1_ChORF1241_s_at	*pstB*	Phosphate transport ATP-binding protein pstB	Membrane transport	Cytoplasmic Membrane	SPy1241	292	369	367	320	1.58	0.0405	0.2314	
M5005_Spy0952	SpM1_ChORF1242_s_at	*pstB2*	Phosphate transport ATP-binding protein pstB	Membrane transport	Cytoplasmic Membrane	SPy1242	435	209	561	161	1.66	0.0327	0.2123	
M5005_Spy0954	SpM1_ChORF1243_s_at	*pstC*	Phosphate transport system permease protein pstC	Membrane transport	Cytoplasmic Membrane	SPy1243	130	840	172	672	1.77	0.2257	0.4208	
M5005_Spy0954	SpM1_ChORF1244_s_at	*pstC*	Phosphate transport system permease protein pstC	Membrane transport	Cytoplasmic Membrane	SPy1244	152	760	217	554	2.02	0.0273	0.1982	
M5005_Spy0955	SpM1_ChORF1245_s_at	*pstS*	Phosphate-binding protein	Membrane transport	Unknown	SPy1245	256	411	328	339	1.65	0.0311	0.2067	
M5005_Spy0956	SpM1_ChORF1246_s_at	-	16S rRNA m(5)C 967 methyltransferase (EC 2.1.1.-)	Cellular processing	Cytoplasmic	SPy1246	165	698	213	582	1.67	0.5412	0.5688	
M5005_Spy0957	SpM1_ChORF1247_s_at	-	Myo-inositol-1(or 4)-monophosphatase (EC 3.1.3.25)	Carbohydrate metabolism	Cytoplasmic	SPy1247	155	751	149	857	0.92	0.0936	0.3028	
M5005_Spy0957	SpM1_ChORF1248_s_at	-	Myo-inositol-1(or 4)-monophosphatase (EC 3.1.3.25)	Carbohydrate metabolism	Cytoplasmic	SPy1248	243	480	280	453	1.33	0.0596	0.2676	
M5005_Spy0957	SpM18_ChORF1197_s_at	-	Myo-inositol-1(or 4)-monophosphatase (EC 3.1.3.25)	Carbohydrate metabolism	Cytoplasmic	spyM18_1197	271	362	378	308	1.95	0.0131	0.1479	
M5005_Spy0957	SpM3_ChORF0884_s_at	-	Myo-inositol-1(or 4)-monophosphatase (EC 3.1.3.25)	Carbohydrate metabolism	Cytoplasmic	spyM3_0884	310	296	401	262	1.67	0.0205	0.1787	
M5005_Spy0959	SpM1_ChORF1249_s_at	-	Arsenate reductase family protein	Unknown	Cytoplasmic	SPy1249	221	548	233	538	1.11	0.3602	0.4888	
M5005_Spy0960	SpM1_ChORF1250_s_at	*mreA*	Riboflavin kinase (EC 2.7.1.26) / FMN adenylyltransferase (EC 2.7.7.2)	Coenzyme and cofactor metabolism	Cytoplasmic	SPy1250	129	897	158	858	1.50	0.6012	0.5893	
M5005_Spy0961	SpM1_ChORF1251_s_at	*truB*	tRNA pseudouridine synthase B (EC 4.2.1.70)	Protein synthesis	Cytoplasmic	SPy1251	309	377	275	387	0.79	0.3306	0.4776	
M5005_Spy0962	SpM1_ChORF1252_s_at	-	Hypothetical protein	Unknown	Unknown	SPy1252	143	750	129	898	0.81	0.9999	0.6937	

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M5005_Spy0963	SpM1_ChORF1253_s_at	-	Integral membrane protein	Unknown	Cytoplasmic Membrane	SPy1253	94	1288	100	1114	1.13	0.1713	0.3817	
M5005_Spy0964	SpM1_ChORF1254_s_at	-	Type I restriction-modification system specificity subunit	Information processing	Cytoplasmic	SPy1254	59	1466	36	1668	0.38	0.8824	0.6651	
M5005_Spy0966	SpM1_ChORF1255_s_at	-	ABC transporter permease protein	Membrane transport	Cytoplasmic Membrane	SPy1255	156	809	154	809	0.97	0.7916	0.6472	
M5005_Spy0967	SpM1_ChORF1257_s_at	-	ABC transporter ATP-binding protein	Membrane transport	Cytoplasmic Membrane	SPy1257	43	1801	51	1651	1.41	0.0592	0.2676	
M5005_Spy0968	SpM1_ChORF1258_s_at	-	Transcriptional regulator, TetR family	Information processing	Cytoplasmic	SPy1258	14	2466	15	2399	1.19	0.2024	0.4059	
M5005_Spy0969	SpM18_ChORF1209_x_at	-	Hypothetical protein	Unknown	Unknown	spyM18_1209	22	2385	22	2340	1.00	0.7489	0.6347	
M5005_Spy0970	SpM1_ChORF1259_s_at	-	NAD-dependent K+ or Na+ uptake system component / Transcriptional regulator, GntR family	Cellular processing	Cytoplasmic	SPy1259	264	399	216	563	0.67	0.0065	0.1005	
M5005_Spy0971	SpM1_ChORF1260_s_at	-	General stress protein, Gls24 family	Unknown	Unknown	SPy1260	3253	12	3011	18	0.86	0.9513	0.6822	
M5005_Spy0972	SpM1_ChORF1261_s_at	-	Hypothetical protein	Unknown	Unknown	SPy1261	4553	10	4276	12	0.88	0.5481	0.5698	
M5005_Spy0973	SpM1_ChORF1262_s_at	-	General stress protein, Gls24 family	Stress adaptation	Cytoplasmic	SPy1262	6199	5	5530	10	0.80	0.9959	0.6930	
M5005_Spy0974	SpM1_ChORF1263_s_at	-	Small integral membrane protein	Unknown	Cytoplasmic Membrane	SPy1263	1019	59	776	96	0.58	0.4141	0.5164	
M5005_Spy0974	SpM18_ChORF1214_s_at	-	Small integral membrane protein	Unknown	Cytoplasmic Membrane	spyM18_1214	1038	64	773	98	0.56	0.4340	0.5218	
M5005_Spy0975	SpM1_ChORF1264_s_at	-	Hypothetical protein	Unknown	Cytoplasmic Membrane	SPy1264	5467	8	4128	13	0.57	0.0768	0.2905	
M5005_Spy0976	SpM1_ChORF1265_s_at	-	Integral membrane protein	Unknown	Unknown	SPy1265	2764	16	2957	17	1.14	0.5992	0.5893	
M5005_Spy0977	SpM1_ChORF1267_s_at	*pcrA*	DNA helicase II (EC 3.6.1.-)	Cellular processing	Cytoplasmic	SPy1267	202	606	134	893	0.44	0.0776	0.2912	
M5005_Spy0978	SpM1_ChORF1270_s_at	-	Na(+)-linked D-alanine glycine permease	Membrane transport	Cytoplasmic Membrane	SPy1270	36	1964	13	2485	0.14	0.8923	0.6690	
M5005_Spy0978	SpM3_ChORF0902_at	-	Na(+)-linked D-alanine glycine permease	Membrane transport	Cytoplasmic Membrane	spyM3_0902	15	2521	24	2245	2.57	0.8969	0.6690	
M5005_Spy0980	SpM1_ChORF1272_s_at	-	Cobalt-zinc-cadmium resistance protein czcD	Membrane transport	Cytoplasmic Membrane	SPy1272	116	1068	76	1325	0.43	0.5782	0.5829	

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M5005_Spy0981	SpM1_ChORF1273_s_at	*cfa*	CAMP factor	Virulence	Extracellular	SPy1273	24	2235	81	1310	10.99	0.0733	0.2853	
M5005_Spy0982	SpM1_ChORF1274_s_at	-	Histidine-binding protein	Membrane transport	Unknown	SPy1274	168	609	137	821	0.67	0.4115	0.5159	
M5005_Spy0983	SpM1_ChORF1275_s_at	-	Histidine transport ATP-binding protein hisP	Membrane transport	Cytoplasmic Membrane	SPy1275	123	889	122	1059	0.98	0.2061	0.4088	
M5005_Spy0984	SpM1_ChORF1276_s_at	-	Histidine transport system permease protein hisM	Membrane transport	Cytoplasmic Membrane	SPy1276	123	873	144	947	1.36	0.5733	0.5804	
M5005_Spy0985	SpM18_ChORF1226_s_at	-	PhnA protein	Unknown	Unknown	spyM18_1226	228	449	180	784	0.63	0.3149	0.4728	
M5005_Spy0986	SpM1_ChORF1280_s_at	*glmS*	Glucosamine--fructose-6-phosphate aminotransferase [isomerizing] transamidination (EC 2.6.1.16)	Cell wall metabolism	Cytoplasmic	SPy1280	643	137	611	145	0.90	0.6779	0.6136	
M5005_Spy0986	SpM12_ChORF272-9_s_at	*glmS*	Glucosamine--fructose-6-phosphate aminotransferase [isomerizing] (EC 2.6.1.16)	Cell wall metabolism	Cytoplasmic		742	113	727	113	0.96	0.1423	0.3533	
M5005_Spy0987	SpM1_ChORF1281_s_at	*sipC*	Signal peptidase I (EC 3.4.21.89)	Secretion	Unknown	SPy1281	297	354	224	505	0.57	0.1893	0.3986	
M5005_Spy0988	SpM1_ChORF1282_s_at	*pyk, pykA*	Pyruvate kinase (EC 2.7.1.40)	Carbohydrate metabolism	Cytoplasmic	SPy1282	492	203	500	210	1.03	0.3465	0.4836	
M5005_Spy0989	SpM1_ChORF1283_s_at	*pfk*	Non-allosteric 6-phosphofructokinase (EC 2.7.1.11)	Carbohydrate metabolism	Cytoplasmic	SPy1283	304	373	332	356	1.20	0.9598	0.6844	
M5005_Spy0990	SpM1_ChORF1284_s_at	*dnaE*	DNA polymerase III alpha subunit (EC 2.7.7.7)	Information processing	Cytoplasmic	SPy1284	199	652	185	650	0.87	0.3648	0.4889	
M5005_Spy0991	SpM1_ChORF1285_s_at	-	Transcriptional regulator, GntR family	Information processing	Cytoplasmic	SPy1285	125	898	100	1171	0.64	0.2723	0.4449	
M5005_Spy0992	SpM1_ChORF1286_s_at	-	ABC transporter ATP-binding protein	Membrane transport	Cytoplasmic Membrane	SPy1286	59	1425	60	1472	1.03	0.0393	0.2300	
M5005_Spy0993	SpM1_ChORF1287_s_at	-	ABC transporter permease protein	Membrane transport	Cytoplasmic Membrane	SPy1287	83	1251	41	1702	0.25	0.0837	0.2979	
M5005_Spy0994	SpM1_ChORF1288_s_at	-	Putative membrane-associated alkaline phosphatase	Membrane transport	Cytoplasmic Membrane	SPy1288	52	1611	67	1331	1.68	0.3277	0.4776	

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M5005_Spy0994	SpM1_ChORF1289_s_at	-	Putative membrane-associated alkaline phosphatase	Membrane transport	Cytoplasmic Membrane	SPy1289	183	632	191	685	1.09	0.9311	0.6750	
M5005_Spy0995	SpM18_ChORF0394_x_at	-	Phage protein	Phage	Cytoplasmic	spyM18_0394	81	1294	75	1307	0.87	0.5376	0.5672	
M5005_Spy0996	SpM18_ChORF0393_s_at	*speA2*	Pyrogenic toxin superantigen exotoxin type A precursor, A2 allele	Virulence	Extracellular	spyM18_0393	101	1035	163	710	2.63	0.0979	0.3076	
M5005_Spy0997	SpM49_ChORF7585-43_at	-	Phage protein	Phage	Unknown		40	1737	71	1371	3.19	0.0103	0.1289	
M5005_Spy0998	SpyM3_1303_at	-	Phage protein	Phage	Unknown	spyM3_1303	13	2454	18	2244	1.97	0.8567	0.6602	
M5005_Spy0999	SpM49_ChORF7585-42_at	-	Phage protein	Phage	Unknown		57	1209	25	2176	0.20	0.4817	0.5443	
M5005_Spy1002	SpM49_ChORF7585-39_at	-	N-acetylmuramoyl-L-alanine amidase (EC 3.5.1.28)	Phage	Cytoplasmic		29	2145	34	1792	1.38	0.6072	0.5926	
M5005_Spy1003	SpM49_ChORF7585-38_at	-	Phage protein	Phage	Unknown		34	2075	35	1854	1.08	0.1330	0.3410	
M5005_Spy1004	SpyM3_1308_x_at	-	Phage protein	Phage	Cytoplasmic	spyM3_1308	25	2190	15	2530	0.37	0.6593	0.6081	
M5005_Spy1005	SpM49_ChORF7585-37_at	-	Phage protein	Phage	Cytoplasmic		41	1721	38	1824	0.83	0.7804	0.6442	
M5005_Spy1006	SpM49_ChORF7585-2_at	-	Phage structural protein	Phage	Unknown		22	2368	23	2057	1.17	0.0840	0.2979	
M5005_Spy1006	SpM49_ChORF7585-34_s_at	-	Phage structural protein	Phage	Unknown		18	2382	21	2115	1.50	0.5026	0.5512	
M5005_Spy1006	SpM49_ChORF7585-35_at	-	Phage structural protein	Phage	Unknown		25	2127	14	2559	0.31	0.0263	0.1949	
M5005_Spy1007	SpM49_ChORF7585-3_at	-	Phage protein	Phage	Extracellular		22	2328	41	1629	3.63	0.2838	0.4537	
M5005_Spy1007	SpM49_ChORF7585-33_at	-	Phage protein	Phage	Extracellular		16	2499	12	2501	0.56	0.8295	0.6540	
M5005_Spy1007	SpM49_ChORF7585-4_at	-	Phage protein	Phage	Extracellular		19	2437	16	2379	0.72	0.0744	0.2853	
M5005_Spy1008	SpM49_ChORF7585-32_at	-	Phage-related protein	Phage	Unknown		33	1944	57	1398	2.90	0.8187	0.6519	
M5005_Spy1009	SpM49_ChORF7585-30_at	-	Phage protein	Phage	Unknown		39	1662	39	1751	1.00	0.7939	0.6483	
M5005_Spy1009	SpM49_ChORF7585-31_at	-	Phage protein	Phage	Unknown		97	1230	68	1516	0.49	0.0305	0.2054	

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M5005_Spy1009	SpM49_ChORF7585-5_at	-	Phage protein	Phage	Unknown		21	2209	21	2183	1.00	0.2852	0.4541	
M5005_Spy1009	SpM49_ChORF7585-6_at	-	Phage protein	Phage	Unknown		22	1823	37	1820	2.68	0.6757	0.6129	
M5005_Spy1009	SpM49_ChORF7585-7_at	-	Phage protein	Phage	Unknown		12	2578	8	2648	0.50	0.1834	0.3901	
M5005_Spy1010	SpM49_ChORF7585-29_at	-	Phage protein	Phage	Cytoplasmic		16	2417	17	2420	1.22	0.4021	0.5118	
M5005_Spy1011	SpM49_ChORF7585-28_at	-	Phage protein	Phage	Unknown		47	1693	27	2047	0.34	0.6614	0.6081	
M5005_Spy1012	SpM49_ChORF7585-27_at	-	Antigen A	Phage	Cytoplasmic		27	2163	43	1746	2.59	0.1253	0.3349	
M5005_Spy1013	SpM49_ChORF7585-26_at	-	Antigen B	Phage	Cytoplasmic		51	1446	59	1399	1.34	0.3595	0.4888	
M5005_Spy1014	SpM49_ChORF7585-24_at	-	Antigen C	Phage	Unknown		39	1760	26	1912	0.44	0.3331	0.4779	
M5005_Spy1015	SpM49_ChORF7585-8_at	-	Phage protein	Phage	Unknown		31	2021	20	2185	0.40	0.4718	0.5394	
M5005_Spy1016	SpM49_ChORF7585-23_at	-	Phage protein	Phage	Cytoplasmic		20	2315	25	2130	1.56	0.1643	0.3754	
M5005_Spy1017	SpyM3_1321_at	-	Phage protein	Phage	Cytoplasmic	spyM3_1321	21	2249	31	1801	2.16	0.2680	0.4436	
M5005_Spy1018	SpM49_ChORF7585-22_at	-	Phage protein	Phage	Cytoplasmic		21	2288	17	2325	0.64	0.0709	0.2830	
M5005_Spy1019	SpM49_ChORF7585-21_at	-	Phage scaffold protein	Phage	Cytoplasmic		10	2643	24	2138	5.45	0.1358	0.3459	
M5005_Spy1019	SpM49_ChORF7585-9_at	-	Phage scaffold protein	Phage	Cytoplasmic		38	1663	40	1766	1.11	0.9216	0.6743	
M5005_Spy1020	SpM1_ChORF0685_s_at	-	Phage protein	Phage	Unknown	SPy0685	14	2485	21	2316	2.24	0.5935	0.5880	
M5005_Spy1021	SpM49_ChORF7585-20_at	-	Phage protein	Phage	Unknown		18	2467	11	2532	0.38	0.4634	0.5348	
M5005_Spy1022	SpM49_ChORF7585-19_at	-	Portal protein	Phage	Cytoplasmic		48	1689	19	2273	0.16	0.0241	0.1908	
M5005_Spy1024	SpM49_ChORF7585-17_at	-	Phage protein	Phage	Cytoplasmic		41	1677	26	2068	0.42	0.4425	0.5248	
M5005_Spy1024	SpM49_ChORF7585-18_at	-	Phage protein	Phage	Cytoplasmic		39	1914	21	2239	0.30	0.4388	0.5231	
M5005_Spy1025	SpM1_ChORF0677_s_at	-	Phage encoded transcriptional regulator, ArpU family	Phage	Cytoplasmic	SPy0677	25	2144	39	1817	2.50	0.1640	0.3752	
M5005_Spy1026	M12_1466_s_at	-	Phage protein	Phage	Extracellular		30	2192	36	1726	1.45	0.1422	0.3533	

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M5005_Spy1026	SpM18_ChORF1787_at	-	Phage protein	Phage	Extracellular	spyM18_1787	95	1216	121	996	1.63	0.7769	0.6419	
M5005_Spy1027	SpM18_ChORF1786_at	-	Phage protein	Phage	Cytoplasmic	spyM18_1786	18	2399	17	2526	0.84	0.8146	0.6512	
M5005_Spy1029	SpM18_ChORF0740_x_at	-	Phage protein	Phage	Unknown	spyM18_0740	64	1488	52	1618	0.66	0.1946	0.3993	
M5005_Spy1029	SpM18_ChORF1790_s_at	-	Phage protein	Phage	Unknown	spyM18_1790	14	2563	32	1784	5.00	0.4859	0.5443	
M5005_Spy1029	SpM3_ChORF0954_s_at	-	Phage protein	Phage	Unknown	spyM3_0954	13	2420	17	2486	1.65	0.8836	0.6655	
M5005_Spy1030	SpM18_ChORF1789_s_at	-	Phage protein	Phage	Unknown	spyM18_1789	20	2422	10	2601	0.23	0.0035	0.0713	
M5005_Spy1034	SpM18_ChORF1794_s_at	-	Phage protein	Phage	Unknown	spyM18_1794	53	1465	89	1239	2.85	0.8212	0.6525	
M5005_Spy1037	SpM18_ChORF1795_s_at	-	Phage single-strand DNA binding protein	Phage	Unknown	spyM18_1795	13	2605	10	2631	0.57	0.2940	0.4577	
M5005_Spy1037	SpM18_ChORF1796_s_at	-	Phage single-strand DNA binding protein	Phage	Unknown	spyM18_1796	39	1655	32	1982	0.71	0.2859	0.4541	
M5005_Spy1039	SpM18_ChORF1798_at	-	Phage protein	Phage	Cytoplasmic	spyM18_1798	33	1683	43	1782	1.69	0.1211	0.3279	
M5005_Spy1040	SpM5_ChORF270b-7_at	-	Phage protein	Phage	Cytoplasmic		44	1816	31	1909	0.49	0.6950	0.6184	
M5005_Spy1041	SpM18_ChORF1800_at	-	Phage protein	Phage	Cytoplasmic	spyM18_1800	25	2189	30	1963	1.38	0.2311	0.4227	
M5005_Spy1042	SpM5_ChORF270b-6_at	-	Phage replication protein	Phage	Cytoplasmic		37	1920	58	1552	2.44	0.0690	0.2789	
M5005_Spy1044	SpM18_ChORF1301_at	-	Phage protein	Phage	Unknown	spyM18_1301	15	2510	22	2281	2.06	0.9650	0.6850	
M5005_Spy1044	SpM3_ChORF0964_at	-	Phage protein	Phage	Unknown	spyM3_0964	24	2297	14	2557	0.32	0.2293	0.4227	
M5005_Spy1045	SpM18_ChORF1302_at	-	Transcriptional regulator	Phage	Unknown	spyM18_1302	51	1548	58	1523	1.30	0.3451	0.4836	
M5005_Spy1045	SpM18_ChORF1303_at	-	Transcriptional regulator	Phage	Unknown	spyM18_1303	11	2618	21	2263	3.91	0.6303	0.6000	
M5005_Spy1046	SpM3_ChORF0972_at	-	Phage protein	Phage	Unknown	spyM3_0972	44	1669	51	1612	1.33	0.4999	0.5512	
M5005_Spy1047	SpM3_ChORF0973_at	-	Phage protein	Phage	Unknown	spyM3_0973	51	1547	60	1454	1.39	0.3807	0.4981	
M5005_Spy1049	SpM18_ChORF1305_s_at	-	Phage protein	Phage	Unknown	spyM18_1305	60	1491	30	1866	0.26	0.8719	0.6632	

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M5005_Spy1049	SpM3_ChORF0976_s_at	-	Phage protein	Phage	Unknown	spyM3_0976	60	1483	35	1811	0.34	0.4848	0.5443	
M5005_Spy1050	SpM18_ChORF1306_at	-	Phage transcriptional repressor	Phage	Cytoplasmic	spyM18_1306	65	1243	80	1319	1.53	0.6726	0.6123	
M5005_Spy1052	SpM18_ChORF1309_s_at	*int.1*	DNA integration/recombination/invertion protein phi5005.1 int	Phage	Cytoplasmic	spyM18_1309	20	2364	24	1983	1.43	0.7032	0.6200	
M5005_Spy1054	SpM1_ChORF1290_s_at	-	Phage protein	Phage	Unknown	SPy1290	41	1508	52	1551	1.57	0.8730	0.6632	
M5005_Spy1055	SpM1_ChORF1291_s_at	*malP, glgP*	Maltodextrin (glycogen) phosphorylase (EC 2.4.1.1)	Carbohydrate metabolism	Cytoplasmic	SPy1291	71	1369	110	969	2.40	0.2400	0.4266	
M5005_Spy1056	SpM1_ChORF1292_s_at	*malM*	Amylomaltase/4-alpha-glucanotransferase (EC 2.4.1.25)	Carbohydrate metabolism	Cytoplasmic	SPy1292	111	1065	121	974	1.18	0.3322	0.4779	
M5005_Spy1057	SpM1_ChORF1293_s_at	*malR*	Maltose Operon Transcriptional repressor, LacI family	Information processing	Cytoplasmic	SPy1293	81	1261	52	1550	0.42	0.1097	0.3154	
M5005_Spy1058	SpM1_ChORF1294_s_at	*malE*	Maltose/maltodextrin (ABC transporter) substrate binding protein	Membrane transport	Unknown	SPy1294	167	561	259	405	2.39	0.5934	0.5880	
M5005_Spy1059	SpM1_ChORF1295_s_at	*malF*	Maltose/maltosaccharide/maltodextrin ABC transport system (permease) protein	Membrane transport	Cytoplasmic Membrane	SPy1295	51	1502	82	1283	2.60	0.1035	0.3143	
M5005_Spy1060	SpM1_ChORF1296_s_at	*malG*	Maltose/maltosaccharide/maltodextrin ABC transport system (permease) protein	Membrane transport	Cytoplasmic Membrane	SPy1296	25	2076	65	1536	7.06	0.1797	0.3887	
M5005_Spy1061	SpM1_ChORF1297_at	*malT*	Transcriptional regulator, LacI family	Information processing	Unknown	SPy1297	54	1490	76	1387	1.99	0.7593	0.6368	
M5005_Spy1061	SpM3_ChORF0986_x_at	*malT*	Transcriptional regulator, LacI family	Information processing	Unknown	spyM3_0986	51	1459	22	2169	0.18	0.2701	0.4441	
M5005_Spy1062	SpM1_ChORF1298_at	*malA*	Maltodextrose utilization protein malA	Carbohydrate metabolism	Cytoplasmic Membrane	SPy1298	2074	22	2505	20	1.46	0.1433	0.3546	
M5005_Spy1063	SpM1_ChORF1301_at	*malC*	Maltodextrin/cyclodextrin ABC transport system (permease) protein	Membrane transport	Cytoplasmic Membrane	SPy1301	4720	9	5222	9	1.22	0.0359	0.2201	

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M5005_Spy1064	SpM1_ChORF1299_at	*malD*	Maltodextrin/cyclodextrin ABC transport system (permease) protein	Membrane transport	Cytoplasmic Membrane	SPy1299	2522	21	2641	19	1.10	0.2264	0.4208	
M5005_Spy1065	SpM1_ChORF1302_at	*amyA*	Cyclomaltodextrin glucanotransferase/Alpha-amylase (EC 3.2.1.1), putative cyclomaltodextrin glucanotransferase (EC 3.2.1.19)	Carbohydrate metabolism	Extracellular	SPy1302	4898	4	6299	7	1.65	0.3626	0.4888	
M5005_Spy1066	SpM1_ChORF1304_at	*amyB*	Cyclomaltodextrinase/Neopullulanase (EC 3.2.1.135) / Cyclomaltodextrinase (EC 3.2.1.54) / Maltogenic alpha-amylase (EC 3.2.1.133)	Carbohydrate metabolism	Cytoplasmic	SPy1304	2258	20	2030	26	0.81	0.0852	0.2979	
M5005_Spy1067	SpM1_ChORF1306_at	*malX*	Maltose/maltodextrin-binding protein	Membrane transport	Unknown	SPy1306	1017	44	1130	44	1.23	0.9272	0.6750	
M5005_Spy1069	SpM1_ChORF1308_s_at	*dltD*	Esterase (EC 3.1.1.-)	Cell wall metabolism	Cytoplasmic	SPy1308	276	437	254	448	0.85	0.6556	0.6065	
M5005_Spy1070	SpM1_ChORF1310_s_at	*dltC*	Putative D-alanyl carrier protein	Cell wall metabolism	Unknown	SPy1310	226	582	197	586	0.76	0.0600	0.2677	
M5005_Spy1072	SpM1_ChORF1311_s_at	*dltB*	Putative integral membrane protein	Cell wall metabolism	Cytoplasmic Membrane	SPy1311	135	730	134	939	0.98	0.0920	0.3002	
M5005_Spy1073	SpM1_ChORF1312_s_at	*dltA*	Putative D-alanine-D-alanyl carrier protein ligase (EC 6.3.2.-); D-alanine-activating enzyme	Cell wall metabolism	Cytoplasmic	SPy1312	360	290	411	256	1.30	0.3384	0.4798	
M5005_Spy1074	SpM3_ChORF0995_at	-	Hypothetical protein	Unknown	Unknown	spyM3_0995	130	943	182	640	1.95	0.5256	0.5623	
M5005_Spy1075	SpM1_ChORF1314_s_at	*uvrB*	Excinuclease ABC subunit B	Information processing	Cytoplasmic	SPy1314	420	227	469	224	1.24	0.3116	0.4706	
M5005_Spy1076	SpM1_ChORF1315_s_at	*glnH*	Transporter	Membrane transport	Cytoplasmic Membrane	SPy1315	322	339	297	377	0.85	0.3302	0.4776	
M5005_Spy1077	SpM1_ChORF1316_s_at	*glnQ.2*	Glutamine transport ATP-binding protein glnQ	Membrane transport	Cytoplasmic Membrane	SPy1316	245	481	217	621	0.79	0.3303	0.4776	

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M5005_Spy1077	SpM12_ChORF236-7_s_at	*glnQ.2*	Glutamine transport ATP-binding protein glnQ	Membrane transport	Cytoplasmic Membrane		93	1144	70	1414	0.56	0.8708	0.6632	
M5005_Spy1078	SpM18_ChORF1329_s_at	-	Hypothetical protein	Unknown	Unknown	spyM18_1329	112	766	111	1006	0.98	0.0667	0.2767	
M5005_Spy1079	SpM18_ChORF1331_s_at	-	PTS system, cellobiose-specific IIC component	Carbohydrate metabolism	Cytoplasmic Membrane	spyM18_1331	91	1086	81	1314	0.80	0.4916	0.5472	
M5005_Spy1080	SpM1_ChORF1323_s_at	-	Hypothetical protein	Unknown	Cytoplasmic	SPy1323	95	1174	133	865	1.97	0.1148	0.3225	
M5005_Spy1081	SpM1_ChORF1322_s_at	-	PTS system, cellobiose-specific IIA component (EC 2.7.1.69)	Carbohydrate metabolism	Cytoplasmic	SPy1322	129	880	141	927	1.19	0.7467	0.6340	
M5005_Spy1082	SpM1_ChORF1324_s_at	-	PTS system, cellobiose-specific IIB component (EC 2.7.1.69)	Carbohydrate metabolism	Cytoplasmic	SPy1324	38	1775	55	1511	2.07	0.0345	0.2168	
M5005_Spy1083	SpM1_ChORF1325_s_at	-	Transcription antiterminator, BglG family / PTS system, mannitol (Cryptic)-specific IIA component (EC 2.7.1.69)	Information processing	Cytoplasmic	SPy1325	120	1064	132	774	1.21	0.1218	0.3283	
M5005_Spy1083	SpM3_ChORF1004_s_at	-	Transcription antiterminator, BglG family / PTS system, mannitol (Cryptic)-specific IIA component (EC 2.7.1.69)	Information processing	Cytoplasmic	spyM3_1004	35	1911	42	1715	1.50	0.0300	0.2042	
M5005_Spy1084	SpM1_ChORF1326_s_at	-	Outer surface protein	Unknown	Cytoplasmic	SPy1326	49	1544	82	1261	2.83	0.1329	0.3410	
M5005_Spy1085	SpM1_ChORF1328_s_at	*bglA.2*	Beta-glucosidase (EC 3.2.1.21)	Carbohydrate metabolism	Cytoplasmic	SPy1328	36	1942	62	1474	2.97	0.7004	0.6186	
M5005_Spy1086	SpM1_ChORF1329_s_at	-	Nicotinamide mononucleotide transporter	Membrane transport	Cytoplasmic Membrane	SPy1329	95	1185	65	1451	0.47	0.2241	0.4201	
M5005_Spy1087	SpM18_ChORF1340_at	*int*	Hypothetical cytosolic protein	Unknown	Extracellular	spyM18_1340	58	1440	97	1122	2.80	0.1216	0.3283	
M5005_Spy1088	SpM1_ChORF1333_s_at	*obg*	GTP-binding protein OBG family	Unknown	Cytoplasmic	SPy1333	255	408	279	406	1.20	0.0633	0.2737	

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M5005_Spy1092	SpM1_ChORF1337_s_at	*rsuA*	Ribosomal small subunit pseudouridine synthase A (EC 4.2.1.70)	Protein synthesis	Unknown	SPy1337	81	1178	67	1443	0.68	0.1581	0.3712	
M5005_Spy1093	SpM1_ChORF1339_s_at	-	Hypothetical protein	Unknown	Unknown	SPy1339	184	658	222	540	1.46	0.1445	0.3563	
M5005_Spy1094	SpM1_ChORF1340_s_at	-	Transporter, MFS superfamily	Membrane transport	Cytoplasmic Membrane	SPy1340	36	1897	29	1957	0.67	0.5200	0.5590	
M5005_Spy1095	SpM1_ChORF1343_s_at	-	Hypothetical cytosolic protein	Unknown	Cytoplasmic	SPy1343	39	1554	124	1011	10.29	0.2273	0.4215	
M5005_Spy1096	SpM1_ChORF1344_s_at	-	Thioesterase superfamily protein	Unknown	Cytoplasmic	SPy1344	80	1222	85	1241	1.13	0.6362	0.6019	
M5005_Spy1097	SpM1_ChORF1345_s_at	-	Phosphorylase, Pnp/Udp family	Unknown	Cytoplasmic	SPy1345	219	484	212	548	0.94	0.8849	0.6662	
M5005_Spy1097	SpM49_ChORF903-3_s_at	-	Phosphorylase, Pnp/Udp family	Unknown	Cytoplasmic		88	1236	104	1074	1.38	0.1187	0.3253	
M5005_Spy1098	SpM1_ChORF1346_s_at	-	tRNA (Uracil-5-) -methyltransferase (EC 2.1.1.35)	Protein synthesis	Cytoplasmic	SPy1346	86	1241	89	1217	1.07	0.4318	0.5207	
M5005_Spy1098	SpM18_ChORF1359_at	-	tRNA (Uracil-5-) -methyltransferase (EC 2.1.1.35)	Protein synthesis	Cytoplasmic	spyM18_1359	39	1910	55	1567	2.01	0.3025	0.4645	
M5005_Spy1098	SpM49_ChORF903-2_s_at	-	tRNA (Uracil-5-) -methyltransferase (EC 2.1.1.35)	Protein synthesis	Cytoplasmic		165	804	163	712	0.98	0.8330	0.6551	
M5005_Spy1100	SpM1_ChORF1351_s_at	*aroK*	Shikimate kinase (EC 2.7.1.71)	Amino acid metabolism	Cytoplasmic	SPy1351	56	1566	67	1382	1.44	0.9742	0.6874	
M5005_Spy1100	SpM1_ChORF1352_s_at	*aroK*	Shikimate kinase (EC 2.7.1.71)	Amino acid metabolism	Cytoplasmic	SPy1352	93	1126	105	1108	1.29	0.2682	0.4436	
M5005_Spy1102	SpM1_ChORF1353_s_at	-	Ribonuclease BN (EC 3.1.-.-)	Cellular processing	Cytoplasmic Membrane	SPy1353	167	719	155	782	0.86	0.5995	0.5893	
M5005_Spy1103	SpM1_ChORF1354_s_at	*map*	Methionine aminopeptidase (EC 3.4.11.18)	Unknown	Cytoplasmic	SPy1354	213	473	276	430	1.67	0.1902	0.3986	
M5005_Spy1104	SpM1_ChORF1355_s_at	-	Cytosolic protein containing multiple CBS domains	Unknown	Cytoplasmic	SPy1355	268	431	291	390	1.18	0.4174	0.5169	
M5005_Spy1105	SpM1_ChORF1356_s_at	-	Ribosomal-protein-alanine acetyltransferase (EC 2.3.1.128)	Protein synthesis	Cytoplasmic	SPy1356	91	1229	93	1076	1.04	0.1542	0.3672	

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M5005_Spy1106	SpM1_ChORF1357_s_at	*grab*	Protein G-related alpha 2M-binding protein	Virulence	Cell Wall	SPy1357	46	1697	233	479	25.97	1.5E-09	**3.1E-07**	**Significant**
M5005_Spy1106	SpM5_ChORF270b-528_at	*grab*	Protein G-related alpha 2M-binding protein	Virulence	Cell Wall		27	2069	36	1863	1.82	0.0784	0.2918	
M5005_Spy1107	SpM1_ChORF1358_s_at	*murZ*	UDP-N-acetylglucosamine 1-carboxyvinyltransferase (EC 2.5.1.7)	Cell wall metabolism	Cytoplasmic	SPy1358	205	578	240	514	1.37	0.8105	0.6512	
M5005_Spy1108	SpM1_ChORF1359_s_at	*metK*	S-adenosylmethionine synthetase (EC 2.5.1.6)	Cellular processing	Cytoplasmic	SPy1359	321	367	291	404	0.82	0.0007	**0.0208**	**Significant**
M5005_Spy1109	SpM1_ChORF1361_s_at	*inlA*	Internalin protein	Virulence	Cell Wall	SPy1361	209	598	159	715	0.58	0.5633	0.5763	
M5005_Spy1110	SpM1_ChORF1362_s_at	*birA*	Biotin operon repressor / Biotin--[acetyl-CoA-carboxylase] synthetase (EC 6.3.4.15)	Coenzyme and cofactor metabolism	Unknown	SPy1362	143	816	150	752	1.11	0.5868	0.5868	
M5005_Spy1111	SpM1_ChORF1363_s_at	-	Hypothetical protein	Unknown	Unknown	SPy1363	91	1151	109	1029	1.43	0.1074	0.3149	
M5005_Spy1111	SpM1_ChORF1364_s_at	-	Hypothetical protein	Unknown	Unknown	SPy1364	200	581	207	603	1.07	0.4577	0.5317	
M5005_Spy1113	SpM1_ChORF1365_s_at	-	GAF domain-containing proteins	Cellular processing	Unknown	SPy1365	231	513	242	494	1.09	0.2262	0.4208	
M5005_Spy1114	SpM1_ChORF1366_s_at	-	Hypothetical membrane spanning protein	Unknown	Cytoplasmic Membrane	SPy1366	48	1641	45	1773	0.91	0.4530	0.5308	
M5005_Spy1115	SpM1_ChORF1367_s_at	-	Hypothetical membrane spanning protein	Unknown	Cytoplasmic Membrane	SPy1367	14	2603	19	2256	1.84	0.3550	0.4878	
M5005_Spy1116	SpM1_ChORF1368_s_at	*udk*	Uridine kinase (EC 2.7.1.48)	Nucleotide metabolism	Cytoplasmic	SPy1368	94	1173	86	1272	0.84	0.6161	0.5962	
M5005_Spy1117	SpM1_ChORF1369_s_at	*deaD2*	ATP-dependent RNA helicase	Stress adaptation	Cytoplasmic	SPy1369	415	236	357	334	0.74	0.8294	0.6540	
M5005_Spy1118	SpM1_ChORF1370_s_at	-	Peptidoglycan N-acetylglucosamine deacetylase (EC 3.5.1.33)	Cell wall metabolism	Cytoplasmic	SPy1370	602	139	669	118	1.23	0.0842	0.2979	

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M5005_Spy1119	SpM1_ChORF1371_s_at	*gapN*	NADP-dependent glyceraldehyde-3-phosphate dehydrogenase (EC 1.2.1.9)	Carbohydrate metabolism	Cytoplasmic	SPy1371	266	464	257	474	0.93	0.1509	0.3626	
M5005_Spy1120	SpM1_ChORF1372_s_at	*pstI*	Phosphoenolpyruvate-protein phosphotransferase (EC 2.7.3.9)	Carbohydrate metabolism	Cytoplasmic	SPy1372	407	267	384	288	0.89	0.7984	0.6494	
M5005_Spy1121	SpM1_ChORF1373_s_at	*ptsH*	Phosphocarrier protein HPr	Carbohydrate metabolism	Cytoplasmic	SPy1373	319	356	411	249	1.66	0.3324	0.4779	
M5005_Spy1123	SpM1_ChORF1375_s_at	*nrdE.2*	Ribonucleoside-diphosphate reductase alpha chain (EC 1.17.4.1)	Nucleotide metabolism	Cytoplasmic	SPy1375	159	692	162	728	1.04	0.2432	0.4278	
M5005_Spy1123	SpM12_ChORF227-1_at	-	Ribonucleoside-diphosphate reductase alpha chain (EC 1.17.4.1)	Nucleotide metabolism	Cytoplasmic		18	2486	14	2424	0.61	0.0092	0.1209	
M5005_Spy1123	SpM5_ChORF270b-538_s_at	-	Ribonucleoside-diphosphate reductase alpha chain (EC 1.17.4.1)	Nucleotide metabolism	Cytoplasmic		135	849	102	1039	0.57	0.0963	0.3058	
M5005_Spy1124	SpM1_ChORF1378_s_at	*nrdF.2*	Ribonucleoside-diphosphate reductase beta chain (EC 1.17.4.1)	Nucleotide metabolism	Unknown	SPy1378	205	505	157	789	0.59	0.0177	0.1674	
M5005_Spy1125	SpM1_ChORF1379_s_at	-	Chloride channel protein	Membrane transport	Cytoplasmic Membrane	SPy1379	91	1110	98	1144	1.16	0.0158	0.1619	
M5005_Spy1126	SpM1_ChORF0195_x_at	-	Transposase	Mobile genetic element	Unknown	SPy0195	16	2572	26	2338	2.75	0.5822	0.5849	
M5005_Spy1126	SpM18_ChORF1348_x_at	-	Transposase	Mobile genetic element	Unknown	spyM18_1348	24	2129	41	1855	2.91	0.1364	0.3469	
M5005_Spy1128	SpM3_ChORF1017_s_at	-	Transposase	Mobile genetic element	Cytoplasmic	spyM3_1017	259	387	214	542	0.69	0.1992	0.4020	
M5005_Spy1129	SpM1_ChORF1384_s_at	-	CAAX amino terminal protease family	Information processing	Cytoplasmic Membrane	SPy1384	35	1921	48	1615	1.89	0.3468	0.4836	
M5005_Spy1131	SpM1_ChORF1385_s_at	-	Transcriptional regulator, Cro/CI family	Information processing	Cytoplasmic	SPy1385	45	1709	42	1800	0.87	0.0636	0.2743	
M5005_Spy1131	SpM1_ChORF1386_s_at	-	Transcriptional regulator, Cro/CI family	Information processing	Cytoplasmic	SPy1386	35	1637	74	1321	4.46	0.2758	0.4472	

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M5005_Spy1132	SpM1_ChORF1389_s_at	*alaS*	Alanyl-tRNA synthetase (EC 6.1.1.7)	Protein synthesis	Cytoplasmic	SPy1389	131	753	188	628	2.07	0.1711	0.3817	
M5005_Spy1132	SpM18_ChORF1397_at	*alaS*	Alanyl-tRNA synthetase (EC 6.1.1.7)	Protein synthesis	Cytoplasmic	spyM18_1397	20	2414	23	2113	1.26	0.3645	0.4889	
M5005_Spy1133	SpM1_ChORF1390_s_at	*surA, prsA*	Peptidyl-prolyl cis-trans isomerase (EC 5.2.1.8)	Unknown	Unknown	SPy1390	673	121	619	104	0.85	0.5153	0.5562	
M5005_Spy1134	SpM1_ChORF1391_s_at	-	O-methyltransferase (EC 2.1.1.-)	Unknown	Cytoplasmic	SPy1391	119	921	109	903	0.84	0.0509	0.2541	
M5005_Spy1135	SpM1_ChORF1392_s_at	-	Oxalate/formate antiporter	Unknown	Cytoplasmic Membrane	SPy1392	51	1640	54	1502	1.13	0.3806	0.4981	
M5005_Spy1136	SpM1_ChORF1393_s_at	*pepB*	Oligoendopeptidase F (EC 3.4.24.-)	Amino acid metabolism	Cytoplasmic	SPy1393	99	1020	127	1018	1.66	0.1805	0.3887	
M5005_Spy1137	SpM1_ChORF1395_s_at	-	Putative competence protein/transcription factor	Information processing	Cytoplasmic	SPy1395	88	1256	116	1081	1.74	0.7576	0.6368	
M5005_Spy1138	SpM1_ChORF1398_s_at	-	Ribosomal small subunit pseudouridine synthase A (EC 4.2.1.70)	Protein synthesis	Cytoplasmic	SPy1398	261	428	308	357	1.40	0.0236	0.1908	
M5005_Spy1139	SpM1_ChORF1399_s_at	*nagB*	Glucosamine-6-phosphate isomerase (EC 3.5.99.6)	Carbohydrate metabolism	Unknown	SPy1399	181	697	212	605	1.36	0.0034	0.0700	
M5005_Spy1140	SpM1_ChORF1400_s_at	*queA*	S-adenosylmethionine:tRNA ribosyltransferase-isomerase (EC 5.-.-.-)	Protein synthesis	Cytoplasmic	SPy1400	137	855	112	1067	0.67	0.0715	0.2838	
M5005_Spy1141	SpM1_ChORF1401_s_at	-	Hypothetical cytosolic protein	Unknown	Cytoplasmic	SPy1401	108	1060	98	1096	0.82	0.0842	0.2979	
M5005_Spy1143	SpM1_ChORF1402_s_at	-	Hypothetical protein	Unknown	Unknown	SPy1402	58	1522	315	388	29.55	4.1E-09	**6.8E-07**	**Significant**
M5005_Spy1143	SpM1_ChORF1404_s_at	-	Hypothetical protein	Unknown	Unknown	SPy1404	57	1494	274	369	23.39	1.1E-08	**1.6E-06**	**Significant**
M5005_Spy1144	SpM1_ChORF1405_s_at	-	Hypothetical protein	Unknown	Unknown	SPy1405	61	1701	224	515	13.51	1.1E-08	**1.6E-06**	**Significant**
M5005_Spy1144	SpM3_ChORF1070_s_at	-	Hypothetical protein	Unknown	Unknown	spyM3_1070	38	2103	259	459	47.38	1.5E-09	**3.1E-07**	**Significant**
M5005_Spy1145	SpM1_ChORF1406_s_at	*sodA*	Superoxide dismutase (EC 1.15.1.1)	Stress adaptation	Extracellular	SPy1406	689	114	691	122	1.00	0.9655	0.6850	

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M5005_Spy1146	SpM3_ChORF1072_s_at	-	DNA polymerase III, delta subunit (EC 2.7.7.7)	Information processing	Cytoplasmic	spyM3_1072	129	963	106	999	0.68	0.9918	0.6918	
M5005_Spy1147	SpM1_ChORF1408_s_at	*comEC*	ComE operon protein 3	Unknown	Cytoplasmic Membrane	SPy1408	46	1422	29	1992	0.39	0.6754	0.6129	
M5005_Spy1147	SpM1_ChORF1409_s_at	*comEC*	ComE operon protein 4	Unknown	Cytoplasmic Membrane	SPy1409	49	1900	40	1850	0.66	0.6093	0.5930	
M5005_Spy1149	SpM1_ChORF1410_s_at	-	1-acyl-sn-glycerol-3-phosphate acyltransferase (EC 2.3.1.51)	Unknown	Cytoplasmic Membrane	SPy1410	151	813	160	744	1.13	0.1356	0.3458	
M5005_Spy1150	SpM1_ChORF1411_s_at	-	Methyltransferase (EC 2.1.1.-)	Unknown	Cytoplasmic	SPy1411	47	1529	39	1632	0.69	0.9114	0.6743	
M5005_Spy1151	SpM1_ChORF1412_s_at	-	Hypothetical protein with endo/excinuclease domain	Unknown	Cytoplasmic	SPy1412	22	2300	20	2329	0.81	0.0468	0.2467	
M5005_Spy1153	SpM1_ChORF1414_s_at	-	Kup system potassium uptake protein	Unknown	Cytoplasmic Membrane	SPy1414	42	1727	96	1213	5.36	0.2881	0.4544	
M5005_Spy1154	SpM1_ChORF1415_s_at	*deaD*	ATP-dependent RNA helicase	Stress adaptation	Cytoplasmic	SPy1415	799	95	740	105	0.86	0.1951	0.3995	
M5005_Spy1155	SpM1_ChORF1416_s_at	*prfC*	Bacterial Peptide Chain Release Factor 3 (RF-3)	Protein synthesis	Cytoplasmic	SPy1416	536	196	518	188	0.93	0.5029	0.5512	
M5005_Spy1155	SpM3_ChORF1081_s_at	*prfC*	Bacterial Peptide Chain Release Factor 3 (RF-3)	Cellular processing	Cytoplasmic	spyM3_1081	32	1880	45	1699	1.94	0.9855	0.6910	
M5005_Spy1156	SpM1_ChORF1419_s_at	-	Hypothetical Membrane Spanning Protein	Unknown	Cytoplasmic Membrane	SPy1419	166	646	195	645	1.39	0.7956	0.6488	
M5005_Spy1157	SpM1_ChORF1420_s_at	*murF*	UDP-N-acetylmuramoylalanine-D-glutamyl-lysine--D-alanyl-D-alanine ligase (EC 6.3.2.10)	Cell wall metabolism	Cytoplasmic	SPy1420	391	300	426	235	1.19	0.0620	0.2713	
M5005_Spy1158	SpM1_ChORF1421_s_at	*ddlA*	D-alanine--D-alanine ligase (EC 6.3.2.4)	Cell wall metabolism	Cytoplasmic	SPy1421	70	1510	68	1349	0.94	0.9690	0.6859	
M5005_Spy1158	SpM12_ChORF247-14_s_at	*ddlA*	D-alanine--D-alanine ligase (EC 6.3.2.4)	Cell wall metabolism	Cytoplasmic		11	2639	9	2636	0.64	0.0019	**0.0442**	**Significant**
M5005_Spy1159	SpM1_ChORF1422_s_at	*recR*	Recombination protein recR	Information processing	Cytoplasmic	SPy1422	91	1267	92	1206	1.01	0.3386	0.4798	

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M5005_Spy1160	SpM3_ChORF1086_at	-	Penicillin-binding protein	Unknown	Unknown	spyM3_1086	121	811	129	1021	1.13	0.1662	0.3767	
M5005_Spy1161	SpM1_ChORF1424_s_at	-	Formate transporter	Membrane transport	Cytoplasmic Membrane	SPy1424	139	908	84	1267	0.37	0.5713	0.5801	
M5005_Spy1162	SpM1_ChORF1425_s_at	-	Hypothetical protein	Unknown	Cytoplasmic Membrane	SPy1425	140	787	175	681	1.55	0.0044	0.0836	
M5005_Spy1163	SpM1_ChORF1427_s_at	-	Transcriptional regulator, biotin repressor family	Information processing	Cytoplasmic	SPy1427	65	1478	56	1608	0.74	0.6425	0.6036	
M5005_Spy1164	SpM1_ChORF1429_s_at	*gpmA*	Phosphoglycerate mutase (EC 5.4.2.1)	Carbohydrate metabolism	Cytoplasmic	SPy1429	293	386	281	417	0.92	0.6671	0.6097	
M5005_Spy1165	SpM1_ChORF1432_s_at	*pyrD*	Dihydroorotate dehydrogenase (EC 1.3.3.1)	Nucleotide metabolism	Cytoplasmic	SPy1432	101	1091	124	942	1.50	0.4504	0.5295	
M5005_Spy1166	SpM18_ChORF1442_s_at	-	Hypothetical protein	Unknown	Unknown	spyM18_1442	408	273	377	307	0.85	0.3436	0.4826	
M5005_Spy1166	SpM3_ChORF1092_s_at	-	Hypothetical protein	Unknown	Unknown	spyM3_1092	442	229	388	295	0.77	0.3673	0.4908	
M5005_Spy1167	SpM1_ChORF1434_s_at	-	Lead, cadmium, zinc and mercury transporting ATPase (EC 3.6.3.-)	Membrane transport	Cytoplasmic Membrane	SPy1434	79	1132	76	1220	0.92	0.8029	0.6501	
M5005_Spy1168	SpM18_ChORF1444_x_at	-	Phage protein	Phage	Cytoplasmic	spyM18_1444	34	1936	19	2191	0.33	0.3305	0.4776	
M5005_Spy1169	SpM1_ChORF1436_s_at	*spd3*	Streptodornase (EC 3.1.21.1)	Virulence	Unknown	SPy1436	460	210	525	163	1.30	0.0279	0.1982	
M5005_Spy1170	SpM1_ChORF1437_s_at	-	Hypothetical membrane associated protein	Phage	Cytoplasmic Membrane	SPy1437	30	2115	40	1684	1.85	0.5065	0.5532	
M5005_Spy1171	SpM1_ChORF1438_s_at	-	Phage-associated cell wall hydrolase	Phage	Cytoplasmic	SPy1438	32	2116	30	2046	0.91	0.4500	0.5295	
M5005_Spy1173	SpM1_ChORF0706_s_at	-	Phage protein	Phage	Unknown	SPy0706	36	1848	23	2148	0.42	0.2908	0.4558	
M5005_Spy1173	SpM1_ChORF1440_x_at	-	Phage protein	Phage	Unknown	SPy1440	8	2660	11	2606	2.23	0.8720	0.6632	
M5005_Spy1173	SpM1_ChORF1441_s_at	-	Phage protein	Phage	Unknown	SPy1441	33	2067	34	1631	1.06	0.3218	0.4755	
M5005_Spy1175	SpM1_ChORF1443_s_at	-	Phage protein	Phage	Cytoplasmic	SPy1443	75	1361	70	1225	0.85	0.2600	0.4390	
M5005_Spy1176	SpM1_ChORF1444_s_at	-	Phage infection protein	Phage	Unknown	SPy1444	45	1619	39	1736	0.74	0.1789	0.3887	

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M5005_Spy1176	SpM5_ChORF270b-554_at	-	Phage infection protein	Phage	Unknown		29	1941	17	2354	0.34	0.4812	0.5442	
M5005_Spy1177	SpM1_ChORF1447_at	-	Phage protein	Phage	Cytoplasmic	SPy1447	31	2077	43	1640	1.85	0.7359	0.6294	
M5005_Spy1177	SpM1_ChORF1448_s_at	-	Phage protein	Phage	Cytoplasmic	SPy1448	58	1520	51	1488	0.77	0.1814	0.3887	
M5005_Spy1178	SpM18_ChORF1460_s_at	-	Phage protein	Phage	Cytoplasmic Membrane	spyM18_1460	16	2566	14	2426	0.77	0.9583	0.6844	
M5005_Spy1178	SpM5_ChORF270b-557_at	-	Phage protein	Phage	Cytoplasmic Membrane		17	2511	14	2509	0.67	0.2693	0.4436	
M5005_Spy1179	SpM1_ChORF1449_s_at	-	Phage protein	Phage	Unknown	SPy1449	24	1958	22	2294	0.78	0.8805	0.6649	
M5005_Spy1180	SpM1_ChORF1450_s_at	-	Phage protein	Phage	Cytoplasmic	SPy1450	11	2646	13	2544	1.46	0.4181	0.5169	
M5005_Spy1181	SpM1_ChORF1451_s_at	-	Phage major tail protein	Phage	Cytoplasmic	SPy1451	29	2122	21	2108	0.53	0.4842	0.5443	
M5005_Spy1182	SpM1_ChORF1452_s_at	-	Phage protein	Phage	Cytoplasmic	SPy1452	18	2340	14	2489	0.59	0.4990	0.5512	
M5005_Spy1184	SpM1_ChORF1453_s_at	-	Phage protein	Phage	Cytoplasmic	SPy1453	241	416	161	769	0.45	0.4871	0.5443	
M5005_Spy1184	SpM1_ChORF1454_s_at	-	Phage protein	Phage	Cytoplasmic	SPy1454	22	2353	19	2295	0.75	0.9080	0.6729	
M5005_Spy1184	SpM1_ChORF1455_s_at	-	Phage protein	Phage	Cytoplasmic	SPy1455	32	1798	46	1581	2.12	0.0272	0.1982	
M5005_Spy1186	SpM1_ChORF1456_s_at	-	Phage protein	Phage	Unknown	SPy1456	36	1882	20	2153	0.31	0.6558	0.6065	
M5005_Spy1187	SpM1_ChORF1457_s_at	-	Phage structural protein	Phage	Cytoplasmic	SPy1457	25	2171	71	1308	8.36	0.0922	0.3002	
M5005_Spy1187	SpM5_ChORF270b-559_at	-	Phage structural protein	Phage	Cytoplasmic		57	1458	48	1667	0.71	0.2103	0.4110	
M5005_Spy1188	SpM1_ChORF1459_s_at	-	Phage protein	Phage	Cytoplasmic	SPy1459	18	2276	51	1571	8.33	0.6817	0.6146	
M5005_Spy1189	SpM1_ChORF1460_s_at	-	Phage terminase	Phage	Unknown	SPy1460	85	1253	78	1369	0.84	0.6401	0.6031	
M5005_Spy1189	SpM5_ChORF270b-141_at	-	Phage terminase	Phage	Unknown		33	2134	22	2174	0.44	0.1176	0.3242	
M5005_Spy1190	SpM1_ChORF1461_x_at	-	Phage protein	Phage	Unknown	SPy1461	27	2228	20	2103	0.55	0.9860	0.6910	
M5005_Spy1190	SpM1_ChORF1462_x_at	-	Phage protein	Phage	Unknown	SPy1462	35	1698	45	1753	1.67	0.6539	0.6061	
M5005_Spy1190	SpM3_ChORF1118_s_at	-	Phage protein	Phage	Unknown	spyM3_1118	10	2651	11	2615	1.36	0.2389	0.4255	

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M5005_Spy1192	SpM1_ChORF1463_s_at	-	Phage protein	Phage	Cytoplasmic	SPy1463	163	797	154	734	0.89	0.8039	0.6505	
M5005_Spy1193	SpM1_ChORF1464_s_at	-	Phage protein	Phage	Cytoplasmic	SPy1464	139	762	110	1098	0.62	0.3004	0.4623	
M5005_Spy1193	SpM1_ChORF1465_s_at	-	Phage protein	Phage	Cytoplasmic	SPy1465	60	1535	65	1340	1.21	0.0572	0.2639	
M5005_Spy1196	SpM1_ChORF1468_s_at	-	HNH endonuclease family protein	Phage	Unknown	SPy1468	10	2609	8	2649	0.79	0.6338	0.6012	
M5005_Spy1197	SpM3_ChORF1124_s_at	-	Phage protein	Phage	Cytoplasmic	spyM3_1124	20	2410	39	1737	3.73	0.1612	0.3722	
M5005_Spy1198	SpM1_ChORF0676_s_at	-	Phage protein	Phage	Unknown	SPy0676	31	2030	65	1436	4.44	0.1071	0.3149	
M5005_Spy1199	SpM1_ChORF1471_x_at	-	Phage protein	Phage	Unknown	SPy1471	26	2170	33	1842	1.62	0.1458	0.3573	
M5005_Spy1200	SpM1_ChORF1474_s_at	-	Phage protein	Phage	Unknown	SPy1474	21	2205	49	1718	5.31	0.4781	0.5421	
M5005_Spy1201	SpM1_ChORF1473_s_at	-	Phage protein	Phage	Cytoplasmic	SPy1473	71	1403	41	1601	0.34	0.1020	0.3116	
M5005_Spy1202	SpM18_ChORF1493_at	-	Phage protein	Phage	Cytoplasmic	spyM18_1493	45	1674	25	1780	0.30	0.1147	0.3225	
M5005_Spy1205	SpM1_ChORF0957_s_at	-	Phage protein	Phage	Unknown	SPy0957	9	2547	16	2505	2.99	0.0470	0.2467	
M5005_Spy1205	SpM1_ChORF1478_s_at	-	Phage protein	Phage	Unknown	SPy1478	21	2221	25	2235	1.41	0.4349	0.5221	
M5005_Spy1205	SpM12_ChORF278-26_s_at	-	Phage protein	Phage	Unknown		19	2397	47	1591	6.25	0.2326	0.4227	
M5005_Spy1205	SpM3_ChORF1136_s_at	-	Phage protein	Phage	Unknown	spyM3_1136	16	2408	13	2472	0.72	0.4046	0.5120	
M5005_Spy1205	SpM49_ChORF7585-10_s_at	-	Phage protein	Phage	Unknown		22	2278	18	2352	0.64	0.8069	0.6512	
M5005_Spy1205	SpM49_ChORF7585-11_s_at	-	Phage protein	Phage	Unknown		26	2044	18	2462	0.48	0.4723	0.5394	
M5005_Spy1205	SpM5_ChORFJ7578C-203_s_at	-	Phage protein	Phage	Unknown		39	1802	31	2069	0.62	0.2633	0.4400	
M5005_Spy1206	SpM1_ChORF1479_s_at	-	Phage protein	Phage	Cytoplasmic	SPy1479	63	1563	43	1645	0.47	0.5895	0.5874	
M5005_Spy1208	SpM18_ChORF1498_x_at	-	Phage protein	Phage	Unknown	spyM18_1498	69	1416	40	1623	0.34	0.3609	0.4888	
M5005_Spy1211	SpM1_ChORF0952_at	-	Phage protein	Phage	Unknown	SPy0952	31	1877	19	2326	0.37	0.3049	0.4656	
M5005_Spy1212	SpM1_ChORF1484_s_at	*xis*	Excisionase	Phage	Unknown	SPy1484	161	671	137	872	0.72	0.3454	0.4836	

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M5005_Spy1213	SpM3_ChORF0967_at	-	Phage protein	Phage	Cytoplasmic	spyM3_0967	17	2380	20	2202	1.34	0.0085	0.1150	
M5005_Spy1214	SpM1_ChORF0949_s_at	-	Phage protein	Phage	Unknown	SPy0949	164	743	133	843	0.65	0.0181	0.1696	
M5005_Spy1215	SpM1_ChORF0948_s_at	-	Phage protein	Phage	Cytoplasmic	SPy0948	121	854	105	1079	0.75	0.1210	0.3279	
M5005_Spy1216	SpM1_ChORF0947_s_at	-	Phage protein	Phage	Cytoplasmic	SPy0947	32	2092	26	2219	0.69	0.0670	0.2767	
M5005_Spy1221	SpM5_ChORF4P31a-199_at	-	Phage protein	Phage	Unknown		23	2273	15	2417	0.40	0.9656	0.6850	
M5005_Spy1222	SpM1_ChORF1488_s_at	*int.2*	DNA integration/recombination/invertion protein phi5005.2 int	Phage	Cytoplasmic	SPy1488	47	1588	42	1740	0.79	0.0240	0.1908	
M5005_Spy1223	SpM1_ChORF1489_s_at	*hlpA*	DNA-binding protein HU	Cellular processing	Cytoplasmic	SPy1489	553	165	590	140	1.14	0.2073	0.4090	
M5005_Spy1225	SpM1_ChORF1491_s_at	-	Lipase/Acylhydrolase with GDSL-like motif	Unknown	Unknown	SPy1491	203	588	189	694	0.86	0.4047	0.5120	
M5005_Spy1225	SpM1_ChORF1492_s_at	-	Lipase/Acylhydrolase with GDSL-like motif	Unknown	Unknown	SPy1492	240	493	208	565	0.75	0.9550	0.6835	
M5005_Spy1225	SpM1_ChORF1493_s_at	-	Lipase/Acylhydrolase with GDSL-like motif	Unknown	Unknown	SPy1493	239	412	266	463	1.24	0.4163	0.5169	
M5005_Spy1227	SpM1_ChORF1494_s_at	-	Hypothetical protein	Unknown	Cell Wall	SPy1494	412	271	522	187	1.60	0.0059	0.0952	
M5005_Spy1228	SpM1_ChORF1495_s_at	*recN*	DNA repair protein recN	Cellular processing	Cytoplasmic	SPy1495	384	308	444	230	1.34	0.0091	0.1203	
M5005_Spy1229	SpM1_ChORF1496_s_at	*argR1*	Arginine repressor, argR	Information processing	Unknown	SPy1496	151	746	127	909	0.71	0.9627	0.6850	
M5005_Spy1229	SpM1_ChORF1497_s_at	*argR1*	Arginine repressor, argR	Information processing	Unknown	SPy1497	309	313	381	277	1.51	0.1699	0.3817	
M5005_Spy1231	SpM1_ChORF1498_s_at	*fps*	Dimethylallyltransferase (EC 2.5.1.1) / Geranyltranstransferase (EC 2.5.1.10)	Lipid metabolism	Cytoplasmic	SPy1498	188	669	189	671	1.01	0.2221	0.4185	
M5005_Spy1232	SpM1_ChORF1499_s_at	*xseB*	Exodeoxyribonuclease VII small subunit (EC 3.1.11.6)	Information processing	Unknown	SPy1499	214	488	260	449	1.48	0.0081	0.1126	
M5005_Spy1232	SpM1_ChORF1500_s_at	*xseB*	Exodeoxyribonuclease VII small subunit (EC 3.1.11.6)	Information processing	Unknown	SPy1500	250	397	287	386	1.32	0.9886	0.6915	

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M5005_Spy1234	SpM1_ChORF1502_s_at	*folD*	Methylenetetrahydrofolate dehydrogenase (NADP+) (EC 1.5.1.5) / Methenyltetrahydrofolate cyclohydrolase (EC 3.5.4.9)	Coenzyme and cofactor metabolism	Cytoplasmic	SPy1502	65	1341	87	1279	1.80	0.2102	0.4110	
M5005_Spy1235	SpM1_ChORF1503_s_at	-	Phosphglucomutase (EC 5.4.2.2) / Phosphomannomutase (EC 5.4.2.8)	Carbohydrate metabolism	Cytoplasmic	SPy1503	1029	50	1072	49	1.09	0.0785	0.2918	
M5005_Spy1236	SpM1_ChORF1505_s_at	*phr*	Deoxyribodipyrimidine photolyase (EC 4.1.99.3)	Information processing	Cytoplasmic	SPy1505	45	1795	40	1723	0.79	0.9739	0.6874	
M5005_Spy1237	SpM1_ChORF1506_s_at	-	Arginine transport ATP-binding protein artP	Membrane transport	Cytoplasmic Membrane	SPy1506	44	1764	62	1493	2.05	0.5631	0.5763	
M5005_Spy1238	SpM1_ChORF1507_s_at	-	Arginine transport system permease protein artQ	Membrane transport	Cytoplasmic Membrane	SPy1507	26	2199	30	1831	1.31	0.0850	0.2979	
M5005_Spy1239	SpM1_ChORF1508_s_at	-	Hypothetical cytosolic protein	Unknown	Cytoplasmic	SPy1508	214	554	245	467	1.31	0.1749	0.3853	
M5005_Spy1240	SpM1_ChORF1509_s_at	*clpE*	ATP-dependent clp protease ATP-binding subunit clpE	Stress adaptation	Cytoplasmic	SPy1509	1465	27	1079	47	0.54	0.0020	**0.0465**	**Significant**
M5005_Spy1241	SpM1_ChORF1510_s_at	*mutT*	Mutator mutT protein (7,8-dihydro-8-oxoguanine-triphosphatase) (EC 3.6.1.-)	Cellular processing	Unknown	SPy1510	130	934	132	980	1.04	0.6448	0.6041	
M5005_Spy1242	SpM1_ChORF1511_s_at	-	Hypothetical cytosolic protein	Unknown	Cytoplasmic	SPy1511	512	190	428	227	0.70	0.4151	0.5169	
M5005_Spy1243	SpM1_ChORF1513_s_at	*ileS*	Isoleucyl-tRNA synthetase (EC 6.1.1.5)	Protein synthesis	Cytoplasmic	SPy1513	105	1104	130	1007	1.56	0.2829	0.4537	
M5005_Spy1244	SpM1_ChORF1514_s_at	*divIVAS*	Cell division initiation protein DivIVA	Cellular processing	Unknown	SPy1514	439	228	427	222	0.95	0.7817	0.6442	
M5005_Spy1245	SpM1_ChORF1515_s_at	-	RNA binding protein	Unknown	Cytoplasmic	SPy1515	304	430	295	380	0.95	0.3738	0.4941	
M5005_Spy1246	SpM1_ChORF1516_s_at	-	Integral membrane protein	Unknown	Unknown	SPy1516	153	791	148	918	0.95	0.4711	0.5390	
M5005_Spy1247	SpM1_ChORF1518_s_at	-	Hypothetical cytosolic protein	Unknown	Cytoplasmic	SPy1518	879	82	886	74	1.02	0.8137	0.6512	

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M5005_Spy1248	SpM1_ChORF1519_s_at	-	Pyridoxal-5'-phosphate family protein	Unknown	Cytoplasmic	SPy1519	524	175	484	171	0.85	0.7229	0.6262	
M5005_Spy1249	SpM1_ChORF1520_s_at	*ftsZ*	Cell division protein ftsZ	Cellular processing	Unknown	SPy1520	810	87	930	68	1.32	0.2317	0.4227	
M5005_Spy1250	SpM1_ChORF1521_s_at	*ftsA*	Cell division protein ftsA	Cellular processing	Cytoplasmic	SPy1521	1190	41	1311	33	1.21	0.4119	0.5159	
M5005_Spy1251	SpM1_ChORF1523_s_at	*divIB*	Cell division protein ftsQ	Cellular processing	Unknown	SPy1523	316	326	267	409	0.71	0.7588	0.6368	
M5005_Spy1252	SpM1_ChORF1524_s_at	*murG*	UDP-N-acetylglucosamine--N-acetylmuramyl-(pentapeptide) pyrophosphoryl-undecaprenol N-acetylglucosamine transferase (EC 2.4.1.227)	Cellular processing	Cytoplasmic Membrane	SPy1524	137	832	163	735	1.41	0.3377	0.4798	
M5005_Spy1253	SpM1_ChORF1525_s_at	*murD*	UDP-N-acetylmuramoylalanine--D-glutamate ligase (EC 6.3.2.9)	Cell wall metabolism	Cytoplasmic	SPy1525	220	443	242	503	1.21	0.2283	0.4222	
M5005_Spy1254	SpM1_ChORF1526_s_at	-	Hypothetical membrane spanning protein	Unknown	Cytoplasmic Membrane	SPy1526	86	1276	100	1172	1.37	0.1089	0.3154	
M5005_Spy1255	SpM1_ChORF1527_s_at	*typA*	GTP-binding protein TypA/BipA	Information processing	Cytoplasmic	SPy1527	441	226	339	299	0.59	0.4681	0.5372	
M5005_Spy1256	SpM1_ChORF1528_s_at	-	Rhodanese-related sulfurtransferases	Unknown	Cytoplasmic	SPy1528	66	1358	78	1347	1.40	0.6170	0.5962	
M5005_Spy1257	SpM1_ChORF1529_s_at	*glcK*	Glucokinase (EC 2.7.1.2)	Carbohydrate metabolism	Cytoplasmic	SPy1529	138	901	134	945	0.94	0.2529	0.4334	
M5005_Spy1258	SpM1_ChORF1530_s_at	-	Hypothetical cytosolic protein	Unknown	Cytoplasmic	SPy1530	69	1397	82	1301	1.44	0.0645	0.2748	
M5005_Spy1259	SpM1_ChORF1531_s_at	*dpr*	Non-specific DNA-binding protein Dps / Iron-binding ferritin-like antioxidant protein	Stress adaptation	Unknown	SPy1531	806	76	1120	48	1.93	0.7854	0.6463	
M5005_Spy1260	SpM1_ChORF1532_s_at	-	Prepilin peptidase family (EC 3.4.99.-)	Unknown	Cytoplasmic Membrane	SPy1532	15	2555	11	2593	0.54	0.7355	0.6294	
M5005_Spy1261	SpM1_ChORF1533_s_at	-	Radical SAM family enzyme	Unknown	Cytoplasmic	SPy1533	185	688	206	608	1.23	0.9223	0.6743	

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M5005_Spy1262	SpM1_ChORF1534_s_at	-	Transcriptional regulator	Unknown	Unknown	SPy1534	147	708	141	781	0.92	0.9840	0.6907	
M5005_Spy1264	SpM1_ChORF1535_s_at	-	Ribose operon repressor	Information processing	Cytoplasmic	SPy1535	78	1355	69	1391	0.78	0.4499	0.5295	
M5005_Spy1266	SpM1_ChORF1536_s_at	-	ATP-dependent protease La (EC 3.4.21.53)	Unknown	Unknown	SPy1536	313	380	315	310	1.01	0.8459	0.6565	
M5005_Spy1266	SpM1_ChORF1537_s_at	-	ATP-dependent protease La (EC 3.4.21.53)	Unknown	Unknown	SPy1537	45	1788	51	1604	1.27	0.0594	0.2676	
M5005_Spy1268	SpM1_ChORF1538_s_at	-	Methyltransferase (EC 2.1.1.-)	Unknown	Cytoplasmic	SPy1538	106	945	111	1049	1.10	0.1354	0.3458	
M5005_Spy1269	SpM1_ChORF1539_s_at	*asnA*	Aspartate--ammonia ligase (EC 6.3.1.1)	Amino acid metabolism	Cytoplasmic	SPy1539	40	1694	73	1293	3.41	0.0646	0.2748	
M5005_Spy1270	SpM1_ChORF1541_s_at	*arcC*	Carbamate kinase (EC 2.7.2.2)	Carbohydrate metabolism	Unknown	SPy1541	318	325	327	311	1.06	0.1571	0.3712	
M5005_Spy1271	SpM1_ChORF1542_s_at	-	Xaa-His dipeptidase (EC 3.4.13.3)	Amino acid metabolism	Cytoplasmic	SPy1542	282	364	244	557	0.74	0.0875	0.3002	
M5005_Spy1272	SpM1_ChORF1543_s_at	-	Arginine/ornithine antiporter	Membrane transport	Cytoplasmic Membrane	SPy1543	184	540	207	584	1.26	0.1210	0.3279	
M5005_Spy1273	SpM1_ChORF1544_s_at	*arcB*	Ornithine carbamoyltransferase (EC 2.1.3.3)	Amino acid metabolism	Cytoplasmic	SPy1544	615	118	839	97	1.86	0.7473	0.6341	
M5005_Spy1274	SpM1_ChORF1546_s_at	-	Acetyltransferase (EC 2.3.1.-)	Cellular processing	Cytoplasmic	SPy1546	634	133	780	87	1.52	0.3919	0.5061	
M5005_Spy1275	SpM1_ChORF1547_s_at	*arcA*	Arginine deiminase (EC 3.5.3.6)	Amino acid metabolism	Cytoplasmic	SPy1547	444	177	588	154	1.75	0.0517	0.2541	
M5005_Spy1275	SpM49_ChORF356-2_s_at	*arcA*	Arginine deiminase (EC 3.5.3.6)	Amino acid metabolism	Cytoplasmic		135	925	133	801	0.98	0.6468	0.6041	
M5005_Spy1276	SpM1_ChORF1548_s_at	-	Transcription regulator, Crp/Fnrfamily	Unknown	Cytoplasmic	SPy1548	137	775	134	950	0.95	0.1861	0.3936	
M5005_Spy1277	SpM1_ChORF1549_s_at	*ahrC.2*	Arginine repressor, argR	Information processing	Unknown	SPy1549	35	1808	51	1558	2.19	0.1604	0.3722	
M5005_Spy1278	SpM1_ChORF1551_s_at	-	Hypothetical protein	Unknown	Unknown	SPy1551	139	714	147	874	1.12	0.0866	0.3002	
M5005_Spy1278	SpM12_ChORF301-71_s_at	-	Hypothetical protein	Unknown	Unknown		41	1739	44	1858	1.14	0.9194	0.6743	
M5005_Spy1279	SpM1_ChORF1552_s_at	-	Hypothetical cytosolic protein	Unknown	Cytoplasmic	SPy1552	78	1162	71	1190	0.82	0.2209	0.4181	
M5005_Spy1280	SpM12_ChORF301-33_at	*zmpR*	Two-component histidine sensor kinase	Signal transduction	Cytoplasmic Membrane		56	1657	39	1868	0.49	0.1120	0.3186	

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M5005_Spy1281	SpM1_ChORF1556_s_at	*zmpS*	Two-component response regulator	Signal transduction	Cytoplasmic	SPy1556	54	1455	37	1812	0.48	0.9974	0.6931	
M5005_Spy1282	SpM1_ChORF1557_s_at	*msrA*	Peptide methionine sulfoxide reductase msrA/msrB (EC 1.8.4.6)	Cellular processing	Unknown	SPy1557	54	1617	53	1540	0.99	0.7717	0.6395	
M5005_Spy1283	SpM1_ChORF1558_s_at	-	Thiol:disulfide interchange protein tlpA	Cellular processing	Unknown	SPy1558	21	2206	25	1975	1.40	0.6055	0.5923	
M5005_Spy1284	SpM5_ChORF270b-69_s_at	-	Cytochrome C-type biogenesis protein ccdA	Unknown	Cytoplasmic Membrane		39	1905	43	1659	1.22	0.0534	0.2552	
M5005_Spy1285	M12_1348_s_at	-	Hypothetical cytosolic protein	Unknown	Cytoplasmic		29	2022	32	1809	1.18	0.4861	0.5443	
M5005_Spy1285	SpM1_ChORF1561_s_at	-	Hypothetical cytosolic protein	Unknown	Cytoplasmic	SPy1561	107	1038	131	847	1.52	0.5731	0.5804	
M5005_Spy1286	SpM1_ChORF1563_s_at	-	Conserved hypothetical protein; RexB-like involved in DNA replication, recombination, and repair	Unknown	Cytoplasmic	SPy1563	53	1493	82	1205	2.41	0.0055	0.0940	
M5005_Spy1287	SpM1_ChORF1562_s_at	-	Hypothetical protein	Unknown	Cytoplasmic	SPy1562	89	1190	139	866	2.48	0.0482	0.2502	
M5005_Spy1288	SpM1_ChORF1564_s_at	-	Hypothetical cytosolic protein	Unknown	Cytoplasmic	SPy1564	33	2054	79	1342	5.92	0.0279	0.1982	
M5005_Spy1289	SpM1_ChORF1565_s_at	-	Hypothetical protein	Unknown	Cytoplasmic	SPy1565	97	1067	127	998	1.70	0.0004	**0.0132**	**Significant**
M5005_Spy1290	SpM1_ChORF1566_s_at	-	Hypothetical protein	Unknown	Unknown	SPy1566	94	1082	68	1421	0.52	0.3330	0.4779	
M5005_Spy1291	SpM1_ChORF1567_s_at	-	ATP-dependent RNA helicase	Stress adaptation	Cytoplasmic	SPy1567	50	1661	75	1334	2.27	0.9910	0.6918	
M5005_Spy1292	SpM1_ChORF1568_s_at	*valS*	Valyl-tRNA synthetase (EC 6.1.1.9)	Protein synthesis	Cytoplasmic	SPy1568	57	1408	50	1509	0.78	0.2256	0.4208	
M5005_Spy1294	SpM1_ChORF1569_s_at	-	Ribosomal-protein-serine acetyltransferase (EC 2.3.1.-)	Protein synthesis	Unknown	SPy1569	27	2123	43	1788	2.56	0.2714	0.4449	

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M5005_Spy1294	SpM1_ChORF1570_at	-	Ribosomal-protein-serine acetyltransferase (EC 2.3.1.-)	Protein synthesis	Unknown	SPy1570	284	441	209	654	0.54	0.2837	0.4537	
M5005_Spy1295	SpM1_ChORF1571_s_at	-	Hypothetical cytosolic protein	Unknown	Cytoplasmic	SPy1571	70	1354	83	1376	1.38	0.5107	0.5539	
M5005_Spy1296	SpM1_ChORF1572_s_at	-	Hypothetical protein	Unknown	Cytoplasmic	SPy1572	95	1137	70	1440	0.53	0.4548	0.5310	
M5005_Spy1297	SpM1_ChORF1575_s_at	-	Phospho-2-dehydro-3-deoxyheptonate aldolase (EC 4.1.2.15)	Amino acid metabolism	Cytoplasmic	SPy1575	81	1081	85	1113	1.12	0.9976	0.6931	
M5005_Spy1297	SpM1_ChORF1576_s_at	-	Phospho-2-dehydro-3-deoxyheptonate aldolase (EC 4.1.2.15)	Amino acid metabolism	Cytoplasmic	SPy1576	110	1134	72	1363	0.43	0.0965	0.3058	
M5005_Spy1298	SpM1_ChORF1577_s_at	*aroB*	3-dehydroquinate synthase (EC 4.6.1.3)	Amino acid metabolism	Cytoplasmic	SPy1577	134	886	129	1015	0.92	0.4229	0.5176	
M5005_Spy1300	SpM1_ChORF1580_s_at	-	Hypothetical cytosolic protein	Unknown	Cytoplasmic	SPy1580	119	724	134	934	1.26	0.1259	0.3353	
M5005_Spy1301	SpM1_ChORF1581_s_at	-	Hypothetical cytosolic protein	Unknown	Cytoplasmic	SPy1581	197	559	347	309	3.10	0.0036	0.0713	
M5005_Spy1302	SpM1_ChORF1582_s_at	-	SAM-dependent methyltransferase	Unknown	Cytoplasmic	SPy1582	131	689	250	452	3.64	0.0361	0.2208	
M5005_Spy1303	SpM1_ChORF1584_s_at	*aroE*	Shikimate 5-dehydrogenase (EC 1.1.1.25)	Amino acid metabolism	Cytoplasmic	SPy1584	192	624	310	396	2.62	0.0050	0.0897	
M5005_Spy1303	SpM18_ChORF1591_s_at	*aroE*	Shikimate 5-dehydrogenase (EC 1.1.1.25)	Amino acid metabolism	Cytoplasmic	spyM18_1591	36	1719	36	1895	1.02	0.5818	0.5849	
M5005_Spy1304	SpM1_ChORF1586_s_at	*lacZ*	Beta-galactosidase (EC 3.2.1.23)	Carbohydrate metabolism	Unknown	SPy1586	616	112	1354	35	4.83	0.0067	0.1020	
M5005_Spy1305	SpM1_ChORF1587_s_at	*lytR*	Two-component response regulator	Signal transduction	Cytoplasmic	SPy1587	326	278	665	115	4.17	0.0064	0.0991	
M5005_Spy1306	SpM1_ChORF1588_s_at	*lytS*	Two-component sensor kinase	Signal transduction	Cytoplasmic	SPy1588	324	281	479	192	2.19	0.0074	0.1081	
M5005_Spy1307	SpM1_ChORF1589_s_at	-	Hypothetical membrane spanning protein	Unknown	Cytoplasmic Membrane	SPy1589	159	705	192	648	1.46	0.0190	0.1707	
M5005_Spy1308	SpM1_ChORF1591_s_at	-	Sugar-binding protein	Membrane transport	Unknown	SPy1591	465	240	723	110	2.43	0.0114	0.1377	
M5005_Spy1308	SpM1_ChORF1592_s_at	-	Sugar-binding protein	Membrane transport	Unknown	SPy1592	1186	33	2151	23	3.29	0.0021	**0.0471**	**Significant**

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M5005_Spy1309	SpM1_ChORF1593_s_at	-	Sugar transport system permease protein	Unknown	Cytoplasmic Membrane	SPy1593	547	127	1037	58	3.60	0.0169	0.1652	
M5005_Spy1310	SpM1_ChORF1595_s_at	-	Sugar transport system permease protein	Unknown	Cytoplasmic Membrane	SPy1595	323	274	435	213	1.81	0.0006	**0.0179**	**Significant**
M5005_Spy1311	SpM1_ChORF1596_s_at	-	Glucokinase (EC 2.7.1.2) / transcription regulator	Information processing	Cytoplasmic	SPy1596	70	1516	104	1153	2.21	0.3470	0.4836	
M5005_Spy1313	SpM1_ChORF1599_s_at	-	Beta-glucosidase (EC 3.2.1.21)	Carbohydrate metabolism	Cytoplasmic	SPy1599	262	465	325	350	1.54	0.1901	0.3986	
M5005_Spy1314	SpM1_ChORF1600_s_at	*hyl*	Hyaluronoglucosaminidase (EC 3.2.1.35)	Carbohydrate metabolism	Extracellular	SPy1600	254	450	288	457	1.28	0.2597	0.4390	
M5005_Spy1315	SpM1_ChORF1602_s_at	-	Transcriptional regulator, GntR family / Transcriptional regulator, LacI family	Information processing	Cytoplasmic	SPy1602	279	383	260	444	0.86	0.4198	0.5172	
M5005_Spy1316	SpM1_ChORF1603_s_at	-	Hypothetical protein	Unknown	Unknown	SPy1603	229	545	303	434	1.75	0.0544	0.2568	
M5005_Spy1317	SpM1_ChORF1604_s_at	-	Alpha-mannosidase (EC 3.2.1.24)	Carbohydrate metabolism	Unknown	SPy1604	501	193	629	133	1.58	0.0074	0.1081	
M5005_Spy1318	SpM1_ChORF1605_s_at	*rocA*	Sensory transduction protein kinase-like transcriptional regulator	Information processing	Cytoplasmic Membrane	SPy1605	61	1442	43	1777	0.48	0.9148	0.6743	
M5005_Spy1319	SpM49_ChORF7585-45_s_at	-	tRNA (Uracil-5-) -methyltransferase (EC 2.1.1.35)	Protein synthesis	Cytoplasmic		40	1622	75	1432	3.45	0.8240	0.6525	
M5005_Spy1320	SpM1_ChORF1607_s_at	-	Regulatory protein recX	Information processing	Unknown	SPy1607	50	1526	46	1626	0.85	0.6856	0.6155	
M5005_Spy1321	SpM1_ChORF1608_s_at	-	Hypothetical cytosolic protein	Unknown	Cytoplasmic	SPy1608	286	357	280	349	0.96	0.2408	0.4269	
M5005_Spy1323	SpM1_ChORF1610_s_at	-	Transposase	Mobile genetic element	Cytoplasmic	SPy1610	25	1935	24	2109	0.90	0.8672	0.6623	
M5005_Spy1324	SpM18_ChORF1620_x_at	-	Hypothetical protein	Unknown	Unknown	spyM18_1620	23	2275	29	2119	1.70	0.2924	0.4565	
M5005_Spy1324	SpM18_ChORF1621_s_at	-	Hypothetical protein	Unknown	Unknown	spyM18_1621	2366	19	2823	21	1.42	0.1827	0.3892	
M5005_Spy1326	SpM1_ChORF1615_s_at	*comFC*	ComF operon protein 3	Membrane transport	Unknown	SPy1615	14	2430	14	2415	1.01	0.2965	0.4589	
M5005_Spy1327	SpM1_ChORF1616_s_at	*comFA*	ComF operon protein 1	Membrane transport	Cytoplasmic	SPy1616	140	865	103	1281	0.55	0.4094	0.5147	
M5005_Spy1328	SpM1_ChORF1617_s_at	-	Xaa-Pro dipeptidase (EC 3.4.13.9)	Unknown	Cytoplasmic	SPy1617	43	1620	50	1607	1.37	0.6538	0.6061	

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M5005_Spy1329	SpM1_ChORF1618_s_at	*cysM*	Cysteine synthase (EC 4.2.99.8)	Amino acid metabolism	Cytoplasmic	SPy1618	82	1350	87	1245	1.12	0.8666	0.6623	
M5005_Spy1330	SpM1_ChORF1619_s_at	-	S1-type RNA-binding domain	Unknown	Unknown	SPy1619	165	710	121	1010	0.54	0.9368	0.6775	
M5005_Spy1331	SpM18_ChORF1629_s_at	-	Peptidyl-prolyl cis-trans isomerase (EC 5.2.1.8)	Unknown	Cytoplasmic	spyM18_1629	143	814	138	913	0.92	0.7559	0.6366	
M5005_Spy1332	SpM1_ChORF1621_s_at	*rr03*	Two-component response regulator yvqC	Signal transduction	Cytoplasmic	SPy1621	193	651	185	631	0.92	0.5482	0.5698	
M5005_Spy1332	SpM1_ChORF1622_s_at	*hk03*	Two-component histidine sesnor kinase	Signal transduction	Cytoplasmic	SPy1622	95	1043	132	995	1.91	0.3921	0.5061	
M5005_Spy1334	SpM1_ChORF1623_s_at	-	Transporter yvqF	Unknown	Cytoplasmic Membrane	SPy1623	32	2169	50	1673	2.54	0.6973	0.6184	
M5005_Spy1335	SpM5_ChORF-b16C31-7_s_at	-	Serine/threonine protein kinase (EC 2.7.1.37)	Unknown	Cytoplasmic Membrane		174	522	213	639	1.51	0.5020	0.5512	
M5005_Spy1336	SpM1_ChORF1626_s_at	*pppL/stp1*	Protein phosphatase 2C (EC 3.1.3.16)	Cellular processing	Cytoplasmic	SPy1626	365	310	305	366	0.70	0.7280	0.6287	
M5005_Spy1337	SpM1_ChORF1627_s_at	*sunL*	16S rRNA m(5)C 967 methyltransferase (EC 2.1.1.-)	Information processing	Cytoplasmic	SPy1627	209	618	200	523	0.92	0.2195	0.4175	
M5005_Spy1337	SpM1_ChORF1628_s_at	*sunL*	16S rRNA m(5)C 967 methyltransferase (EC 2.1.1.-)	Information processing	Cytoplasmic	SPy1628	249	459	262	415	1.10	0.5443	0.5695	
M5005_Spy1339	SpM1_ChORF1629_s_at	*priA*	Primosomal protein N'	Information processing	Cytoplasmic	SPy1629	119	1004	128	889	1.16	0.2642	0.4407	
M5005_Spy1340	SpM1_ChORF1630_s_at	-	DNA-directed RNA polymerase omega chain (EC 2.7.7.6)	Unknown	Cytoplasmic	SPy1630	267	445	252	399	0.89	0.1826	0.3892	
M5005_Spy1341	SpM1_ChORF1632_s_at	*gmk*	Guanylate kinase (EC 2.7.4.8)	Nucleotide metabolism	Cytoplasmic	SPy1632	177	604	171	695	0.93	0.4665	0.5363	
M5005_Spy1342	SpM1_ChORF1633_s_at	-	Hydrolase (HAD superfamily)	Unknown	Cytoplasmic	SPy1633	907	61	927	69	1.04	0.3303	0.4776	
M5005_Spy1343	SpM1_ChORF1634_s_at	-	Transcriptional regulators, LysR family	Information processing	Cytoplasmic	SPy1634	112	1072	128	920	1.29	0.0810	0.2961	
M5005_Spy1344	SpM1_ChORF1637_s_at	*atoB*	Acetyl-CoA acetyltransferase (EC 2.3.1.9)	Lipid metabolism	Cytoplasmic	SPy1637	31	1996	30	1878	0.93	0.6834	0.6147	
M5005_Spy1345	SpM1_ChORF1638_s_at	*atoD.1*	Acetate CoA-transferase alpha subunit (EC 2.8.3.8)	Cell wall metabolism	Cytoplasmic	SPy1638	25	2252	23	2127	0.85	0.7658	0.6382	

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M5005_Spy1346	SpM1_ChORF1639_s_at	*atoA*	Acetate CoA-transferase beta subunit (EC 2.8.3.8)	Cell wall metabolism	Cytoplasmic	SPy1639	33	2016	34	1791	1.05	0.2361	0.4227	
M5005_Spy1347	SpM1_ChORF1640_s_at	-	D-beta-hydroxybutyrate dehydrogenase (EC 1.1.1.30)	Unknown	Cytoplasmic	SPy1640	29	2068	18	2356	0.39	0.4159	0.5169	
M5005_Spy1347	SpM12_ChORF289-13_s_at	-	D-beta-hydroxybutyrate dehydrogenase (EC 1.1.1.30)	Unknown	Cytoplasmic		12	2606	12	2471	1.12	0.2308	0.4227	
M5005_Spy1348	SpM1_ChORF1641_s_at	-	D-beta-hydroxybutyrate permease	Unknown	Cytoplasmic Membrane	SPy1641	63	1392	53	1555	0.72	0.6277	0.5996	
M5005_Spy1348	SpM5_ChORF169a-188_s_at	-	D-beta-hydroxybutyrate permease	Unknown	Cytoplasmic Membrane		31	2038	53	1664	2.97	0.0891	0.3002	
M5005_Spy1349	SpM1_ChORF1642_s_at	*luxS*	Autoinducer-2 production protein luxS (EC 3.13.1.-)	Information processing	Cytoplasmic	SPy1642	135	823	148	861	1.21	0.6743	0.6128	
M5005_Spy1350	SpM1_ChORF1643_s_at	-	Hypothetical protein	Unknown	Unknown	SPy1643	611	136	569	199	0.87	0.1219	0.3283	
M5005_Spy1351	SpM1_ChORF1644_s_at	-	Methyltransferase (EC 2.1.1.-)	Unknown	Cytoplasmic	SPy1644	509	185	389	244	0.58	0.0551	0.2582	
M5005_Spy1352	SpM1_ChORF1646_s_at	-	Cell division initiation protein DivIVA	Unknown	Cytoplasmic	SPy1646	297	351	302	402	1.04	0.3241	0.4769	
M5005_Spy1352	SpM12_ChORF289-43_s_at	-	Cell division initiation protein DivIVA	Unknown	Cytoplasmic		55	1482	76	1243	1.94	0.2880	0.4544	
M5005_Spy1353	SpM1_ChORF1647_s_at	-	Hypothetical cytosolic protein	Unknown	Cytoplasmic	SPy1647	66	1417	86	1082	1.70	0.6856	0.6155	
M5005_Spy1354	SpM1_ChORF1648_s_at	*recU*	Recombination protein recU	Cellular processing	Unknown	SPy1648	725	116	580	153	0.64	0.6191	0.5962	
M5005_Spy1355	SpM1_ChORF1649_s_at	*pbp1A; ponA*	Multimodular transpeptidase-transglycosylase PBP 1A	Cell wall metabolism	Extracellular	SPy1649	1497	29	1585	31	1.12	0.8612	0.6613	
M5005_Spy1356	SpM1_ChORF1651_s_at	*pepC*	Aminopeptidase C (EC 3.4.22.40)	Amino acid metabolism	Cytoplasmic	SPy1651	324	315	485	206	2.24	0.0335	0.2148	
M5005_Spy1357	SpM18_ChORF1663_s_at	-	NH(3)-dependent NAD(+) synthetase (EC 6.3.5.1)	Unknown	Cytoplasmic	spyM18_1663	143	790	120	993	0.70	0.9640	0.6850	
M5005_Spy1358	SpM1_ChORF1653_s_at	*nadE*	Nicotinate phosphoribosyltransferase (EC 2.4.2.11)	Phage	Cytoplasmic	SPy1652	177	673	188	676	1.13	0.6366	0.6019	

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M5005_Spy1359	SpM1_ChORF1654_s_at	-	Amino acid permease	Unknown	Cytoplasmic Membrane	SPy1653	101	1119	107	1103	1.12	0.0198	0.1745	
M5005_Spy1360	SpM18_ChORF1666_s_at	*trxB*	Thioredoxin reductase (EC 1.8.1.9)	Amino acid metabolism	Cytoplasmic	spyM18_1666	125	796	105	1107	0.70	0.8204	0.6525	
M5005_Spy1361	SpM1_ChORF1656_s_at	*aapA*	Hypothetical membrane associated protein	Unknown	Cytoplasmic Membrane	SPy1654	30	1977	36	1892	1.43	0.8815	0.6650	
M5005_Spy1362	SpM1_ChORF1657_s_at	-	Transporter	Unknown	Cytoplasmic Membrane	SPy1656	104	979	134	907	1.68	0.8048	0.6509	
M5005_Spy1363	SpM1_ChORF1658_s_at	-	Amino acid ABC transporter permease protein	Membrane transport	Cytoplasmic Membrane	SPy1657	89	1125	131	868	2.17	0.0257	0.1923	
M5005_Spy1364	SpM1_ChORF1659_s_at	-	ATP-dependent RNA helicase	Stress adaptation	Cytoplasmic	SPy1658	282	433	207	571	0.54	0.3750	0.4947	
M5005_Spy1364	SpM12_ChORF274-19_s_at	-	ATP-dependent RNA helicase	Stress adaptation	Cytoplasmic		113	851	136	890	1.44	0.3902	0.5057	
M5005_Spy1365	SpM1_ChORF1662_s_at	-	Phospho-N-acetylmuramoyl-pentapeptide-transferase (EC 2.7.8.13)	Cell wall metabolism	Cytoplasmic Membrane	SPy1659	83	1193	116	1038	1.96	0.3638	0.4889	
M5005_Spy1366	SpM1_ChORF1664_s_at	*mraY*	Division specific D,D-transpeptidase / Cell division protein ftsI	Cellular processing	Cytoplasmic Membrane	SPy1662	269	341	295	333	1.20	0.9883	0.6915	
M5005_Spy1367	SpM1_ChORF1665_s_at	*pbpX*	Cell division protein ftsL	Cellular processing	Unknown	SPy1664	29	2040	15	2371	0.26	0.6285	0.5999	
M5005_Spy1368	SpM1_ChORF1666_s_at	*ftsL*	S-adenosyl-methyltransferase mraW (EC 2.1.1.-)	Unknown	Cytoplasmic	SPy1665	237	514	188	649	0.63	0.0537	0.2552	
M5005_Spy1370	SpM1_ChORF1670_s_at	-	Gamma-glutamyl phosphate reductase (EC 1.2.1.41)	Unknown	Cytoplasmic	SPy1666	171	704	147	915	0.74	0.4059	0.5120	
M5005_Spy1370	SpM1_ChORF1672_s_at	*proA*	Gamma-glutamyl phosphate reductase (EC 1.2.1.41)	Amino acid metabolism	Cytoplasmic	SPy1670	36	2139	22	2225	0.37	0.4545	0.5310	
M5005_Spy1372	SpM1_ChORF1673_at	*proB*	ABC transporter permease protein	Membrane transport	Cytoplasmic Membrane	SPy1672	149	752	212	559	2.03	0.0295	0.2028	
M5005_Spy1372	SpM1_ChORF1673_s_at	*proB*	ABC transporter permease protein	Membrane transport	Cytoplasmic Membrane	SPy1673	170	637	208	624	1.51	0.0251	0.1923	
M5005_Spy1373	SpM1_ChORF1674_s_at	-	ABC transporter ATP-binding protein	Membrane transport	Cytoplasmic Membrane	SPy1674	103	980	172	763	2.80	0.8404	0.6563	

M5005_gene	RML Probeset	Gene	Description	Function	Predicted Cellular Localization *	Synonym †	Normalized Expression (WT) ‡	Transcript Rank (WT) §	Normalized Expression (Mutant) ‡	Transcript Rank (Mutant) §	Fold Change (Mutant : WT) **	*P* -value (Strain)	*Q* -value (Strain)††	Strain Significance (FDR=0.05)
M5005_Spy1374	SpM1_ChORF1675_s_at	-	Hypothetical protein	Unknown	Cytoplasmic	SPy1675	107	1074	102	1145	0.92	0.0940	0.3033	
M5005_Spy1375	SpM1_ChORF1676_s_at	*tkt*	Transketolase (EC 2.2.1.1)	Carbohydrate metabolism	Cytoplasmic	SPy1676	1006	45	1148	41	1.30	0.2799	0.4510	
M5005_Spy1376	SpM1_ChORF1678_s_at	*tkt*	Transketolase (EC 2.2.1.1)	Carbohydrate metabolism	Cytoplasmic	SPy1678	744	93	741	92	0.99	0.9047	0.6715	
M5005_Spy1377	SpM1_ChORF1680_s_at	-	Trans-acting positive transcriptional regulator	Information processing	Cytoplasmic	SPy1680	372	289	335	355	0.81	0.8056	0.6510	
M5005_Spy1377	SpM1_ChORF1681_s_at	-	Trans-acting positive transcriptional regulator	Information processing	Cytoplasmic	SPy1681	667	132	587	165	0.77	0.5243	0.5615	
M5005_Spy1379	SpM1_ChORF1682_s_at	*glpF*	Glycerol uptake facilitator protein	Carbohydrate metabolism	Cytoplasmic Membrane	SPy1682	239	492	225	501	0.89	0.6798	0.6139	
M5005_Spy1380	SpM1_ChORF1683_s_at	*glpO*	Alpha-glycerophosphate oxidase (EC 1.1.3.21)	Carbohydrate metabolism	Extracellular	SPy1683	554	150	409	205	0.55	0.6346	0.6013	
M5005_Spy1381	SpM1_ChORF1684_s_at	*glpK*	Glycerol kinase (EC 2.7.1.30)	Carbohydrate metabolism	Unknown	SPy1684	314	360	243	506	0.60	0.0060	0.0952	
M5005_Spy1382	SpM1_ChORF1686_s_at	-	Hypothetical membrane associated protein	Unknown	Unknown	SPy1686	1065	49	692	117	0.42	0.1529	0.3657	
M5005_Spy1383	SpM1_ChORF1687_s_at	-	Hypothetical cytosolic protein	Unknown	Cytoplasmic	SPy1687	215	567	229	578	1.14	0.0995	0.3083	
M5005_Spy1384	SpM1_ChORF1688_at	*glyS*	Glycyl-tRNA synthetase beta chain (EC 6.1.1.14)	Protein synthesis	Unknown	SPy1688	160	883	130	954	0.65	0.0084	0.1150	
M5005_Spy1384	SpM5_ChORF169a-196_at	*glyS*	Glycyl-tRNA synthetase beta chain (EC 6.1.1.14)	Protein synthesis	Unknown		33	1718	73	1269	4.79	0.1577	0.3712	
M5005_Spy1385	SpM1_ChORF1689_s_at	*glyQ*	Glycyl-tRNA synthetase alpha chain (EC 6.1.1.14)	Protein synthesis	Cytoplasmic	SPy1689	142	764	134	896	0.89	0.1097	0.3154	
M5005_Spy1386	SpM1_ChORF1691_s_at	-	Hypothetical membrane spanning protein	Unknown	Cytoplasmic Membrane	SPy1691	406	244	313	361	0.60	0.5318	0.5655	
M5005_Spy1387	SpM1_ChORF1693_s_at	-	Aldo/keto reductase family	Carbohydrate metabolism	Cytoplasmic	SPy1693	1366	31	1055	36	0.60	0.2685	0.4436	
M5005_Spy1388	SpM1_ChORF1694_s_at	*nagA*	N-acetylglucosamine-6-phosphate deacetylase (EC 3.5.1.25)	Carbohydrate metabolism	Unknown	SPy1694	513	191	654	107	1.63	0.0620	0.2713	
M5005_Spy1389	SpM1_ChORF1695_s_at	-	Sodium-dependent phosphate transporter	Membrane transport	Cytoplasmic Membrane	SPy1695	163	788	160	749	0.97	0.3531	0.4869	

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M5005_Spy1390	SpM1_ChORF1697_s_at	-	Hypothetical protein	Unknown	Extracellular	SPy1697	83	1323	96	1231	1.34	0.4931	0.5486	
M5005_Spy1391	SpM1_ChORF1698_s_at	-	DegV family protein	Unknown	Cytoplasmic	SPy1698	162	675	167	826	1.05	0.1612	0.3722	
M5005_Spy1392	SpM1_ChORF1699_s_at	-	Transcriptional regulator, TetR family	Unknown	Cytoplasmic	SPy1699	89	1398	73	1312	0.68	0.4132	0.5162	
M5005_Spy1393	SpM1_ChORF1700_s_at	-	Hydrolase (HAD superfamily)	Unknown	Cytoplasmic	SPy1700	229	512	252	394	1.21	0.2265	0.4208	
M5005_Spy1394	SpM1_ChORF1701_s_at	-	Hypothetical membrane spanning protein	Unknown	Cytoplasmic Membrane	SPy1701	216	621	290	431	1.80	0.8236	0.6525	
M5005_Spy1395	SpM1_ChORF1704_s_at	*lacD.1*	Tagatose-bisphosphate aldolase (EC 4.1.2.40)	Carbohydrate metabolism	Unknown	SPy1704	143	844	271	441	3.59	0.0001	**0.0043**	**Significant**
M5005_Spy1396	SpM18_ChORF1715_at	*nadE*	Tagatose-6-phosphate kinase (EC 2.7.1.144)	Carbohydrate metabolism	Unknown	spyM18_1715	53	1601	103	1066	3.84	0.0139	0.1497	
M5005_Spy1397	SpM1_ChORF1707_at	*lacB.1*	Galactose-6-phosphate isomerase lacB subunit (EC 5.3.1.26)	Carbohydrate metabolism	Cytoplasmic	SPy1707	63	1321	156	755	6.10	0.0086	0.1157	
M5005_Spy1397	SpM1_ChORF1707_s_at	*lacB.1*	Galactose-6-phosphate isomerase lacB subunit (EC 5.3.1.26)	Carbohydrate metabolism	Cytoplasmic	SPy1708	100	975	149	793	2.20	0.1153	0.3225	
M5005_Spy1398	SpM1_ChORF1708_s_at	*lacA.1*	Galactose-6-phosphate isomerase lacA subunit (EC 5.3.1.26)	Carbohydrate metabolism	Unknown	SPy1709	101	1023	174	757	2.93	0.0046	0.0858	
M5005_Spy1399	SpM18_ChORF1719_s_at	-	PTS system, galactose-specific IIC component (EC 2.7.1.69)	Carbohydrate metabolism	Cytoplasmic Membrane	spyM18_1719	137	805	327	331	5.69	2.9E-05	**0.0012**	**Significant**
M5005_Spy1401	SpM1_ChORF1710_s_at	-	PTS system, galactose-specific IIA component (EC 2.7.1.69)	Carbohydrate metabolism	Cytoplasmic	SPy1710	153	728	309	325	4.08	0.0003	**0.0105**	**Significant**
M5005_Spy1401	SpM1_ChORF1711_s_at	-	PTS system, galactose-specific IIA component (EC 2.7.1.69)	Carbohydrate metabolism	Cytoplasmic	SPy1711	107	899	112	940	1.09	0.0019	**0.0454**	**Significant**
M5005_Spy1402	SpM1_ChORF1712_s_at	*lacR.1*	Lactose phosphotransferase system repressor	Information processing	Cytoplasmic	SPy1712	37	1832	48	1764	1.65	0.5112	0.5539	
M5005_Spy1404	SpM1_ChORF1714_s_at	*copZ*	Copper chaperone	Membrane transport	Unknown	SPy1714	265	385	237	556	0.80	0.3504	0.4854	
M5005_Spy1405	SpM1_ChORF1715_s_at	*copA*	Copper-exporting ATPase (EC 3.6.3.4)	Membrane transport	Cytoplasmic Membrane	SPy1715	238	446	202	638	0.72	0.0569	0.2635	

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M5005_Spy1406	SpM1_ChORF1717_at	*copY*	CopAB ATPases metal-fist type repressor	Information processing	Cytoplasmic	SPy1717	116	932	104	1032	0.80	0.7997	0.6497	
M5005_Spy1407	SpM1_ChORF1718_s_at	-	Esterase (EC 3.1.1.-)	Unknown	Unknown	SPy1718	50	1672	71	1370	2.03	0.9668	0.6854	
M5005_Spy1408	SpM1_ChORF1719_s_at	*rbfA*	Ribosome-binding factor A	Cellular processing	Cytoplasmic	SPy1719	215	544	307	423	2.04	0.7046	0.6200	
M5005_Spy1409	SpM1_ChORF1721_s_at	*infB*	Bacterial Protein Translation Initiation Factor 2 (IF-2)	Cellular processing	Cytoplasmic	SPy1721	405	238	385	264	0.91	0.0694	0.2797	
M5005_Spy1411	SpM1_ChORF1722_s_at	-	Hypothetical cytosolic protein	Unknown	Cytoplasmic	SPy1722	142	741	147	971	1.07	0.3117	0.4706	
M5005_Spy1411	SpM1_ChORF1723_s_at	-	Hypothetical cytosolic protein	Unknown	Cytoplasmic	SPy1723	175	709	169	675	0.93	0.4239	0.5176	
M5005_Spy1412	SpM1_ChORF1724_s_at	*nusA*	N utilization substance protein A	Cellular processing	Cytoplasmic	SPy1724	442	182	456	201	1.06	0.2418	0.4269	
M5005_Spy1413	SpM1_ChORF1725_s_at	-	Hypothetical cytosolic protein	Unknown	Cytoplasmic	SPy1725	159	640	181	647	1.30	0.2971	0.4589	
M5005_Spy1415	SpM12_ChORF251-6_at	*sdaD2*	Phage-encoded streptodornase (EC 3.1.21.1)	Virulence	Unknown		210	579	253	400	1.45	0.1092	0.3154	
M5005_Spy1415	SpM12_ChORF251-8_at	*sdaD2*	Phage-encoded streptodornase (EC 3.1.21.1)	Virulence	Unknown		17	2487	14	2538	0.75	0.8322	0.6548	
M5005_Spy1416	SpM12_ChORF251-7_at	-	N-acetylmuramoyl-L-alanine amidase (EC 3.5.1.28)	Phage	Cytoplasmic		114	1066	89	1140	0.61	0.0801	0.2939	
M5005_Spy1420	SpM1_ChORF0999_at	-	Phage protein	Phage	Cytoplasmic	SPy0999	28	1981	25	2184	0.80	0.7127	0.6214	
M5005_Spy1420	SpM12_ChORF299-66_at	-	Phage protein	Phage	Cytoplasmic		92	1109	59	1492	0.41	0.6621	0.6081	
M5005_Spy1421	SpM12_ChORF299-1_at	-	Phage infection protein	Phage	Unknown		10	2614	16	2456	2.34	0.3602	0.4888	
M5005_Spy1421	SpM12_ChORF299-65_at	-	Phage infection protein	Phage	Unknown		60	1412	49	1593	0.65	0.9030	0.6707	
M5005_Spy1422	SpM12_ChORF299-64_at	-	Phage protein	Phage	Unknown		100	1073	69	1383	0.48	0.8453	0.6565	
M5005_Spy1423	SpM12_ChORF299-63_at	-	Hyaluronoglucosaminidase (EC 3.2.1.35)	Phage	Cytoplasmic		48	1713	50	1517	1.07	0.6864	0.6159	
M5005_Spy1424	SpM12_ChORF299-2_x_at	-	Phage endopeptidase	Phage	Cytoplasmic		42	1743	31	1867	0.53	0.3293	0.4776	
M5005_Spy1424	SpM12_ChORF299-62_at	-	Phage endopeptidase	Phage	Cytoplasmic		13	2565	11	2580	0.82	0.1432	0.3546	

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M5005_Spy1425	SpM12_ChORF299-61_s_at	-	Phage protein	Phage	Cytoplasmic		29	2173	24	2083	0.70	0.1806	0.3887	
M5005_Spy1426	SpM12_ChORF299-3_s_at	-	Phage protein	Phage	Cell Wall		20	2341	11	2596	0.29	0.2437	0.4278	
M5005_Spy1426	SpM12_ChORF299-4_at	-	Phage protein	Phage	Cell Wall		21	2260	22	2278	1.08	0.6129	0.5951	
M5005_Spy1426	SpM12_ChORF299-5_s_at	-	Phage protein	Phage	Cell Wall		57	1452	42	1748	0.53	0.2186	0.4166	
M5005_Spy1426	SpM12_ChORF299-60_at	-	Phage protein	Phage	Cell Wall		27	2187	15	2402	0.30	0.4377	0.5231	
M5005_Spy1427	SpM12_ChORF299-59_s_at	-	Phage protein	Phage	Cytoplasmic		20	2390	14	2440	0.48	0.5607	0.5750	
M5005_Spy1428	SpM12_ChORF299-58_s_at	-	Phage protein	Phage	Cytoplasmic		26	2239	41	1627	2.51	0.5070	0.5532	
M5005_Spy1428	SpM12_ChORF299-6_s_at	-	Phage protein	Phage	Cytoplasmic		36	1649	31	1861	0.77	0.1289	0.3379	
M5005_Spy1429	SpM12_ChORF299-57_s_at	-	Phage protein	Phage	Cytoplasmic		31	1979	48	1735	2.41	0.1596	0.3721	
M5005_Spy1430	SpM12_ChORF299-56_s_at	-	Phage protein	Phage	Cytoplasmic		29	2047	36	1779	1.56	0.9553	0.6835	
M5005_Spy1432	SpM12_ChORF299-55_s_at	-	Phage protein	Phage	Unknown		20	2429	14	2470	0.48	0.2321	0.4227	
M5005_Spy1432	SpyM3_1427_at	-	Phage protein	Phage	Unknown	spyM3_1427	39	1556	29	1928	0.55	0.3642	0.4889	
M5005_Spy1433	SpM12_ChORF299-54_s_at	-	Phage protein	Phage	Cytoplasmic		17	2457	20	2175	1.32	0.3504	0.4854	
M5005_Spy1434	SpM12_ChORF299-53_s_at	-	Phage protein	Phage	Unknown		26	2274	25	2178	0.96	0.9895	0.6916	
M5005_Spy1435	SpM12_ChORF299-52_s_at	-	Phage scaffold protein	Phage	Cytoplasmic		37	1751	47	1805	1.59	0.6113	0.5941	
M5005_Spy1435	SpM12_ChORF299-7_at	-	Phage scaffold protein	Phage	Cytoplasmic		109	1111	98	1236	0.80	0.1415	0.3533	
M5005_Spy1437	SpyM3_1432_at	-	Hypothetical phage protein	Phage	Unknown	spyM3_1432	39	1872	22	2222	0.33	0.1399	0.3519	
M5005_Spy1438	SpM12_ChORF299-51_s_at	-	Phage protein	Phage	Cytoplasmic		29	2174	17	2377	0.34	0.6761	0.6129	
M5005_Spy1439	SpM12_ChORF299-50_at	-	Portal protein	Phage	Unknown		21	2455	19	2152	0.85	0.7889	0.6469	
M5005_Spy1440	SpM12_ChORF299-48_at	-	Terminase large subunit	Phage	Cytoplasmic		14	2601	15	2510	1.06	0.3350	0.4792	
M5005_Spy1440	SpM12_ChORF299-49_at	-	Terminase large subunit	Phage	Cytoplasmic		52	1596	51	1559	0.99	0.0314	0.2078	

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M5005_Spy1440	SpM12_ChORF299-49_s_at	-	Terminase large subunit	Phage	Cytoplasmic		31	1904	35	1730	1.26	0.6749	0.6129	
M5005_Spy1440	SpM12_ChORF299-8_s_at	-	Terminase large subunit	Phage	Cytoplasmic		19	2360	21	2303	1.20	0.4763	0.5413	
M5005_Spy1442	SpM12_ChORF299-47_s_at	-	Phage transcriptional activator	Phage	Unknown		69	1265	48	1633	0.49	0.0214	0.1827	
M5005_Spy1443	M12_1752_at	-	Phage protein	Phage	Unknown		17	2331	15	2388	0.71	0.1817	0.3888	
M5005_Spy1444	SpM12_ChORF299-46_at	-	Adenine-specific methyltransferase (EC 2.1.1.72)	Phage	Cytoplasmic		36	1975	37	1775	1.03	0.6647	0.6091	
M5005_Spy1444	SpM12_ChORF299-9_at	-	Adenine-specific methyltransferase (EC 2.1.1.72)	Phage	Cytoplasmic		18	2445	39	1754	4.72	0.5993	0.5893	
M5005_Spy1446	SpyM3_1439_at	-	Phage protein	Phage	Extracellular	spyM3_1439	30	1968	33	1970	1.22	0.5481	0.5698	
M5005_Spy1447	SpM12_ChORF299-45_s_at	-	Phage-related DNA helicase	Phage	Unknown		15	2478	18	2394	1.35	0.2294	0.4227	
M5005_Spy1449	SpM12_ChORF299-10_at	-	DNA primase	Phage	Unknown		57	1450	47	1697	0.68	0.4740	0.5403	
M5005_Spy1449	SpM12_ChORF299-44_at	-	DNA primase	Phage	Unknown		40	1901	25	1790	0.38	0.0057	0.0949	
M5005_Spy1450	SpM12_ChORF299-43_at	-	Phage-encoded DNA polymerase (EC 2.7.7.7)	Phage	Cytoplasmic		37	1918	34	1900	0.86	0.1649	0.3758	
M5005_Spy1451	SpM12_ChORF299-42_at	-	Phage protein	Phage	Cytoplasmic		71	1298	100	1033	2.00	0.1434	0.3546	
M5005_Spy1452	SpM12_ChORF299-41_at	-	Phage protein	Phage	Unknown		23	2186	35	1795	2.28	0.0656	0.2754	
M5005_Spy1453	SpM12_ChORF299-40_at	-	Phage protein	Phage	Cytoplasmic		52	1678	47	1564	0.82	0.2388	0.4255	
M5005_Spy1454	SpM12_ChORF299-39_s_at	-	Phage protein	Phage	Cytoplasmic		51	1559	94	1176	3.41	0.7748	0.6410	
M5005_Spy1456	SpyM3_1447_at	-	Phage protein	Phage	Unknown	spyM3_1447	34	1976	30	1952	0.78	0.7867	0.6466	
M5005_Spy1457	SpM12_ChORF299-38_at	-	Phage protein	Phage	Cytoplasmic		19	2286	29	2062	2.27	0.9561	0.6838	
M5005_Spy1458	M12_1767_at	-	Phage protein	Phage	Cytoplasmic		68	1319	55	1427	0.64	0.6463	0.6041	
M5005_Spy1460	M12_1769_at	-	Phage protein	Phage	Cytoplasmic		101	1127	74	1218	0.54	0.8164	0.6512	
M5005_Spy1461	M12_1770_at	-	Phage protein	Phage	Unknown		102	978	105	1186	1.06	0.2351	0.4227	
M5005_Spy1462	SpM12_ChORF299-11_at	-	Phage protein	Phage	Unknown		17	2208	12	2584	0.46	0.0914	0.3002	
M5005_Spy1463	M12_1772_x_at	-	Phage protein	Phage	Extracellular		37	1632	38	1678	1.03	0.5825	0.5849	

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M5005_Spy1464	SpM12_ChORF299-12_at	-	Phage transcriptional regulator, Cro/CI family	Phage	Unknown		21	2452	16	2337	0.62	0.0943	0.3033	
M5005_Spy1465	SpM12_ChORF299-13_at	-	Phage protein	Phage	Cytoplasmic		50	1626	37	1802	0.56	0.4410	0.5244	
M5005_Spy1466	SpM12_ChORF299-14_at	-	Phage protein	Phage	Cytoplasmic		107	1155	138	816	1.66	0.5340	0.5665	
M5005_Spy1467	SpM12_ChORF299-15_at	*int.3*	DNA integration/recombination /invertion protein phi5005.3 int	Phage	Cytoplasmic		45	1658	47	1643	1.06	0.2557	0.4345	
M5005_Spy1468	SpM1_ChORF1726_s_at	-	tRNA (m(7)G46) methyltransferase (EC 2.1.1.-)	Protein synthesis	Unknown	SPy1726	159	717	123	935	0.60	0.7696	0.6391	
M5005_Spy1469	SpM1_ChORF1727_s_at	-	Phosphotransferase enzyme family	Unknown	Cytoplasmic	SPy1727	378	270	385	255	1.04	0.8005	0.6499	
M5005_Spy1470	SpM1_ChORF1728_s_at	-	Protein ecsB	Membrane transport	Cytoplasmic Membrane	SPy1728	86	1100	92	1110	1.14	0.3509	0.4854	
M5005_Spy1471	SpM1_ChORF1729_s_at	-	ABC-type transporter ATP-binding protein ecsA	Membrane transport	Cytoplasmic Membrane	SPy1729	125	843	124	1009	0.99	0.2044	0.4077	
M5005_Spy1472	SpM1_ChORF1730_s_at	*hit*	Bis(5'-nucleosyl)-tetraphosphatase (asymmetrical) (EC 3.6.1.17)	Cellular processing	Cytoplasmic	SPy1730	162	732	187	655	1.33	0.9733	0.6874	
M5005_Spy1473	SpM1_ChORF1731_s_at	-	Hypothetical protein	Unknown	Unknown	SPy1731	142	831	138	887	0.94	0.7167	0.6231	
M5005_Spy1474	SpM1_ChORF1733_s_at	*lytR*	Transcriptional regulator, LytR family	Information processing	Unknown	SPy1733	128	826	110	1004	0.74	0.6399	0.6031	
M5005_Spy1474	SpM12_ChORF299-19_s_at	*lytR*	Transcriptional regulator, LytR family	Information processing	Unknown		9	2588	11	2560	1.66	0.3381	0.4798	
M5005_Spy1476	SpM1_ChORF1734_s_at	-	ATP/GTP hydrolase	Cellular processing	Cytoplasmic	SPy1734	64	1384	65	1479	1.04	0.0618	0.2713	
M5005_Spy1476	SpM1_ChORF1735_s_at	-	ATP/GTP hydrolase	Cellular processing	Cytoplasmic	SPy1735	96	1049	120	1090	1.55	0.4399	0.5235	
M5005_Spy1477	SpM1_ChORF1736_s_at	-	Guanine-hypoxanthine permease	Membrane transport	Cytoplasmic Membrane	SPy1736	45	1623	60	1569	1.77	0.0262	0.1949	
M5005_Spy1478	SpM1_ChORF1737_s_at	-	Hydrolase (HAD superfamily)	Unknown	Unknown	SPy1737	221	555	187	701	0.72	0.2533	0.4334	

M5005_gene	RML Probeset	Gene	Description	Function	Predicted Cellular Localization *	Synonym †	Normalized Expression (WT) ‡	Transcript Rank (WT) §	Normalized Expression (Mutant) ‡	Transcript Rank (Mutant) §	Fold Change (Mutant : WT) **	*P* -value (Strain)	*Q* -value (Strain)††	Strain Significance (FDR=0.05)
M5005_Spy1479	SpM1_ChORF1738_s_at	*manL*	PTS system, mannose-specific IIAB component (EC 2.7.1.69)	Carbohydrate metabolism	Cytoplasmic	SPy1738	178	725	130	853	0.53	0.4424	0.5248	
M5005_Spy1480	SpM1_ChORF1739_s_at	*manM*	PTS system, mannose-specific IIC component (EC 2.7.1.69)	Carbohydrate metabolism	Cytoplasmic Membrane	SPy1739	181	614	161	777	0.79	0.0523	0.2541	
M5005_Spy1481	SpM1_ChORF1740_s_at	*manN*	PTS system, mannose-specific IID component (EC 2.7.1.69)	Carbohydrate metabolism	Cytoplasmic Membrane	SPy1740	125	1028	111	1102	0.79	0.5431	0.5695	
M5005_Spy1482	SpM1_ChORF1741_s_at	*manO*	Hypothetical cytosolic protein	Membrane transport	Unknown	SPy1741	87	1269	37	1652	0.19	0.4468	0.5280	
M5005_Spy1483	SpM1_ChORF1742_s_at	*serS*	Seryl-tRNA synthetase (EC 6.1.1.11)	Protein synthesis	Cytoplasmic	SPy1742	118	967	141	785	1.43	0.6515	0.6058	
M5005_Spy1484	SpM1_ChORF1744_s_at	*accD*	Acetyl-coenzyme A carboxylase carboxyl transferase subunit alpha (EC 6.4.1.2)	Lipid metabolism	Cytoplasmic	SPy1744	62	1391	80	1315	1.66	0.1006	0.3098	
M5005_Spy1485	SpM1_ChORF1743_s_at	*accA*	Acetyl-coenzyme A carboxylase carboxyl transferase subunit beta (EC 6.4.1.2)	Lipid metabolism	Cytoplasmic	SPy1743	52	1399	83	1483	2.53	0.8143	0.6512	
M5005_Spy1486	SpM1_ChORF1745_s_at	*accC*	Biotin carboxylase (EC 6.3.4.14)	Cell wall metabolism	Cytoplasmic	SPy1745	101	938	130	929	1.65	0.7476	0.6341	
M5005_Spy1487	SpM1_ChORF1746_s_at	*fabZ*	(3R)-hydroxymyristoyl-[acyl carrier protein] dehydratase (EC 4.2.1.-)	Lipid metabolism	Cytoplasmic	SPy1746	38	1411	53	1642	1.97	0.5068	0.5532	
M5005_Spy1488	SpM1_ChORF1747_s_at	*accB*	Biotin carboxyl carrier protein of acetyl-CoA carboxylase	Lipid metabolism	Cytoplasmic	SPy1747	71	1360	57	1655	0.64	0.0536	0.2552	
M5005_Spy1489	SpM1_ChORF1748_s_at	*fabF*	3-oxoacyl-[acyl-carrier-protein] synthase (EC 2.3.1.41)	Lipid metabolism	Cytoplasmic	SPy1748	87	1044	91	1167	1.10	0.5882	0.5874	
M5005_Spy1491	SpM1_ChORF1749_s_at	*fabD*	Malonyl-CoA-[acyl-carrier-protein] transacylase (EC 2.3.1.39)	Lipid metabolism	Cytoplasmic	SPy1749	114	1029	80	1259	0.49	0.6346	0.6013	

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M5005_Spy1491	SpM1_ChORF1750_s_at	*fabD*	Malonyl-CoA-[acyl-carrier-protein] transacylase (EC 2.3.1.39)	Lipid metabolism	Cytoplasmic	SPy1750	49	1580	73	1372	2.26	0.4796	0.5430	
M5005_Spy1492	SpM1_ChORF1751_s_at	*fabK*	Enoyl-[acyl-carrier protein] reductase (NADH) (EC 1.3.1.9)	Lipid metabolism	Cytoplasmic Membrane	SPy1751	86	744	129	985	2.28	0.4484	0.5287	
M5005_Spy1493	SpM1_ChORF1753_s_at	*acpP*	Acyl carrier protein	Lipid metabolism	Cytoplasmic	SPy1753	61	1196	41	1741	0.45	0.2286	0.4222	
M5005_Spy1494	SpM1_ChORF1754_s_at	*fabH*	3-oxoacyl-[acyl-carrier-protein] synthase III (EC 2.3.1.41)	Lipid metabolism	Cytoplasmic Membrane	SPy1754	182	727	128	983	0.50	0.0054	0.0926	
M5005_Spy1495	SpM1_ChORF1755_s_at	-	Transcriptional regulator, MarR family	Information processing	Cytoplasmic	SPy1755	225	520	171	683	0.58	0.2544	0.4334	
M5005_Spy1496	SpM1_ChORF1758_s_at	*phaB*	Enoyl-CoA hydratase (EC 4.2.1.17)	Cell wall metabolism	Cytoplasmic	SPy1758	46	1449	73	1396	2.52	0.3355	0.4792	
M5005_Spy1497	SpM1_ChORF1759_s_at	*dnaJ*	Chaperone protein DnaJ	Stress adaptation	Cytoplasmic	SPy1759	578	174	429	280	0.55	0.0041	0.0803	
M5005_Spy1498	SpM1_ChORF1760_s_at	*dnaK*	Chaperone protein DnaK	Stress adaptation	Cytoplasmic	SPy1760	4152	11	2084	24	0.25	1.8E-07	**1.4E-05**	**Significant**
M5005_Spy1499	SpM1_ChORF1761_s_at	*grpE*	Chaperone protein GrpE	Stress adaptation	Cytoplasmic	SPy1761	2117	23	1086	51	0.26	3.9E-08	**4.2E-06**	**Significant**
M5005_Spy1500	SpM1_ChORF1763_s_at	*hrcA*	Heat-inducible, Class I Heat shock transcriptional repressor	Information processing	Cytoplasmic	SPy1763	1917	15	1006	42	0.28	1.9E-07	**1.4E-05**	**Significant**
M5005_Spy1501	SpM1_ChORF1765_s_at	-	N-acetylmuramoyl-L-alanine amidase (EC 3.5.1.28)	Unknown	Unknown	SPy1765	33	2082	61	1434	3.46	0.9816	0.6906	
M5005_Spy1502	SpM1_ChORF1764_s_at	-	D-alanyl-D-alanine carboxypeptidase (EC 3.4.16.4)	Cell wall metabolism	Cytoplasmic	SPy1764	72	1292	54	1600	0.55	0.4841	0.5443	
M5005_Spy1503	SpM1_ChORF1766_s_at	-	Phosphoglycerate mutase (EC 5.4.2.1)	Carbohydrate metabolism	Cytoplasmic	SPy1766	80	1115	92	1216	1.34	0.5986	0.5893	
M5005_Spy1504	SpM1_ChORF1768_s_at	-	Hypothetical membrane spanning protein	Unknown	Cytoplasmic Membrane	SPy1768	42	1636	54	1522	1.65	0.8238	0.6525	
M5005_Spy1506	SpM1_ChORF1769_s_at	*gatB*	Aspartyl/glutamyl-tRNA(Asn/Gln) amidotransferase subunit B (EC 6.3.5.-)	Protein synthesis	Cytoplasmic	SPy1769	26	2140	31	1804	1.46	0.7675	0.6382	

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M5005_Spy1506	SpM1_ChORF1770_s_at	*gatB*	Aspartyl/glutamyl-tRNA(Asn/Gln) amidotransferase subunit B (EC 6.3.5.-)	Protein synthesis	Cytoplasmic	SPy1770	151	850	199	641	1.73	0.5555	0.5728	
M5005_Spy1507	SpM1_ChORF1771_s_at	*gatA*	Aspartyl/glutamyl-tRNA(Asn/Gln) amidotransferase subunit A (EC 6.3.5.-)	Protein synthesis	Cytoplasmic	SPy1771	163	793	162	739	0.98	0.1778	0.3875	
M5005_Spy1508	SpM1_ChORF1772_s_at	*gatC*	Glutamyl-tRNA(Gln) amidotransferase subunit C (EC 6.3.5.-)	Protein synthesis	Unknown	SPy1772	40	1849	51	1646	1.65	0.6966	0.6184	
M5005_Spy1510	SpyM3_1542_at	-	Pyruvate,phosphate dikinase (EC 2.7.9.1)	Unknown	Extracellular	#N/A	68	1469	71	1393	1.10	0.0290	0.2024	
M5005_Spy1511	M12_1829_s_at	-	Pyrazinamidase (EC 3.5.1.-) / Nicotinamidase (EC 3.5.1.19)	Coenzyme and cofactor metabolism	Unknown		11	2658	9	2620	0.61	0.8460	0.6565	
M5005_Spy1511	SpM1_ChORF1776_s_at	-	Pyrazinamidase (EC 3.5.1.-) / Nicotinamidase (EC 3.5.1.19)	Coenzyme and cofactor metabolism	Unknown	SPy1776	95	1186	73	1377	0.59	0.6238	0.5981	
M5005_Spy1512	SpM1_ChORF1777_s_at	*codY*	Pleiotropic transcriptional repressor codY	Information processing	Unknown	SPy1777	463	207	363	303	0.61	0.0131	0.1479	
M5005_Spy1513	SpM1_ChORF1779_s_at	-	Aspartate aminotransferase (EC 2.6.1.1)	Carbohydrate metabolism	Cytoplasmic	SPy1779	164	695	165	849	1.01	0.4340	0.5218	
M5005_Spy1514	SpM1_ChORF1780_s_at	-	Universal stress protein family	Stress adaptation	Cytoplasmic	SPy1780	168	713	118	871	0.49	0.1737	0.3845	
M5005_Spy1515	SpM1_ChORF1781_s_at	-	Hydrolase (HAD superfamily)	Unknown	Cytoplasmic	SPy1781	83	1210	81	1286	0.95	0.0961	0.3058	
M5005_Spy1516	SpM1_ChORF1782_s_at	*asnB*	L-asparaginase (EC 3.5.1.1)	Amino acid metabolism	Cytoplasmic	SPy1782	68	1353	76	1306	1.27	0.8013	0.6499	
M5005_Spy1517	SpM1_ChORF1783_s_at	-	Lantibiotic transport permease protein	Membrane transport	Cytoplasmic Membrane	SPy1783	18	2336	13	2476	0.57	0.9481	0.6811	
M5005_Spy1518	SpM1_ChORF1784_s_at	-	Transporter	Membrane transport	Cytoplasmic Membrane	SPy1784	20	2373	21	2351	1.02	0.4183	0.5169	
M5005_Spy1519	SpM1_ChORF1785_s_at	*recG*	ATP-dependent DNA helicase recG (EC 3.6.1.-)	Information processing	Cytoplasmic	SPy1785	189	645	172	760	0.83	0.0680	0.2773	

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M5005_Spy1519	SpM12_ChORF294-6_s_at	*recG*	ATP-dependent DNA helicase recG (EC 3.6.1.-)	Information processing	Cytoplasmic		133	782	126	830	0.90	0.0279	0.1982	
M5005_Spy1521	SpM1_ChORF1788_s_at	-	Cobalt transport ATP-binding protein cbiO	Membrane transport	Cytoplasmic Membrane	SPy1788	72	1198	71	1401	0.98	0.6198	0.5962	
M5005_Spy1522	SpM1_ChORF1787_s_at	-	Cobalt transport protein cbiQ	Membrane transport	Cytoplasmic Membrane	SPy1787	212	510	229	555	1.17	0.9801	0.6904	
M5005_Spy1523	SpM1_ChORF1789_s_at	-	Permease	Unknown	Cytoplasmic Membrane	SPy1789	151	774	142	895	0.88	0.1827	0.3892	
M5005_Spy1524	SpM1_ChORF1790_s_at	-	ABC transporter ATP-binding protein	Membrane transport	Cytoplasmic Membrane	SPy1790	89	1317	70	1381	0.62	0.8942	0.6690	
M5005_Spy1524	SpM1_ChORF1791_s_at	-	ABC transporter ATP-binding protein	Membrane transport	Cytoplasmic Membrane	SPy1791	41	1740	59	1477	2.10	0.2360	0.4227	
M5005_Spy1525	SpM1_ChORF1793_s_at	-	ABC transporter ATP-binding protein	Membrane transport	Cytoplasmic Membrane	SPy1793	21	2238	47	1530	5.13	0.5712	0.5801	
M5005_Spy1527	SpM1_ChORF1794_s_at	-	Ferrichrome transport system permease protein fhuB	Membrane transport	Cytoplasmic Membrane	SPy1794	140	684	155	787	1.22	0.9964	0.6930	
M5005_Spy1528	SpM1_ChORF1795_s_at	*htsA, siaA*	Putative heme binding protein	Membrane transport	Unknown	SPy1795	114	984	116	977	1.05	0.6285	0.5999	
M5005_Spy1529	SpM1_ChORF1796_s_at	*shp*	Putative heme binding protein	Membrane transport	Unknown	SPy1796	33	1576	50	1575	2.27	0.9629	0.6850	
M5005_Spy1530	SpM1_ChORF1798_s_at	-	Putative Fe3+-siderophore transport protein	Membrane transport	Extracellular	SPy1798	117	1033	197	614	2.83	0.0948	0.3037	
M5005_Spy1531	SpM1_ChORF1801_s_at	*isp2*	Immunogenic secreted protein	Virulence	Unknown	SPy1801	472	188	1863	29	15.56	1.4E-13	**5.3E-11**	**Significant**
M5005_Spy1532	SpM1_ChORF1804_s_at	*acpS*	Alanine racemase (EC 5.1.1.1)	Cellular processing	Cytoplasmic	SPy1804	57	1501	53	1518	0.89	0.7463	0.6339	
M5005_Spy1533	SpM1_ChORF1802_s_at	*alr*	Holo-[acyl-carrier protein] synthase (EC 2.7.8.7)	Cellular processing	Cytoplasmic	SPy1802	129	902	140	901	1.17	0.7440	0.6328	
M5005_Spy1534	SpM1_ChORF1805_s_at	*secA*	Protein translocase subunit secA	Secretion	Cytoplasmic	SPy1805	701	103	738	95	1.11	0.9490	0.6811	
M5005_Spy1538	SpM1_ChORF1810_s_at	*pmi*	Mannose-6-phosphate isomerase (EC 5.3.1.8)	Carbohydrate metabolism	Cytoplasmic	SPy1810	225	562	283	372	1.58	0.2914	0.4558	
M5005_Spy1539	SpM1_ChORF1811_s_at	*scrK*	Fructokinase (EC 2.7.1.4)	Carbohydrate metabolism	Cytoplasmic	SPy1811	105	825	241	502	5.25	0.0368	0.2229	

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M5005_Spy1540	SpM1_ChORF1813_at	*endoS*	Endo-beta-N-acetylglucosaminidase F2 precursor (EC 3.2.1.96); mannosyl-glycoprotein endo-b-N-acetylglucosaminidase	Carbohydrate metabolism	Extracellular	SPy1813	244	538	456	273	3.49	0.0004	**0.0132**	**Significant**
M5005_Spy1542	SpM1_ChORF1815_s_at	*scrA*	PTS system, sucrose-specific IIABC component (EC 2.7.1.69)	Carbohydrate metabolism	Cytoplasmic Membrane	SPy1815	207	533	255	429	1.51	0.0481	0.2502	
M5005_Spy1543	SpM1_ChORF1816_s_at	*scrB*	Sucrose-6-phosphate hydrolase (EC 3.2.1.26)	Carbohydrate metabolism	Cytoplasmic	SPy1816	193	602	280	492	2.10	0.2425	0.4277	
M5005_Spy1544	SpM1_ChORF1817_s_at	*scrR*	Sucrose operon repressor	Information processing	Cytoplasmic	SPy1817	117	1002	121	1024	1.07	0.3274	0.4776	
M5005_Spy1546	SpM1_ChORF1818_s_at	*nusB*	General stress protein, Gls24 family	Stress adaptation	Cytoplasmic	SPy1818	249	395	243	528	0.95	0.6161	0.5962	
M5005_Spy1546	SpM1_ChORF1820_s_at	*nusB*	General stress protein, Gls24 family	Stress adaptation	Cytoplasmic	SPy1820	149	769	173	754	1.34	0.8185	0.6519	
M5005_Spy1547	SpM1_ChORF1821_s_at	*efp*	Protein Translation Elongation Factor P (EF-P)	Cellular processing	Cytoplasmic	SPy1821	1108	43	1166	40	1.11	0.2939	0.4577	
M5005_Spy1548	SpM1_ChORF1823_s_at	*comEB*	ComE operon protein 2	Membrane transport	Cytoplasmic	SPy1823	99	1095	104	1129	1.09	0.6246	0.5983	
M5005_Spy1549	SpM12_ChORF283-25_s_at	-	Xaa-Pro dipeptidase (EC 3.4.13.9)	Amino acid metabolism	Cytoplasmic		151	772	134	834	0.79	0.0228	0.1884	
M5005_Spy1550	SpM1_ChORF1825_at	*uvrA*	Excinuclease ABC subunit A	Cellular processing	Cytoplasmic	SPy1825	185	659	157	886	0.72	0.8279	0.6539	
M5005_Spy1551	SpM1_ChORF1827_s_at	-	Magnesium and cobalt transport protein corA	Unknown	Cytoplasmic Membrane	SPy1827	102	1136	107	1030	1.10	0.9920	0.6918	
M5005_Spy1552	SpM1_ChORF1828_s_at	-	Hypothetical membrane spanning protein	Unknown	Cytoplasmic Membrane	SPy1828	101	1045	102	973	1.02	0.9190	0.6743	
M5005_Spy1553	SpM1_ChORF1829_s_at	*rpsR*	SSU ribosomal protein S18P	Protein synthesis	Unknown	SPy1829	218	474	235	469	1.16	0.2133	0.4110	
M5005_Spy1553	SpM5_ChORF169a-232_at	*rpsR*	SSU ribosomal protein S18P	Protein synthesis	Unknown		10	2641	9	2600	0.86	0.0340	0.2163	
M5005_Spy1554	SpM1_ChORF1830_s_at	*ssb2*	Phage single-strand DNA binding protein	Phage	Unknown	SPy1830	551	172	535	191	0.94	0.7459	0.6339	
M5005_Spy1555	SpM1_ChORF1831_s_at	*rpsF*	SSU ribosomal protein S6P	Protein synthesis	Cytoplasmic	SPy1831	1907	26	2198	25	1.33	0.0172	0.1652	

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M5005_Spy1556	SpM1_ChORF1832_s_at	-	Hypothetical protein	Unknown	Cytoplasmic Membrane	SPy1832	243	434	365	294	2.27	9.0E-05	**0.0035**	**Significant**
M5005_Spy1557	SpM1_ChORF1833_s_at	*mutY*	A/G-specific adenine DNA glycosylase (EC 3.2.2.-)	Unknown	Cytoplasmic	SPy1833	280	389	277	454	0.97	0.8600	0.6609	
M5005_Spy1558	SpM1_ChORF1834_s_at	-	Transcriptional regulator	Information processing	Cytoplasmic Membrane	SPy1834	28	1741	17	2372	0.35	0.3987	0.5106	
M5005_Spy1559	SpM1_ChORF1835_s_at	*trx*	Thioredoxin	Amino acid metabolism	Cytoplasmic	SPy1835	140	835	95	1075	0.47	0.4314	0.5207	
M5005_Spy1560	SpM1_ChORF1836_s_at	-	Phosphatidylglycerophosphatase B (EC 3.1.3.27)	Unknown	Cytoplasmic Membrane	SPy1836	94	1306	91	1182	0.94	0.7399	0.6311	
M5005_Spy1561	SpM1_ChORF1837_s_at	*mutS2*	DNA mismatch repair protein mutS	Information processing	Cytoplasmic	SPy1837	182	656	220	566	1.46	0.7767	0.6419	
M5005_Spy1562	SpM1_ChORF1839_s_at	-	Colicin V production protein	Unknown	Cytoplasmic Membrane	SPy1839	100	993	105	1020	1.11	0.4207	0.5176	
M5005_Spy1563	SpM1_ChORF1840_s_at	-	Hypothetical cytosolic protein	Unknown	Cytoplasmic	SPy1840	45	1843	45	1838	1.01	0.0485	0.2502	
M5005_Spy1564	SpM1_ChORF1841_s_at	-	Ribonuclease HIII (EC 3.1.26.4)	Cellular processing	Unknown	SPy1841	128	879	126	855	0.96	0.8405	0.6563	
M5005_Spy1565	SpM1_ChORF1842_s_at	*spi*	Signal peptidase I (EC 3.4.21.89)	Cellular processing	Unknown	SPy1842	215	531	222	576	1.06	0.5594	0.5749	
M5005_Spy1566	SpM1_ChORF1844_s_at	*recD*	Exodeoxyribonuclease V alpha chain (EC 3.1.11.5)	Cellular processing	Cytoplasmic	SPy1844	182	649	171	670	0.89	0.0670	0.2767	
M5005_Spy1567	SpM1_ChORF1845_s_at	-	Hypothetical protein	Unknown	Cytoplasmic Membrane	SPy1845	134	842	182	643	1.87	0.0281	0.1982	
M5005_Spy1568	SpM1_ChORF1846_s_at	*dinP*	DNA polymerase IV (EC 2.7.7.7)	Cellular processing	Cytoplasmic	SPy1846	113	1021	126	1068	1.23	0.2158	0.4142	
M5005_Spy1569	SpM1_ChORF1849_s_at	*pfl*	Formate acetyltransferase (EC 2.3.1.54) acetyl-CoA + formate = CoA + pyruvate	Carbohydrate metabolism	Cytoplasmic	SPy1849	777	81	615	138	0.63	0.0232	0.1901	
M5005_Spy1570	SpM1_ChORF1850_s_at	-	Penicillin-binding protein	Unknown	Unknown	SPy1850	96	1122	108	1105	1.28	0.6352	0.6015	
M5005_Spy1570	SpM1_ChORF1851_s_at	-	Penicillin-binding protein	Unknown	Unknown	SPy1851	114	892	129	937	1.28	0.3923	0.5061	
M5005_Spy1572	SpM1_ChORF1852_s_at	-	Hypothetical membrane spanning protein	Unknown	Cytoplasmic Membrane	SPy1852	85	1296	57	1521	0.45	0.0964	0.3058	

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M5005_Spy1572	SpM12_ChORF260-3_s_at	-	Hypothetical membrane spanning protein	Unknown	Cytoplasmic Membrane		89	1201	55	1455	0.39	0.6613	0.6081	
M5005_Spy1573	SpM1_ChORF1854_s_at	*glpF.2*	Aquaporin / Glycerol uptake facilitator protein	Membrane transport	Cytoplasmic Membrane	SPy1854	67	1514	87	1177	1.69	0.4152	0.5169	
M5005_Spy1575	SpM1_ChORF1856_s_at	*norA*	Quinolone resistance protein NorA	Membrane transport	Cytoplasmic Membrane	SPy1856	24	2333	48	1561	3.95	0.1242	0.3335	
M5005_Spy1576	SpM1_ChORF1857_s_at	-	Transcription regulator, crp family	Information processing	Cytoplasmic	SPy1857	171	699	147	807	0.73	0.5689	0.5795	
M5005_Spy1577	SpM1_ChORF1858_s_at	*pepXP*	Xaa-Pro dipeptidyl-peptidase (EC 3.4.14.11)	Amino acid metabolism	Cytoplasmic	SPy1858	84	1248	112	1071	1.80	0.7555	0.6366	
M5005_Spy1578	SpM18_ChORF1923_at	-	Transcriptional regulator, Cro/CI family	Information processing	Cytoplasmic	spyM18_1923	49	1728	19	2257	0.16	0.5756	0.5812	
M5005_Spy1579	SpM1_ChORF1861_s_at	-	Transcriptional regulator	Phage	Unknown	SPy1861	89	1135	83	1305	0.87	0.4245	0.5176	
M5005_Spy1580	SpM1_ChORF1862_s_at	-	Hypothetical cytosolic protein	Unknown	Unknown	SPy1862	151	818	139	824	0.84	0.2449	0.4287	
M5005_Spy1581	SpM1_ChORF1863_s_at	-	Transcriptional regulator, MerR family	Information processing	Cytoplasmic Membrane	SPy1863	45	1634	31	1839	0.49	0.7283	0.6287	
M5005_Spy1582	SpM1_ChORF1864_s_at	*dnaQ*	DNA polymerase III, epsilon chain (EC 2.7.7.7)	Cellular processing	Unknown	SPy1864	73	1310	51	1584	0.49	0.0522	0.2541	
M5005_Spy1582	SpM12_ChORF217-7_s_at	*dnaQ*	DNA polymerase III, epsilon chain (EC 2.7.7.7)	Cellular processing	Unknown		38	1759	25	2049	0.43	0.6986	0.6184	
M5005_Spy1583	SpM1_ChORF1865_s_at	-	Hypothetical cytosolic protein	Unknown	Cytoplasmic	SPy1865	164	757	179	707	1.18	0.4827	0.5443	
M5005_Spy1584	SpM1_ChORF1866_s_at	-	NAD(FAD)-utilizing dehydrogenases	Unknown	Unknown	SPy1866	165	765	162	823	0.96	0.9307	0.6750	
M5005_Spy1584	SpM12_ChORF217-5_at	-	NAD(FAD)-utilizing dehydrogenases	Unknown	Unknown		32	2062	28	1948	0.76	0.2097	0.4110	
M5005_Spy1585	SpM1_ChORF1867_s_at	*deoC*	Deoxyribose-phosphate aldolase (EC 4.1.2.4)	Carbohydrate metabolism	Cytoplasmic	SPy1867	1145	42	1001	43	0.76	0.7058	0.6200	
M5005_Spy1586	SpM1_ChORF1868_s_at	*nupC*	Nucleoside permease nupC	Membrane transport	Cytoplasmic Membrane	SPy1868	670	126	490	190	0.54	0.9960	0.6930	
M5005_Spy1587	SpM1_ChORF1869_s_at	*udp*	Uridine phosphorylase (EC 2.4.2.3)	Nucleotide metabolism	Cytoplasmic	SPy1869	934	54	935	53	1.00	0.9191	0.6743	
M5005_Spy1589	SpM12_ChORF217-1_at	*crgR*	Transcriptional regulator, GntR family	Information processing	Unknown		47	1692	80	1200	2.89	0.1409	0.3530	

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M5005_Spy1589	SpM12_ChORF217-10_s_at	*crgR*	Transcriptional regulator, GntR family	Information processing	Unknown		153	742	133	916	0.76	0.7097	0.6201	
M5005_Spy1590	SpM1_ChORF1871_s_at	*rpsN2*	SSU ribosomal protein S14P	Protein synthesis	Unknown	SPy1871	2251	17	2955	15	1.72	0.0353	0.2190	
M5005_Spy1592	SpM1_ChORF1872_s_at	-	Ribosomal-protein-alanine acetyltransferase (EC 2.3.1.128)	Protein synthesis	Cytoplasmic	SPy1872	331	353	237	489	0.51	0.5086	0.5532	
M5005_Spy1592	SpM1_ChORF1873_s_at	-	Ribosomal-protein-alanine acetyltransferase (EC 2.3.1.128)	Protein synthesis	Cytoplasmic	SPy1873	62	1413	56	1573	0.81	0.2631	0.4400	
M5005_Spy1593	SpM1_ChORF1874_s_at	-	Glycoprotease protein family	Amino acid metabolism	Unknown	SPy1874	124	936	124	943	1.00	0.3098	0.4702	
M5005_Spy1594	SpM1_ChORF1875_s_at	-	Putative transcriptional regulator	Unknown	Cytoplasmic	SPy1875	510	199	457	254	0.80	0.6267	0.5994	
M5005_Spy1595	SpM1_ChORF1876_s_at	-	Zn-dependent hydrolase (EC 3.-.-.-)	Cellular processing	Cytoplasmic	SPy1876	792	67	685	135	0.75	0.9241	0.6750	
M5005_Spy1596	SpM1_ChORF1877_s_at	*glnA*	Glutamine synthetase (EC 6.3.1.2)	Amino acid metabolism	Cytoplasmic	SPy1877	358	303	371	300	1.07	0.9980	0.6931	
M5005_Spy1597	SpM1_ChORF1878_s_at	-	Transcriptional regulator, MerR family	Information processing	Cytoplasmic	SPy1878	322	336	319	304	0.98	0.9831	0.6906	
M5005_Spy1598	SpM1_ChORF1879_s_at	-	Hypothetical protein	Unknown	Cytoplasmic Membrane	SPy1879	45	1724	51	1539	1.29	0.5338	0.5665	
M5005_Spy1599	SpM1_ChORF1881_s_at	*pgk*	Phosphoglycerate kinase (EC 2.7.2.3)	Carbohydrate metabolism	Cytoplasmic	SPy1881	325	302	263	442	0.66	0.5964	0.5889	
M5005_Spy1600	SpM1_ChORF1882_s_at	*lppC*	Acid phosphatase (EC 3.1.3.2)	Cellular processing	Unknown	SPy1882	382	257	342	298	0.80	0.7558	0.6366	
M5005_Spy1601	SpM1_ChORF1884_s_at	-	Membrane protease protein family	Unknown	Unknown	SPy1884	328	321	306	382	0.87	0.8118	0.6512	
M5005_Spy1602	SpM1_ChORF1885_s_at	-	Predicted kinase related to hydroxyacetone kinase	Unknown	Unknown	SPy1885	602	157	583	162	0.94	0.2362	0.4227	
M5005_Spy1603	SpM1_ChORF1886_s_at	*asp*	Putative alkaline-shock protein	Stress adaptation	Unknown	SPy1886	477	220	484	207	1.03	0.8393	0.6563	
M5005_Spy1605	SpM1_ChORF0303_s_at	-	Transposase	Mobile genetic element	Cytoplasmic	SPy0303	223	535	287	413	1.65	0.0162	0.1619	
M5005_Spy1606	SpM1_ChORF1888_s_at	*rpmB*	LSU ribosomal protein L28P	Protein synthesis	Unknown	SPy1888	529	194	540	152	1.04	0.6549	0.6065	
M5005_Spy1607	SpM1_ChORF1889_s_at	*fba*	Fructose-bisphosphate aldolase (EC 4.1.2.13)	Carbohydrate metabolism	Cytoplasmic	SPy1889	321	334	318	351	0.98	0.0383	0.2282	

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M5005_Spy1608	SpM1_ChORF1892_s_at	-	Alpha/beta hydrolase	Unknown	Cytoplasmic Membrane	SPy1892	145	802	131	741	0.81	0.5781	0.5829	
M5005_Spy1610	SpM1_ChORF1894_s_at	*pyrG*	CTP synthase (EC 6.3.4.2)	Nucleotide metabolism	Unknown	SPy1894	135	815	118	944	0.76	0.6672	0.6097	
M5005_Spy1611	SpM1_ChORF1895_s_at	*rpoE*	DNA-directed RNA polymerase delta chain (EC 2.7.7.6)	Cellular processing	Cytoplasmic	SPy1895	240	657	220	564	0.84	0.9754	0.6877	
M5005_Spy1612	SpM1_ChORF1896_s_at	*ropA*	Trigger factor, ppiase (EC 5.2.1.8)	Cellular processing	Cytoplasmic	SPy1896	415	233	380	292	0.83	0.6426	0.6036	
M5005_Spy1613	SpM1_ChORF1897_s_at	-	Mechanosensitive ion channel	Unknown	Cytoplasmic Membrane	SPy1897	30	2226	23	2165	0.59	0.6300	0.6000	
M5005_Spy1614	SpM1_ChORF1898_s_at	-	Hypothetical protein	Unknown	Cytoplasmic	SPy1898	94	1164	114	1058	1.49	0.7311	0.6294	
M5005_Spy1615	SpM1_ChORF1899_s_at	-	Hypothetical membrane spanning protein	Unknown	Cytoplasmic Membrane	SPy1899	96	1258	114	1027	1.42	0.8100	0.6512	
M5005_Spy1616	SpM1_ChORF1900_s_at	*thiD*	Phosphomethylpyrimidine kinase (EC 2.7.4.7) / Hydroxymethylpyrimidine kinase (EC 2.7.1.49)	Coenzyme and cofactor metabolism	Unknown	SPy1900	80	1107	102	1152	1.62	0.2943	0.4577	
M5005_Spy1616	SpM1_ChORF1901_s_at	*thiD*	Phosphomethylpyrimidine kinase (EC 2.7.4.7) / Hydroxymethylpyrimidine kinase (EC 2.7.1.49)	Coenzyme and cofactor metabolism	Unknown	SPy1901	160	716	140	914	0.77	0.2346	0.4227	
M5005_Spy1620	SpM1_ChORF1903_s_at	-	Glycerate kinase (EC 2.7.1.31)	Unknown	Cytoplasmic	SPy1903	44	1404	29	1950	0.45	0.1377	0.3489	
M5005_Spy1621	SpM1_ChORF1904_s_at	*hsdR*	Type I restriction-modification system restriction subunit (EC 3.1.21.3)	Information processing	Unknown	SPy1904	142	803	179	703	1.58	0.7508	0.6354	
M5005_Spy1622	SpM1_ChORF1905_s_at	*hsdS*	Type I restriction-modification system specificity subunit	Information processing	Cytoplasmic	SPy1905	39	1755	39	1727	0.98	0.8698	0.6629	
M5005_Spy1623	SpM1_ChORF1906_s_at	*hsdM*	Type I restriction-modification system methylation subunit	Information processing	Unknown	SPy1906	105	1055	102	1149	0.94	0.0985	0.3081	

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M5005_Spy1624	SpM18_ChORF1977_at	-	Hypothetical protein	Unknown	Unknown	spyM18_1977	25	2102	18	2190	0.56	0.6055	0.5923	
M5005_Spy1625	SpM1_ChORF1908_s_at	*salR*	Transcriptional regulatory protein degU	Information processing	Cytoplasmic	SPy1908	34	1868	53	1532	2.44	0.5865	0.5868	
M5005_Spy1627	SpM1_ChORF1911_s_at	*salY*	ABC transporter permease protein	Membrane transport	Cytoplasmic Membrane	SPy1911	47	1600	51	1505	1.15	0.8617	0.6614	
M5005_Spy1627	SpM49_ChORF6658-4_s_at	*salY*	ABC transporter permease protein	Membrane transport	Cytoplasmic Membrane		31	2141	20	2291	0.41	0.7377	0.6298	
M5005_Spy1629	SpM1_ChORF1912_s_at	*salX*	Lantibiotic transport ATP-binding protein	Membrane transport	Cytoplasmic Membrane	SPy1912	52	1351	61	1373	1.41	0.9447	0.6801	
M5005_Spy1630	SpM1_ChORF1914_s_at	*salB*	Serine (threonine) dehydratase (lantibiotic biosynthesis)	Virulence	Cytoplasmic	SPy1914	13	2541	10	2514	0.62	0.7531	0.6362	
M5005_Spy1631	SpM1_ChORF1915_at	*salA*	Lantibiotic salivaricin A	Virulence	Unknown	SPy1915	77	1220	91	1063	1.39	0.8577	0.6602	
M5005_Spy1632	SpM1_ChORF1916_s_at	*lacG*	6-phospho-beta-galactosidase (EC 3.2.1.85)	Carbohydrate metabolism	Cytoplasmic	SPy1916	62	1443	61	1537	0.96	0.2688	0.4436	
M5005_Spy1633	SpM1_ChORF1917_s_at	*lacE*	PTS system, lactose-specific IIBC component (EC 2.7.1.69)	Carbohydrate metabolism	Cytoplasmic Membrane	SPy1917	87	1040	135	864	2.38	0.0165	0.1628	
M5005_Spy1633	SpM49_ChORF6658-6_s_at	*lacE*	PTS system, lactose-specific IIBC component (EC 2.7.1.69)	Carbohydrate metabolism	Cytoplasmic Membrane		28	1991	38	1787	1.74	0.4607	0.5330	
M5005_Spy1634	SpM1_ChORF1918_s_at	*lacF*	PTS system, lactose-specific IIA component (EC 2.7.1.69)	Carbohydrate metabolism	Cytoplasmic	SPy1918	159	693	161	772	1.02	0.0216	0.1827	
M5005_Spy1635	SpM1_ChORF1919_s_at	*lacD.2*	Tagatose-bisphosphate aldolase (EC 4.1.2.40)	Carbohydrate metabolism	Cytoplasmic	SPy1919	225	701	209	570	0.87	0.0558	0.2607	
M5005_Spy1636	SpM1_ChORF1921_s_at	*lacC.2*	Tagatose-6-phosphate kinase (EC 2.7.1.144)	Carbohydrate metabolism	Unknown	SPy1921	88	1283	101	1092	1.33	0.3276	0.4776	
M5005_Spy1637	SpM1_ChORF1922_s_at	*lacB.2*	Galactose-6-phosphate isomerase lacB subunit (EC 5.3.1.26)	Carbohydrate metabolism	Cytoplasmic	SPy1922	116	1063	83	1133	0.52	0.2879	0.4544	
M5005_Spy1638	SpM1_ChORF1923_s_at	*lacA.2*	Galactose-6-phosphate isomerase lacA subunit (EC 5.3.1.26)	Carbohydrate metabolism	Cytoplasmic	SPy1923	104	1325	102	1128	0.96	0.9651	0.6850	

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M5005_Spy1639	SpM1_ChORF1924_s_at	*lacR.2*	Lactose phosphotransferase system repressor	Information processing	Cytoplasmic	SPy1924	77	1316	93	1178	1.46	0.0038	0.0744	
M5005_Spy1639	SpM5_ChORF125g-147_at	*lacR.2*	Lactose phosphotransferase system repressor	Information processing	Cytoplasmic		33	1787	20	2228	0.35	0.8450	0.6565	
M5005_Spy1640	SpM1_ChORF1926_s_at	-	DNA-damage-inducible protein J	Stress adaptation	Unknown	SPy1926	31	1758	78	1264	6.45	0.0546	0.2571	
M5005_Spy1641	SpM1_ChORF1927_s_at	-	Hypothetical cytosolic protein	Unknown	Cytoplasmic	SPy1927	42	1803	45	1676	1.16	0.0979	0.3076	
M5005_Spy1642	SpM12_ChORF257-16_s_at	-	DNA integration/recombination/invertion protein	Information processing	Unknown		16	2495	23	2211	2.10	0.4335	0.5218	
M5005_Spy1645	SpM12_ChORF257-17_s_at	-	DNA integration/recombination/invertion protein	Information processing	Unknown		52	1586	26	1884	0.25	0.0319	0.2095	
M5005_Spy1646	SpM1_ChORF1931_s_at	*rpsI*	SSU ribosomal protein S9P	Protein synthesis	Unknown	SPy1931	238	460	218	562	0.83	0.5484	0.5698	
M5005_Spy1647	SpM1_ChORF1932_s_at	*rplM*	LSU ribosomal protein L13P	Protein synthesis	Unknown	SPy1932	532	166	377	267	0.50	0.1070	0.3149	
M5005_Spy1647	SpM5_ChORF125g-172_at	*rplM*	LSU ribosomal protein L13P	Protein synthesis	Unknown		27	1947	29	1978	1.16	0.6450	0.6041	
M5005_Spy1648	SpM1_ChORF1935_s_at	-	Transcriptional regulator, Cro/CI family	Information processing	Unknown	SPy1935	25	2183	50	1619	4.02	0.3626	0.4888	
M5005_Spy1649	SpM1_ChORF1934_s_at	-	Hypothetical membrane spanning protein	Unknown	Cytoplasmic Membrane	SPy1934	93	1203	76	1290	0.67	0.0328	0.2123	
M5005_Spy1650	SpM1_ChORF1936_s_at	-	DegV family protein	Unknown	Cytoplasmic	SPy1936	42	1589	48	1587	1.32	0.4522	0.5302	
M5005_Spy1651	SpM1_ChORF1937_s_at	-	Hypothetical cytosolic protein	Unknown	Cytoplasmic	SPy1937	254	414	210	539	0.69	0.7086	0.6201	
M5005_Spy1652	SpM1_ChORF1938_s_at	-	23S rRNA methyltransferase (EC 2.1.1.-)	Cellular processing	Cytoplasmic	SPy1938	351	368	278	389	0.63	0.3741	0.4941	
M5005_Spy1653	SpM1_ChORF1939_s_at	-	Hypothetical membrane associated protein	Unknown	Unknown	SPy1939	37	1820	73	1457	3.98	0.8594	0.6607	
M5005_Spy1655	SpM1_ChORF1940_s_at	*cysS*	Cysteinyl-tRNA synthetase (EC 6.1.1.16)	Protein synthesis	Cytoplasmic	SPy1940	102	1054	97	1124	0.90	0.2502	0.4334	

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M5005_Spy1655	SpM1_ChORF1941_s_at	*cysS*	Cysteinyl-tRNA synthetase (EC 6.1.1.16)	Protein synthesis	Cytoplasmic	SPy1941	112	1118	105	1143	0.88	0.3409	0.4806	
M5005_Spy1656	SpM1_ChORF1942_s_at	-	Hypothetical protein	Unknown	Cytoplasmic Membrane	SPy1942	65	1381	23	2275	0.12	0.0246	0.1908	
M5005_Spy1658	SpM1_ChORF1944_s_at	*cysE*	Serine acetyltransferase (EC 2.3.1.30)	Amino acid metabolism	Cytoplasmic	SPy1944	277	447	294	455	1.12	0.8731	0.6632	
M5005_Spy1659	SpM1_ChORF1945_s_at	-	Hypothetical protein	Unknown	Unknown	SPy1945	139	761	156	758	1.26	0.0663	0.2762	
M5005_Spy1659	SpM1_ChORF1946_s_at	-	Hypothetical protein	Unknown	Unknown	SPy1946	207	506	275	407	1.76	0.0870	0.3002	
M5005_Spy1661	SpM1_ChORF1947_s_at	-	Transaldolase (EC 2.2.1.2)	Carbohydrate metabolism	Cytoplasmic	SPy1947	64	1336	63	1495	0.96	0.0422	0.2363	
M5005_Spy1662	SpM1_ChORF1949_s_at	-	Putative transport protein sgaT	Membrane transport	Cytoplasmic Membrane	SPy1949	75	1212	108	1037	2.08	0.0025	0.0539	
M5005_Spy1663	SpM1_ChORF1950_s_at	-	PTS system, IIB component (EC 2.7.1.69)	Carbohydrate metabolism	Cytoplasmic	SPy1950	27	1953	44	1654	2.65	0.8076	0.6512	
M5005_Spy1663	SpM1_ChORF1952_s_at	-	PTS system, IIB component (EC 2.7.1.69)	Carbohydrate metabolism	Cytoplasmic	SPy1952	21	2317	32	1949	2.27	0.8132	0.6512	
M5005_Spy1665	SpM1_ChORF1955_s_at	-	Hypothetical protein	Cellular processing	Unknown	SPy1955	98	944	120	894	1.51	0.8633	0.6616	
M5005_Spy1665	SpM18_ChORF2020_at	-	Hypothetical protein	Unknown	Unknown	spyM18_2020	25	2185	21	2270	0.68	0.8501	0.6580	
M5005_Spy1667	SpM1_ChORF1956_s_at	-	Hypothetical protein	Unknown	Unknown	SPy1956	13	2550	16	2409	1.65	0.9279	0.6750	
M5005_Spy1668	SpM1_ChORF1957_s_at	-	Putative transcriptional regulator	Unknown	Cytoplasmic	SPy1957	18	2329	7	2643	0.16	0.4304	0.5200	
M5005_Spy1669	SpM1_ChORF1958_s_at	*def*	Peptide deformylase (EC 3.5.1.88)	Cellular processing	Cytoplasmic	SPy1958	63	1485	79	1244	1.60	0.0138	0.1497	
M5005_Spy1670	SpM1_ChORF1959_s_at	-	Oxidoreductase (EC 1.1.1.-)	Unknown	Unknown	SPy1959	167	747	200	652	1.45	0.7345	0.6294	
M5005_Spy1671	SpM1_ChORF1960_s_at	-	Transcriptional regulator, MarR family	Information processing	Cytoplasmic	SPy1960	78	1364	134	948	2.97	0.0170	0.1652	
M5005_Spy1672	SpM1_ChORF1961_s_at	*polC*	DNA polymerase III alpha subunit (EC 2.7.7.7)	Information processing	Cytoplasmic	SPy1961	219	596	273	433	1.55	0.0744	0.2853	

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M5005_Spy1672	SpM12_ChORF285-3_s_at	-	DNA polymerase III alpha subunit (EC 2.7.7.7)	Information processing	Cytoplasmic		49	1652	69	1527	2.01	0.6855	0.6155	
M5005_Spy1673	SpM1_ChORF1962_s_at	*proS*	Prolyl-tRNA synthetase (EC 6.1.1.15)	Protein synthesis	Cytoplasmic	SPy1962	426	252	374	291	0.77	0.1422	0.3533	
M5005_Spy1673	SpM5_ChORF125g-177_at	*proS*	Prolyl-tRNA synthetase (EC 6.1.1.15)	Protein synthesis	Cytoplasmic		16	2545	14	2391	0.75	0.2108	0.4110	
M5005_Spy1674	SpM1_ChORF1963_s_at	-	Pheromone-processing membrane metalloprotease	Cellular processing	Cytoplasmic Membrane	SPy1963	297	343	266	497	0.80	0.6408	0.6034	
M5005_Spy1675	SpM1_ChORF1964_s_at	*cdsA*	Phosphatidate cytidylyltransferase (EC 2.7.7.41)	Lipid metabolism	Cytoplasmic Membrane	SPy1964	263	406	209	589	0.63	0.5853	0.5864	
M5005_Spy1676	SpM1_ChORF1965_s_at	*uppS*	Undecaprenyl pyrophosphate synthetase (EC 2.5.1.31)	Lipid metabolism	Unknown	SPy1965	450	222	383	285	0.73	0.2464	0.4308	
M5005_Spy1677	SpM1_ChORF1968_s_at	-	Protein translocase subunit YajC	Secretion	Unknown	SPy1968	502	178	490	214	0.95	0.8566	0.6602	
M5005_Spy1677	SpM5_ChORF125g-178_at	-	Protein translocase subunit YajC	Secretion	Unknown		25	2243	23	2084	0.85	0.3105	0.4706	
M5005_Spy1678	SpM1_ChORF1971_s_at	-	Thioredoxin	Stress adaptation	Unknown	SPy1971	352	292	334	323	0.90	0.4490	0.5291	
M5005_Spy1680	SpM1_ChORF1972_s_at	*pulA*	Pullulanase/Amylopullulanase (EC 3.2.1.41)	Carbohydrate metabolism	Unknown	SPy1972	79	1048	153	891	3.70	0.5604	0.5750	
M5005_Spy1681	SpM1_ChORF1973_at	*dexB*	Dextran glucosidase/Glucan 1,6-alpha-glucosidase (EC 3.2.1.70)	Carbohydrate metabolism	Cytoplasmic	SPy1973	131	792	171	708	1.72	0.2707	0.4447	
M5005_Spy1681	SpM18_ChORF2039_s_at	*dexB*	Dextran glucosidase/Glucan 1,6-alpha-glucosidase (EC 3.2.1.70)	Carbohydrate metabolism	Cytoplasmic	spyM18_2039	208	560	225	553	1.17	0.0673	0.2770	
M5005_Spy1682	SpM1_ChORF1976_s_at	*msmK*	Multiple sugar-binding ABC transporter protein	Membrane transport	Cytoplasmic Membrane	SPy1976	228	529	351	286	2.37	0.0451	0.2434	
M5005_Spy1682	SpM12_ChORF292-19_s_at	*msmK*	Multiple sugar-binding ABC transporter protein	Membrane transport	Cytoplasmic Membrane		22	2337	22	2017	0.95	0.4565	0.5316	
M5005_Spy1683	SpM1_ChORF1978_s_at	*lrp*	Leucine rich protein	Virulence	Cytoplasmic	SPy1978	100	1015	119	1013	1.42	0.1904	0.3986	
M5005_Spy1684	SpM1_ChORF1979_at	*ska*	Streptokinase	Virulence	Unknown	SPy1979	258	453	811	99	9.88	2.9E-08	**3.3E-06**	**Significant**

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M5005_Spy1685	SpM1_ChORF1980_s_at	-	D-tyrosyl-tRNA(Tyr) deacylase (EC 3.1.-.-)	Protein synthesis	Unknown	SPy1980	37	1907	41	1650	1.20	0.6329	0.6008	
M5005_Spy1686	SpM1_ChORF1981_s_at	*relA*	GTP pyrophosphokinase (EC 2.7.6.5)	Stress adaptation	Cytoplasmic	SPy1981	228	500	231	526	1.03	0.2183	0.4166	
M5005_Spy1687	SpM1_ChORF1983_at	*sclA*	Collagen-like surface protein A	Virulence	Cell Wall	SPy1983	127	937	195	688	2.35	0.1126	0.3200	
M5005_Spy1690	SpM1_ChORF1984_s_at	*nrdI.1*	NrdI protein	Nucleotide metabolism	Cytoplasmic	SPy1984	196	591	187	680	0.91	0.6626	0.6081	
M5005_Spy1691	SpM1_ChORF1985_s_at	-	Exodeoxyribonuclease III (EC 3.1.11.2)	Unknown	Cytoplasmic	SPy1985	78	1233	97	1137	1.54	0.1167	0.3229	
M5005_Spy1692	SpM1_ChORF1986_s_at	-	PTS system, glucose-specific IIABC component (EC 2.7.1.69)	Carbohydrate metabolism	Cytoplasmic Membrane	SPy1986	265	407	326	359	1.52	0.1066	0.3149	
M5005_Spy1694	SpM1_ChORF1987_s_at	-	Hypothetical cytosolic protein	Unknown	Cytoplasmic	SPy1987	232	570	155	786	0.45	0.0190	0.1707	
M5005_Spy1695	SpM1_ChORF1988_s_at	-	Ribosomal protein L11 methyltransferase (EC 2.1.1.-)	Protein synthesis	Unknown	SPy1988	179	754	170	761	0.90	0.8790	0.6643	
M5005_Spy1696	SpM1_ChORF1989_s_at	-	Hypothetical protein	Unknown	Unknown	SPy1989	132	962	144	815	1.20	0.2234	0.4196	
M5005_Spy1697	SpM49_ChORF391-1_s_at	-	Para-aminobenzoate synthetase component I (EC 4.1.3.-) /4-amino-4-deoxychorismate lyase (EC 4.-.-.-)	Unknown	Cytoplasmic		335	348	435	276	1.69	0.3026	0.4645	
M5005_Spy1697	SpM5_ChORF125g-189_s_at	-	Para-aminobenzoate synthetase component I (EC 4.1.3.-) /4-amino-4-deoxychorismate lyase (EC 4.-.-.-)	Unknown	Cytoplasmic		136	870	99	1041	0.53	0.0116	0.1377	
M5005_Spy1698	SpM1_ChORF1991_s_at	*trpG*	Anthranilate synthase component II (EC 4.1.3.27) / Para-aminobenzoate synthase glutamine amidotransferase component II (EC 4.1.3.-)	Unknown	Cytoplasmic	SPy1991	119	852	172	724	2.06	0.0538	0.2552	

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M5005_Spy1699	SpM1_ChORF1992_s_at	-	ATPase, AAA family	Unknown	Cytoplasmic	SPy1992	240	509	201	636	0.70	0.4660	0.5362	
M5005_Spy1700	SpM1_ChORF1994_s_at	-	Acetyltransferase (EC 2.3.1.-)	Cellular processing	Cytoplasmic	SPy1994	11	2621	12	2474	1.20	0.0098	0.1250	
M5005_Spy1701	SpM1_ChORF1995_s_at	*flaR*	DNA topology modulation protein flar-related protein	Unknown	Unknown	SPy1995	33	1680	70	1385	4.38	0.7295	0.6294	
M5005_Spy1702	SpM1_ChORF1998_at	*smeZ*	Streptococcal mitogenic exotoxin Z; Pyrogenic toxin superantigen exotoxin type Z	Virulence	Extracellular	SPy1998	33	2084	45	1675	1.94	0.9523	0.6824	
M5005_Spy1702	SpM12_ChORF291-40_s_at	*smeZ*	Streptococcal mitogenic exotoxin Z; Pyrogenic toxin superantigen exotoxin type Z	Virulence	Extracellular		22	2150	18	2331	0.68	0.6622	0.6081	
M5005_Spy1702	SpM18_ChORF2063_at	*smeZ*	Streptococcal mitogenic exotoxin Z; Pyrogenic toxin superantigen exotoxin type Z	Virulence	Extracellular	spyM18_2063	35	1752	27	2008	0.58	0.3111	0.4706	
M5005_Spy1703	SpM1_ChORF1999_at	-	Hypothetical cytosolic protein	Unknown	Unknown	SPy1999	33	2011	40	1663	1.50	0.0528	0.2551	
M5005_Spy1704	SpM1_ChORF2000_s_at	*dppA*	Dipeptide-binding protein	Membrane transport	Cell Wall	SPy2000	1044	47	512	167	0.24	3.1E-05	**0.0013**	**Significant**
M5005_Spy1705	SpM1_ChORF2001_s_at	*dppB*	Dipeptide transport system permease protein dppB	Membrane transport	Cytoplasmic Membrane	SPy2001	77	1221	59	1410	0.58	0.9421	0.6793	
M5005_Spy1706	SpM1_ChORF2002_s_at	*dppC*	Dipeptide transport system permease protein dppC	Membrane transport	Cytoplasmic Membrane	SPy2002	83	1047	48	1572	0.34	0.6842	0.6151	
M5005_Spy1707	SpM1_ChORF2003_s_at	*dppD*	Dipeptide transport ATP-binding protein dppD	Membrane transport	Cytoplasmic Membrane	SPy2003	148	703	98	1127	0.43	0.0127	0.1453	
M5005_Spy1708	SpM1_ChORF2004_s_at	*dppE*	Dipeptide transport ATP-binding protein dppF	Membrane transport	Cytoplasmic Membrane	SPy2004	56	1285	58	1420	1.09	0.9432	0.6796	
M5005_Spy1709	SpM1_ChORF2005_s_at	-	Hypothetical protein	Unknown	Cytoplasmic	SPy2005	1948	24	2187	22	1.26	1.7E-05	**0.0008**	**Significant**

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M5005_Spy1710	SpM1_ChORF2006_s_at	-	Streptococcal histidine triad protein	Unknown	Unknown (This protein may have multiple localization sites.)	SPy2006	878	52	982	45	1.25	0.7349	0.6294	
M5005_Spy1711	SpM1_ChORF2007_s_at	*lbp, lmb*	Laminin binding protein	Virulence	Cytoplasmic	SPy2007	517	192	467	215	0.82	0.4188	0.5169	
M5005_Spy1713	M12_2021_x_at	-	Hypothetical protein	Unknown	Unknown		110	1022	75	1380	0.47	0.1298	0.3379	
M5005_Spy1715	SpM1_ChORF2010_s_at	*scpA*	C5A peptidase precursor (EC 3.4.21.-)	Virulence	Cell Wall	SPy2010	887	84	935	66	1.11	0.8969	0.6690	
M5005_Spy1715	SpM12_ChORF248-6_s_at	*scpA*	C5A peptidase precursor (EC 3.4.21.-)	Virulence	Cell Wall		826	80	1044	62	1.60	0.0882	0.3002	
M5005_Spy1716	SpM1_ChORF2013_s_at	*tnp*	Transposase	Mobile genetic element	Cytoplasmic	SPy2013	144	783	152	762	1.11	0.3309	0.4778	
M5005_Spy1718	SpM1_ChORF2016_at	*sic1.01*	Streptococcal inhibitor of complement	Virulence	Unknown	SPy2016	7407	1	9688	3	1.71	1.7E-05	**0.0008**	**Significant**
M5005_Spy1719	SpM1_ChORF2018_at	*emm1.0*	M protein	Virulence	Cell Wall	SPy2018	4623	7	4968	11	1.15	0.7485	0.6346	
M5005_Spy1719	SpM12_ChORF248-4_s_at	*emm1.0*	M protein	Virulence	Cell Wall		7336	2	7878	6	1.15	0.3641	0.4889	
M5005_Spy1720	SpM1_ChORF2019_s_at	*mga*	Multiple gene activator; Trans-acting positive transcriptional regulator	Information processing	Cytoplasmic	SPy2019	259	418	213	569	0.68	0.7326	0.6294	
M5005_Spy1723	SpM1_ChORF2025_s_at	*isp*	Immunogenic secreted protein	Virulence	Cell Wall	SPy2025	791	85	562	158	0.50	0.1545	0.3672	
M5005_Spy1723	SpM12_ChORF249-5_s_at	*isp*	Immunogenic secreted protein	Virulence	Cell Wall		829	55	625	124	0.57	0.1990	0.4020	
M5005_Spy1724	SpM1_ChORF2026_s_at	*ihk*	Two-component system histidine kinase	Signal transduction	Cytoplasmic Membrane	SPy2026	483	162	329	341	0.47	0.3564	0.4882	
M5005_Spy1725	SpM1_ChORF2027_s_at	*irr*	Two-component response regulator	Signal transduction	Cytoplasmic	SPy2027	340	288	267	477	0.62	0.1653	0.3758	
M5005_Spy1726	SpM1_ChORF2029_s_at	-	ABC transporter permease protein	Membrane transport	Cytoplasmic Membrane	SPy2029	277	358	226	487	0.67	0.1764	0.3864	
M5005_Spy1727	SpM1_ChORF2031_s_at	-	ABC transporter ATP-binding protein	Membrane transport	Cytoplasmic Membrane	SPy2031	221	507	166	699	0.57	0.1068	0.3149	
M5005_Spy1728	SpM1_ChORF2032_s_at	-	Periplasmic component of efflux system	Membrane transport	Unknown	SPy2032	1029	35	659	112	0.41	0.0495	0.2521	
M5005_Spy1729	SpM12_ChORF265-2_s_at	-	Hypothetical protein	Unknown	Unknown		15	2490	13	2444	0.78	0.3834	0.4999	

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M5005_Spy1730	SpM1_ChORF2034_s_at	-	Hypothetical protein	Unknown	Cytoplasmic	SPy2034	92	1359	82	1297	0.80	0.5889	0.5874	
M5005_Spy1731	SpM18_ChORF2095_s_at	-	Hypothetical cytosolic protein	Unknown	Unknown	spyM18_2095	225	472	250	451	1.23	0.8142	0.6512	
M5005_Spy1732	SpM12_ChORF265-4_s_at	-	Protein export protein prsA precursor	Unknown	Unknown		335	279	1212	39	13.06	2.5E-12	**6.6E-10**	**Significant**
M5005_Spy1733	SpM12_ChORF221-3_s_at	-	Hypothetical protein	Unknown	Unknown		100	1128	712	83	50.33	5.1E-18	**3.2E-15**	**Significant**
M5005_Spy1734	SpM12_ChORF221-2_s_at	-	Streptopain precursor fragment	Unknown	Extracellular		379	246	20129	1	2822.23	4.9E-20	**4.5E-17**	**Significant**
M5005_Spy1735	SpM1_ChORF2039_s_at	*speB*	Pyrogenic toxin superantigen exotoxin B (EC 3.4.22.10)	Virulence	Extracellular	SPy2039	301	304	13615	2	2052.68	6.1E-21	**1.1E-17**	**Significant**
M5005_Spy1736	SpM1_ChORF2040_at	-	Hypothetical protein	Unknown	Extracellular	SPy2040	83	1340	1872	28	508.48	2.2E-16	**9.9E-14**	**Significant**
M5005_Spy1736	SpM1_ChORF2041_s_at	-	Hypothetical protein	Unknown	Extracellular	SPy2041	29	2258	11	2464	0.15	0.3193	0.4745	
M5005_Spy1737	SpM1_ChORF2042_s_at	*rgg*	Transcriptional regulator	Information processing	Cytoplasmic	SPy2042	41	2046	65	1392	2.53	0.6268	0.5994	
M5005_Spy1738	SpM1_ChORF2043_s_at	*spd*	Streptodornase (EC 3.1.21.1)	Virulence	Unknown	SPy2043	3255	14	7915	5	5.92	1.9E-08	**2.5E-06**	**Significant**
M5005_Spy1740	SpM1_ChORF2045_s_at	-	Low temperature requirement C protein	Unknown	Unknown	SPy2045	122	807	128	967	1.10	0.5123	0.5546	
M5005_Spy1741	SpM1_ChORF2047_s_at	*gldA*	Glycerol dehydrogenase (EC 1.1.1.6)	Carbohydrate metabolism	Cytoplasmic	SPy2047	218	650	218	611	1.00	0.8234	0.6525	
M5005_Spy1742	SpM1_ChORF2048_s_at	*mipB*	Transaldolase (EC 2.2.1.2)	Carbohydrate metabolism	Cytoplasmic	SPy2048	65	1215	96	1156	2.19	0.8721	0.6632	
M5005_Spy1743	SpM1_ChORF2049_s_at	*pflD*	Formate acetyltransferase (EC 2.3.1.54)	Carbohydrate metabolism	Cytoplasmic	SPy2049	187	601	181	616	0.94	0.2895	0.4558	
M5005_Spy1744	SpM1_ChORF2050_at	-	PTS system, cellobiose-specific IIC component	Carbohydrate metabolism	Cytoplasmic Membrane	SPy2050	48	1821	33	1846	0.47	0.3672	0.4908	
M5005_Spy1744	SpM1_ChORF2050_s_at	-	PTS system, cellobiose-specific IIC component	Carbohydrate metabolism	Cytoplasmic Membrane	SPy2051	48	1696	55	1547	1.33	0.0083	0.1150	
M5005_Spy1745	SpM1_ChORF2051_s_at	-	PTS system, cellobiose-specific IIB component (EC 2.7.1.69)	Carbohydrate metabolism	Cytoplasmic	SPy2051	62	1448	53	1628	0.75	0.2081	0.4102	

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M5005_Spy1746	SpM1_ChORF2052_s_at	-	PTS system, cellobiose-specific IIA component (EC 2.7.1.69)	Carbohydrate metabolism	Cytoplasmic	SPy2052	76	1180	65	1486	0.73	0.4605	0.5330	
M5005_Spy1747	SpM1_ChORF2053_s_at	-	Sorbitol operon regulator	Information processing	Cytoplasmic	SPy2053	210	498	163	733	0.60	0.1510	0.3626	
M5005_Spy1748	SpM5_ChORF125g-81_s_at	-	Transcriptional regulator, DeoR family	Unknown	Unknown		142	859	116	885	0.67	0.2328	0.4227	
M5005_Spy1749	SpM1_ChORF2055_s_at	-	Pyruvate formate-lyase activating enzyme (EC 1.97.1.4)	Unknown	Cytoplasmic	SPy2055	125	801	99	1094	0.63	0.0080	0.1126	
M5005_Spy1750	SpyM3_1756_s_at	-	Hypothetical protein	Unknown	Unknown	#N/A	15	2580	19	2378	1.63	0.3996	0.5106	
M5005_Spy1751	SpM1_ChORF2058_s_at	*secE*	Protein translocase subunit secE	Secretion	Unknown	SPy2058	63	1346	99	1118	2.45	0.4123	0.5159	
M5005_Spy1753	SpM1_ChORF2059_s_at	*pbp2A*	Multimodular transpeptidase-transglycosylase PBP 2A	Cell wall metabolism	Extracellular	SPy2059	593	149	559	144	0.89	0.7206	0.6254	
M5005_Spy1754	SpM1_ChORF2060_s_at	-	Translation initiation inhibitor	Unknown	Cytoplasmic	SPy2060	353	282	368	293	1.08	0.1954	0.3995	
M5005_Spy1755	SpM18_ChORF2122_s_at	-	Hypothetical cytosolic protein	Unknown	Unknown	spyM18_2122	453	230	437	221	0.93	0.1761	0.3862	
M5005_Spy1756	SpM1_ChORF2063_s_at	-	Ribosomal large subunit pseudouridine synthase D (EC 4.2.1.70)	Protein synthesis	Cytoplasmic	SPy2063	233	573	244	525	1.10	0.5494	0.5698	
M5005_Spy1757	SpM1_ChORF2065_s_at	-	Hypothetical protein	Unknown	Unknown	SPy2065	251	470	189	604	0.57	0.0616	0.2713	
M5005_Spy1758	SpM1_ChORF2066_s_at	-	Probable dipeptidase B (EC 3.4.-.-)	Amino acid metabolism	Unknown (This protein may have multiple localization sites.)	SPy2066	111	1010	162	692	2.13	0.0299	0.2042	
M5005_Spy1760	SpyM3_1764_at	-	Transcriptional regulator, MutR family	Unknown	Unknown	-	15	2558	10	2623	0.43	0.1810	0.3887	
M5005_Spy1761	SpM1_ChORF2070_s_at	*groEL*	60 kDa chaperonin GroEL	Stress adaptation	Cytoplasmic	SPy2070	699	101	531	182	0.58	1.1E-05	**0.0006**	**Significant**
M5005_Spy1762	SpM1_ChORF2072_s_at	*groES*	10 kDa chaperonin GroES	Stress adaptation	Cytoplasmic	SPy2072	574	123	343	296	0.36	2.0E-06	**0.0001**	**Significant**

M5005_gene	RML Probeset	Gene	Description	Function	Predicted Cellular Localization *	Synonym †	Normalized Expression (WT) ‡	Transcript Rank (WT) §	Normalized Expression (Mutant) ‡	Transcript Rank (Mutant) §	Fold Change (Mutant : WT) **	*P* -value (Strain)	*Q* -value (Strain)††	Strain Significance (FDR=0.05)
M5005_Spy1763	SpM1_ChORF2073_s_at	*clpC*	Negative regulator of genetic competence clpC/mecB	Information processing	Cytoplasmic	SPy2073	509	158	471	217	0.86	0.0817	0.2979	
M5005_Spy1764	SpM1_ChORF2074_s_at	*ctsR*	Transcriptional regulator ctsR	Information processing	Cytoplasmic	SPy2074	211	525	170	704	0.65	0.0751	0.2867	
M5005_Spy1765	SpM1_ChORF2077_x_at	*csp*	Cold shock protein	Stress adaptation	Cytoplasmic	SPy2077	1151	38	889	64	0.60	0.0520	0.2541	
M5005_Spy1768	SpM1_ChORF2079_s_at	*ahpC*	Peroxiredoxin reductase (NAD(P)H) (EC 1.6.4.-)	Stress adaptation	Cytoplasmic	SPy2079	648	115	468	220	0.52	0.0995	0.3083	
M5005_Spy1769	SpM1_ChORF2080_s_at	*ahpF*	Peroxiredoxin reductase (NAD(P)H) (EC 1.6.4.-)	Stress adaptation	Cytoplasmic	SPy2080	602	147	419	229	0.48	0.1621	0.3727	
M5005_Spy1770	SpM1_ChORF2081_s_at	*hutI*	Imidazolonepropionase (EC 3.5.2.7)	Amino acid metabolism	Cytoplasmic	SPy2081	396	208	406	272	1.05	0.8626	0.6616	
M5005_Spy1771	SpM1_ChORF2082_at	*hutU*	Urocanate hydratase (EC 4.2.1.49)	Amino acid metabolism	Cytoplasmic	SPy2082	475	181	674	108	2.01	0.3721	0.4933	
M5005_Spy1771	SpM12_ChORF298-25_s_at	*hutU*	Urocanate hydratase (EC 4.2.1.49)	Amino acid metabolism	Cytoplasmic		38	1817	28	1984	0.56	0.8227	0.6525	
M5005_Spy1772	SpM1_ChORF2083_s_at	-	Glutamate formiminotransferase(EC 2.1.2.5)	Unknown	Cytoplasmic	SPy2083	437	239	579	170	1.75	0.0524	0.2541	
M5005_Spy1773	SpM1_ChORF2084_s_at	-	Formiminotetrahydrofolate cyclodeaminase (EC 4.3.1.4)	Nucleotide metabolism	Unknown	SPy2084	203	641	250	522	1.51	0.3967	0.5094	
M5005_Spy1774	SpM1_ChORF2085_s_at	*fhs.2*	Formate--tetrahydrofolate ligase (EC 6.3.4.3)	Carbohydrate metabolism	Cytoplasmic	SPy2085	774	99	897	67	1.34	0.1959	0.3998	
M5005_Spy1775	SpM1_ChORF2087_s_at	-	Hypothetical cytosolic protein	Unknown	Unknown	SPy2087	422	259	418	253	0.98	0.2225	0.4188	
M5005_Spy1776	SpM1_ChORF2088_s_at	-	putative cationic amino acid transporter protein	Membrane transport	Cytoplasmic Membrane	SPy2088	488	145	806	82	2.73	0.1292	0.3379	
M5005_Spy1776	SpM12_ChORF298-21_at	-	putative cationic amino acid transporter protein	Membrane transport	Cytoplasmic Membrane		22	2283	18	2445	0.63	0.2745	0.4461	
M5005_Spy1777	SpM1_ChORF2089_s_at	*hutH*	Histidine ammonia-lyase (EC 4.3.1.3)	Amino acid metabolism	Cytoplasmic	SPy2089	805	90	1132	46	1.98	0.0582	0.2665	
M5005_Spy1778	SpM1_ChORF2090_s_at	*hutG*	Formiminoglutamase (EC 3.5.3.8)	Amino acid metabolism	Cytoplasmic	SPy2090	336	337	491	200	2.14	0.1161	0.3229	
M5005_Spy1779	SpM1_ChORF2091_s_at	-	Transcriptional regulator, LuxR family	Information processing	Cytoplasmic	SPy2091	72	1184	75	1275	1.10	0.4648	0.5358	

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M5005_Spy1780	SpM1_ChORF2092_s_at	*rpsB*	SSU ribosomal protein S2P	Protein synthesis	Cytoplasmic	SPy2092	376	263	293	408	0.61	0.0656	0.2754	
M5005_Spy1781	SpM1_ChORF2093_s_at	*tsf*	Protein Translation Elongation Factor Ts (EF-Ts)	Cellular processing	Cytoplasmic	SPy2093	338	286	314	358	0.86	0.1465	0.3575	
M5005_Spy1782	SpM1_ChORF2095_s_at	*pepO*	Neutral endopeptidase (EC 3.4.24.-)	Amino acid metabolism	Cytoplasmic	SPy2095	354	276	384	263	1.18	0.3224	0.4759	
M5005_Spy1782	SpM5_ChORF125g-225_at	*pepO*	Neutral endopeptidase (EC 3.4.24.-)	Cellular processing	Cytoplasmic		17	2355	22	2181	1.71	0.1316	0.3393	
M5005_Spy1783	SpM1_ChORF2096_s_at	*dexS*	Trehalose-6-phosphate hydrolase (EC 3.2.1.93)	Carbohydrate metabolism	Cytoplasmic	SPy2096	78	1177	84	1409	1.16	0.9671	0.6854	
M5005_Spy1784	SpM1_ChORF2097_s_at	-	PTS system, trehalose-specific IIBC component (EC 2.7.1.69)	Carbohydrate metabolism	Cytoplasmic Membrane	SPy2097	102	1309	86	1199	0.71	0.1260	0.3353	
M5005_Spy1784	SpM12_ChORF297-3_s_at	-	PTS system, trehalose-specific IIBC component (EC 2.7.1.69)	Carbohydrate metabolism	Cytoplasmic Membrane		17	2415	14	2412	0.70	0.9088	0.6729	
M5005_Spy1785	SpM1_ChORF2099_s_at	-	Trehalose operon transcriptional repressor	Information processing	Cytoplasmic	SPy2099	36	1761	48	1482	1.82	0.3545	0.4878	
M5005_Spy1786	SpM18_ChORF2160_s_at	-	Transcriptional regulator, MarR family	Information processing	Cytoplasmic	spyM18_2160	47	1553	66	1466	1.94	0.4100	0.5148	
M5005_Spy1787	SpM18_ChORF2161_s_at	-	Glyoxalase family protein	Cellular processing	Cytoplasmic	spyM18_2161	16	2507	17	2304	1.11	0.1271	0.3368	
M5005_Spy1788	SpM1_ChORF2104_s_at	-	Protein yaaA	Cellular processing	Cytoplasmic	SPy2104	125	795	133	902	1.14	0.8515	0.6586	
M5005_Spy1789	SpM1_ChORF2105_s_at	*nrdG*	Anaerobic ribonucleoside-triphosphate reductase activating protein (EC 1.97.1.4)	Cellular processing	Unknown	SPy2105	184	587	167	721	0.82	0.1811	0.3887	
M5005_Spy1790	SpM1_ChORF2106_s_at	-	Acetyltransferase (EC 2.3.1.-)	Cellular processing	Cytoplasmic	SPy2106	415	216	337	283	0.66	0.1297	0.3379	
M5005_Spy1791	SpM1_ChORF2107_s_at	-	Virulence factor mviM	Unknown	Unknown	SPy2107	233	461	167	697	0.52	0.5541	0.5726	
M5005_Spy1792	SpM18_ChORF2167_x_at	-	Hypothetical protein	Unknown	Extracellular	spyM18_2167	165	720	153	799	0.86	0.0002	**0.0080**	**Significant**

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M5005_Spy1793	SpM1_ChORF2110_s_at	*nrdD*	Anaerobic ribonucleoside-triphosphate reductase (EC 1.17.4.2)	Unknown	Cytoplasmic	SPy2110	769	65	512	177	0.44	0.0112	0.1377	
M5005_Spy1794	SpM1_ChORF2111_s_at	-	Hypothetical membrane spanning protein	Unknown	Cytoplasmic Membrane	SPy2111	76	995	84	1136	1.22	0.2179	0.4166	
M5005_Spy1795	SpM1_ChORF2112_s_at	-	Hypothetical cytosolic protein	Unknown	Cytoplasmic	SPy2112	387	283	441	284	1.30	0.2626	0.4400	
M5005_Spy1797	SpM1_ChORF2113_s_at	-	Hypothetical cytosolic protein	Unknown	Cytoplasmic	SPy2113	1299	37	1006	50	0.60	0.4855	0.5443	
M5005_Spy1797	SpM1_ChORF2114_s_at	-	Hypothetical cytosolic protein	Unknown	Cytoplasmic	SPy2114	1045	53	1046	52	1.00	0.8644	0.6620	
M5005_Spy1798	SpM1_ChORF2115_s_at	-	Arsenate reductase family protein	Unknown	Cytoplasmic	SPy2115	534	152	785	119	2.16	0.0767	0.2905	
M5005_Spy1799	SpM1_ChORF2116_s_at	*recA*	RecA protein	Information processing	Cytoplasmic	SPy2116	509	169	576	155	1.28	0.4045	0.5120	
M5005_Spy1800	SpM1_ChORF2117_s_at	*cinA*	Colligrin	Information processing	Cytoplasmic	SPy2117	109	1034	124	986	1.30	0.8607	0.6612	
M5005_Spy1801	SpM1_ChORF2118_s_at	*tag*	DNA-3-methyladenine glycosylase (EC 3.2.2.20)	Information processing	Unknown	SPy2118	22	2263	46	1731	4.67	0.5928	0.5880	
M5005_Spy1802	SpM1_ChORF2119_s_at	*ruvA*	Holliday junction DNA helicase ruvA	Information processing	Unknown	SPy2119	131	871	142	828	1.17	0.3579	0.4885	
M5005_Spy1803	SpM1_ChORF2120_s_at	*lmrP*	Multidrug resistance protein B	Membrane transport	Cytoplasmic Membrane	SPy2120	80	1124	74	1348	0.86	0.1377	0.3489	
M5005_Spy1804	SpM1_ChORF2121_s_at	*mutL*	DNA mismatch repair protein mutL	Information processing	Cytoplasmic	SPy2121	190	592	184	651	0.94	0.6479	0.6046	
M5005_Spy1805	SpM1_ChORF2148_s_at	*mutS*	DNA mismatch repair protein mutS	Information processing	Cytoplasmic	SPy2148	136	821	132	1053	0.95	0.1598	0.3721	
M5005_Spy1806	SpM1_ChORF2149_s_at	-	Hypothetical cytosolic protein	Unknown	Unknown	SPy2149	77	1426	64	1338	0.68	0.6420	0.6036	
M5005_Spy1807	SpM1_ChORF2150_s_at	*ahrC, argR2*	Arginine repressor, argR	Information processing	Cytoplasmic	SPy2150	143	834	130	955	0.83	0.1455	0.3573	
M5005_Spy1808	SpM1_ChORF2151_s_at	*argS*	Arginyl-tRNA synthetase (EC 6.1.1.19)	Protein synthesis	Cytoplasmic	SPy2151	574	164	580	172	1.02	0.6076	0.5926	
M5005_Spy1809	SpM1_ChORF2152_s_at	*uviB*	Bacteriocin uviB	Stress adaptation	Unknown	SPy2152	39	1747	45	1661	1.37	0.4363	0.5231	

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M5005_Spy1810	SpM1_ChORF2153_s_at	-	Hypothetical membrane spanning protein	Unknown	Cytoplasmic Membrane	SPy2153	166	643	156	706	0.88	0.1503	0.3618	
M5005_Spy1811	SpM1_ChORF2154_s_at	-	Hypothetical membrane spanning protein	Unknown	Cytoplasmic Membrane	SPy2154	206	526	206	677	1.00	0.0124	0.1426	
M5005_Spy1811	SpM1_ChORF2155_s_at	-	Hypothetical membrane spanning protein	Unknown	Cytoplasmic Membrane	SPy2155	173	597	173	678	0.99	0.4561	0.5316	
M5005_Spy1813	SpM1_ChORF2156_s_at	*aspS*	Aspartyl-tRNA synthetase (EC 6.1.1.12)	Protein synthesis	Cytoplasmic	SPy2156	158	759	140	800	0.80	0.8117	0.6512	
M5005_Spy1814	SpM1_ChORF2157_s_at	*hisS*	Histidyl-tRNA synthetase (EC 6.1.1.21)	Protein synthesis	Cytoplasmic	SPy2157	65	1441	58	1441	0.82	0.5686	0.5795	
M5005_Spy1815	SpM1_ChORF2159_s_at	*rpmF*	LSU ribosomal protein L32P	Protein synthesis	Unknown	SPy2159	705	111	532	157	0.57	0.0159	0.1619	
M5005_Spy1815	SpM18_ChORF2196_x_at	*rpmF*	LSU ribosomal protein L32P	Protein synthesis	Unknown	spyM18_2196	874	75	578	164	0.44	0.0414	0.2330	
M5005_Spy1816	SpM1_ChORF2160_x_at	*rpmG*	LSU ribosomal protein L33P	Protein synthesis	Extracellular	SPy2160	416	221	321	336	0.60	0.0164	0.1628	
M5005_Spy1816	SpM18_ChORF2197_x_at	*rpmG*	LSU ribosomal protein L33P	Protein synthesis	Extracellular	spyM18_2197	359	272	294	398	0.67	0.0100	0.1261	
M5005_Spy1817	SpM1_ChORF2162_s_at	*cadD*	Cadmium resistance protein	Membrane transport	Cytoplasmic Membrane	SPy2162	23	2133	31	1942	1.76	0.1612	0.3722	
M5005_Spy1817	SpM12_ChORF218-1_s_at	*cadD*	Cadmium resistance protein	Membrane transport	Cytoplasmic Membrane		13	2595	10	2632	0.58	0.7611	0.6372	
M5005_Spy1818	SpM1_ChORF2163_s_at	*cadC*	Cadmium efflux system accessory protein	Membrane transport	Unknown	SPy2163	15	2509	13	2454	0.70	0.3044	0.4656	
M5005_Spy1818	SpM18_ChORF2199_s_at	*cadC*	Cadmium efflux system accessory protein	Membrane transport	Unknown	spyM18_2199	10	2607	35	1918	11.38	0.7646	0.6382	
M5005_Spy1819	SpM1_ChORF2164_s_at	-	Hypothetical phage protein	Phage	Cytoplasmic	SPy2164	31	2000	22	2032	0.49	0.4139	0.5164	
M5005_Spy1820	SpM1_ChORF2165_s_at	-	FtsK/SpoIIIE family	Phage	Unknown	SPy2165	34	1850	27	2092	0.63	0.2201	0.4177	
M5005_Spy1820	SpM18_ChORF2202_s_at	-	FtsK/SpoIIIE family	Phage	Unknown	spyM18_2202	134	789	109	1054	0.66	0.0240	0.1908	
M5005_Spy1821	SpM1_ChORF2166_s_at	-	Hypothetical phage protein	Phage	Unknown	SPy2166	14	2551	33	1929	5.36	0.7063	0.6200	
M5005_Spy1822	SpM12_ChORF218-7_s_at	-	Transcriptional regulator	Information processing	Cytoplasmic		76	1337	68	1300	0.80	0.6960	0.6184	

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M5005_Spy1823	SpM1_ChORF2169_s_at	-	Integral membrane protein	Phage	Cytoplasmic Membrane	SPy2169	53	1608	38	1616	0.52	0.4636	0.5348	
M5005_Spy1823	SpyM3_1824_at	-	Integral membrane protein	Phage	Cytoplasmic Membrane	#N/A	18	2473	27	2301	2.26	0.8391	0.6563	
M5005_Spy1824	SpM1_ChORF2170_at	-	Phosphohydrolase (MutT/nudix family protein)	Phage	Cytoplasmic	SPy2170	45	1748	57	1610	1.60	0.7611	0.6372	
M5005_Spy1825	SpM1_ChORF2172_s_at	-	Transcriptional regulator, PadR family	Phage	Unknown	SPy2172	43	1671	32	1911	0.57	0.9154	0.6743	
M5005_Spy1826	SpM1_ChORF2173_s_at	-	Hypothetical membrane associated protein	Phage	Cytoplasmic Membrane	SPy2173	51	1533	77	1345	2.27	0.5496	0.5698	
M5005_Spy1827	SpM1_ChORF2174_s_at	-	Hypothetical membrane associated protein	Phage	Unknown	SPy2174	48	1912	29	1798	0.37	0.6501	0.6051	
M5005_Spy1829	SpM1_ChORF2176_s_at	-	Phage infection protein	Phage	Cytoplasmic Membrane	SPy2176	61	1595	97	1142	2.54	0.8460	0.6565	
M5005_Spy1830	SpM1_ChORF2177_s_at	-	Transcriptional regulator, TetR family	Information processing	Unknown	SPy2177	23	2280	15	2439	0.44	0.9037	0.6711	
M5005_Spy1831	SpM1_ChORF2178_s_at	*rpsD*	SSU ribosomal protein S4P	Protein synthesis	Cytoplasmic	SPy2178	244	451	279	411	1.31	0.0949	0.3037	
M5005_Spy1834	SpM1_ChORF2181_s_at	-	Hypothetical protein	Unknown	Cytoplasmic	SPy2181	121	894	107	1181	0.78	0.2107	0.4110	
M5005_Spy1835	SpM1_ChORF2182_s_at	*holB*	Replicative DNA helicase (EC 3.6.1.-)	Cellular processing	Cytoplasmic	SPy2182	640	141	388	329	0.37	0.0004	**0.0137**	**Significant**
M5005_Spy1836	SpM1_ChORF2183_s_at	*rplI*	LSU ribosomal protein L9P	Protein synthesis	Cytoplasmic	SPy2183	453	200	345	306	0.58	0.0010	**0.0256**	**Significant**
M5005_Spy1836	SpM1_ChORF2184_s_at	*rplI*	LSU ribosomal protein L9P	Protein synthesis	Cytoplasmic	SPy2184	591	140	421	266	0.51	0.0011	**0.0294**	**Significant**
M5005_Spy1838	SpM1_ChORF2185_at	*gidA*	Glucose inhibited division protein A	Cellular processing	Cytoplasmic	SPy2185	28	1855	54	1599	3.73	0.2033	0.4066	
M5005_Spy1839	SpM1_ChORF2186_s_at	-	Phosphohydrolase (MutT/nudix family protein)	Unknown	Cytoplasmic	SPy2186	81	1264	87	1252	1.15	0.7564	0.6366	
M5005_Spy1840	SpM1_ChORF2188_s_at	*trmU*	tRNA (5-methylaminomethyl-2-thiouridylate)-methyltransferase (EC 2.1.1.61)	Protein synthesis	Cytoplasmic	SPy2188	196	491	177	625	0.81	0.0058	0.0952	
M5005_Spy1841	SpM1_ChORF2189_s_at	*sdhB*	L-serine dehydratase (EC 4.2.1.13)	Amino acid metabolism	Unknown	SPy2189	109	1112	165	788	2.29	0.6203	0.5963	

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M5005_Spy1842	SpM1_ChORF2190_s_at	*sdhA*	L-serine dehydratase (EC 4.2.1.13)	Amino acid metabolism	Cytoplasmic Membrane	SPy2190	103	1062	101	1014	0.96	0.0685	0.2779	
M5005_Spy1843	SpM1_ChORF2191_s_at	-	Transglycosylase SLT domain family protein	Virulence	Extracellular	SPy2191	224	454	174	791	0.60	0.0183	0.1703	
M5005_Spy1845	SpM1_ChORF2193_s_at	*cbiO2*	ATP-binding protein involved in export of hyaluronan capsule	Membrane transport	Cytoplasmic Membrane	SPy2193	150	833	119	960	0.63	0.3252	0.4776	
M5005_Spy1845	SpM1_ChORF2194_s_at	*cbiO2*	ATP-binding protein involved in export of hyaluronan capsule	Membrane transport	Cytoplasmic Membrane	SPy2194	95	1024	94	1227	0.99	0.5921	0.5877	
M5005_Spy1846	SpM1_ChORF2195_s_at	*cbiO1*	ATP-binding protein involved in export of hyaluronan capsule	Membrane transport	Cytoplasmic Membrane	SPy2195	145	776	155	804	1.14	0.3189	0.4745	
M5005_Spy1846	SpM1_ChORF2196_s_at	*pgsA*	CDP-diacylglycerol--glycerol-3-phosphate 3-phosphatidyltransferase	Membrane transport	Cytoplasmic Membrane	SPy2196	137	882	135	838	0.98	0.7338	0.6294	
M5005_Spy1848	SpM1_ChORF2197_s_at	-	Hypothetical membrane associated protein	Unknown	Unknown	SPy2197	225	557	215	599	0.91	0.5793	0.5833	
M5005_Spy1849	SpM1_ChORF2198_s_at	-	Zinc protease (EC 3.4.99.-)	Unknown	Cytoplasmic	SPy2198	111	982	141	820	1.61	0.0397	0.2310	
M5005_Spy1850	SpM1_ChORF2199_s_at	-	Zinc protease (EC 3.4.99.-)	Cellular processing	Cytoplasmic	SPy2199	67	1414	97	1016	2.12	0.4703	0.5387	
M5005_Spy1851	SpM1_ChORF2200_s_at	*hasA*	Hyaluronan synthase (EC 2.4.1.212)	Carbohydrate metabolism	Cytoplasmic Membrane	SPy2200	148	824	211	596	2.04	0.0001	**0.0021**	**Significant**
M5005_Spy1852	SpM1_ChORF2201_s_at	*hasB*	UDP-glucose 6-dehydrogenase (EC 1.1.1.22)	Carbohydrate metabolism	Unknown	SPy2201	127	1014	155	742	1.49	0.0053	0.0926	
M5005_Spy1853	SpM1_ChORF2202_s_at	*hasC*	UTP--glucose-1-phosphate uridylyltransferase (EC 2.7.7.9)	Carbohydrate metabolism	Cytoplasmic	SPy2202	244	442	325	330	1.77	0.0454	0.2434	
M5005_Spy1854	SpM1_ChORF2203_s_at	-	Hypothetical cytosolic protein	Cellular processing	Unknown	SPy2203	144	839	115	970	0.64	0.6080	0.5926	
M5005_Spy1855	SpM1_ChORF2204_s_at	*recF*	DNA replication and repair protein recF	Information processing	Cytoplasmic	SPy2204	147	794	204	610	1.92	0.4653	0.5360	
M5005_Spy1856	SpM1_ChORF2205_s_at	-	Glucose uptake protein homolog	Membrane transport	Cytoplasmic Membrane	SPy2205	578	146	431	243	0.56	0.0138	0.1497	

M5005_gene	RML Probeset	Gene	Description	Function	Predicted Cellular Localization *	Synonym †	Normalized Expression (WT) ‡	Transcript Rank (WT) §	Normalized Expression (Mutant) ‡	Transcript Rank (Mutant) §	Fold Change (Mutant : WT) **	*P* -value (Strain)	*Q* -value (Strain)††	Strain Significance (FDR=0.05)
M5005_Spy1857	SpM1_ChORF2206_s_at	*guaB*	Inosine-5'-monophosphate dehydrogenase (EC 1.1.1.205)	Nucleotide metabolism	Cytoplasmic	SPy2206	171	634	174	700	1.03	0.2095	0.4110	
M5005_Spy1858	SpM1_ChORF2207_s_at	*trsA/trpA*	Tryptophanyl-tRNA synthetase (EC 6.1.1.2)	Protein synthesis	Cytoplasmic	SPy2207	113	1050	98	1119	0.74	0.1944	0.3993	
M5005_Spy1860	SpM1_ChORF2209_s_at	-	Hypothetical membrane spanning protein	Membrane transport	Cytoplasmic Membrane	SPy2209	45	1625	23	2052	0.26	0.3771	0.4968	
M5005_Spy1861	SpM1_ChORF2210_s_at	-	ABC transporter ATP-binding protein	Membrane transport	Cytoplasmic Membrane	SPy2210	87	1140	107	1056	1.52	0.9741	0.6874	
M5005_Spy1863	SpM12_ChORF236-4_s_at	-	Transposase	Mobile genetic element	Unknown	spyM18_2254	36	1720	52	1578	2.13	0.5283	0.5631	
M5005_Spy1863	SpM18_ChORF2254_s_at	-	Transposase	Mobile genetic element	Unknown	spyM18_2254	42	1659	57	1542	1.88	0.2361	0.4227	
M5005_Spy1864	SpM1_ChORF2215_s_at	-	Hypothetical cytosolic protein	Unknown	Unknown	SPy2215	26	2301	27	2151	1.11	0.4752	0.5410	
M5005_Spy1865	SpM1_ChORF2216_s_at	*htrA*	Protease Do (EC 3.4.21.-); Secreted protein chaperone	Stress adaptation	Unknown	SPy2216	306	388	238	609	0.61	0.0014	**0.0353**	**Significant**
M5005_Spy1866	SpM1_ChORF2217_s_at	*spoJ*	Chromosome partitioning protein parB	Cellular processing	Cytoplasmic	SPy2217	228	589	156	770	0.47	0.0027	0.0570	

*Predicted Cellular Localization according to psortb (available at: http://www.psort.org/genomes/genomes.pl)

†Synonym in M1 SF370, M3 MGAS315 or M18 MGAS8232 GAS strains.

‡Normalized expression values following (1) an absolute square root transform normalization and (2) array scaling to center array means and obtain a standard deviation of 1.0.

§Transcript rank for most abundant transcript is valued at 1. Rank increases arithmetically with decreasing transcript detection, according to the normalized expression estimates.

**Fold change calculated on the square of the normalized expression estimates.

††Bootstrapped Q-values assessing the treatment (strain) effect in RMLChip microarrays using ANOVA model (with wash batch effect removed by linear sliding scaling)

Supplementary Table 4. Correlated transcript expression in GAS *in vivo* transcriptome microarrays reveals co-regulation.

Region	ORF #	Gene	Synonym	Description
I	M5005_Spy0562	*sagA*	*spy0738*	Streptolysin S precursor
	M5005_Spy0563	*sagB*	*spy0739*	Streptolysin S biosynthesis protein
	M5005_Spy0564	*sagC*	*spy0740*	Streptolysin S biosynthesis protein
	M5005_Spy0565	*sagD*	*spy0741*	Streptolysin S biosynthesis protein
	M5005_Spy0566	*sagE*	*spy0742*	Streptolysin S self-immunity protein
	M5005_Spy0567	*sagF*	*spy0743*	Streptolysin S biosynthesis protein
	M5005_Spy0568	*sagG*	*spy0744*	Streptolysin S export ATP-binding protein
	M5005_Spy0569	*sagH*	*spy0745*	Streptolysin S export transmembrane protein
	M5005_Spy0570	*sagI*	*spy0746*	Streptolysin S export transmembrane protein
II	M5005_Spy0751	*acoA*	*spy1026*	Pyruvate Dehydrogenase E1 (EC 1.2.4.1)
	M5005_Spy0752	*acoB*	*spy1027*	Pyruvate Dehydrogenase E1 (EC 1.2.4.1)
III	M5005_Spy0926	-	*spy1212*	Cardiolipin synthetase (EC 2.7.8.-)
	M5005_Spy0927	*fhs.1*	*spy1213*	Formate--tetrahydrofolate ligase (EC 6.3.4.3)
	M5005_Spy0928	*lplA*	*spy1214*	Lipoate-protein ligase A (EC 6.-.-.-)
	M5005_Spy0929	-	*spy1215*	SIR2 family protein
	M5005_Spy0930	-	*spy1216*	ATPase
IV	M5005_Spy0971	-	*spy1260*	General stress protein, Gls24 family
	M5005_Spy0972	-	*spy1261*	Hypothetical protein
	M5005_Spy0973	-	*spy1262*	General stress protein, Gls24 family
	M5005_Spy0974	-	*spy1263*	Small integral membrane protein

	M5005_Spy0975	-	*spy1264*	Small integral membrane protein
V	M5005_Spy1062	*malA*	*spy1298*	Maltodextrose utilization protein
	M5005_Spy1063	*malC*	*spy1299*	Maltose transport system permease protein
	M5005_Spy1064	*malD*	*spy1301*	Maltose transport system permease protein
	M5005_Spy1065	*amyA*	*spy1302*	Alpha-amylase (EC 3.2.1.1)
	M5005_Spy1066	*amyB*	*spy1304*	Cyclomaltodextrinase (EC 3.2.1.54)
	M5005_Spy1067	*malX*	*spy1306*	Maltose/maltodextrin-binding protein
VI	M5005_Spy1303	*aroE*	*spy1584*	Shikimate 5-dehydrogenase (EC 1.1.1.25)
	M5005_Spy1304	*lacZ*	*spy1586*	Beta-galactosidase (EC 3.2.1.23)
	M5005_Spy1305	*lytR*	*spy1587*	Two-component response regulator
	M5005_Spy1306	*lytS*	*spy1588*	Two-component sensor kinase
	M5005_Spy1307	-	*spy1589*	Hypothetical membrane spanning protein
	M5005_Spy1308	-	*spy1591*	Sugar-binding protein
	M5005_Spy1309	-	*spy1592*	Sugar-binding protein
	M5005_Spy1310	-	*spy1593*	Sugar transport system permease protein
VII	M5005_Spy1718	*sic1.01*	*spy2016*	Streptococcal Inhibitor of Complement
	M5005_Spy1719	*emm1.0*	*spy2018*	M protein
	M5005_Spy1720	*mga*	*spy2019*	Multiple Gene Activator
	M5005_Spy1721	-		Hypothetical protein
	M5005_Spy1722	-	*spy2023*	Hypothetical protein
	M5005_Spy1723	*isp*	*spy2025*	Immunogenic secreted protein
	M5005_Spy1724	*ihk*	*spy2026*	Two-component histidine kinase
	M5005_Spy1725	*irr*	*spy2027*	Two-component response regulator

	M5005_Spy1726	-	*spy2029*	ABC transporter permease protein
	M5005_Spy1727	-	*spy2031*	ABC transporter ATP-binding protein
	M5005_Spy1728	-	*spy2032*	ABC transporter
VIII	M5005_Spy1732	-		Protein export protein prsA precursor
	M5005_Spy1733	-		Hypothetical protein
	M5005_Spy1734	-		Streptopain precursor fragment
	M5005_Spy1735	*speB*	*spy2039*	Streptococcal PTSAg Exotoxin B
	M5005_Spy1736	-	*spy2040*	Hypothetical protein
IX	M5005_Spy1771	*hutI*	*spy2081*	Imidazolonepropionase (EC 3.5.2.7)
	M5005_Spy1772	*hutU*	*spy2082*	Urocanate hydratase (EC 4.2.1.49)
	M5005_Spy1773	-	*spy2083*	Glutamate formiminotransferase (EC 2.1.2.5)
	M5005_Spy1774	-	*spy2084*	Formiminotetrahydrofolate cyclodeaminase (EC 4.3.1.4)
	M5005_Spy1775	*fhs.2*	*spy2085*	Formate--tetrahydrofolate ligase (EC 6.3.4.3)
	M5005_Spy1776	-	*spy2087*	Hypothetical cytosolic protein
	M5005_Spy1777	*hutH*	*spy2089*	Histidine ammonia-lyase (EC 4.3.1.3)
	M5005_Spy1778	*hutG*	*spy2090*	Formiminoglutamase (EC 3.5.3.8)

Supplementary Table 5. Correlation of GAS gene expression with *covR* /*S* two-component regulatory system (TCS) transcripts.

M5005_Spy#	Gene	Synonym *	WT Transcript Rank †	Mutant Transcript Rank †	*r* Correlation (*covR*) ‡	*P*-value Correlation (*covR*)	*Q*-value Correlation (*covR*) §	*r* Correlation (*covS*) ‡	*P*-value Correlation (*covS*)	*Q*-value Correlation (*covS*) §
M5005_Spy0282	*covR*	spyM18_0328	283	639	1.0000	N/A	**N/A**	0.6780	8.7E-08	**0.0055**
M5005_Spy1684	*ska*	spy1979	431	86	0.8571	3.9E-15	0.0027	0.7046	1.6E-08	**0.0055**
M5005_Spy0500	-	spy0601	398	286	0.8295	1.8E-13	0.0027	0.6337	1.0E-06	**0.0055**
M5005_Spy0281	-	spy0334	484	347	0.7947	9.3E-12	0.0027	0.6396	7.5E-07	**0.0055**
M5005_Spy1733	-		1077	110	0.7545	3.8E-10	0.0027	0.7114	1.0E-08	**0.0055**
M5005_Spy1531	*isp2*	spy1801	203	29	0.7502	5.5E-10	0.0027	0.7286	3.0E-09	**0.0055**
M5005_Spy1734	-		275	1	0.7371	1.5E-09	0.0027	0.7352	1.8E-09	**0.0055**
M5005_Spy1106	*grab*	spy1357	1639	519	0.7316	2.4E-09	0.0027	0.4928	3.21E-04	**0.0057**
M5005_Spy1143	-	spy1402	1468	359	0.7079	1.3E-08	0.0027	0.7538	4.1E-10	**0.0055**
M5005_Spy0568	*sagG*	spy0744	397	207	0.7071	1.4E-08	0.0027	0.6412	6.9E-07	**0.0055**
M5005_Spy0115	-	spy0136	1203	366	0.7029	1.8E-08	0.0027	0.5796	1.3E-05	**0.0055**
M5005_Spy0531	*ftsE*	spy0644	239	144	0.6979	2.5E-08	0.0027	0.4849	4.13E-04	**0.0059**
M5005_Spy1735	*speB*	spy2039	360	2	0.692	3.6E-08	0.0027	0.7635	1.8E-10	**0.0055**
M5005_Spy1736	-	spy2040	1220	28	0.692	3.7E-08	0.0027	0.6957	2.9E-08	**0.0055**
M5005_Spy0618	*cmk*	spy0803	154	72	0.6904	4.1E-08	0.0027	0.6687	1.5E-07	**0.0055**
M5005_Spy1732	-		309	36	0.6832	6.3E-08	0.0027	0.5934	7.0E-06	**0.0055**
M5005_Spy0283	*covS*	spy0337	759	328	0.678	8.7E-08	0.0027	1.0000	N/A	**N/A**
M5005_Spy0562	*sagA*	spy0738	30	8	0.676	9.8E-08	0.0027	0.5757	1.5E-05	**0.0055**
M5005_Spy0952	*pstB2*	spy1242	229	166	0.6718	1.3E-07	0.0027	0.4653	7.54E-04	**0.0067**
M5005_Spy1143	-	spy1404	1483	432	0.6712	1.3E-07	0.0027	0.5597	2.9E-05	**0.0055**
M5005_Spy0614	*pepT*	spy0799	211	146	0.6437	6.1E-07	0.0027	0.5396	6.3E-05	**0.0055**
M5005_Spy0832	*malP*	spy1109	603	229	0.638	8.2E-07	0.0027	0.6477	4.9E-07	**0.0055**
M5005_Spy1144	-	spy1405	1441	540	0.6242	1.6E-06	0.0027	0.5243	1.10E-04	**0.0055**
M5005_Spy0385	-	spy0470	128	61	0.6236	1.7E-06	0.0027	0.4674	7.10E-04	**0.0067**
M5005_Spy1356	*pepC*	spy1651	326	202	0.6218	1.8E-06	0.0027	0.4362	0.0017	**0.0097**
M5005_Spy0530	*prfB*	spy0643	455	405	0.6202	2.0E-06	0.0027	0.4596	8.94E-04	**0.0071**
M5005_Spy0161	*perR*	spy0187	130	99	0.617	2.3E-06	0.0027	0.4876	3.80E-04	**0.0059**
M5005_Spy0279	*lemA*	spy0330	190	137	0.6146	2.6E-06	0.0027	0.4194	0.0027	0.0131
M5005_Spy0955	*pstS*	spy1245	436	340	0.6134	2.8E-06	0.0027	0.4114	0.0033	0.0144
M5005_Spy0564	*sagC*	spy0740	396	130	0.6067	3.8E-06	0.0027	0.6700	1.4E-07	**0.0055**

M5005_Spy#	Gene	Synonym *	WT Transcript Rank †	Mutant Transcript Rank †	*r* Correlation (*covR*) ‡	*P*-value Correlation (*covR*)	*Q*-value Correlation (*covR*) §	*r* Correlation (*covS*) ‡	*P*-value Correlation (*covS*)	*Q*-value Correlation (*covS*) §
M5005_Spy0525	-	spy0637	1711	705	0.6065	3.9E-06	0.0027	0.5654	2.3E-05	**0.0055**
M5005_Spy1540	*endoS*	spy1813	462	222	0.6038	4.4E-06	0.0027	0.6097	3.3E-06	**0.0055**
M5005_Spy0559	-		1666	1050	0.6034	4.5E-06	0.0027	0.5296	9.1E-05	**0.0055**
M5005_Spy0524	*idnO*	spy0636	1068	350	0.598	5.7E-06	0.0027	0.4033	0.0041	0.0166
M5005_Spy0563	*sagB*	spy0739	430	266	0.591	7.8E-06	0.0027	0.5548	3.5E-05	**0.0055**
M5005_Spy0959	-	spy1249	530	518	0.5838	1.1E-05	0.0027	0.2398	0.0970	0.1155
M5005_Spy0192	*hasC.2*	spy0224	314	232	0.5814	1.2E-05	0.0027	0.3197	0.0252	0.0506
M5005_Spy1303	*aroE*	spy1584	620	367	0.5806	1.2E-05	0.0027	0.5667	2.2E-05	**0.0055**
M5005_Spy0615	*ebsA*	spy0800	359	264	0.5804	1.2E-05	0.0027	0.4138	0.0031	0.0141
M5005_Spy0011	-	spy0013	2103	2211	0.578	1.4E-05	0.0027	0.2602	0.0710	0.0946
M5005_Spy0351	*spyA*	spy0428	195	129	0.5774	1.4E-05	0.0027	0.6548	3.3E-07	**0.0055**
M5005_Spy0567	*sagF*	spy0743	802	308	0.5773	1.4E-05	0.0027	0.5138	1.59E-04	**0.0055**
M5005_Spy0820	*folC.1*	spy1096	344	336	0.5765	1.5E-05	0.0027	0.5014	2.42E-04	**0.0055**
M5005_Spy0565	*sagD*	spy0741	357	147	0.5754	1.5E-05	0.0027	0.6003	5.1E-06	**0.0055**
M5005_Spy0531	*ftsE*	spy0645	449	310	0.5733	1.7E-05	0.0027	0.4968	2.83E-04	**0.0056**
M5005_Spy0415	-	spy0504	137	125	0.5725	1.7E-05	0.0027	0.5001	2.53E-04	**0.0055**
M5005_Spy1851	*hasA*	spy2200	767	578	0.5687	2.0E-05	0.0027	0.6559	3.1E-07	**0.0055**
M5005_Spy0833	-	spy1110	368	174	0.5632	2.5E-05	0.0027	0.5985	5.6E-06	**0.0055**
M5005_Spy0568	*sagG*		961	409	0.5622	2.6E-05	0.0027	0.4838	4.29E-04	**0.0059**
M5005_Spy0570	*sagI*		580	265	0.5621	2.6E-05	0.0027	0.6324	1.1E-06	**0.0055**
M5005_Spy0366	-		497	466	0.5541	3.6E-05	0.0027	0.2503	0.0828	0.1040
M5005_Spy0673	*papS*	spy0866	674	566	0.5526	3.8E-05	0.0027	0.3207	0.0247	0.0500
M5005_Spy0352	-	spy0430	896	276	0.5503	4.2E-05	0.0027	0.4217	0.0025	0.0126
M5005_Spy1547	*efp*	spy1821	44	38	0.5494	4.4E-05	0.0027	0.3426	0.0160	0.0397
M5005_Spy0249	*oppA*	spyM18_0281	207	184	0.5486	4.5E-05	0.0027	0.4674	7.08E-04	**0.0067**
M5005_Spy1262	-	spy1534	772	839	0.5483	4.5E-05	0.0027	0.2804	0.0510	0.0773
M5005_Spy0527	*kgdA*	spy0639	1229	682	0.5475	4.7E-05	0.0027	0.3594	0.0112	0.0315
M5005_Spy0571	-	spy0747	146	73	0.5466	4.8E-05	0.0027	0.5255	1.06E-04	**0.0055**
M5005_Spy1415	*sdaD2*		569	477	0.5441	5.3E-05	0.0027	0.2125	0.1426	0.1510
M5005_Spy0519	*agaD*	spy0629	2197	1411	0.5436	5.4E-05	0.0027	0.2761	0.0548	0.0805
M5005_Spy0569	*sagH*	spy0745	663	457	0.5419	5.8E-05	0.0027	0.5368	7.0E-05	**0.0055**
M5005_Spy1308	-	spy1592	38	24	0.5403	6.1E-05	0.0027	0.5060	2.08E-04	**0.0055**

M5005_Spy#	Gene	Synonym *	WT Transcript Rank †	Mutant Transcript Rank †	*r* Correlation (*covR*) ‡	*P*-value Correlation (*covR*)	*Q*-value Correlation (*covR*) §	*r* Correlation (*covS*) ‡	*P*-value Correlation (*covS*)	*Q*-value Correlation (*covS*) §
M5005_Spy0368	*mtsA*	spy0453	103	116	0.5396	6.3E-05	0.0027	0.3219	0.0241	0.0492
M5005_Spy1144	-	SpyM3_1070	1830	464	0.538	6.7E-05	0.0027	0.7624	2.0E-10	**0.0055**
M5005_Spy1555	*rpsF*	spy1831	25	22	0.5378	6.7E-05	0.0027	0.5470	4.8E-05	**0.0055**
M5005_Spy1605	-	spy0303	523	403	0.535	7.5E-05	0.0027	0.4193	0.0027	0.0131
M5005_Spy1639	*lacR.2*	spy1924	1283	1165	0.5345	7.6E-05	0.0027	0.2990	0.0369	0.0632
M5005_Spy0949	*pepN*	spy1239	193	149	0.5337	7.8E-05	0.0027	0.5449	5.2E-05	**0.0055**
M5005_Spy0707	-	spy0904	1664	1457	0.5323	8.3E-05	0.0027	0.3538	0.0126	0.0341
M5005_Spy0702	-	spy0899	824	732	0.531	8.7E-05	0.0027	0.6461	5.3E-07	**0.0055**
M5005_Spy0526	-	spyM18_0701	1302	431	0.527	0.0001	0.0027	0.4211	0.0026	0.0128
M5005_Spy1232	*xseB*	spy1499	557	460	0.5269	0.0001	0.0027	0.6328	1.1E-06	**0.0055**
M5005_Spy0218	-	spy0258	1491	976	0.5252	0.0001	0.0027	0.3349	0.0187	0.0424
M5005_Spy0595	*rexA*	spy0777	851	579	0.5244	0.0001	0.0027	0.2412	0.0950	0.1137
M5005_Spy1782	*pepO*	spy2095	295	279	0.5236	0.0001	0.0027	0.3308	0.0203	0.0447
M5005_Spy0721	-	spy0919	106	89	0.5233	0.0001	0.0027	0.4739	5.82E-04	**0.0064**
M5005_Spy1596	*glnA*	spy1877	293	293	0.521	0.0001	0.0027	0.2506	0.0824	0.1038
M5005_Spy1542	*scrA*	spy1815	579	473	0.5195	0.0001	0.0027	0.3921	0.0053	0.0197
M5005_Spy0950	*phoU*	spy1240	375	292	0.5194	0.0001	0.0027	0.3900	0.0056	0.0204
M5005_Spy1316	-	spy1603	500	376	0.5187	0.0001	0.0027	0.3414	0.0164	0.0401
M5005_Spy0556	*eno*	spy0731	116	101	0.5177	0.0001	0.0027	0.3621	0.0106	0.0303
M5005_Spy0287	*pgdA*	spy0341	358	260	0.5169	0.0001	0.0027	0.3978	0.0046	0.0181
M5005_Spy0280	-		401	389	0.5151	0.0002	0.0027	0.4893	3.59E-04	**0.0058**
M5005_Spy1310	-	spy1595	327	231	0.5137	0.0002	0.0027	0.5454	5.1E-05	**0.0055**
M5005_Spy0951	*pstB*	spy1241	370	298	0.5134	0.0002	0.0027	0.5487	4.5E-05	**0.0055**
M5005_Spy1849	-	spy2198	989	844	0.5133	0.0002	0.0027	0.2438	0.0914	0.1105
M5005_Spy1309	-	spy1593	160	52	0.5131	0.0002	0.0027	0.5291	9.3E-05	**0.0055**
M5005_Spy1304	*lacZ*	spy1586	134	33	0.512	0.0002	0.0027	0.4719	6.19E-04	**0.0065**
M5005_Spy1399	-	spyM18_1719	827	343	0.51	0.0002	0.0027	0.5198	1.29E-04	**0.0055**
M5005_Spy1556	-	spy1832	468	301	0.5081	0.0002	0.0027	0.5399	6.2E-05	**0.0055**
M5005_Spy1357	-	spyM18_1663	789	978	0.5071	0.0002	0.0027	0.1626	0.2643	0.2264
M5005_Spy0546	*rpmE*	spy0717	122	108	0.5047	0.0002	0.0027	0.2931	0.0409	0.0664
M5005_Spy0160	-	spy0186	212	208	0.5031	0.0002	0.0027	0.5313	8.6E-05	**0.0055**
M5005_Spy0954	*pstC*	spy1244	749	558	0.5014	0.0002	0.0027	0.5699	1.9E-05	**0.0055**

M5005_Spy#	Gene	Synonym *	WT Transcript Rank †	Mutant Transcript Rank †	*r* Correlation (*covR*) ‡	*P*-value Correlation (*covR*)	*Q*-value Correlation (*covR*) §	*r* Correlation (*covS*) ‡	*P*-value Correlation (*covS*)	*Q*-value Correlation (*covS*) §
M5005_Spy1242	-	spy1511	179	236	0.501	0.0002	0.0027	0.3537	0.0127	0.0341
M5005_Spy0229	*prgA*	spy0269	35	43	0.5009	0.0002	0.0027	0.2585	0.0729	0.0964
M5005_Spy0598	*mscL*	spy0780	537	433	0.4997	0.0003	0.0027	0.3475	0.0144	0.0372
M5005_Spy0957	-	spy1247	739	811	0.4986	0.0003	0.0027	0.4915	3.35E-04	**0.0058**
M5005_Spy1395	*lacD.1*	spy1704	793	439	0.4982	0.0003	0.0027	0.5731	1.7E-05	**0.0055**
M5005_Spy0222	*ksgA*	spy0262	611	624	0.4978	0.0003	0.0027	0.3921	0.0053	0.0197
M5005_Spy0364	-	spy0446	321	311	0.4973	0.0003	0.0027	0.3267	0.0220	0.0468
M5005_Spy0020	*plsX*	spy0022	549	445	0.4972	0.0003	0.0027	0.3693	0.0090	0.0278
M5005_Spy0285	*dnaB*	spy0339	232	214	0.4951	0.0003	0.0027	0.1797	0.2168	0.1971
M5005_Spy0672	-	spy0865	525	438	0.4951	0.0003	0.0027	0.3689	0.0091	0.0279
M5005_Spy1164	*gpmA*	spy1429	369	412	0.4916	0.0003	0.0027	0.1897	0.1918	0.1821
M5005_Spy0986	*glmS*		102	104	0.4886	0.0004	0.0028	0.3639	0.0102	0.0297
M5005_Spy1306	*lytS*	spy1588	325	205	0.4884	0.0004	0.0028	0.5117	1.72E-04	**0.0055**
M5005_Spy1715	*scpA*		79	51	0.4857	0.0004	0.0028	0.3481	0.0142	0.0370
M5005_Spy0761	-	spy1036	1215	1305	0.485	0.0004	0.0028	0.2445	0.0905	0.1096
M5005_Spy0082	*pbp1b*	spy0097	376	349	0.4842	0.0004	0.0028	0.2873	0.0453	0.0710
M5005_Spy1375	*tkt*	spy1676	55	40	0.4836	0.0004	0.0028	0.3768	0.0076	0.0247
M5005_Spy0691	*clpX*	spy0885	598	539	0.4828	0.0004	0.0028	0.5042	2.21E-04	**0.0055**
M5005_Spy0292	-	spy0348	132	138	0.4827	0.0004	0.0028	0.4892	3.62E-04	**0.0058**
M5005_Spy1401	-	spy1710	746	368	0.4819	0.0005	0.0028	0.3848	0.0063	0.0217
M5005_Spy1738	*sda*	spy2043	12	4	0.481	0.0005	0.0028	0.6088	3.5E-06	**0.0055**
M5005_Spy0129	*ntpC*	spy0151	1097	669	0.4792	0.0005	0.0028	0.3688	0.0091	0.0279
M5005_Spy0335	-	spy0406	204	132	0.4778	0.0005	0.0029	0.5626	2.6E-05	**0.0055**
M5005_Spy0196	-	spy0229	775	710	0.4774	0.0005	0.0029	0.5656	2.3E-05	**0.0055**
M5005_Spy0956	-	spy1246	703	571	0.4767	0.0005	0.0029	0.0989	0.4989	0.3365
M5005_Spy1305	*lytR*	spy1587	320	124	0.4759	0.0005	0.0029	0.5199	1.29E-04	**0.0055**
M5005_Spy1554	*ssb2*	spy1830	157	173	0.4754	0.0006	0.0029	0.1595	0.2736	0.2309
M5005_Spy1289	-	spy1565	1099	937	0.4753	0.0006	0.0029	0.5253	1.06E-04	**0.0055**
M5005_Spy1250	*ftsA*	spy1521	37	34	0.4748	0.0006	0.0029	0.2951	0.0396	0.0654
M5005_Spy1227	-	spy1494	250	181	0.4732	0.0006	0.0030	0.4466	0.0013	**0.0083**
M5005_Spy0545	*agaS*	spy0716	1087	600	0.4727	0.0006	0.0030	0.6687	1.5E-07	**0.0055**
M5005_Spy1567	-	spy1845	846	667	0.4726	0.0006	0.0030	0.3542	0.0125	0.0340

M5005_Spy#	Gene	Synonym *	WT Transcript Rank †	Mutant Transcript Rank †	*r* Correlation (*covR*) ‡	*P*-value Correlation (*covR*)	*Q*-value Correlation (*covR*) §	*r* Correlation (*covS*) ‡	*P*-value Correlation (*covS*)	*Q*-value Correlation (*covS*) §
M5005_Spy0098	-	spy0116	121	131	0.4719	0.0006	0.0030	0.2939	0.0404	0.0660
M5005_Spy1413	-	spy1725	726	671	0.4717	0.0006	0.0030	0.2793	0.0520	0.0781
M5005_Spy1594	-	spy1875	180	218	0.4713	0.0006	0.0030	0.3944	0.0050	0.0191
M5005_Spy1073	*dltA*	spy1311	835	886	0.4704	0.0006	0.0030	0.4224	0.0025	0.0125
M5005_Spy1671	-	spy1960	1276	895	0.4684	0.0007	0.0031	0.2122	0.1433	0.1512
M5005_Spy0270	-	spy0317	145	80	0.4666	0.0007	0.0032	0.3146	0.0277	0.0537
M5005_Spy0362	*gcaD*	spy0443	412	467	0.4664	0.0007	0.0032	0.1889	0.1936	0.1829
M5005_Spy1391	-	spy1698	719	722	0.4652	0.0008	0.0032	0.2090	0.1496	0.1545
M5005_Spy1302	-	spy1582	860	487	0.4648	0.0008	0.0032	0.4993	2.60E-04	**0.0055**
M5005_Spy0988	*pyk, pykA*	spy1282	189	190	0.4633	0.0008	0.0033	0.3270	0.0218	0.0467
M5005_Spy0947	*ciaH*	spy1236	426	529	0.4618	0.0008	0.0033	0.3949	0.0050	0.0189
M5005_Spy1235	-	spy1503	50	47	0.461	0.0009	0.0034	0.4123	0.0032	0.0143
M5005_Spy0572	-	spy0749	560	533	0.4608	0.0009	0.0034	0.5874	9.1E-06	**0.0055**
M5005_Spy1301	-	spy1581	606	307	0.4592	0.0009	0.0034	0.5052	2.14E-04	**0.0055**
M5005_Spy0331	*dnaX*	spy0400	810	634	0.4591	0.0009	0.0034	0.3270	0.0218	0.0467
M5005_Spy0233	*plr, gap*	spy0274	73	85	0.4586	0.0009	0.0034	0.2035	0.1608	0.1615
M5005_Spy0541	-	spy0654	586	348	0.4583	0.0009	0.0034	0.3711	0.0087	0.0271
M5005_Spy1719	*emm1*		2	5	0.4583	0.0009	0.0034	0.3039	0.0338	0.0606
M5005_Spy0330	*tmk*	spy0399	864	715	0.4567	0.0010	0.0035	0.4576	9.48E-04	**0.0073**
M5005_Spy0169	-	spy0196	2366	1979	0.4562	0.0010	0.0036	0.2351	0.1039	0.1208
M5005_Spy0320	-	spy0382	404	400	0.4561	0.0010	0.0036	0.2343	0.1052	0.1214
M5005_Spy1133	*surA, prsA*	spy1390	115	139	0.4556	0.0010	0.0036	0.3518	0.0132	0.0351
M5005_Spy0844	*nifS, yrvO*	spy1123	435	441	0.4531	0.0011	0.0037	0.2127	0.1423	0.1509
M5005_Spy0872	*nox*	spy1150	124	112	0.453	0.0011	0.0037	0.2874	0.0452	0.0710
M5005_Spy1718	*sic*	spy2016	1	3	0.4529	0.0011	0.0037	0.5539	3.7E-05	**0.0055**
M5005_Spy0414	-	spy0503	141	157	0.4528	0.0011	0.0037	0.5821	1.1E-05	**0.0055**
M5005_Spy0844	*nifS, yrvO*	spy1122	187	223	0.4528	0.0011	0.0037	0.3223	0.0239	0.0489
M5005_Spy0067	*rpmJ*	spy0076	226	198	0.4523	0.0011	0.0037	0.5219	1.20E-04	**0.0055**
M5005_Spy0662	*fruA*	spy0855	371	334	0.4516	0.0011	0.0038	0.3355	0.0184	0.0422
M5005_Spy0942	-	spy1228	131	169	0.4513	0.0011	0.0038	0.4154	0.0030	0.0139
M5005_Spy0163	-	spy0189	288	227	0.4509	0.0011	0.0038	0.4453	0.0013	**0.0085**
M5005_Spy1553	*rpsR*	spy1829	544	515	0.4504	0.0012	0.0038	0.4518	0.0011	**0.0077**

M5005_Spy#	Gene	Synonym *	WT Transcript Rank †	Mutant Transcript Rank †	*r* Correlation (*covR*) ‡	*P*-value Correlation (*covR*)	*Q*-value Correlation (*covR*) §	*r* Correlation (*covS*) ‡	*P*-value Correlation (*covS*)	*Q*-value Correlation (*covS*) §
M5005_Spy1538	*pmi*	spy1810	517	407	0.4503	0.0012	0.0038	0.3897	0.0056	0.0204
M5005_Spy0043	*rpsJ*	spy0047	552	616	0.448	0.0012	0.0040	0.3508	0.0135	0.0355
M5005_Spy0954	*pstC*	spy1243	867	696	0.448	0.0012	0.0040	0.1150	0.4314	0.3076
M5005_Spy0709	*pyrC*	spy0907	1181	1151	0.4464	0.0013	0.0041	0.1274	0.3832	0.2871
M5005_Spy1248	-	spy1519	170	203	0.4459	0.0013	0.0041	0.3072	0.0318	0.0582
M5005_Spy0153	*araD*	spy0179	475	351	0.4431	0.0014	0.0043	0.5566	3.3E-05	**0.0055**
M5005_Spy0637	*lsp*	spy0826	1356	1375	0.4422	0.0015	0.0044	0.3118	0.0292	0.0554
M5005_Spy0289	-	spy0343	278	356	0.4421	0.0015	0.0044	0.3874	0.0060	0.0211
M5005_Spy1715	*scpA*	spy2010	63	66	0.4413	0.0015	0.0044	0.2766	0.0544	0.0802
M5005_Spy0818	-	spy1094	693	803	0.4412	0.0015	0.0044	0.5769	1.4E-05	**0.0055**
M5005_Spy0243	-	spy0287	487	505	0.4412	0.0015	0.0044	0.1002	0.4934	0.3340
M5005_Spy0424	*ccpA*	spy0514	302	237	0.4397	0.0016	0.0045	0.5057	2.10E-04	**0.0055**
M5005_Spy0566	*sagE*	spy0742	1344	761	0.4394	0.0016	0.0045	0.4184	0.0028	0.0132
M5005_Spy0228	*purR*	spy0268	255	256	0.4392	0.0016	0.0045	0.3176	0.0262	0.0517
M5005_Spy1073	*dltA*	spy1312	289	249	0.439	0.0016	0.0046	0.2781	0.0530	0.0790
M5005_Spy1589	*crgR*		747	900	0.4386	0.0016	0.0046	0.2526	0.0799	0.1022
M5005_Spy1300	-	spy1580	935	888	0.4381	0.0016	0.0046	0.4067	0.0037	0.0156
M5005_Spy0558	-	spy0733	2506	1230	0.438	0.0016	0.0046	0.1765	0.2251	0.2033
M5005_Spy0627	*gor, gpoA, gshR*	spy0813	929	774	0.4375	0.0017	0.0047	0.3872	0.0060	0.0212
M5005_Spy1756	-	spy2063	488	490	0.4373	0.0017	0.0047	0.1472	0.3128	0.2528
M5005_Spy0065	*adk*	spy0074	909	1009	0.437	0.0017	0.0047	0.3131	0.0285	0.0546
M5005_Spy1317	-	spy1604	186	135	0.4369	0.0017	0.0047	0.4971	2.80E-04	**0.0056**
M5005_Spy1308	-	spy1591	205	106	0.4368	0.0017	0.0047	0.5164	1.46E-04	**0.0055**
M5005_Spy1354	*recU*	spy1648	105	156	0.4364	0.0017	0.0047	0.1580	0.2783	0.2330
M5005_Spy1709	-	spy2005	23	23	0.4361	0.0017	0.0047	0.6249	1.6E-06	**0.0055**
M5005_Spy1682	*msmK*	spy1976	507	305	0.4358	0.0017	0.0047	0.3256	0.0224	0.0474
M5005_Spy0423	*pepQ*	spy0513	820	728	0.4356	0.0018	0.0047	0.4401	0.0016	**0.0092**
M5005_Spy1155	*prfC*	spy1416	164	185	0.4349	0.0018	0.0048	0.2467	0.0874	0.1074
M5005_Spy1409	*infB*	spy1721	257	274	0.4343	0.0018	0.0048	0.4997	2.56E-04	**0.0055**
M5005_Spy0674	-	spy0867	410	382	0.434	0.0018	0.0049	0.2360	0.1025	0.1197
M5005_Spy1373	-	spy1674	1048	698	0.4325	0.0019	0.0050	0.0076	0.9587	0.4888

M5005_Spy#	Gene	Synonym *	WT Transcript Rank †	Mutant Transcript Rank †	*r* Correlation (*covR*) ‡	*P*-value Correlation (*covR*)	*Q*-value Correlation (*covR*) §	*r* Correlation (*covS*) ‡	*P*-value Correlation (*covS*)	*Q*-value Correlation (*covS*) §
M5005_Spy0062	*rpmD*	spy0071	297	248	0.4321	0.0019	0.0050	0.2411	0.0952	0.1138
M5005_Spy1139	*nagB*	spy1399	652	576	0.4312	0.0020	0.0051	0.2782	0.0529	0.0790
M5005_Spy1659	-	spy1946	578	430	0.4285	0.0021	0.0055	0.2068	0.1539	0.1573
M5005_Spy0315	-	spy0376	463	577	0.4272	0.0022	0.0056	0.5200	1.28E-04	**0.0055**
M5005_Spy1374	-	spy1675	1024	1101	0.4265	0.0022	0.0057	0.2682	0.0624	0.0878
M5005_Spy1799	*recA*	spy2116	183	162	0.426	0.0023	0.0057	0.3714	0.0086	0.0271
M5005_Spy1119	*gapN*	spy1371	415	471	0.4258	0.0023	0.0057	0.1813	0.2124	0.1940
M5005_Spy0855	*proV*	spy1133	1384	969	0.4255	0.0023	0.0057	0.2794	0.0519	0.0781
M5005_Spy0290	*murC*	spy0345	163	183	0.4254	0.0023	0.0057	0.2235	0.1227	0.1355
M5005_Spy1104	-	spy1355	413	398	0.4234	0.0024	0.0060	0.2488	0.0848	0.1057
M5005_Spy1249	*ftsZ*	spy1520	82	68	0.4221	0.0025	0.0061	0.4544	0.0010	**0.0075**
M5005_Spy0197	-	spy0230	1809	1585	0.4216	0.0026	0.0061	0.3042	0.0336	0.0606
M5005_Spy0602	*rmlD*	spy0784	730	604	0.4212	0.0026	0.0062	0.4206	0.0026	0.0128
M5005_Spy1377	-	spy1681	119	151	0.4205	0.0026	0.0062	0.3206	0.0247	0.0501
M5005_Spy1621	*hsdR*	spy1904	801	681	0.4201	0.0027	0.0063	-0.0181	0.9020	0.4751
M5005_Spy0162	*vlg*	spy0188	197	170	0.42	0.0027	0.0063	0.3646	0.0100	0.0296
M5005_Spy0822	*folP*	spy1098	222	221	0.4198	0.0027	0.0063	0.2500	0.0832	0.1043
M5005_Spy1118	-	spy1370	138	122	0.4194	0.0027	0.0063	0.2858	0.0465	0.0723
M5005_Spy0539	-	spy0652	287	258	0.4181	0.0028	0.0065	0.4061	0.0038	0.0158
M5005_Spy0603	*rgpAc*	spy0786	351	358	0.4173	0.0029	0.0066	0.1713	0.2392	0.2117
M5005_Spy1388	*nagA*	spy1694	178	127	0.4165	0.0029	0.0067	0.2620	0.0690	0.0931
M5005_Spy0821	*folE*	spy1097	336	337	0.4163	0.0029	0.0067	0.3074	0.0317	0.0581
M5005_Spy1141	-	spy1401	1014	1135	0.4148	0.0030	0.0069	0.4523	0.0011	**0.0077**
M5005_Spy0696	*deoB*	spy0890	114	84	0.4146	0.0031	0.0069	0.3824	0.0067	0.0227
M5005_Spy1473	-	spy1731	799	866	0.4138	0.0031	0.0071	0.0558	0.7033	0.4127
M5005_Spy0374	*rplK*	spy0460	494	563	0.4132	0.0032	0.0071	0.2353	0.1036	0.1207
M5005_Spy1377	-	spy1680	280	332	0.4128	0.0032	0.0072	0.2813	0.0502	0.0764
M5005_Spy0915	*ffh*	spy1200	686	641	0.4123	0.0032	0.0072	0.1606	0.2702	0.2298
M5005_Spy1270	*arcC*	spy1541	334	342	0.411	0.0034	0.0074	0.2705	0.0601	0.0861
M5005_Spy1121	*ptsH*	spy1373	333	250	0.4108	0.0034	0.0074	0.3100	0.0302	0.0562
M5005_Spy1778	*hutG*	spy2090	308	195	0.408	0.0036	0.0079	0.2953	0.0394	0.0654
M5005_Spy1539	*scrK*	spy1811	1032	501	0.408	0.0036	0.0079	0.4802	4.80E-04	**0.0061**

M5005_Spy#	Gene	Synonym *	WT Transcript Rank †	Mutant Transcript Rank †	*r* Correlation (*covR*) ‡	*P*-value Correlation (*covR*)	*Q*-value Correlation (*covR*) §	*r* Correlation (*covS*) ‡	*P*-value Correlation (*covS*)	*Q*-value Correlation (*covS*) §
M5005_Spy0668	*ideS, mac*	spy0861	1600	1492	0.4074	0.0037	0.0079	0.3069	0.0320	0.0584
M5005_Spy1228	*recN*	spy1495	271	224	0.4073	0.0037	0.0079	0.5135	1.61E-04	**0.0055**
M5005_Spy1095	-	spy1343	1792	951	0.4071	0.0037	0.0079	0.0409	0.7800	0.4386
M5005_Spy0251	*oppC*	spy0295	648	618	0.4069	0.0037	0.0079	0.6759	9.9E-08	**0.0055**
M5005_Spy0164	-	spy0190	303	257	0.4055	0.0039	0.0081	0.5800	1.3E-05	**0.0055**
M5005_Spy0540	-	spy0653	337	234	0.4052	0.0039	0.0082	0.5783	1.3E-05	**0.0055**
M5005_Spy0069	*rpsK*	spy0078	104	109	0.4051	0.0039	0.0082	0.3247	0.0228	0.0480
M5005_Spy1156	-	spy1419	701	636	0.4041	0.0040	0.0083	0.2774	0.0537	0.0797
M5005_Spy0937	-	spy1223	1400	1543	0.404	0.0040	0.0083	0.3032	0.0342	0.0610
M5005_Spy0194	*gpsA*	spy0226	246	164	0.4023	0.0042	0.0086	0.3667	0.0096	0.0289
M5005_Spy0986	*glmS*	spy1280	125	142	0.402	0.0042	0.0086	0.2259	0.1187	0.1318
M5005_Spy0214	-	spy0254	1205	1001	0.4016	0.0042	0.0086	0.2637	0.0672	0.0915
M5005_Spy1401	-	spy1711	1022	1032	0.4011	0.0043	0.0087	0.3010	0.0356	0.0621
M5005_Spy1355	*pbp1A*	spy1649	27	31	0.401	0.0043	0.0087	0.2690	0.0616	0.0871
M5005_Spy0047	*rplB*	spy0052	199	251	0.3998	0.0044	0.0089	0.3182	0.0259	0.0513
M5005_Spy1223	*hlpA*	spy1489	156	148	0.3993	0.0045	0.0090	0.5019	2.38E-04	**0.0055**
M5005_Spy0836	-	spy1113	483	381	0.3987	0.0045	0.0091	0.3936	0.0051	0.0193
M5005_Spy0242	-	spy0285	886	814	0.3976	0.0047	0.0093	0.3331	0.0193	0.0434
M5005_Spy1557	*mutY*	spy1833	386	423	0.3976	0.0047	0.0093	0.0563	0.7009	0.4120
M5005_Spy0038	-	spy0041	367	330	0.3969	0.0047	0.0094	0.3876	0.0059	0.0210
M5005_Spy1550	*uvrA*	spy1825	634	771	0.3968	0.0048	0.0094	0.3444	0.0154	0.0387
M5005_Spy1600	*lppC*	spy1882	273	315	0.3968	0.0048	0.0094	0.1989	0.1707	0.1686
M5005_Spy0649	-	spy0841	959	1174	0.3965	0.0048	0.0094	0.2224	0.1246	0.1367
M5005_Spy0763	*femD*	spy1038	677	755	0.3964	0.0048	0.0094	0.2505	0.0826	0.1038
M5005_Spy0996	*speA2*	spyM18_0393	1071	736	0.3964	0.0048	0.0094	0.1968	0.1754	0.1715
M5005_Spy1534	*secA*	spy1805	109	102	0.3961	0.0048	0.0094	0.2401	0.0965	0.1152
M5005_Spy0841	-	spy1119	1216	1111	0.3947	0.0050	0.0097	0.2533	0.0791	0.1016
M5005_Spy0777		spy1054	1040	862	0.3945	0.0050	0.0097	0.2447	0.0902	0.1096
M5005_Spy1138	-	spy1398	425	369	0.3943	0.0051	0.0098	0.2980	0.0376	0.0638
M5005_Spy1797	-	spy2114	47	49	0.3941	0.0051	0.0098	0.2115	0.1445	0.1516
M5005_Spy1271	-	spy1542	384	492	0.3935	0.0052	0.0099	0.3693	0.0090	0.0278
M5005_Spy0661	*fruB*	spy0854	294	215	0.393	0.0052	0.0099	0.3623	0.0105	0.0303

M5005_Spy#	Gene	Synonym *	WT Transcript Rank †	Mutant Transcript Rank †	*r* Correlation (*covR*) ‡	*P*-value Correlation (*covR*)	*Q*-value Correlation (*covR*) §	*r* Correlation (*covS*) ‡	*P*-value Correlation (*covS*)	*Q*-value Correlation (*covS*) §
M5005_Spy0634	-	spy0821	322	306	0.3925	0.0053	0.0100	0.3118	0.0292	0.0554
M5005_Spy1253	*murD*	spy1525	534	496	0.3905	0.0055	0.0104	0.1167	0.4247	0.3056
M5005_Spy1093	-	spy1339	640	544	0.3905	0.0055	0.0104	0.4562	9.86E-04	**0.0074**
M5005_Spy0715	-	spy0913	69	67	0.3901	0.0056	0.0104	0.2749	0.0559	0.0816
M5005_Spy1247	-	spy1518	65	75	0.3901	0.0056	0.0104	0.4528	0.0011	**0.0076**
M5005_Spy0930	-	spy1216	97	113	0.39	0.0056	0.0104	0.2907	0.0427	0.0684
M5005_Spy0325	*murE*	spy0388	521	516	0.3897	0.0056	0.0105	0.4153	0.0030	0.0139
M5005_Spy0068	*rpsM*	spy0077	312	291	0.3893	0.0057	0.0105	0.2488	0.0847	0.1057
M5005_Spy0341	-		2280	1873	0.3892	0.0057	0.0105	0.0527	0.7190	0.4183
M5005_Spy1846	-	spy2196	829	879	0.3889	0.0057	0.0106	0.0797	0.5862	0.3698
M5005_Spy1634	*lacF*	spy1918	727	756	0.3882	0.0058	0.0107	0.3070	0.0319	0.0584
M5005_Spy1376	-	spy1678	101	98	0.388	0.0059	0.0107	0.2426	0.0931	0.1119
M5005_Spy0698	*punA*	spy0892	175	141	0.3878	0.0059	0.0107	0.1748	0.2295	0.2061
M5005_Spy0791	*uvrC*		1540	1485	0.3871	0.0060	0.0108	0.2680	0.0627	0.0880
M5005_Spy0147	*leuS*	spy0173	565	638	0.3868	0.0060	0.0109	0.1341	0.3583	0.2761
M5005_Spy1633	*lacE*	spy1917	1178	882	0.3868	0.0060	0.0109	0.4093	0.0035	0.0150
M5005_Spy1337	*sunL*	spy1627	572	621	0.3865	0.0061	0.0109	-0.0971	0.5067	0.3398
M5005_Spy0317	*hlyX*	spy0378	219	272	0.386	0.0062	0.0110	0.0790	0.5895	0.3710
M5005_Spy0410	-	spy0500	399	312	0.3859	0.0062	0.0110	0.3376	0.0177	0.0414
M5005_Spy0823	*folQ*	spy1099	716	602	0.3857	0.0062	0.0110	0.2463	0.0879	0.1079
M5005_Spy0135	-	spy0159	437	489	0.3847	0.0064	0.0113	0.0795	0.5873	0.3700
M5005_Spy1103	*map*	spy1354	562	427	0.3845	0.0064	0.0113	0.6160	2.5E-06	**0.0055**
M5005_Spy0137	-	spy0163	794	897	0.3841	0.0064	0.0114	0.2446	0.0902	0.1096
M5005_Spy0875	*srtA*	spy1154	133	145	0.384	0.0065	0.0114	0.3186	0.0257	0.0511
M5005_Spy0372	-	spy0458	992	1029	0.3838	0.0065	0.0114	0.4147	0.0031	0.0139
M5005_Spy0624	*aroD*	spy0809	714	623	0.3829	0.0066	0.0116	0.2856	0.0467	0.0724
M5005_Spy1831	*rpsD*	spy2178	464	418	0.3826	0.0067	0.0117	0.1732	0.2341	0.2083
M5005_Spy0106	*rofA*	spy0124	29	32	0.3819	0.0068	0.0118	0.3370	0.0179	0.0417
M5005_Spy0132	*ntpB*	spy0155	912	500	0.3813	0.0069	0.0119	0.4484	0.0012	**0.0081**
M5005_Spy0208	-	spy0247	502	463	0.3808	0.0069	0.0120	0.1056	0.4702	0.3247
M5005_Spy0660	*fruR*	spy0853	574	408	0.3801	0.0071	0.0122	0.3528	0.0129	0.0345
M5005_Spy1275	*arcA*		841	898	0.3799	0.0071	0.0122	0.3194	0.0253	0.0506

M5005_Spy#	Gene	Synonym *	WT Transcript Rank †	Mutant Transcript Rank †	*r* Correlation (*covR*) ‡	*P*-value Correlation (*covR*)	*Q*-value Correlation (*covR*) §	*r* Correlation (*covS*) ‡	*P*-value Correlation (*covS*)	*Q*-value Correlation (*covS*) §
M5005_Spy0019	-	spy0021	2013	1592	0.3795	0.0072	0.0123	0.0943	0.5192	0.3453
M5005_Spy0899	*citG*	spy1179	1619	1425	0.3794	0.0072	0.0123	0.3274	0.0217	0.0466
M5005_Spy1241	*mutT*	spy1510	865	905	0.3788	0.0073	0.0123	0.4179	0.0028	0.0133
M5005_Spy1852	*hasB*	spy2201	888	785	0.3788	0.0073	0.0123	0.2271	0.1166	0.1300
M5005_Spy0178	-	spy0208	1168	1260	0.3784	0.0073	0.0124	0.3317	0.0199	0.0441
M5005_Spy0066	*infA*	spy0075	68	76	0.378	0.0074	0.0125	0.2693	0.0613	0.0871
M5005_Spy0930	-	spy1217	95	63	0.3779	0.0074	0.0125	0.3031	0.0343	0.0610
M5005_Spy1274	-	spy1546	129	92	0.3767	0.0076	0.0128	0.2344	0.1049	0.1213
M5005_Spy1275	*arcA*	spy1547	218	150	0.3765	0.0077	0.0128	0.2326	0.1077	0.1233
M5005_Spy0508	*tufA*	spy0611	14	15	0.3756	0.0078	0.0130	0.2427	0.0929	0.1119
M5005_Spy0935	*dpfB*	spy1221	2087	1800	0.3753	0.0079	0.0131	0.4210	0.0026	0.0128
M5005_Spy0411	-	spy0501	445	551	0.3745	0.0080	0.0133	-0.0403	0.7833	0.4393
M5005_Spy0609	-	spy0793	622	482	0.374	0.0081	0.0134	0.5962	6.2E-06	**0.0055**
M5005_Spy1755	-	spyM18_2122	214	228	0.3729	0.0083	0.0137	0.3014	0.0354	0.0621
M5005_Spy1773	-	spy2084	590	485	0.3728	0.0083	0.0137	0.2701	0.0605	0.0864
M5005_Spy0701	*cpsY*	spy0898	1599	1344	0.3721	0.0085	0.0138	0.0282	0.8475	0.4575
M5005_Spy0275	-	spy0324	928	835	0.3716	0.0086	0.0139	0.2600	0.0712	0.0947
M5005_Spy1635	*lacD.2*	spy1919	518	584	0.3715	0.0086	0.0139	0.3445	0.0153	0.0387
M5005_Spy0213	-	SpyM3_0181	1145	677	0.3712	0.0086	0.0140	0.3658	0.0098	0.0293
M5005_Spy0232	*fus*	spy0273	64	79	0.3705	0.0088	0.0142	0.3363	0.0182	0.0420
M5005_Spy1136	*pepB*	spy1393	1092	938	0.3702	0.0088	0.0143	0.1347	0.3560	0.2752
M5005_Spy1808	*argS*	spy2151	151	158	0.3701	0.0089	0.0143	0.3817	0.0068	0.0229
M5005_Spy0626	-	spy0811	633	538	0.3697	0.0089	0.0144	0.3181	0.0259	0.0513
M5005_Spy1272	-	spy1543	638	594	0.3695	0.0090	0.0144	0.3170	0.0265	0.0521
M5005_Spy1776	-	spy2088	192	88	0.3694	0.0090	0.0144	0.3508	0.0135	0.0355
M5005_Spy1798	-	spy2115	165	91	0.3691	0.0091	0.0145	0.2942	0.0402	0.0660
M5005_Spy0304	-	spy0362	774	909	0.369	0.0091	0.0145	0.2282	0.1148	0.1284
M5005_Spy0471	-	spy0568	1134	1242	0.3682	0.0092	0.0147	0.0543	0.7109	0.4153
M5005_Spy0994	-	spy1288	1537	1397	0.3668	0.0095	0.0151	0.2105	0.1467	0.1530
M5005_Spy0957	-	spyM18_1197	407	285	0.3663	0.0096	0.0152	0.3643	0.0101	0.0297
M5005_Spy0061	*rpsE*	spy0069	373	385	0.3657	0.0098	0.0154	0.1968	0.1752	0.1715
M5005_Spy1777	*hutH*	spy2089	85	41	0.3653	0.0098	0.0155	0.3053	0.0329	0.0598

M5005_Spy#	Gene	Synonym *	WT Transcript Rank †	Mutant Transcript Rank †	*r* Correlation (*covR*) ‡	*P* -value Correlation (*covR*)	*Q*- value Correlation (*covR*) §	*r* Correlation (*covS*) ‡	*P* -value Correlation (*covS*)	*Q*- value Correlation (*covS*) §
M5005_Spy0824	*folK*	spy1100	635	640	0.3642	0.0101	0.0157	0.1782	0.2205	0.1999
M5005_Spy1064	*malC*	spy1301	8	10	0.3638	0.0102	0.0158	0.4494	0.0012	**0.0080**
M5005_Spy0521	*agaV*	spy0631	1502	1177	0.3619	0.0106	0.0164	0.3863	0.0061	0.0213
M5005_Spy0792	-	spy1069	240	247	0.3612	0.0108	0.0166	0.2043	0.1592	0.1611
M5005_Spy1599	*pgk*	spy1881	323	451	0.361	0.0108	0.0166	0.1320	0.3661	0.2794
M5005_Spy1245	-	spy1515	355	390	0.3609	0.0109	0.0166	0.1981	0.1724	0.1694
M5005_Spy1795	-	spy2112	267	225	0.3601	0.0110	0.0169	0.5642	2.4E-05	**0.0055**
M5005_Spy0070	*rpoA*	spy0080	71	64	0.3595	0.0112	0.0170	0.3004	0.0359	0.0624
M5005_Spy1314	*hyl*	spy1600	441	401	0.3587	0.0114	0.0172	0.4545	0.0010	**0.0075**
M5005_Spy0793	-	spy1070	159	178	0.3569	0.0118	0.0177	0.1749	0.2294	0.2061
M5005_Spy1145	*sodA*	spy1406	113	115	0.3568	0.0119	0.0177	0.2562	0.0756	0.0986
M5005_Spy1362	-	spy1656	1045	887	0.3562	0.0120	0.0179	0.0108	0.9415	0.4845
M5005_Spy1731	-	spyM18_2095	513	486	0.3553	0.0122	0.0182	0.1168	0.4240	0.3054
M5005_Spy1544	*scrR*	spy1817	947	970	0.3551	0.0123	0.0182	0.2112	0.1451	0.1521
M5005_Spy1612	*ropA*	spy1896	245	284	0.3551	0.0123	0.0182	0.2949	0.0397	0.0654
M5005_Spy1288	-	spy1564	1962	1280	0.3548	0.0124	0.0183	0.2657	0.0650	0.0899
M5005_Spy0516	*pacL*	spy0623	252	239	0.3547	0.0124	0.0183	0.3077	0.0315	0.0579
M5005_Spy1677	-	spy1968	185	197	0.3542	0.0125	0.0185	0.3048	0.0332	0.0602
M5005_Spy0697	*arsC*	spy0891	281	283	0.3538	0.0126	0.0186	0.2589	0.0724	0.0959
M5005_Spy0140	-	spy0166	1037	1113	0.3536	0.0127	0.0187	0.2986	0.0371	0.0633
M5005_Spy0656	*trmD*	spy0849	950	1014	0.3535	0.0127	0.0187	-0.0118	0.9357	0.4835
M5005_Spy0681	-	spy0875	543	521	0.3516	0.0132	0.0194	0.2822	0.0495	0.0755
M5005_Spy1775	-	spy2087	237	244	0.3508	0.0135	0.0196	0.3763	0.0077	0.0249
M5005_Spy0597	*rplU*	spyM18_0838	532	503	0.3507	0.0135	0.0196	0.1272	0.3837	0.2872
M5005_Spy1062	*malA*	spy1298	22	21	0.3502	0.0136	0.0198	0.4100	0.0034	0.0148
M5005_Spy0144	-	spyM18_0167	2359	1287	0.3501	0.0136	0.0198	0.4832	4.36E-04	**0.0059**
M5005_Spy0152	-	spy0178	952	712	0.35	0.0137	0.0198	0.3940	0.0051	0.0191
M5005_Spy0576	*atpB*	spy0755	911	949	0.3495	0.0138	0.0200	0.2094	0.1487	0.1541
M5005_Spy0147	*leuS*		986	1034	0.3491	0.0139	0.0201	0.2692	0.0615	0.0871
M5005_Spy1162	-	spy1425	809	689	0.3488	0.0140	0.0201	0.2170	0.1342	0.1445
M5005_Spy1855	*recF*	spy2204	770	606	0.3484	0.0142	0.0203	0.2134	0.1410	0.1498
M5005_Spy0426	-	spy0516	81	154	0.3479	0.0143	0.0205	0.1452	0.3194	0.2567

M5005_Spy#	Gene	Synonym *	WT Transcript Rank †	Mutant Transcript Rank †	*r* Correlation (*covR*) ‡	*P* -value Correlation (*covR*)	*Q-* value Correlation (*covR*) §	*r* Correlation (*covS*) ‡	*P* -value Correlation (*covS*)	*Q-* value Correlation (*covS*) §
M5005_Spy0479	-	spy0577	536	660	0.3477	0.0144	0.0205	0.2298	0.1122	0.1265
M5005_Spy1122	*nrdH*	spy1374	871	995	0.3468	0.0146	0.0208	0.1583	0.2772	0.2325
M5005_Spy1169	*spd3*	spy1436	210	179	0.3449	0.0152	0.0215	0.3726	0.0084	0.0267
M5005_Spy1144	-	spyM18_1413	1936	1209	0.3431	0.0158	0.0222	0.4591	9.07E-04	**0.0071**
M5005_Spy0635	*rpmA*	spy0822	349	375	0.3425	0.0160	0.0224	0.2997	0.0364	0.0627
M5005_Spy0375	*rplA*	spy0461	965	950	0.3409	0.0165	0.0230	0.3263	0.0221	0.0470
M5005_Spy1364	-	spy1658	385	593	0.3405	0.0167	0.0231	0.0831	0.5701	0.3638
M5005_Spy0150	-	spy0176	1292	1127	0.339	0.0172	0.0236	0.5214	1.22E-04	**0.0055**
M5005_Spy1157	*murF*	spy1420	266	241	0.3388	0.0173	0.0237	0.3459	0.0149	0.0381
M5005_Spy0735	*cpsFP*	spy0935	673	611	0.3385	0.0174	0.0238	0.6260	1.5E-06	**0.0055**
M5005_Spy1358	*nadE*	spy1652	660	654	0.3358	0.0183	0.0250	0.1282	0.3799	0.2856
M5005_Spy0593	-	spy0775	1274	1188	0.3346	0.0188	0.0255	0.1378	0.3451	0.2698
M5005_Spy0619	*infC*	spy0804	301	320	0.3345	0.0188	0.0255	0.0356	0.8079	0.4457
M5005_Spy0932	-	spy1219	169	143	0.334	0.0190	0.0257	0.2564	0.0754	0.0986
M5005_Spy0529	-	spy0642	1003	628	0.3338	0.0191	0.0258	0.3296	0.0207	0.0451
M5005_Spy1719	*emm1*	spy2018	9	11	0.3337	0.0191	0.0258	0.2375	0.1004	0.1179
M5005_Spy1472	*hit*	spy1730	720	658	0.333	0.0194	0.0261	0.0599	0.6825	0.4058
M5005_Spy1570	-	spy1851	966	925	0.3327	0.0195	0.0262	0.0115	0.9376	0.4837
M5005_Spy0957	-	SpyM3_0884	346	259	0.3323	0.0197	0.0264	0.3171	0.0264	0.0520
M5005_Spy0361	-	spy0442	352	353	0.332	0.0198	0.0264	0.2997	0.0365	0.0627
M5005_Spy1698	*trpG*	spy1991	934	700	0.3319	0.0198	0.0265	0.2658	0.0649	0.0898
M5005_Spy1669	*def*	spy1958	1424	1279	0.3317	0.0199	0.0265	0.2830	0.0488	0.0751
M5005_Spy1754	-	spy2060	296	296	0.3316	0.0199	0.0265	0.1928	0.1844	0.1781
M5005_Spy0795	*rplJ*	spy1072	605	553	0.3314	0.0200	0.0266	0.3280	0.0214	0.0462
M5005_Spy0929	-	spy1215	59	50	0.331	0.0202	0.0267	0.2573	0.0743	0.0976
M5005_Spy1398	*lacA.1*	spy1709	1061	692	0.3307	0.0203	0.0268	0.2796	0.0517	0.0778
M5005_Spy1469	-	spy1727	276	275	0.3305	0.0204	0.0269	0.2472	0.0868	0.1072
M5005_Spy0554	-	spy0728	110	134	0.3303	0.0205	0.0270	0.0988	0.4994	0.3365
M5005_Spy1117	*deaD2*	spy1369	247	303	0.3284	0.0212	0.0278	0.2092	0.1491	0.1543
M5005_Spy0830	-	spy1106	1492	1207	0.3276	0.0216	0.0281	0.2237	0.1222	0.1351
M5005_Spy0127	*ntpK*	spy0149	1879	1243	0.3273	0.0217	0.0282	0.4345	0.0018	0.0101
M5005_Spy1311	-	spy1596	1332	1086	0.3263	0.0221	0.0286	0.0724	0.6212	0.3819

M5005_Spy#	Gene	Synonym *	WT Transcript Rank †	Mutant Transcript Rank †	*r* Correlation (*covR*) ‡	*P* -value Correlation (*covR*)	*Q-* value Correlation (*covR*) §	*r* Correlation (*covS*) ‡	*P* -value Correlation (*covS*)	*Q-* value Correlation (*covS*) §
M5005_Spy0790	*gabD*	spy1067	491	530	0.3262	0.0222	0.0286	0.2671	0.0636	0.0886
M5005_Spy1064	*malC*	spy1299	16	20	0.3258	0.0223	0.0287	0.3615	0.0107	0.0305
M5005_Spy1140	*queA*	spy1400	825	1026	0.3258	0.0223	0.0287	0.3420	0.0162	0.0399
M5005_Spy0388	*dgk*	spy0473	618	608	0.3257	0.0224	0.0287	0.3331	0.0194	0.0434
M5005_Spy0874	*gyrA*	spy1152	62	77	0.3256	0.0224	0.0287	0.1272	0.3839	0.2872
M5005_Spy1532	*acpS*	spy1804	1484	1534	0.3247	0.0228	0.0291	0.1010	0.4897	0.3325
M5005_Spy1307	-	spy1589	732	644	0.3244	0.0230	0.0293	0.4558	9.97E-04	**0.0074**
M5005_Spy1389	-	spy1695	717	757	0.324	0.0231	0.0294	0.2132	0.1413	0.1500
M5005_Spy1132	*alaS*	spy1389	859	653	0.3238	0.0232	0.0295	0.3868	0.0060	0.0212
M5005_Spy1503	-	spy1766	1252	1168	0.3232	0.0235	0.0297	0.2482	0.0855	0.1061
M5005_Spy0536	*dinG*	spy0649	910	808	0.3226	0.0238	0.0299	0.1087	0.4572	0.3195
M5005_Spy0326	-	spy0390	546	649	0.322	0.0241	0.0302	0.1435	0.3254	0.2601
M5005_Spy0016	-	M12_0555	20	27	0.3215	0.0243	0.0304	0.0717	0.6245	0.3834
M5005_Spy0384	-	spy0469	541	520	0.3215	0.0243	0.0304	0.1026	0.4829	0.3295
M5005_Spy0628	*folC.2*	spy0814	893	816	0.3209	0.0246	0.0307	0.1615	0.2676	0.2279
M5005_Spy0700	*cpsX*	spy0895	374	435	0.3207	0.0247	0.0307	0.3201	0.0249	0.0502
M5005_Spy1222	*int.2*	spy1488	1625	1711	0.3201	0.0250	0.0310	0.2771	0.0539	0.0798
M5005_Spy0705	*amiC*	spy0902	1253	1163	0.3196	0.0252	0.0312	0.1528	0.2945	0.2412
M5005_Spy1595	-	spy1876	91	118	0.3195	0.0252	0.0312	0.2965	0.0386	0.0649
M5005_Spy0651	-	spy0843	1622	1680	0.3193	0.0253	0.0313	0.0440	0.7638	0.4327
M5005_Spy1342	-	spy1633	61	69	0.3183	0.0258	0.0317	0.1334	0.3610	0.2771
M5005_Spy1052	*int.1*	spyM18_1309	2343	2117	0.3167	0.0266	0.0325	0.2087	0.1501	0.1548
M5005_Spy0528	-	spy0640	1746	1527	0.3164	0.0268	0.0326	0.1959	0.1773	0.1726
M5005_Spy0682	*mvaK1*	spy0876	972	927	0.3157	0.0271	0.0330	0.1249	0.3926	0.2912
M5005_Spy0286	*dnaI*	spy0340	194	177	0.3153	0.0274	0.0332	0.1207	0.4088	0.2993
M5005_Spy0358	-	spy0439	1059	1016	0.3151	0.0274	0.0332	0.0350	0.8115	0.4468
M5005_Spy0814	-	M12_0090	1046	1190	0.314	0.0280	0.0337	0.1579	0.2786	0.2330
M5005_Spy1774	*fhs.2*	spy2085	98	71	0.3128	0.0286	0.0344	0.2233	0.1231	0.1357
M5005_Spy0244	*nifS, csd*	spy0288	573	642	0.3119	0.0291	0.0347	0.4857	4.04E-04	**0.0059**
M5005_Spy1411	-	spy1723	664	714	0.3117	0.0292	0.0348	0.1716	0.2385	0.2113
M5005_Spy1137	-	spy1395	1175	1005	0.3114	0.0294	0.0349	0.0662	0.6511	0.3934
M5005_Spy0547	-	spy0720	380	425	0.3103	0.0300	0.0354	0.2665	0.0641	0.0890

M5005_Spy#	Gene	Synonym *	WT Transcript Rank †	Mutant Transcript Rank †	*r* Correlation (*covR*) ‡	*P*-value Correlation (*covR*)	*Q*-value Correlation (*covR*) §	*r* Correlation (*covS*) ‡	*P*-value Correlation (*covS*)	*Q*-value Correlation (*covS*) §
M5005_Spy0946	*rpsT*	spy1234	636	769	0.3101	0.0301	0.0355	0.0039	0.9787	0.4934
M5005_Spy0360	-	spy0441	1190	1278	0.3093	0.0306	0.0358	-0.1184	0.4179	0.3034
M5005_Spy1154	*deaD*	spy1415	88	100	0.3093	0.0306	0.0358	0.0942	0.5195	0.3453
M5005_Spy1337	*sunL*	spy1628	452	454	0.3089	0.0308	0.0360	0.4464	0.0013	**0.0083**
M5005_Spy0699	*deoD2*	spy0894	117	111	0.3087	0.0309	0.0360	0.2309	0.1104	0.1251
M5005_Spy0617	-		528	378	0.3086	0.0310	0.0361	0.2957	0.0391	0.0653
M5005_Spy0053	*rpsQ*	spy0060	241	294	0.3079	0.0314	0.0364	0.2039	0.1600	0.1615
M5005_Spy0776	*lepA*	spy1053	339	327	0.3073	0.0317	0.0366	0.0650	0.6572	0.3956
M5005_Spy1646	*rpsI*	spy1931	480	555	0.3072	0.0318	0.0366	0.0127	0.9312	0.4829
M5005_Spy0472	*ftsY*	spy0569	432	329	0.3067	0.0321	0.0369	0.3353	0.0185	0.0422
M5005_Spy0139	*nga*	spy0165	785	766	0.3066	0.0321	0.0369	0.4427	0.0014	**0.0089**
M5005_Spy1225	-	spy1492	471	588	0.3054	0.0328	0.0376	0.2354	0.1035	0.1207
M5005_Spy1266	-	spy1537	1655	1570	0.3051	0.0330	0.0377	0.3796	0.0071	0.0237
M5005_Spy0692	-	spy0886	733	744	0.3047	0.0333	0.0378	0.4186	0.0028	0.0132
M5005_Spy1593	-	spy1874	901	953	0.3047	0.0333	0.0378	0.0616	0.6743	0.4021
M5005_Spy1340	-	spy1630	414	478	0.3045	0.0334	0.0378	0.6160	2.5E-06	**0.0055**
M5005_Spy0873	*ldh*	spy1151	559	524	0.3045	0.0334	0.0378	0.2552	0.0768	0.0997
M5005_Spy1696	-	spy1989	856	831	0.3045	0.0334	0.0378	0.0847	0.5627	0.3611
M5005_Spy1372	*proB*	spy1672	765	575	0.3043	0.0335	0.0379	0.2621	0.0689	0.0931
M5005_Spy0612	*amrA*	spy0797	782	819	0.3041	0.0336	0.0380	0.6167	2.4E-06	**0.0055**
M5005_Spy0736	*cpsFQ*	spy0936	903	801	0.3029	0.0344	0.0387	0.2117	0.1442	0.1514
M5005_Spy0263	*nadD*		316	339	0.3028	0.0344	0.0387	0.3384	0.0174	0.0409
M5005_Spy0334	-	spy0405	812	861	0.3027	0.0345	0.0387	0.0237	0.8715	0.4650
M5005_Spy0580	*atpG*	spy0759	1233	1011	0.3024	0.0347	0.0389	0.1836	0.2067	0.1909
M5005_Spy0928	*lplA*	spy1214	93	78	0.3023	0.0347	0.0389	0.2675	0.0631	0.0881
M5005_Spy1372	*proB*	spy1673	685	589	0.3021	0.0349	0.0390	0.5182	1.37E-04	**0.0055**
M5005_Spy0319	*ppaC*	spy0380	286	281	0.302	0.0350	0.0390	0.1617	0.2669	0.2278
M5005_Spy0230	*rpsL*	spy0271	284	360	0.3019	0.0350	0.0390	0.1077	0.4614	0.3211
M5005_Spy0522	-		1531	957	0.3018	0.0351	0.0391	0.2398	0.0971	0.1155
M5005_Spy1330	-	spy1619	707	968	0.3015	0.0353	0.0392	0.4455	0.0013	**0.0085**
M5005_Spy0892	*satE*	spy1172	741	1006	0.3014	0.0353	0.0392	0.0566	0.6995	0.4119
M5005_Spy0040	*adhA*	spy0044	235	189	0.3009	0.0356	0.0395	0.2949	0.0397	0.0654

M5005_Spy#	Gene	Synonym *	WT Transcript Rank †	Mutant Transcript Rank †	*r* Correlation (*covR*) ‡	*P* -value Correlation (*covR*)	*Q*- value Correlation (*covR*) §	*r* Correlation (*covS*) ‡	*P* -value Correlation (*covS*)	*Q*- value Correlation (*covS*) §
M5005_Spy0633	*rplU*	spy0819	269	246	0.3008	0.0357	0.0396	0.3388	0.0172	0.0408
M5005_Spy0648	*rpsP*	spy0840	489	549	0.3003	0.0360	0.0398	0.2901	0.0432	0.0688
M5005_Spy1411	-	spy1722	800	822	0.3002	0.0361	0.0398	0.0703	0.6313	0.3865
M5005_Spy0134	-	spy0158	454	417	0.3001	0.0362	0.0398	0.2082	0.1511	0.1556
M5005_Spy0608	*rgpFc*	spy0792	585	537	0.3	0.0363	0.0399	0.2734	0.0573	0.0828
M5005_Spy1772	-	spy2083	228	160	0.2998	0.0364	0.0399	0.2890	0.0440	0.0696
M5005_Spy0933	-	spy1220	233	240	0.2996	0.0365	0.0401	0.4268	0.0022	0.0116
M5005_Spy0329	-	spy0397	641	517	0.2986	0.0372	0.0407	0.2699	0.0607	0.0866
M5005_Spy1065	*amyA*	spy1302	7	7	0.2986	0.0372	0.0407	0.2985	0.0372	0.0634
M5005_Spy0039	*purK*	spyM18_0043	1034	668	0.2985	0.0372	0.0407	0.1302	0.3727	0.2826
M5005_Spy0738	-	spy1011	1351	1109	0.298	0.0376	0.0411	0.3788	0.0073	0.0240
M5005_Spy1606	*rpmB*	spy1888	167	172	0.2971	0.0382	0.0417	0.3378	0.0176	0.0413
M5005_Spy1651	-	spy1937	442	582	0.2968	0.0384	0.0418	0.3262	0.0222	0.0470
M5005_Spy1690	*nrdI.1*	spy1984	610	657	0.2967	0.0384	0.0418	0.0119	0.9354	0.4835
M5005_Spy0071	*rplQ*	spy0080a	372	354	0.2962	0.0388	0.0421	0.0640	0.6621	0.3971
M5005_Spy0124	*sloR*	spy0146	1184	994	0.2962	0.0388	0.0421	0.1801	0.2156	0.1964
M5005_Spy0863	*prfA*	spy1141	1036	987	0.2962	0.0388	0.0421	0.4443	0.0014	**0.0087**
M5005_Spy0246	-	spy0290	998	805	0.2957	0.0391	0.0423	0.2949	0.0397	0.0654
M5005_Spy0625	*aroF*	spy0810	698	546	0.2951	0.0395	0.0427	-0.0085	0.9536	0.4874
M5005_Spy1670	-	spy1959	695	620	0.2951	0.0396	0.0427	0.0420	0.7747	0.4363
M5005_Spy0056	*rplE*	spy0063	274	295	0.2946	0.0399	0.0430	0.1653	0.2563	0.2216
M5005_Spy0927	*fhs.1*	spy1213	76	83	0.2944	0.0401	0.0430	0.1453	0.3192	0.2567
M5005_Spy0948	*ciaR*	spy1237	915	958	0.2941	0.0403	0.0431	0.2605	0.0706	0.0943
M5005_Spy0141	*slo*	spy0167	265	201	0.2928	0.0412	0.0439	0.2746	0.0562	0.0817
M5005_Spy1665	-	spy1955	1095	973	0.2927	0.0413	0.0439	0.0390	0.7904	0.4414
M5005_Spy0291	-	spy0346	563	532	0.2922	0.0416	0.0442	0.2065	0.1545	0.1577
M5005_Spy0917	-	spy1202	1285	1331	0.2921	0.0417	0.0442	0.1201	0.4112	0.2997
M5005_Spy0574	-	spy0752	1421	1116	0.2917	0.0420	0.0444	0.4364	0.0017	**0.0097**
M5005_Spy0327	*upp*	spy0392	1001	873	0.2916	0.0421	0.0444	0.0952	0.5150	0.3438
M5005_Spy1771	*hutU*	spy2082	201	120	0.2913	0.0423	0.0446	0.2951	0.0395	0.0654
M5005_Spy1468	-	spy1726	728	959	0.2896	0.0436	0.0458	0.3087	0.0309	0.0572
M5005_Spy0483	-	spy0583	120	152	0.2882	0.0447	0.0466	0.0825	0.5729	0.3650

M5005_Spy#	Gene	Synonym *	WT Transcript Rank †	Mutant Transcript Rank †	*r* Correlation (*covR*) ‡	*P*-value Correlation (*covR*)	*Q*-value Correlation (*covR*) §	*r* Correlation (*covS*) ‡	*P*-value Correlation (*covS*)	*Q*-value Correlation (*covS*) §
M5005_Spy0221	-	spy0261	602	568	0.2881	0.0447	0.0466	0.3407	0.0166	0.0402
M5005_Spy1659	-	spy1945	816	773	0.2871	0.0455	0.0472	0.6260	1.5E-06	**0.0055**
M5005_Spy1259	*dpr*	spy1531	84	44	0.2864	0.0461	0.0477	0.1842	0.2051	0.1899
M5005_Spy0051	*rplP*	spy0057	87	95	0.2857	0.0466	0.0482	0.1986	0.1713	0.1689
M5005_Spy0842	-	spy1120	650	632	0.2856	0.0467	0.0482	0.5388	6.5E-05	**0.0055**
M5005_Spy1585	*deoC*	spy1867	41	55	0.2854	0.0468	0.0482	0.1887	0.1942	0.1833
M5005_Spy0175	*tgt*	spy0203	1512	1161	0.2853	0.0469	0.0482	0.2562	0.0755	0.0986
M5005_Spy1681	*dexB*	spyM18_2039	575	536	0.2853	0.0469	0.0482	0.2987	0.0371	0.0633
M5005_Spy0550	-	spy0723	1776	1465	0.2852	0.0470	0.0483	0.0315	0.8301	0.4526
M5005_Spy0382	*msrA.2*	spy0466	1206	1299	0.2847	0.0474	0.0485	0.1905	0.1898	0.1817
M5005_Spy0425	-	spy0515	57	70	0.284	0.0480	0.0489	0.1984	0.1718	0.1690
M5005_Spy0983	-	spy1275	907	963	0.2835	0.0484	0.0492	0.1556	0.2857	0.2362
M5005_Spy1083	-	spy1325	932	906	0.2828	0.0490	0.0497	0.1948	0.1799	0.1746
M5005_Spy1697	-		310	230	0.2826	0.0491	0.0498	0.3727	0.0084	0.0267
M5005_Spy1424	-		2360	2406	0.2825	0.0492	0.0498	0.0912	0.5332	0.3512
M5005_Spy1602	-	spy1885	139	153	0.2821	0.0496	0.0500	0.0888	0.5438	0.3546
M5005_Spy0990	*dnaE*	spy1284	604	663	0.2819	0.0497	0.0500	0.2630	0.0679	0.0921
M5005_Spy1770	*hutI*	spy2081	263	255	0.2819	0.0497	0.0500	0.0851	0.5609	0.3607
M5005_Spy1386	-	spy1691	256	363	0.2811	0.0504	0.0506	0.2387	0.0986	0.1167
M5005_Spy0311	-	spy0370	1921	2000	0.2809	0.0505	0.0507	0.2454	0.0892	0.1089
M5005_Spy0591	-	spy0772	416	560	0.2806	0.0508	0.0509	0.1322	0.3653	0.2790
M5005_Spy1045	-	spyM18_1302	1556	1478	0.2806	0.0508	0.0509	0.0496	0.7353	0.4239
M5005_Spy0737	*mutX*	spy1010	1223	1227	0.2805	0.0509	0.0509	0.4666	7.27E-04	**0.0067**
M5005_Spy0484	*ptsK, hprK*	spy0584	381	449	0.2794	0.0519	0.0516	0.3226	0.0238	0.0489
M5005_Spy0600	*rpoD*	spy0782	510	506	0.2793	0.0519	0.0517	-0.0136	0.9262	0.4812
M5005_Spy0231	*rpsG*	spy0272	80	119	0.2792	0.0521	0.0517	0.1963	0.1764	0.1718
M5005_Spy0437	*vicX*	spy0530	1039	858	0.2787	0.0525	0.0519	0.1860	0.2006	0.1876
M5005_Spy1636	*lacC.2*	spy1921	1177	1107	0.2787	0.0525	0.0519	0.0836	0.5678	0.3629
M5005_Spy1379	*glpF*	spy1682	479	535	0.278	0.0531	0.0524	0.0946	0.5178	0.3448
M5005_Spy0074	-		564	543	0.2749	0.0559	0.0549	0.0170	0.9075	0.4760
M5005_Spy0938	*pgmA*	spy1224	503	472	0.2748	0.0560	0.0550	0.1789	0.2189	0.1986
M5005_Spy0295	-	spy0351	224	324	0.2747	0.0562	0.0551	0.1225	0.4016	0.2964

M5005_Spy#	Gene	Synonym *	WT Transcript Rank †	Mutant Transcript Rank †	*r* Correlation (*covR*) ‡	*P*-value Correlation (*covR*)	*Q*-value Correlation (*covR*) §	*r* Correlation (*covS*) ‡	*P*-value Correlation (*covS*)	*Q*-value Correlation (*covS*) §
M5005_Spy0477	-	spy0575	849	789	0.2741	0.0567	0.0555	0.0124	0.9324	0.4829
M5005_Spy0957	-	spy1248	465	414	0.2738	0.0569	0.0557	0.3353	0.0185	0.0422
M5005_Spy0302	-	spy0359	531	664	0.2737	0.0570	0.0557	0.0014	0.9926	0.4973
M5005_Spy0753	*acoC*	spy1029	90	59	0.2734	0.0573	0.0559	0.3421	0.0161	0.0399
M5005_Spy0726	-	spy0925	925	934	0.2723	0.0584	0.0569	0.3961	0.0048	0.0186
M5005_Spy0108	-	spy0127	1391	1304	0.272	0.0587	0.0571	0.4663	7.32E-04	**0.0067**
M5005_Spy1845	-	spy2194	1114	1159	0.2713	0.0594	0.0576	-0.0778	0.5953	0.3736
M5005_Spy0662	*fruA*		2507	2318	0.2708	0.0599	0.0579	0.3813	0.0069	0.0230
M5005_Spy0487	-	spy0588	317	388	0.2706	0.0600	0.0580	0.2312	0.1100	0.1250
M5005_Spy0552	-	spy0726	345	424	0.27	0.0606	0.0585	0.0928	0.5258	0.3483
M5005_Spy1580	-	spy1862	752	859	0.2696	0.0610	0.0587	0.3288	0.0211	0.0457
M5005_Spy1120	*pstI*	spy1372	254	277	0.2692	0.0614	0.0590	0.2669	0.0638	0.0887
M5005_Spy1611	*rpoE*	spy1895	470	547	0.2692	0.0615	0.0590	0.2859	0.0464	0.0722
M5005_Spy0083	*rpoB*	spy0098	171	199	0.2685	0.0621	0.0596	0.2065	0.1545	0.1577
M5005_Spy0217	*nanH*	spy0257	591	607	0.2685	0.0622	0.0596	0.0645	0.6597	0.3965
M5005_Spy1178	-	spyM18_1460	2500	2494	0.2682	0.0624	0.0597	0.0983	0.5017	0.3377
M5005_Spy0266	-	spy0312	887	961	0.2681	0.0625	0.0597	0.0831	0.5704	0.3638
M5005_Spy1318	*rocA*	spy1605	1438	1700	0.2677	0.0630	0.0601	0.2035	0.1609	0.1615
M5005_Spy0349	*nrdE.1*	spy0427	217	200	0.2674	0.0632	0.0602	0.1713	0.2393	0.2117
M5005_Spy1339	*priA*	spy1629	937	931	0.2665	0.0641	0.0607	0.1875	0.1970	0.1848
M5005_Spy1813	*aspS*	spy2156	734	846	0.2665	0.0642	0.0607	0.0172	0.9068	0.4758
M5005_Spy0943	*cdd*	spy1230	236	252	0.2664	0.0642	0.0607	0.1889	0.1937	0.1829
M5005_Spy1359	-	spy1653	1066	1065	0.2663	0.0644	0.0608	0.4401	0.0016	**0.0092**
M5005_Spy0780	-	spy1057	319	404	0.2662	0.0645	0.0608	0.0549	0.7077	0.4146
M5005_Spy0542	*pepD*	spy0713	1136	857	0.2661	0.0646	0.0609	0.3156	0.0272	0.0530
M5005_Spy0462	-	spy0559	955	883	0.2658	0.0649	0.0611	0.3684	0.0092	0.0281
M5005_Spy0442	-	spy0535	2404	2512	0.2655	0.0652	0.0613	-0.0419	0.7748	0.4363
M5005_Spy0606	*rgpDc*	spy0790	446	455	0.2649	0.0659	0.0618	0.2459	0.0886	0.1084
M5005_Spy0493	-	spy0593	616	554	0.2645	0.0663	0.0621	0.6426	6.4E-07	**0.0055**
M5005_Spy1678	-	spy1971	298	333	0.264	0.0668	0.0625	0.1895	0.1921	0.1821
M5005_Spy0126	*ntpI*		1616	1155	0.264	0.0668	0.0625	0.4081	0.0036	0.0153
M5005_Spy1166	-	SpyM3_1092	221	271	0.2638	0.0670	0.0626	0.0805	0.5825	0.3687

M5005_Spy#	Gene	Synonym *	WT Transcript Rank †	Mutant Transcript Rank †	*r* Correlation (*covR*) ‡	*P*-value Correlation (*covR*)	*Q*-value Correlation (*covR*) §	*r* Correlation (*covS*) ‡	*P*-value Correlation (*covS*)	*Q*-value Correlation (*covS*) §
M5005_Spy1131	-	spy1386	1881	1330	0.2627	0.0682	0.0636	0.0015	0.9917	0.4972
M5005_Spy1069	-	spy1308	400	475	0.2623	0.0687	0.0639	0.2304	0.1112	0.1257
M5005_Spy0342	*prtS*	spy0416	94	103	0.262	0.0689	0.0641	0.1134	0.4377	0.3108
M5005_Spy1363	-	spy1657	1165	912	0.2613	0.0698	0.0647	0.1681	0.2483	0.2166
M5005_Spy1158	*ddlA*	spy1421	1336	1393	0.2607	0.0704	0.0652	0.0094	0.9491	0.4859
M5005_Spy0751	*acoA*	spy1026	86	97	0.2602	0.0710	0.0654	0.1845	0.2043	0.1898
M5005_Spy1082	-	spy1324	1821	1521	0.2601	0.0711	0.0655	0.5841	1.1E-05	**0.0055**
M5005_Spy1587	*udp*	spy1869	58	65	0.2601	0.0711	0.0655	0.2023	0.1633	0.1632
M5005_Spy1067	*malX*	spy1306	53	42	0.2598	0.0715	0.0657	0.1509	0.3008	0.2452
M5005_Spy1229	*argR*	spy1496	756	936	0.2595	0.0718	0.0660	-0.1129	0.4399	0.3119
M5005_Spy0328	*clpP*	spy0395	36	62	0.2587	0.0727	0.0665	0.0915	0.5317	0.3507
M5005_Spy0961	*truB*	spy1251	348	429	0.2586	0.0727	0.0665	0.1542	0.2900	0.2388
M5005_Spy0421	*gloA*	spy0511	1173	1126	0.2571	0.0746	0.0678	0.1479	0.3104	0.2514
M5005_Spy0981	*cfa*	spy1273	2215	1262	0.2569	0.0747	0.0678	0.1140	0.4354	0.3100
M5005_Spy0858	*xpt*	spy1136	1450	1384	0.256	0.0758	0.0686	0.0460	0.7534	0.4291
M5005_Spy1229	*argR*	spy1497	347	282	0.2556	0.0763	0.0690	0.1160	0.4275	0.3062
M5005_Spy0676	-	SpyM3_0589	2133	1507	0.2553	0.0767	0.0692	0.4206	0.0026	0.0128
M5005_Spy0504	*pepF*	spy0606	1017	889	0.2551	0.0769	0.0693	0.1182	0.4186	0.3034
M5005_Spy0331	*dnaX*	spyM18_0450	1869	2283	0.255	0.0771	0.0694	0.3689	0.0091	0.0279
M5005_Spy0037	-	spy0040	251	314	0.2548	0.0772	0.0694	0.2369	0.1013	0.1187
M5005_Spy1737	*rgg*	spy2042	1742	1423	0.254	0.0782	0.0702	0.1390	0.3409	0.2675
M5005_Spy0365	*pfs*	spy0447	290	267	0.2532	0.0791	0.0707	0.5304	8.9E-05	**0.0055**
M5005_Spy0324	*fhuA*	spy0386	2054	2383	0.2531	0.0794	0.0708	0.0151	0.9182	0.4791
M5005_Spy0128	*ntpE*	spy0150	1345	1115	0.2528	0.0797	0.0710	0.3457	0.0150	0.0381
M5005_Spy1335	-		671	569	0.2527	0.0798	0.0710	-0.0075	0.9592	0.4888
M5005_Spy1559	*trx*	spy1835	813	1154	0.2525	0.0801	0.0712	0.2826	0.0491	0.0751
M5005_Spy1251	*divIB*	spy1523	338	444	0.2515	0.0813	0.0719	0.2459	0.0885	0.1084
M5005_Spy0725	*elaC*	spy0924	230	226	0.2514	0.0814	0.0720	0.1916	0.1873	0.1800
M5005_Spy0908	*citX*	spy1190	1726	1410	0.2509	0.0821	0.0722	-0.1832	0.2077	0.1910
M5005_Spy0978	-	SpyM3_0902	2527	2121	0.2509	0.0821	0.0722	0.0887	0.5446	0.3547
M5005_Spy1546	*nusB*	spy1820	763	695	0.2509	0.0821	0.0722	0.2326	0.1078	0.1233
M5005_Spy0436	*vicK*	spy0529	511	615	0.2504	0.0827	0.0727	0.1800	0.2160	0.1965

M5005_Spy#	Gene	Synonym *	WT Transcript Rank †	Mutant Transcript Rank †	*r* Correlation (*covR*) ‡	*P*-value Correlation (*covR*)	*Q*-value Correlation (*covR*) §	*r* Correlation (*covS*) ‡	*P*-value Correlation (*covS*)	*Q*-value Correlation (*covS*) §
M5005_Spy0422	-	spy0512	665	591	0.2499	0.0833	0.0731	0.1893	0.1926	0.1824
M5005_Spy0760	-		1530	1551	0.2499	0.0834	0.0731	0.3634	0.0103	0.0298
M5005_Spy0496	-	spy0596	769	750	0.2498	0.0834	0.0731	0.1163	0.4263	0.3060
M5005_Spy0509	*tpi*	spy0613	402	426	0.2496	0.0838	0.0732	0.2614	0.0696	0.0933
M5005_Spy1675	*cdsA*	spy1964	421	586	0.2494	0.0840	0.0734	0.1295	0.3752	0.2839
M5005_Spy1255	*typA*	spy1527	223	321	0.2492	0.0842	0.0735	0.0485	0.7406	0.4252
M5005_Spy1590	*rpsN2*	spy1871	19	18	0.2484	0.0852	0.0740	0.1576	0.2795	0.2334
M5005_Spy0226	-	spy0266	107	128	0.248	0.0858	0.0744	0.0360	0.8062	0.4451
M5005_Spy0926	-	spy1212	127	107	0.2469	0.0872	0.0754	0.2715	0.0592	0.0852
M5005_Spy0870	-	spy1148	424	452	0.2466	0.0877	0.0757	0.2690	0.0616	0.0871
M5005_Spy0925	*rnhB*	spy1211	143	180	0.2465	0.0877	0.0757	0.1494	0.3056	0.2480
M5005_Spy1687	*sclA*	spy1983	885	637	0.246	0.0884	0.0762	0.1407	0.3349	0.2644
M5005_Spy1225	-	spy1491	592	652	0.2452	0.0894	0.0769	0.5470	4.8E-05	**0.0055**
M5005_Spy0850	*pta*	spy1128	112	155	0.2451	0.0897	0.0770	0.0957	0.5132	0.3429
M5005_Spy1012	-		2120	1682	0.2449	0.0899	0.0771	0.2496	0.0837	0.1048
M5005_Spy1603	*asp*	spy1886	198	204	0.2446	0.0903	0.0774	0.1517	0.2982	0.2437
M5005_Spy0429	-	spy0519	2291	2132	0.2445	0.0904	0.0774	0.2643	0.0665	0.0908
M5005_Spy1173	-	spyM18_0389	2122	2068	0.2445	0.0905	0.0774	0.2524	0.0802	0.1024
M5005_Spy1390	-	spy1697	1227	1153	0.2428	0.0928	0.0790	0.3516	0.0132	0.0352
M5005_Spy0008	*divIC*	spy0010	2153	1973	0.2426	0.0931	0.0791	0.1249	0.3924	0.2912
M5005_Spy0804	*srtR*	spy1081	2594	2033	0.2425	0.0932	0.0792	0.2010	0.1662	0.1649
M5005_Spy0131	*ntpA*	spy0154	1258	776	0.2421	0.0937	0.0795	0.2580	0.0734	0.0969
M5005_Spy1396	*nadE*	spyM18_1715	1521	1092	0.2407	0.0958	0.0809	0.3405	0.0167	0.0404
M5005_Spy1601	-	spy1884	318	372	0.2404	0.0961	0.0810	0.1787	0.2193	0.1989
M5005_Spy0811	-	spy1088	2403	1929	0.2399	0.0969	0.0815	-0.0045	0.9753	0.4926
M5005_Spy0910	*citC*	spy1192	498	626	0.239	0.0981	0.0821	-0.0227	0.8770	0.4664
M5005_Spy1815	*rpmF*	spyM18_2196	67	161	0.2386	0.0988	0.0826	-0.0564	0.7005	0.4120
M5005_Spy0551	*rplS*	spy0724	612	666	0.2384	0.0991	0.0827	-0.1132	0.4388	0.3114
M5005_Spy0175	*tgt*	M12_0671	2231	1702	0.2379	0.0997	0.0832	0.3327	0.0195	0.0436
M5005_Spy0165	-	spy0191	1659	1707	0.237	0.1010	0.0842	0.0058	0.9682	0.4911
M5005_Spy0989	*pfk*	spy1283	356	335	0.2369	0.1012	0.0842	0.1477	0.3113	0.2519
M5005_Spy0313	-	spy0373	2418	1796	0.2368	0.1014	0.0843	-0.0536	0.7147	0.4168

M5005_Spy#	Gene	Synonym *	WT Transcript Rank †	Mutant Transcript Rank †	*r* Correlation (*covR*) ‡	*P*-value Correlation (*covR*)	*Q*-value Correlation (*covR*) §	*r* Correlation (*covS*) ‡	*P*-value Correlation (*covS*)	*Q*-value Correlation (*covS*) §
M5005_Spy0592	-	spy0773	758	1022	0.2368	0.1014	0.0843	-0.0124	0.9327	0.4829
M5005_Spy1564	-	spy1841	877	945	0.2364	0.1019	0.0846	0.3714	0.0086	0.0271
M5005_Spy1683	*lrp*	spy1978	1079	982	0.2357	0.1030	0.0853	0.1696	0.2441	0.2138
M5005_Spy0747	-	spy1020	177	219	0.2353	0.1036	0.0857	0.2827	0.0490	0.0751
M5005_Spy1702	*smeZ*	spy1998	1959	1648	0.2349	0.1042	0.0860	0.0104	0.9434	0.4849
M5005_Spy1691	-	spy1985	1263	1142	0.2346	0.1047	0.0861	0.1632	0.2625	0.2253
M5005_Spy1380	*glpO*	spy1683	155	253	0.234	0.1056	0.0868	0.1667	0.2523	0.2184
M5005_Spy0271	-	spy0319	392	331	0.2338	0.1059	0.0869	0.5087	1.90E-04	**0.0055**
M5005_Spy1638	*lacA.2*	spy1923	1041	1098	0.2337	0.1061	0.0869	-0.1108	0.4486	0.3162
M5005_Spy1857	*guaB*	spy2206	683	693	0.2337	0.1061	0.0869	-0.2186	0.1314	0.1424
M5005_Spy0308	-	spy0366	1010	1169	0.2336	0.1063	0.0870	0.1040	0.4770	0.3283
M5005_Spy0004	-	spy0006	589	688	0.2333	0.1067	0.0872	0.0730	0.6182	0.3817
M5005_Spy0695	*rpiA*	spy0889	172	192	0.2319	0.1089	0.0887	0.4145	0.0031	0.0139
M5005_Spy0247	-	spyM18_0279	822	813	0.2315	0.1095	0.0890	-0.0310	0.8323	0.4532
M5005_Spy0012	*hpt*	spyM18_0013	642	751	0.2314	0.1096	0.0891	0.3265	0.0221	0.0469
M5005_Spy0495	*lysS*	spy0595	202	245	0.2313	0.1099	0.0892	0.1080	0.4603	0.3208
M5005_Spy1006	-		2303	2155	0.231	0.1102	0.0894	0.2616	0.0694	0.0933
M5005_Spy1057	*malR*	spy1293	1246	1545	0.2305	0.1111	0.0900	0.3570	0.0118	0.0325
M5005_Spy0336	-	spy0407	876	739	0.2304	0.1112	0.0900	0.1945	0.1804	0.1748
M5005_Spy1811	-	spy2154	583	599	0.2303	0.1114	0.0900	0.2330	0.1071	0.1230
M5005_Spy0594	*rexB*	spy0776	852	1028	0.2296	0.1125	0.0907	0.2647	0.0660	0.0906
M5005_Spy0363	-	spy0444	387	411	0.229	0.1135	0.0914	0.0191	0.8964	0.4724
M5005_Spy1319	-		1747	1322	0.2288	0.1138	0.0916	-0.1012	0.4889	0.3321
M5005_Spy0052	*rpmC*	spy0059	447	512	0.2285	0.1142	0.0917	0.4485	0.0012	**0.0081**
M5005_Spy1367	*pbpX*	spy1664	2050	2448	0.2284	0.1145	0.0919	0.0246	0.8666	0.4635
M5005_Spy1170	-	spy1437	2027	1735	0.2281	0.1149	0.0921	0.1549	0.2879	0.2374
M5005_Spy0277	*ntpJ*	spy0327	492	514	0.2279	0.1152	0.0922	0.0542	0.7117	0.4156
M5005_Spy1113	-	spy1365	496	497	0.227	0.1167	0.0933	0.0365	0.8033	0.4443
M5005_Spy0348	*nrdI*	spy0426	875	884	0.2262	0.1181	0.0943	0.3820	0.0068	0.0228
M5005_Spy1402	*lacR.1*	spy1712	1832	1612	0.2256	0.1190	0.0949	0.2656	0.0651	0.0899
M5005_Spy1163	-	spy1427	1396	1505	0.2252	0.1197	0.0952	0.3095	0.0305	0.0567
M5005_Spy1488	*accB*	spy1747	1323	1486	0.2249	0.1203	0.0956	0.3135	0.0283	0.0544

M5005_Spy#	Gene	Synonym *	WT Transcript Rank †	Mutant Transcript Rank †	*r* Correlation (*covR*) ‡	*P*-value Correlation (*covR*)	*Q*-value Correlation (*covR*) §	*r* Correlation (*covS*) ‡	*P*-value Correlation (*covS*)	*Q*-value Correlation (*covS*) §
M5005_Spy1331	-	spyM18_1629	790	867	0.2248	0.1204	0.0956	0.2584	0.0730	0.0964
M5005_Spy0044	*rplC*	spy0049	268	384	0.2247	0.1207	0.0957	0.0755	0.6061	0.3777
M5005_Spy0046	*rplW*	spy0051	383	410	0.2246	0.1207	0.0957	0.2576	0.0739	0.0972
M5005_Spy1838	*gidA*	spy2185	2083	1524	0.2239	0.1220	0.0966	0.1327	0.3632	0.2781
M5005_Spy0976	-	spy1265	15	17	0.2238	0.1222	0.0967	0.2780	0.0531	0.0790
M5005_Spy1037	-	spyM18_1795	2574	2610	0.2237	0.1222	0.0967	-0.0363	0.8044	0.4444
M5005_Spy1208	-	spyM18_0728	2637	2466	0.2236	0.1225	0.0968	0.1980	0.1727	0.1696
M5005_Spy0236	-	spy0277	1210	1245	0.2231	0.1233	0.0972	-0.1330	0.3621	0.2776
M5005_Spy1165	*pyrD*	spy1432	1064	952	0.2227	0.1240	0.0976	0.0270	0.8539	0.4602
M5005_Spy0805	*srtK*	spy1082	1365	1152	0.2223	0.1247	0.0978	0.2661	0.0646	0.0895
M5005_Spy1699	-	spy1992	472	619	0.2218	0.1257	0.0985	0.5284	9.5E-05	**0.0055**
M5005_Spy1066	*amyB*	spy1304	18	26	0.2217	0.1258	0.0985	0.3694	0.0090	0.0278
M5005_Spy1804	*mutL*	spy2121	624	665	0.2213	0.1265	0.0988	-0.0396	0.7871	0.4408
M5005_Spy1797	-	spy2113	34	54	0.2212	0.1267	0.0988	0.2558	0.0761	0.0989
M5005_Spy1277	*ahrC.2*	spy1549	1892	1557	0.2208	0.1273	0.0990	0.2007	0.1667	0.1652
M5005_Spy0209	-	spy0248	486	687	0.2202	0.1284	0.0995	0.0300	0.8376	0.4550
M5005_Spy1631	*salA*	spy1915	1282	1176	0.2201	0.1286	0.0995	0.0756	0.6057	0.3777
M5005_Spy0933	-	spy1218	74	39	0.2198	0.1292	0.0998	0.2644	0.0664	0.0907
M5005_Spy0994	-	spy1289	643	645	0.2197	0.1293	0.0998	0.3778	0.0074	0.0244
M5005_Spy1070	*dltD*	spy1310	512	629	0.2197	0.1293	0.0998	0.3187	0.0256	0.0511
M5005_Spy0671	-	spy0864	613	603	0.2196	0.1295	0.0998	0.0472	0.7472	0.4271
M5005_Spy0579	*atpA*	spy0758	678	713	0.2195	0.1296	0.0998	0.0704	0.6306	0.3864
M5005_Spy0642	*carA*	spy0833	745	829	0.2194	0.1298	0.0998	0.1411	0.3336	0.2643
M5005_Spy1167	-	spy1434	1260	1312	0.2193	0.1300	0.0999	0.1056	0.4702	0.3247
M5005_Spy0581	*atpD*		1186	1066	0.2191	0.1304	0.1002	0.2608	0.0703	0.0939
M5005_Spy1809	-	spy2152	1802	1656	0.2175	0.1334	0.1017	0.3283	0.0213	0.0460
M5005_Spy0097	*pepA*	spy0115	313	428	0.2167	0.1348	0.1026	0.3014	0.0353	0.0621
M5005_Spy0146	*metB*	spy0172	1871	784	0.2163	0.1355	0.1031	0.1590	0.2753	0.2315
M5005_Spy1020	-	spy0685	2549	2216	0.2162	0.1356	0.1031	-0.0234	0.8731	0.4654
M5005_Spy0684	*mvaK2*	spy0878	954	1031	0.2161	0.1359	0.1031	0.3161	0.0269	0.0527
M5005_Spy0104	-	spy0122	509	459	0.2151	0.1377	0.1042	0.2517	0.0810	0.1029
M5005_Spy1239	-	spy1508	555	488	0.215	0.1380	0.1043	0.0881	0.5473	0.3555

M5005_Spy#	Gene	Synonym *	WT Transcript Rank †	Mutant Transcript Rank †	*r* Correlation (*covR*) ‡	*P*-value Correlation (*covR*)	*Q*-value Correlation (*covR*) §	*r* Correlation (*covS*) ‡	*P*-value Correlation (*covS*)	*Q*-value Correlation (*covS*) §
M5005_Spy0827	*potB*	spy1103	1159	1317	0.2146	0.1386	0.1047	0.0907	0.5355	0.3518
M5005_Spy0073	-	spyM18_0084	3	6	0.2143	0.1392	0.1051	0.4295	0.0021	0.0111
M5005_Spy1652	-	spy1938	299	419	0.214	0.1398	0.1055	0.1617	0.2669	0.2278
M5005_Spy1751	*secE*	spy2058	1414	1128	0.2138	0.1402	0.1057	0.3566	0.0119	0.0326
M5005_Spy1781	*tsf*	spy2093	307	362	0.2138	0.1403	0.1057	0.1088	0.4569	0.3195
M5005_Spy0474	*licT*	spy0571	1506	2082	0.2137	0.1404	0.1057	-0.1817	0.2114	0.1933
M5005_Spy0865	-	spy1143	627	743	0.2133	0.1411	0.1060	0.1060	0.4685	0.3242
M5005_Spy0703	*pyrF*	spy0900	1236	1666	0.2125	0.1426	0.1068	0.4226	0.0025	0.0124
M5005_Spy1546	*nusB*	spy1818	453	493	0.2113	0.1449	0.1081	0.4999	2.55E-04	**0.0055**
M5005_Spy0690	-	spy0884	1147	1204	0.2111	0.1453	0.1083	0.5066	2.04E-04	**0.0055**
M5005_Spy0772	-	spy1049	1723	1835	0.2106	0.1463	0.1088	0.3278	0.0215	0.0463
M5005_Spy0476	*bglA*	spy0574	1297	1285	0.2099	0.1477	0.1098	0.0259	0.8599	0.4612
M5005_Spy0284	-	spy0338	978	821	0.2086	0.1503	0.1112	0.0228	0.8763	0.4664
M5005_Spy0187	-		740	753	0.2084	0.1507	0.1113	0.1741	0.2315	0.2070
M5005_Spy0167	-		1902	1944	0.2083	0.1509	0.1113	0.1096	0.4535	0.3186
M5005_Spy0720	-		1338	1313	0.2082	0.1512	0.1113	0.0857	0.5581	0.3597
M5005_Spy0339	*exoA*	spy0412	547	614	0.2081	0.1513	0.1113	-0.0426	0.7716	0.4356
M5005_Spy1568	*dinP*	spy1846	973	943	0.2068	0.1540	0.1131	0.4228	0.0025	0.0124
M5005_Spy1244	*divIVAS*	spy1514	227	238	0.2065	0.1546	0.1133	0.3273	0.0217	0.0466
M5005_Spy1269	*asnA*	spy1539	1758	1341	0.2064	0.1548	0.1134	0.4555	0.0010	**0.0074**
M5005_Spy0779	-	spy1056	1306	1783	0.2061	0.1554	0.1137	0.4050	0.0039	0.0162
M5005_Spy0960	*mreA*	spy1250	869	765	0.206	0.1556	0.1137	-0.0431	0.7685	0.4343
M5005_Spy1533	*alr*	spy1802	870	849	0.2055	0.1567	0.1142	0.1156	0.4289	0.3065
M5005_Spy0713	*bcaT*	spy0911	1573	1584	0.2049	0.1578	0.1148	-0.0522	0.7219	0.4189
M5005_Spy1406	*copY*	spy1717	951	1089	0.2042	0.1593	0.1155	-0.0030	0.9838	0.4948
M5005_Spy1853	*hasC*	spy2202	461	346	0.2033	0.1612	0.1167	0.3679	0.0093	0.0283
M5005_Spy0548	-	spy0721	505	675	0.2029	0.1621	0.1171	-0.1343	0.3577	0.2758
M5005_Spy0561	*epf*		2244	2157	0.2027	0.1625	0.1171	-0.0337	0.8184	0.4491
M5005_Spy1779	-	spy2091	1319	1321	0.2027	0.1625	0.1171	-0.1222	0.4030	0.2971
M5005_Spy1829	-	spy2176	1440	1144	0.2027	0.1625	0.1171	0.0164	0.9109	0.4769
M5005_Spy1387	-	spy1693	31	48	0.2021	0.1637	0.1176	0.1200	0.4113	0.2997
M5005_Spy0413	*secG*	spy0502	343	394	0.2009	0.1664	0.1194	0.3502	0.0136	0.0358

M5005_Spy#	Gene	Synonym *	WT Transcript Rank †	Mutant Transcript Rank †	*r* Correlation (*covR*) ‡	*P*-value Correlation (*covR*)	*Q*-value Correlation (*covR*) §	*r* Correlation (*covS*) ‡	*P*-value Correlation (*covS*)	*Q*-value Correlation (*covS*) §
M5005_Spy0433	-	spy0526	2204	1971	0.2003	0.1676	0.1202	0.2452	0.0895	0.1091
M5005_Spy1177	-	spy1448	1466	1558	0.2002	0.1677	0.1202	0.0333	0.8205	0.4498
M5005_Spy1286	-	spy1563	1518	1256	0.2	0.1682	0.1205	0.1335	0.3603	0.2769
M5005_Spy0866	-	spy1144	881	1141	0.1996	0.1690	0.1207	0.1829	0.2084	0.1911
M5005_Spy1586	*nupC*	spy1868	118	196	0.1993	0.1697	0.1211	0.2432	0.0923	0.1114
M5005_Spy0111	-	spy0130	1446	1292	0.1982	0.1723	0.1221	0.1985	0.1715	0.1689
M5005_Spy0945	*coaA*	spy1233	2093	1546	0.1978	0.1732	0.1227	0.2513	0.0816	0.1032
M5005_Spy0557	-	spy0732	2485	1370	0.1975	0.1739	0.1230	0.3360	0.0182	0.0421
M5005_Spy1397	*lacB.1*	spy1707	1416	775	0.1973	0.1743	0.1232	0.3711	0.0087	0.0271
M5005_Spy0868	-	spy1146	485	510	0.197	0.1750	0.1235	0.3040	0.0337	0.0606
M5005_Spy0973	-	spy1262	4	9	0.1966	0.1758	0.1240	0.1174	0.4220	0.3050
M5005_Spy1674	-	spy1963	364	446	0.196	0.1770	0.1245	0.3240	0.0232	0.0484
M5005_Spy0641	*pyrB*	spy0832	1070	880	0.1958	0.1776	0.1249	0.5515	4.0E-05	**0.0055**
M5005_Spy0099	-	spy0117	1405	1503	0.1945	0.1805	0.1266	0.0313	0.8310	0.4527
M5005_Spy1530	-	spy1798	946	631	0.1934	0.1831	0.1281	0.0348	0.8126	0.4468
M5005_Spy0087	*comYB*	spy0102	2143	1984	0.1923	0.1855	0.1295	0.0841	0.5655	0.3620
M5005_Spy0753	*acoC*		2111	2013	0.192	0.1864	0.1297	0.1574	0.2802	0.2337
M5005_Spy1726	-	spy2029	395	534	0.1914	0.1876	0.1304	-0.0972	0.5063	0.3397
M5005_Spy0683	*mvaD*	spy0877	815	878	0.1906	0.1895	0.1312	0.3326	0.0195	0.0436
M5005_Spy0263	*nadD*	spy0308	599	627	0.1904	0.1900	0.1315	0.2497	0.0836	0.1048
M5005_Spy0055	*rplX*	spy0062	191	209	0.19	0.1909	0.1320	0.1250	0.3921	0.2912
M5005_Spy0689	*dyr*	spy0883	1380	1222	0.1892	0.1930	0.1331	-0.1300	0.3734	0.2829
M5005_Spy0890	*ddh*	spy1170	2422	2015	0.1891	0.1931	0.1331	0.3300	0.0206	0.0450
M5005_Spy1521	-	spy1788	1316	1360	0.1881	0.1956	0.1344	0.1833	0.2075	0.1910
M5005_Spy1579	-	spy1861	1163	1244	0.1878	0.1964	0.1349	0.0318	0.8283	0.4521
M5005_Spy0752	*acoB*	spy1028	60	60	0.1874	0.1972	0.1352	0.1628	0.2638	0.2261
M5005_Spy0921	-	spy1206	1897	2167	0.1867	0.1989	0.1363	0.0472	0.7474	0.4271
M5005_Spy0367	*scaR*	spy0450	365	422	0.1862	0.2003	0.1371	0.2073	0.1529	0.1567
M5005_Spy0091	*comYD*	spy0106	2340	2253	0.1861	0.2005	0.1372	0.0512	0.7269	0.4202
M5005_Spy0553	*gyrB*	spy0727	161	182	0.1858	0.2011	0.1375	0.1152	0.4305	0.3071
M5005_Spy0354	-	spy0433	1404	1249	0.1857	0.2015	0.1376	0.0860	0.5570	0.3596
M5005_Spy0632	*capA*	spy0818	776	799	0.1841	0.2054	0.1396	0.0024	0.9871	0.4956

M5005_Spy#	Gene	Synonym *	WT Transcript Rank †	Mutant Transcript Rank †	*r* Correlation (*covR*) ‡	*P*-value Correlation (*covR*)	*Q*-value Correlation (*covR*) §	*r* Correlation (*covS*) ‡	*P*-value Correlation (*covS*)	*Q*-value Correlation (*covS*) §
M5005_Spy1079	-	spyM18_1331	1148	1261	0.1833	0.2073	0.1406	0.0203	0.8900	0.4703
M5005_Spy0405	*silE*	spyM18_0551	2633	2232	0.1832	0.2076	0.1407	-0.0662	0.6512	0.3934
M5005_Spy1291	-	spy1567	1575	1319	0.1827	0.2088	0.1413	0.1109	0.4481	0.3161
M5005_Spy1348	-		2006	1538	0.1826	0.2091	0.1414	0.2188	0.1309	0.1421
M5005_Spy0815	-	M12_0089	1651	1416	0.1824	0.2097	0.1418	0.3318	0.0199	0.0441
M5005_Spy1097	-		1174	1090	0.1812	0.2129	0.1432	0.4600	8.84E-04	**0.0071**
M5005_Spy1768	*ahpC*	spy2079	123	212	0.181	0.2133	0.1434	-0.0466	0.7508	0.4281
M5005_Spy1758	-	spy2066	990	746	0.1809	0.2136	0.1434	0.2033	0.1611	0.1617
M5005_Spy1190	-	spy1461	2112	2249	0.1807	0.2140	0.1435	-0.0545	0.7098	0.4150
M5005_Spy1625	*salR*	spy1908	1910	1540	0.1805	0.2146	0.1438	0.1835	0.2070	0.1909
M5005_Spy0013	*ftsH*	spy0015	147	171	0.1801	0.2155	0.1442	0.0369	0.8013	0.4440
M5005_Spy0582	*atpC*	spy0761	443	509	0.1798	0.2164	0.1446	0.3117	0.0292	0.0554
M5005_Spy1753	*pbp2A*	spy2059	142	167	0.1794	0.2175	0.1451	0.0456	0.7558	0.4300
M5005_Spy0435	*vicR*	spy0528	440	527	0.1764	0.2252	0.1493	0.2168	0.1346	0.1448
M5005_Spy0517	*regR*	spy0627	1151	1267	0.1755	0.2278	0.1508	0.2039	0.1599	0.1615
M5005_Spy1615	-	spy1899	1106	1017	0.175	0.2291	0.1513	0.0671	0.6469	0.3919
M5005_Spy0817	*dacA*	spy1093	1558	1875	0.1749	0.2295	0.1514	0.0447	0.7602	0.4318
M5005_Spy0048	*rpsS*	spy0053	330	341	0.1744	0.2307	0.1518	-0.0494	0.7360	0.4240
M5005_Spy0488	-	spy0589	987	1054	0.1744	0.2307	0.1518	0.1507	0.3014	0.2454
M5005_Spy1632	*lacG*	spy1916	1428	1454	0.1742	0.2313	0.1519	0.0793	0.5883	0.3704
M5005_Spy0478	-	spy0576	1082	1121	0.1739	0.2322	0.1524	0.5638	2.5E-05	**0.0055**
M5005_Spy0620	*rpl36*	spy0805	243	268	0.1733	0.2337	0.1530	0.2108	0.1460	0.1529
M5005_Spy0578	*atpH*	spy0757	1053	1068	0.1732	0.2341	0.1530	0.2624	0.0686	0.0928
M5005_Spy0014	-	spy0016	1415	1434	0.1731	0.2342	0.1530	0.2477	0.0861	0.1067
M5005_Spy0195	-	spy0228	1296	1255	0.1731	0.2342	0.1530	-0.0269	0.8546	0.4602
M5005_Spy1328	-	spy1617	1698	1583	0.1724	0.2361	0.1541	-0.1096	0.4536	0.3186
M5005_Spy0092	-	spy0107	2377	1850	0.1723	0.2364	0.1541	-0.0838	0.5669	0.3626
M5005_Spy1791	-	spy2107	490	719	0.1723	0.2366	0.1542	0.0645	0.6598	0.3965
M5005_Spy0408	*fpg*	spy0497	1508	1438	0.1713	0.2392	0.1555	0.0008	0.9956	0.4982
M5005_Spy0963	-	spy1253	1127	1120	0.1712	0.2396	0.1556	0.2560	0.0758	0.0987
M5005_Spy0891	*satD*	spy1171	1683	1651	0.1709	0.2403	0.1559	-0.0599	0.6828	0.4058
M5005_Spy0001	*dnaA*	spy0002	390	479	0.17	0.2428	0.1569	0.1299	0.3737	0.2829

M5005_Spy#	Gene	Synonym *	WT Transcript Rank †	Mutant Transcript Rank †	*r* Correlation (*covR*) ‡	*P* -value Correlation (*covR*)	*Q*- value Correlation (*covR*) §	*r* Correlation (*covS*) ‡	*P* -value Correlation (*covS*)	*Q*- value Correlation (*covS*) §
M5005_Spy0327	*upp*	spyM18_0444	1519	1852	0.1698	0.2435	0.1572	0.0101	0.9453	0.4850
M5005_Spy0323	*fhuD*	spy0385	1971	2413	0.1683	0.2476	0.1596	-0.0044	0.9759	0.4926
M5005_Spy0750	-	spy1025	845	780	0.1681	0.2482	0.1599	0.3122	0.0290	0.0554
M5005_Spy1160	-	SpyM3_1086	920	920	0.1678	0.2490	0.1602	0.3488	0.0140	0.0366
M5005_Spy1292	*valS*	spy1568	1479	1572	0.1673	0.2505	0.1610	0.3652	0.0099	0.0294
M5005_Spy0924	-	spy1210	2236	1807	0.1672	0.2509	0.1611	0.0876	0.5497	0.3565
M5005_Spy1313	-	spy1599	423	345	0.1669	0.2519	0.1617	0.2427	0.0930	0.1119
M5005_Spy0962	-	spy1252	791	924	0.1662	0.2537	0.1625	0.0915	0.5317	0.3507
M5005_Spy0816	-		1011	996	0.166	0.2544	0.1625	0.0137	0.9255	0.4812
M5005_Spy1408	*rbfA*	spy1719	551	371	0.166	0.2543	0.1625	0.3084	0.0311	0.0573
M5005_Spy0144	-	spy0170	1630	876	0.1658	0.2549	0.1627	0.1413	0.3328	0.2638
M5005_Spy0685	-	spy0879	388	319	0.1657	0.2551	0.1627	0.1156	0.4292	0.3065
M5005_Spy0584	*murA*	spy0763	277	323	0.1655	0.2558	0.1630	0.1334	0.3610	0.2771
M5005_Spy1575	*norA*	spy1856	2221	1610	0.1646	0.2583	0.1642	0.2959	0.0390	0.0653
M5005_Spy1026	-	spyM18_1787	1120	972	0.1644	0.2591	0.1646	0.1073	0.4630	0.3217
M5005_Spy0867	*glyA*	spy1145	366	383	0.1631	0.2627	0.1667	-0.0435	0.7664	0.4333
M5005_Spy0987	*sipC*	spy1281	363	541	0.1623	0.2654	0.1678	0.0563	0.7009	0.4120
M5005_Spy0057	*rpsN*	spy0064	158	191	0.162	0.2662	0.1682	0.2802	0.0511	0.0774
M5005_Spy0942	-		2557	2138	0.1619	0.2663	0.1682	0.1293	0.3758	0.2840
M5005_Spy1257	*glcK*	spy1529	823	892	0.1619	0.2663	0.1682	-0.0048	0.9737	0.4926
M5005_Spy0719	-		1737	1739	0.1618	0.2666	0.1682	0.0957	0.5130	0.3429
M5005_Spy0356	*speJ*	spy0436	2499	1672	0.1617	0.2669	0.1683	0.0379	0.7962	0.4434
M5005_Spy0800	-	spy1077	2094	2222	0.1617	0.2670	0.1683	0.2882	0.0446	0.0704
M5005_Spy0250	*oppB*	spy0294	1096	944	0.1616	0.2672	0.1683	0.5116	1.72E-04	**0.0055**
M5005_Spy1266	-	spy1536	341	361	0.1607	0.2700	0.1697	-0.2676	0.0630	0.0881
M5005_Spy0274	*braB*		1212	1389	0.1601	0.2718	0.1705	0.0928	0.5258	0.3483
M5005_Spy1592	-	spy1873	1433	1504	0.1596	0.2733	0.1709	-0.0142	0.9231	0.4808
M5005_Spy0758	*lplB*	spy1033	926	997	0.1594	0.2739	0.1712	-0.1431	0.3267	0.2605
M5005_Spy1322	-	spyM18_1618	2478	2551	0.159	0.2751	0.1718	0.0324	0.8253	0.4514
M5005_Spy1630	*salB*	spy1914	2577	2604	0.159	0.2751	0.1718	0.0857	0.5584	0.3597
M5005_Spy0093	-	spy0108	405	556	0.1581	0.2779	0.1728	0.0084	0.9544	0.4874
M5005_Spy0538	*asnS*		1006	828	0.1573	0.2803	0.1739	-0.0354	0.8092	0.4461

M5005_Spy#	Gene	Synonym *	WT Transcript Rank †	Mutant Transcript Rank †	*r* Correlation (*covR*) ‡	*P*-value Correlation (*covR*)	*Q*-value Correlation (*covR*) §	*r* Correlation (*covS*) ‡	*P*-value Correlation (*covS*)	*Q*-value Correlation (*covS*) §
M5005_Spy1123	*nrdE.2*	spy1375	729	745	0.1572	0.2808	0.1741	0.0525	0.7202	0.4184
M5005_Spy0198	-	spy0233	2309	1643	0.1567	0.2823	0.1747	0.4017	0.0042	0.0170
M5005_Spy0439	*smc*	spy0532	1029	731	0.1555	0.2861	0.1769	0.2170	0.1342	0.1445
M5005_Spy1323	-	spy1610	2196	2135	0.1554	0.2863	0.1769	0.0700	0.6325	0.3871
M5005_Spy0386	*phoH*	spy0471	1222	975	0.1553	0.2866	0.1770	0.6204	2.0E-06	**0.0055**
M5005_Spy0332	-	spy0401	1162	948	0.1546	0.2890	0.1783	0.1435	0.3254	0.2601
M5005_Spy1598	-	spy1879	1652	1559	0.1542	0.2902	0.1790	0.0479	0.7436	0.4262
M5005_Spy0252	*oppD*	spy0296	473	476	0.1536	0.2920	0.1793	0.0291	0.8429	0.4563
M5005_Spy1744	-	spy2051	1611	1512	0.1535	0.2924	0.1794	0.2121	0.1434	0.1512
M5005_Spy0123	-	spy0145	2060	1838	0.1526	0.2953	0.1804	0.0726	0.6201	0.3817
M5005_Spy0084	*rpoC*	spy0099	70	90	0.1525	0.2954	0.1804	0.0262	0.8580	0.4607
M5005_Spy0207	*fasX*	spy0246	553	717	0.1525	0.2955	0.1804	-0.0052	0.9717	0.4920
M5005_Spy0045	*rplD*	spy0050	311	374	0.1523	0.2960	0.1806	0.0907	0.5354	0.3518
M5005_Spy1846	-	spy2195	780	782	0.1522	0.2966	0.1806	0.0751	0.6082	0.3787
M5005_Spy1432	-		2369	2502	0.1514	0.2992	0.1819	-0.0286	0.8455	0.4571
M5005_Spy0463	-		927	942	0.1504	0.3023	0.1831	0.2182	0.1319	0.1428
M5005_Spy1616	*thiD*	spy1901	725	848	0.1504	0.3022	0.1831	-0.2154	0.1371	0.1468
M5005_Spy0427	*thrS*	spy0517	837	550	0.1502	0.3028	0.1832	0.2741	0.0567	0.0821
M5005_Spy1514	-	spy1780	690	990	0.1491	0.3064	0.1851	-0.2170	0.1342	0.1445
M5005_Spy0203	*gltX*	spy0239	777	946	0.1488	0.3076	0.1856	0.1260	0.3884	0.2891
M5005_Spy0202	-	spy0238	1265	1236	0.1487	0.3080	0.1857	0.1896	0.1919	0.1821
M5005_Spy0438	*acpA*	spy0531	2216	2274	0.1485	0.3086	0.1859	0.2125	0.1428	0.1510
M5005_Spy0296	-	spy0352	679	802	0.148	0.3102	0.1867	-0.0180	0.9022	0.4751
M5005_Spy0882	-	spy1161	1767	1985	0.1477	0.3111	0.1869	-0.0656	0.6542	0.3944
M5005_Spy1769	*ahpF*	spy2080	140	243	0.1477	0.3112	0.1869	-0.0325	0.8245	0.4512
M5005_Spy0714	-	spy0912	1517	2041	0.1476	0.3115	0.1869	0.2690	0.0616	0.0871
M5005_Spy1720	*mga*	spy2019	428	570	0.1476	0.3115	0.1869	0.0899	0.5392	0.3533
M5005_Spy1174	-	spy1442	2105	2384	0.147	0.3134	0.1878	0.1723	0.2364	0.2097
M5005_Spy1474	*lytR*		2651	2583	0.1463	0.3158	0.1889	0.0290	0.8430	0.4563
M5005_Spy1700	-	spy1994	2615	2547	0.1459	0.3171	0.1895	0.0919	0.5300	0.3502
M5005_Spy0643	*carB*	spy0835	842	885	0.1458	0.3176	0.1896	-0.0713	0.6264	0.3844
M5005_Spy0755	*acoL, pdhD*	spy1031	174	193	0.1457	0.3177	0.1896	0.1216	0.4054	0.2984

M5005_Spy#	Gene	Synonym *	WT Transcript Rank †	Mutant Transcript Rank †	*r* Correlation (*covR*) ‡	*P*-value Correlation (*covR*)	*Q*-value Correlation (*covR*) §	*r* Correlation (*covS*) ‡	*P*-value Correlation (*covS*)	*Q*-value Correlation (*covS*) §
M5005_Spy0523	-	spy0634	2071	1690	0.1456	0.3181	0.1898	0.1954	0.1786	0.1737
M5005_Spy0050	*rpsC*	spy0056	153	188	0.1453	0.3193	0.1902	0.1269	0.3850	0.2876
M5005_Spy1529	*shp*	spy1796	1942	1586	0.1446	0.3215	0.1911	-0.2145	0.1389	0.1481
M5005_Spy1336	*pppL, stp1*	spy1626	285	373	0.1444	0.3223	0.1912	0.1732	0.2341	0.2083
M5005_Spy0404	-	M12_0889	1050	1385	0.1441	0.3232	0.1916	0.1001	0.4937	0.3340
M5005_Spy1364	-		977	877	0.144	0.3235	0.1916	0.1471	0.3132	0.2528
M5005_Spy1802	*ruvA*	spy2119	858	836	0.144	0.3234	0.1916	0.1130	0.4395	0.3118
M5005_Spy0586	*endA*	spy0766	1569	1455	0.1439	0.3240	0.1918	0.2406	0.0959	0.1146
M5005_Spy0711	*parE*	spy0909	1199	1057	0.1434	0.3255	0.1923	0.0161	0.9126	0.4773
M5005_Spy0581	*atpD*	spy0760	723	617	0.1423	0.3295	0.1942	0.1674	0.2502	0.2181
M5005_Spy0941	-	spy1226	261	316	0.1418	0.3312	0.1948	-0.0904	0.5369	0.3521
M5005_Spy1273	*arcB*	spy1544	135	81	0.1415	0.3323	0.1952	0.0634	0.6652	0.3986
M5005_Spy0223	-	spy0263	225	273	0.141	0.3337	0.1957	-0.0179	0.9028	0.4751
M5005_Spy0381	-	spy0464	1305	1541	0.1397	0.3384	0.1977	0.3233	0.0235	0.0485
M5005_Spy0213	-	spy0252	855	567	0.1393	0.3398	0.1984	0.1553	0.2867	0.2368
M5005_Spy0060	*rplR*	spy0067	42	56	0.1391	0.3406	0.1988	0.3374	0.0177	0.0414
M5005_Spy0665	-	M12_1091	2614	2419	0.1389	0.3411	0.1989	-0.0038	0.9795	0.4935
M5005_Spy0577	*atpF*	spy0756	1126	1015	0.1385	0.3427	0.1996	0.0178	0.9033	0.4751
M5005_Spy0003	-	spy0004	1524	1509	0.1382	0.3436	0.2001	-0.1395	0.3390	0.2663
M5005_Spy0407	*mutR*	spy0496	1968	1870	0.1381	0.3440	0.2002	0.0104	0.9434	0.4849
M5005_Spy1225	-	spy1493	478	447	0.138	0.3444	0.2003	0.0386	0.7926	0.4424
M5005_Spy0018	*prsA.2*	spy0020	735	703	0.1379	0.3445	0.2003	0.0223	0.8791	0.4669
M5005_Spy1180	-	spy1450	2625	2527	0.1368	0.3486	0.2022	0.0515	0.7255	0.4198
M5005_Spy1701	*flaR*	spy1995	1934	1379	0.1362	0.3507	0.2030	-0.3021	0.0349	0.0620
M5005_Spy0941	-	spy1227	270	297	0.1357	0.3526	0.2035	0.1035	0.4791	0.3284
M5005_Spy1677	-		2213	2169	0.1344	0.3573	0.2058	0.0550	0.7073	0.4146
M5005_Spy0869	-	spy1147	588	561	0.1328	0.3631	0.2085	-0.0598	0.6830	0.4058
M5005_Spy0502	-	spy0604	300	370	0.1321	0.3656	0.2093	0.0817	0.5767	0.3662
M5005_Spy1350	-	spy1643	136	163	0.1321	0.3657	0.2093	0.0158	0.9144	0.4779
M5005_Spy1647	*rplM*	spy1932	166	288	0.132	0.3659	0.2093	-0.0656	0.6544	0.3944
M5005_Spy0796	*rplL*	spy1073	979	985	0.1317	0.3670	0.2098	0.1984	0.1717	0.1689
M5005_Spy0353	-	spy0432	914	1096	0.1316	0.3675	0.2100	-0.0196	0.8936	0.4715

M5005_Spy#	Gene	Synonym *	WT Transcript Rank †	Mutant Transcript Rank †	*r* Correlation (*covR*) ‡	*P*-value Correlation (*covR*)	*Q*-value Correlation (*covR*) §	*r* Correlation (*covS*) ‡	*P*-value Correlation (*covS*)	*Q*-value Correlation (*covS*) §
M5005_Spy0718	-	spy0916	974	1179	0.1312	0.3689	0.2105	0.3661	0.0097	0.0291
M5005_Spy0133	*ntpD*	spy0157	1493	1334	0.131	0.3697	0.2108	-0.0349	0.8121	0.4468
M5005_Spy1246	-	spy1516	748	818	0.1295	0.3753	0.2132	-0.2355	0.1033	0.1205
M5005_Spy1006	-		2436	2213	0.1293	0.3759	0.2134	0.1431	0.3265	0.2605
M5005_Spy0130	*msmRL*	spyM18_0148	1469	1316	0.129	0.3769	0.2139	0.2772	0.0538	0.0797
M5005_Spy1351	-	spy1644	181	269	0.1289	0.3775	0.2140	-0.0124	0.9324	0.4829
M5005_Spy0383	-	spy0467	1065	1012	0.1286	0.3785	0.2142	0.2225	0.1244	0.1367
M5005_Spy0391	-	spy0477	1098	992	0.1283	0.3798	0.2147	-0.0909	0.5344	0.3516
M5005_Spy1324	-	spyM18_1621	17	19	0.1278	0.3816	0.2153	0.1267	0.3858	0.2879
M5005_Spy0690	-	spyM18_0945	1339	1428	0.1273	0.3835	0.2162	0.1705	0.2416	0.2124
M5005_Spy1258	-	spy1530	1352	1253	0.1272	0.3837	0.2162	0.1250	0.3920	0.2912
M5005_Spy0534	*bsaA*	spyM18_0709	736	697	0.1251	0.3917	0.2194	0.3462	0.0148	0.0379
M5005_Spy1321	-	spy1608	377	415	0.1251	0.3916	0.2194	0.0705	0.6301	0.3863
M5005_Spy0909	*oadA*	spy1191	2129	1871	0.1245	0.3942	0.2204	0.2344	0.1049	0.1213
M5005_Spy1076	*glnH*	spy1315	329	387	0.1242	0.3953	0.2208	-0.0164	0.9111	0.4769
M5005_Spy0599	*dnaG*	spy0781	353	379	0.1241	0.3956	0.2208	0.1558	0.2850	0.2359
M5005_Spy1159	*recR*	spy1422	1153	1171	0.1241	0.3957	0.2208	0.1425	0.3286	0.2612
M5005_Spy0031	*purK*		1498	1613	0.1239	0.3962	0.2210	-0.0097	0.9475	0.4853
M5005_Spy0717	-	spy0915	527	679	0.1236	0.3973	0.2212	-0.0722	0.6218	0.3821
M5005_Spy0971	-	spy1260	13	16	0.1236	0.3974	0.2212	0.0930	0.5248	0.3481
M5005_Spy1686	*relA*	spy1981	506	522	0.1234	0.3984	0.2212	0.1004	0.4925	0.3338
M5005_Spy0380	*rrf*	spy0463	675	742	0.1233	0.3985	0.2212	0.0527	0.7190	0.4183
M5005_Spy0837	-	spy1114	1150	966	0.1233	0.3987	0.2212	0.0559	0.7028	0.4126
M5005_Spy1176	-		2049	2377	0.1225	0.4017	0.2219	0.1829	0.2085	0.1911
M5005_Spy0269	-	spy0316	594	523	0.1224	0.4020	0.2219	-0.0669	0.6477	0.3920
M5005_Spy1349	*luxS*	spy1642	836	815	0.1222	0.4028	0.2219	-0.0784	0.5923	0.3724
M5005_Spy0974	-	spy1263	52	93	0.1221	0.4033	0.2220	0.0085	0.9539	0.4874
M5005_Spy0482	-	spy0581	1593	1464	0.1214	0.4060	0.2234	0.2283	0.1146	0.1283
M5005_Spy0809	*srtE*	spy1086	2157	1898	0.1211	0.4070	0.2234	0.1404	0.3359	0.2649
M5005_Spy0939	-	spy1225	403	494	0.1211	0.4071	0.2234	0.2777	0.0533	0.0793
M5005_Spy0613	-	spy0798	1268	1248	0.1209	0.4079	0.2237	0.0149	0.9190	0.4794
M5005_Spy1083	-	SpyM3_1004	1893	1703	0.1197	0.4127	0.2257	0.2519	0.0807	0.1029

M5005_Spy#	Gene	Synonym *	WT Transcript Rank †	Mutant Transcript Rank †	*r* Correlation (*covR*) ‡	*P*-value Correlation (*covR*)	*Q*-value Correlation (*covR*) §	*r* Correlation (*covS*) ‡	*P*-value Correlation (*covS*)	*Q*-value Correlation (*covS*) §
M5005_Spy0369	*mtsB*	spy0454	477	448	0.1192	0.4146	0.2264	0.0140	0.9241	0.4809
M5005_Spy0441	*aroE.2*	spy0534	1834	1748	0.1192	0.4148	0.2264	0.3005	0.0359	0.0624
M5005_Spy1546	*nusB*		2116	1966	0.1187	0.4166	0.2272	0.2446	0.0903	0.1096
M5005_Spy1680	*pulA*	spy1972	1257	796	0.1186	0.4172	0.2273	-0.0347	0.8128	0.4468
M5005_Spy0791	*uvrC*	spy1068	173	206	0.1175	0.4212	0.2291	0.0290	0.8432	0.4563
M5005_Spy1440	-		2374	2220	0.1172	0.4224	0.2293	-0.0674	0.6452	0.3914
M5005_Spy1512	*codY*	spy1777	209	302	0.1168	0.4241	0.2299	-0.0928	0.5261	0.3483
M5005_Spy1478	-	spy1737	533	656	0.1164	0.4257	0.2306	-0.0841	0.5654	0.3620
M5005_Spy0879	-	spy1158	215	365	0.1157	0.4284	0.2318	-0.1309	0.3700	0.2815
M5005_Spy1320	-	spy1607	1570	1636	0.1155	0.4294	0.2319	-0.2280	0.1150	0.1285
M5005_Spy1188	-	spy1459	2430	1560	0.1152	0.4308	0.2321	-0.0366	0.8026	0.4442
M5005_Spy1347	-	spy1640	2061	2350	0.1149	0.4318	0.2323	-0.0632	0.6662	0.3989
M5005_Spy0089	-	spy0104	1901	1650	0.1147	0.4327	0.2327	-0.0267	0.8556	0.4603
M5005_Spy0199	-	spy0235	902	1036	0.1146	0.4329	0.2327	0.3583	0.0115	0.0320
M5005_Spy1190	-	SpyM3_1118	2643	2582	0.1144	0.4337	0.2328	0.2153	0.1374	0.1469
M5005_Spy0216	-		1722	1629	0.1139	0.4359	0.2334	0.0668	0.6484	0.3923
M5005_Spy1264	-	spy1535	1271	1388	0.1134	0.4380	0.2341	0.1901	0.1908	0.1821
M5005_Spy0871	-	spy1149	524	609	0.1124	0.4421	0.2358	0.2919	0.0418	0.0673
M5005_Spy1525	-	spy1793	2333	1632	0.112	0.4438	0.2364	-0.0923	0.5281	0.3492
M5005_Spy0513	-	spy0619	988	1297	0.111	0.4479	0.2384	-0.2232	0.1231	0.1357
M5005_Spy1548	*comEB*	spy1823	1084	1091	0.1108	0.4486	0.2384	-0.0029	0.9843	0.4948
M5005_Spy0085	-	spy0100	249	317	0.1105	0.4496	0.2384	0.0515	0.7255	0.4198
M5005_Spy1189	-	spy1460	1209	1294	0.1105	0.4499	0.2384	0.1329	0.3628	0.2780
M5005_Spy1705	*dppB*	spy2001	1281	1468	0.1105	0.4499	0.2384	0.0592	0.6860	0.4072
M5005_Spy0486	-	spy0587	808	778	0.1103	0.4505	0.2385	0.0242	0.8691	0.4645
M5005_Spy1382	-	spy1686	45	114	0.1102	0.4511	0.2386	0.0351	0.8106	0.4467
M5005_Spy1107	*murZ*	spy1358	584	502	0.1098	0.4525	0.2392	0.1031	0.4807	0.3287
M5005_Spy0901	-	spyM18_1133	2378	2478	0.1094	0.4544	0.2396	-0.0568	0.6985	0.4115
M5005_Spy0179	-	spyM18_0196	409	456	0.1089	0.4565	0.2405	-0.1104	0.4503	0.3170
M5005_Spy0372	-		2460	2472	0.1088	0.4566	0.2405	-0.0007	0.9962	0.4982
M5005_Spy1597	-	spy1878	328	355	0.1077	0.4614	0.2421	0.0858	0.5576	0.3596
M5005_Spy0054	*rplN*	spy0061	150	194	0.1076	0.4616	0.2421	0.1287	0.3783	0.2849

M5005_Spy#	Gene	Synonym *	WT Transcript Rank †	Mutant Transcript Rank †	*r* Correlation (*covR*) ‡	*P* -value Correlation (*covR*)	*Q*- value Correlation (*covR*) §	*r* Correlation (*covS*) ‡	*P* -value Correlation (*covS*)	*Q*- value Correlation (*covS*) §
M5005_Spy0746	-	spy1019	2319	2314	0.1076	0.4619	0.2421	-0.2309	0.1105	0.1251
M5005_Spy0264	-	spy0309	787	718	0.1075	0.4622	0.2422	0.2044	0.1589	0.1610
M5005_Spy1402	*lacR.1*		2388	2553	0.1069	0.4645	0.2432	-0.0394	0.7880	0.4408
M5005_Spy0122	-	spy0144	1408	1258	0.1068	0.4652	0.2434	0.2379	0.0997	0.1173
M5005_Spy0680	-	spy0874	710	725	0.1062	0.4679	0.2447	0.0167	0.9094	0.4764
M5005_Spy1823	-	spy2169	1513	1772	0.105	0.4729	0.2471	-0.0424	0.7726	0.4357
M5005_Spy1111	-	spy1364	600	592	0.1047	0.4741	0.2477	-0.2221	0.1251	0.1369
M5005_Spy0826	*potA*	spy1102	906	759	0.1041	0.4767	0.2486	0.1472	0.3130	0.2528
M5005_Spy0914	-	spy1198	1571	1728	0.1035	0.4792	0.2496	0.1700	0.2429	0.2129
M5005_Spy1315	-	spy1602	389	461	0.1027	0.4826	0.2510	0.1409	0.3341	0.2644
M5005_Spy1205	-	SpyM3_1135	1789	1861	0.1021	0.4849	0.2519	0.0796	0.5865	0.3698
M5005_Spy0064	*secY*	spy0073	168	262	0.1015	0.4878	0.2531	-0.0314	0.8303	0.4526
M5005_Spy1524	-	spy1791	1745	1469	0.1011	0.4893	0.2535	0.1731	0.2343	0.2084
M5005_Spy0021	*acpP.2*	spy0023	1430	1352	0.101	0.4900	0.2538	0.0368	0.8018	0.4440
M5005_Spy0729	*dnaD*	spy0928	623	690	0.0997	0.4954	0.2557	0.4107	0.0034	0.0146
M5005_Spy1676	*uppS*	spy1965	216	280	0.0995	0.4964	0.2560	-0.0240	0.8700	0.4646
M5005_Spy1077	*glnQ.2*		1140	1376	0.0989	0.4990	0.2568	0.2715	0.0592	0.0852
M5005_Spy0177	-	spy0207	1735	1733	0.0982	0.5019	0.2581	0.1637	0.2612	0.2244
M5005_Spy1624	-	spyM18_1977	2210	2328	0.0977	0.5041	0.2585	-0.1035	0.4790	0.3284
M5005_Spy1465	-		1578	1793	0.0974	0.5055	0.2586	0.2100	0.1475	0.1536
M5005_Spy1543	*scrB*	spy1816	614	413	0.0968	0.5080	0.2598	0.0022	0.9881	0.4959
M5005_Spy0781	*ptsB*	spy1058	89	133	0.0968	0.5084	0.2599	0.0470	0.7485	0.4275
M5005_Spy1764	*ctsR*	spy2074	567	711	0.0962	0.5107	0.2608	-0.1531	0.2936	0.2406
M5005_Spy0911	-		2336	2630	0.0959	0.5121	0.2611	0.1610	0.2691	0.2290
M5005_Spy1213	-	SpyM3_0967	2454	2278	0.0951	0.5156	0.2623	0.1211	0.4072	0.2988
M5005_Spy0659	*apbA*		1545	2048	0.0941	0.5203	0.2642	0.2956	0.0392	0.0653
M5005_Spy0555	-	spy0729	1983	1604	0.0938	0.5216	0.2646	0.0044	0.9759	0.4926
M5005_Spy1815	*rpmF*	spy2159	108	175	0.0938	0.5216	0.2646	-0.1049	0.4734	0.3265
M5005_Spy0881	-	spy1159	350	676	0.0935	0.5228	0.2651	0.1596	0.2732	0.2308
M5005_Spy1501	-	spy1765	1949	1452	0.0931	0.5247	0.2659	-0.0774	0.5970	0.3743
M5005_Spy0767	-	spy1043	872	1010	0.0927	0.5265	0.2666	-0.1709	0.2403	0.2120
M5005_Spy1757	-	spy2065	448	650	0.0924	0.5277	0.2670	0.0906	0.5356	0.3518

M5005_Spy#	Gene	Synonym *	WT Transcript Rank †	Mutant Transcript Rank †	*r* Correlation (*covR*) ‡	*P*-value Correlation (*covR*)	*Q*-value Correlation (*covR*) §	*r* Correlation (*covS*) ‡	*P*-value Correlation (*covS*)	*Q*-value Correlation (*covS*) §
M5005_Spy0035	*ruvB*	spy0038	99	123	0.0914	0.5322	0.2684	0.0222	0.8797	0.4669
M5005_Spy0512	-	spy0617	458	462	0.0914	0.5323	0.2684	-0.0304	0.8358	0.4543
M5005_Spy1763	*clpC*	spy2073	182	210	0.09	0.5387	0.2709	0.0604	0.6801	0.4050
M5005_Spy0518	-	spy0628	2058	1934	0.0896	0.5405	0.2711	-0.0034	0.9815	0.4939
M5005_Spy0974	-	spyM18_1214	49	94	0.0894	0.5413	0.2713	0.0051	0.9724	0.4922
M5005_Spy1187	-	spy1457	2211	1363	0.0892	0.5424	0.2717	0.3590	0.0113	0.0317
M5005_Spy0589	-	spy0770	1868	1487	0.087	0.5521	0.2760	0.0525	0.7201	0.4184
M5005_Spy0759	-		2326	2005	0.0865	0.5547	0.2764	0.2971	0.0381	0.0645
M5005_Spy1080	-	spy1323	1117	899	0.0861	0.5564	0.2771	0.2299	0.1120	0.1264
M5005_Spy0452	-	spy0544	2023	1396	0.0856	0.5586	0.2781	-0.0127	0.9307	0.4829
M5005_Spy0241	*rgpG*	spy0282	721	686	0.0854	0.5597	0.2784	0.4014	0.0043	0.0171
M5005_Spy1443	-	M12_1752	2441	2459	0.0852	0.5604	0.2786	0.0447	0.7603	0.4318
M5005_Spy1116	*udk*	spy1368	1124	1215	0.0849	0.5619	0.2788	0.2533	0.0791	0.1016
M5005_Spy1616	*thiD*	spy1900	1248	1100	0.0844	0.5640	0.2794	0.0443	0.7624	0.4324
M5005_Spy1861	-	spy2210	1180	1064	0.0839	0.5663	0.2802	-0.0395	0.7876	0.4408
M5005_Spy0723	-	spy0922	467	596	0.0833	0.5692	0.2812	-0.2098	0.1480	0.1539
M5005_Spy0262	-	spy0307	1275	1069	0.0831	0.5701	0.2815	-0.0047	0.9744	0.4926
M5005_Spy0968	-	spy1258	2554	2424	0.083	0.5709	0.2816	-0.0442	0.7628	0.4324
M5005_Spy1008	-		1935	1496	0.083	0.5709	0.2816	0.0280	0.8485	0.4579
M5005_Spy0782	*ptsC*	spy1059	264	380	0.0829	0.5712	0.2817	0.0110	0.9402	0.4845
M5005_Spy0838	-	spy1115	1093	1302	0.0812	0.5790	0.2847	0.3521	0.0131	0.0350
M5005_Spy1015	-		2005	2279	0.0812	0.5791	0.2847	-0.0613	0.6755	0.4026
M5005_Spy0676	-	spyM18_0930	1286	1599	0.0801	0.5844	0.2867	0.1861	0.2005	0.1876
M5005_Spy1234	*folD*	spy1502	1397	1210	0.08	0.5846	0.2867	0.0054	0.9704	0.4919
M5005_Spy0508	*tufA*	spyM18_0678	2270	2372	0.08	0.5849	0.2867	0.2291	0.1133	0.1274
M5005_Spy0300	-	spy0357	466	572	0.0793	0.5878	0.2877	0.1034	0.4794	0.3284
M5005_Spy0088	*comYC*	spy0103	2271	2181	0.079	0.5895	0.2881	0.0683	0.6412	0.3902
M5005_Spy1232	*xseB*	spy1500	451	402	0.0775	0.5965	0.2911	0.1508	0.3011	0.2453
M5005_Spy0167	-	SpyM3_1054	495	528	0.0771	0.5984	0.2917	0.2505	0.0825	0.1038
M5005_Spy0919	*guaA*	spy1204	561	595	0.077	0.5991	0.2919	-0.1396	0.3388	0.2663
M5005_Spy1174	-	spyM18_0774	2591	2585	0.0765	0.6013	0.2926	0.0340	0.8166	0.4485
M5005_Spy0081	*tyrS*	spy0096	1888	1646	0.0761	0.6033	0.2933	-0.0354	0.8092	0.4461

M5005_Spy#	Gene	Synonym *	WT Transcript Rank †	Mutant Transcript Rank †	*r* Correlation (*covR*) ‡	*P*-value Correlation (*covR*)	*Q*-value Correlation (*covR*) §	*r* Correlation (*covS*) ‡	*P*-value Correlation (*covS*)	*Q*-value Correlation (*covS*) §
M5005_Spy0896	-	spy1176	1733	1769	0.0758	0.6047	0.2939	0.0748	0.6096	0.3790
M5005_Spy1742	*mipB*		2578	2544	0.0749	0.6092	0.2950	0.3214	0.0243	0.0495
M5005_Spy1850	-	spy2199	1367	1143	0.0749	0.6090	0.2950	-0.0508	0.7287	0.4209
M5005_Spy0727	*recJ*	spy0926	540	581	0.0748	0.6094	0.2950	0.0626	0.6690	0.4000
M5005_Spy1256	-	spy1528	1374	1290	0.0745	0.6111	0.2956	0.1879	0.1960	0.1846
M5005_Spy0889	-	spy1169	2288	2634	0.0719	0.6234	0.2997	0.0741	0.6129	0.3800
M5005_Spy1348	-	spy1641	1425	1542	0.0718	0.6240	0.2998	0.1669	0.2518	0.2184
M5005_Spy0765	*hemN, hemC*	spy1040	1785	1426	0.0707	0.6292	0.3016	0.0163	0.9115	0.4770
M5005_Spy1361	*aapA*	spy1654	2026	1824	0.0698	0.6337	0.3029	-0.0048	0.9740	0.4926
M5005_Spy0785	*yesN*	spy1062	1020	1220	0.069	0.6375	0.3040	-0.0456	0.7557	0.4300
M5005_Spy0855	*proV*	spy1134	499	480	0.0687	0.6390	0.3043	0.0956	0.5134	0.3429
M5005_Spy0610	-	spy0794	991	1203	0.0681	0.6421	0.3052	0.4789	5.00E-04	**0.0062**
M5005_Spy0015	-	M12_0138	2645	2571	0.0669	0.6477	0.3068	-0.0373	0.7990	0.4436
M5005_Spy0114	-	spy0135	2396	2267	0.0669	0.6478	0.3068	-0.0675	0.6452	0.3914
M5005_Spy0499	-	spy0600	1375	1018	0.0669	0.6478	0.3068	0.1009	0.4902	0.3326
M5005_Spy1842	*sdhA*	spy2190	1049	1110	0.0662	0.6512	0.3078	0.0665	0.6500	0.3931
M5005_Spy0344	-	spy0421	1929	2322	0.0652	0.6560	0.3095	0.0445	0.7616	0.4322
M5005_Spy0168	-		1021	988	0.0651	0.6568	0.3098	0.4080	0.0036	0.0153
M5005_Spy1126	-	spyM18_1348	2226	1725	0.0647	0.6586	0.3103	0.2036	0.1605	0.1615
M5005_Spy1044	-	spyM18_1804	2161	2541	0.0634	0.6650	0.3126	-0.2651	0.0657	0.0903
M5005_Spy1710	-	spy2006	66	58	0.0632	0.6663	0.3131	0.0146	0.9206	0.4800
M5005_Spy1274	-		1750	1705	0.0627	0.6687	0.3140	0.2043	0.1591	0.1611
M5005_Spy1009	-		2260	1804	0.0625	0.6699	0.3143	-0.0257	0.8608	0.4612
M5005_Spy1452	-		2243	1842	0.0624	0.6699	0.3143	0.1597	0.2732	0.2308
M5005_Spy1503	-	spyM18_1836	2373	2558	0.062	0.6720	0.3148	0.1019	0.4860	0.3306
M5005_Spy0276	-	spy0326	1062	830	0.0613	0.6756	0.3159	0.1765	0.2251	0.2033
M5005_Spy1184	-	spy1454	2264	2286	0.0609	0.6778	0.3161	-0.1002	0.4932	0.3340
M5005_Spy1334	-	spy1623	1988	1578	0.0609	0.6778	0.3161	0.0100	0.9459	0.4850
M5005_Spy1450	-		1984	2632	0.0609	0.6779	0.3161	0.0012	0.9934	0.4975
M5005_Spy0991	-	spy1285	895	1122	0.0605	0.6798	0.3166	0.0123	0.9332	0.4830
M5005_Spy1205	-		2285	2360	0.0601	0.6816	0.3173	-0.0213	0.8844	0.4690
M5005_Spy1477	-	spy1736	1650	1458	0.0595	0.6848	0.3180	0.3102	0.0301	0.0562

M5005_Spy#	Gene	Synonym *	WT Transcript Rank †	Mutant Transcript Rank †	*r* Correlation (*covR*) ‡	*P*-value Correlation (*covR*)	*Q*-value Correlation (*covR*) §	*r* Correlation (*covS*) ‡	*P*-value Correlation (*covS*)	*Q*-value Correlation (*covS*) §
M5005_Spy0305	-	spy0363	718	800	0.0585	0.6896	0.3196	-0.1576	0.2796	0.2334
M5005_Spy1050	-	spyM18_1306	1393	1268	0.0583	0.6906	0.3198	-0.0267	0.8557	0.4603
M5005_Spy0353	-	spy0431	1606	1480	0.0579	0.6928	0.3202	0.0292	0.8424	0.4563
M5005_Spy0322	*fhuB*	spy0383	2172	1714	0.0577	0.6939	0.3205	0.0813	0.5787	0.3669
M5005_Spy0191	-		1803	1519	0.0574	0.6954	0.3205	-0.0928	0.5259	0.3483
M5005_Spy0630	*nifS, yrvO*	spy0816	1078	1134	0.0574	0.6952	0.3205	-0.1211	0.4074	0.2988
M5005_Spy1450	-		1856	1867	0.0558	0.7033	0.3230	-0.0813	0.5786	0.3669
M5005_Spy1287	-	spy1562	1171	852	0.0554	0.7053	0.3237	0.0528	0.7188	0.4183
M5005_Spy1563	-	spy1840	1660	1658	0.055	0.7073	0.3240	0.0290	0.8432	0.4563
M5005_Spy0201	-	spy0237	1057	1291	0.0539	0.7132	0.3259	-0.1589	0.2755	0.2315
M5005_Spy1816	*rpmG*	spyM18_2197	292	392	0.0539	0.7132	0.3259	-0.1168	0.4240	0.3054
M5005_Spy1009	-		2603	2647	0.0537	0.7140	0.3261	0.1166	0.4250	0.3057
M5005_Spy0096	*proC*	spy0112	361	513	0.0536	0.7145	0.3262	-0.1747	0.2299	0.2061
M5005_Spy1365	-	spy1659	1219	1004	0.0534	0.7157	0.3266	-0.0906	0.5357	0.3518
M5005_Spy0734	*cpsFO*	spy0933	444	450	0.0529	0.7179	0.3272	0.0368	0.8016	0.4440
M5005_Spy0918	-	spy1203	1195	1232	0.0528	0.7187	0.3274	-0.2647	0.0661	0.0906
M5005_Spy0079	*adcB*	spy0094	262	364	0.0526	0.7197	0.3276	-0.0308	0.8336	0.4535
M5005_Spy1826	-	spy2173	1542	1301	0.0525	0.7199	0.3276	0.0068	0.9632	0.4894
M5005_Spy0049	*rplV*	spy0055	474	605	0.0523	0.7211	0.3276	-0.0498	0.7341	0.4237
M5005_Spy1102	-	spy1353	696	786	0.0521	0.7220	0.3278	0.1977	0.1733	0.1700
M5005_Spy0664	*mur1.2*	spy0857	206	395	0.0515	0.7251	0.3288	-0.0931	0.5245	0.3481
M5005_Spy1412	*nusA*	spy1724	220	220	0.0513	0.7261	0.3289	-0.1036	0.4787	0.3284
M5005_Spy1864	-	spy2215	2169	2026	0.0513	0.7262	0.3289	-0.0320	0.8274	0.4521
M5005_Spy1740	-	spy2045	918	933	0.051	0.7279	0.3294	-0.1459	0.3173	0.2555
M5005_Spy0646	-	spy0838	1330	1329	0.0505	0.7302	0.3300	-0.2675	0.0632	0.0881
M5005_Spy0503	-	spyM18_0672	1235	1296	0.0503	0.7315	0.3304	-0.0849	0.5621	0.3609
M5005_Spy1166	-	spyM18_1442	253	289	0.0488	0.7391	0.3332	0.0822	0.5744	0.3655
M5005_Spy0136	*purA*	spy0160	582	483	0.0481	0.7429	0.3345	-0.1623	0.2652	0.2270
M5005_Spy1584	-		1964	1995	0.0477	0.7449	0.3350	0.0497	0.7346	0.4238
M5005_Spy1650	-	spy1936	1708	1602	0.0474	0.7465	0.3353	-0.1524	0.2959	0.2423
M5005_Spy0834	-	spy1111	1541	1407	0.0468	0.7497	0.3359	0.1408	0.3347	0.2644
M5005_Spy1622	*hsdS*	spy1905	1784	1771	0.0466	0.7504	0.3359	-0.0396	0.7873	0.4408

M5005_Spy#	Gene	Synonym *	WT Transcript Rank †	Mutant Transcript Rank †	*r* Correlation (*covR*) ‡	*P* -value Correlation (*covR*)	*Q-* value Correlation (*covR*) §	*r* Correlation (*covS*) ‡	*P* -value Correlation (*covS*)	*Q-* value Correlation (*covS*) §
M5005_Spy0333	-	spyM18_0453	1985	2259	0.0464	0.7517	0.3363	0.2166	0.1349	0.1450
M5005_Spy0400	*silD*	spyM18_0547	1715	1899	0.046	0.7538	0.3369	0.0115	0.9374	0.4837
M5005_Spy1657	-	spyM18_2010	2429	2244	0.0458	0.7549	0.3371	-0.2495	0.0839	0.1048
M5005_Spy1682	*msmK*		2266	2199	0.0458	0.7546	0.3371	0.2188	0.1309	0.1421
M5005_Spy0077	*adcR*	spy0092	83	105	0.0447	0.7602	0.3385	0.0895	0.5408	0.3536
M5005_Spy1629	*salX*	spy1912	1539	1453	0.0447	0.7603	0.3385	-0.1182	0.4185	0.3034
M5005_Spy0998	-	SpyM3_1303	2588	2361	0.0445	0.7613	0.3386	0.0904	0.5366	0.3521
M5005_Spy0353	-	SpyM3_0306	1456	1515	0.0438	0.7653	0.3397	-0.0952	0.5153	0.3438
M5005_Spy0430	-	spy0521	2308	2293	0.0438	0.7650	0.3397	0.1583	0.2775	0.2326
M5005_Spy1784	-		2459	2483	0.0429	0.7699	0.3412	-0.1900	0.1909	0.1821
M5005_Spy1054	-	spy1290	1729	1550	0.0428	0.7703	0.3412	0.0982	0.5020	0.3377
M5005_Spy1791	-		2452	2426	0.0422	0.7732	0.3424	-0.2127	0.1423	0.1509
M5005_Spy0878	-	spy1157	5	14	0.0418	0.7754	0.3431	0.0007	0.9963	0.4982
M5005_Spy1098	-	spy1346	1189	1192	0.0416	0.7766	0.3434	0.2095	0.1485	0.1541
M5005_Spy1254	-	spy1526	1194	1119	0.0412	0.7785	0.3439	0.4593	9.01E-04	**0.0071**
M5005_Spy0234	-	spyM18_0262	1406	1339	0.0398	0.7860	0.3465	0.0926	0.5269	0.3486
M5005_Spy1506	*gatB*	spy1770	753	625	0.0397	0.7864	0.3465	-0.0680	0.6423	0.3905
M5005_Spy1856	-	spy2205	148	233	0.0392	0.7893	0.3472	-0.0630	0.6670	0.3992
M5005_Spy0575	*atpE*	SpyM3_0493	1457	1695	0.0372	0.7999	0.3504	0.1701	0.2425	0.2128
M5005_Spy0808	*srtF*	spy1085	1780	1449	0.0372	0.7997	0.3504	0.0755	0.6060	0.3777
M5005_Spy0602	*rmlD*		1687	1859	0.037	0.8007	0.3505	-0.1305	0.3713	0.2817
M5005_Spy1780	*rpsB*	spy2092	279	396	0.037	0.8006	0.3505	-0.2265	0.1176	0.1309
M5005_Spy0904	-	spyM18_1136	2529	1892	0.036	0.8062	0.3525	-0.1300	0.3734	0.2829
M5005_Spy1077	*glnQ.2*	spy1316	459	557	0.0357	0.8078	0.3529	-0.0373	0.7991	0.4436
M5005_Spy0058	*rpsH*	spy0065	378	597	0.0355	0.8084	0.3530	0.0687	0.6389	0.3895
M5005_Spy0159	*polA*	spy0185	1496	1582	0.0352	0.8104	0.3537	0.0079	0.9572	0.4882
M5005_Spy1495	-	spy1755	514	706	0.0348	0.8126	0.3545	0.0206	0.8883	0.4698
M5005_Spy0090	-	spy0105	1966	2533	0.0345	0.8141	0.3551	0.2248	0.1205	0.1334
M5005_Spy0094	*ackA*	spy0109	570	683	0.0333	0.8201	0.3568	0.0403	0.7834	0.4393
M5005_Spy1420	-	spy0999	2078	2081	0.0333	0.8201	0.3568	0.0071	0.9616	0.4894
M5005_Spy0345	*metS*	spy0422	821	854	0.0331	0.8212	0.3570	-0.2629	0.0680	0.0922
M5005_Spy1741	*gldA*	spy2047	542	552	0.0328	0.8227	0.3575	0.0959	0.5121	0.3427

M5005_Spy#	Gene	Synonym *	WT Transcript Rank †	Mutant Transcript Rank †	*r* Correlation (*covR*) ‡	*P* -value Correlation (*covR*)	*Q*- value Correlation (*covR*) §	*r* Correlation (*covS*) ‡	*P* -value Correlation (*covS*)	*Q*- value Correlation (*covS*) §
M5005_Spy1486	*accC*	spy1745	1063	915	0.0319	0.8278	0.3591	-0.1164	0.4256	0.3058
M5005_Spy1192	-	spy1463	713	791	0.0308	0.8336	0.3614	-0.0733	0.6165	0.3813
M5005_Spy0754	-		2380	2463	0.0298	0.8389	0.3632	-0.0075	0.9595	0.4888
M5005_Spy1173	-	spyM18_1247	2597	2115	0.0296	0.8398	0.3633	-0.2348	0.1045	0.1212
M5005_Spy0783	*ptsD*	spy1060	200	261	0.029	0.8431	0.3643	0.0866	0.5541	0.3582
M5005_Spy1399	-		2543	2205	0.0285	0.8461	0.3654	-0.0726	0.6199	0.3817
M5005_Spy1115	-	spy1367	2561	2319	0.0281	0.8481	0.3659	0.0659	0.6526	0.3941
M5005_Spy1098	-		708	735	0.028	0.8483	0.3659	0.0319	0.8275	0.4521
M5005_Spy0173	-	spy0201	904	871	0.0275	0.8511	0.3667	-0.1413	0.3328	0.2638
M5005_Spy1096	-	spy1344	1249	1224	0.0271	0.8534	0.3674	0.0315	0.8297	0.4526
M5005_Spy1124	*nrdF.2*	spy1378	587	770	0.0248	0.8656	0.3708	-0.1409	0.3344	0.2644
M5005_Spy1562	-	spy1839	1080	1078	0.0242	0.8689	0.3714	-0.2537	0.0785	0.1011
M5005_Spy1208	-	spyM18_1498	1347	1736	0.0241	0.8693	0.3714	0.2386	0.0987	0.1168
M5005_Spy1784	-	spy2097	1060	1218	0.0236	0.8721	0.3725	-0.1690	0.2458	0.2149
M5005_Spy1824	-	spy2170	1657	1493	0.0234	0.8734	0.3726	0.2973	0.0381	0.0644
M5005_Spy1074	-	SpyM3_0995	866	670	0.0233	0.8736	0.3726	0.1764	0.2252	0.2033
M5005_Spy1474	*lytR*	spy1733	884	1044	0.0224	0.8788	0.3742	-0.0404	0.7831	0.4393
M5005_Spy0224	*rpe*	spy0264	420	491	0.0217	0.8821	0.3750	0.0884	0.5456	0.3552
M5005_Spy1060	*malG*	spy1296	2206	1417	0.0211	0.8858	0.3756	-0.0462	0.7526	0.4288
M5005_Spy1295	-	spy1571	1331	1251	0.0208	0.8870	0.3760	-0.1086	0.4576	0.3195
M5005_Spy1462	-		2449	2570	0.0207	0.8880	0.3762	-0.0279	0.8488	0.4579
M5005_Spy1507	*gatA*	spy1771	715	747	0.0206	0.8885	0.3762	0.0437	0.7654	0.4331
M5005_Spy0916	*ylxM*	spy1201	1303	1114	0.0201	0.8909	0.3769	0.3037	0.0339	0.0608
M5005_Spy0982	-	spy1274	691	869	0.0187	0.8984	0.3792	0.2027	0.1625	0.1628
M5005_Spy1123	-		838	1105	0.0187	0.8987	0.3792	-0.0618	0.6732	0.4017
M5005_Spy0400	*silD*	SpyM3_0341	1607	1494	0.0183	0.9008	0.3797	-0.2699	0.0607	0.0866
M5005_Spy1570	-	spy1850	1108	1058	0.0179	0.9027	0.3802	0.2161	0.1358	0.1458
M5005_Spy1439	-		2327	2295	0.0174	0.9056	0.3812	-0.0696	0.6349	0.3883
M5005_Spy1366	*mraY*	spy1662	411	391	0.0173	0.9061	0.3812	0.0233	0.8735	0.4654
M5005_Spy0309	-	spy0367	1213	1225	0.017	0.9078	0.3818	-0.0836	0.5680	0.3629
M5005_Spy1592	-	spy1872	315	508	0.0169	0.9083	0.3818	0.0485	0.7405	0.4252
M5005_Spy0638	-	spy0827	609	767	0.0162	0.9121	0.3828	-0.0817	0.5769	0.3662

M5005_Spy#	Gene	Synonym *	WT Transcript Rank †	Mutant Transcript Rank †	*r* Correlation (*covR*) ‡	*P*-value Correlation (*covR*)	*Q*-value Correlation (*covR*) §	*r* Correlation (*covS*) ‡	*P*-value Correlation (*covS*)	*Q*-value Correlation (*covS*) §
M5005_Spy1736	-	spy2041	2063	2593	0.0162	0.9123	0.3828	-0.1570	0.2813	0.2339
M5005_Spy1444	-		2426	1765	0.0161	0.9127	0.3828	0.0053	0.9713	0.4920
M5005_Spy1487	*fabZ*	spy1746	1827	1539	0.0152	0.9176	0.3843	-0.2121	0.1434	0.1512
M5005_Spy0552	-		1793	1949	0.015	0.9187	0.3845	-0.1197	0.4127	0.3003
M5005_Spy1088	*obg*		1552	2051	0.0148	0.9195	0.3846	-0.0224	0.8783	0.4669
M5005_Spy1280	*zmpR*		1488	1759	0.014	0.9242	0.3860	-0.2518	0.0809	0.1029
M5005_Spy0126	*ntpI*	spy0148	1094	845	0.0137	0.9254	0.3863	-0.0198	0.8923	0.4712
M5005_Spy1480	*manM*	spy1739	653	754	0.0122	0.9336	0.3887	-0.2704	0.0602	0.0861
M5005_Spy1494	*fabH*	spy1754	649	932	0.0122	0.9339	0.3887	-0.2186	0.1313	0.1424
M5005_Spy1370	*proA*	spy1670	1866	2194	0.0118	0.9358	0.3890	0.0339	0.8174	0.4487
M5005_Spy1583	-	spy1865	711	680	0.0109	0.9406	0.3901	0.1230	0.3999	0.2955
M5005_Spy1155	*prfC*	SpyM3_1081	1970	1661	0.0107	0.9420	0.3904	-0.1857	0.2014	0.1879
M5005_Spy0008	*divIC*	spy0009	1557	1617	0.0104	0.9433	0.3907	0.0579	0.6930	0.4097
M5005_Spy1816	*rpmG*	spy2160	244	352	0.0101	0.9451	0.3910	-0.1067	0.4658	0.3231
M5005_Spy1694	-	spy1987	493	781	0.01	0.9454	0.3910	-0.1169	0.4239	0.3054
M5005_Spy0884	*smf*	spy1163	2015	1621	0.0099	0.9459	0.3910	0.2757	0.0552	0.0808
M5005_Spy0035	-		2123	2074	0.0098	0.9468	0.3910	-0.0191	0.8963	0.4724
M5005_Spy1002	-		2045	1865	0.0098	0.9470	0.3910	-0.2093	0.1490	0.1543
M5005_Spy1724	*ihk*	spy2026	196	338	0.0098	0.9467	0.3910	-0.1431	0.3267	0.2605
M5005_Spy1231	*fps*	spy1498	626	651	0.0085	0.9538	0.3930	-0.2788	0.0524	0.0786
M5005_Spy0732	-	spy0930	1298	1404	0.0075	0.9593	0.3936	0.0999	0.4947	0.3345
M5005_Spy1765	*csp*	spy2077	40	74	0.0073	0.9602	0.3938	0.0385	0.7930	0.4425
M5005_Spy0561	*epf*		2453	2550	0.0071	0.9616	0.3942	-0.2263	0.1179	0.1311
M5005_Spy1426	-		2346	2591	0.0069	0.9626	0.3944	-0.3256	0.0225	0.0474
M5005_Spy1392	-	spy1699	1166	1345	0.0065	0.9644	0.3946	0.2394	0.0976	0.1160
M5005_Spy0205	*fasC*		2493	1963	0.0063	0.9659	0.3949	-0.0377	0.7969	0.4434
M5005_Spy0819	-	SpyM3_0757	2088	1917	0.0059	0.9680	0.3949	0.0100	0.9458	0.4850
M5005_Spy1037	-	spyM18_1796	1806	1894	0.0059	0.9678	0.3949	0.2567	0.0750	0.0983
M5005_Spy1013	-		1553	1473	0.0057	0.9687	0.3950	0.0521	0.7220	0.4189
M5005_Spy1817	*cadD*	spy2162	2242	1924	0.0052	0.9717	0.3959	0.0484	0.7412	0.4254
M5005_Spy1748	-		2041	1941	0.0043	0.9767	0.3972	-0.1541	0.2903	0.2390
M5005_Spy0615	*ebsA*	spy0801	2560	2442	0.0041	0.9778	0.3972	0.0993	0.4974	0.3358

M5005_Spy#	Gene	Synonym *	WT Transcript Rank †	Mutant Transcript Rank †	*r* Correlation (*covR*) ‡	*P*-value Correlation (*covR*)	*Q*-value Correlation (*covR*) §	*r* Correlation (*covS*) ‡	*P*-value Correlation (*covS*)	*Q*-value Correlation (*covS*) §
M5005_Spy0078	*adcC*	spy0093	162	254	0.0039	0.9787	0.3972	-0.1091	0.4556	0.3189
M5005_Spy1647	*rplM*		2107	1961	0.0039	0.9788	0.3972	0.1095	0.4539	0.3186
M5005_Spy0922	*pdxK*	spyM18_1158	1858	2480	0.0034	0.9813	0.3978	0.1966	0.1757	0.1715
M5005_Spy0227	*cbf*	spy0267	272	263	0.0024	0.9869	0.3995	0.0224	0.8786	0.4669
M5005_Spy0463	-	spyM18_0630	680	764	0.0018	0.9900	0.4002	-0.0103	0.9439	0.4849
M5005_Spy0225	-	spy0265	324	434	0.0016	0.9910	0.4003	-0.1331	0.3617	0.2775
M5005_Spy1655	*cysS*	spy1941	983	1081	0.0014	0.9922	0.4006	-0.0359	0.8065	0.4452
M5005_Spy0002	*dnaN*	spy0003	688	792	0.001	0.9945	0.4011	-0.0569	0.6979	0.4115
M5005_Spy0905	*citD*	spy1186	2376	2415	0.001	0.9946	0.4011	0.0850	0.5616	0.3608
M5005_Spy1211	-	spy0952	2011	2324	0.0009	0.9951	0.4011	-0.1245	0.3941	0.2922
M5005_Spy0212	-	spy0251	596	583	-0.002	0.9894	0.4001	-0.1316	0.3674	0.2802
M5005_Spy1721	-	#N/A	2444	2388	-0.0024	0.9871	0.3995	0.0621	0.6719	0.4012
M5005_Spy0607	*rgpEc*	spy0791	558	643	-0.0029	0.9842	0.3987	-0.0208	0.8872	0.4696
M5005_Spy1482	*manO*	spy1741	1185	1787	-0.0038	0.9796	0.3973	-0.3640	0.0101	0.0297
M5005_Spy0301	-	spy0358	429	610	-0.0042	0.9773	0.3972	0.0087	0.9526	0.4873
M5005_Spy1435	-		1836	1626	-0.0042	0.9773	0.3972	-0.0934	0.5233	0.3474
M5005_Spy1834	-	spy2181	922	1067	-0.0048	0.9741	0.3966	0.0099	0.9459	0.4850
M5005_Spy1848	-	spy2197	516	562	-0.0061	0.9669	0.3949	-0.0539	0.7132	0.4163
M5005_Spy0768	-	spy1044	1390	1354	-0.0066	0.9643	0.3946	-0.1538	0.2913	0.2396
M5005_Spy1085	*bglA.2*	spy1328	1863	1448	-0.0068	0.9628	0.3944	-0.1450	0.3201	0.2571
M5005_Spy1087	*int*	spyM18_1340	1470	1147	-0.0075	0.9590	0.3936	-0.0488	0.7392	0.4248
M5005_Spy1236	*phr*	spy1505	1649	1738	-0.0077	0.9583	0.3934	-0.1724	0.2362	0.2097
M5005_Spy1046	-	SpyM3_0972	1669	1561	-0.0078	0.9576	0.3933	-0.1383	0.3432	0.2690
M5005_Spy0017	*sibA*	spy0019	184	287	-0.0079	0.9568	0.3931	-0.1236	0.3974	0.2943
M5005_Spy0446	-	spy0539	1472	1665	-0.008	0.9563	0.3931	-0.0332	0.8207	0.4498
M5005_Spy0274	*braB*	spy0323	1310	1386	-0.008	0.9567	0.3931	-0.4505	0.0012	**0.0079**
M5005_Spy0265	-	spy0310	670	709	-0.0082	0.9556	0.3931	0.0111	0.9396	0.4845
M5005_Spy1565	*spi*	spy1842	550	545	-0.0084	0.9543	0.3930	0.0684	0.6403	0.3901
M5005_Spy0245	*nifU, yurV*	spy0289	593	531	-0.0087	0.9526	0.3928	-0.1703	0.2422	0.2128
M5005_Spy0972	-	spy1261	10	12	-0.0092	0.9498	0.3921	-0.0576	0.6941	0.4102
M5005_Spy0271	-	M12_0652	2185	2517	-0.01	0.9458	0.3910	-0.1820	0.2108	0.1929
M5005_Spy1427	-		2352	2476	-0.01	0.9458	0.3910	0.0318	0.8283	0.4521

M5005_Spy#	Gene	Synonym *	WT Transcript Rank †	Mutant Transcript Rank †	*r* Correlation (*covR*) ‡	*P*-value Correlation (*covR*)	*Q*-value Correlation (*covR*) §	*r* Correlation (*covS*) ‡	*P*-value Correlation (*covS*)	*Q*-value Correlation (*covS*) §
M5005_Spy0944	-	spy1232	676	926	-0.0106	0.9422	0.3904	-0.0109	0.9407	0.4845
M5005_Spy1344	*atoB*	spy1637	1991	1936	-0.0111	0.9398	0.3899	-0.1732	0.2339	0.2083
M5005_Spy1516	*asnB*	spy1782	1360	1307	-0.0111	0.9397	0.3899	0.1708	0.2407	0.2122
M5005_Spy0620	*rpl35*	spyM18_0867	258	325	-0.0116	0.9371	0.3892	-0.0988	0.4992	0.3365
M5005_Spy1002	-		2252	1957	-0.0116	0.9367	0.3892	0.1327	0.3634	0.2781
M5005_Spy0925	*rnhB*	spyM18_1162	1581	1472	-0.0118	0.9359	0.3890	0.0880	0.5474	0.3555
M5005_Spy1668	-	spy1957	2421	2652	-0.0121	0.9340	0.3887	0.0749	0.6089	0.3787
M5005_Spy0337	-		1051	993	-0.0126	0.9313	0.3883	0.1195	0.4136	0.3008
M5005_Spy1723	*isp*		78	136	-0.0126	0.9317	0.3883	-0.1105	0.4499	0.3169
M5005_Spy1782	*pepO*		2458	2187	-0.0127	0.9309	0.3883	0.1968	0.1754	0.1715
M5005_Spy1394	-	spy1701	548	399	-0.013	0.9295	0.3879	-0.0479	0.7436	0.4262
M5005_Spy1860	-	spy2209	1643	2151	-0.0143	0.9223	0.3853	0.0227	0.8769	0.4664
M5005_Spy1845	-	spy2193	761	984	-0.0155	0.9159	0.3837	0.1147	0.4324	0.3082
M5005_Spy0447	-	spy0540	2225	2070	-0.0164	0.9109	0.3825	0.2011	0.1659	0.1649
M5005_Spy0063	*rplO*	spy0072	56	82	-0.0168	0.9090	0.3819	0.0672	0.6463	0.3919
M5005_Spy1653	-	spy1939	1850	1340	-0.0178	0.9036	0.3804	0.2016	0.1648	0.1641
M5005_Spy1801	*tag*	spy2118	2302	1633	-0.018	0.9021	0.3801	-0.0783	0.5930	0.3725
M5005_Spy0027	-	spyM18_0030	1270	1186	-0.0188	0.8981	0.3792	-0.2158	0.1365	0.1464
M5005_Spy1578	-	spyM18_1923	1590	2291	-0.0191	0.8965	0.3788	0.0394	0.7881	0.4408
M5005_Spy0901	-	spy1181	2525	1884	-0.0195	0.8944	0.3781	-0.1057	0.4697	0.3247
M5005_Spy0268	-	spy0315	1572	1406	-0.0205	0.8886	0.3762	-0.1899	0.1912	0.1821
M5005_Spy0712	*parC*		2195	1799	-0.0214	0.8842	0.3752	-0.0685	0.6402	0.3901
M5005_Spy0787	-	spy1064	1994	2127	-0.0215	0.8837	0.3752	0.2011	0.1659	0.1649
M5005_Spy1100	*aroK*	spy1352	1142	1075	-0.0216	0.8827	0.3750	-0.4167	0.0029	0.0136
M5005_Spy0154	-	spy0180	1547	1314	-0.022	0.8808	0.3747	0.2213	0.1265	0.1381
M5005_Spy0444	-		1500	1600	-0.022	0.8806	0.3747	-0.1052	0.4718	0.3256
M5005_Spy1041	-	spyM18_1800	2176	1950	-0.0228	0.8762	0.3732	0.1852	0.2027	0.1887
M5005_Spy0080	-	spy0095	2018	1909	-0.023	0.8752	0.3729	0.2085	0.1505	0.1551
M5005_Spy1425	-		2062	2128	-0.023	0.8752	0.3729	-0.3993	0.0045	0.0177
M5005_Spy0678	-	spy0872	1113	1175	-0.0233	0.8736	0.3726	-0.2707	0.0599	0.0860
M5005_Spy0802	-	M12_1862	2273	2297	-0.0233	0.8737	0.3726	0.0105	0.9429	0.4849
M5005_Spy0498	-	spy0599	1028	793	-0.0242	0.8686	0.3714	0.3304	0.0204	0.0448

M5005_Spy#	Gene	Synonym *	WT Transcript Rank †	Mutant Transcript Rank †	*r* Correlation (*covR*) ‡	*P* -value Correlation (*covR*)	*Q*- value Correlation (*covR*) §	*r* Correlation (*covS*) ‡	*P* -value Correlation (*covS*)	*Q*- value Correlation (*covS*) §
M5005_Spy0155	-	spy0181	1156	1196	-0.0244	0.8680	0.3714	-0.0689	0.6379	0.3891
M5005_Spy0519	*agaD*	spy0630	1944	1103	-0.0244	0.8679	0.3714	0.1870	0.1982	0.1857
M5005_Spy1479	*manL*	spy1738	658	918	-0.0248	0.8658	0.3708	-0.1572	0.2806	0.2338
M5005_Spy1730	-	spy2034	1146	1257	-0.0253	0.8631	0.3699	0.3410	0.0165	0.0402
M5005_Spy0186	-	SpyM3_0158	1773	1537	-0.0257	0.8609	0.3691	-0.1315	0.3678	0.2804
M5005_Spy0158	*opuABC*	spy0184	208	386	-0.0259	0.8597	0.3688	-0.1747	0.2298	0.2061
M5005_Spy0322	*fhuB*	spy0384	1515	2109	-0.026	0.8592	0.3687	-0.0154	0.9165	0.4787
M5005_Spy0720	-	spy0918	1511	1217	-0.0262	0.8582	0.3684	0.0739	0.6139	0.3801
M5005_Spy1836	*rplI*	spy2184	144	242	-0.0264	0.8569	0.3682	-0.1890	0.1933	0.1829
M5005_Spy1019	-		1828	1745	-0.0266	0.8559	0.3679	-0.2192	0.1302	0.1417
M5005_Spy1136	*pepB*		2484	2235	-0.0268	0.8549	0.3676	-0.0412	0.7784	0.4380
M5005_Spy0034	-		1054	1202	-0.0269	0.8547	0.3676	0.0378	0.7967	0.4434
M5005_Spy0303	*glr*	spy0361	630	919	-0.027	0.8540	0.3675	-0.2814	0.0501	0.0763
M5005_Spy0745	-	spy1018	2084	1856	-0.0272	0.8526	0.3672	0.0562	0.7013	0.4121
M5005_Spy0293	*greA*	spy0349	601	659	-0.0297	0.8393	0.3632	0.1024	0.4839	0.3300
M5005_Spy1385	*glyQ*	spy1689	804	890	-0.0311	0.8320	0.3608	-0.2115	0.1445	0.1516
M5005_Spy1508	*gatC*		2442	2445	-0.0319	0.8277	0.3591	-0.3585	0.0114	0.0319
M5005_Spy0373	-	spy0459	945	1088	-0.032	0.8270	0.3591	-0.1933	0.1832	0.1771
M5005_Spy0440	-	spy0533	2619	2496	-0.0324	0.8248	0.3583	-0.0745	0.6109	0.3794
M5005_Spy0449	-	spy0542	1709	1580	-0.0333	0.8201	0.3568	-0.0410	0.7796	0.4385
M5005_Spy0419	-	spy0508	916	733	-0.0357	0.8074	0.3528	0.3615	0.0107	0.0305
M5005_Spy0743	-	spy1016	1997	2130	-0.0367	0.8023	0.3509	-0.1289	0.3774	0.2849
M5005_Spy1045	-	spyM18_1303	2628	2228	-0.0376	0.7973	0.3496	-0.1168	0.4242	0.3054
M5005_Spy1221	-		2250	2457	-0.0378	0.7967	0.3495	-0.0325	0.8246	0.4512
M5005_Spy1360	*trxB*	spyM18_1666	898	1080	-0.038	0.7954	0.3490	-0.0069	0.9625	0.4894
M5005_Spy0157	*opuAA*	spy0183	188	300	-0.0381	0.7949	0.3490	-0.1060	0.4687	0.3242
M5005_Spy1075	*uvrB*	spy1314	238	211	-0.0386	0.7925	0.3483	-0.1671	0.2511	0.2184
M5005_Spy1240	*clpE*	spy1509	28	46	-0.0396	0.7872	0.3465	-0.0957	0.5129	0.3429
M5005_Spy1279	-	spy1552	1262	1358	-0.0396	0.7870	0.3465	-0.1534	0.2928	0.2404
M5005_Spy0458	-	spyM18_0618	2361	2103	-0.0397	0.7865	0.3465	-0.0618	0.6734	0.4017
M5005_Spy0640	*pyrP*	spy0831	1144	1027	-0.0403	0.7836	0.3457	-0.2283	0.1146	0.1283
M5005_Spy0041	-	spy0045	1495	1364	-0.0406	0.7819	0.3452	0.3617	0.0107	0.0305

M5005_Spy#	Gene	Synonym *	WT Transcript Rank †	Mutant Transcript Rank †	*r* Correlation (*covR*) ‡	*P*-value Correlation (*covR*)	*Q*-value Correlation (*covR*) §	*r* Correlation (*covS*) ‡	*P*-value Correlation (*covS*)	*Q*-value Correlation (*covS*) §
M5005_Spy0575	*atpE*	spy0754	1317	1544	-0.0413	0.7780	0.3438	0.1438	0.3242	0.2596
M5005_Spy1404	*copZ*	spy1714	417	507	-0.0416	0.7768	0.3434	-0.1152	0.4304	0.3071
M5005_Spy1508	*gatC*		2003	2254	-0.042	0.7744	0.3427	-0.1322	0.3654	0.2790
M5005_Spy0975	-	spy1264	6	13	-0.0434	0.7671	0.3401	-0.0995	0.4966	0.3354
M5005_Spy1196	-	spy1468	2644	2642	-0.0435	0.7666	0.3400	0.0894	0.5414	0.3538
M5005_Spy1663	-	spy1950	2127	1678	-0.0438	0.7652	0.3397	-0.2860	0.0463	0.0722
M5005_Spy1283	-	spy1558	2314	2091	-0.0442	0.7631	0.3392	-0.0478	0.7443	0.4262
M5005_Spy0886	-		2249	2260	-0.0443	0.7624	0.3390	-0.2960	0.0389	0.0652
M5005_Spy1818	*cadC*	spyM18_2199	2630	1846	-0.0448	0.7599	0.3385	-0.2462	0.0882	0.1081
M5005_Spy1711	*lmb*	spy2007	176	213	-0.0452	0.7577	0.3377	0.0799	0.5854	0.3698
M5005_Spy1744	-	spy2050	1612	1888	-0.0454	0.7567	0.3377	-0.1307	0.3709	0.2817
M5005_Spy0533	-	spy0646	962	962	-0.0462	0.7528	0.3365	-0.1536	0.2921	0.2400
M5005_Spy0583	-	spy0762	891	809	-0.0462	0.7525	0.3365	-0.0621	0.6715	0.4012
M5005_Spy0657	*trxB, yumC*	spy0850	1193	1162	-0.0467	0.7503	0.3359	0.1789	0.2187	0.1986
M5005_Spy0636	*epuA*	spyM18_0886	2207	2548	-0.0468	0.7493	0.3359	-0.1439	0.3239	0.2595
M5005_Spy1642	-		2476	2150	-0.0468	0.7495	0.3359	-0.0683	0.6411	0.3902
M5005_Spy0340	*lctO*	spy0414	75	159	-0.047	0.7482	0.3357	-0.0205	0.8886	0.4698
M5005_Spy1034	-	spyM18_1794	1516	1187	-0.0477	0.7446	0.3350	-0.1860	0.2007	0.1876
M5005_Spy0679	-	spy0873	889	983	-0.0479	0.7438	0.3347	-0.3850	0.0063	0.0217
M5005_Spy0839	-	spyM18_1077	1694	1862	-0.0484	0.7412	0.3339	0.1827	0.2088	0.1914
M5005_Spy1282	*msrA*	spy1557	1505	1535	-0.049	0.7379	0.3328	-0.2688	0.0618	0.0872
M5005_Spy0828	*potC*	spy1104	1562	1439	-0.0501	0.7326	0.3307	0.0717	0.6243	0.3834
M5005_Spy0450	*mefE*	spy0543	1584	1532	-0.0506	0.7300	0.3300	-0.0992	0.4977	0.3358
M5005_Spy1009	-		2310	2218	-0.0511	0.7274	0.3293	0.1427	0.3282	0.2612
M5005_Spy0517	*regR*	spy0627	1383	1277	-0.0513	0.7263	0.3289	0.1403	0.3363	0.2649
M5005_Spy0515	-	spy0622	1823	1295	-0.0517	0.7241	0.3286	-0.3040	0.0337	0.0606
M5005_Spy0448	-	spyM18_0607	1761	1741	-0.0523	0.7212	0.3276	-0.0750	0.6087	0.3787
M5005_Spy1177	-	spy1447	1992	1701	-0.0523	0.7213	0.3276	-0.0003	0.9982	0.4987
M5005_Spy1830	-	spy2177	2255	2441	-0.0523	0.7213	0.3276	0.0880	0.5475	0.3555
M5005_Spy0220	-	spy0260	535	458	-0.0527	0.7192	0.3275	-0.1093	0.4545	0.3187
M5005_Spy0314	-	spy0374	964	864	-0.0529	0.7179	0.3272	-0.0819	0.5757	0.3658
M5005_Spy0883	-	spyM18_1122	1480	1491	-0.0533	0.7161	0.3266	0.1338	0.3593	0.2764

M5005_Spy#	Gene	Synonym *	WT Transcript Rank †	Mutant Transcript Rank †	*r* Correlation (*covR*) ‡	*P* -value Correlation (*covR*)	*Q-* value Correlation (*covR*) §	*r* Correlation (*covS*) ‡	*P* -value Correlation (*covS*)	*Q-* value Correlation (*covS*) §
M5005_Spy0728	*apt*	spy0927	1131	1199	-0.054	0.7122	0.3259	-0.1271	0.3842	0.2872
M5005_Spy0299	-	spy0356	744	956	-0.0548	0.7084	0.3242	0.1834	0.2072	0.1909
M5005_Spy1684	*ska*	spyM18_2042	2258	2493	-0.0549	0.7081	0.3242	-0.0436	0.7661	0.4333
M5005_Spy0830	-	spy1107	1250	965	-0.0551	0.7070	0.3240	0.0778	0.5952	0.3736
M5005_Spy1447	-		2522	2358	-0.0558	0.7036	0.3230	0.0531	0.7169	0.4177
M5005_Spy0260	-	spy0305	260	278	-0.0559	0.7026	0.3230	-0.0197	0.8933	0.4715
M5005_Spy1243	*ileS*	spy1513	1038	914	-0.056	0.7024	0.3230	0.2827	0.0490	0.0751
M5005_Spy0101	*adhE*	spyM18_0118	1138	1019	-0.0564	0.7005	0.3223	-0.0510	0.7277	0.4205
M5005_Spy0371	-	spy0457	519	612	-0.0565	0.6998	0.3221	0.1877	0.1966	0.1846
M5005_Spy0881	-	spy1160	1007	1235	-0.0566	0.6995	0.3221	-0.1420	0.3306	0.2625
M5005_Spy0455	-	SpyM3_0391	997	840	-0.057	0.6973	0.3212	-0.2118	0.1441	0.1514
M5005_Spy0711	*parE*		1648	1288	-0.0576	0.6944	0.3205	-0.0200	0.8915	0.4710
M5005_Spy1126	-	SpyM3_1015	2503	2346	-0.0576	0.6942	0.3205	-0.0394	0.7883	0.4408
M5005_Spy1016	-		2364	2104	-0.0577	0.6936	0.3205	-0.1615	0.2676	0.2279
M5005_Spy1800	*cinA*	spy2117	1012	954	-0.058	0.6921	0.3202	-0.2876	0.0451	0.0709
M5005_Spy0448	-		2425	2615	-0.0584	0.6904	0.3198	0.0518	0.7238	0.4193
M5005_Spy1817	*cadD*		2573	2609	-0.0587	0.6888	0.3194	-0.1531	0.2935	0.2406
M5005_Spy0629	-	spy0815	1577	1727	-0.0593	0.6859	0.3183	-0.1430	0.3269	0.2605
M5005_Spy0906	*citE*	spy1188	1685	1547	-0.0594	0.6849	0.3180	-0.3062	0.0324	0.0591
M5005_Spy0236	-	spy0276	1112	1166	-0.0598	0.6833	0.3175	-0.3252	0.0226	0.0477
M5005_Spy1011	-		1628	2017	-0.0599	0.6827	0.3174	-0.0569	0.6979	0.4115
M5005_Spy0877	-	spy1156	43	117	-0.0605	0.6796	0.3166	-0.0893	0.5419	0.3538
M5005_Spy0206	*fasA*	spy0245	1774	1563	-0.0607	0.6786	0.3163	-0.1710	0.2400	0.2118
M5005_Spy1858	*trsA, trpA*	spy2207	975	1137	-0.0608	0.6780	0.3161	-0.1640	0.2602	0.2239
M5005_Spy0273	-	spy0321	940	1226	-0.0613	0.6755	0.3159	-0.1425	0.3287	0.2612
M5005_Spy0537	*aspC*	spy0650	259	217	-0.0618	0.6729	0.3150	0.0690	0.6373	0.3891
M5005_Spy1794	-	spy2111	1289	1233	-0.0619	0.6725	0.3149	0.0491	0.7376	0.4248
M5005_Spy1017	-	SpyM3_1321	2325	1930	-0.062	0.6720	0.3148	-0.3950	0.0050	0.0189
M5005_Spy0462	-	spyM18_0626	1047	1286	-0.0631	0.6669	0.3133	0.0383	0.7939	0.4428
M5005_Spy1421	-		1449	1597	-0.0644	0.6601	0.3105	0.1232	0.3988	0.2950
M5005_Spy1821	-	spy2166	2555	1889	-0.0647	0.6588	0.3103	-0.1112	0.4469	0.3157
M5005_Spy1303	*aroE*	spyM18_1591	1872	1821	-0.0662	0.6515	0.3078	-0.1426	0.3283	0.2612

M5005_Spy#	Gene	Synonym *	WT Transcript Rank †	Mutant Transcript Rank †	*r* Correlation (*covR*) ‡	*P*-value Correlation (*covR*)	*Q*-value Correlation (*covR*) §	*r* Correlation (*covS*) ‡	*P*-value Correlation (*covS*)	*Q*-value Correlation (*covS*) §
M5005_Spy1637	*lacB.2*	spy1922	958	1241	-0.0664	0.6501	0.3074	-0.2150	0.1379	0.1472
M5005_Spy1523	-	spy1789	754	837	-0.0668	0.6485	0.3069	0.1370	0.3479	0.2706
M5005_Spy0456	-	spy0550	1907	1681	-0.067	0.6472	0.3068	-0.1694	0.2447	0.2142
M5005_Spy0719	-	spy0917	1554	1674	-0.0672	0.6465	0.3067	-0.2291	0.1134	0.1274
M5005_Spy1581	-	spy1863	1661	1914	-0.0675	0.6449	0.3062	-0.2105	0.1465	0.1530
M5005_Spy1146	-		2563	2225	-0.0677	0.6437	0.3057	-0.1308	0.3704	0.2817
M5005_Spy0110	*eftLSL.B*	spy0129	942	1158	-0.0691	0.6369	0.3039	-0.2617	0.0693	0.0933
M5005_Spy0677	*fms*	spy0870	1341	1336	-0.0696	0.6344	0.3029	-0.0834	0.5690	0.3634
M5005_Spy1836	*rplI*	spy2183	213	309	-0.0699	0.6334	0.3029	-0.2563	0.0755	0.0986
M5005_Spy1483	*serS*	spy1742	944	843	-0.0702	0.6317	0.3023	-0.2140	0.1398	0.1487
M5005_Spy1863	-		1873	1549	-0.0704	0.6309	0.3020	0.0758	0.6049	0.3775
M5005_Spy1088	*obg*	spy1333	438	416	-0.0707	0.6293	0.3016	-0.1936	0.1826	0.1768
M5005_Spy1179	-	spy1449	2219	2212	-0.0708	0.6289	0.3016	-0.0825	0.5732	0.3650
M5005_Spy0461	-	spy0558	1465	1490	-0.0709	0.6285	0.3016	-0.1118	0.4442	0.3143
M5005_Spy0031	*purK*		1582	1552	-0.0723	0.6214	0.2991	-0.0969	0.5079	0.3403
M5005_Spy1110	*birA*	spy1362	795	806	-0.0724	0.6211	0.2991	-0.1652	0.2567	0.2216
M5005_Spy0312	-	spy0371	1107	1094	-0.0725	0.6206	0.2990	-0.3011	0.0355	0.0621
M5005_Spy1381	*glpK*	spy1684	340	495	-0.0727	0.6196	0.2988	-0.2426	0.0930	0.1119
M5005_Spy1010	-		2508	2371	-0.0732	0.6170	0.2977	-0.2640	0.0669	0.0912
M5005_Spy1061	-	spy1297	1509	1315	-0.0735	0.6157	0.2972	-0.1616	0.2674	0.2279
M5005_Spy1438	-		2033	2366	-0.0737	0.6148	0.2969	-0.3149	0.0275	0.0535
M5005_Spy1200	-	spy0962	2656	2654	-0.074	0.6135	0.2964	-0.1038	0.4779	0.3284
M5005_Spy1496	*phaB*	spy1758	1635	1346	-0.074	0.6135	0.2964	-0.0079	0.9569	0.4882
M5005_Spy0360	-	spyM18_0484	2443	2460	-0.0748	0.6094	0.2950	0.0690	0.6378	0.3891
M5005_Spy1039	-	spyM18_1798	1924	1684	-0.0751	0.6083	0.2950	-0.3014	0.0353	0.0621
M5005_Spy0900	-	spy1180	1605	1368	-0.0753	0.6071	0.2946	0.1224	0.4020	0.2965
M5005_Spy0370	*mtsC*	spy0456	1033	1020	-0.0754	0.6067	0.2945	-0.2781	0.0530	0.0790
M5005_Spy1827	-	spy2174	1602	1960	-0.0761	0.6034	0.2933	0.0002	0.9989	0.4987
M5005_Spy0156	-	spy0182	242	322	-0.0765	0.6012	0.2926	0.0258	0.8604	0.4612
M5005_Spy0993	-	spy1287	1218	1718	-0.0766	0.6006	0.2925	-0.3000	0.0362	0.0627
M5005_Spy1111	-	spy1363	1154	1055	-0.0775	0.5964	0.2911	-0.2849	0.0473	0.0730
M5005_Spy0428	-	spy0518	2212	1467	-0.0786	0.5912	0.2889	-0.1488	0.3076	0.2493

M5005_Spy#	Gene	Synonym *	WT Transcript Rank †	Mutant Transcript Rank †	*r* Correlation (*covR*) ‡	*P* -value Correlation (*covR*)	*Q-* value Correlation (*covR*) §	*r* Correlation (*covS*) ‡	*P* -value Correlation (*covS*)	*Q-* value Correlation (*covS*) §
M5005_Spy0506	*ftsW*	spy0609	853	989	-0.0793	0.5883	0.2877	-0.3913	0.0054	0.0200
M5005_Spy1727	-	spy2031	529	724	-0.0793	0.5882	0.2877	-0.2473	0.0867	0.1071
M5005_Spy0712	*parC*	spy0910	1044	1000	-0.0799	0.5854	0.2868	-0.3707	0.0087	0.0272
M5005_Spy0655	-	spyM18_0907	1960	2315	-0.0801	0.5842	0.2867	0.1621	0.2659	0.2274
M5005_Spy0113	-	spy0133	1829	1327	-0.0805	0.5825	0.2860	-0.2886	0.0444	0.0701
M5005_Spy0543	*adcA*	spy0714	77	168	-0.0805	0.5825	0.2860	-0.0893	0.5417	0.3538
M5005_Spy1260	-	spy1532	2533	2592	-0.0812	0.5792	0.2847	-0.2120	0.1436	0.1513
M5005_Spy0416	-	spy0505	608	646	-0.0815	0.5777	0.2844	-0.1176	0.4208	0.3045
M5005_Spy0864	*hemK*	spy1142	890	981	-0.082	0.5755	0.2835	-0.0298	0.8389	0.4555
M5005_Spy0653	*czcD*	spy0845	1528	1696	-0.0827	0.5722	0.2820	-0.0108	0.9414	0.4845
M5005_Spy1471	-	spy1729	900	955	-0.0837	0.5677	0.2806	-0.1367	0.3490	0.2711
M5005_Spy1835	*holB*	spy2182	126	270	-0.0843	0.5647	0.2795	-0.2222	0.1250	0.1369
M5005_Spy0015	-		2214	1933	-0.0845	0.5637	0.2794	0.1263	0.3871	0.2886
M5005_Spy0185	*pgi*		1658	2034	-0.0845	0.5638	0.2794	-0.1310	0.3698	0.2815
M5005_Spy0936	*dfp*	spy1222	687	881	-0.0846	0.5633	0.2794	-0.2578	0.0737	0.0972
M5005_Spy1524	-	spy1790	1170	1372	-0.0849	0.5618	0.2788	-0.0097	0.9475	0.4853
M5005_Spy0409	-	spy0498	1202	1130	-0.0856	0.5587	0.2781	-0.1228	0.4006	0.2959
M5005_Spy1353	-	spy1647	1378	1216	-0.0865	0.5546	0.2764	-0.2090	0.1494	0.1544
M5005_Spy1805	*mutS*	spy2148	834	908	-0.0867	0.5535	0.2764	-0.1927	0.1846	0.1782
M5005_Spy1058	*malE*	spy1294	692	465	-0.0869	0.5526	0.2761	-0.0213	0.8844	0.4690
M5005_Spy0239	*mecA*	spy0281	706	863	-0.0886	0.5448	0.2725	-0.2081	0.1514	0.1556
M5005_Spy1627	*salY*		2007	2275	-0.089	0.5431	0.2719	-0.0529	0.7181	0.4183
M5005_Spy1558	-	spy1834	2076	2381	-0.0894	0.5411	0.2713	-0.1904	0.1901	0.1818
M5005_Spy0237	-	spy0278	857	870	-0.0897	0.5401	0.2711	-0.0545	0.7100	0.4150
M5005_Spy0999	-		1475	2072	-0.0898	0.5393	0.2709	-0.1592	0.2745	0.2313
M5005_Spy1171	-	spy1438	1977	1932	-0.0904	0.5369	0.2701	0.0547	0.7089	0.4149
M5005_Spy0801	-	M12_1863	2516	2484	-0.0905	0.5364	0.2700	-0.1039	0.4776	0.3284
M5005_Spy1728	-	spy2032	51	126	-0.0911	0.5336	0.2689	-0.2153	0.1374	0.1469
M5005_Spy1049	-	SpyM3_0976	1452	1845	-0.0915	0.5316	0.2684	0.0739	0.6136	0.3801
M5005_Spy0485	*lgt*	spy0585	291	468	-0.0924	0.5278	0.2670	-0.0896	0.5403	0.3536
M5005_Spy0844	*nifS, yrvO*	spy1121	1444	1395	-0.0928	0.5260	0.2665	-0.1188	0.4162	0.3023
M5005_Spy0149	-	spy0175	976	980	-0.0942	0.5197	0.2640	0.1035	0.4790	0.3284

M5005_Spy#	Gene	Synonym *	WT Transcript Rank †	Mutant Transcript Rank †	*r* Correlation (*covR*) ‡	*P*-value Correlation (*covR*)	*Q*-value Correlation (*covR*) §	*r* Correlation (*covS*) ‡	*P*-value Correlation (*covS*)	*Q*-value Correlation (*covS*) §
M5005_Spy0125	-	spy0147	1786	2237	-0.095	0.5160	0.2623	0.0208	0.8874	0.4696
M5005_Spy1197	-	SpyM3_1124	2353	1762	-0.095	0.5160	0.2623	-0.2068	0.1539	0.1573
M5005_Spy1629	*salX*		2126	2271	-0.0953	0.5147	0.2621	-0.1445	0.3217	0.2581
M5005_Spy1369	-	SpyM3_1404	1769	1390	-0.0957	0.5130	0.2614	-0.2021	0.1638	0.1633
M5005_Spy0059	*rplF*	spy0066	433	601	-0.0959	0.5122	0.2611	0.0250	0.8644	0.4626
M5005_Spy0803	*srtI*	spy1080	1890	2107	-0.0961	0.5112	0.2609	-0.2775	0.0535	0.0795
M5005_Spy0645	-	spy0837	1439	1403	-0.0961	0.5114	0.2609	-0.2752	0.0557	0.0813
M5005_Spy1445	-	spyM18_1282	2581	2662	-0.0976	0.5045	0.2585	-0.0641	0.6617	0.3971
M5005_Spy1716	*tnp*		2124	2391	-0.0976	0.5047	0.2585	-0.0447	0.7604	0.4318
M5005_Spy1825	-	spy2172	1689	1896	-0.0976	0.5048	0.2585	-0.0423	0.7730	0.4357
M5005_Spy1703	-	spyM18_2065	1603	2349	-0.098	0.5030	0.2581	-0.1877	0.1965	0.1846
M5005_Spy0073	-		941	727	-0.0981	0.5025	0.2581	0.0037	0.9799	0.4935
M5005_Spy0757	*hylA*	spy1032	1779	1526	-0.0985	0.5007	0.2575	-0.0910	0.5342	0.3516
M5005_Spy0663	*mur1.1*	spy0856	1157	1021	-0.0992	0.4976	0.2563	-0.1200	0.4114	0.2997
M5005_Spy1440	-		2556	2462	-0.0994	0.4967	0.2560	0.1165	0.4255	0.3058
M5005_Spy0338	-	spy0410	1447	1383	-0.0997	0.4953	0.2557	0.1952	0.1790	0.1739
M5005_Spy0507	-	spyM18_0677	1632	1676	-0.0999	0.4945	0.2555	0.2389	0.0984	0.1167
M5005_Spy1511	-	spy1776	1119	1351	-0.1001	0.4938	0.2553	-0.1550	0.2877	0.2374
M5005_Spy0970	-	spy1259	419	559	-0.1003	0.4931	0.2551	-0.1022	0.4847	0.3304
M5005_Spy1457	-		2390	1990	-0.1012	0.4892	0.2535	0.0304	0.8355	0.4543
M5005_Spy1176	-	spy1444	1642	1764	-0.1016	0.4872	0.2529	0.2894	0.0437	0.0693
M5005_Spy0195	-	spy0227	1353	1456	-0.1033	0.4801	0.2500	0.0371	0.8002	0.4439
M5005_Spy1149	-	spy1410	755	758	-0.1035	0.4791	0.2496	0.0192	0.8957	0.4724
M5005_Spy1346	*atoA*	spy1639	1953	1869	-0.1041	0.4768	0.2486	0.0071	0.9615	0.4894
M5005_Spy1561	*mutS2*	spy1837	647	548	-0.1045	0.4750	0.2480	-0.0097	0.9473	0.4853
M5005_Spy0114	-	spy0135	2400	1709	-0.1074	0.4626	0.2423	-0.2788	0.0524	0.0786
M5005_Spy1613	-	spy1897	2022	2165	-0.108	0.4601	0.2415	-0.2107	0.1463	0.1530
M5005_Spy1788	-	spy2104	899	903	-0.1083	0.4588	0.2411	-0.0017	0.9906	0.4968
M5005_Spy1685	-	spy1980	1833	1724	-0.1096	0.4533	0.2392	0.2074	0.1527	0.1567
M5005_Spy1706	*dppC*	spy2002	1228	1605	-0.1096	0.4536	0.2393	0.0372	0.7998	0.4439
M5005_Spy1692	-	spy1986	418	344	-0.1098	0.4527	0.2392	0.1073	0.4632	0.3217
M5005_Spy0103	-	spy0121	797	838	-0.1104	0.4501	0.2384	0.1911	0.1884	0.1806

M5005_Spy#	Gene	Synonym *	WT Transcript Rank †	Mutant Transcript Rank †	*r* Correlation (*covR*) ‡	*P*-value Correlation (*covR*)	*Q*-value Correlation (*covR*) §	*r* Correlation (*covS*) ‡	*P*-value Correlation (*covS*)	*Q*-value Correlation (*covS*) §
M5005_Spy0621	*rplT*	spy0806	1663	2522	-0.1106	0.4494	0.2384	-0.1591	0.2748	0.2313
M5005_Spy1153	-	spy1414	1727	1150	-0.1106	0.4494	0.2384	0.0767	0.6003	0.3757
M5005_Spy1518	-	spy1784	2344	2236	-0.1107	0.4487	0.2384	-0.2419	0.0940	0.1129
M5005_Spy0922	*pdxK*	spy1208	2428	1923	-0.1109	0.4482	0.2384	0.2838	0.0482	0.0742
M5005_Spy1276	-	spy1548	826	894	-0.1116	0.4454	0.2372	0.0284	0.8463	0.4571
M5005_Spy1097	-	spy1345	538	573	-0.1126	0.4413	0.2355	-0.1605	0.2706	0.2299
M5005_Spy0980	-	spy1272	957	1311	-0.1129	0.4397	0.2348	0.2509	0.0821	0.1036
M5005_Spy0722	*miaA*	spy0921	1461	1495	-0.1136	0.4370	0.2336	-0.0731	0.6175	0.3816
M5005_Spy0744	-	spy1017	1818	1910	-0.1137	0.4367	0.2336	-0.3662	0.0097	0.0291
M5005_Spy0859	-	spy1137	2044	1999	-0.1137	0.4366	0.2336	-0.0376	0.7978	0.4435
M5005_Spy1440	-		1993	1841	-0.1141	0.4350	0.2330	0.0675	0.6449	0.3914
M5005_Spy1517	-	spy1783	2427	2515	-0.1143	0.4340	0.2328	0.0950	0.5162	0.3441
M5005_Spy1818	*cadC*	spy2163	2514	2532	-0.1144	0.4339	0.2328	-0.2851	0.0471	0.0729
M5005_Spy1819	-	spy2164	2004	2206	-0.1144	0.4337	0.2328	0.1370	0.3479	0.2706
M5005_Spy1723	*isp*	spy2025	92	165	-0.1145	0.4333	0.2328	-0.2305	0.1111	0.1257
M5005_Spy0170	*nadC*	spy0197	2108	2302	-0.1152	0.4306	0.2321	-0.3417	0.0163	0.0400
M5005_Spy1506	*gatB*	spy1769	2160	1915	-0.1152	0.4305	0.2321	-0.1736	0.2330	0.2080
M5005_Spy0511	*murM*	spy0615	760	678	-0.1153	0.4302	0.2321	0.0326	0.8240	0.4512
M5005_Spy0182	*speG*	spy0212	1853	1905	-0.1155	0.4294	0.2319	-0.0109	0.9410	0.4845
M5005_Spy1423	-		1608	1589	-0.1156	0.4290	0.2319	-0.0069	0.9627	0.4894
M5005_Spy0102	-	spyM18_0120	2106	1826	-0.1157	0.4287	0.2319	-0.0571	0.6966	0.4113
M5005_Spy1042	-		1841	1479	-0.1164	0.4259	0.2306	0.2226	0.1242	0.1366
M5005_Spy1278	-		1734	1677	-0.1166	0.4249	0.2303	-0.1409	0.3341	0.2644
M5005_Spy1806	-	spy2149	1279	1429	-0.1173	0.4224	0.2293	-0.1550	0.2877	0.2374
M5005_Spy0387	-	spy0472	1182	1008	-0.1175	0.4215	0.2291	0.0728	0.6193	0.3817
M5005_Spy0847	-	spy1125	697	853	-0.1177	0.4205	0.2288	0.0222	0.8794	0.4669
M5005_Spy0687	*mvaS.1*	spy0880	878	635	-0.1184	0.4176	0.2275	0.2097	0.1481	0.1539
M5005_Spy0966	-	spy1255	737	787	-0.1186	0.4170	0.2273	-0.0126	0.9317	0.4829
M5005_Spy1614	-	spy1898	1129	1013	-0.1193	0.4144	0.2264	-0.0887	0.5447	0.3547
M5005_Spy1173	-	spy1440	2659	2584	-0.1195	0.4135	0.2261	-0.1001	0.4936	0.3340
M5005_Spy0475	-	spy0572	939	999	-0.1197	0.4126	0.2257	-0.2826	0.0491	0.0751
M5005_Spy0497	-	spy0598	963	1030	-0.1203	0.4103	0.2246	-0.1162	0.4267	0.3061

M5005_Spy#	Gene	Synonym *	WT Transcript Rank †	Mutant Transcript Rank †	*r* Correlation (*covR*) ‡	*P*-value Correlation (*covR*)	*Q*-value Correlation (*covR*) §	*r* Correlation (*covS*) ‡	*P*-value Correlation (*covS*)	*Q*-value Correlation (*covS*) §
M5005_Spy0152	-		2032	2136	-0.1211	0.4071	0.2234	0.0694	0.6355	0.3885
M5005_Spy1100	*aroK*	spy1351	1490	1401	-0.1213	0.4065	0.2234	0.0297	0.8396	0.4557
M5005_Spy1409	*infB*	spyM18_1729	2372	2240	-0.1213	0.4065	0.2234	-0.1180	0.4193	0.3038
M5005_Spy0744	-	spyM18_1000	1837	1603	-0.1222	0.4029	0.2219	0.0169	0.9080	0.4761
M5005_Spy0992	-	spy1286	1464	1461	-0.1224	0.4022	0.2219	-0.2593	0.0720	0.0955
M5005_Spy0899	*citG*	spy1178	1499	1652	-0.1225	0.4016	0.2219	-0.2551	0.0769	0.0997
M5005_Spy1771	*hutU*		1822	1992	-0.1226	0.4015	0.2219	-0.0373	0.7989	0.4436
M5005_Spy1237	-	spy1506	1682	1445	-0.1231	0.3994	0.2213	-0.0583	0.6906	0.4085
M5005_Spy0910	*citC*		2362	2351	-0.1233	0.3986	0.2212	-0.0767	0.6006	0.3757
M5005_Spy1147	*comEC*	spy1408	1636	1986	-0.1234	0.3984	0.2212	-0.3211	0.0245	0.0497
M5005_Spy1863	-	SpyM3_0989	2306	2617	-0.1234	0.3981	0.2212	-0.2076	0.1523	0.1565
M5005_Spy0211	*rpmH*	spy0250	1278	1347	-0.1244	0.3943	0.2204	0.0120	0.9348	0.4834
M5005_Spy0666	-		2090	1231	-0.1247	0.3932	0.2200	-0.2340	0.1056	0.1218
M5005_Spy1641	-	spy1927	1719	1659	-0.1256	0.3898	0.2188	-0.1991	0.1702	0.1684
M5005_Spy1432	-	SpyM3_1427	1801	1989	-0.1257	0.3896	0.2188	0.0029	0.9840	0.4948
M5005_Spy1610	*pyrG*	spy1894	840	991	-0.1269	0.3848	0.2165	-0.0507	0.7296	0.4213
M5005_Spy1081	-	spy1322	873	842	-0.1272	0.3836	0.2162	-0.0914	0.5321	0.3509
M5005_Spy1181	-	SpyM3_1107	1845	2131	-0.1278	0.3816	0.2153	-0.1505	0.3021	0.2456
M5005_Spy0121	-	spy0142	1930	2062	-0.1281	0.3805	0.2149	-0.1565	0.2829	0.2349
M5005_Spy1050	-		2590	2332	-0.1287	0.3782	0.2142	-0.1987	0.1710	0.1688
M5005_Spy1294	-	spy1569	2132	1697	-0.1288	0.3776	0.2140	-0.0518	0.7238	0.4193
M5005_Spy1458	-	M12_1767	1355	1517	-0.1305	0.3713	0.2114	-0.2202	0.1284	0.1399
M5005_Spy1667	-	spyM18_2023	2406	2407	-0.1305	0.3713	0.2114	0.2095	0.1486	0.1541
M5005_Spy0138	*nusG*	spy0164	1132	1056	-0.1306	0.3711	0.2114	0.0482	0.7422	0.4258
M5005_Spy0357	-	spy0437	1707	1477	-0.1315	0.3679	0.2100	0.0725	0.6207	0.3818
M5005_Spy1368	*ftsL*	spy1665	482	655	-0.1323	0.3649	0.2091	-0.2560	0.0758	0.0987
M5005_Spy1205	-		1775	1922	-0.1325	0.3639	0.2087	0.0973	0.5059	0.3396
M5005_Spy1109	*inlA*	spy1361	571	762	-0.1342	0.3579	0.2059	-0.0605	0.6795	0.4048
M5005_Spy1854	-	spy2203	786	1007	-0.1343	0.3575	0.2058	0.2938	0.0405	0.0660
M5005_Spy0219	-	spy0259	1183	1237	-0.1347	0.3561	0.2054	-0.1442	0.3228	0.2588
M5005_Spy0852	-	SpyM3_0788	662	820	-0.1356	0.3528	0.2035	-0.2677	0.0629	0.0881
M5005_Spy1434	-		2168	2089	-0.1359	0.3517	0.2032	-0.1034	0.4795	0.3284

M5005_Spy#	Gene	Synonym *	WT Transcript Rank †	Mutant Transcript Rank †	*r* Correlation (*covR*) ‡	*P*-value Correlation (*covR*)	*Q*-value Correlation (*covR*) §	*r* Correlation (*covS*) ‡	*P*-value Correlation (*covS*)	*Q*-value Correlation (*covS*) §
M5005_Spy1504	-	spy1768	1710	1525	-0.1359	0.3517	0.2032	-0.1198	0.4124	0.3002
M5005_Spy0639	*pyrR*		2098	2153	-0.136	0.3516	0.2032	-0.1667	0.2522	0.2184
M5005_Spy1451	-		2299	2064	-0.1361	0.3510	0.2031	0.1813	0.2125	0.1940
M5005_Spy1243	*ileS*	SpyM3_1166	1538	1594	-0.1365	0.3498	0.2027	-0.0672	0.6466	0.3919
M5005_Spy0272	-	spy0320	231	304	-0.1388	0.3415	0.1991	-0.2277	0.1156	0.1291
M5005_Spy1332	*hk03*	spy1622	1111	907	-0.1398	0.3380	0.1976	-0.1365	0.3496	0.2713
M5005_Spy1633	*lacE*		2072	1786	-0.1403	0.3364	0.1970	-0.2617	0.0694	0.0933
M5005_Spy1146	-	SpyM3_1072	874	1071	-0.1409	0.3344	0.1960	-0.1589	0.2756	0.2315
M5005_Spy0514	-	spy0621	1402	1432	-0.1411	0.3335	0.1957	-0.0382	0.7943	0.4428
M5005_Spy0479	-	spy0578	2339	2428	-0.1414	0.3325	0.1952	-0.0775	0.5966	0.3742
M5005_Spy0460	-	spy0556	1455	1791	-0.142	0.3304	0.1945	-0.2920	0.0418	0.0672
M5005_Spy0885	-	SpyM3_0820	731	896	-0.1425	0.3288	0.1939	-0.2293	0.1130	0.1273
M5005_Spy1424	-		2394	2477	-0.1429	0.3275	0.1933	-0.3390	0.0172	0.0408
M5005_Spy1182	-	spy1452	2410	2479	-0.1436	0.3249	0.1920	0.0477	0.7446	0.4262
M5005_Spy0183	-	spyM18_0202	1141	1420	-0.1444	0.3221	0.1912	-0.3034	0.0341	0.0609
M5005_Spy0452	-	SpyM3_0388	2544	2298	-0.145	0.3203	0.1905	-0.1287	0.3783	0.2849
M5005_Spy1352	-		1497	1310	-0.1455	0.3186	0.1899	-0.1203	0.4102	0.2997
M5005_Spy0828	*potC*		948	964	-0.1463	0.3159	0.1889	-0.1282	0.3801	0.2856
M5005_Spy1178	-		2469	2508	-0.1464	0.3157	0.1889	-0.2562	0.0756	0.0986
M5005_Spy1029	-	spyM18_1790	2547	1897	-0.1466	0.3148	0.1885	0.0469	0.7490	0.4276
M5005_Spy1811	-	spy2155	672	694	-0.1473	0.3124	0.1873	-0.0725	0.6203	0.3817
M5005_Spy0254	-	M12_0466	2657	2623	-0.1479	0.3106	0.1867	0.0560	0.7023	0.4125
M5005_Spy1007	-		2491	2560	-0.1482	0.3096	0.1865	0.0897	0.5398	0.3534
M5005_Spy1203	-	spy1475	2227	1951	-0.1488	0.3076	0.1856	-0.0783	0.5927	0.3725
M5005_Spy1793	*nrdD*	spy2110	100	186	-0.1503	0.3025	0.1831	-0.2321	0.1085	0.1236
M5005_Spy1285	-	M12_1348	2035	1902	-0.1512	0.2996	0.1821	0.0303	0.8362	0.4544
M5005_Spy1206	-	spy0956	1073	1366	-0.1517	0.2983	0.1815	-0.0478	0.7445	0.4262
M5005_Spy1750	-	#N/A	2542	2321	-0.1523	0.2962	0.1806	-0.2483	0.0854	0.1061
M5005_Spy0180	-	spy0210	1533	1497	-0.1528	0.2945	0.1803	-0.3412	0.0164	0.0401
M5005_Spy0355	-	spy0435	2171	2139	-0.1531	0.2937	0.1799	-0.1926	0.1849	0.1783
M5005_Spy0762	-	spy1037	982	1140	-0.1539	0.2912	0.1792	-0.1640	0.2601	0.2239
M5005_Spy1205	-	spyM18_1496	2052	2435	-0.1541	0.2904	0.1790	-0.2516	0.0812	0.1030

M5005_Spy#	Gene	Synonym *	WT Transcript Rank †	Mutant Transcript Rank †	*r* Correlation (*covR*) ‡	*P*-value Correlation (*covR*)	*Q*-value Correlation (*covR*) §	*r* Correlation (*covS*) ‡	*P*-value Correlation (*covS*)	*Q*-value Correlation (*covS*) §
M5005_Spy1025	-	spy0677	2199	1758	-0.157	0.2815	0.1743	-0.1094	0.4541	0.3186
M5005_Spy1055	*glgP*	spy1291	1324	1042	-0.1571	0.2811	0.1742	-0.3176	0.0262	0.0517
M5005_Spy0417	*pcp*	spy0506	666	622	-0.1577	0.2792	0.1734	0.0172	0.9067	0.4758
M5005_Spy1453	-		1535	1625	-0.1583	0.2775	0.1726	-0.0442	0.7628	0.4324
M5005_Spy1569	*pfl*	spy1849	96	140	-0.1584	0.2770	0.1725	-0.2471	0.0869	0.1072
M5005_Spy0447	-		2055	2266	-0.1586	0.2763	0.1722	-0.0490	0.7381	0.4248
M5005_Spy1173	-	spy1441	1922	1854	-0.1588	0.2756	0.1720	0.0984	0.5010	0.3374
M5005_Spy0353	-	spyM18_0479	1673	1998	-0.1597	0.2730	0.1709	-0.1031	0.4810	0.3287
M5005_Spy1044	-	spyM18_1301	2523	2195	-0.1598	0.2728	0.1708	-0.1391	0.3406	0.2674
M5005_Spy1397	*lacB.1*	spy1708	1076	812	-0.1599	0.2724	0.1706	-0.0797	0.5863	0.3698
M5005_Spy0390	*era*	spy0476	408	436	-0.1606	0.2702	0.1697	0.0655	0.6550	0.3946
M5005_Spy1049	-	spyM18_1305	1451	1937	-0.1607	0.2700	0.1697	0.1202	0.4106	0.2997
M5005_Spy1708	*dppE*	spy2004	1489	1475	-0.161	0.2692	0.1694	-0.0208	0.8873	0.4696
M5005_Spy0670	*rpsU*	SpyM3_0584	1088	947	-0.1615	0.2677	0.1685	-0.0378	0.7963	0.4434
M5005_Spy1725	*irr*	spy2027	306	443	-0.1625	0.2645	0.1674	-0.1399	0.3377	0.2658
M5005_Spy1449	-		1782	2306	-0.1627	0.2640	0.1672	-0.1915	0.1874	0.1800
M5005_Spy1697	-		832	1129	-0.1629	0.2633	0.1668	-0.2622	0.0688	0.0931
M5005_Spy0455	-	spy0549	2610	1996	-0.163	0.2630	0.1668	0.1017	0.4870	0.3309
M5005_Spy1147	*comEC*	spy1409	1587	1744	-0.1654	0.2560	0.1630	-0.1208	0.4084	0.2991
M5005_Spy1508	*gatC*	spy1772	1755	1556	-0.1656	0.2555	0.1628	-0.1638	0.2607	0.2241
M5005_Spy0639	*pyrR*		778	834	-0.1657	0.2551	0.1627	0.1284	0.3792	0.2852
M5005_Spy0176	-	spy0205	1348	1634	-0.166	0.2544	0.1625	-0.1835	0.2070	0.1909
M5005_Spy1007	-		2296	1720	-0.166	0.2544	0.1625	-0.2155	0.1369	0.1467
M5005_Spy0740	*fbp*	spy1013	1072	1038	-0.1662	0.2537	0.1625	-0.1176	0.4211	0.3045
M5005_Spy1695	-	spy1988	657	708	-0.1663	0.2535	0.1625	0.0085	0.9540	0.4874
M5005_Spy0112	-	spy0131	807	1076	-0.1664	0.2533	0.1625	-0.3189	0.0255	0.0510
M5005_Spy1783	*dexS*	spy2096	1273	1238	-0.1674	0.2503	0.1609	-0.2631	0.0678	0.0921
M5005_Spy1459	-	spyM18_0725	1860	1831	-0.1688	0.2463	0.1588	0.1899	0.1914	0.1821
M5005_Spy1589	*crgR*		1631	1275	-0.1691	0.2455	0.1584	-0.0056	0.9696	0.4917
M5005_Spy0204	*fasB*	spy0242	1796	2365	-0.1702	0.2425	0.1568	0.0842	0.5651	0.3620
M5005_Spy1481	*manN*	spy1740	897	1037	-0.1704	0.2418	0.1564	-0.0903	0.5372	0.3521
M5005_Spy1014	-		1797	2059	-0.1706	0.2413	0.1562	0.0233	0.8740	0.4654

M5005_Spy#	Gene	Synonym *	WT Transcript Rank †	Mutant Transcript Rank †	*r* Correlation (*covR*) ‡	*P*-value Correlation (*covR*)	*Q*-value Correlation (*covR*) §	*r* Correlation (*covS*) ‡	*P*-value Correlation (*covS*)	*Q*-value Correlation (*covS*) §
M5005_Spy1197	-	SpyM3_1124	2158	2247	-0.1707	0.2409	0.1560	-0.1829	0.2084	0.1911
M5005_Spy1489	*fabF*	spy1748	1187	1178	-0.1707	0.2409	0.1560	-0.2496	0.0837	0.1048
M5005_Spy1029	-	SpyM3_0954	2571	2373	-0.1708	0.2406	0.1560	0.0952	0.5155	0.3438
M5005_Spy1841	*sdhB*	spy2189	1009	730	-0.1712	0.2396	0.1556	-0.3130	0.0286	0.0547
M5005_Spy0897	-	spy1177	779	967	-0.1713	0.2392	0.1555	0.0102	0.9445	0.4850
M5005_Spy0600	*rpoD*		1967	2201	-0.1721	0.2370	0.1543	-0.0786	0.5912	0.3719
M5005_Spy1047	-	SpyM3_0973	1555	1463	-0.1732	0.2341	0.1530	-0.3428	0.0159	0.0396
M5005_Spy1771	*hutU*		1013	1183	-0.1734	0.2335	0.1530	-0.2338	0.1059	0.1221
M5005_Spy1298	*aroB*	spy1577	844	921	-0.1736	0.2328	0.1527	-0.0709	0.6284	0.3854
M5005_Spy0104	-	spy0123	637	826	-0.1742	0.2312	0.1519	-0.1079	0.4606	0.3209
M5005_Spy1776	-		2263	2355	-0.1743	0.2311	0.1519	0.1285	0.3789	0.2852
M5005_Spy1032	-	spyM18_1286	984	1332	-0.1747	0.2298	0.1515	-0.3365	0.0181	0.0419
M5005_Spy1515	-	spy1781	1221	1263	-0.1752	0.2284	0.1510	-0.3113	0.0294	0.0556
M5005_Spy0400	*silD*	spy0486	46	87	-0.1753	0.2283	0.1510	-0.3306	0.0203	0.0448
M5005_Spy1442	-		2367	2250	-0.1755	0.2278	0.1508	-0.0761	0.6032	0.3768
M5005_Spy1421	-		2634	2414	-0.1775	0.2224	0.1476	-0.1183	0.4181	0.3034
M5005_Spy0601	-	spy0783	1259	1061	-0.1779	0.2212	0.1468	-0.0840	0.5662	0.3623
M5005_Spy0023	-		2159	2519	-0.1782	0.2205	0.1465	-0.2587	0.0727	0.0962
M5005_Spy1284	-		1787	1685	-0.1785	0.2197	0.1461	-0.0858	0.5576	0.3596
M5005_Spy1729	-		2526	2516	-0.1791	0.2182	0.1453	-0.2054	0.1568	0.1594
M5005_Spy1672	-		1586	1380	-0.1792	0.2180	0.1453	-0.0920	0.5297	0.3502
M5005_Spy0318	*pflC*	spy0379	382	511	-0.1797	0.2165	0.1446	-0.1559	0.2848	0.2359
M5005_Spy0876	-	spy1155	1299	1430	-0.1801	0.2155	0.1442	-0.2140	0.1397	0.1487
M5005_Spy0402	-	spy0488	1473	1412	-0.1809	0.2135	0.1434	-0.0813	0.5788	0.3669
M5005_Spy0803	*srtI*		1327	1619	-0.1815	0.2121	0.1429	-0.0440	0.7642	0.4328
M5005_Spy1584	-	spy1866	705	748	-0.1817	0.2114	0.1426	0.0059	0.9680	0.4911
M5005_Spy1667	-	spy1956	2585	2390	-0.1821	0.2104	0.1420	-0.1834	0.2071	0.1909
M5005_Spy1040	-		1672	1925	-0.1822	0.2102	0.1420	0.1670	0.2515	0.2184
M5005_Spy1573	*glpF.2*	spy1854	1364	1206	-0.1827	0.2088	0.1413	-0.0514	0.7258	0.4198
M5005_Spy0730	*nth*	spy0929	956	939	-0.1836	0.2066	0.1402	-0.0046	0.9748	0.4926
M5005_Spy1393	-	spy1700	501	481	-0.1843	0.2049	0.1394	0.0601	0.6817	0.4056
M5005_Spy0903	*oadB*	spy1184	1085	1247	-0.1846	0.2042	0.1390	0.0472	0.7473	0.4271

M5005_Spy#	Gene	Synonym *	WT Transcript Rank †	Mutant Transcript Rank †	*r* Correlation (*covR*) ‡	*P*-value Correlation (*covR*)	*Q*-value Correlation (*covR*) §	*r* Correlation (*covS*) ‡	*P*-value Correlation (*covS*)	*Q*-value Correlation (*covS*) §
M5005_Spy0732	-	spy0931	1110	1124	-0.1852	0.2027	0.1380	-0.1260	0.3882	0.2891
M5005_Spy0654	-	spy0846	2167	2038	-0.1853	0.2025	0.1380	0.2450	0.0898	0.1093
M5005_Spy1814	*hisS*	spy2157	1398	1474	-0.1853	0.2024	0.1380	-0.2228	0.1239	0.1365
M5005_Spy0006	*trcF*	spy0008	1287	1303	-0.1863	0.2000	0.1370	-0.2050	0.1577	0.1601
M5005_Spy1006	-		2174	2475	-0.1875	0.1969	0.1352	-0.2021	0.1638	0.1633
M5005_Spy1352	-	spy1646	362	377	-0.1881	0.1956	0.1344	0.0025	0.9862	0.4955
M5005_Spy0172	-	spy0199	1335	1939	-0.1889	0.1937	0.1334	-0.0730	0.6182	0.3817
M5005_Spy1029	-	spyM18_0740	1409	1548	-0.1896	0.1919	0.1326	0.0521	0.7224	0.4189
M5005_Spy0470	-	spy0567	1002	1070	-0.1898	0.1915	0.1323	-0.3653	0.0098	0.0294
M5005_Spy1106	*grab*		2128	1813	-0.1909	0.1890	0.1310	-0.4132	0.0032	0.0142
M5005_Spy1190	-	spy1462	1887	1660	-0.1913	0.1880	0.1305	0.1069	0.4649	0.3227
M5005_Spy1205	-		2147	2339	-0.1913	0.1879	0.1305	-0.1253	0.3909	0.2906
M5005_Spy1444	-		1857	1794	-0.1919	0.1866	0.1298	-0.2447	0.0901	0.1096
M5005_Spy0114	-		1939	1440	-0.192	0.1863	0.1297	-0.2511	0.0818	0.1034
M5005_Spy1713	-	M12_2021	1005	1323	-0.1923	0.1857	0.1295	-0.1178	0.4201	0.3042
M5005_Spy0109	-	spy0128	830	875	-0.193	0.1840	0.1285	-0.0802	0.5840	0.3693
M5005_Spy1522	-	spy1787	566	526	-0.193	0.1840	0.1285	-0.0726	0.6202	0.3817
M5005_Spy1789	*nrdG*	spy2105	639	720	-0.1935	0.1828	0.1280	-0.2755	0.0553	0.0809
M5005_Spy0858	*xpt*		2569	2640	-0.1953	0.1787	0.1254	-0.3392	0.0171	0.0408
M5005_Spy1194	-	spyM18_1481	2335	2528	-0.1956	0.1781	0.1251	-0.1620	0.2661	0.2275
M5005_Spy0491	-	spy0591	699	901	-0.1961	0.1768	0.1245	-0.0495	0.7354	0.4239
M5005_Spy1584	-		1805	1566	-0.1966	0.1758	0.1240	-0.0138	0.9251	0.4812
M5005_Spy1785	-	spy2099	1874	1614	-0.1977	0.1734	0.1228	-0.2614	0.0696	0.0933
M5005_Spy0840	*radC*	spy1118	2038	1954	-0.1984	0.1719	0.1220	-0.2062	0.1552	0.1582
M5005_Spy1173	-	SpyM3_0729	2202	1622	-0.1988	0.1709	0.1215	0.1672	0.2509	0.2183
M5005_Spy1205	-	SpyM3_1136	2490	2513	-0.1989	0.1707	0.1214	-0.3264	0.0221	0.0469
M5005_Spy0781	*ptsB*	spyM18_1035	2584	2401	-0.1991	0.1702	0.1212	-0.2849	0.0473	0.0730
M5005_Spy1566	*recD*	spy1844	646	701	-0.1991	0.1702	0.1212	-0.3165	0.0267	0.0523
M5005_Spy0911	-	spy1193	669	928	-0.1998	0.1687	0.1206	-0.1505	0.3020	0.2456
M5005_Spy1383	-	spy1687	554	525	-0.1998	0.1686	0.1206	-0.4404	0.0015	**0.0092**
M5005_Spy1467	*int.3*		1641	1630	-0.2012	0.1656	0.1189	-0.1750	0.2290	0.2061
M5005_Spy0186	-	spy0216	1333	1219	-0.2024	0.1631	0.1174	-0.3762	0.0077	0.0249

M5005_Spy#	Gene	Synonym *	WT Transcript Rank †	Mutant Transcript Rank †	*r* Correlation (*covR*) ‡	*P*-value Correlation (*covR*)	*Q*-value Correlation (*covR*) §	*r* Correlation (*covS*) ‡	*P*-value Correlation (*covS*)	*Q*-value Correlation (*covS*) §
M5005_Spy0596	-	spy0778	850	807	-0.2026	0.1626	0.1171	0.0080	0.9563	0.4881
M5005_Spy0516	*pacL*		1894	2101	-0.203	0.1617	0.1169	0.0145	0.9214	0.4802
M5005_Spy1655	*cysS*	spy1940	1056	1145	-0.2043	0.1591	0.1155	-0.3236	0.0233	0.0485
M5005_Spy1702	*smeZ*	spyM18_2063	1889	2039	-0.2045	0.1586	0.1152	-0.1306	0.3711	0.2817
M5005_Spy0744	-	SpyM3_0654	2265	2539	-0.2047	0.1582	0.1150	-0.3294	0.0208	0.0453
M5005_Spy0307	-	spy0365	2034	1623	-0.2051	0.1575	0.1147	-0.2224	0.1246	0.1367
M5005_Spy0545	*agaS*	spyM18_0784	2532	2257	-0.2051	0.1574	0.1147	-0.3795	0.0072	0.0237
M5005_Spy1437	-	SpyM3_1432	1790	2175	-0.2055	0.1567	0.1142	-0.2285	0.1143	0.1281
M5005_Spy1261	-	spy1533	632	598	-0.2065	0.1546	0.1133	-0.2117	0.1441	0.1514
M5005_Spy1491	*fabD*	spy1750	1598	1350	-0.2067	0.1541	0.1131	-0.2011	0.1660	0.1649
M5005_Spy0403	-	spy0489	1443	2023	-0.2074	0.1528	0.1123	0.1953	0.1788	0.1737
M5005_Spy1560	-	spy1836	1128	1173	-0.2081	0.1512	0.1113	-0.2038	0.1602	0.1615
M5005_Spy0121	-	M12_0965	2392	2215	-0.2081	0.1514	0.1113	0.1242	0.3951	0.2928
M5005_Spy1131	-	spy1385	1656	1713	-0.2083	0.1508	0.1113	-0.1209	0.4081	0.2991
M5005_Spy0347	*nrdF.1*	spy0425	661	672	-0.2089	0.1498	0.1110	-0.1973	0.1741	0.1708
M5005_Spy0964	-	spy1254	1460	1808	-0.2096	0.1484	0.1101	-0.2323	0.1082	0.1234
M5005_Spy0708	*ung*	spy0905	1130	1205	-0.2097	0.1482	0.1100	-0.1368	0.3488	0.2711
M5005_Spy1294	-	spy1570	379	585	-0.2108	0.1461	0.1087	-0.1895	0.1921	0.1821
M5005_Spy1645	-		1534	2053	-0.2109	0.1458	0.1086	-0.3223	0.0239	0.0489
M5005_Spy0017	*sibA*		2031	1642	-0.2116	0.1444	0.1078	-0.0682	0.6417	0.3903
M5005_Spy1185	-		2085	2214	-0.2119	0.1438	0.1074	-0.0257	0.8609	0.4612
M5005_Spy0523	-		1961	2221	-0.2126	0.1426	0.1068	-0.1879	0.1961	0.1846
M5005_Spy1790	-	spy2106	248	326	-0.2128	0.1421	0.1067	-0.2184	0.1317	0.1426
M5005_Spy0033	*purB*	spy0036	631	590	-0.2154	0.1372	0.1039	-0.2968	0.0384	0.0647
M5005_Spy1370	-	spy1666	681	824	-0.2158	0.1365	0.1034	-0.1913	0.1879	0.1803
M5005_Spy1551	-	spy1827	1055	1062	-0.2158	0.1364	0.1034	-0.1189	0.4160	0.3023
M5005_Spy0913	-	spy1196	656	833	-0.2161	0.1358	0.1031	-0.1021	0.4849	0.3304
M5005_Spy0036	-	spy0039	882	1118	-0.2177	0.1330	0.1015	-0.0550	0.7076	0.4146
M5005_Spy0043	*rpsJ*		2351	2345	-0.2178	0.1327	0.1013	-0.2212	0.1266	0.1381
M5005_Spy0985	-	spyM18_1226	508	674	-0.2179	0.1325	0.1013	-0.3417	0.0163	0.0400
M5005_Spy1577	*pepXP*	spy1858	1214	1025	-0.2183	0.1319	0.1010	-0.1080	0.4601	0.3208
M5005_Spy0583	-	M12_0158	2653	2574	-0.2188	0.1309	0.1003	-0.0964	0.5101	0.3416

M5005_Spy#	Gene	Synonym *	WT Transcript Rank †	Mutant Transcript Rank †	*r* Correlation (*covR*) ‡	*P*-value Correlation (*covR*)	*Q*-value Correlation (*covR*) §	*r* Correlation (*covS*) ‡	*P*-value Correlation (*covS*)	*Q*-value Correlation (*covS*) §
M5005_Spy1502	-	spy1764	1313	1531	-0.2189	0.1308	0.1003	0.0333	0.8204	0.4498
M5005_Spy1296	-	spy1572	1109	1378	-0.219	0.1305	0.1002	-0.3347	0.0187	0.0424
M5005_Spy1422	-		1083	1387	-0.2197	0.1294	0.0998	-0.1683	0.2478	0.2163
M5005_Spy0468	-	spyM18_0635	2238	1876	-0.2205	0.1278	0.0991	-0.0745	0.6111	0.3794
M5005_Spy1094	-	spy1340	1875	1977	-0.221	0.1271	0.0989	-0.2412	0.0950	0.1137
M5005_Spy1098	-	spyM18_1359	1791	1510	-0.221	0.1270	0.0989	-0.1289	0.3776	0.2849
M5005_Spy1527	-	spy1794	811	783	-0.221	0.1270	0.0989	-0.1306	0.3712	0.2817
M5005_Spy1665	-	spyM18_2020	2198	2239	-0.2213	0.1266	0.0988	-0.0039	0.9790	0.4934
M5005_Spy1476	-	spy1735	1102	977	-0.2214	0.1263	0.0987	-0.1641	0.2599	0.2239
M5005_Spy0622	-	spy0807	342	406	-0.2224	0.1245	0.0978	-0.1374	0.3464	0.2703
M5005_Spy1716	*tnp*	spy2013	784	798	-0.2227	0.1240	0.0976	-0.3120	0.0291	0.0554
M5005_Spy1126	-	spy0195	2509	2065	-0.2233	0.1230	0.0970	-0.0589	0.6879	0.4075
M5005_Spy0037	-		1862	2289	-0.2234	0.1229	0.0970	0.0152	0.9174	0.4789
M5005_Spy1497	*dnaJ*	spy1759	149	235	-0.2253	0.1196	0.0952	-0.1208	0.4084	0.2991
M5005_Spy1203	-	spyM18_0733	2056	2231	-0.2261	0.1182	0.0943	-0.4715	0.0006	**0.0065**
M5005_Spy1627	*salY*	spy1911	1617	1569	-0.227	0.1168	0.0933	-0.1376	0.3459	0.2702
M5005_Spy0825	*murB*	spy1101	1309	1276	-0.2274	0.1160	0.0928	-0.2938	0.0404	0.0660
M5005_Spy1493	*acpP*	spy1753	1442	1726	-0.2286	0.1141	0.0917	-0.2910	0.0425	0.0682
M5005_Spy1582	*dnaQ*		1820	2099	-0.2292	0.1131	0.0912	-0.1170	0.4235	0.3054
M5005_Spy1203	-	SpyM3_1132	1928	2094	-0.23	0.1118	0.0903	-0.2367	0.1015	0.1188
M5005_Spy0902	-	spy1183	1176	1308	-0.2304	0.1112	0.0900	-0.3087	0.0309	0.0572
M5005_Spy1278	-	spy1551	819	823	-0.2324	0.1081	0.0882	-0.4401	0.0016	**0.0092**
M5005_Spy0687	*mvaS.1*	spy0881	1412	1367	-0.2331	0.1070	0.0874	-0.1031	0.4810	0.3287
M5005_Spy1552	-	spy1828	1074	1104	-0.2333	0.1066	0.0872	-0.2544	0.0777	0.1006
M5005_Spy1200	-	spy1474	2305	1595	-0.2344	0.1050	0.0863	-0.0855	0.5592	0.3599
M5005_Spy0652	-	spy0844	993	1269	-0.2348	0.1044	0.0860	-0.4076	0.0037	0.0154
M5005_Spy1281	*zmpS*	spyM18_1569	1945	1687	-0.2348	0.1044	0.0860	-0.1896	0.1920	0.1821
M5005_Spy1193	-	spy1464	817	1045	-0.2353	0.1037	0.0857	-0.1602	0.2714	0.2299
M5005_Spy1150	-	spy1411	1627	1763	-0.2356	0.1031	0.0854	0.2333	0.1066	0.1227
M5005_Spy0261	-	spyM18_0302	2397	1956	-0.2362	0.1023	0.0848	-0.2726	0.0581	0.0838
M5005_Spy1658	*cysE*	spy1944	394	393	-0.2365	0.1018	0.0845	-0.0632	0.6662	0.3989
M5005_Spy1205	-	spy0957	2648	2410	-0.2385	0.0989	0.0827	-0.4671	0.0007	**0.0067**

M5005_Spy#	Gene	Synonym *	WT Transcript Rank †	Mutant Transcript Rank †	*r* Correlation (*covR*) ‡	*P*-value Correlation (*covR*)	*Q*-value Correlation (*covR*) §	*r* Correlation (*covS*) ‡	*P*-value Correlation (*covS*)	*Q*-value Correlation (*covS*) §
M5005_Spy1513	-	spy1779	712	729	-0.2392	0.0979	0.0820	-0.2323	0.1082	0.1234
M5005_Spy0895	-	spy1175	1560	1641	-0.2393	0.0977	0.0819	-0.2126	0.1425	0.1510
M5005_Spy1672	*polC*	spy1961	539	437	-0.2401	0.0966	0.0813	-0.3988	0.0045	0.0178
M5005_Spy0306	-	spy0364	933	1281	-0.2403	0.0963	0.0811	-0.2667	0.0639	0.0888
M5005_Spy0588	*pheT*	spy0769	1122	1170	-0.2405	0.0960	0.0810	-0.0770	0.5989	0.3750
M5005_Spy1702	*smeZ*		2290	2344	-0.2405	0.0960	0.0810	-0.0522	0.7218	0.4189
M5005_Spy1415	*sdaD2*		2468	2468	-0.241	0.0952	0.0805	-0.0264	0.8571	0.4606
M5005_Spy0789	-	spy1066	1158	1095	-0.2438	0.0914	0.0779	-0.2143	0.1392	0.1483
M5005_Spy0185	*pgi*	spy0215	917	841	-0.2439	0.0912	0.0779	-0.1843	0.2049	0.1899
M5005_Spy1840	*trmU*	spy2188	607	685	-0.2439	0.0912	0.0779	-0.5545	3.6E-05	**0.0055**
M5005_Spy0769	-	spy1046	1086	1108	-0.2451	0.0896	0.0770	-0.2365	0.1018	0.1190
M5005_Spy0605	*rgpCc*	spy0789	1240	851	-0.2456	0.0890	0.0765	-0.1378	0.3452	0.2698
M5005_Spy0104	-		2253	1683	-0.246	0.0884	0.0762	-0.1618	0.2668	0.2278
M5005_Spy1822	-		1290	1392	-0.2487	0.0849	0.0738	0.0589	0.6875	0.4075
M5005_Spy0969	-	spyM18_1209	2274	2183	-0.2489	0.0846	0.0736	0.1203	0.4102	0.2997
M5005_Spy1281	*zmpS*	spy1556	1501	1788	-0.2489	0.0846	0.0736	-0.2023	0.1633	0.1632
M5005_Spy1529	*htsA, siaA*	spy1795	970	1003	-0.2509	0.0820	0.0722	-0.0236	0.8723	0.4653
M5005_Spy1470	-	spy1728	1191	1172	-0.2516	0.0811	0.0719	-0.2977	0.0378	0.0640
M5005_Spy1639	*lacR.2*		1927	2269	-0.2516	0.0811	0.0719	-0.1233	0.3986	0.2950
M5005_Spy1782	*pepO*		2152	2439	-0.2526	0.0799	0.0711	-0.1020	0.4856	0.3305
M5005_Spy1004	-	SpyM3_1308	2203	2440	-0.2528	0.0796	0.0710	0.0269	0.8546	0.4602
M5005_Spy1761	*groEL*	spy2070	111	176	-0.2532	0.0791	0.0707	-0.3441	0.0155	0.0388
M5005_Spy1006	-		1544	1686	-0.2533	0.0791	0.0707	-0.1604	0.2711	0.2299
M5005_Spy1663	-	spy1952	2323	1907	-0.2533	0.0791	0.0707	-0.0948	0.5172	0.3446
M5005_Spy1839	-	spy2186	1243	1211	-0.2535	0.0788	0.0707	-0.2119	0.1438	0.1514
M5005_Spy1172	-	spy0707	1736	1853	-0.2539	0.0784	0.0703	-0.0670	0.6472	0.3919
M5005_Spy1428	-		2149	1719	-0.2548	0.0772	0.0694	0.0569	0.6976	0.4115
M5005_Spy1178	-	spyM18_1462	2356	2525	-0.2549	0.0772	0.0694	-0.2008	0.1665	0.1650
M5005_Spy0327	*upp*	spy0393	1520	1774	-0.2555	0.0764	0.0690	-0.4092	0.0035	0.0150
M5005_Spy0030	*purE*	spy0033	1543	1798	-0.256	0.0758	0.0686	-0.0291	0.8429	0.4563
M5005_Spy0445	*metK*	spy0538	2321	2488	-0.2566	0.0751	0.0681	-0.3681	0.0093	0.0282
M5005_Spy1208	-	spyM18_0727	2014	2158	-0.257	0.0746	0.0678	-0.0320	0.8273	0.4521

M5005_Spy#	Gene	Synonym *	WT Transcript Rank †	Mutant Transcript Rank †	*r* Correlation (*covR*) ‡	*P*-value Correlation (*covR*)	*Q*-value Correlation (*covR*) §	*r* Correlation (*covS*) ‡	*P*-value Correlation (*covS*)	*Q*-value Correlation (*covS*) §
M5005_Spy0213	-		1963	2002	-0.2572	0.0744	0.0677	-0.2104	0.1467	0.1530
M5005_Spy0885	-	SpyM3_0820	1386	1502	-0.2582	0.0733	0.0668	-0.1603	0.2713	0.2299
M5005_Spy0775	-	M12_1893	1225	1405	-0.2586	0.0728	0.0665	-0.2676	0.0631	0.0881
M5005_Spy0848	-	spy1126	617	633	-0.2586	0.0728	0.0665	-0.3900	0.0056	0.0204
M5005_Spy0550	-	spy0723	1752	1611	-0.2591	0.0722	0.0662	0.0798	0.5857	0.3698
M5005_Spy1198	-	spy0676	2012	1427	-0.2607	0.0705	0.0652	-0.3649	0.0099	0.0296
M5005_Spy0893	*gid*	spy1173	750	810	-0.2614	0.0696	0.0647	-0.5166	0.0001	**0.0055**
M5005_Spy0573	*lig*	spy0751	1090	1041	-0.2637	0.0671	0.0627	-0.1877	0.1964	0.1846
M5005_Spy0261	-	spy0306	930	960	-0.2643	0.0665	0.0623	0.1017	0.4870	0.3309
M5005_Spy1685	-	#N/A	1583	2185	-0.2668	0.0639	0.0605	-0.0392	0.7889	0.4410
M5005_Spy1061	-	SpyM3_0986	1559	2204	-0.2669	0.0638	0.0605	-0.2897	0.0434	0.0691
M5005_Spy1151	-	spy1412	2279	2263	-0.2699	0.0608	0.0586	-0.3341	0.0190	0.0428
M5005_Spy0238	*bacA*	spy0280	1081	1139	-0.2711	0.0595	0.0576	0.0821	0.5749	0.3655
M5005_Spy0360	-	SpyM3_0310	2446	2105	-0.2743	0.0565	0.0554	-0.0141	0.9235	0.4808
M5005_Spy0396	-		1315	1689	-0.275	0.0558	0.0549	-0.2532	0.0792	0.1016
M5005_Spy1681	*dexB*	spy1973	862	704	-0.275	0.0558	0.0549	-0.1427	0.3280	0.2612
M5005_Spy1456	-	SpyM3_1447	1913	1946	-0.2789	0.0523	0.0518	-0.1091	0.4554	0.3189
M5005_Spy1326	*comFC*	spy1615	2564	2501	-0.2791	0.0521	0.0518	-0.1903	0.1903	0.1818
M5005_Spy1460	-	M12_1769	1067	1328	-0.2797	0.0516	0.0515	-0.1602	0.2714	0.2299
M5005_Spy0920	-	spy1205	2535	2019	-0.28	0.0514	0.0513	-0.1725	0.2359	0.2095
M5005_Spy0846	-	spy1124	2125	2133	-0.2816	0.0500	0.0502	-0.3013	0.0354	0.0621
M5005_Spy1630	*salB*		1958	2080	-0.2818	0.0498	0.0501	-0.1092	0.4552	0.3189
M5005_Spy0010	-		1322	1353	-0.282	0.0496	0.0500	-0.1859	0.2010	0.1877
M5005_Spy0645	-	spy0836	694	738	-0.282	0.0496	0.0500	0.0537	0.7138	0.4165
M5005_Spy0882	-	spy1161	1759	1664	-0.284	0.0480	0.0489	-0.3385	0.0174	0.0409
M5005_Spy1519	*recG*	spy1785	625	699	-0.2841	0.0479	0.0489	-0.5341	7.7E-05	**0.0055**
M5005_Spy1430	-		2051	1815	-0.2842	0.0478	0.0488	0.1265	0.3863	0.2882
M5005_Spy1384	*glyS*		1925	1349	-0.2844	0.0476	0.0487	-0.3425	0.0160	0.0397
M5005_Spy1215	-	spy0948	924	1079	-0.2847	0.0474	0.0485	-0.2384	0.0990	0.1170
M5005_Spy1347	-		2604	2549	-0.2847	0.0474	0.0485	-0.2762	0.0547	0.0805
M5005_Spy1863	-	spyM18_2254	1718	1482	-0.2872	0.0454	0.0472	-0.2879	0.0449	0.0707
M5005_Spy1384	*glyS*		2467	2499	-0.2881	0.0447	0.0466	-0.3234	0.0234	0.0485

M5005_Spy#	Gene	Synonym *	WT Transcript Rank †	Mutant Transcript Rank †	*r* Correlation (*covR*) ‡	*P*-value Correlation (*covR*)	*Q*-value Correlation (*covR*) §	*r* Correlation (*covS*) ‡	*P*-value Correlation (*covS*)	*Q*-value Correlation (*covS*) §
M5005_Spy0759	-		1550	1516	-0.289	0.0440	0.0461	-0.3472	0.0145	0.0373
M5005_Spy1485	*accA*	spy1743	1532	1250	-0.289	0.0440	0.0461	-0.1911	0.1884	0.1806
M5005_Spy1429	-		2009	1616	-0.2895	0.0436	0.0458	-0.3234	0.0234	0.0485
M5005_Spy1005	-		1732	1780	-0.2921	0.0417	0.0442	-0.0262	0.8583	0.4607
M5005_Spy1433	-		2447	2268	-0.2924	0.0415	0.0440	-0.1517	0.2980	0.2436
M5005_Spy0259	-	spy1806	1179	1234	-0.2928	0.0412	0.0439	-0.1702	0.2423	0.2128
M5005_Spy0636	*epuA*	spy0824	773	1189	-0.2935	0.0407	0.0435	-0.3058	0.0326	0.0593
M5005_Spy0784	*yesM*		1529	1433	-0.2939	0.0404	0.0432	-0.4150	0.0030	0.0139
M5005_Spy0148	-	spy0174	1342	1033	-0.2941	0.0403	0.0431	-0.3576	0.0116	0.0322
M5005_Spy1464	-		2341	2398	-0.2943	0.0401	0.0430	-0.4343	0.0018	0.0101
M5005_Spy1511	-	M12_1829	2621	2638	-0.2945	0.0400	0.0430	-0.1933	0.1832	0.1771
M5005_Spy1168	-	spyM18_1444	1911	2282	-0.2957	0.0392	0.0423	-0.3011	0.0355	0.0621
M5005_Spy1284	-		1810	1940	-0.3001	0.0361	0.0398	-0.3304	0.0204	0.0448
M5005_Spy1420	-		1143	1466	-0.3014	0.0353	0.0392	0.0872	0.5515	0.3572
M5005_Spy0101	*adhE*	spyM18_0119	1089	1132	-0.3026	0.0346	0.0388	-0.4498	0.0012	**0.0080**
M5005_Spy1623	*hsdM*	spy1906	1031	1102	-0.3027	0.0345	0.0387	-0.4396	0.0016	**0.0093**
M5005_Spy0862	*tdk2*	spy1140	768	904	-0.3036	0.0339	0.0383	-0.2903	0.0430	0.0687
M5005_Spy0550	-		2166	2177	-0.3051	0.0331	0.0377	-0.2955	0.0392	0.0653
M5005_Spy0894	*oadA*	spy1174	1952	1694	-0.3053	0.0329	0.0376	-0.2758	0.0551	0.0807
M5005_Spy0793	-		2140	1879	-0.3056	0.0327	0.0375	-0.2332	0.1069	0.1228
M5005_Spy1252	*murG*	spy1524	828	741	-0.3056	0.0327	0.0375	-0.4546	0.0010	**0.0075**
M5005_Spy1186	-	spy1456	1870	2265	-0.3058	0.0326	0.0375	-0.2335	0.1063	0.1224
M5005_Spy0420	-	spy0510	1329	1246	-0.3073	0.0317	0.0366	-0.2242	0.1214	0.1343
M5005_Spy0466	-	spyM18_0633	1702	1829	-0.3074	0.0317	0.0366	-0.1275	0.3828	0.2870
M5005_Spy1134	-	spy1391	936	1051	-0.3091	0.0307	0.0358	-0.3899	0.0056	0.0204
M5005_Spy1722	-	spy2023	621	721	-0.3091	0.0307	0.0358	-0.0870	0.5524	0.3576
M5005_Spy0480	-		2070	2084	-0.3094	0.0305	0.0358	0.0250	0.8645	0.4626
M5005_Spy0659	*apbA*	spy0852	1104	1180	-0.31	0.0302	0.0355	-0.1096	0.4535	0.3186
M5005_Spy0739	-	spy1012	1211	788	-0.3102	0.0301	0.0354	-0.1584	0.2771	0.2325
M5005_Spy1029	-	SpyM3_0696	1751	1590	-0.3102	0.0300	0.0354	-0.3336	0.0191	0.0431
M5005_Spy1466	-		1025	868	-0.3107	0.0298	0.0352	-0.0746	0.6104	0.3793
M5005_Spy1549	-		757	893	-0.3108	0.0297	0.0352	-0.3743	0.0081	0.0260

M5005_Spy#	Gene	Synonym *	WT Transcript Rank †	Mutant Transcript Rank †	*r* Correlation (*covR*) ‡	*P*-value Correlation (*covR*)	*Q*-value Correlation (*covR*) §	*r* Correlation (*covS*) ‡	*P*-value Correlation (*covS*)	*Q*-value Correlation (*covS*) §
M5005_Spy0631	*thiI*	spy0817	764	772	-0.3111	0.0295	0.0350	-0.4158	0.0030	0.0138
M5005_Spy1125	-	spy1379	1149	1133	-0.3113	0.0295	0.0350	-0.4646	0.0008	**0.0068**
M5005_Spy0706	-	spy0903	1016	1073	-0.3122	0.0290	0.0346	-0.1851	0.2029	0.1888
M5005_Spy1205	-		2486	2418	-0.3124	0.0289	0.0345	-0.2806	0.0508	0.0771
M5005_Spy0454	-	spy0546	1840	1668	-0.3125	0.0288	0.0345	-0.1418	0.3310	0.2627
M5005_Spy1742	*mipB*	spy2048	1389	1149	-0.3126	0.0288	0.0345	-0.1158	0.4284	0.3065
M5005_Spy1056	*malM*	spy1292	985	971	-0.3127	0.0287	0.0344	-0.2855	0.0468	0.0725
M5005_Spy1345	*atoD.1*	spy1638	2177	2146	-0.3127	0.0287	0.0344	-0.1663	0.2533	0.2191
M5005_Spy1167	-	SpyM3_1093	2101	1906	-0.3135	0.0283	0.0340	0.1169	0.4237	0.3054
M5005_Spy0480	-		1208	1185	-0.3143	0.0278	0.0336	0.0691	0.6373	0.3891
M5005_Spy1297	-	spy1576	996	1356	-0.3144	0.0278	0.0336	-0.3641	0.0101	0.0297
M5005_Spy1172	-	spyM18_0776	2284	2334	-0.3155	0.0272	0.0331	-0.4424	0.0015	**0.0089**
M5005_Spy1114	-	spy1366	1614	1653	-0.3165	0.0267	0.0326	-0.2511	0.0818	0.1034
M5005_Spy1824	*rpmF*	spyM18_2209	1680	1381	-0.3168	0.0266	0.0325	-0.1291	0.3766	0.2845
M5005_Spy1285	-	spy1561	1026	910	-0.3181	0.0259	0.0318	-0.2692	0.0614	0.0871
M5005_Spy0117	-	spyM18_0135	839	1053	-0.319	0.0255	0.0313	-0.2491	0.0844	0.1054
M5005_Spy1184	-	spy1453	469	752	-0.3191	0.0254	0.0313	-0.2722	0.0584	0.0843
M5005_Spy1746	-	spy2052	1288	1422	-0.3199	0.0250	0.0310	-0.1967	0.1756	0.1715
M5005_Spy0029	*purD*	spy0032	684	662	-0.3201	0.0250	0.0310	-0.3314	0.0200	0.0443
M5005_Spy1329	*cysM*	spy1618	1231	1208	-0.3207	0.0246	0.0307	-0.1343	0.3576	0.2758
M5005_Spy1748	-		803	1002	-0.3215	0.0243	0.0304	-0.2274	0.1160	0.1294
M5005_Spy0724	-	spy0923	831	930	-0.3224	0.0238	0.0300	-0.0065	0.9647	0.4899
M5005_Spy0316	-	spy0377	742	804	-0.3225	0.0238	0.0299	-0.1706	0.2411	0.2122
M5005_Spy1024	-		1794	2217	-0.3228	0.0237	0.0299	-0.0042	0.9772	0.4929
M5005_Spy0544	-		2494	2411	-0.323	0.0236	0.0298	-0.2949	0.0397	0.0654
M5005_Spy1620	-	spy1903	1679	1959	-0.3237	0.0233	0.0295	-0.4419	0.0015	**0.0090**
M5005_Spy1176	-		2368	2317	-0.3237	0.0233	0.0295	-0.1669	0.2517	0.2184
M5005_Spy1576	-	spy1857	682	827	-0.3237	0.0233	0.0295	-0.0488	0.7393	0.4248
M5005_Spy1803	*lmrP*	spy2120	1255	1335	-0.3241	0.0231	0.0294	-0.4197	0.0027	0.0131
M5005_Spy1553	*rpsR*		2642	2622	-0.3249	0.0227	0.0290	-0.5658	2.3E-05	**0.0055**
M5005_Spy1424	-		1705	1926	-0.3253	0.0225	0.0288	-0.2300	0.1118	0.1263
M5005_Spy0658	-	spy0851	476	499	-0.326	0.0223	0.0287	-0.4234	0.0024	0.0123

M5005_Spy#	Gene	Synonym *	WT Transcript Rank †	Mutant Transcript Rank †	*r* Correlation (*covR*) ‡	*P*-value Correlation (*covR*)	*Q*-value Correlation (*covR*) §	*r* Correlation (*covS*) ‡	*P*-value Correlation (*covS*)	*Q*-value Correlation (*covS*) §
M5005_Spy0501	-	spy0603	450	723	-0.3261	0.0222	0.0286	-0.3550	0.0123	0.0335
M5005_Spy1202	-	spyM18_1493	1647	2111	-0.3262	0.0222	0.0286	-0.2890	0.0440	0.0696
M5005_Spy1703	-	spy1999	1948	1734	-0.3267	0.0220	0.0285	-0.4147	0.0031	0.0139
M5005_Spy1510	-	#N/A	1362	1361	-0.3271	0.0218	0.0283	-0.5106	0.0002	**0.0055**
M5005_Spy0997	-		1764	1365	-0.3292	0.0209	0.0274	-0.4164	0.0029	0.0137
M5005_Spy1021	-		2411	2580	-0.3296	0.0208	0.0272	-0.3775	0.0075	0.0245
M5005_Spy0694	*clpL*	spy0888	33	121	-0.3297	0.0207	0.0272	-0.3139	0.0281	0.0542
M5005_Spy0984	-	spy1276	908	832	-0.3299	0.0206	0.0271	-0.0545	0.7099	0.4150
M5005_Spy0468	*tnpA*	spy0565	1918	2575	-0.3309	0.0202	0.0267	-0.1362	0.3509	0.2722
M5005_Spy1461	-	M12_1770	1052	1074	-0.3313	0.0201	0.0266	-0.2826	0.0491	0.0751
M5005_Spy1491	*fabD*	spy1749	968	1272	-0.3314	0.0200	0.0266	-0.1965	0.1760	0.1716
M5005_Spy0024	*purF*	spy0026	1204	794	-0.3329	0.0194	0.0261	-0.3301	0.0205	0.0449
M5005_Spy0280	-		1169	1337	-0.333	0.0194	0.0261	-0.3496	0.0138	0.0362
M5005_Spy0490	-	spy0590	1091	1239	-0.3355	0.0184	0.0251	-0.3283	0.0213	0.0460
M5005_Spy0770	-	spy1047	2312	2436	-0.3374	0.0177	0.0242	-0.0568	0.6983	0.4115
M5005_Spy0031	*purK*	spy0034	1467	1451	-0.3385	0.0174	0.0238	-0.2688	0.0619	0.0872
M5005_Spy0518	-	spy0628	2138	1983	-0.3387	0.0173	0.0237	-0.3411	0.0165	0.0402
M5005_Spy0978	-	spy1270	1864	2511	-0.3395	0.0170	0.0235	-0.2379	0.0997	0.1173
M5005_Spy1022	-		1610	2281	-0.3396	0.0170	0.0234	-0.3602	0.0110	0.0311
M5005_Spy1184	-	SpyM3_1109	1385	1797	-0.3398	0.0169	0.0234	-0.3445	0.0154	0.0387
M5005_Spy1787	-	spyM18_2161	2473	2370	-0.3398	0.0169	0.0234	-0.4128	0.0032	0.0142
M5005_Spy0278	*gidB*	spy0329	1388	1506	-0.3408	0.0166	0.0230	-0.4240	0.0024	0.0122
M5005_Spy1823	-	#N/A	2431	2036	-0.3411	0.0165	0.0229	0.0771	0.5985	0.3749
M5005_Spy0358	-		1198	1146	-0.3412	0.0164	0.0229	-0.0860	0.5566	0.3595
M5005_Spy0749	-	spy1024	1334	1581	-0.3433	0.0157	0.0221	-0.1837	0.2064	0.1908
M5005_Spy1089	-	spyM18_1343	439	734	-0.3438	0.0156	0.0219	-0.2576	0.0740	0.0972
M5005_Spy1786	-	spyM18_2160	1621	1414	-0.3439	0.0155	0.0219	-0.2021	0.1638	0.1633
M5005_Spy1132	*alaS*	spyM18_1397	2347	2166	-0.3441	0.0155	0.0219	-0.1139	0.4357	0.3100
M5005_Spy0465	-	spyM18_0631	667	865	-0.345	0.0152	0.0215	-0.0400	0.7848	0.4399
M5005_Spy1863	-	spyM18_1319	2609	2641	-0.3451	0.0152	0.0215	-0.3171	0.0264	0.0520
M5005_Spy0806	*srtA*	spy1083	1343	1573	-0.3465	0.0147	0.0209	-0.1380	0.3443	0.2697
M5005_Spy1407	-	spy1718	1576	1362	-0.3471	0.0146	0.0207	0.0937	0.5219	0.3467

M5005_Spy#	Gene	Synonym *	WT Transcript Rank †	Mutant Transcript Rank †	*r* Correlation (*covR*) ‡	*P*-value Correlation (*covR*)	*Q*-value Correlation (*covR*) §	*r* Correlation (*covS*) ‡	*P*-value Correlation (*covS*)	*Q*-value Correlation (*covS*) §
M5005_Spy0505	*ppc*	spy0608	597	702	-0.3472	0.0145	0.0207	-0.3306	0.0203	0.0448
M5005_Spy1649	-	spy1934	1135	1306	-0.3492	0.0139	0.0201	-0.4566	0.0010	**0.0074**
M5005_Spy1027	-	spyM18_1786	2417	2387	-0.3498	0.0138	0.0199	-0.0726	0.6202	0.3817
M5005_Spy1201	-	spy1473	1325	1723	-0.351	0.0134	0.0196	-0.3560	0.0120	0.0329
M5005_Spy1435	-		1008	1136	-0.3518	0.0132	0.0193	-0.3422	0.0161	0.0399
M5005_Spy0857	*guaC*	spy1135	995	1024	-0.3522	0.0131	0.0192	-0.2480	0.0858	0.1064
M5005_Spy1216	-	spy0947	1987	2049	-0.3539	0.0126	0.0186	-0.3272	0.0217	0.0466
M5005_Spy1205	-	spy1478	2311	2078	-0.3552	0.0123	0.0182	-0.2527	0.0799	0.1022
M5005_Spy0459	-	spy0555	2010	1810	-0.357	0.0118	0.0177	-0.2763	0.0547	0.0805
M5005_Spy1161	-	spy1424	818	1228	-0.3575	0.0117	0.0175	-0.3231	0.0235	0.0485
M5005_Spy1499	*grpE*	spy1761	21	45	-0.3578	0.0116	0.0175	-0.4937	0.0003	**0.0057**
M5005_Spy0710	-	spy0908	1116	986	-0.358	0.0115	0.0174	-0.2742	0.0566	0.0821
M5005_Spy0215	-		1105	1214	-0.3581	0.0115	0.0174	-0.3137	0.0282	0.0543
M5005_Spy1343	-	spy1634	980	935	-0.3581	0.0115	0.0174	-0.5083	0.0002	**0.0055**
M5005_Spy0151	-	spy0177	971	580	-0.3582	0.0115	0.0174	-0.1213	0.4063	0.2987
M5005_Spy1214	-	spy0949	709	902	-0.3587	0.0114	0.0172	-0.1563	0.2834	0.2350
M5005_Spy1187	-		1476	1607	-0.3591	0.0113	0.0172	-0.3911	0.0055	0.0200
M5005_Spy0253	*oppF*	spy0297	456	442	-0.3608	0.0109	0.0166	-0.1094	0.4543	0.3186
M5005_Spy1189	-		1946	2196	-0.3623	0.0105	0.0162	-0.5322	8.3E-05	**0.0055**
M5005_Spy1476	-	spy1734	1411	1424	-0.3645	0.0100	0.0156	-0.3992	0.0045	0.0177
M5005_Spy0248	*dacA*	spy0292	833	1063	-0.3648	0.0100	0.0156	-0.3949	0.0050	0.0189
M5005_Spy0788	-	spy1065	1019	1318	-0.3655	0.0098	0.0154	-0.1597	0.2731	0.2308
M5005_Spy0256	*comX1.1*	spy0300	1314	1409	-0.3664	0.0096	0.0152	-0.1064	0.4668	0.3235
M5005_Spy1572	-	spy1852	1207	1481	-0.3673	0.0094	0.0150	-0.4861	0.0004	**0.0059**
M5005_Spy0418	-	spy0507	751	630	-0.368	0.0093	0.0148	-0.3445	0.0153	0.0387
M5005_Spy1843	-	spy2191	520	691	-0.369	0.0091	0.0145	-0.2967	0.0385	0.0648
M5005_Spy0544	-	spyM18_0783	2451	2605	-0.3693	0.0090	0.0145	-0.3569	0.0118	0.0325
M5005_Spy1681	*dexB*		854	1309	-0.3716	0.0086	0.0139	-0.2895	0.0436	0.0693
M5005_Spy0807	*srtT*	spy1084	1957	1757	-0.3725	0.0084	0.0137	-0.1403	0.3363	0.2649
M5005_Spy1384	*glyS*	spy1688	724	917	-0.3733	0.0082	0.0135	-0.4752	0.0006	**0.0063**
M5005_Spy0861	-	spy1139	1448	1201	-0.3735	0.0082	0.0135	-0.1278	0.3816	0.2866
M5005_Spy0759	-	spy1034	1851	1882	-0.3746	0.0080	0.0133	-0.1353	0.3540	0.2742

M5005_Spy#	Gene	Synonym *	WT Transcript Rank †	Mutant Transcript Rank †	*r* Correlation (*covR*) ‡	*P*-value Correlation (*covR*)	*Q*-value Correlation (*covR*) §	*r* Correlation (*covS*) ‡	*P*-value Correlation (*covS*)	*Q*-value Correlation (*covS*) §
M5005_Spy1656	-	spy1942	1387	2162	-0.3754	0.0079	0.0131	-0.4492	0.0012	**0.0080**
M5005_Spy0005	*pth*	spy0007	1304	1343	-0.3766	0.0076	0.0128	-0.3077	0.0315	0.0579
M5005_Spy1673	*proS*		2479	2487	-0.3778	0.0075	0.0125	-0.4119	0.0033	0.0143
M5005_Spy1399	-		2492	2450	-0.3787	0.0073	0.0123	-0.3976	0.0047	0.0181
M5005_Spy1324	-	spyM18_1620	2259	1967	-0.3791	0.0072	0.0123	-0.2936	0.0406	0.0662
M5005_Spy0849	-	spy1127	1251	1265	-0.3792	0.0072	0.0123	-0.5265	0.0001	**0.0055**
M5005_Spy0693	-	spy0887	460	542	-0.3793	0.0072	0.0123	-0.3390	0.0172	0.0408
M5005_Spy0611	-	spy0796	1256	1326	-0.3797	0.0071	0.0122	-0.2614	0.0697	0.0933
M5005_Spy0454	-	spy0547	2538	2347	-0.3801	0.0071	0.0122	-0.3430	0.0158	0.0395
M5005_Spy1500	*hrcA*	spy1763	24	53	-0.3802	0.0071	0.0122	-0.4529	0.0011	**0.0076**
M5005_Spy0432	-	spy0524	1724	1952	-0.3817	0.0068	0.0118	0.0856	0.5586	0.3597
M5005_Spy1341	*gmk*	spy1632	659	707	-0.3824	0.0067	0.0117	-0.1747	0.2298	0.2061
M5005_Spy1297	-	spy1575	1242	1223	-0.3836	0.0065	0.0114	-0.2343	0.1051	0.1214
M5005_Spy1572	-		1172	1513	-0.3836	0.0065	0.0114	-0.1710	0.2400	0.2118
M5005_Spy1060	*malG*	spy1295	1546	1254	-0.386	0.0062	0.0110	-0.3399	0.0169	0.0405
M5005_Spy1405	*copA*		2228	1730	-0.3862	0.0061	0.0110	-0.4388	0.0016	**0.0094**
M5005_Spy1449	-		1482	1628	-0.3862	0.0061	0.0110	-0.3388	0.0173	0.0408
M5005_Spy0817	*dacA*	spyM18_1051	1363	1675	-0.3876	0.0059	0.0108	-0.1337	0.3597	0.2766
M5005_Spy0288	*snf*	spy0342	393	647	-0.3884	0.0058	0.0106	-0.2537	0.0785	0.1011
M5005_Spy1648	-	spy1935	2189	1575	-0.3885	0.0058	0.0106	-0.1633	0.2622	0.2252
M5005_Spy0511	*murM*	spy0616	806	797	-0.3889	0.0057	0.0106	-0.4278	0.0022	0.0115
M5005_Spy1426	-		1478	1717	-0.3891	0.0057	0.0106	-0.2948	0.0398	0.0655
M5005_Spy1492	*fabK*		2539	2608	-0.3897	0.0056	0.0105	-0.1160	0.4275	0.3062
M5005_Spy1749	-	spy2055	894	1125	-0.3908	0.0055	0.0104	-0.3508	0.0135	0.0355
M5005_Spy1608	-	spy1892	781	913	-0.391	0.0055	0.0103	-0.3055	0.0328	0.0596
M5005_Spy1129	-	spy1384	1882	1608	-0.3932	0.0052	**0.0099**	-0.2893	0.0438	0.0695
M5005_Spy1426	-		2320	2192	-0.3935	0.0052	**0.0099**	-0.2784	0.0527	0.0790
M5005_Spy0587	*pheS*	spy0768	1201	1273	-0.3936	0.0051	**0.0099**	-0.3241	0.0231	0.0484
M5005_Spy1044	-	SpyM3_0964	2229	2503	-0.395	0.0050	**0.0097**	-0.1842	0.2052	0.1899
M5005_Spy1745	-	spy2051	1434	1533	-0.3956	0.0049	**0.0095**	-0.3358	0.0183	0.0422
M5005_Spy0443	-	spy0536	1241	1338	-0.3967	0.0048	**0.0094**	-0.0643	0.6608	0.3969
M5005_Spy0688	*thyA*	spy0882	883	825	-0.3973	0.0047	**0.0093**	-0.3463	0.0148	0.0379

M5005_Spy#	Gene	Synonym *	WT Transcript Rank †	Mutant Transcript Rank †	*r* Correlation (*covR*) ‡	*P* -value Correlation (*covR*)	*Q-* value Correlation (*covR*) §	*r* Correlation (*covS*) ‡	*P* -value Correlation (*covS*)	*Q-* value Correlation (*covS*) §
M5005_Spy0073	-	spy0084	304	216	-0.4007	0.0043	**0.0087**	-0.1886	0.1945	0.1834
M5005_Spy0812	-		1920	1488	-0.4012	0.0043	**0.0087**	-0.3539	0.0126	0.0341
M5005_Spy0119	-	spy0140	1358	1284	-0.4013	0.0043	**0.0087**	-0.3041	0.0336	0.0606
M5005_Spy0810	*srtG*	spy1087	1931	1921	-0.4018	0.0042	**0.0086**	-0.2929	0.0411	0.0665
M5005_Spy1000	-		1844	2092	-0.4023	0.0042	**0.0086**	-0.3051	0.0330	0.0598
M5005_Spy0778	*csrA*	spy1055	913	929	-0.4026	0.0041	**0.0086**	-0.3355	0.0184	0.0422
M5005_Spy1327	*comFA*	spy1616	814	1093	-0.4029	0.0041	**0.0085**	-0.2930	0.0411	0.0665
M5005_Spy0393	-	spy0479	1382	1369	-0.4046	0.0039	**0.0082**	-0.2696	0.0611	0.0869
M5005_Spy1771	*hutU*	spyM18_2141	1574	2031	-0.4049	0.0039	**0.0082**	-0.2325	0.1079	0.1233
M5005_Spy0561	*epf*	spy0737	1618	1191	-0.4067	0.0037	**0.0079**	-0.0035	0.9809	0.4938
M5005_Spy1208	-	SpyM3_1138	1432	1520	-0.4069	0.0037	**0.0079**	-0.1769	0.2241	0.2026
M5005_Spy1463	-	M12_1772	1838	1778	-0.4069	0.0037	**0.0079**	-0.0811	0.5794	0.3671
M5005_Spy0116	*atoE*	spy0137	1232	1501	-0.4072	0.0037	**0.0079**	-0.3508	0.0134	0.0355
M5005_Spy0766	-	spy1042	1035	847	-0.408	0.0036	**0.0079**	-0.2956	0.0392	0.0653
M5005_Spy1519	*recG*		848	941	-0.4082	0.0036	**0.0079**	-0.4835	0.0004	**0.0059**
M5005_Spy0028	-	spy0031	1916	2012	-0.4091	0.0035	**0.0077**	-0.1742	0.2313	0.2069
M5005_Spy1332	*rr03*	spy1621	615	661	-0.4104	0.0034	**0.0075**	-0.2378	0.0999	0.1174
M5005_Spy1747	-	spy2053	568	737	-0.4118	0.0033	**0.0073**	-0.3696	0.0090	0.0278
M5005_Spy0764	-	spy1039	1743	2400	-0.4125	0.0032	**0.0072**	-0.5175	0.0001	**0.0055**
M5005_Spy0590	-	spyM18_0831	1596	1816	-0.4168	0.0029	**0.0067**	-0.3576	0.0116	0.0322
M5005_Spy0570	*sagI*		788	911	-0.4169	0.0029	**0.0067**	-0.2351	0.1039	0.1208
M5005_Spy0457	-	spy0552	1549	1638	-0.4176	0.0028	**0.0066**	-0.3366	0.0180	0.0419
M5005_Spy1238	-	spy1507	2144	1942	-0.4177	0.0028	**0.0066**	-0.1352	0.3544	0.2742
M5005_Spy1707	*dppD*	spy2003	766	1138	-0.4193	0.0027	**0.0063**	-0.4685	0.0007	**0.0067**
M5005_Spy1184	-	spy1455	1982	1639	-0.4198	0.0027	**0.0063**	-0.5213	0.0001	**0.0055**
M5005_Spy0995	-	spyM18_0394	1244	1320	-0.4212	0.0026	**0.0062**	-0.2395	0.0974	0.1159
M5005_Spy1332	*hk03*	spyM18_1630	2387	2356	-0.4217	0.0025	**0.0061**	-0.2877	0.0450	0.0708
M5005_Spy1454	-		1548	1160	-0.4217	0.0025	**0.0061**	-0.0845	0.5635	0.3614
M5005_Spy1697	-		1730	1654	-0.4219	0.0025	**0.0061**	-0.3395	0.0170	0.0407
M5005_Spy1331	-		1843	2116	-0.4228	0.0025	**0.0060**	-0.1116	0.4453	0.3149
M5005_Spy1492	*fabK*	spy1751	1200	923	-0.4235	0.0024	**0.0060**	-0.3722	0.0085	0.0267
M5005_Spy1542	*scrA*		2148	2433	-0.424	0.0024	**0.0059**	-0.3017	0.0351	0.0621

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M5005_Spy0585	*epuA*	SpyM3_0503	861	817	-0.4257	0.0023	**0.0057**	-0.3666	0.0096	0.0289
M5005_Spy1607	*fba*	spy1889	332	357	-0.4258	0.0023	**0.0057**	-0.4227	0.0025	0.0124
M5005_Spy0231	*rpsG*		1422	1802	-0.4263	0.0023	**0.0057**	-0.1733	0.2336	0.2083
M5005_Spy0967	-	spy1257	1688	1562	-0.4271	0.0022	**0.0056**	-0.2862	0.0462	0.0720
M5005_Spy1173	-	spy0706	1865	2148	-0.4272	0.0022	**0.0056**	-0.2526	0.0800	0.1022
M5005_Spy0392	-	spy0478	2462	2309	-0.4295	0.0021	**0.0053**	-0.2656	0.0651	0.0899
M5005_Spy0473	-	spy0570	921	763	-0.4305	0.0020	**0.0052**	-0.3132	0.0284	0.0545
M5005_Spy1009	-		1768	1754	-0.4309	0.0020	**0.0052**	-0.2551	0.0769	0.0997
M5005_Spy1866	*spoJ*	spy2217	504	777	-0.4311	0.0020	**0.0051**	-0.3058	0.0326	0.0593
M5005_Spy1457	-		1471	1761	-0.4327	0.0019	**0.0050**	-0.3608	0.0109	0.0308
M5005_Spy1290	-	spy1566	1133	1394	-0.433	0.0019	**0.0050**	-0.3088	0.0309	0.0572
M5005_Spy0604	*rgpBc*	spy0787	457	470	-0.4358	0.0017	**0.0047**	-0.5593	2.9E-05	**0.0055**
M5005_Spy0200	*sms*	spy0236	762	1043	-0.4366	0.0017	**0.0047**	-0.2908	0.0427	0.0684
M5005_Spy1416	-		969	1197	-0.4372	0.0017	**0.0047**	-0.4285	0.0021	0.0113
M5005_Spy0076	-	M12_1023	305	318	-0.4388	0.0016	**0.0046**	-0.3858	0.0062	0.0214
M5005_Spy1792	-	spyM18_2167	704	795	-0.4389	0.0016	**0.0046**	-0.4648	0.0008	**0.0068**
M5005_Spy0189	-	spy0219	335	299	-0.4395	0.0016	**0.0045**	-0.2547	0.0773	0.1002
M5005_Spy1218	-	SpyM3_1262	2559	2639	-0.4414	0.0015	**0.0044**	-0.3598	0.0111	0.0313
M5005_Spy0716	-	spy0914	949	979	-0.4419	0.0015	**0.0044**	-0.3380	0.0175	0.0411
M5005_Spy1024	-		1741	2046	-0.4433	0.0014	**0.0043**	-0.4334	0.0019	0.0102
M5005_Spy0083	*rpoB*		1311	1471	-0.4446	0.0014	**0.0042**	-0.4034	0.0041	0.0166
M5005_Spy1174	-	spy0705	1294	1148	-0.4446	0.0014	**0.0042**	-0.3139	0.0281	0.0542
M5005_Spy0860	-	spy1138	1413	1460	-0.4452	0.0013	**0.0042**	-0.2217	0.1257	0.1373
M5005_Spy0216	-	spy0256	1058	855	-0.446	0.0013	**0.0041**	-0.2639	0.0670	0.0912
M5005_Spy1177	-		863	1184	-0.446	0.0013	**0.0041**	-0.3352	0.0186	0.0422
M5005_Spy1405	*copA*	spy1715	481	613	-0.4463	0.0013	**0.0041**	-0.3393	0.0171	0.0408
M5005_Spy1704	*dppA*	spy2000	48	187	-0.4495	0.0012	**0.0039**	-0.4131	0.0032	0.0142
M5005_Spy1240	*clpE*		2620	2653	-0.4504	0.0012	**0.0038**	-0.4253	0.0023	0.0119
M5005_Spy0434	-	spy0527	1754	1536	-0.4513	0.0011	**0.0038**	-0.3012	0.0354	0.0621
M5005_Spy0771	-	spy1048	798	648	-0.4527	0.0011	**0.0037**	-0.2471	0.0869	0.1072
M5005_Spy0977	*pcrA*	spy1267	595	891	-0.4542	0.0010	**0.0037**	-0.2360	0.1025	0.1197
M5005_Spy0549	-	spy0722	1445	1919	-0.4548	0.0010	**0.0036**	-0.3769	0.0076	0.0247

M5005_Spy#	Gene	Synonym *	WT Transcript Rank †	Mutant Transcript Rank †	*r* Correlation (*covR*) ‡	*P* -value Correlation (*covR*)	*Q-* value Correlation (*covR*) §	*r* Correlation (*covS*) ‡	*P* -value Correlation (*covS*)	*Q-* value Correlation (*covS*) §
M5005_Spy0623	-	spy0808	422	469	-0.4581	9.34E-04	**0.0034**	-0.5210	0.0001	**0.0055**
M5005_Spy1640	-	spy1926	2002	1289	-0.4583	9.28E-04	**0.0034**	-0.3647	0.0100	0.0296
M5005_Spy0586	*endA*		1943	2063	-0.4584	9.24E-04	**0.0034**	-0.3861	0.0061	0.0214
M5005_Spy0651	-		1224	1157	-0.4591	9.07E-04	**0.0034**	-0.4316	0.0020	0.0106
M5005_Spy0025	*purM*	spy0027	1266	1156	-0.4599	8.86E-04	**0.0034**	-0.1493	0.3060	0.2482
M5005_Spy1484	*accD*	spy1744	1427	1270	-0.461	8.57E-04	**0.0034**	-0.2325	0.1079	0.1233
M5005_Spy1455	-	SpyM3_1448	738	860	-0.4613	8.50E-04	**0.0034**	-0.3932	0.0052	0.0194
M5005_Spy1158	*ddlA*		2611	2626	-0.463	8.08E-04	**0.0033**	-0.3545	0.0125	0.0338
M5005_Spy1807	*ahrC*	spy2150	796	916	-0.4636	7.95E-04	**0.0033**	-0.4114	0.0033	0.0144
M5005_Spy1175	-	spy1443	1291	1377	-0.4637	7.92E-04	**0.0033**	-0.3291	0.0209	0.0454
M5005_Spy1654	-		892	1046	-0.4639	7.88E-04	**0.0033**	-0.3534	0.0127	0.0342
M5005_Spy1428	-		1867	1911	-0.4645	7.73E-04	**0.0032**	-0.3947	0.0050	0.0189
M5005_Spy1370	-	spyM18_1678	2470	2029	-0.465	7.63E-04	**0.0032**	-0.4786	0.0005	**0.0062**
M5005_Spy0378	*pyrH*	spy0462	406	420	-0.4661	7.38E-04	**0.0032**	-0.2900	0.0432	0.0688
M5005_Spy0798	-	spy1075	1814	2055	-0.4673	7.11E-04	**0.0031**	-0.2745	0.0563	0.0818
M5005_Spy1440	-		1536	1555	-0.4721	6.16E-04	**0.0030**	-0.4991	0.0003	**0.0055**
M5005_Spy0748	*estA*	spy1022	644	740	-0.4743	5.75E-04	**0.0029**	-0.4655	0.0008	**0.0067**
M5005_Spy0394	-	spy0480	879	1097	-0.4756	5.52E-04	**0.0029**	-0.2939	0.0404	0.0660
M5005_Spy1086	-	spy1329	1118	1419	-0.479	4.98E-04	**0.0028**	-0.3573	0.0117	0.0323
M5005_Spy1084	-	spy1326	1597	1259	-0.4809	4.69E-04	**0.0028**	-0.3904	0.0056	0.0203
M5005_Spy0854	-	spy1131	1217	1229	-0.4812	4.65E-04	**0.0028**	-0.3195	0.0252	0.0506
M5005_Spy0022	-		1069	1264	-0.4827	4.44E-04	**0.0028**	-0.5236	0.0001	**0.0055**
M5005_Spy0786	-	spy1063	1023	1087	-0.484	4.26E-04	**0.0028**	-0.4075	0.0037	0.0154
M5005_Spy1026	-	M12_1466	2029	1823	-0.4854	4.07E-04	**0.0028**	-0.3228	0.0237	0.0487
M5005_Spy1449	-		1760	2110	-0.4865	3.93E-04	**0.0028**	-0.4375	0.0017	**0.0096**
M5005_Spy1212	*xis*	spy1484	722	872	-0.4876	3.81E-04	**0.0028**	-0.2417	0.0942	0.1130
M5005_Spy1820	-	spy2165	1908	2025	-0.4878	3.78E-04	**0.0028**	-0.4048	0.0039	0.0162
M5005_Spy1181	-	spy1451	2053	2230	-0.491	3.41E-04	**0.0027**	-0.1461	0.3165	0.2551
M5005_Spy1582	*dnaQ*	spy1864	1308	1567	-0.4916	3.34E-04	**0.0027**	-0.4243	0.0024	0.0121
M5005_Spy1743	*pflD*	spy2049	628	673	-0.4923	3.27E-04	**0.0027**	-0.3399	0.0169	0.0405
M5005_Spy0733	-	spy0932	1284	1355	-0.4939	3.10E-04	**0.0027**	-0.2679	0.0627	0.0880
M5005_Spy1206	-	spy1479	1426	1692	-0.4944	3.06E-04	**0.0027**	-0.2904	0.0429	0.0687

M5005_Spy#	Gene	Synonym *	WT Transcript Rank †	Mutant Transcript Rank †	*r* Correlation (*covR*) ‡	*P* -value Correlation (*covR*)	*Q-* value Correlation (*covR*) §	*r* Correlation (*covS*) ‡	*P* -value Correlation (*covS*)	*Q-* value Correlation (*covS*) §
M5005_Spy1205	-		2393	1627	-0.4953	2.97E-04	**0.0027**	-0.3889	0.0058	0.0207
M5005_Spy0670	*rpsU*	spyM18_0924	2257	2337	-0.498	2.72E-04	**0.0027**	-0.4605	0.0009	**0.0071**
M5005_Spy0360	-		2046	2597	-0.4986	2.66E-04	**0.0027**	-0.2577	0.0738	0.0972
M5005_Spy0590	-	spy0771	1155	1099	-0.4991	2.62E-04	**0.0027**	-0.2704	0.0602	0.0861
M5005_Spy1268	-	spy1538	1027	1035	-0.4993	2.60E-04	**0.0027**	-0.2662	0.0645	0.0894
M5005_Spy0655	-	spy0847	2104	1609	-0.4998	2.55E-04	**0.0027**	-0.3400	0.0168	0.0405
M5005_Spy1451	-		1326	1123	-0.5031	2.29E-04	**0.0027**	-0.4022	0.0042	0.0168
M5005_Spy1199	-	spy1471	2154	1880	-0.504	2.22E-04	**0.0027**	-0.3721	0.0085	0.0267
M5005_Spy1762	*groES*	spy2072	152	313	-0.5051	2.14E-04	**0.0027**	-0.4590	0.0009	**0.0071**
M5005_Spy0544	-	spy0715	581	440	-0.5064	2.05E-04	**0.0027**	-0.3009	0.0356	0.0621
M5005_Spy1018	-		2316	2374	-0.5064	2.05E-04	**0.0027**	-0.4040	0.0040	0.0164
M5005_Spy1439	-		2193	2273	-0.5076	1.97E-04	**0.0027**	-0.3103	0.0300	0.0562
M5005_Spy1673	*proS*	spy1962	234	290	-0.5077	1.96E-04	**0.0027**	-0.3498	0.0137	0.0361
M5005_Spy0794	*thdF*	spy1071	943	1194	-0.5097	1.84E-04	**0.0027**	-0.3909	0.0055	0.0201
M5005_Spy1003	-		1917	1840	-0.5097	1.84E-04	**0.0027**	-0.3724	0.0084	0.0267
M5005_Spy0026	*purN*	spy0028	1646	1371	-0.5098	1.83E-04	**0.0027**	-0.2346	0.1046	0.1213
M5005_Spy1550	*uvrA*	spyM18_1890	2021	2073	-0.5098	1.83E-04	**0.0027**	-0.2654	0.0653	0.0900
M5005_Spy1662	-	spy1949	1295	1060	-0.5109	1.76E-04	**0.0027**	-0.5158	0.0001	**0.0055**
M5005_Spy0907	*citF*	spy1189	1714	1866	-0.5129	1.64E-04	**0.0027**	-0.3832	0.0066	0.0223
M5005_Spy1030	-	spyM18_1789	2365	2620	-0.5136	1.60E-04	**0.0027**	-0.5384	6.6E-05	**0.0055**
M5005_Spy1175	-	spy0703	2142	2197	-0.519	1.33E-04	**0.0027**	-0.4488	0.0012	**0.0081**
M5005_Spy1135	-	spy1392	1551	1528	-0.5194	1.31E-04	**0.0027**	-0.2374	0.1005	0.1180
M5005_Spy0310	-	spy0369	847	1077	-0.5204	1.26E-04	**0.0027**	-0.3969	0.0047	0.0183
M5005_Spy0171	-	spy0198	2407	2311	-0.521	1.24E-04	**0.0027**	-0.4119	0.0033	0.0143
M5005_Spy0031	*purK*	spyM18_0034	1318	1577	-0.5214	1.22E-04	**0.0027**	-0.3929	0.0052	0.0195
M5005_Spy1446	-	SpyM3_1439	2030	1887	-0.5234	1.14E-04	**0.0027**	-0.2468	0.0873	0.1073
M5005_Spy1426	-		2121	2453	-0.5237	1.13E-04	**0.0027**	-0.2934	0.0407	0.0662
M5005_Spy1697	-	spyM18_2056	689	1193	-0.5269	1.01E-04	**0.0027**	-0.3347	0.0188	0.0424
M5005_Spy1661	-	spy1947	1403	1441	-0.5272	9.9E-05	**0.0027**	-0.3697	0.0089	0.0278
M5005_Spy1078	-	spyM18_1329	981	1039	-0.5285	9.5E-05	**0.0027**	-0.3838	0.0065	0.0222
M5005_Spy0398	-	spyM18_0544	960	1112	-0.5289	9.3E-05	**0.0027**	-0.3836	0.0065	0.0222
M5005_Spy1092	*rsuA*	spy1337	1239	1399	-0.5313	8.6E-05	**0.0027**	-0.2983	0.0374	0.0636

M5005_Spy#	Gene	Synonym *	WT Transcript Rank †	Mutant Transcript Rank †	*r* Correlation (*covR*) ‡	*P*-value Correlation (*covR*)	*Q*-value Correlation (*covR*) §	*r* Correlation (*covS*) ‡	*P*-value Correlation (*covS*)	*Q*-value Correlation (*covS*) §
M5005_Spy0922	*pdxK*	spy1209	1601	1849	-0.5328	8.1E-05	**0.0027**	-0.4256	0.0023	0.0119
M5005_Spy1123	-		2437	2498	-0.5331	8.0E-05	**0.0027**	-0.4864	0.0004	**0.0059**
M5005_Spy0399	-	spy0484	880	1048	-0.5345	7.6E-05	**0.0027**	-0.4753	0.0006	**0.0063**
M5005_Spy0095	-	spy0110	1254	1271	-0.5355	7.4E-05	**0.0027**	-0.3517	0.0132	0.0351
M5005_Spy0346	-	M12_0056	702	768	-0.5368	7.0E-05	**0.0027**	-0.3432	0.0158	0.0395
M5005_Spy0828	*potC*		1898	1781	-0.5374	6.8E-05	**0.0027**	-0.4185	0.0028	0.0132
M5005_Spy1176	-		1701	1900	-0.538	6.7E-05	**0.0027**	-0.4153	0.0030	0.0139
M5005_Spy0647	-		1139	1374	-0.5381	6.7E-05	**0.0027**	-0.4389	0.0016	**0.0094**
M5005_Spy0389	*dgk*	spy0475	905	856	-0.5404	6.1E-05	**0.0027**	-0.4544	0.0010	**0.0075**
M5005_Spy0031	*purK*		1423	1618	-0.5409	6.0E-05	**0.0027**	-0.4128	0.0032	0.0142
M5005_Spy1168	-	SpyM3_1094	1192	1443	-0.545	5.1E-05	**0.0027**	-0.4327	0.0019	0.0103
M5005_Spy1459	-	spy1483	1381	1833	-0.5489	4.4E-05	**0.0027**	-0.3968	0.0048	0.0184
M5005_Spy0086	*comYA*	spy0101	1675	1747	-0.5505	4.2E-05	**0.0027**	-0.4303	0.0020	0.0109
M5005_Spy1128	-	SpyM3_1017	427	564	-0.5516	4.0E-05	**0.0027**	-0.3777	0.0075	0.0244
M5005_Spy1193	-	spy1465	1453	1415	-0.5541	3.6E-05	**0.0027**	-0.3456	0.0150	0.0381
M5005_Spy1498	*dnaK*	spy1760	11	25	-0.5557	3.4E-05	**0.0027**	-0.5175	0.0001	**0.0055**
M5005_Spy1271	-	spyM18_1560	1629	1591	-0.5559	3.4E-05	**0.0027**	-0.3638	0.0102	0.0297
M5005_Spy1820	-	spyM18_2202	843	1052	-0.5586	3.0E-05	**0.0027**	-0.4776	0.0005	**0.0062**
M5005_Spy1637	*lacB.2*	spyM18_1990	1261	1047	-0.5592	3.0E-05	**0.0027**	-0.3137	0.0282	0.0543
M5005_Spy1365	-	spyM18_1673	1591	1770	-0.5617	2.7E-05	**0.0027**	-0.4668	0.0007	**0.0067**
M5005_Spy1760	-	-	2534	2613	-0.5639	2.5E-05	**0.0027**	-0.4848	0.0004	**0.0059**
M5005_Spy0561	*epf*		2414	2497	-0.5643	2.4E-05	**0.0027**	-0.3325	0.0196	0.0436
M5005_Spy0120	*atoD.2*	spy0141	1463	1293	-0.5689	2.0E-05	**0.0027**	-0.4131	0.0032	0.0142
M5005_Spy1424	-		2589	2576	-0.5698	1.9E-05	**0.0027**	-0.2923	0.0416	0.0671
M5005_Spy0466	-	spyM18_0632	434	474	-0.571	1.8E-05	**0.0027**	-0.4465	0.0013	**0.0083**
M5005_Spy1865	*htrA*	spy2216	354	504	-0.5716	1.8E-05	**0.0027**	-0.4178	0.0028	0.0133
M5005_Spy1810	-	spy2153	700	779	-0.5723	1.7E-05	**0.0027**	-0.2328	0.1074	0.1233
M5005_Spy0144	-	SpyM3_0132	2641	2305	-0.5725	1.7E-05	**0.0027**	-0.5322	8.3E-05	**0.0055**
M5005_Spy1019	-		2631	2125	-0.5826	1.1E-05	**0.0027**	-0.4575	0.0010	**0.0073**
M5005_Spy1105	-	spy1356	1152	1167	-0.5903	8.0E-06	**0.0027**	-0.4336	0.0019	0.0102
M5005_Spy0585	*epuA*	spy0764	576	760	-0.5907	7.9E-06	**0.0027**	-0.3672	0.0095	0.0287
M5005_Spy1007	-		2384	2397	-0.592	7.4E-06	**0.0027**	-0.4613	0.0008	**0.0070**

M5005_Spy#	Gene	Synonym *	WT Transcript Rank †	Mutant Transcript Rank †	*r* Correlation (*covR*) ‡	*P*-value Correlation (*covR*)	*Q*-value Correlation (*covR*) §	*r* Correlation (*covS*) ‡	*P*-value Correlation (*covS*)	*Q*-value Correlation (*covS*) §
M5005_Spy0147	*leuS*	spyM18_0171	526	587	-0.6065	3.9E-06	**0.0027**	-0.3654	0.0098	0.0294
M5005_Spy1442	-		1350	1601	-0.6203	2.0E-06	**0.0027**	-0.5394	6.4E-05	**0.0055**
M5005_Spy1108	*metK*	spy1359	331	397	-0.6236	1.7E-06	**0.0027**	-0.4661	0.0007	**0.0067**
M5005_Spy0704	*pyrE*	spy0901	1103	1059	-0.6314	1.2E-06	**0.0027**	-0.5143	0.0002	**0.0055**
M5005_Spy1009	-		1101	1391	-0.6352	9.4E-07	**0.0027**	-0.4627	0.0008	**0.0070**
M5005_Spy0585	*epuA*	spyM18_0822	655	684	-0.652	3.9E-07	**0.0027**	-0.5004	0.0003	**0.0055**

*Synonym in M1 SF370, M3 MGAS315 or M18 MGAS8232 GAS strains.

†Transcript rank for most abundant transcript is valued at 1. Rank increases arithmetically with decreasing transcript detection, according to the normalized expression estimates.

‡Pearson correlation coefficient assessing the association of transcript expression.

§Bootstrapped *Q*-values assessing correlations in RMLChip microarrays. Bolded text denote correlations with *Q* values of less than 0.01.

Supplementary Table 6. Significance analysis of function and expression (SAFE) of GAS RMLChip *in vivo* transcriptome data.

M5005_gene	RML Probeset	*T*-statistic *	Empirical *P*-value †	Gene	Synonym	Description	Function	Q-value (Strain) ‡
M5005_Spy0340	SpM1_ChORF0414_s_at	3.50	**0.0001**	*lctO*	SPy0414	L-lactate oxidase (EC 1.13.12.4)	Carbohydrate metabolism	0.1745
M5005_Spy0407	SpM1_ChORF0496_s_at	-2.47	**0.0001**	*mutR*	SPy0496	Transcriptional regulator	Information processing	0.3712
M5005_Spy0521	SpM1_ChORF0631_s_at	-3.20	**0.0001**	*agaV*	SPy0631	PTS system, N-acetylgalactosamine-specific IIB component (EC 2.7.1.69)	Carbohydrate metabolism	0.0421
M5005_Spy0522	SpM5_ChORFJ7578C-260_s_at	-2.73	**0.0001**	-		Unsaturated glucuronyl hydrolase (EC 3.2.1.-)	Unknown	0.1745
M5005_Spy0627	SpM1_ChORF0813_at	-2.56	**0.0001**	*gor, gshR*	SPy0813	Glutathione reductase (EC 1.8.1.7)	Stress adaptation	0.0405
M5005_Spy0782	SpM1_ChORF1059_s_at	3.10	**0.0001**	*ptsC*	SPy1059	PTS system, mannose/fructose family IIC component	Carbohydrate metabolism	0.2979
M5005_Spy0826	SpM1_ChORF1102_s_at	-2.54	**0.0001**	*potA*	SPy1102	Spermidine/putrescine transport ATP-binding protein potA	Membrane transport	0.1512
M5005_Spy0877	SpM1_ChORF1156_s_at	3.76	**0.0001**	-	SPy1156	Hypothetical protein	Unknown	0.1231
M5005_Spy0922	SpM18_ChORF1158_s_at	-2.47	**0.0001**	*pdxK*	spyM18_1158	Hypothetical membrane spanning protein	Unknown	0.3379
M5005_Spy1082	SpM1_ChORF1324_s_at	-2.13	**0.0001**	-	SPy1324	PTS system, cellobiose-specific IIB component (EC 2.7.1.69)	Carbohydrate metabolism	0.2168
M5005_Spy1704	SpM1_ChORF2000_s_at	3.86	**0.0001**	*dppA*	SPy2000	Dipeptide-binding protein	Membrane transport	0.0013
M5005_Spy1835	SpM1_ChORF2182_s_at	3.88	**0.0001**	*holB*	SPy2182	Replicative DNA helicase (EC 3.6.1.-)	Cellular processing	0.0137
M5005_Spy0527	SpM1_ChORF0639_s_at	-3.08	**0.0002**	*kgdA*	SPy0639	4-Hydroxy-2-oxoglutarate aldolase (EC 4.1.3.16) / 2-dehydro-3-deoxyphosphogluconate aldolase (EC 4.1.2.14) Reaction: 2-dehydro-3-deoxy-D-gluconate 6-phosphate = pyruvate + D-glyceraldehyde 3-phosphate	Carbohydrate metabolism	0.0859
M5005_Spy0783	SpM1_ChORF1060_s_at	3.40	**0.0002**	*ptsD*	SPy1060	PTS system, mannose/fructose family IID component	Carbohydrate metabolism	0.4151
M5005_Spy0899	SpM1_ChORF1179_s_at	-2.63	**0.0002**	*citG*	SPy1179	Transcriptional regulator, GntR family	Information processing	0.1231

M5005_gene	RML Probeset	*T* -statistic *	Empirical *P* -value †	Gene	Synonym	Description	Function	Q-value (Strain) ‡
M5005_Spy0971	SpM1_ChORF1260_s_at	4.04	**0.0002**	-	SPy1260	General stress protein, Gls24 family	Unknown	0.6822
M5005_Spy0974	SpM1_ChORF1263_s_at	3.97	**0.0002**	-	SPy1263	Small integral membrane protein	Unknown	0.5164
M5005_Spy1381	SpM1_ChORF1684_s_at	3.29	**0.0002**	*glpK*	SPy1684	Glycerol kinase (EC 2.7.1.30)	Carbohydrate metabolism	0.0952
M5005_Spy1395	SpM1_ChORF1704_s_at	-3.23	**0.0002**	*lacD.1*	SPy1704	Tagatose-bisphosphate aldolase (EC 4.1.2.40)	Carbohydrate metabolism	0.0043
M5005_Spy1399	SpM18_ChORF1719_s_at	-3.27	**0.0002**	-	spyM18_1719	PTS system, galactose-specific IIC component (EC 2.7.1.69)	Carbohydrate metabolism	0.0012
M5005_Spy1512	SpM1_ChORF1777_s_at	3.00	**0.0002**	*codY*	SPy1777	Pleiotropic transcriptional repressor codY	Information processing	0.1479
M5005_Spy1782	SpM5_ChORF125g-225_at	-2.31	**0.0002**	*pepO*		Neutral endopeptidase (EC 3.4.24.-)	Amino acid metabolism	0.3393
M5005_Spy0198	SpM1_ChORF0233_s_at	-2.30	**0.0003**	-	SPy0233	Hypothetical cytosolic protein	Unknown	0.1913
M5005_Spy0447	SpM1_ChORF0540_s_at	-2.68	**0.0003**	-	SPy0540	Glycosyltransferase involved in cell wall biogenesis (EC 2.4.-.-)	Cell wall metabolism	0.1377
M5005_Spy0558	SpM1_ChORF0733_at	-2.58	**0.0003**	-	SPy0733	Transposase	Mobile genetic element	0.1209
M5005_Spy0830	SpM1_ChORF1106_s_at	-2.48	**0.0003**	-	SPy1106	Transcriptional regulatory protein dpiA	Information processing	0.1497
M5005_Spy0878	SpM1_ChORF1157_s_at	3.86	**0.0003**	-	SPy1157	Hypothetical protein	Unknown	0.2979
M5005_Spy0974	SpM18_ChORF1214_s_at	3.65	**0.0003**	-	spyM18_1214	Small integral membrane protein	Unknown	0.5218
M5005_Spy1041	SpM18_ChORF1800_at	-2.32	**0.0003**	-	spyM18_1800	Phage protein	Phage	0.4227
M5005_Spy1205	SpM5_ChORFJ7578C-203_s_at	-1.86	**0.0003**	-		Phage protein	Phage	0.4400
M5005_Spy1359	SpM1_ChORF1654_s_at	-2.40	**0.0003**	-	SPy1653	Amino acid permease	Unknown	0.1745
M5005_Spy1363	SpM1_ChORF1658_s_at	-2.66	**0.0003**	-	SPy1657	Amino acid ABC transporter permease protein	Membrane transport	0.1923
M5005_Spy1398	SpM1_ChORF1708_s_at	-2.90	**0.0003**	*lacA.1*	SPy1709	Galactose-6-phosphate isomerase lacA subunit (EC 5.3.1.26)	Carbohydrate metabolism	0.0858
M5005_Spy1849	SpM1_ChORF2198_s_at	-2.49	**0.0003**	-	SPy2198	Zinc protease (EC 3.4.99.-)	Unknown	0.2310
M5005_Spy0501	SpM1_ChORF0603_s_at	2.74	**0.0004**	-	SPy0603	Hypothetical integral membrane protein	Unknown	0.0253

M5005_gene	RML Probeset	*T* -statistic *	Empirical *P* -value †	Gene	Synonym	Description	Function	Q-value (Strain) ‡
M5005_Spy0620	SpM18_ChORF0867_s_at	3.09	**0.0004**	*rpl35*	spyM18_0867	LSU ribosomal protein L35P	Protein synthesis	0.1674
M5005_Spy0695	SpM1_ChORF0889_s_at	2.95	**0.0004**	*rpiA*	SPy0889	Ribose 5-phosphate isomerase (EC 5.3.1.6)	Carbohydrate metabolism	0.6743
M5005_Spy0753	SpM12_ChORF281-7_s_at	-2.52	**0.0004**	*acoC*		Dihydrolipoamide acetyltransferase component of pyruvate dehydrogenase complex (EC 2.3.1.12)	Information processing	0.2332
M5005_Spy0791	SpM1_ChORF1068_s_at	3.11	**0.0004**	*uvrC*	SPy1068	Excinuclease ABC subunit C	Information processing	0.3266
M5005_Spy0890	SpM1_ChORF1170_s_at	-3.01	**0.0004**	*ddh*	SPy1170	D-lactate dehydrogenase (EC 1.1.1.28)	Carbohydrate metabolism	0.1908
M5005_Spy0922	SpM1_ChORF1208_s_at	-2.49	**0.0004**	*pdxK*	SPy1208	Hypothetical membrane spanning protein	Unknown	0.3492
M5005_Spy1286	SpM1_ChORF1563_s_at	-2.43	**0.0004**	-	SPy1563	Conserved hypothetical protein; RexB-like involved in DNA replication, recombination, and repair	Unknown	0.0940
M5005_Spy1348	SpM5_ChORF169a-188_s_at	-2.27	**0.0004**	-		D-beta-hydroxybutyrate permease	Unknown	0.3002
M5005_Spy1439	SpM12_ChORF299-50_at	-2.16	**0.0004**	-		Portal protein	Phage	0.6469
M5005_Spy0126	SpM12_ChORF175-2_s_at	-2.45	**0.0005**	*ntpI*		V-type sodium ATP synthase subunit I (EC 3.6.3.15)	Membrane transport	0.1577
M5005_Spy0433	SpM1_ChORF0526_s_at	-2.59	**0.0005**	-	SPy0526	Long-chain-fatty-acid--CoA ligase (EC 6.2.1.3)	Lipid metabolism	0.3892
M5005_Spy1115	SpM1_ChORF1367_s_at	-2.30	**0.0005**	-	SPy1367	Hypothetical membrane spanning protein	Unknown	0.4878
M5005_Spy1283	SpM1_ChORF1558_s_at	-2.20	**0.0005**	-	SPy1558	Thiol:disulfide interchange protein tlpA	Cellular processing	0.5923
M5005_Spy1397	SpM1_ChORF1707_at	-2.59	**0.0005**	*lacB.1*	SPy1707	Galactose-6-phosphate isomerase lacB subunit (EC 5.3.1.26)	Carbohydrate metabolism	0.1157
M5005_Spy1586	SpM1_ChORF1868_s_at	3.12	**0.0005**	*nupC*	SPy1868	Nucleoside permease nupC	Membrane transport	0.6930
M5005_Spy1700	SpM1_ChORF1994_s_at	-2.54	**0.0005**	-	SPy1994	Acetyltransferase (EC 2.3.1.-)	Cellular processing	0.1250
M5005_Spy1792	SpM18_ChORF2167_x_at	2.60	**0.0005**	-	spyM18_2167	Hypothetical protein	Unknown	0.0080
M5005_Spy0064	SpM1_ChORF0073_s_at	3.17	**0.0006**	*secY*	SPy0073	Protein translocase subunit secY	Secretion	0.1908

M5005_gene	RML Probeset	*T* -statistic *	Empirical *P* -value †	Gene	Synonym	Description	Function	Q-value (Strain) ‡
M5005_Spy0282	SpM18_ChORF0328_s_at	-3.22	**0.0006**	*covR*	spyM18_0328	Two-component response regulator CovR (CsrR)	Signal transduction	1.3E-05
M5005_Spy0662	SpM5_ChORF4P31a-19_s_at	-2.38	**0.0006**	*fruA*		PTS system, fructose-specific IIABC component (EC 2.7.1.69)	Carbohydrate metabolism	0.2095
M5005_Spy0720	SpM1_ChORF0918_s_at	-2.24	**0.0006**	-	SPy0918	Putative exfoliative toxin	Virulence	0.2770
M5005_Spy0791	SpM5_ChORF270b-333_s_at	-2.22	**0.0006**	*uvrC*		Excinuclease ABC subunit C	Information processing	0.0826
M5005_Spy1012	SpM49_ChORF7585-27_at	-2.30	**0.0006**	-		Antigen A	Phage	0.3349
M5005_Spy1222	SpM1_ChORF1488_s_at	-2.78	**0.0006**	*int.2*	SPy1488	DNA integration/recombination/invertion protein phi5005.2 int	Phage	0.1908
M5005_Spy1396	SpM18_ChORF1715_at	-2.54	**0.0006**	*nadE*	spyM18_1715	Tagatose-6-phosphate kinase (EC 2.7.1.144)	Carbohydrate metabolism	0.1497
M5005_Spy1477	SpM1_ChORF1736_s_at	-2.31	**0.0006**	-	SPy1736	Guanine-hypoxanthine permease	Membrane transport	0.1949
M5005_Spy1765	SpM1_ChORF2077_x_at	3.57	**0.0006**	*csp*	SPy2077	Cold shock protein	Stress adaptation	0.2541
M5005_Spy1819	SpM1_ChORF2164_s_at	-2.16	**0.0006**	-	SPy2164	Hypothetical phage protein	Phage	0.5164
M5005_Spy0050	SpM1_ChORF0056_s_at	3.16	**0.0007**	*rpsC*	SPy0056	SSU ribosomal protein S3P	Protein synthesis	0.2917
M5005_Spy0063	SpM1_ChORF0072_s_at	3.24	**0.0007**	*rplO*	SPy0072	LSU ribosomal protein L15P	Protein synthesis	0.2979
M5005_Spy0386	SpM1_ChORF0471_s_at	-2.16	**0.0007**	*phoH*	SPy0471	PhoH protein	Unknown	0.1479
M5005_Spy0574	SpM1_ChORF0752_s_at	-2.23	**0.0007**	-	SPy0752	Diacylglycerol kinase family	Cellular processing	0.2439
M5005_Spy1006	SpM49_ChORF7585-2_at	-2.89	**0.0007**	-		Phage structural protein	Phage	0.2979
M5005_Spy1452	SpM12_ChORF299-41_at	-2.78	**0.0007**	-		Phage protein	Phage	0.2754
M5005_Spy1836	SpM1_ChORF2184_s_at	3.16	**0.0007**	*rplI*	SPy2184	LSU ribosomal protein L9P	Protein synthesis	0.0294
M5005_Spy0196	SpM1_ChORF0229_s_at	-2.25	**0.0008**	-	SPy0229	Multidrug resistance ABC transporter ATP-binding and permease protein	Membrane transport	0.0991
M5005_Spy0352	SpM1_ChORF0430_at	-2.82	**0.0008**	-	SPy0430	Hypothetical membrane associated protein	Unknown	0.0003
M5005_Spy0441	SpM1_ChORF0534_s_at	-2.44	**0.0008**	*aroE.2*	SPy0534	Shikimate 5-dehydrogenase (EC 1.1.1.25)	Amino acid metabolism	0.3379

M5005_gene	RML Probeset	*T* -statistic *	Empirical *P* -value †	Gene	Synonym	Description	Function	Q-value (Strain) ‡
M5005_Spy0528	SpM1_ChORF0640_s_at	-2.30	**0.0008**	-	SPy0640	Beta-phosphoglucomutase (EC 5.4.2.6) / Glucose-1-phosphate phosphodismutase (EC 2.7.1.41)	Unknown	0.2979
M5005_Spy0529	SpM1_ChORF0642_s_at	-2.33	**0.0008**	-	SPy0642	Conserved hypothetical protein	Unknown	0.0179
M5005_Spy0734	SpM1_ChORF0933_s_at	2.59	**0.0008**	*cpsFO*	SPy0933	Glucose-1-phosphate thymidylyltransferase (EC 2.7.7.24)	Carbohydrate metabolism	0.4334
M5005_Spy1769	SpM1_ChORF2080_s_at	3.00	**0.0008**	*ahpF*	SPy2080	Peroxiredoxin reductase (NAD(P)H) (EC 1.6.4.-)	Stress adaptation	0.3727
M5005_Spy1793	SpM1_ChORF2110_s_at	3.05	**0.0008**	*nrdD*	SPy2110	Anaerobic ribonucleoside-triphosphate reductase (EC 1.17.4.2)	Unknown	0.1377
M5005_Spy0909	SpM1_ChORF1191_s_at	-2.75	**0.0009**	*oadA*	SPy1191	Oxaloacetate decarboxylase alpha chain (EC 4.1.1.3)	Carbohydrate metabolism	0.2541
M5005_Spy1258	SpM1_ChORF1530_s_at	-2.09	**0.0009**	-	SPy1530	Hypothetical cytosolic protein	Unknown	0.2748
M5005_Spy1401	SpM1_ChORF1710_s_at	-2.85	**0.0009**	-	SPy1710	PTS system, galactose-specific IIA component (EC 2.7.1.69)	Carbohydrate metabolism	0.0105
M5005_Spy0059	SpM1_ChORF0066_s_at	2.83	**0.001**	*rplF*	SPy0066	LSU ribosomal protein L6P	Protein synthesis	0.2057
M5005_Spy0157	SpM1_ChORF0183_s_at	2.92	**0.001**	*opuAA*	SPy0183	Glycine betaine transport ATP-binding protein	Membrane transport	0.0897
M5005_Spy0972	SpM1_ChORF1261_s_at	3.40	**0.001**	-	SPy1261	Hypothetical protein	Unknown	0.5698
M5005_Spy1126	SpM18_ChORF1348_x_at	-2.25	**0.001**	-	spyM18_1348	Transposase	Mobile genetic element	0.3469
M5005_Spy1744	SpM1_ChORF2050_s_at	-2.38	**0.001**	-	SPy2051	PTS system, cellobiose-specific IIC component	Carbohydrate metabolism	0.1150
M5005_Spy0495	SpM1_ChORF0595_s_at	2.50	**0.0011**	*lysS*	SPy0595	Lysyl-tRNA synthetase (EC 6.1.1.6)	Protein synthesis	0.3098
M5005_Spy0619	SpM1_ChORF0804_s_at	3.07	**0.0011**	*infC*	SPy0804	Bacterial Protein Translation Initiation Factor 3 (IF-3)	Information processing	0.5602
M5005_Spy1556	SpM1_ChORF1832_s_at	-2.28	**0.0011**	-	SPy1832	Hypothetical protein	Unknown	0.0035
M5005_Spy0231	SpM1_ChORF0272_s_at	2.93	**0.0012**	*rpsG*	SPy0272	SSU ribosomal protein S7P	Protein synthesis	0.4460
M5005_Spy0720	SpM12_ChORF2489_s_at	-1.93	**0.0012**	-		Putative exfoliative toxin	Virulence	0.4269
M5005_Spy0743	SpM1_ChORF1016_s_at	-2.10	**0.0012**	-	SPy1016	ABC transporter substrate-binding protein	Membrane transport	0.5512

M5005_gene	RML Probeset	*T* -statistic *	Empirical *P* -value †	Gene	Synonym	Description	Function	Q-value (Strain) ‡
M5005_Spy0973	SpM1_ChORF1262_s_at	3.27	**0.0012**	-	SPy1262	General stress protein, Gls24 family	Stress adaptation	0.6930
M5005_Spy1288	SpM1_ChORF1564_s_at	-2.46	**0.0012**	-	SPy1564	Hypothetical cytosolic protein	Unknown	0.1982
M5005_Spy1432	SpM12_ChORF299-55_s_at	-2.30	**0.0012**	-		Phage protein	Phage	0.4227
M5005_Spy1602	SpM1_ChORF1885_s_at	2.91	**0.0013**	-	SPy1885	Predicted kinase related to hydroxyacetone kinase	Unknown	0.4227
M5005_Spy1671	SpM1_ChORF1960_s_at	-2.53	**0.0013**	-	SPy1960	Transcriptional regulator, MarR family	Information processing	0.1652
M5005_Spy0676	SpM3_ChORF0589_s_at	-2.10	**0.0014**	-	spyM3_0589	Hypothetical protein	Unknown	0.2057
M5005_Spy0800	SpM1_ChORF1077_s_at	-2.60	**0.0014**	-	SPy1077	DNA-cytosine methyltransferase (EC 2.1.1.73)	Cellular processing	0.2979
M5005_Spy0809	SpM1_ChORF1086_s_at	-2.32	**0.0014**	*srtE*	SPy1086	Lantibiotic transport permease protein	Membrane transport	0.3002
M5005_Spy1295	SpM1_ChORF1571_s_at	-1.98	**0.0014**	-	SPy1571	Hypothetical cytosolic protein	Unknown	0.5539
M5005_Spy0051	SpM1_ChORF0057_s_at	3.01	**0.0015**	*rplP*	SPy0057	LSU ribosomal protein L16P	Protein synthesis	0.4166
M5005_Spy0056	SpM1_ChORF0063_s_at	3.11	**0.0015**	*rplE*	SPy0063	LSU ribosomal protein L5P	Protein synthesis	0.4110
M5005_Spy0804	SpM1_ChORF1081_at	-2.13	**0.0015**	*srtR*	SPy1081	Nisin biosynthesis two-component response regulator nisR	Signal transduction	0.3167
M5005_Spy1171	SpM1_ChORF1438_s_at	-2.43	**0.0015**	-	SPy1438	Phage-associated cell wall hydrolase	Phage	0.5295
M5005_Spy0772	SpM1_ChORF1049_s_at	-2.22	**0.0016**	-	SPy1049	Hypothetical protein	Unknown	0.3722
M5005_Spy1780	SpM1_ChORF2092_s_at	2.37	**0.0016**	*rpsB*	SPy2092	SSU ribosomal protein S2P	Protein synthesis	0.2754
M5005_Spy0090	SpM1_ChORF0105_s_at	-2.21	**0.0017**	-	SPy0105	Hypothetical protein	Unknown	0.4394
M5005_Spy0153	SpM1_ChORF0179_s_at	-2.67	**0.0017**	*araD*	SPy0179	L-ribulose-5-phosphate 4-epimerase (EC 5.1.3.4)	Carbohydrate metabolism	0.0087
M5005_Spy0233	SpM1_ChORF0274_s_at	3.05	**0.0017**	*plr, gap*	SPy0274	Glyceraldehyde 3-phosphate dehydrogenase (EC 1.2.1.12); plasmin receptor	Carbohydrate metabolism	0.6691
M5005_Spy0716	SpM1_ChORF0914_s_at	-2.56	**0.0018**	-	SPy0914	Hypothetical protein	Unknown	0.6918
M5005_Spy0712	SpM5_ChORF4P31a-8_s_at	-1.99	**0.0019**	*parC*		Topoisomerase IV subunit A (EC 5.99.1.-)	Information processing	0.4888

M5005_gene	RML Probeset	*T* -statistic *	Empirical *P* -value †	Gene	Synonym	Description	Function	Q-value (Strain) ‡
M5005_Spy1108	SpM1_ChORF1359_s_at	2.87	**0.0019**	*metK*	SPy1359	S-adenosylmethionine synthetase (EC 2.5.1.6)	Cellular processing	0.0208
M5005_Spy1187	SpM1_ChORF1457_s_at	-2.03	**0.0019**	-	SPy1457	Phage structural protein	Phage	0.3002
M5005_Spy0058	SpM1_ChORF0065_s_at	2.29	**0.002**	*rpsH*	SPy0065	SSU ribosomal protein S8P	Protein synthesis	0.1923
M5005_Spy0832	SpM1_ChORF1109_s_at	-2.66	**0.002**	*malP*	SPy1109	Malate-sodium symport	Membrane transport	0.0010
M5005_Spy0531	SpM1_ChORF0645_s_at	-2.59	**0.0021**	*ftsE*	SPy0645	Cell division ATP-binding protein ftsE	Cellular processing	0.0442
M5005_Spy0905	SpM1_ChORF1186_s_at	-2.24	**0.0021**	*citD*	SPy1186	Citrate lyase acyl carrier protein	Carbohydrate metabolism	0.4110
M5005_Spy1213	SpM3_ChORF0967_at	-2.45	**0.0021**	-	spyM3_0967	Phage protein	Phage	0.1150
M5005_Spy1816	SpM18_ChORF2197_x_at	2.75	**0.0021**	*rpmG*	spyM18_2197	LSU ribosomal protein L33P	Protein synthesis	0.1261
M5005_Spy1347	SpM1_ChORF1640_s_at	-2.08	**0.0022**	-	SPy1640	D-beta-hydroxybutyrate dehydrogenase (EC 1.1.1.30)	Unknown	0.5169
M5005_Spy1488	SpM1_ChORF1747_s_at	-2.30	**0.0022**	*accB*	SPy1747	Biotin carboxyl carrier protein of acetyl-CoA carboxylase	Lipid metabolism	0.2552
M5005_Spy0372	SpM1_ChORF0458_s_at	-1.77	**0.0023**	*ftsK*	SPy0458	Cell division protein ftsK	Unknown	0.3492
M5005_Spy1190	SpM3_ChORF1118_s_at	-2.23	**0.0023**	-	spyM3_1118	Phage protein	Phage	0.4255
M5005_Spy1816	SpM1_ChORF2160_x_at	2.76	**0.0023**	*rpmG*	SPy2160	LSU ribosomal protein L33P	Protein synthesis	0.1628
M5005_Spy0409	SpM1_ChORF0498_s_at	-1.97	**0.0024**	-	SPy0498	Dephospho-CoA kinase (EC 2.7.1.24)	Coenzyme and cofactor metabolism	0.3546
M5005_Spy0583	SpM1_ChORF0762_s_at	-1.93	**0.0024**	-	SPy0762	Hypothetical membrane associated protein	Unknown	0.3379
M5005_Spy1097	SpM49_ChORF9033_s_at	-2.04	**0.0024**	-		Phosphorylase, Pnp/Udp family	Unknown	0.3253
M5005_Spy1494	SpM1_ChORF1754_s_at	2.20	**0.0024**	*fabH*	SPy1754	3-oxoacyl-[acyl-carrier-protein] synthase III (EC 2.3.1.41)	Lipid metabolism	0.0926
M5005_Spy1768	SpM1_ChORF2079_s_at	2.60	**0.0024**	*ahpC*	SPy2079	Peroxiredoxin reductase (NAD(P)H) (EC 1.6.4.-)	Stress adaptation	0.3083
M5005_Spy1815	SpM18_ChORF2196_x_at	2.96	**0.0024**	*rpmF*	spyM18_2196	LSU ribosomal protein L32P	Protein synthesis	0.2330
M5005_Spy1817	SpM1_ChORF2162_s_at	-2.13	**0.0024**	*cadD*	SPy2162	Cadmium resistance protein	Membrane transport	0.3722

M5005_gene	RML Probeset	*T*-statistic *	Empirical *P*-value †	Gene	Synonym	Description	Function	Q-value (Strain) ‡
M5005_Spy1852	SpM1_ChORF2201_s_at	-2.00	**0.0024**	*hasB*	SPy2201	UDP-glucose 6-dehydrogenase (EC 1.1.1.22)	Carbohydrate metabolism	0.0926
M5005_Spy1865	SpM1_ChORF2216_s_at	2.92	**0.0024**	*htrA*	SPy2216	Protease Do (EC 3.4.21.-); Secreted protein chaperone	Stress adaptation	0.0353
M5005_Spy1524	SpM1_ChORF1791_s_at	-2.13	**0.0025**	-	SPy1791	ABC transporter ATP-binding protein	Membrane transport	0.4227
M5005_Spy1570	SpM1_ChORF1850_s_at	-1.77	**0.0026**	-	SPy1850	Penicillin-binding protein	Unknown	0.6015
M5005_Spy0935	SpM1_ChORF1221_s_at	-2.23	**0.0027**	*dpfB*	SPy1221	Phosphopantothenate--cysteine ligase (EC 6.3.2.5)	Unknown	0.2051
M5005_Spy0281	SpM1_ChORF0334_s_at	-2.39	**0.0028**	-	SPy0334	Hypothetical cytosolic protein	Unknown	0.0008
M5005_Spy0665	M12_1091_at	-1.98	**0.0028**	-		Transposase	Mobile genetic element	0.4310
M5005_Spy0021	SpM1_ChORF0023_s_at	-1.79	**0.0029**	*acpP.2*	SPy0023	Acyl carrier protein	Cellular processing	0.4463
M5005_Spy0850	SpM1_ChORF1128_s_at	2.61	**0.0029**	*pta*	SPy1128	Putative phosphotransacetylase	Cellular processing	0.4227
M5005_Spy0889	SpM1_ChORF1169_s_at	-2.19	**0.0029**	-	SPy1169	Regulatory protein (pfoS/R)	Unknown	0.4854
M5005_Spy1244	SpM1_ChORF1514_s_at	2.56	**0.0029**	*divIVAS*	SPy1514	Cell division initiation protein DivIVA	Cellular processing	0.6442
M5005_Spy1525	SpM1_ChORF1793_s_at	-1.95	**0.0029**	-	SPy1793	ABC transporter ATP-binding protein	Membrane transport	0.5801
M5005_Spy0224	SpM1_ChORF0264_s_at	2.27	**0.003**	*rpe*	SPy0264	Ribulose-phosphate 3-epimerase (EC 5.1.3.1)	Carbohydrate metabolism	0.3410
M5005_Spy0250	SpM1_ChORF0294_s_at	-1.73	**0.003**	*oppB*	SPy0294	Oligopeptide transport system permease protein oppB	Membrane transport	0.3225
M5005_Spy0553	SpM1_ChORF0727_s_at	2.38	**0.003**	*gyrB*	SPy0727	DNA gyrase subunit B (EC 5.99.1.3)	Cellular processing	0.4334
M5005_Spy0485	SpM1_ChORF0585_s_at	2.04	**0.0031**	*lgt*	SPy0585	Prolipoprotein diacylglyceryl transferase (EC 2.4.99.-)	Information processing	0.2054
M5005_Spy0738	SpM1_ChORF1011_s_at	-2.06	**0.0031**	-	SPy1011	Hypothetical membrane spanning protein	Unknown	0.1982
M5005_Spy1083	SpM3_ChORF1004_s_at	-2.63	**0.0031**	-	spyM3_1004	Transcription antiterminator, BglG family / PTS system, mannitol (Cryptic)-specific IIA component (EC 2.7.1.69)	Information processing	0.2042
M5005_Spy1401	SpM1_ChORF1711_s_at	-2.37	**0.0031**	-	SPy1711	PTS system, galactose-specific IIA component (EC 2.7.1.69)	Carbohydrate metabolism	0.0454

M5005_gene	RML Probeset	*T* -statistic *	Empirical *P* -value †	Gene	Synonym	Description	Function	Q-value (Strain) ‡
M5005_Spy0127	SpM1_ChORF0149_s_at	-2.08	**0.0032**	*ntpK*	SPy0149	V-type sodium ATP synthase subunit K (EC 3.6.3.15)	Membrane transport	0.2676
M5005_Spy0332	SpM1_ChORF0401_s_at	-2.73	**0.0033**	-	SPy0401	Tpl protein	Unknown	0.2853
M5005_Spy0550	SpM1_ChORF0723_s_at	-1.76	**0.0033**	-	SPy0723	Chloride channel protein	Membrane transport	0.6540
M5005_Spy0709	SpM1_ChORF0907_s_at	-2.01	**0.0033**	*pyrC*	SPy0907	Dihydroorotase (EC 3.5.2.3)	Nucleotide metabolism	0.3116
M5005_Spy0942	SpM12_ChORF290 9_s_at	-1.86	**0.0033**	-		Nucleoside-binding protein	Unknown	0.6662
M5005_Spy1342	SpM1_ChORF1633_s_at	2.75	**0.0033**	-	SPy1633	Hydrolase (HAD superfamily)	Unknown	0.4776
M5005_Spy1866	SpM1_ChORF2217_s_at	2.39	**0.0033**	*spoJ*	SPy2217	Chromosome partitioning protein parB	Cellular processing	0.0570
M5005_Spy0083	SpM1_ChORF0098_s_at	2.69	**0.0034**	*rpoB*	SPy0098	DNA-directed RNA polymerase beta chain (EC 2.7.7.6)	Cellular processing	0.6328
M5005_Spy0322	SpM1_ChORF0383_s_at	-1.94	**0.0034**	*ftsB*	SPy0384	Ferrichrome transport system permease protein fhuB	Membrane transport	0.6200
M5005_Spy0423	SpM1_ChORF0513_s_at	-2.35	**0.0034**	*pepQ*	SPy0513	Xaa-Pro dipeptidase (EC 3.4.13.9)	Amino acid metabolism	0.0381
M5005_Spy1440	SpM12_ChORF299 8_s_at	-2.11	**0.0034**	-		Terminase large subunit	Phage	0.5413
M5005_Spy1578	SpM18_ChORF1923_at	-1.91	**0.0034**	-	spyM18_1923	Transcriptional regulator, Cro/CI family	Information processing	0.5812
M5005_Spy1677	SpM5_ChORF125g 178_at	-2.01	**0.0034**	-		Protein translocase subunit YajC	Secretion	0.4706
M5005_Spy0765	SpM1_ChORF1040_s_at	-2.10	**0.0035**	*emN, hem*	SPy1040	Coproporphyrinogen oxidase, anaerobic (EC 1.-.-.-)	Coenzyme and cofactor metabolism	0.4883
M5005_Spy0054	SpM1_ChORF0061_s_at	2.45	**0.0036**	*rplN*	SPy0061	LSU ribosomal protein L14P	Protein synthesis	0.3758
M5005_Spy1763	SpM1_ChORF2073_s_at	2.42	**0.0036**	*clpC*	SPy2073	Negative regulator of genetic competence clpC/mecB	Information processing	0.2979
M5005_Spy1856	SpM1_ChORF2205_s_at	2.82	**0.0036**	-	SPy2205	Glucose uptake protein homolog	Membrane transport	0.1497
M5005_Spy0696	SpM1_ChORF0890_s_at	2.70	**0.0037**	*deoB*	SPy0890	Phosphopentomutase (EC 5.4.2.7)	Carbohydrate metabolism	0.3906
M5005_Spy1443	M12_1752_at	-2.12	**0.0037**	-		Phage protein	Phage	0.3888
M5005_Spy0152	SpM1_ChORF0178_s_at	-2.45	**0.0038**	-	SPy0178	L-xylulose 5-phosphate 3-epimerase (EC 5.3.1.-)	Carbohydrate metabolism	0.0315
M5005_Spy1387	SpM1_ChORF1693_s_at	2.74	**0.0038**	-	SPy1693	Aldo/keto reductase family	Carbohydrate metabolism	0.4436

M5005_gene	RML Probeset	*T* -statistic *	Empirical *P* -value †	Gene	Synonym	Description	Function	Q-value (Strain) ‡
M5005_Spy1702	SpM1_ChORF1998_at	-1.83	**0.0038**	*smeZ*	SPy1998	Streptococcal mitogenic exotoxin Z; Pyrogenic toxin superantigen exotoxin type Z	Virulence	0.6824
M5005_Spy1840	SpM1_ChORF2188_s_at	2.51	**0.0039**	*trmU*	SPy2188	tRNA (5-methylaminomethyl-2-thiouridylate)-methyltransferase (EC 2.1.1.61)	Protein synthesis	0.0952
M5005_Spy0508	SpM1_ChORF0611_s_at	2.89	**0.0041**	*tufA*	SPy0611	Protein Translation Elongation Factor Tu (EF-TU)	Cellular processing	0.6750
M5005_Spy0705	SpM1_ChORF0902_s_at	-1.86	**0.0041**	*amiC*	SPy0902	Amidase family protein	Unknown	0.5080
M5005_Spy0146	SpM1_ChORF0172_s_at	-2.03	**0.0043**	*metB*	SPy0172	Cystathionine beta-lyase (EC 4.4.1.8)	Amino acid metabolism	0.2314
M5005_Spy0333	SpM18_ChORF0453_at	-2.13	**0.0043**	-	spyM18_0453	Hypothetical signal peptidase-like protein	Unknown	0.6382
M5005_Spy1587	SpM1_ChORF1869_s_at	2.73	**0.0043**	*udp*	SPy1869	Uridine phosphorylase (EC 2.4.2.3)	Nucleotide metabolism	0.6743
M5005_Spy0921	SpM1_ChORF1206_s_at	-2.17	**0.0044**	-	SPy1206	ABC transporter ATP-binding protein	Membrane transport	0.5231
M5005_Spy1067	SpM1_ChORF1306_at	2.78	**0.0044**	*malX*	SPy1306	Maltose/maltodextrin-binding protein	Membrane transport	0.6750
M5005_Spy1575	SpM1_ChORF1856_s_at	-1.84	**0.0044**	*norA*	SPy1856	Quinolone resistance protein NorA	Membrane transport	0.3335
M5005_Spy1243	SpM1_ChORF1513_s_at	-1.80	**0.0045**	*ileS*	SPy1513	Isoleucyl-tRNA synthetase (EC 6.1.1.5)	Protein synthesis	0.4537
M5005_Spy0108	SpM1_ChORF0127_at	-1.83	**0.0046**	-	SPy0127	Signal peptidase I (EC 3.4.21.89)	Secretion	0.2028
M5005_Spy0752	SpM1_ChORF1028_s_at	2.72	**0.0046**	*acoB*	SPy1028	Pyruvate dehydrogenase E1 component beta subunit (EC 1.2.4.1)	Carbohydrate metabolism	0.4687
M5005_Spy0714	SpM1_ChORF0912_s_at	-1.91	**0.0047**	-	SPy0912	Hypothetical cytosolic protein	Unknown	0.4888
M5005_Spy0828	SpM1_ChORF1104_s_at	-2.05	**0.0047**	*potC*	SPy1104	Spermidine/putrescine transport system permease protein potC	Membrane transport	0.4227
M5005_Spy1245	SpM1_ChORF1515_s_at	2.51	**0.0048**	-	SPy1515	RNA binding protein	Unknown	0.4941
M5005_Spy1839	SpM1_ChORF2186_s_at	-1.80	**0.0048**	-	SPy2186	Phosphohydrolase (MutT/nudix family protein)	Unknown	0.6366
M5005_Spy0318	SpM1_ChORF0379_s_at	2.04	**0.0049**	*pflC*	SPy0379	Pyruvate formate-lyase activating enzyme (EC 1.97.1.4)	Carbohydrate metabolism	0.2979

M5005_gene	RML Probeset	*T* -statistic *	Empirical *P* -value †	Gene	Synonym	Description	Function	Q-value (Strain) ‡
M5005_Spy1060	SpM1_ChORF1296_s_at	-1.76	**0.0049**	*malG*	SPy1296	Maltose/maltosaccharide/maltodextrin ABC transport system (permease) protein	Membrane transport	0.3887
M5005_Spy1320	SpM1_ChORF1607_s_at	-1.80	**0.0049**	-	SPy1607	Regulatory protein recX	Information processing	0.6155
M5005_Spy1190	SpM1_ChORF1462_x_at	-1.96	**0.005**	-	SPy1462	Phage protein	Phage	0.6061
M5005_Spy1496	SpM1_ChORF1758_s_at	-1.85	**0.005**	*phaB*	SPy1758	Enoyl-CoA hydratase (EC 4.2.1.17)	Cell wall metabolism	0.4792
M5005_Spy0517	SpM1_ChORF0627_s_at	-2.00	**0.0052**	*regR*	SPy0627	Transcriptional regulator, LacI family	Information processing	0.2541
M5005_Spy0830	SpM1_ChORF1107_s_at	-1.72	**0.0052**	-	SPy1107	Transcriptional regulatory protein dpiA	Information processing	0.4208
M5005_Spy1009	SpM49_ChORF7585-5_at	-1.89	**0.0052**	-		Phage protein	Phage	0.4541
M5005_Spy1131	SpM1_ChORF1386_s_at	-1.73	**0.0052**	-	SPy1386	Transcriptional regulator, Cro/CI family	Information processing	0.4472
M5005_Spy1382	SpM1_ChORF1686_s_at	2.77	**0.0053**	-	SPy1686	Hypothetical membrane associated protein	Unknown	0.3657
M5005_Spy0536	SpM1_ChORF0649_s_at	-1.78	**0.0054**	*dinG*	SPy0649	ATP-dependent helicase, DinG family	Cellular processing	0.3887
M5005_Spy0615	SpM1_ChORF0800_s_at	-2.20	**0.0054**	*ebsA*	SPy0800	Hypothetical pore-forming peptide	Unknown	0.0175
M5005_Spy0867	SpM1_ChORF1145_s_at	1.90	**0.0054**	*glyA*	SPy1145	Serine hydroxymethyltransferase (EC 2.1.2.1)	Cellular processing	0.3149
M5005_Spy0941	SpM1_ChORF1227_s_at	2.47	**0.0054**	-	SPy1227	Nucleoside transport ATP-binding protein	Membrane transport	0.5364
M5005_Spy1269	SpM1_ChORF1539_s_at	-1.91	**0.0054**	*asnA*	SPy1539	Aspartate--ammonia ligase (EC 6.3.1.1)	Amino acid metabolism	0.2748
M5005_Spy0057	SpM1_ChORF0064_s_at	2.44	**0.0055**	*rpsN*	SPy0064	SSU ribosomal protein S14P	Protein synthesis	0.4792
M5005_Spy0620	SpM1_ChORF0805_s_at	2.15	**0.0055**	*rpl36*	SPy0805	LSU ribosomal protein L35P	Protein synthesis	0.4828
M5005_Spy0404	M12_0889_at	-1.99	**0.0056**	-		Hypothetical protein	Unknown	0.2853
M5005_Spy0438	SpM1_ChORF0531_s_at	-2.24	**0.0056**	*acpA*	SPy0531	Ribonuclease III (EC 3.1.26.3)	Information processing	0.4888
M5005_Spy0601	SpM1_ChORF0783_s_at	-1.68	**0.0056**	-	SPy0783	Hypothetical cytosolic protein	Unknown	0.5176
M5005_Spy0802	M12_1862_s_at	-2.10	**0.0056**	-		Relaxase	Information processing	0.5962

M5005_gene	RML Probeset	*T*-statistic *	Empirical *P*-value †	Gene	Synonym	Description	Function	Q-value (Strain) ‡
M5005_Spy0425	SpM1_ChORF0515_s_at	2.67	**0.0057**	-	SPy0515	Glycosyltransferase (EC 2.4.1.-)	Carbohydrate metabolism	0.4745
M5005_Spy1613	SpM1_ChORF1897_s_at	-1.70	**0.0057**	-	SPy1897	Mechanosensitive ion channel	Unknown	0.6000
M5005_Spy0354	SpM1_ChORF0433_at	-1.71	**0.0059**	-	SPy0433	Hypothetical protein	Unknown	0.4110
M5005_Spy0641	SpM1_ChORF0832_s_at	-1.81	**0.0059**	*pyrB*	SPy0832	Aspartate carbamoyltransferase (EC 2.1.3.2)	Cellular processing	0.3524
M5005_Spy0962	SpM1_ChORF1252_s_at	-1.65	**0.0059**	-	SPy1252	Hypothetical protein	Unknown	0.6937
M5005_Spy1087	SpM18_ChORF1340_at	-1.79	**0.0061**	*int*	spyM18_1340	Hypothetical cytosolic protein	Unknown	0.3283
M5005_Spy1676	SpM1_ChORF1965_s_at	2.06	**0.0061**	*uppS*	SPy1965	Undecaprenyl pyrophosphate synthetase (EC 2.5.1.31)	Lipid metabolism	0.4308
M5005_Spy0781	SpM1_ChORF1058_s_at	2.45	**0.0063**	*ptsB*	SPy1058	PTS system, mannose/fructose family IIB component	Carbohydrate metabolism	0.5231
M5005_Spy1287	SpM1_ChORF1562_s_at	-1.87	**0.0064**	-	SPy1562	Hypothetical protein	Unknown	0.2502
M5005_Spy0344	SpM1_ChORF0421_s_at	-1.76	**0.0065**	-	SPy0421	Permease	Unknown	0.5886
M5005_Spy1530	SpM1_ChORF1798_s_at	-1.93	**0.0065**	-	SPy1798	Putative Fe3+-siderophore transport protein	Membrane transport	0.3037
M5005_Spy1830	SpM1_ChORF2177_s_at	-1.85	**0.0065**	-	SPy2177	Transcriptional regulator, TetR family	Information processing	0.6711
M5005_Spy0997	SpM49_ChORF7585-43_at	2.49	**0.0066**	-		Phage protein	Phage	0.1289
M5005_Spy1384	SpM1_ChORF1688_at	2.65	**0.0067**	*glyS*	SPy1688	Glycyl-tRNA synthetase beta chain (EC 6.1.1.14)	Protein synthesis	0.1150
M5005_Spy1423	SpM12_ChORF299-63_at	-2.27	**0.0067**	-		Hyaluronoglucosaminidase (EC 3.2.1.35)	Phage	0.6159
M5005_Spy0383	SpM1_ChORF0467_s_at	-1.52	**0.0069**	-	SPy0467	D-alanyl-D-alanine carboxypeptidase (EC 3.4.16.4)	Cell wall metabolism	0.5551
M5005_Spy0462	SpM18_ChORF0626_s_at	-1.58	**0.0069**	-	spyM18_0626	Hypothetical protein	Unknown	0.6690
M5005_Spy0981	SpM1_ChORF1273_s_at	-2.44	**0.0069**	*cfa*	SPy1273	AMP factor	Virulence	0.2853
M5005_Spy0732	SpM1_ChORF0930_s_at	-1.79	**0.007**	-	SPy0930	NIF3-related protein	Information processing	0.4776
M5005_Spy1254	SpM1_ChORF1526_s_at	-1.63	**0.007**	-	SPy1526	Hypothetical membrane spanning protein	Unknown	0.3154
M5005_Spy1177	SpM1_ChORF1448_s_at	-2.05	**0.0071**	-	SPy1448	Phage protein	Phage	0.3887

M5005_gene	RML Probeset	*T*-statistic *	Empirical *P*-value †	Gene	Synonym	Description	Function	Q-value (Strain) ‡
M5005_Spy1221	SpM5_ChORF4P31a-199_at	-1.97	**0.0071**	-		Phage protein	Phage	0.6850
M5005_Spy0858	SpM1_ChORF1136_s_at	-1.88	**0.0072**	*xpt*	SPy1136	Xanthine phosphoribosyltransferase (EC 2.4.2.-)	Unknown	0.5932
M5005_Spy0711	SpM1_ChORF0909_s_at	-1.81	**0.0073**	*parE*	SPy0909	Topoisomerase IV subunit B (EC 5.99.1.-)	Information processing	0.5494
M5005_Spy0760	SpM12_ChORF281-1_s_at	-1.79	**0.0073**	-		UDP-N-acetylmuramoylalanyl-D-glutamate--2,6-diaminopimelate ligase (EC 6.3.2.13)	Cell wall metabolism	0.4278
M5005_Spy0859	SpM1_ChORF1137_s_at	-2.02	**0.0074**	-	SPy1137	Xanthine permease	Membrane transport	0.6743
M5005_Spy0456	SpM1_ChORF0550_s_at	-1.58	**0.0075**	-	SPy0550	Plasmid stabilization system antitoxin protein	Unknown	0.6512
M5005_Spy1037	SpM18_ChORF1795_s_at	-2.07	**0.0075**	-	spyM18_1795	Phage single-strand DNA binding protein	Phage	0.4577
M5005_Spy1176	SpM5_ChORF270b-554_at	-1.82	**0.0075**	-		Phage infection protein	Phage	0.5442
M5005_Spy1266	SpM1_ChORF1537_s_at	-1.90	**0.0076**	-	SPy1537	ATP-dependent protease La (EC 3.4.21.53)	Unknown	0.2676
M5005_Spy1180	SpM1_ChORF1450_s_at	-2.12	**0.0077**	-	SPy1450	Phage protein	Phage	0.5169
M5005_Spy0114	SpM1_ChORF0135_s_at	-2.22	**0.0079**	-	SPy0135	Sortase	Cell wall metabolism	0.4990
M5005_Spy0158	SpM1_ChORF0184_s_at	2.30	**0.008**	*opuABC*	SPy0184	Glycine betaine-binding protein / Glycine betaine transport system permease protein	Membrane transport	0.0846
M5005_Spy0328	SpM1_ChORF0395_s_at	2.59	**0.008**	*clpP*	SPy0395	ATP-dependent Clp protease proteolytic subunit (EC 3.4.21.92)	Information processing	0.3933
M5005_Spy0084	SpM1_ChORF0099_s_at	2.48	**0.0081**	*rpoC*	SPy0099	DNA-directed RNA polymerase beta' chain (EC 2.7.7.6)	Cellular processing	0.6928
M5005_Spy0937	SpM1_ChORF1223_s_at	-1.74	**0.0081**	-	SPy1223	Transporter	Unknown	0.3361
M5005_Spy1824	SpM1_ChORF2170_at	-1.68	**0.0081**	-	SPy2170	Phosphohydrolase (MutT/nudix family protein)	Phage	0.6372
M5005_Spy0077	SpM1_ChORF0092_s_at	2.46	**0.0084**	*adcR*	SPy0092	Transcriptional regulator, MarR family	Information processing	0.5310
M5005_Spy0114	SpM1_ChORF0135_at	-1.78	**0.0084**	-	SPy0135	Sortase	Cell wall metabolism	0.6184
M5005_Spy0439	SpM1_ChORF0532_s_at	-1.77	**0.0084**	*smc*	SPy0532	Chromosome partition protein smc	Information processing	0.3977

M5005_gene	RML Probeset	*T*-statistic *	Empirical *P*-value †	Gene	Synonym	Description	Function	Q-value (Strain) ‡
M5005_Spy1815	SpM1_ChORF2159_s_at	2.53	**0.0084**	*rpmF*	SPy2159	LSU ribosomal protein L32P	Protein synthesis	0.1619
M5005_Spy0761	SpM1_ChORF1036_s_at	-1.78	**0.0085**	-	SPy1036	Hypothetical membrane spanning protein	Unknown	0.3817
M5005_Spy1154	SpM1_ChORF1415_s_at	2.42	**0.0085**	*deaD*	SPy1415	ATP-dependent RNA helicase	Stress adaptation	0.3995
M5005_Spy1179	SpM1_ChORF1449_s_at	-1.93	**0.0087**	-	SPy1449	Phage protein	Phage	0.6649
M5005_Spy1019	SpM49_ChORF7585-9_at	-1.71	**0.0088**	-		Phage scaffold protein	Phage	0.6743
M5005_Spy0561	SpM12_ChORF262 3_s_at	-1.75	**0.0089**	*epf*		Putative extracellular matrix binding protein	Virulence	0.6563
M5005_Spy0275	SpM1_ChORF0324_s_at	-2.12	**0.009**	-	SPy0324	Serine/threonine sodium symporter	Membrane transport	0.1081
M5005_Spy1585	SpM1_ChORF1867_s_at	2.47	**0.009**	*deoC*	SPy1867	Deoxyribose-phosphate aldolase (EC 4.1.2.4)	Carbohydrate metabolism	0.6200
M5005_Spy1465	SpM12_ChORF299 13_at	-1.71	**0.0092**	-		Phage protein	Phage	0.5244
M5005_Spy0968	SpM1_ChORF1258_s_at	-1.97	**0.0093**	-	SPy1258	Transcriptional regulator, TetR family	Information processing	0.4059
M5005_Spy1549	SpM12_ChORF283 25_s_at	2.22	**0.0093**	-		Xaa-Pro dipeptidase (EC 3.4.13.9)	Amino acid metabolism	0.1884
M5005_Spy1450	SpM12_ChORF299 43_at	-1.85	**0.0094**	-		Phage-encoded DNA polymerase (EC 2.7.7.7)	Phage	0.3758
M5005_Spy0091	SpM1_ChORF0106_s_at	-1.90	**0.0095**	*comYD*	SPy0106	ComG operon protein 6	Membrane transport	0.4888
M5005_Spy1818	SpM18_ChORF2199_s_at	-1.65	**0.0095**	*cadC*	spyM18_2199	Cadmium efflux system accessory protein	Membrane transport	0.6382
M5005_Spy1037	SpM18_ChORF1796_s_at	-1.89	**0.0096**	-	spyM18_1796	Phage single-strand DNA binding protein	Phage	0.4541
M5005_Spy0517	SpM1_ChORF0627_at	-1.60	**0.0097**	*regR*	SPy0627	Transcriptional regulator, LacI family	Information processing	0.6295
M5005_Spy0737	SpM1_ChORF1010_s_at	-1.85	**0.0097**	*mutX*	SPy1010	Mutator mutT protein (7,8-dihydro-8-oxoguanine-triphosphatase) (EC 3.6.1.-)	Information processing	0.3721
M5005_Spy0719	SpM5_ChORF4P31a-181_x_at	-1.70	**0.0098**	-		Glutathione S-transferase (EC 2.5.1.18)	Unknown	0.4248
M5005_Spy0125	SpM1_ChORF0147_s_at	-1.67	**0.01**	-	SPy0147	Hypothetical protein	Unknown	0.6512
M5005_Spy1162	SpM1_ChORF1425_s_at	-1.86	0.0101	-	SPy1425	Hypothetical protein	Unknown	0.0836

M5005_gene	RML Probeset	*T* -statistic *	Empirical *P* -value †	Gene	Synonym	Description	Function	Q-value (Strain) ‡
M5005_Spy0049	SpM1_ChORF0055_s_at	1.72	0.0102	*rplV*	SPy0055	LSU ribosomal protein L22P	Protein synthesis	0.1081
M5005_Spy1351	SpM1_ChORF1644_s_at	2.31	0.0102	-	SPy1644	Methyltransferase (EC 2.1.1.-)	Unknown	0.2582
M5005_Spy0226	SpM1_ChORF0266_s_at	2.05	0.0103	-	SPy0266	RmuC family protein	Unknown	0.4110
M5005_Spy0413	SpM1_ChORF0502_s_at	2.05	0.0103	*secG*	SPy0502	Protein translocase subunit secG	Secretion	0.6879
M5005_Spy1838	SpM1_ChORF2185_at	-1.81	0.0103	*gidA*	SPy2185	Glucose inhibited division protein A	Cellular processing	0.4066
M5005_Spy0925	SpM1_ChORF1211_s_at	2.43	0.0104	*rnhB*	SPy1211	Anaerobic ribonucleoside-triphosphate reductase (EC 1.17.4.2)	Unknown	0.4798
M5005_Spy0034	SpM49_ChORF8094-24_s_at	-1.36	0.0106	-		Transcriptional regulator	Information processing	0.5539
M5005_Spy0232	SpM1_ChORF0273_s_at	2.39	0.0106	*fus*	SPy0273	Protein Translation Elongation Factor G (EF-G)	Cellular processing	0.6842
M5005_Spy1718	SpM1_ChORF2016_at	-2.56	0.0107	*sic1.01*	SPy2016	Streptococcal inhibitor of complement	Virulence	0.0008
M5005_Spy0976	SpM1_ChORF1265_s_at	2.54	0.0108	-	SPy1265	Integral membrane protein	Unknown	0.5893
M5005_Spy1853	SpM1_ChORF2202_s_at	-2.23	0.0108	*hasC*	SPy2202	UTP--glucose-1-phosphate uridylyltransferase (EC 2.7.7.9)	Carbohydrate metabolism	0.2434
M5005_Spy0088	SpM1_ChORF0103_s_at	-1.94	0.0109	*comYC*	SPy0103	ComG operon protein 3	Membrane transport	0.6690
M5005_Spy0186	SpM3_ChORF0158_s_at	-1.70	0.0109	-	spyM3_0158	Transcriptional regulator	Information processing	0.5708
M5005_Spy1633	SpM1_ChORF1917_s_at	-1.86	0.011	*lacE*	SPy1917	PTS system, lactose-specific IIBC component (EC 2.7.1.69)	Carbohydrate metabolism	0.1628
M5005_Spy1662	SpM1_ChORF1949_s_at	2.13	0.0111	-	SPy1949	Putative transport protein sgaT	Membrane transport	0.0539
M5005_Spy0699	SpM1_ChORF0894_s_at	2.30	0.0112	*deoD2*	SPy0894	Purine nucleoside phosphorylase (EC 2.4.2.1)	Nucleotide metabolism	0.6844
M5005_Spy1444	SpM12_ChORF299 46_at	-1.74	0.0114	-		Adenine-specific methyltransferase (EC 2.1.1.72)	Phage	0.6091
M5005_Spy0169	SpM1_ChORF0196_s_at	-2.12	0.0115	-	SPy0196	Malonate permease	Membrane transport	0.3875
M5005_Spy0060	SpM1_ChORF0067_s_at	2.41	0.0116	*rplR*	SPy0067	LSU ribosomal protein L18P	Protein synthesis	0.6201
M5005_Spy1524	SpM1_ChORF1790_s_at	-1.62	0.0116	-	SPy1790	ABC transporter ATP-binding protein	Membrane transport	0.6690

M5005_gene	RML Probeset	*T* -statistic *	Empirical *P* -value †	Gene	Synonym	Description	Function	Q-value (Strain) ‡
M5005_Spy1238	SpM1_ChORF1507_s_at	2.29	0.0117	-	SPy1507	Arginine transport system permease protein artQ	Membrane transport	0.2979
M5005_Spy0595	SpM1_ChORF0777_s_at	-1.81	0.0118	*rexA*	SPy0777	ATP-dependent nuclease subunit A	Information processing	0.2287
M5005_Spy0917	SpM1_ChORF1202_s_at	-1.72	0.0118	-	SPy1202	Transcriptional regulator, GntR family	Information processing	0.5504
M5005_Spy1392	SpM1_ChORF1699_s_at	-1.66	0.0119	-	SPy1699	Transcriptional regulator, TetR family	Unknown	0.5162
M5005_Spy1650	SpM1_ChORF1936_s_at	-1.66	0.0119	-	SPy1936	DegV family protein	Unknown	0.5302
M5005_Spy0172	SpM1_ChORF0199_s_at	-1.66	0.012	-	SPy0199	Transposase	Mobile genetic element	0.6874
M5005_Spy0874	SpM1_ChORF1152_s_at	2.32	0.012	*gyrA*	SPy1152	DNA gyrase subunit A (EC 5.99.1.3)	Information processing	0.5874
M5005_Spy0400	SpM18_ChORF0547_s_at	-1.89	0.0121	*silD*	spyM18_0547	Hypothetical protein	Virulence	0.4436
M5005_Spy1141	SpM1_ChORF1401_s_at	-1.61	0.0121	-	SPy1401	Hypothetical cytosolic protein	Unknown	0.2979
M5005_Spy0891	SpM1_ChORF1171_s_at	-2.08	0.0122	*satD*	SPy1171	Hypothetical protein	Unknown	0.6811
M5005_Spy1440	SpM12_ChORF299-49_at	2.45	0.0122	-		Terminase large subunit	Phage	0.2078
M5005_Spy0128	SpM1_ChORF0150_s_at	-1.83	0.0123	*ntpE*	SPy0150	V-type sodium ATP synthase subunit E (EC 3.6.3.14)	Membrane transport	0.0952
M5005_Spy0839	SpM18_ChORF1077_s_at	-1.61	0.0125	-	spyM18_1077	Hypothetical membrane spanning protein	Unknown	0.6665
M5005_Spy1016	SpM49_ChORF7585-23_at	-1.69	0.0125	-		Phage protein	Phage	0.3754
M5005_Spy1123	SpM12_ChORF227-1_at	2.12	0.0128	-		Ribonucleoside-diphosphate reductase alpha chain (EC 1.17.4.1)	Nucleotide metabolism	0.1209
M5005_Spy1554	SpM1_ChORF1830_s_at	2.41	0.0128	*ssb2*	SPy1830	Phage single-strand DNA binding protein	Phage	0.6339
M5005_Spy0468	SpM1_ChORF0565_s_at	-1.74	0.0129	*tnpA*	SPy0565	Transposase	Mobile genetic element	0.5655
M5005_Spy0500	SpM1_ChORF0601_s_at	-2.09	0.0129	-	SPy0601	N-acetylmuramoyl-L-alanine amidase (EC 3.5.1.28)	Cell wall metabolism	0.0043
M5005_Spy1208	SpM18_ChORF1498_x_at	-1.78	0.0129	-	spyM18_1498	Phage protein	Phage	0.4888
M5005_Spy0519	SpM1_ChORF0629_s_at	-2.38	0.0133	*agaD*	SPy0629	PTS system, N-acetylgalactosamine-specific IID component (EC 2.7.1.69)	Carbohydrate metabolism	0.2713

M5005_gene	RML Probeset	*T*-statistic *	Empirical *P*-value †	Gene	Synonym	Description	Function	Q-value (Strain) ‡
M5005_Spy0819	SpM3_ChORF0757_s_at	-1.78	0.0134	-	spyM3_0757	Hypothetical protein	Unknown	0.4227
M5005_Spy0197	SpM1_ChORF0230_s_at	-1.71	0.0135	-	SPy0230	Multidrug resistance ABC transporter ATP-binding and permease protein	Membrane transport	0.5106
M5005_Spy1170	SpM1_ChORF1437_s_at	-1.64	0.0135	-	SPy1437	Hypothetical membrane associated protein	Phage	0.5532
M5005_Spy1321	SpM1_ChORF1608_s_at	2.34	0.0136	-	SPy1608	Hypothetical cytosolic protein	Unknown	0.4269
M5005_Spy0837	SpM1_ChORF1114_s_at	-1.62	0.0137	-	SPy1114	Chloride channel protein	Membrane transport	0.4656
M5005_Spy1374	SpM1_ChORF1675_s_at	-1.59	0.0137	-	SPy1675	Hypothetical protein	Unknown	0.3033
M5005_Spy1079	SpM18_ChORF1331_s_at	-1.76	0.0138	-	spyM18_1331	PTS system, cellobiose-specific IIC component	Carbohydrate metabolism	0.5472
M5005_Spy1811	SpM1_ChORF2154_s_at	-1.91	0.0139	-	SPy2154	Hypothetical membrane spanning protein	Unknown	0.1426
M5005_Spy1045	SpM18_ChORF1302_at	-1.56	0.0141	-	spyM18_1302	Transcriptional regulator	Phage	0.4836
M5005_Spy0629	SpM1_ChORF0815_s_at	-1.41	0.0142	-	SPy0815	Hypothetical protein	Unknown	0.6565
M5005_Spy1009	SpM49_ChORF7585-6_at	-1.63	0.0143	-		Phage protein	Phage	0.6129
M5005_Spy0751	SpM1_ChORF1026_s_at	2.19	0.0146	*acoA*	SPy1026	Pyruvate dehydrogenase E1 component alpha subunit (EC 1.2.4.1)	Carbohydrate metabolism	0.5698
M5005_Spy1332	SpM1_ChORF1622_s_at	-1.31	0.0146	*hk03*	SPy1622	Two-component response regulator yvqC	Signal transduction	0.5061
M5005_Spy1652	SpM1_ChORF1938_s_at	2.17	0.0146	-	SPy1938	23S rRNA methyltransferase (EC 2.1.1.-)	Cellular processing	0.4941
M5005_Spy0382	SpM1_ChORF0466_s_at	-1.67	0.0147	*msrA.2*	SPy0466	Peptide methionine sulfoxide reductase msrA (EC 1.8.4.6)	Cellular processing	0.4394
M5005_Spy0502	SpM1_ChORF0604_s_at	2.18	0.0147	-	SPy0604	Hypothetical exported protein	Unknown	0.2246
M5005_Spy1683	SpM1_ChORF1978_s_at	-1.62	0.0147	*lrp*	SPy1978	Leucine rich protein	Virulence	0.3986
M5005_Spy0471	SpM1_ChORF0568_s_at	-1.68	0.0148	-	SPy0568	Hydrolase (HAD superfamily)	Unknown	0.3989
M5005_Spy1075	SpM1_ChORF1314_s_at	2.39	0.0148	*uvrB*	SPy1314	Excinuclease ABC subunit B	Information processing	0.4706
M5005_Spy0405	SpM18_ChORF0551_s_at	-1.83	0.0149	*silE*	spyM18_0551	Hypothetical protein	Virulence	0.5164

M5005_gene	RML Probeset	*T* -statistic *	Empirical *P* -value †	Gene	Synonym	Description	Function	Q-value (Strain) ‡
M5005_Spy0954	SpM1_ChORF1244_s_at	-1.65	0.0149	*pstC*	SPy1244	Phosphate transport system permease protein pstC	Membrane transport	0.1982
M5005_Spy0955	SpM1_ChORF1245_s_at	-1.86	0.0149	*pstS*	SPy1245	Phosphate-binding protein	Membrane transport	0.2067
M5005_Spy0293	SpM1_ChORF0349_s_at	1.82	0.015	*greA*	SPy0349	Transcription elongation factor greA	Information processing	0.5169
M5005_Spy1820	SpM18_ChORF2202_s_at	2.33	0.015	-	spyM18_2202	FtsK/SpoIIIE family	Phage	0.1908
M5005_Spy0129	SpM1_ChORF0151_s_at	-1.72	0.0153	*ntpC*	SPy0151	V-type ATP synthase subunit C (EC 3.6.3.14)	Membrane transport	0.1976
M5005_Spy1020	SpM1_ChORF0685_s_at	-1.84	0.0153	-	SPy0685	Phage protein	Phage	0.5880
M5005_Spy1708	SpM1_ChORF2004_s_at	-1.43	0.0155	*dppE*	SPy2004	Dipeptide transport ATP-binding protein dppF	Membrane transport	0.6796
M5005_Spy0719	SpM1_ChORF0917_s_at	-1.46	0.0156	-	SPy0917	Glutathione S-transferase (EC 2.5.1.18)	Unknown	0.5624
M5005_Spy1639	SpM1_ChORF1924_s_at	-1.91	0.0156	*lacR.2*	SPy1924	Lactose phosphotransferase system repressor	Information processing	0.0744
M5005_Spy0683	SpM1_ChORF0877_s_at	-1.71	0.0157	*mvaD*	SPy0877	Diphosphomevalonate decarboxylase (EC 4.1.1.33)	Lipid metabolism	0.3727
M5005_Spy0338	SpM1_ChORF0410_s_at	-1.57	0.0158	-	SPy0410	Arsenate reductase family protein	Unknown	0.3002
M5005_Spy1719	SpM1_ChORF2018_at	2.55	0.0158	*emm1.0*	SPy2018	M protein	Virulence	0.6346
M5005_Spy0078	SpM1_ChORF0093_s_at	2.11	0.016	*adcC*	SPy0093	High-affinity zinc uptake system ATP-binding protein znuC	Membrane transport	0.3002
M5005_Spy0893	SpM1_ChORF1173_s_at	2.12	0.0162	*gid*	SPy1173	Glucose inhibited division protein A	Cellular processing	0.1659
M5005_Spy1184	SpM1_ChORF1454_s_at	-1.64	0.0162	-	SPy1454	Phage protein	Phage	0.6729
M5005_Spy0271	M12_0652_at	-1.54	0.0163	-		ABC transporter substrate-binding protein	Membrane transport	0.6509
M5005_Spy0745	SpM1_ChORF1018_s_at	-2.01	0.0163	-	SPy1018	ABC transporter permease protein	Membrane transport	0.4227
M5005_Spy0896	SpM1_ChORF1176_s_at	-1.69	0.0165	-	SPy1176	Biotin carboxyl carrier protein of oxaloacetate decarboxylase (EC 4.1.1.3)	Carbohydrate metabolism	0.6123
M5005_Spy0948	SpM1_ChORF1237_s_at	-1.54	0.0166	*ciaR*	SPy1237	Two-component response regulator ciaR	Signal transduction	0.4882
M5005_Spy0615	SpM1_ChORF0801_s_at	-1.77	0.0167	*ebsA*	SPy0801	Pore forming protein ebsA	Unknown	0.5317

M5005_gene	RML Probeset	*T* -statistic *	Empirical *P* -value †	Gene	Synonym	Description	Function	Q-value (Strain) ‡
M5005_Spy0924	SpM1_ChORF1210_s_at	-1.93	0.0167	-	SPy1210	Transcriptional regulator, GntR family	Information processing	0.5965
M5005_Spy0202	SpM1_ChORF0238_s_at	-2.04	0.017	-	SPy0238	Hypothetical protein	Unknown	0.4736
M5005_Spy1372	SpM1_ChORF1673_at	-1.80	0.017	*proB*	SPy1672	ABC transporter permease protein	Membrane transport	0.2028
M5005_Spy0561	SpM12_ChORF262-4_s_at	-1.94	0.0172	*epf*		Putative extracellular matrix binding protein	Virulence	0.6602
M5005_Spy1630	SpM1_ChORF1914_s_at	-1.62	0.0173	*salB*	SPy1914	Serine (threonine) dehydratase (lantibiotic biosynthesis)	Virulence	0.6362
M5005_Spy1264	SpM1_ChORF1535_s_at	-1.54	0.0174	-	SPy1535	Ribose operon repressor	Information processing	0.5295
M5005_Spy0139	SpM1_ChORF0165_s_at	-1.66	0.0175	*nga*	SPy0165	NAD glycohydrolase; NADase (EC 3.2.2.5)	Virulence	0.2502
M5005_Spy0945	SpM1_ChORF1233_s_at	-1.66	0.0176	*coaA*	SPy1233	Pantothenate kinase (EC 2.7.1.33)	Coenzyme and cofactor metabolism	0.4776
M5005_Spy0892	SpM1_ChORF1172_s_at	-1.61	0.0177	*satE*	SPy1172	Hypothetical protein	Unknown	0.3986
M5005_Spy1147	SpM1_ChORF1409_s_at	-1.62	0.0177	*comEC*	SPy1409	ComE operon protein 3	Unknown	0.5930
M5005_Spy1633	SpM49_ChORF6658-6_s_at	-1.42	0.0177	*lacE*		PTS system, lactose-specific IIBC component (EC 2.7.1.69)	Carbohydrate metabolism	0.5330
M5005_Spy0195	SpM1_ChORF0228_s_at	-1.63	0.0179	-	SPy0228	Transcriptional regulator, MarR family	Information processing	0.5962
M5005_Spy0229	SpM1_ChORF0269_s_at	2.26	0.0179	*prgA*	SPy0269	Surface exclusion protein	Virulence	0.5838
M5005_Spy0613	SpM1_ChORF0798_s_at	-1.40	0.0179	-	SPy0798	Hypothetical membrane spanning protein	Unknown	0.5678
M5005_Spy1126	SpM1_ChORF0195_x_at	-1.67	0.0179	-	SPy0195	Transposase	Mobile genetic element	0.5849
M5005_Spy1352	SpM12_ChORF289-43_s_at	-1.63	0.0181	-		Cell division initiation protein DivIVA	Unknown	0.4544
M5005_Spy1480	SpM1_ChORF1739_s_at	1.89	0.0181	*manM*	SPy1739	PTS system, mannose-specific IIC component (EC 2.7.1.69)	Carbohydrate metabolism	0.2541
M5005_Spy0668	SpM1_ChORF0861_s_at	-2.21	0.0183	*mac, ideS*	SPy0861	IgG-degrading protease of GAS	Virulence	0.2676
M5005_Spy0726	SpM1_ChORF0925_s_at	-1.73	0.0183	-	SPy0925	Short chain dehydrogenase	Unknown	0.2939
M5005_Spy1074	SpM3_ChORF0995_at	-1.55	0.0186	-	spyM3_0995	Hypothetical protein	Unknown	0.5623

M5005_gene	RML Probeset	*T* -statistic *	Empirical *P* -value †	Gene	Synonym	Description	Function	Q-value (Strain) ‡
M5005_Spy0987	SpM1_ChORF1281_s_at	2.08	0.0188	*sipC*	SPy1281	Signal peptidase I (EC 3.4.21.89)	Secretion	0.3986
M5005_Spy1094	SpM1_ChORF1340_s_at	-1.58	0.0188	-	SPy1340	Transporter, MFS superfamily	Membrane transport	0.5590
M5005_Spy0704	SpM1_ChORF0901_s_at	1.89	0.019	*pyrE*	SPy0901	Orotate phosphoribosyltransferase (EC 2.4.2.10)	Nucleotide metabolism	0.0898
M5005_Spy0914	SpM1_ChORF1198_s_at	-1.69	0.0192	-	SPy1198	Phage transcriptional repressor	Phage	0.3752
M5005_Spy1784	SpM12_ChORF2973_s_at	-1.69	0.0192	-		PTS system, trehalose-specific IIBC component (EC 2.7.1.69)	Carbohydrate metabolism	0.6729
M5005_Spy0251	SpM1_ChORF0295_s_at	-1.73	0.0194	*oppC*	SPy0295	Oligopeptide transport system permease protein oppC	Membrane transport	0.0566
M5005_Spy0458	SpM18_ChORF0618_s_at	-1.51	0.0194	-	spyM18_0618	Hypothetical cytosolic protein	Unknown	0.5443
M5005_Spy1691	SpM1_ChORF1985_s_at	-1.76	0.0195	-	SPy1985	Exodeoxyribonuclease III (EC 3.1.11.2)	Unknown	0.3229
M5005_Spy0554	SpM1_ChORF0728_s_at	1.98	0.0196	-	SPy0728	Septation ring formation regulator	Information processing	0.5148
M5005_Spy0963	SpM1_ChORF1253_s_at	-1.45	0.0196	-	SPy1253	Integral membrane protein	Unknown	0.3817
M5005_Spy1647	SpM1_ChORF1932_s_at	2.07	0.0196	*rplM*	SPy1932	LSU ribosomal protein L13P	Protein synthesis	0.3149
M5005_Spy0542	SpM1_ChORF0713_s_at	-1.56	0.0197	*pepD*	SPy0713	Dipeptidase (EC 3.4.-.-)	Amino acid metabolism	0.2979
M5005_Spy1088	SpM1_ChORF1333_s_at	1.75	0.0198	*obg*	SPy1333	GTP-binding protein OBG family	Unknown	0.2737
M5005_Spy0295	SpM1_ChORF0351_s_at	2.17	0.0199	-	SPy0351	60 kDa inner membrane protein YIDC	Cellular processing	0.5176
M5005_Spy0017	SpM1_ChORF0019_s_at	2.05	0.0204	*sibA*	SPy0019	Secreted protein	Cellular processing	0.2682
M5005_Spy0324	SpM1_ChORF0386_s_at	-1.96	0.0204	*ftsD*	SPy0386	Ferrichrome transport ATP-binding protein fhuC	Membrane transport	0.4255
M5005_Spy1368	SpM1_ChORF1666_s_at	1.86	0.0206	*ftsL*	SPy1665	S-adenosyl-methyltransferase mraW (EC 2.1.1.-)	Unknown	0.2552
M5005_Spy0019	SpM1_ChORF0021_s_at	-1.61	0.0207	-	SPy0021	DNA repair protein recO	Cellular processing	0.5064
M5005_Spy0182	SpM1_ChORF0212_s_at	-1.49	0.0207	*speG*	SPy0212	Exotoxin type G precursor	Virulence	0.6705
M5005_Spy0805	SpM1_ChORF1082_at	-1.56	0.021	*srtK*	SPy1082	Two-component nisin biosynthesis sensor protein nisK	Signal transduction	0.4278
M5005_Spy0998	SpyM3_1303_at	-1.81	0.0211	-	spyM3_1303	Phage protein	Phage	0.6602

M5005_gene	RML Probeset	*T* -statistic *	Empirical *P* -value †	Gene	Synonym	Description	Function	Q-value (Strain) ‡
M5005_Spy0124	SpM1_ChORF0146_s_at	-1.72	0.0213	*sloR*	SPy0146	Transcriptional regulator	Information processing	0.1830
M5005_Spy0331	SpM1_ChORF0400_s_at	-1.68	0.0213	*dnaX*	SPy0400	DNA polymerase III, delta' subunit (EC 2.7.7.7)	Information processing	0.2408
M5005_Spy0523	SpM1_ChORF0634_s_at	-1.57	0.0214	-	SPy0634	Hypothetical protein	Membrane transport	0.3938
M5005_Spy0045	SpM1_ChORF0050_s_at	1.90	0.0215	*rplD*	SPy0050	LSU ribosomal protein L1E (= L4P)	Protein synthesis	0.4968
M5005_Spy0593	SpM1_ChORF0775_s_at	-1.53	0.0215	-	SPy0775	Neutral zinc metallopeptidase family	Unknown	0.4175
M5005_Spy1486	SpM1_ChORF1745_s_at	-1.47	0.0216	*accC*	SPy1745	Biotin carboxylase (EC 6.3.4.14)	Cell wall metabolism	0.6341
M5005_Spy1326	SpM1_ChORF1615_s_at	-1.52	0.0217	*comFC*	SPy1615	ComF operon protein 3	Membrane transport	0.4589
M5005_Spy1634	SpM1_ChORF1918_s_at	-1.75	0.0218	*lacF*	SPy1918	PTS system, lactose-specific IIA component (EC 2.7.1.69)	Carbohydrate metabolism	0.1827
M5005_Spy1096	SpM1_ChORF1344_s_at	-1.65	0.0219	-	SPy1344	Thioesterase superfamily protein	Unknown	0.6019
M5005_Spy1323	SpM1_ChORF1610_s_at	-1.45	0.0221	-	SPy1610	Transposase	Mobile genetic element	0.6623
M5005_Spy1622	SpM1_ChORF1905_s_at	-1.56	0.0223	*hsdS*	SPy1905	Type I restriction-modification system specificity subunit	Information processing	0.6629
M5005_Spy1365	SpM1_ChORF1662_s_at	-1.40	0.0224	-	SPy1659	Phospho-N-acetylmuramoyl-pentapeptide-transferase (EC 2.7.8.13)	Cell wall metabolism	0.4889
M5005_Spy0933	SpM1_ChORF1218_s_at	2.18	0.0226	-	SPy1218	Probable NADH-dependent flavin oxidoreductase yqiG (EC 1.-.-.-)	Unknown	0.5893
M5005_Spy0013	SpM1_ChORF0015_s_at	2.13	0.0228	*ftsH*	SPy0015	Cell division protein ftsH (EC 3.4.24.-)	Cellular processing	0.3109
M5005_Spy0095	SpM1_ChORF0110_s_at	1.99	0.0229	-	SPy0110	Hypothetical protein	Unknown	0.1798
M5005_Spy0552	SpM1_ChORF0726_s_at	1.67	0.0229	-	SPy0726	DNA gyrase related protein (probably a hydrolase/phosphatase)	Unknown	0.5231
M5005_Spy0753	SpM1_ChORF1029_s_at	2.18	0.0229	*acoC*	SPy1029	Dihydrolipoamide acetyltransferase component of pyruvate dehydrogenase complex (EC 2.3.1.12)	Information processing	0.6184
M5005_Spy1348	SpM1_ChORF1641_s_at	-1.62	0.0229	-	SPy1641	D-beta-hydroxybutyrate permease	Unknown	0.5996

M5005_gene	RML Probeset	*T* -statistic *	Empirical *P* -value †	Gene	Synonym	Description	Function	Q-value (Strain) ‡
M5005_Spy1843	SpM1_ChORF2191_s_at	1.78	0.023	-	SPy2191	Transglycosylase SLT domain family protein	Virulence	0.1703
M5005_Spy0122	SpM1_ChORF0144_s_at	-1.53	0.0231	-	SPy0144	Putative DNA-binding protein	Information processing	0.4110
M5005_Spy1353	SpM1_ChORF1647_s_at	-1.36	0.0231	-	SPy1647	Hypothetical cytosolic protein	Unknown	0.6155
M5005_Spy0353	SpM1_ChORF0431_at	-2.01	0.0232	-	SPy0431	Hypothetical membrane spanning protein	Unknown	0.4269
M5005_Spy0385	SpM1_ChORF0470_s_at	-1.99	0.0232	-	SPy0470	67 kDa Myosin-crossreactive streptococcal antigen	Virulence	0.0239
M5005_Spy0540	SpM1_ChORF0653_s_at	-1.78	0.0233	-	SPy0653	Transporter	Membrane transport	0.0395
M5005_Spy1615	SpM1_ChORF1899_s_at	-1.47	0.0233	-	SPy1899	Hypothetical membrane spanning protein	Unknown	0.6512
M5005_Spy0076	M12_1023_s_at	1.84	0.0234	-		4-diphosphocytidyl-2-C-methyl-D-erythritol kinase (EC 2.7.1.148)	Lipid metabolism	0.2853
M5005_Spy1703	SpM1_ChORF1999_at	2.24	0.0235	-	SPy1999	Hypothetical cytosolic protein	Unknown	0.2551
M5005_Spy1300	SpM1_ChORF1580_s_at	-1.50	0.0237	-	SPy1580	Hypothetical cytosolic protein	Unknown	0.3353
M5005_Spy1659	SpM1_ChORF1945_s_at	-1.37	0.0238	-	SPy1945	Hypothetical protein	Unknown	0.2762
M5005_Spy0618	SpM1_ChORF0803_s_at	-2.04	0.0241	*cmk*	SPy0803	Cytidylate kinase (EC 2.7.4.14)	Nucleotide metabolism	0.0060
M5005_Spy0348	SpM1_ChORF0426_s_at	-1.62	0.0242	*nrdI*	SPy0426	NrdI protein	Nucleotide metabolism	0.3083
M5005_Spy0442	SpM1_ChORF0535_s_at	-1.68	0.0242	-	SPy0535	Hypothetical cytosolic protein	Unknown	0.4889
M5005_Spy1116	SpM1_ChORF1368_s_at	-1.35	0.0242	*udk*	SPy1368	Uridine kinase (EC 2.7.1.48)	Nucleotide metabolism	0.5962
M5005_Spy0855	SpM1_ChORF1133_s_at	-2.13	0.0243	*proV*	SPy1133	Glycine betaine transport ATP-binding protein	Membrane transport	0.5061
M5005_Spy1386	SpM1_ChORF1691_s_at	2.09	0.0243	-	SPy1691	Hypothetical membrane spanning protein	Unknown	0.5655
M5005_Spy0156	SpM1_ChORF0182_s_at	1.99	0.0245	-	SPy0182	Metal-dependent hydrolase (EC 3.-.-.-)	Cellular processing	0.4999
M5005_Spy0170	SpM1_ChORF0197_s_at	-1.47	0.0245	*nadC*	SPy0197	Nicotinate-nucleotide pyrophosphorylase [carboxylating] (EC 2.4.2.19)	Coenzyme and cofactor metabolism	0.6184
M5005_Spy0864	SpM1_ChORF1142_s_at	-1.30	0.0245	*hemK*	SPy1142	Peptide release factor-glutamine N5-methyltransferase (EC 2.1.1.-)	Information processing	0.4589

M5005_gene	RML Probeset	*T* -statistic *	Empirical *P* -value †	Gene	Synonym	Description	Function	Q-value (Strain) ‡
M5005_Spy0031	SpM1_ChORF0034_at	1.94	0.0248	*purK*	SPy0034	Phosphoribosylaminoimidazole carboxylase ATPase subunit (EC 4.1.1.21)	Nucleotide metabolism	0.1949
M5005_Spy1277	SpM1_ChORF1549_s_at	-1.40	0.0248	*ahrC.2*	SPy1549	Arginine repressor, argR	Information processing	0.3722
M5005_Spy1412	SpM1_ChORF1724_s_at	2.06	0.0248	*nusA*	SPy1724	N utilization substance protein A	Cellular processing	0.4269
M5005_Spy1801	SpM1_ChORF2118_s_at	-1.50	0.0251	*tag*	SPy2118	DNA-3-methyladenine glycosylase (EC 3.2.2.20)	Information processing	0.5880
M5005_Spy0367	SpM1_ChORF0450_s_at	1.88	0.0253	*scaR*	SPy0450	Iron-dependent repressor	Information processing	0.5106
M5005_Spy1607	SpM1_ChORF1889_s_at	2.08	0.0253	*fba*	SPy1889	Fructose-bisphosphate aldolase (EC 4.1.2.13)	Carbohydrate metabolism	0.2282
M5005_Spy0918	SpM1_ChORF1203_s_at	-1.44	0.0256	-	SPy1203	Hypothetical protein	Unknown	0.6743
M5005_Spy0602	SpM1_ChORF0784_s_at	-1.58	0.0258	*rmlD*	SPy0784	dTDP-4-dehydrorhamnose reductase (EC 1.1.1.133)	Cell wall metabolism	0.2190
M5005_Spy0587	SpM1_ChORF0768_s_at	2.21	0.0261	*pheS*	SPy0768	Phenylalanyl-tRNA synthetase alpha chain (EC 6.1.1.20)	Protein synthesis	0.3002
M5005_Spy1349	SpM1_ChORF1642_s_at	-1.27	0.0261	*luxS*	SPy1642	Autoinducer-2 production protein luxS (EC 3.13.1.-)	Information processing	0.6128
M5005_Spy0755	SpM1_ChORF1031_s_at	1.98	0.0263	*acoL, pdhD*	SPy1031	Dihydrolipoamide dehydrogenase (EC 1.8.1.4)	Carbohydrate metabolism	0.5301
M5005_Spy1376	SpM1_ChORF1678_s_at	2.05	0.0264	*tkt*	SPy1678	Transketolase (EC 2.2.1.1)	Carbohydrate metabolism	0.6715
M5005_Spy0167	SpM3_ChORF1054_s_at	-1.83	0.0267	-	spyM3_1054	Transposase	Mobile genetic element	0.3225
M5005_Spy0327	SpM1_ChORF0393_x_at	-1.30	0.0268	*upp*	SPy0393	Uracil phosphoribosyltransferase (EC 2.4.2.9)	Nucleotide metabolism	0.3081
M5005_Spy0123	SpM1_ChORF0145_s_at	-1.50	0.027	-	SPy0145	Translation initiation inhibitor	Cellular processing	0.6489
M5005_Spy0342	SpM1_ChORF0416_s_at	2.14	0.0271	*prtS*	SPy0416	Lactocepin (EC 3.4.21.96)	Amino acid metabolism	0.4745
M5005_Spy1111	SpM1_ChORF1364_s_at	1.98	0.0271	-	SPy1364	Hypothetical protein	Unknown	0.5317
M5005_Spy1402	SpM1_ChORF1712_s_at	-1.54	0.0271	*lacR.1*	SPy1712	Lactose phosphotransferase system repressor	Information processing	0.5539
M5005_Spy0085	SpM1_ChORF0100_s_at	2.02	0.0272	-	SPy0100	Putative DNA binding protein	Unknown	0.3076
M5005_Spy1707	SpM1_ChORF2003_s_at	1.70	0.0275	*dppD*	SPy2003	Dipeptide transport ATP-binding protein dppD	Membrane transport	0.1453

M5005_gene	RML Probeset	*T*-statistic *	Empirical *P*-value †	Gene	Synonym	Description	Function	Q-value (Strain) ‡
M5005_Spy1809	SpM1_ChORF2152_s_at	-1.48	0.0275	*uviB*	SPy2152	Bacteriocin uviB	Stress adaptation	0.5231
M5005_Spy1182	SpM1_ChORF1452_s_at	-1.43	0.0276	-	SPy1452	Phage protein	Phage	0.5512
M5005_Spy0806	SpM1_ChORF1083_at	-1.64	0.0278	*srtA*	SPy1083	Lantibiotic srtA precursor	Virulence	0.6061
M5005_Spy1426	SpM12_ChORF2993_s_at	-1.53	0.0278	-		Phage protein	Phage	0.4278
M5005_Spy0684	SpM1_ChORF0878_s_at	-1.59	0.0281	*mvaK2*	SPy0878	Phosphomevalonate kinase (EC 2.7.4.2)	Lipid metabolism	0.2853
M5005_Spy1389	SpM1_ChORF1695_s_at	-1.42	0.0281	-	SPy1695	Sodium-dependent phosphate transporter	Membrane transport	0.4869
M5005_Spy1817	SpM12_ChORF2181_s_at	-1.56	0.0286	*cadD*		Cadmium resistance protein	Membrane transport	0.6372
M5005_Spy1318	SpM1_ChORF1605_s_at	-1.38	0.0287	*rocA*	SPy1605	Sensory transduction protein kinase-like transcriptional regulator	Information processing	0.6743
M5005_Spy1698	SpM1_ChORF1991_s_at	-1.54	0.0287	*trpG*	SPy1991	Anthranilate synthase component II (EC 4.1.3.27) / Para-aminobenzoate synthase glutamine amidotransferase component II (EC 4.1.3.-)	Unknown	0.2552
M5005_Spy0646	SpM1_ChORF0838_s_at	-1.44	0.0293	-	SPy0838	ABC transporter permease protein	Membrane transport	0.6200
M5005_Spy1095	SpM1_ChORF1343_s_at	-1.56	0.0293	-	SPy1343	Hypothetical cytosolic protein	Unknown	0.4215
M5005_Spy0080	SpM1_ChORF0095_s_at	-1.47	0.0295	-	SPy0095	Bis(5'-nucleosyl)-tetraphosphatase (asymmetrical) (EC 3.6.1.17)	Virulence	0.6910
M5005_Spy0609	SpM1_ChORF0793_s_at	-1.51	0.0301	-	SPy0793	Phosphoglycerol transferase	Unknown	0.1081
M5005_Spy0943	SpM1_ChORF1230_s_at	2.01	0.0302	*cdd*	SPy1230	Cytidine deaminase (EC 3.5.4.5)	Nucleotide metabolism	0.6572
M5005_Spy0499	SpM1_ChORF0600_s_at	-1.38	0.0304	-	SPy0600	Thiamine transporter	Membrane transport	0.5745
M5005_Spy0673	SpM1_ChORF0866_s_at	-1.49	0.0304	*papS*	SPy0866	Poly(A) polymerase (EC 2.7.7.19) / tRNA nucleotidyltransferase (EC 2.7.7.25)	Protein synthesis	0.4088
M5005_Spy0113	SpM1_ChORF0133_at	-1.43	0.0305	-	SPy0133	Transposase	Mobile genetic element	0.6743

M5005_gene	RML Probeset	*T*-statistic *	Empirical *P*-value †	Gene	Synonym	Description	Function	Q-value (Strain) ‡
M5005_Spy0658	SpM1_ChORF0851_s_at	1.75	0.0305	-	SPy0851	Regulatory protein (pfoS/R)	Information processing	0.1557
M5005_Spy1860	SpM1_ChORF2209_s_at	-1.25	0.0305	-	SPy2209	Hypothetical membrane spanning protein	Membrane transport	0.4968
M5005_Spy0053	SpM1_ChORF0060_s_at	1.98	0.0307	*rpsQ*	SPy0060	SSU ribosomal protein S17P	Protein synthesis	0.4184
M5005_Spy0218	SpM1_ChORF0258_s_at	-1.91	0.0308	-	SPy0258	N-acetylmannosamine kinase (EC 2.7.1.60)	Carbohydrate metabolism	0.1923
M5005_Spy0483	SpM1_ChORF0583_s_at	2.01	0.031	-	SPy0583	Stress-responsive transcriptional regulator PspC	Stress adaptation	0.5626
M5005_Spy1140	SpM1_ChORF1400_s_at	-1.91	0.031	*queA*	SPy1400	S-adenosylmethionine:tRNA ribosyltransferase-isomerase (EC 5.-.-.-)	Protein synthesis	0.2838
M5005_Spy0381	SpM1_ChORF0464_s_at	-1.50	0.0311	-	SPy0464	S1 RNA binding domain	Cellular processing	0.5864
M5005_Spy0325	SpM1_ChORF0388_s_at	-1.58	0.0312	*murE*	SPy0388	UDP-N-acetylmuramoyl-L-alanyl-D-glutamate--lysine ligase (EC 6.3.2.7)	Cellular processing	0.1656
M5005_Spy1247	SpM1_ChORF1518_s_at	1.98	0.0313	-	SPy1518	Hypothetical cytosolic protein	Unknown	0.6512
M5005_Spy0167	SpM12_ChORF286-28_s_at	-1.66	0.0315	-		Transposase	Mobile genetic element	0.6586
M5005_Spy0378	SpM1_ChORF0462_s_at	2.00	0.0315	*pyrH*	SPy0462	Uridylate kinase (EC 2.7.4.-)	Cellular processing	0.2297
M5005_Spy1517	SpM1_ChORF1783_s_at	-1.48	0.0315	-	SPy1783	Lantibiotic transport permease protein	Membrane transport	0.6811
M5005_Spy1790	SpM1_ChORF2106_s_at	1.87	0.0317	-	SPy2106	Acetyltransferase (EC 2.3.1.-)	Cellular processing	0.3379
M5005_Spy1155	SpM3_ChORF1081_s_at	-1.54	0.0318	*prfC*	spyM3_1081	Bacterial Peptide Chain Release Factor 3 (RF-3)	Protein synthesis	0.6910
M5005_Spy1004	SpyM3_1308_x_at	-1.35	0.032	-	spyM3_1308	Phage protein	Phage	0.6081
M5005_Spy0603	SpM1_ChORF0786_s_at	1.79	0.0323	*rgpAc*	SPy0786	Alpha-(1,2)-rhamnosyltransferase (EC 2.4.1.-)	Cell wall metabolism	0.4981
M5005_Spy1324	SpM18_ChORF1620_x_at	-1.40	0.0324	-	spyM18_1620	Hypothetical protein	Unknown	0.4565
M5005_Spy0327	SpM18_ChORF0444_x_at	-1.87	0.0328	*upp*	spyM18_0444	Uracil phosphoribosyltransferase (EC 2.4.2.9)	Nucleotide metabolism	0.4110
M5005_Spy1166	SpM18_ChORF1442_s_at	1.95	0.0328	-	spyM18_1442	Hypothetical protein	Unknown	0.4826

M5005_gene	RML Probeset	*T*-statistic *	Empirical *P*-value †	Gene	Synonym	Description	Function	Q-value (Strain) ‡
M5005_Spy1377	SpM1_ChORF1681_s_at	1.96	0.0328	-	SPy1681	Trans-acting positive transcriptional regulator	Information processing	0.5615
M5005_Spy1814	SpM1_ChORF2157_s_at	-1.33	0.0332	*hisS*	SPy2157	Histidyl-tRNA synthetase (EC 6.1.1.21)	Protein synthesis	0.5795
M5005_Spy1006	SpM49_ChORF7585-34_s_at	-1.56	0.0334	-		Phage structural protein	Phage	0.5512
M5005_Spy0507	SpM18_ChORF0677_x_at	-1.37	0.0335	-	spyM18_0677	Hypothetical cytosolic protein	Unknown	0.6641
M5005_Spy0927	SpM1_ChORF1213_s_at	1.95	0.0335	*fhs.1*	SPy1213	Formate--tetrahydrofolate ligase (EC 6.3.4.3)	Carbohydrate metabolism	0.6372
M5005_Spy0236	SpM1_ChORF0276_s_at	1.53	0.0336	-	SPy0276	ABC transporter amino acid-binding protein / Amino acid ABC transporter permease protein	Membrane transport	0.1511
M5005_Spy0817	SpM1_ChORF1093_s_at	-1.31	0.0339	*dacA*	SPy1093	D-alanyl-D-alanine carboxypeptidase (EC 3.4.16.4)	Cell wall metabolism	0.6843
M5005_Spy1447	SpM12_ChORF299-45_s_at	-1.49	0.034	-		Phage-related DNA helicase	Phage	0.4227
M5005_Spy0236	SpM1_ChORF0277_s_at	-1.53	0.0342	-	SPy0277	ABC transporter amino acid-binding protein / Amino acid ABC transporter permease protein	Membrane transport	0.5626
M5005_Spy1236	SpM1_ChORF1505_s_at	-1.31	0.0342	*phr*	SPy1505	Deoxyribodipyrimidine photolyase (EC 4.1.99.3)	Information processing	0.6874
M5005_Spy1259	SpM1_ChORF1531_s_at	2.06	0.0343	*dpr*	SPy1531	Non-specific DNA-binding protein Dps / Iron-binding ferritin-like antioxidant protein	Stress adaptation	0.6463
M5005_Spy1503	SpM1_ChORF1766_s_at	-1.48	0.0344	-	SPy1766	Phosphoglycerate mutase (EC 5.4.2.1)	Carbohydrate metabolism	0.5893
M5005_Spy1603	SpM1_ChORF1886_s_at	1.84	0.0344	*asp*	SPy1886	Putative alkaline-shock protein	Stress adaptation	0.6563
M5005_Spy0503	SpM18_ChORF0672_s_at	-1.35	0.0346	*gpoA*	spyM18_0672	Glutathione peroxidase (EC 1.11.1.9)	Stress adaptation	0.6470
M5005_Spy1584	SpM12_ChORF217-5_at	-1.67	0.0346	-		NAD(FAD)-utilizing dehydrogenases	Unknown	0.4110
M5005_Spy1139	SpM1_ChORF1399_s_at	-1.77	0.0347	*nagB*	SPy1399	Glucosamine-6-phosphate isomerase (EC 3.5.99.6)	Carbohydrate metabolism	0.0700
M5005_Spy0311	SpM1_ChORF0370_s_at	-1.91	0.0348	-	SPy0370	Hypothetical cytosolic protein	Unknown	0.4541
M5005_Spy1601	SpM1_ChORF1884_s_at	1.63	0.0349	-	SPy1884	Membrane protease protein family	Unknown	0.6512

M5005_gene	RML Probeset	*T*-statistic *	Empirical *P*-value †	Gene	Synonym	Description	Function	Q-value (Strain) ‡
M5005_Spy0941	SpM1_ChORF1226_s_at	1.77	0.0353	-	SPy1226	Nucleoside transport ATP-binding protein	Membrane transport	0.2867
M5005_Spy0048	SpM1_ChORF0053_x_at	1.80	0.0356	*rpsS*	SPy0053	SSU ribosomal protein S19P	Protein synthesis	0.3859
M5005_Spy0602	SpM5_ChORF4P31a-86_s_at	-1.40	0.0356	*rmlD*		dTDP-4-dehydrorhamnose reductase (EC 1.1.1.133)	Cell wall metabolism	0.6743
M5005_Spy1260	SpM1_ChORF1532_s_at	-1.45	0.0359	-	SPy1532	Prepilin peptidase family (EC 3.4.99.-)	Unknown	0.6294
M5005_Spy1624	SpM18_ChORF1977_at	-1.49	0.0359	-	spyM18_1977	Hypothetical protein	Unknown	0.5923
M5005_Spy0530	SpM1_ChORF0643_s_at	-1.60	0.0363	*prfB*	SPy0643	Bacterial Peptide Chain Release Factor 2 (RF-2)	Information processing	0.2393
M5005_Spy0926	SpM1_ChORF1212_s_at	1.90	0.0364	-	SPy1212	Cardiolipin synthetase (EC 2.7.8.-)	Lipid metabolism	0.6743
M5005_Spy0149	SpM1_ChORF0175_s_at	-1.31	0.0365	-	SPy0175	PTS system, 3-keto-L-gulonate specific IIB component (EC 2.7.1.69)	Carbohydrate metabolism	0.6623
M5005_Spy0219	SpM1_ChORF0259_s_at	-1.80	0.0367	-	SPy0259	Transcriptional regulator, RpiR family	Information processing	0.5864
M5005_Spy0792	SpM1_ChORF1069_s_at	1.88	0.0367	-	SPy1069	NAD(P)H-dependent quinone reductase (EC 1.-.-.-)	Carbohydrate metabolism	0.6368
M5005_Spy0531	SpM1_ChORF0644_s_at	-1.81	0.0369	*ftsE*	SPy0644	Cell division ATP-binding protein ftsE	Cellular processing	0.0132
M5005_Spy0884	SpM1_ChORF1163_s_at	-1.43	0.037	*smf*	SPy1163	Smf protein	Cellular processing	0.4798
M5005_Spy1614	SpM1_ChORF1898_s_at	-1.30	0.037	-	SPy1898	Hypothetical protein	Unknown	0.6294
M5005_Spy1420	SpM1_ChORF0999_at	-1.46	0.0373	-	SPy0999	Phage protein	Phage	0.6214
M5005_Spy1375	SpM1_ChORF1676_s_at	1.97	0.0377	*tkt*	SPy1676	Transketolase (EC 2.2.1.1)	Carbohydrate metabolism	0.4510
M5005_Spy0581	SpM12_ChORF269-12_s_at	-1.39	0.038	*atpD*		ATPase, beta subunit	Carbohydrate metabolism	0.5159
M5005_Spy0844	SpM1_ChORF1122_s_at	1.75	0.038	*nifS, yrvO*	SPy1122	Cysteine desulfhydrase (EC 4.4.1.-) / Selenocysteine lyase (EC 4.4.1.16)	Coenzyme and cofactor metabolism	0.6775
M5005_Spy1487	SpM1_ChORF1746_s_at	-1.30	0.038	*fabZ*	SPy1746	(3R)-hydroxymyristoyl-[acyl carrier protein] dehydratase (EC 4.2.1.-)	Lipid metabolism	0.5532
M5005_Spy0070	SpM1_ChORF0080_s_at	1.91	0.0382	*rpoA*	SPy0080	DNA-directed RNA polymerase alpha chain (EC 2.7.7.6)	Cellular processing	0.6463

M5005_gene	RML Probeset	*T*-statistic *	Empirical *P*-value †	Gene	Synonym	Description	Function	Q-value (Strain) ‡
M5005_Spy1100	SpM1_ChORF1351_s_at	-1.32	0.0383	*aroK*	SPy1351	Shikimate kinase (EC 2.7.1.71)	Amino acid metabolism	0.6874
M5005_Spy0707	SpM1_ChORF0904_s_at	-1.39	0.0384	-	SPy0904	Cystine transport system permease protein	Membrane transport	0.4544
M5005_Spy0164	SpM1_ChORF0190_s_at	-1.78	0.0385	-	SPy0190	ParB-like nuclease	Unknown	0.0105
M5005_Spy0272	SpM1_ChORF0320_s_at	1.66	0.0386	-	SPy0320	ABC transporter ATP-binding protein	Membrane transport	0.2754
M5005_Spy0073	SpM18_ChORF0084_s_at	-2.10	0.0388	-	spyM18_0084	Hypothetical protein	Unknown	0.0976
M5005_Spy0555	SpM1_ChORF0729_s_at	-1.37	0.0389	-	SPy0729	Hypothetical cytosolic protein	Unknown	0.6294
M5005_Spy0254	M12_0466_at	-1.49	0.039	-		Transposase	Mobile genetic element	0.5800
M5005_Spy0427	SpM1_ChORF0517_s_at	-1.59	0.0392	*thrS*	SPy0517	Threonyl-tRNA synthetase (EC 6.1.1.3)	Protein synthesis	0.3149
M5005_Spy0996	SpM18_ChORF0393_s_at	-1.61	0.0392	*speA2*	spyM18_0393	Pyrogenic toxin superantigen exotoxin type A precursor, A2 allele	Virulence	0.3076
M5005_Spy1009	SpM49_ChORF7585-31_at	1.96	0.0394	-		Phage protein	Phage	0.2054
M5005_Spy1625	SpM1_ChORF1908_s_at	-1.45	0.0394	*salR*	SPy1908	Transcriptional regulatory protein degU	Information processing	0.5868
M5005_Spy0676	SpM18_ChORF0930_s_at	-1.27	0.0395	-	spyM18_0930	Hypothetical protein	Unknown	0.6184
M5005_Spy0068	SpM1_ChORF0077_s_at	1.81	0.0396	*rpsM*	SPy0077	SSU ribosomal protein S13P	Protein synthesis	0.5891
M5005_Spy0319	SpM1_ChORF0380_s_at	1.67	0.0401	*ppaC*	SPy0380	Manganese-dependent inorganic pyrophosphatase (EC 3.6.1.1)	Cellular processing	0.5400
M5005_Spy0300	SpM1_ChORF0357_s_at	1.66	0.0402	-	SPy0357	Hydrolase (HAD superfamily)	Unknown	0.2024
M5005_Spy0701	SpM1_ChORF0898_s_at	-1.32	0.0402	*cpsY*	SPy0898	Transcriptional regulators, LysR family	Information processing	0.6184
M5005_Spy1647	SpM5_ChORF125g-172_at	-1.52	0.0403	*rplM*		LSU ribosomal protein L13P	Protein synthesis	0.6041
M5005_Spy0014	SpM1_ChORF0016_s_at	-1.63	0.0405	-	SPy0016	Amino acid permease	Membrane transport	0.3719
M5005_Spy0664	SpM1_ChORF0857_s_at	1.84	0.0405	*mur1.2*	SPy0857	Autolysin (EC 3.5.1.28)	Cell wall metabolism	0.2028
M5005_Spy1685	SpM1_ChORF1980_s_at	-1.43	0.0405	-	SPy1980	D-tyrosyl-tRNA(Tyr) deacylase (EC 3.1.-.-)	Protein synthesis	0.6008

M5005_gene	RML Probeset	*T* -statistic *	Empirical *P* -value †	Gene	Synonym	Description	Function	Q-value (Strain) ‡
M5005_Spy0763	SpM1_ChORF1038_s_at	-1.56	0.0409	*femD*	SPy1038	Phosphoglucosamine mutase (EC 5.4.2.10)	Cell wall metabolism	0.1377
M5005_Spy1540	SpM1_ChORF1813_at	-1.95	0.0409	*endoS*	SPy1813	Endo-beta-N-acetylglucosaminidase F2 precursor (EC 3.2.1.96); mannosyl-glycoprotein endo-b-N-acetylglucosaminidase	Carbohydrate metabolism	0.0132
M5005_Spy1546	SpM1_ChORF1818_s_at	1.63	0.0414	*nusB*	SPy1818	General stress protein, Gls24 family	Stress adaptation	0.5962
M5005_Spy1256	SpM1_ChORF1528_s_at	-1.35	0.0416	-	SPy1528	Rhodanese-related sulfurtransferases	Unknown	0.5962
M5005_Spy0154	SpM1_ChORF0180_s_at	-1.40	0.0419	-	SPy0180	Hypothetical protein	Unknown	0.6488
M5005_Spy1178	SpM5_ChORF270b-557_at	-1.41	0.0419	-		Phage protein	Phage	0.4436
M5005_Spy0341	SpM5_ChORFJ7578C-323_s_at	-1.42	0.042	*prtS*		Lactocepin (EC 3.4.21.96)	Unknown	0.6727
M5005_Spy0504	SpM1_ChORF0606_s_at	-1.62	0.042	*pepF*	SPy0606	Oligoendopeptidase F (EC 3.4.24.-)	Amino acid metabolism	0.4345
M5005_Spy1042	SpM5_ChORF270b-6_at	-1.57	0.042	-		Phage replication protein	Phage	0.2789
M5005_Spy0702	SpM1_ChORF0899_s_at	-1.39	0.0421	-	SPy0899	Hypothetical protein	Unknown	0.1908
M5005_Spy0389	SpM1_ChORF0475_s_at	1.59	0.0424	*dgk*	SPy0475	Diacylglycerol kinase (EC 2.7.1.107)	Lipid metabolism	0.1707
M5005_Spy1066	SpM1_ChORF1304_at	1.98	0.0424	*amyB*	SPy1304	Cyclomaltodextrinase/Neopullulanase (EC 3.2.1.135) / Cyclomaltodextrinase (EC 3.2.1.54) / Maltogenic alpha-amylase (EC 3.2.1.133)	Carbohydrate metabolism	0.2979
M5005_Spy0147	SpM12_ChORF286-3_s_at	-1.29	0.0427	*leuS*		Leucyl-tRNA synthetase (EC 6.1.1.4)	Protein synthesis	0.5540
M5005_Spy0454	SpM1_ChORF0547_s_at	-1.36	0.0427	-	SPy0547	Hypothetical protein	Unknown	0.4558
M5005_Spy0187	SpM12_ChORF197-4_s_at	-1.56	0.0429	-		Transposase	Mobile genetic element	0.2770
M5005_Spy0637	SpM1_ChORF0826_s_at	-1.45	0.043	*lsp*	SPy0826	Lipoprotein signal peptidase (EC 3.4.23.36)	Secretion	0.3002
M5005_Spy0849	SpM1_ChORF1127_s_at	1.63	0.043	-	SPy1127	Ribosomal large subunit pseudouridine synthase D (EC 4.2.1.70)	Protein synthesis	0.1377

M5005_gene	RML Probeset	*T*-statistic *	Empirical *P*-value †	Gene	Synonym	Description	Function	Q-value (Strain) ‡
M5005_Spy0392	SpM1_ChORF0478_s_at	-1.29	0.0431	-	SPy0478	Hypothetical protein	Unknown	0.1707
M5005_Spy1049	SpM3_ChORF0976_s_at	-1.47	0.0431	-	spyM3_0976	Phage protein	Phage	0.5443
M5005_Spy0008	SpM1_ChORF0010_s_at	-1.64	0.0433	*divIC*	SPy0010	Cell division protein	Cellular processing	0.6201
M5005_Spy1310	SpM1_ChORF1595_s_at	-1.95	0.0433	-	SPy1595	Sugar transport system permease protein	Unknown	0.0179
M5005_Spy1821	SpM1_ChORF2166_s_at	-1.27	0.0442	-	SPy2166	Hypothetical phage protein	Phage	0.6200
M5005_Spy0223	SpM1_ChORF0263_s_at	1.55	0.0443	-	SPy0263	GTPase (EC 3.6.1.-)	Unknown	0.3722
M5005_Spy1781	SpM1_ChORF2093_s_at	1.63	0.0445	*tsf*	SPy2093	Protein Translation Elongation Factor Ts (EF-Ts)	Cellular processing	0.3575
M5005_Spy1057	SpM1_ChORF1293_s_at	-1.30	0.0446	*malR*	SPy1293	Maltose Operon Transcriptional repressor, LacI family	Information processing	0.3154
M5005_Spy1188	SpM1_ChORF1459_s_at	-1.26	0.0447	-	SPy1459	Phage protein	Phage	0.6146
M5005_Spy0518	SpM1_ChORF0628_at	-1.25	0.0448	-	SPy0628	Oligohyaluronate lyase (EC 4.2.2.-)	Unknown	0.3719
M5005_Spy0956	SpM1_ChORF1246_s_at	-1.28	0.0452	-	SPy1246	16S rRNA m(5)C 967 methyltransferase (EC 2.1.1.-)	Cellular processing	0.5688
M5005_Spy0793	SpM1_ChORF1070_s_at	1.69	0.0453	-	SPy1070	Xaa-His dipeptidase (EC 3.4.13.3)	Amino acid metabolism	0.6184
M5005_Spy1083	SpM1_ChORF1325_s_at	-1.61	0.0454	-	SPy1325	Transcription antiterminator, BglG family / PTS system, mannitol (Cryptic)-specific IIA component (EC 2.7.1.69)	Information processing	0.3283
M5005_Spy0886	SpM12_ChORF288 15_at	-1.48	0.0455	-		Transcriptional regulators, LysR family	Information processing	0.5698
M5005_Spy0470	SpM1_ChORF0567_s_at	1.67	0.0457	-	SPy0567	Hydrolase (HAD superfamily)	Unknown	0.2748
M5005_Spy0594	SpM1_ChORF0776_s_at	-1.26	0.0464	*rexB*	SPy0776	ATP-dependent nuclease subunit B	Cellular processing	0.5198
M5005_Spy1350	SpM1_ChORF1643_s_at	1.83	0.0468	-	SPy1643	Hypothetical protein	Unknown	0.3283
M5005_Spy0120	SpM1_ChORF0141_s_at	1.68	0.047	*atoD.2*	SPy0141	Acetate CoA-transferase alpha subunit (EC 2.8.3.8)	Carbohydrate metabolism	0.2321
M5005_Spy1826	SpM1_ChORF2173_s_at	-1.47	0.0474	-	SPy2173	Hypothetical membrane associated protein	Phage	0.5698
M5005_Spy1758	SpM1_ChORF2066_s_at	-1.50	0.0479	-	SPy2066	Probable dipeptidase B (EC 3.4.-.-)	Amino acid metabolism	0.2042

M5005_gene	RML Probeset	*T* -statistic *	Empirical *P* -value †	Gene	Synonym	Description	Function	Q-value (Strain) ‡
M5005_Spy1065	SpM1_ChORF1302_at	2.00	0.048	*amyA*	SPy1302	Cyclomaltodextrin glucanotransferase/Alpha-amylase (EC 3.2.1.1), putative cyclomaltodextrin glucanotransferase (EC 3.2.1.19)	Carbohydrate metabolism	0.4888
M5005_Spy1189	SpM1_ChORF1460_s_at	-1.57	0.0481	-	SPy1460	Phage terminase	Phage	0.6031
M5005_Spy0754	SpM5_ChORF270b-343_at	-1.52	0.0482	-		Hypothetical protein	Unknown	0.6811
M5005_Spy1651	SpM1_ChORF1937_s_at	1.63	0.0483	-	SPy1937	Hypothetical cytosolic protein	Unknown	0.6201
M5005_Spy1205	SpM49_ChORF7585-10_s_at	-1.33	0.0489	-		Phage protein	Phage	0.6512
M5005_Spy1673	SpM1_ChORF1962_s_at	1.83	0.0489	*proS*	SPy1962	Prolyl-tRNA synthetase (EC 6.1.1.15)	Protein synthesis	0.3533
M5005_Spy1506	SpM1_ChORF1769_s_at	-1.49	0.049	*gatB*	SPy1769	Aspartyl/glutamyl-tRNA(Asn/Gln) amidotransferase subunit B (EC 6.3.5.-)	Protein synthesis	0.6382
M5005_Spy1842	SpM1_ChORF2190_s_at	-1.51	0.049	*sdhA*	SPy2190	L-serine dehydratase (EC 4.2.1.13)	Amino acid metabolism	0.2779
M5005_Spy0746	SpM1_ChORF1019_s_at	-1.46	0.0492	-	SPy1019	ABC transporter ATP-binding protein	Membrane transport	0.5874
M5005_Spy1009	SpM49_ChORF7585-7_at	-1.32	0.0495	-		Phage protein	Phage	0.3901
M5005_Spy0299	SpM1_ChORF0356_s_at	-1.36	0.0499	-	SPy0356	23S rRNA methyltransferase (EC 2.1.1.-)	Information processing	0.5107
M5005_Spy1518	SpM1_ChORF1784_s_at	-1.32	0.0501	-	SPy1784	Transporter	Membrane transport	0.5169
M5005_Spy0827	SpM1_ChORF1103_s_at	-1.46	0.0502	*potB*	SPy1103	Spermidine/putrescine transport system permease protein potB	Membrane transport	0.5169
M5005_Spy1728	SpM1_ChORF2032_s_at	1.92	0.0504	-	SPy2032	Periplasmic component of efflux system	Membrane transport	0.2521
M5005_Spy0274	SpM5_ChORFJ7578C-342_s_at	-1.29	0.0505	*braB*		Branched-chain amino acid transport system carrier protein	Membrane transport	0.6339
M5005_Spy1391	SpM1_ChORF1698_s_at	-1.58	0.0505	-	SPy1698	DegV family protein	Unknown	0.3722
M5005_Spy1694	SpM1_ChORF1987_s_at	1.29	0.0506	-	SPy1987	Hypothetical cytosolic protein	Unknown	0.1707
M5005_Spy1863	SpM12_ChORF236-4_s_at	-1.47	0.0508	-		Transposase	Mobile genetic element	0.5631

M5005_gene	RML Probeset	*T* -statistic *	Empirical *P* -value †	Gene	Synonym	Description	Function	Q-value (Strain) ‡
M5005_Spy0336	SpM1_ChORF0407_s_at	-1.40	0.0509	-	SPy0407	Hypothetical membrane associated protein	Unknown	0.3181
M5005_Spy0461	SpM1_ChORF0558_s_at	-1.23	0.051	-	SPy0558	Hypothetical cytosolic protein	Unknown	0.4734
M5005_Spy1595	SpM1_ChORF1876_s_at	1.86	0.0516	-	SPy1876	Zn-dependent hydrolase (EC 3.-.-.-)	Cellular processing	0.6750
M5005_Spy0260	SpM1_ChORF0305_s_at	1.53	0.052	-	SPy0305	Putative lipase	Unknown	0.4010
M5005_Spy1715	SpM1_ChORF2010_s_at	1.82	0.0521	*scpA*	SPy2010	C5A peptidase precursor (EC 3.4.21.-)	Virulence	0.6690
M5005_Spy0394	SpM1_ChORF0480_at	1.70	0.0522	-	SPy0480	Hypothetical protein	Unknown	0.1736
M5005_Spy0811	SpM1_ChORF1088_at	-1.45	0.0522	-	SPy1088	Transcriptional regulator, Cro/CI family	Phage	0.5886
M5005_Spy0484	SpM1_ChORF0584_s_at	1.52	0.0523	*ptsK, hprK*	SPy0584	Hpr(ser) kinase (EC 2.7.1.-) / Phosphatase (EC 3.1.3.-)	Cellular processing	0.6035
M5005_Spy1757	SpM1_ChORF2065_s_at	1.41	0.0526	-	SPy2065	Hypothetical protein	Unknown	0.2713
M5005_Spy0628	SpM1_ChORF0814_s_at	-1.84	0.0529	*folC.2*	SPy0814	Folylpolyglutamate synthase (EC 6.3.2.17) / Dihydrofolate synthase (EC 6.3.2.12)	Coenzyme and cofactor metabolism	0.4449
M5005_Spy1723	SpM1_ChORF2025_s_at	1.81	0.0531	*isp*	SPy2025	Immunogenic secreted protein	Virulence	0.3672
M5005_Spy1519	SpM12_ChORF2946_s_at	1.69	0.0534	*recG*		ATP-dependent DNA helicase recG (EC 3.6.1.-)	Information processing	0.1982
M5005_Spy1232	SpM1_ChORF1499_s_at	-1.56	0.0536	*xseB*	SPy1499	Exodeoxyribonuclease VII small subunit (EC 3.1.11.6)	Information processing	0.1126
M5005_Spy1367	SpM1_ChORF1665_s_at	-1.24	0.0541	*pbpX*	SPy1664	Cell division protein ftsL	Cellular processing	0.5999
M5005_Spy0446	SpM1_ChORF0539_s_at	-1.36	0.0542	-	SPy0539	Hypothetical membrane associated protein	Unknown	0.5750
M5005_Spy0722	SpM1_ChORF0921_s_at	-1.28	0.0548	*miaA*	SPy0921	tRNA delta(2)-isopentenylpyrophosphate transferase (EC 2.5.1.8)	Protein synthesis	0.5445
M5005_Spy0175	M12_0671_s_at	-1.43	0.0558	*tgt*		Queuine tRNA-ribosyltransferase (EC 2.4.2.29)	Protein synthesis	0.4110
M5005_Spy0214	SpM1_ChORF0254_s_at	-1.77	0.0562	-	SPy0254	N-acetylneuraminate transport system permease protein	Membrane transport	0.4999
M5005_Spy0561	SpM12_ChORF2621_s_at	1.80	0.0564	*epf*		Putative extracellular matrix binding protein	Virulence	0.2853
M5005_Spy0617	SpM12_ChORF2469_s_at	-1.61	0.0566	-		Hypothetical membrane associated protein	Unknown	0.1081

M5005_gene	RML Probeset	*T* -statistic *	Empirical *P* -value †	Gene	Synonym	Description	Function	Q-value (Strain) ‡
M5005_Spy1663	SpM1_ChORF1950_s_at	-1.40	0.0566	-	SPy1950	PTS system, IIB component (EC 2.7.1.69)	Carbohydrate metabolism	0.6512
M5005_Spy0630	SpM1_ChORF0816_s_at	-1.44	0.0567	*nifS, yrvO*	SPy0816	Cysteine desulfhydrase (EC 4.4.1.-) / Selenocysteine lyase (EC 4.4.1.16)	Amino acid metabolism	0.6906
M5005_Spy0636	SpM1_ChORF0824_s_at	1.05	0.0568	*epuA*	SPy0824	Transcriptional regulators, LysR family	Information processing	0.1619
M5005_Spy0833	SpM1_ChORF1110_s_at	-1.69	0.0576	-	SPy1110	NAD-dependent malic enzyme (EC 1.1.1.38)	Carbohydrate metabolism	0.0539
M5005_Spy1026	SpM18_ChORF1787_at	-1.66	0.0579	-	spyM18_1787	Phage protein	Phage	0.6419
M5005_Spy1190	SpM1_ChORF1461_x_at	-1.48	0.0579	-	SPy1461	Phage protein	Phage	0.6910
M5005_Spy0929	SpM1_ChORF1215_s_at	1.84	0.0587	-	SPy1215	SIR2 family protein	Information processing	0.6790
M5005_Spy0911	SpM1_ChORF1193_s_at	1.15	0.0589	-	SPy1193	Hypothetical protein	Unknown	0.0871
M5005_Spy0842	SpM1_ChORF1120_s_at	-1.27	0.0591	-	SPy1120	Redox-sensitive transcriptional regulator Rex	Unknown	0.2330
M5005_Spy0426	SpM1_ChORF0516_s_at	1.71	0.0593	-	SPy0516	1,2-diacylglycerol 3-glucosyltransferase (EC 2.4.1.157)	Cell wall metabolism	0.4838
M5005_Spy0087	SpM1_ChORF0102_s_at	-1.35	0.0595	*comYB*	SPy0102	ComG operon protein 2	Membrane transport	0.5400
M5005_Spy0612	SpM1_ChORF0797_s_at	-1.38	0.0595	*amrA*	SPy0797	Transcriptional activator amrA	Information processing	0.1707
M5005_Spy0862	SpM1_ChORF1140_s_at	1.25	0.0598	*tdk2*	SPy1140	Thymidine kinase (EC 2.7.1.21)	Unknown	0.0870
M5005_Spy0047	SpM1_ChORF0052_s_at	1.71	0.0601	*rplB*	SPy0052	LSU ribosomal protein L2P	Protein synthesis	0.6700
M5005_Spy0191	SpM12_ChORF279 21_s_at	-1.32	0.0603	-		Integral membrane protein (Rhomboid family)	Unknown	0.5532
M5005_Spy0546	SpM1_ChORF0717_s_at	1.84	0.0603	*rpmE*	SPy0717	LSU ribosomal protein L31P	Protein synthesis	0.5106
M5005_Spy0636	SpM18_ChORF0886_s_at	-1.27	0.0605	*epuA*	spyM18_0886	Transcriptional regulators, LysR family	Information processing	0.5877
M5005_Spy0387	SpM1_ChORF0472_s_at	-1.35	0.0606	-	SPy0472	Uracil DNA glycosylase superfamily protein	Information processing	0.4088
M5005_Spy1405	SpM1_ChORF1715_s_at	1.56	0.0606	*copA*	SPy1715	Copper-exporting ATPase (EC 3.6.3.4)	Membrane transport	0.2635
M5005_Spy1631	SpM1_ChORF1915_at	-1.26	0.0609	*salA*	SPy1915	Lantibiotic salivaricin A	Virulence	0.6602

M5005_gene	RML Probeset	*T*-statistic *	Empirical *P*-value †	Gene	Synonym	Description	Function	Q-value (Strain) ‡
M5005_Spy0928	SpM1_ChORF1214_s_at	1.78	0.0615	*lplA*	SPy1214	Lipoate-protein ligase A (EC 6.-.-.-)	Coenzyme and cofactor metabolism	0.6750
M5005_Spy0904	SpM18_ChORF1136_s_at	-1.32	0.0617	-	spyM18_1136	Hypothetical protein	Unknown	0.6931
M5005_Spy1599	SpM1_ChORF1881_s_at	1.61	0.0617	*pgk*	SPy1881	Phosphoglycerate kinase (EC 2.7.2.3)	Carbohydrate metabolism	0.5889
M5005_Spy1567	SpM1_ChORF1845_s_at	-1.37	0.0621	-	SPy1845	Hypothetical protein	Unknown	0.1982
M5005_Spy0933	SpM1_ChORF1220_s_at	1.73	0.0622	-	SPy1220	Probable NADH-dependent flavin oxidoreductase yqiG (EC 1.-.-.-)	Unknown	0.6824
M5005_Spy1823	SpM1_ChORF2169_s_at	-1.29	0.0623	-	SPy2169	Integral membrane protein	Phage	0.5348
M5005_Spy0942	SpM1_ChORF1228_s_at	1.74	0.0625	-	SPy1228	Nucleoside-binding protein	Unknown	0.4449
M5005_Spy1460	M12_1769_at	-1.31	0.0629	-		Phage protein	Phage	0.6512
M5005_Spy1665	SpM18_ChORF2020_at	-1.30	0.0629	-	spyM18_2020	Hypothetical protein	Cellular processing	0.6580
M5005_Spy0883	SpM18_ChORF1122_s_at	-1.13	0.0634	-	spyM18_1122	Ribonuclease HII (EC 3.1.26.4)	Cellular processing	0.6822
M5005_Spy0908	SpM1_ChORF1190_s_at	-1.26	0.0641	*citX*	SPy1190	Apo-citrate lyase phosphoribosyl-dephospho-CoA transferase (EC 2.7.7.-)	Carbohydrate metabolism	0.6690
M5005_Spy1136	SpM1_ChORF1393_s_at	-1.32	0.0643	*pepB*	SPy1393	Oligoendopeptidase F (EC 3.4.24.-)	Amino acid metabolism	0.3887
M5005_Spy0930	SpM1_ChORF1216_s_at	1.74	0.0649	-	SPy1216	ATPase associated with chromosome architecture/replication	Unknown	0.6563
M5005_Spy0840	SpM1_ChORF1118_s_at	-1.23	0.0652	*radC*	SPy1118	DNA repair protein radC	Information processing	0.6512
M5005_Spy1746	SpM1_ChORF2052_s_at	-1.18	0.0652	-	SPy2052	PTS system, cellobiose-specific IIA component (EC 2.7.1.69)	Carbohydrate metabolism	0.5330
M5005_Spy1806	SpM1_ChORF2149_s_at	-1.17	0.0652	-	SPy2149	Hypothetical cytosolic protein	Unknown	0.6036
M5005_Spy1002	SpM49_ChORF7585-39_at	-1.21	0.066	-		N-acetylmuramoyl-L-alanine amidase (EC 3.5.1.28)	Phage	0.5926
M5005_Spy1605	SpM1_ChORF0303_s_at	-1.41	0.066	-	SPy0303	Transposase	Mobile genetic element	0.1619
M5005_Spy1231	SpM1_ChORF1498_s_at	1.24	0.0663	*fps*	SPy1498	Dimethylallyltransferase (EC 2.5.1.1) / Geranyltranstransferase (EC 2.5.1.10)	Lipid metabolism	0.4185

M5005_gene	RML Probeset	*T* -statistic *	Empirical *P* -value †	Gene	Synonym	Description	Function	Q-value (Strain) ‡
M5005_Spy1211	SpM1_ChORF0952_at	1.61	0.0664	-	SPy0952	Phage protein	Phage	0.4656
M5005_Spy0911	SpM12_ChORF28843_s_at	-1.35	0.0666	-		Hypothetical protein	Unknown	0.5672
M5005_Spy0506	SpM1_ChORF0609_s_at	1.41	0.067	*ftsW*	SPy0609	Cell division protein ftsW	Cellular processing	0.4981
M5005_Spy0578	SpM1_ChORF0757_s_at	-1.29	0.067	*atpH*	SPy0757	ATP synthase delta chain (EC 3.6.3.14)	Carbohydrate metabolism	0.4107
M5005_Spy0808	SpM1_ChORF1085_at	-1.55	0.0675	*srtF*	SPy1085	Lantibiotic transport ATP-binding protein	Membrane transport	0.6781
M5005_Spy0081	SpM1_ChORF0096_s_at	-1.25	0.0676	*tyrS*	SPy0096	Tyrosyl-tRNA synthetase (EC 6.1.1.1)	Protein synthesis	0.6743
M5005_Spy0211	SpM1_ChORF0250_x_at	1.26	0.0678	*rpmH*	SPy0250	LSU ribosomal protein L34P	Protein synthesis	0.5169
M5005_Spy1250	SpM1_ChORF1521_s_at	1.65	0.0679	*ftsA*	SPy1521	Cell division protein ftsA	Cellular processing	0.5159
M5005_Spy1416	SpM12_ChORF2517_at	1.59	0.068	-		N-acetylmuramoyl-L-alanine amidase (EC 3.5.1.28)	Phage	0.2939
M5005_Spy0477	SpM1_ChORF0575_s_at	-1.22	0.0681	-	SPy0575	Hypothetical membrane spanning protein	Unknown	0.4888
M5005_Spy1255	SpM1_ChORF1527_s_at	1.53	0.0682	*typA*	SPy1527	GTP-binding protein TypA/BipA	Information processing	0.5372
M5005_Spy1205	SpM1_ChORF1478_s_at	-1.27	0.0684	-	SPy1478	Phage protein	Phage	0.5221
M5005_Spy1052	SpM18_ChORF1309_s_at	-1.47	0.0685	*int.1*	spyM18_1309	DNA integration/recombination/invertion protein phi5005.1 int	Phage	0.6200
M5005_Spy1469	SpM1_ChORF1727_s_at	1.40	0.0688	-	SPy1727	Phosphotransferase enzyme family	Unknown	0.6499
M5005_Spy1117	SpM1_ChORF1369_s_at	1.43	0.069	*deaD2*	SPy1369	ATP-dependent RNA helicase	Stress adaptation	0.6540
M5005_Spy0313	SpM1_ChORF0373_s_at	-1.51	0.0692	-	SPy0373	Riboflavin transporter	Membrane transport	0.6930
M5005_Spy1193	SpM1_ChORF1465_s_at	1.59	0.0692	-	SPy1465	Phage protein	Phage	0.2639
M5005_Spy0355	SpM1_ChORF0435_at	-1.18	0.0695	-	SPy0435	Hypothetical protein	Unknown	0.5443
M5005_Spy0337	SpM12_ChORF2702_s_at	-1.70	0.0696	*cutC*		Copper homeostasis protein cutC	Unknown	0.4869
M5005_Spy0357	SpM1_ChORF0437_at	-1.17	0.0696	-	SPy0437	Hypothetical protein	Unknown	0.5966

M5005_gene	RML Probeset	*T* -statistic *	Empirical *P* -value †	Gene	Synonym	Description	Function	Q-value (Strain) ‡
M5005_Spy1581	SpM1_ChORF1863_s_at	-1.25	0.0697	-	SPy1863	Transcriptional regulator, MerR family	Information processing	0.6287
M5005_Spy0213	SpM12_ChORF295-17_s_at	-1.20	0.0704	-		N-acetylneuraminate-binding protein	Membrane transport	0.5504
M5005_Spy0991	SpM1_ChORF1285_s_at	-1.13	0.0706	-	SPy1285	Transcriptional regulator, GntR family	Information processing	0.4449
M5005_Spy1149	SpM1_ChORF1410_s_at	-1.34	0.0706	-	SPy1410	1-acyl-sn-glycerol-3-phosphate acyltransferase (EC 2.3.1.51)	Unknown	0.3458
M5005_Spy1292	SpM1_ChORF1568_s_at	-1.33	0.071	*valS*	SPy1568	Valyl-tRNA synthetase (EC 6.1.1.9)	Protein synthesis	0.4208
M5005_Spy1568	SpM1_ChORF1846_s_at	-1.27	0.071	*dinP*	SPy1846	DNA polymerase IV (EC 2.7.7.7)	Cellular processing	0.4142
M5005_Spy1737	SpM1_ChORF2042_s_at	-1.48	0.071	*rgg*	SPy2042	Transcriptional regulator	Information processing	0.5994
M5005_Spy0582	SpM1_ChORF0761_s_at	1.32	0.0713	*atpC*	SPy0761	ATP synthase epsilon chain (EC 3.6.3.14)	Carbohydrate metabolism	0.6034
M5005_Spy1598	SpM1_ChORF1879_s_at	-1.39	0.0715	-	SPy1879	Hypothetical protein	Unknown	0.5665
M5005_Spy1125	SpM1_ChORF1379_s_at	1.36	0.0719	-	SPy1379	Chloride channel protein	Membrane transport	0.1619
M5005_Spy0248	SpM1_ChORF0292_s_at	1.50	0.0721	*dacA*	SPy0292	D-alanyl-D-alanine carboxypeptidase (EC 3.4.16.4)	Cell wall metabolism	0.3149
M5005_Spy1151	SpM1_ChORF1412_s_at	1.46	0.0721	-	SPy1412	Hypothetical protein with endo/excinuclease domain	Unknown	0.2467
M5005_Spy1672	SpM1_ChORF1961_s_at	1.42	0.0721	*polC*	SPy1961	DNA polymerase III alpha subunit (EC 2.7.7.7)	Information processing	0.2853
M5005_Spy1390	SpM1_ChORF1697_s_at	-1.09	0.0722	-	SPy1697	Hypothetical protein	Unknown	0.5486
M5005_Spy0876	SpM1_ChORF1155_s_at	-0.99	0.0723	-	SPy1155	Lactoylglutathione lyase (EC 4.4.1.5)	Carbohydrate metabolism	0.3217
M5005_Spy1054	SpM1_ChORF1290_s_at	-1.15	0.0724	-	SPy1290	Phage protein	Phage	0.6632
M5005_Spy0978	SpM3_ChORF0902_at	-1.37	0.0726	-	spyM3_0902	Na(+)-linked D-alanine glycine permease	Membrane transport	0.6690
M5005_Spy0900	SpM1_ChORF1180_s_at	-1.63	0.073	-	SPy1180	Mg2+/citrate complex secondary transporter	Membrane transport	0.5176
M5005_Spy0575	SpM3_ChORF0493_s_at	-1.35	0.0736	*atpE*	spyM3_0493	ATP synthase C chain (EC 3.6.3.14)	Carbohydrate metabolism	0.5178
M5005_Spy1334	SpM1_ChORF1623_s_at	-1.48	0.0737	-	SPy1623	Transporter yvqF	Unknown	0.6184
M5005_Spy0957	SpM1_ChORF1247_s_at	-1.38	0.0738	-	SPy1247	Myo-inositol-1(or 4)-monophosphatase (EC 3.1.3.25)	Carbohydrate metabolism	0.3028

M5005_gene	RML Probeset	*T* -statistic *	Empirical *P* -value †	Gene	Synonym	Description	Function	Q-value (Strain) ‡
M5005_Spy1166	SpM3_ChORF1092_s_at	1.50	0.0741	-	spyM3_1092	Hypothetical protein	Unknown	0.4908
M5005_Spy0358	SpM12_ChORF2122_s_at	-1.29	0.0742	-		Hypothetical protein	Unknown	0.6294
M5005_Spy1783	SpM1_ChORF2096_s_at	-1.10	0.0745	*dexS*	SPy2096	Trehalose-6-phosphate hydrolase (EC 3.2.1.93)	Carbohydrate metabolism	0.6854
M5005_Spy0516	SpM1_ChORF0623_s_at	1.40	0.0747	*pacL*	SPy0623	Calcium-transporting ATPase (EC 3.6.3.8)	Membrane transport	0.6541
M5005_Spy0967	SpM1_ChORF1257_s_at	1.37	0.0747	-	SPy1257	ABC transporter ATP-binding protein	Membrane transport	0.2676
M5005_Spy0305	SpM1_ChORF0363_s_at	1.14	0.0751	-	SPy0363	Putative phosphoesterase	Unknown	0.2677
M5005_Spy1362	SpM1_ChORF1657_s_at	-1.21	0.0757	-	SPy1656	Transporter	Unknown	0.6509
M5005_Spy1709	SpM1_ChORF2005_s_at	-1.73	0.0757	-	SPy2005	Hypothetical protein	Unknown	0.0008
M5005_Spy1080	SpM1_ChORF1323_s_at	-1.37	0.0761	-	SPy1323	Hypothetical protein	Unknown	0.3225
M5005_Spy0757	SpM1_ChORF1032_s_at	-1.08	0.0763	*hylA*	SPy1032	Hyaluronate lyase precursor (EC 4.2.2.1)	Carbohydrate metabolism	0.5800
M5005_Spy0812	SpM12_ChORF26718_at	1.55	0.0764	-		Hypothetical protein	Unknown	0.2717
M5005_Spy0330	SpM1_ChORF0399_s_at	-1.24	0.077	*tmk*	SPy0399	Thymidylate kinase (EC 2.7.4.9)	Nucleotide metabolism	0.4022
M5005_Spy0592	SpM1_ChORF0773_s_at	1.48	0.077	-	SPy0773	ABC transporter ATP-binding protein	Membrane transport	0.3229
M5005_Spy0266	SpM1_ChORF0312_s_at	-1.38	0.0772	-	SPy0312	Methyltransferase (EC 2.1.1.-)	Unknown	0.4999
M5005_Spy1670	SpM1_ChORF1959_s_at	-1.18	0.0772	-	SPy1959	Oxidoreductase (EC 1.1.1.-)	Unknown	0.6294
M5005_Spy0003	SpM1_ChORF0004_s_at	-1.13	0.0773	-	SPy0004	Hypothetical cytosolic protein	Unknown	0.6368
M5005_Spy0171	SpM1_ChORF0198_s_at	1.68	0.0778	-	SPy0198	Transposase	Mobile genetic element	0.3229
M5005_Spy1764	SpM1_ChORF2074_s_at	1.22	0.0778	*ctsR*	SPy2074	Transcriptional regulator ctsR	Information processing	0.2867
M5005_Spy0801	M12_1863_s_at	-1.15	0.0781	-		Relaxase	Information processing	0.4334
M5005_Spy0882	SpM1_ChORF1161_at	1.27	0.0781	-	SPy1161	GTP-binding protein	Unknown	0.2166
M5005_Spy1364	SpM12_ChORF27419_s_at	-1.38	0.0784	-		ATP-dependent RNA helicase	Stress adaptation	0.5057

M5005_gene	RML Probeset	*T* -statistic *	Empirical *P* -value †	Gene	Synonym	Description	Function	Q-value (Strain) ‡
M5005_Spy1429	SpM12_ChORF299 57_s_at	1.61	0.0784	-		Phage protein	Phage	0.3721
M5005_Spy0703	SpM1_ChORF0900_s_at	-1.44	0.0785	*pyrF*	SPy0900	Orotidine 5'-phosphate decarboxylase (EC 4.1.1.23)	Nucleotide metabolism	0.2538
M5005_Spy1113	SpM1_ChORF1365_s_at	1.40	0.0793	-	SPy1365	GAF domain-containing proteins	Cellular processing	0.4208
M5005_Spy0689	SpM1_ChORF0883_s_at	-1.11	0.0794	*dyr*	SPy0883	Dihydrofolate reductase (EC 1.5.1.3)	Coenzyme and cofactor metabolism	0.6602
M5005_Spy1516	SpM1_ChORF1782_s_at	-1.54	0.0795	*asnB*	SPy1782	L-asparaginase (EC 3.5.1.1)	Amino acid metabolism	0.6499
M5005_Spy0384	SpM1_ChORF0469_s_at	1.52	0.0799	-	SPy0469	Surface antigen	Virulence	0.5886
M5005_Spy0777	SpM1_ChORF1054_at	-1.37	0.08		SPy1054	Collagen-like surface protein	Virulence	0.1901
M5005_Spy0208	SpM1_ChORF0247_s_at	1.52	0.0804	-	SPy0247	60 kDa inner membrane protein YIDC	Cellular processing	0.4929
M5005_Spy1197	SpM3_ChORF1124_s_at	-1.26	0.0806	-	spyM3_1124	Phage protein	Phage	0.3722
M5005_Spy1438	SpM12_ChORF299 51_s_at	-1.22	0.0807	-		Phage protein	Phage	0.6129
M5005_Spy1579	SpM1_ChORF1861_s_at	-1.52	0.0812	-	SPy1861	Transcriptional regulator	Phage	0.5176
M5005_Spy1462	SpM12_ChORF299 11_at	-1.22	0.0813	-		Phage protein	Phage	0.3002
M5005_Spy0916	SpM1_ChORF1201_s_at	-1.13	0.0819	*ylxM*	SPy1201	Signal recognition particle associated protein	Secretion	0.5257
M5005_Spy1407	SpM1_ChORF1718_s_at	-1.17	0.0825	-	SPy1718	Esterase (EC 3.1.1.-)	Unknown	0.6854
M5005_Spy1077	SpM12_ChORF236 7_s_at	-1.11	0.0826	*glnQ.2*		Glutamine transport ATP-binding protein glnQ	Membrane transport	0.6632
M5005_Spy1163	SpM1_ChORF1427_s_at	-1.18	0.0826	-	SPy1427	Transcriptional regulator, biotin repressor family	Information processing	0.6036
M5005_Spy1132	SpM1_ChORF1389_s_at	-1.15	0.083	*alaS*	SPy1389	Alanyl-tRNA synthetase (EC 6.1.1.7)	Protein synthesis	0.3817
M5005_Spy1158	SpM1_ChORF1421_s_at	-1.21	0.0832	*ddlA*	SPy1421	D-alanine--D-alanine ligase (EC 6.3.2.4)	Cell wall metabolism	0.6859
M5005_Spy1201	SpM1_ChORF1473_s_at	1.52	0.0834	-	SPy1473	Phage protein	Phage	0.3116
M5005_Spy1273	SpM1_ChORF1544_s_at	1.56	0.0838	*arcB*	SPy1544	Ornithine carbamoyltransferase (EC 2.1.3.3)	Amino acid metabolism	0.6341

M5005_gene	RML Probeset	*T* -statistic *	Empirical *P* -value †	Gene	Synonym	Description	Function	Q-value (Strain) ‡
M5005_Spy1534	SpM1_ChORF1805_s_at	1.55	0.084	*secA*	SPy1805	Protein translocase subunit secA	Secretion	0.6811
M5005_Spy0815	M12_0089_s_at	-1.21	0.0844	-		DNA integration/recombination/invertion protein	Information processing	0.4192
M5005_Spy1547	SpM1_ChORF1821_s_at	1.60	0.0854	*efp*	SPy1821	Protein Translation Elongation Factor P (EF-P)	Cellular processing	0.4577
M5005_Spy1278	SpM1_ChORF1551_s_at	1.41	0.0856	-	SPy1551	Hypothetical protein	Unknown	0.3002
M5005_Spy0550	SpM1_ChORF0723_at	-1.17	0.0857	-	SPy0723	Chloride channel protein	Membrane transport	0.6676
M5005_Spy0913	SpM1_ChORF1196_s_at	1.08	0.0859	-	SPy1196	Integrase/recombinase xerD	Phage	0.2168
M5005_Spy0519	SpM1_ChORF0630_s_at	-1.21	0.0864	*agaD*	SPy0630	PTS system, N-acetylgalactosamine-specific IID component (EC 2.7.1.69)	Carbohydrate metabolism	0.5590
M5005_Spy0678	SpM1_ChORF0872_s_at	1.14	0.0866	-	SPy0872	5'-nucleotidase (EC 3.1.3.5)	Unknown	0.2815
M5005_Spy1440	SpM12_ChORF299 48_at	-1.37	0.0874	-		Terminase large subunit	Phage	0.4792
M5005_Spy1214	SpM1_ChORF0949_s_at	0.97	0.0875	-	SPy0949	Phage protein	Phage	0.1696
M5005_Spy1649	SpM1_ChORF1934_s_at	1.30	0.0877	-	SPy1934	Hypothetical membrane spanning protein	Unknown	0.2123
M5005_Spy1303	SpM1_ChORF1584_s_at	-1.54	0.0882	*aroE*	SPy1584	Shikimate 5-dehydrogenase (EC 1.1.1.25)	Amino acid metabolism	0.0897
M5005_Spy0268	SpM1_ChORF0315_s_at	-1.44	0.0886	-	SPy0315	Hypothetical protein	Unknown	0.6051
M5005_Spy1818	SpM1_ChORF2163_s_at	-1.13	0.0891	*cadC*	SPy2163	Cadmium efflux system accessory protein	Membrane transport	0.4656
M5005_Spy1846	SpM1_ChORF2196_s_at	-1.15	0.0891	*cbiO1*	SPy2196	ATP-binding protein involved in export of hyaluronan capsule	Membrane transport	0.6294
M5005_Spy0881	SpM1_ChORF1160_s_at	1.33	0.0893	-	SPy1160	Hypothetical cytosolic protein	Unknown	0.3154
M5005_Spy0388	SpM1_ChORF0473_s_at	-1.27	0.0894	*dgk*	SPy0473	Hypothetical Metal-Binding Protein	Unknown	0.1827
M5005_Spy1636	SpM1_ChORF1921_s_at	-1.22	0.0895	*lacC.2*	SPy1921	Tagatose-6-phosphate kinase (EC 2.7.1.144)	Carbohydrate metabolism	0.4776
M5005_Spy1539	SpM1_ChORF1811_s_at	-1.46	0.0897	*scrK*	SPy1811	Fructokinase (EC 2.7.1.4)	Carbohydrate metabolism	0.2229
M5005_Spy1454	SpM12_ChORF299 39_s_at	-1.20	0.09	-		Phage protein	Phage	0.6410

M5005_gene	RML Probeset	*T*-statistic *	Empirical *P*-value †	Gene	Synonym	Description	Function	Q-value (Strain) ‡
M5005_Spy0623	SpM1_ChORF0808_s_at	1.58	0.0901	-	SPy0808	Methyltransferase (EC 2.1.1.-)	Unknown	0.2754
M5005_Spy1380	SpM1_ChORF1683_s_at	1.53	0.0901	*glpO*	SPy1683	Alpha-glycerophosphate oxidase (EC 1.1.3.21)	Carbohydrate metabolism	0.6013
M5005_Spy1659	SpM1_ChORF1946_s_at	-1.22	0.0902	-	SPy1946	Hypothetical protein	Unknown	0.3002
M5005_Spy1316	SpM1_ChORF1603_s_at	-1.35	0.0903	-	SPy1603	Hypothetical protein	Unknown	0.2568
M5005_Spy1339	SpM1_ChORF1629_s_at	-1.25	0.0903	*priA*	SPy1629	Primosomal protein N'	Information processing	0.4407
M5005_Spy1701	SpM1_ChORF1995_s_at	-1.35	0.0904	*flaR*	SPy1995	DNA topology modulation protein flar-related protein	Unknown	0.6294
M5005_Spy0776	SpM1_ChORF1053_s_at	1.29	0.0906	*lepA*	SPy1053	GTP-binding protein lepA	Information processing	0.5590
M5005_Spy1627	SpM49_ChORF6658-4_s_at	-1.29	0.0914	*salY*		ABC transporter permease protein	Membrane transport	0.6298
M5005_Spy0482	SpM1_ChORF0581_s_at	-1.16	0.0915	-	SPy0581	Zinc metalloprotease (EC 3.4.24.-)	Unknown	0.6854
M5005_Spy1594	SpM1_ChORF1875_s_at	1.51	0.0915	-	SPy1875	Putative transcriptional regulator	Unknown	0.5994
M5005_Spy1045	SpM18_ChORF1303_at	-1.19	0.0917	-	spyM18_1303	Transcriptional regulator	Phage	0.6000
M5005_Spy0290	SpM1_ChORF0345_s_at	1.44	0.0923	*murC*	SPy0345	UDP-N-acetylmuramate--alanine ligase (EC 6.3.2.8)	Cell wall metabolism	0.6201
M5005_Spy1424	SpM12_ChORF299-62_at	1.54	0.0924	-		Phage endopeptidase	Phage	0.3546
M5005_Spy0165	SpM1_ChORF0191_at	-1.14	0.0925	-	SPy0191	Transposase	Mobile genetic element	0.6512
M5005_Spy1178	SpM18_ChORF1460_s_at	-1.27	0.093	-	spyM18_1460	Phage protein	Phage	0.6844
M5005_Spy1406	SpM1_ChORF1717_at	-1.12	0.0934	*copY*	SPy1717	CopAB ATPases metal-fist type repressor	Information processing	0.6497
M5005_Spy1635	SpM1_ChORF1919_s_at	-1.39	0.0935	*lacD.2*	SPy1919	Tagatose-bisphosphate aldolase (EC 4.1.2.40)	Carbohydrate metabolism	0.2607
M5005_Spy1620	SpM1_ChORF1903_s_at	-0.94	0.094	-	SPy1903	Glycerate kinase (EC 2.7.1.31)	Unknown	0.3489
M5005_Spy0066	SpM1_ChORF0075_s_at	1.56	0.0942	*infA*	SPy0075	Bacterial Protein Translation Initiation Factor 1 (IF-1)	Cellular processing	0.5695
M5005_Spy0803	SpM12_ChORF284-43_s_at	-1.19	0.0943	*srtI*		Protein involved in lantibiotic (srt) production	Virulence	0.5615
M5005_Spy0651	SpM1_ChORF0843_s_at	-1.24	0.0947	-	SPy0843	Cell surface protein	Unknown	0.6588

M5005_gene	RML Probeset	*T*-statistic *	Empirical *P*-value †	Gene	Synonym	Description	Function	Q-value (Strain) ‡
M5005_Spy1372	SpM1_ChORF1673_s_at	-1.14	0.0948	*proB*	SPy1673	ABC transporter permease protein	Membrane transport	0.1923
M5005_Spy1430	SpM12_ChORF29956_s_at	-1.20	0.0953	-		Phage protein	Phage	0.6835
M5005_Spy1317	SpM1_ChORF1604_s_at	-1.48	0.0954	-	SPy1604	Alpha-mannosidase (EC 3.2.1.24)	Carbohydrate metabolism	0.1081
M5005_Spy1678	SpM1_ChORF1971_s_at	1.40	0.0958	-	SPy1971	Thioredoxin	Stress adaptation	0.5291
M5005_Spy0585	SpM18_ChORF0822_s_at	1.49	0.0959	*epuA*	spyM18_0822	EpuA protein	Virulence	0.2480
M5005_Spy1153	SpM1_ChORF1414_s_at	-1.07	0.0968	-	SPy1414	Kup system potassium uptake protein	Unknown	0.4544
M5005_Spy0779	SpM1_ChORF1056_s_at	-1.10	0.0969	-	SPy1056	Hypothetical membrane spanning protein	Unknown	0.4656
M5005_Spy0289	SpM1_ChORF0343_s_at	1.43	0.0973	-	SPy0343	Hypothetical cytosolic protein	Unknown	0.6041
M5005_Spy0771	SpM1_ChORF1048_s_at	1.52	0.0982	-	SPy1048	Hypothetical cytosolic protein	Unknown	0.4066
M5005_Spy0922	SpM1_ChORF1209_s_at	1.54	0.0983	*pdxK*	SPy1209	Hypothetical membrane spanning protein	Unknown	0.3489
M5005_Spy0583	M12_0158_at	-1.09	0.0984	-		Hypothetical membrane associated protein	Unknown	0.4227
M5005_Spy1160	SpM3_ChORF1086_at	-1.25	0.0984	-	spyM3_1086	Penicillin-binding protein	Unknown	0.3767
M5005_Spy1677	SpM1_ChORF1968_s_at	1.51	0.0985	-	SPy1968	Protein translocase subunit YajC	Secretion	0.6602
M5005_Spy1706	SpM1_ChORF2002_s_at	-1.07	0.0988	*dppC*	SPy2002	Dipeptide transport system permease protein dppC	Membrane transport	0.6151
M5005_Spy1017	SpyM3_1321_at	-1.20	0.099	-	spyM3_1321	Phage protein	Phage	0.4436
M5005_Spy0748	SpM1_ChORF1022_s_at	1.32	0.1008	*estA*	SPy1022	Acetyl esterase (EC 3.1.1.-)	Unknown	0.2541
M5005_Spy1241	SpM1_ChORF1510_s_at	-1.03	0.1012	*mutT*	SPy1510	Mutator mutT protein (7,8-dihydro-8-oxoguanine-triphosphatase) (EC 3.6.1.-)	Cellular processing	0.6041
M5005_Spy0466	SpM18_ChORF0632_s_at	1.54	0.1018	-	spyM18_0632	Hypothetical phage protein	Phage	0.3210
M5005_Spy1137	SpM1_ChORF1395_s_at	-1.06	0.1031	-	SPy1395	Putative competence protein/transcription factor	Information processing	0.6368
M5005_Spy1532	SpM1_ChORF1804_s_at	-1.38	0.1034	*acpS*	SPy1804	Alanine racemase (EC 5.1.1.1)	Cellular processing	0.6339

M5005_gene	RML Probeset	*T* -statistic *	Empirical *P* -value †	Gene	Synonym	Description	Function	Q-value (Strain) ‡
M5005_Spy1064	SpM1_ChORF1299_at	1.53	0.1042	*malD*	SPy1299	Maltodextrin/cyclodextrin ABC transport system (permease) protein	Membrane transport	0.4208
M5005_Spy1360	SpM18_ChORF1666_s_at	-1.06	0.1044	*trxB*	spyM18_1666	Thioredoxin reductase (EC 1.8.1.9)	Amino acid metabolism	0.6525
M5005_Spy1542	SpM1_ChORF1815_s_at	-1.40	0.1048	*scrA*	SPy1815	PTS system, sucrose-specific IIABC component (EC 2.7.1.69)	Carbohydrate metabolism	0.2502
M5005_Spy0452	SpM3_ChORF0388_s_at	-1.04	0.1055	-	spyM3_0388	Chromosome segregation ATPases	Cellular processing	0.6488
M5005_Spy0242	SpM1_ChORF0285_s_at	-1.14	0.106	-	SPy0285	ABC transporter ATP-binding protein	Membrane transport	0.6382
M5005_Spy0474	SpM1_ChORF0571_s_at	-1.25	0.1061	*licT*	SPy0571	Transcription antiterminator, BglG family	Information processing	0.6041
M5005_Spy0715	SpM1_ChORF0913_s_at	1.54	0.1062	-	SPy0913	SSU ribosomal protein S1P	Protein synthesis	0.5376
M5005_Spy1008	SpM49_ChORF7585-32_at	-1.19	0.1065	-		Phage-related protein	Phage	0.6519
M5005_Spy1354	SpM1_ChORF1648_s_at	1.47	0.1071	*recU*	SPy1648	Recombination protein recU	Cellular processing	0.5962
M5005_Spy0682	SpM1_ChORF0876_s_at	-0.99	0.1074	*mvaK1*	SPy0876	Mevalonate kinase (EC 2.7.1.36)	Lipid metabolism	0.5539
M5005_Spy0102	SpM18_ChORF0120_s_at	-1.14	0.1077	-	spyM18_0120	Single-strand DNA binding protein	Phage	0.6564
M5005_Spy1451	SpM12_ChORF299-42_at	1.53	0.1077	-		Phage protein	Phage	0.3546
M5005_Spy0111	SpM1_ChORF0130_at	-1.10	0.108	-	SPy0130	Hypothetical protein	Unknown	0.6690
M5005_Spy1502	SpM1_ChORF1764_s_at	-0.92	0.108	-	SPy1764	D-alanyl-D-alanine carboxypeptidase (EC 3.4.16.4)	Cell wall metabolism	0.5443
M5005_Spy0011	SpM1_ChORF0013_s_at	-1.47	0.1085	-	SPy0013	Cell cycle protein MesJ	Cellular processing	0.5061
M5005_Spy0951	SpM1_ChORF1241_s_at	-1.37	0.1091	*pstB*	SPy1241	Phosphate transport ATP-binding protein pstB	Membrane transport	0.2314
M5005_Spy0585	SpM3_ChORF0503_s_at	1.39	0.1093	*epuA*	spyM3_0503	EpuA protein	Virulence	0.3149
M5005_Spy1435	SpM12_ChORF299-52_s_at	-1.18	0.11	-		Phage scaffold protein	Phage	0.5941
M5005_Spy1397	SpM1_ChORF1707_s_at	-1.18	0.1101	*lacB.1*	SPy1708	Galactose-6-phosphate isomerase lacB subunit (EC 5.3.1.26)	Carbohydrate metabolism	0.3225
M5005_Spy0178	SpM1_ChORF0208_s_at	-0.97	0.1106	-	SPy0208	Metal-dependent hydrolase (EC 3.-.-.-)	Unknown	0.6000

M5005_gene	RML Probeset	*T* -statistic *	Empirical *P* -value †	Gene	Synonym	Description	Function	Q-value (Strain) ‡
M5005_Spy0713	SpM1_ChORF0911_s_at	-1.03	0.1111	*bcaT*	SPy0911	Branched-chain amino acid aminotransferase (EC 2.6.1.42)	Carbohydrate metabolism	0.6743
M5005_Spy0586	SpM1_ChORF0766_s_at	-1.19	0.1117	*endA*	SPy0766	DNA-entry nuclease (EC 3.1.30.-)	Virulence	0.5726
M5005_Spy1176	SpM1_ChORF1444_s_at	-1.34	0.1117	-	SPy1444	Phage infection protein	Phage	0.3887
M5005_Spy1344	SpM1_ChORF1637_s_at	-1.07	0.1126	*atoB*	SPy1637	Acetyl-CoA acetyltransferase (EC 2.3.1.9)	Lipid metabolism	0.6147
M5005_Spy1049	SpM18_ChORF1305_s_at	-1.14	0.113	-	spyM18_1305	Phage protein	Phage	0.6632
M5005_Spy0421	SpM1_ChORF0511_s_at	-1.06	0.1133	*gloA*	SPy0511	Lactoylglutathione lyase (EC 4.4.1.5)	Carbohydrate metabolism	0.6623
M5005_Spy0750	SpM1_ChORF1025_at	-1.07	0.1133	-	SPy1025	ABC transporter ATP-binding protein	Membrane transport	0.5981
M5005_Spy0925	SpM18_ChORF1162_s_at	-1.16	0.1136	*rnhB*	spyM18_1162	Anaerobic ribonucleoside-triphosphate reductase (EC 1.17.4.2)	Unknown	0.6850
M5005_Spy1098	SpM18_ChORF1359_at	-0.92	0.1139	-	spyM18_1359	tRNA (Uracil-5-) -methyltransferase (EC 2.1.1.35)	Protein synthesis	0.4645
M5005_Spy1301	SpM1_ChORF1581_s_at	-1.36	0.1144	-	SPy1581	Hypothetical cytosolic protein	Unknown	0.0713
M5005_Spy1661	SpM1_ChORF1947_s_at	1.28	0.1144	-	SPy1947	Transaldolase (EC 2.2.1.2)	Carbohydrate metabolism	0.2363
M5005_Spy1743	SpM1_ChORF2049_s_at	1.38	0.1148	*pflD*	SPy2049	Formate acetyltransferase (EC 2.3.1.54)	Carbohydrate metabolism	0.4558
M5005_Spy1128	SpM3_ChORF1017_s_at	1.53	0.115	-	spyM3_1017	Transposase	Mobile genetic element	0.4020
M5005_Spy1385	SpM1_ChORF1689_s_at	1.32	0.1151	*glyQ*	SPy1689	Glycyl-tRNA synthetase alpha chain (EC 6.1.1.14)	Protein synthesis	0.3154
M5005_Spy1682	SpM12_ChORF292 19_s_at	-1.16	0.1155	*msmK*		Multiple sugar-binding ABC transporter protein	Membrane transport	0.5316
M5005_Spy1696	SpM1_ChORF1989_s_at	-1.11	0.1158	-	SPy1989	Hypothetical protein	Unknown	0.4196
M5005_Spy1248	SpM1_ChORF1519_s_at	1.32	0.1161	-	SPy1519	Pyridoxal-5'-phosphate family protein	Unknown	0.6262
M5005_Spy0025	SpM1_ChORF0027_s_at	-1.06	0.1164	*purM*	SPy0027	Phosphoribosylformyl-glycinamidine cyclo-ligase (EC 6.3.3.1)	Nucleotide metabolism	0.6108
M5005_Spy1779	SpM1_ChORF2091_s_at	-1.06	0.1166	-	SPy2091	Transcriptional regulator, LuxR family	Information processing	0.5358
M5005_Spy1674	SpM1_ChORF1963_s_at	1.25	0.1168	-	SPy1963	Pheromone-processing membrane metalloprotease	Cellular processing	0.6034

M5005_gene	RML Probeset	*T* -statistic *	Empirical *P* -value †	Gene	Synonym	Description	Function	Q-value (Strain) ‡
M5005_Spy1198	SpM1_ChORF0676_s_at	-1.17	0.1172	-	SPy0676	Phage protein	Phage	0.3149
M5005_Spy1007	SpM49_ChORF7585-33_at	-1.20	0.1174	-		Phage protein	Phage	0.6540
M5005_Spy1060	SpM1_ChORF1295_s_at	1.38	0.1174	*malF*	SPy1295	Maltose/maltosaccharide/maltodextrin ABC transport system (permease) protein	Membrane transport	0.3143
M5005_Spy1544	SpM1_ChORF1817_s_at	-1.10	0.1179	*scrR*	SPy1817	Sucrose operon repressor	Information processing	0.4776
M5005_Spy0957	SpM18_ChORF1197_s_at	-1.27	0.1182	-	spyM18_1197	Myo-inositol-1(or 4)-monophosphatase (EC 3.1.3.25)	Carbohydrate metabolism	0.1479
M5005_Spy0131	SpM1_ChORF0154_s_at	-1.23	0.1183	*ntpA*	SPy0154	V-type sodium ATP synthase subunit A (EC 3.6.3.15)	Membrane transport	0.2838
M5005_Spy1421	SpM12_ChORF299-65_at	-1.09	0.1186	-		Phage infection protein	Phage	0.6707
M5005_Spy0930	SpM1_ChORF1217_s_at	1.48	0.1194	-	SPy1217	ATPase associated with chromosome architecture/replication	Unknown	0.6750
M5005_Spy0700	SpM1_ChORF0895_s_at	1.40	0.1199	*cpsX*	SPy0895	Attenuator of transcription, LytR family regulator	Information processing	0.4755
M5005_Spy0954	SpM1_ChORF1243_s_at	-1.06	0.1199	*pstC*	SPy1243	Phosphate transport system permease protein pstC	Membrane transport	0.4208
M5005_Spy1200	SpM1_ChORF1474_s_at	-1.20	0.1199	-	SPy1474	Phage protein	Phage	0.5421
M5005_Spy1026	M12_1466_s_at	1.41	0.1206	-		Phage protein	Phage	0.3533
M5005_Spy1846	SpM1_ChORF2195_s_at	1.20	0.1208	*cbiO1*	SPy2195	CDP-diacylglycerol--glycerol-3-phosphate 3-phosphatidyltransferase	Membrane transport	0.4745
M5005_Spy0834	SpM1_ChORF1111_s_at	-1.29	0.1215	-	SPy1111	Zn-dependent alcohol dehydrogenases and related dehydrogenases	Unknown	0.4819
M5005_Spy0841	SpM1_ChORF1119_s_at	-1.15	0.1223	-	SPy1119	Glutamine amidotransferase, class I	Unknown	0.4537
M5005_Spy0152	SpM12_ChORF286-31_s_at	-1.28	0.1226	-		L-xylulose 5-phosphate 3-epimerase (EC 5.3.1.-)	Carbohydrate metabolism	0.6690
M5005_Spy1229	SpM1_ChORF1496_s_at	-0.96	0.1231	*argR*	SPy1496	Arginine repressor, argR	Information processing	0.6850
M5005_Spy1861	SpM1_ChORF2210_s_at	-1.00	0.1241	-	SPy2210	ABC transporter ATP-binding protein	Membrane transport	0.6874
M5005_Spy0747	SpM1_ChORF1020_s_at	1.35	0.1243	-	SPy1020	Zn-dependent hydrolase (EC 3.-.-.-)	Unknown	0.6061

M5005_gene	RML Probeset	*T* -statistic *	Empirical *P* -value †	Gene	Synonym	Description	Function	Q-value (Strain) ‡
M5005_Spy1044	SpM3_ChORF0964_at	-1.04	0.1243	-	spyM3_0964	Phage protein	Phage	0.4227
M5005_Spy1723	SpM12_ChORF249 5_s_at	1.48	0.1249	*isp*		Immunogenic secreted protein	Virulence	0.4020
M5005_Spy0666	SpM12_ChORF291 52_s_at	-1.35	0.125	-		Hypothetical protein	Unknown	0.6641
M5005_Spy0648	SpM1_ChORF0840_s_at	1.07	0.1253	*rpsP*	SPy0840	SSU ribosomal protein S16P	Protein synthesis	0.6359
M5005_Spy1501	SpM1_ChORF1765_s_at	-0.95	0.1257	-	SPy1765	N-acetylmuramoyl-L-alanine amidase (EC 3.5.1.28)	Unknown	0.6906
M5005_Spy0310	SpM1_ChORF0369_s_at	1.19	0.1259	-	SPy0369	Ribosomal large subunit pseudouridine synthase B (EC 4.2.1.70)	Protein synthesis	0.2713
M5005_Spy1134	SpM1_ChORF1391_s_at	1.17	0.1266	-	SPy1391	O-methyltransferase (EC 2.1.1.-)	Unknown	0.2541
M5005_Spy1510	SpyM3_1542_at	1.20	0.1267	-	#N/A	Pyruvate,phosphate dikinase (EC 2.7.9.1)	Unknown	0.2024
M5005_Spy0497	SpM1_ChORF0598_s_at	-0.93	0.1268	-	SPy0598	Phosphoglycerate mutase (EC 5.4.2.1)	Carbohydrate metabolism	0.6697
M5005_Spy0515	SpM1_ChORF0622_s_at	-1.16	0.1268	-	SPy0622	Hypothetical cytosolic protein	Unknown	0.6136
M5005_Spy0203	SpM1_ChORF0239_s_at	-1.06	0.127	*gltX*	SPy0239	Glutamyl-tRNA synthetase (EC 6.1.1.17)	Protein synthesis	0.3875
M5005_Spy1425	SpM12_ChORF299 61_s_at	-1.03	0.1279	-		Phage protein	Phage	0.3887
M5005_Spy1308	SpM1_ChORF1592_s_at	-1.48	0.128	-	SPy1592	Sugar-binding protein	Membrane transport	0.0471
M5005_Spy0690	SpM18_ChORF0945_s_at	-1.12	0.1283	-	spyM18_0945	Hypothetical membrane associated protein	Unknown	0.3853
M5005_Spy1570	SpM1_ChORF1851_s_at	-1.01	0.1295	-	SPy1851	Penicillin-binding protein	Unknown	0.5061
M5005_Spy0610	SpM1_ChORF0794_s_at	-1.14	0.1297	-	SPy0794	Glycosyltransferase involved in cell wall biogenesis (EC 2.4.-.-)	Unknown	0.3349
M5005_Spy1120	SpM1_ChORF1372_s_at	1.30	0.1299	*pstI*	SPy1372	Phosphoenolpyruvate-protein phosphotransferase (EC 2.7.3.9)	Carbohydrate metabolism	0.6494
M5005_Spy1577	SpM1_ChORF1858_s_at	-1.00	0.13	*pepXP*	SPy1858	Xaa-Pro dipeptidyl-peptidase (EC 3.4.14.11)	Amino acid metabolism	0.6366
M5005_Spy0175	SpM1_ChORF0203_s_at	-1.09	0.1301	*tgt*	SPy0203	Queuine tRNA-ribosyltransferase (EC 2.4.2.29)	Protein synthesis	0.6007
M5005_Spy1606	SpM1_ChORF1888_s_at	1.34	0.1301	*rpmB*	SPy1888	LSU ribosomal protein L28P	Protein synthesis	0.6065

M5005_gene	RML Probeset	*T*-statistic *	Empirical *P*-value †	Gene	Synonym	Description	Function	Q-value (Strain) ‡
M5005_Spy0576	SpM1_ChORF0755_s_at	-0.89	0.1303	*atpB*	SPy0755	ATP synthase A chain (EC 3.6.3.14)	Carbohydrate metabolism	0.6729
M5005_Spy0870	SpM1_ChORF1148_s_at	1.25	0.1309	-	SPy1148	Multidrug resistance ABC transporter ATP-binding and permease protein	Membrane transport	0.6081
M5005_Spy0611	SpM1_ChORF0796_s_at	1.37	0.1318	-	SPy0796	Hypothetical protein	Unknown	0.3845
M5005_Spy0463	SpM18_ChORF0630_s_at	1.06	0.1321	-	spyM18_0630	Hypothetical cytosolic protein	Phage	0.4321
M5005_Spy0430	SpM1_ChORF0521_s_at	-1.03	0.1324	-	SPy0521	ABC transporter permease protein	Membrane transport	0.6641
M5005_Spy0575	SpM1_ChORF0754_s_at	-1.20	0.1324	*atpE*	SPy0754	ATP synthase C chain (EC 3.6.3.14)	Carbohydrate metabolism	0.6565
M5005_Spy0069	SpM1_ChORF0078_s_at	1.36	0.1326	*rpsK*	SPy0078	SSU ribosomal protein S11P	Protein synthesis	0.6294
M5005_Spy1018	SpM49_ChORF7585-22_at	1.23	0.1328	-		Phage protein	Phage	0.2830
M5005_Spy1864	SpM1_ChORF2215_s_at	-1.02	0.1342	-	SPy2215	Hypothetical cytosolic protein	Unknown	0.5410
M5005_Spy0288	SpM1_ChORF0342_s_at	1.16	0.1344	*snf*	SPy0342	SWF/SNF family helicase	Information processing	0.2979
M5005_Spy0099	SpM1_ChORF0117_s_at	-1.19	0.1348	-	SPy0117	Hypothetical membrane associated protein	Unknown	0.6463
M5005_Spy1034	SpM18_ChORF1794_s_at	-1.00	0.1351	-	spyM18_1794	Phage protein	Phage	0.6525
M5005_Spy1187	SpM5_ChORF270b-559_at	-0.90	0.1353	-		Phage structural protein	Phage	0.4110
M5005_Spy1508	SpM1_ChORF1772_s_at	-1.25	0.1361	*gatC*	SPy1772	Glutamyl-tRNA(Gln) amidotransferase subunit C (EC 6.3.5.-)	Protein synthesis	0.6184
M5005_Spy0448	SpM5_ChORFJ7578C-142_s_at	-1.08	0.137	-		Hypothetical protein	Unknown	0.3740
M5005_Spy0106	SpM1_ChORF0124_s_at	1.44	0.1371	*rofA*	SPy0124	Transcriptional regulator	Information processing	0.5923
M5005_Spy1797	SpM1_ChORF2113_s_at	1.43	0.1376	-	SPy2113	Hypothetical cytosolic protein	Unknown	0.5443
M5005_Spy0957	SpM1_ChORF1248_s_at	-1.19	0.1388	-	SPy1248	Myo-inositol-1(or 4)-monophosphatase (EC 3.1.3.25)	Carbohydrate metabolism	0.2676
M5005_Spy1078	SpM18_ChORF1329_s_at	1.26	0.1395	-	spyM18_1329	Hypothetical protein	Unknown	0.2767
M5005_Spy1304	SpM1_ChORF1586_s_at	-1.45	0.1404	*lacZ*	SPy1586	Beta-galactosidase (EC 3.2.1.23)	Carbohydrate metabolism	0.1020

M5005_gene	RML Probeset	*T* -statistic *	Empirical *P* -value †	Gene	Synonym	Description	Function	Q-value (Strain) ‡
M5005_Spy0185	SpM1_ChORF0215_s_at	1.17	0.1405	*pgi*	SPy0215	Glucose-6-phosphate isomerase (EC 5.3.1.9)	Carbohydrate metabolism	0.4537
M5005_Spy1328	SpM1_ChORF1617_s_at	-1.04	0.1406	-	SPy1617	Xaa-Pro dipeptidase (EC 3.4.13.9)	Unknown	0.6061
M5005_Spy1377	SpM1_ChORF1680_s_at	1.29	0.1411	-	SPy1680	Trans-acting positive transcriptional regulator	Information processing	0.6510
M5005_Spy0303	SpM1_ChORF0361_s_at	1.05	0.1434	*glr*	SPy0361	Glutamate racemase (EC 5.1.1.3)	Cellular processing	0.3002
M5005_Spy0162	SpM1_ChORF0188_s_at	1.26	0.1438	*vlg*	SPy0188	Trans-acting positive regulator Mry	Information processing	0.4706
M5005_Spy1266	SpM1_ChORF1536_s_at	1.25	0.1438	-	SPy1536	ATP-dependent protease La (EC 3.4.21.53)	Unknown	0.6565
M5005_Spy0086	SpM1_ChORF0101_s_at	1.33	0.144	*comYA*	SPy0101	ComG operon protein 1	Membrane transport	0.3618
M5005_Spy0205	SpM5_ChORF275f-139_s_at	-1.10	0.1443	*fasC*		Sensory transduction protein kinase FasC (EC 2.7.3.-)	Signal transduction	0.6750
M5005_Spy0073	SpM5_ChORF270b-605_s_at	-1.41	0.145	-		Hypothetical protein	Unknown	0.4558
M5005_Spy1343	SpM1_ChORF1634_s_at	1.08	0.1453	-	SPy1634	Transcriptional regulators, LysR family	Information processing	0.2961
M5005_Spy0551	SpM1_ChORF0724_s_at	1.20	0.1455	*rplS*	SPy0724	LSU ribosomal protein L19P	Protein synthesis	0.5532
M5005_Spy1285	M12_1348_s_at	-1.09	0.1464	-		Hypothetical cytosolic protein	Unknown	0.5443
M5005_Spy1797	SpM1_ChORF2114_s_at	1.40	0.1464	-	SPy2114	Hypothetical cytosolic protein	Unknown	0.6620
M5005_Spy0213	SpM3_ChORF0181_s_at	-1.10	0.1465	-	spyM3_0181	N-acetylneuraminate-binding protein	Membrane transport	0.2665
M5005_Spy1529	SpM1_ChORF1796_s_at	-1.02	0.1472	*shp*	SPy1796	Putative heme binding protein	Membrane transport	0.6850
M5005_Spy1421	SpM12_ChORF299-1_at	-1.06	0.1475	-		Phage infection protein	Phage	0.4888
M5005_Spy1681	SpM18_ChORF2039_s_at	-1.22	0.1479	*dexB*	spyM18_2039	Dextran glucosidase/Glucan 1,6-alpha-glucosidase (EC 3.2.1.70)	Carbohydrate metabolism	0.2770
M5005_Spy1294	SpM1_ChORF1570_at	1.24	0.1483	-	SPy1570	Ribosomal-protein-serine acetyltransferase (EC 2.3.1.-)	Protein synthesis	0.4537
M5005_Spy1770	SpM1_ChORF2081_s_at	1.34	0.1483	*hutI*	SPy2081	Imidazolonepropionase (EC 3.5.2.7)	Amino acid metabolism	0.6616
M5005_Spy0604	SpM1_ChORF0787_s_at	-1.27	0.1487	*rgpBc*	SPy0787	alpha-L-Rha alpha-1,3-L-rhamnosyltransferase (EC 2.4.1.-)	Cell wall metabolism	0.3154

M5005_gene	RML Probeset	*T* -statistic *	Empirical *P* -value †	Gene	Synonym	Description	Function	Q-value (Strain) ‡
M5005_Spy1307	SpM1_ChORF1589_s_at	-1.16	0.15	-	SPy1589	Hypothetical membrane spanning protein	Unknown	0.1707
M5005_Spy1145	SpM1_ChORF1406_s_at	1.38	0.1513	*sodA*	SPy1406	Superoxide dismutase (EC 1.15.1.1)	Stress adaptation	0.6850
M5005_Spy1736	SpM1_ChORF2041_s_at	-0.98	0.1516	-	SPy2041	Hypothetical protein	Unknown	0.4745
M5005_Spy0952	SpM1_ChORF1242_s_at	-1.23	0.1517	*pstB2*	SPy1242	Phosphate transport ATP-binding protein pstB	Membrane transport	0.2123
M5005_Spy0206	SpM1_ChORF0245_s_at	-0.84	0.1522	*fasA*	SPy0245	Sensory transduction response regulator FasA	Signal transduction	0.4914
M5005_Spy1302	SpM1_ChORF1582_s_at	-1.18	0.1523	-	SPy1582	SAM-dependent methyltransferase	Unknown	0.2208
M5005_Spy0614	SpM1_ChORF0799_s_at	-1.21	0.1532	*pepT*	SPy0799	Peptidase T (EC 3.4.11.14)	Amino acid metabolism	0.0139
M5005_Spy0225	SpM1_ChORF0265_s_at	1.04	0.1543	-	SPy0265	Thiamin pyrophosphokinase (EC 2.7.6.2)	Coenzyme and cofactor metabolism	0.5176
M5005_Spy0487	SpM1_ChORF0588_s_at	1.15	0.1546	-	SPy0588	Hypothetical exported protein	Unknown	0.6364
M5005_Spy0132	SpM1_ChORF0155_s_at	-1.19	0.1556	*ntpB*	SPy0155	V-type sodium ATP synthase subunit B (EC 3.6.3.15)	Membrane transport	0.1538
M5005_Spy0044	SpM1_ChORF0049_s_at	1.16	0.1558	*rplC*	SPy0049	LSU ribosomal protein L3P	Protein synthesis	0.5310
M5005_Spy0452	SpM1_ChORF0544_s_at	-1.22	0.1559	-	SPy0544	Chromosome segregation ATPases	Cellular processing	0.4706
M5005_Spy1015	SpM49_ChORF7585-8_at	-1.03	0.1574	-		Phage protein	Phage	0.5394
M5005_Spy0670	SpM3_ChORF0584_s_at	-0.88	0.1578	*rpsU*	spyM3_0584	Nucleoside diphosphate kinase (EC 2.7.4.6)	Cellular processing	0.5962
M5005_Spy0872	SpM1_ChORF1150_s_at	1.27	0.1581	*nox*	SPy1150	NADH oxidase H2O-forming (EC 1.6.-.-)	Stress adaptation	0.6366
M5005_Spy1352	SpM1_ChORF1646_s_at	1.03	0.1587	-	SPy1646	Cell division initiation protein DivIVA	Unknown	0.4769
M5005_Spy1725	SpM1_ChORF2027_s_at	1.27	0.1597	*irr*	SPy2027	Two-component response regulator	Signal transduction	0.3758
M5005_Spy1223	SpM1_ChORF1489_s_at	1.28	0.1603	*hlpA*	SPy1489	DNA-binding protein HU	Cellular processing	0.4090
M5005_Spy1433	SpM12_ChORF299 54_s_at	-0.91	0.1607	-		Phage protein	Phage	0.4854
M5005_Spy1019	SpM49_ChORF7585-21_at	1.26	0.1613	-		Phage scaffold protein	Phage	0.3459

M5005_gene	RML Probeset	*T* -statistic *	Empirical *P* -value †	Gene	Synonym	Description	Function	Q-value (Strain) ‡
M5005_Spy1072	SpM1_ChORF1311_s_at	-1.06	0.1624	*dltB*	SPy1311	Putative integral membrane protein	Cell wall metabolism	0.3002
M5005_Spy1205	SpM3_ChORF1136_s_at	-1.06	0.1628	-	spyM3_1136	Phage protein	Phage	0.5120
M5005_Spy1227	SpM1_ChORF1494_s_at	-1.21	0.1635	-	SPy1494	Hypothetical protein	Unknown	0.0952
M5005_Spy0253	SpM1_ChORF0297_s_at	1.27	0.1637	*oppF*	SPy0297	Oligopeptide transport ATP-binding protein oppF	Membrane transport	0.5698
M5005_Spy0511	SpM1_ChORF0616_s_at	1.11	0.1637	*murM*	SPy0616	UDP-N-acetylmuramoylpentapeptide-lysine N(6)-alanyltransferase (EC 2.3.2.10)	Cell wall metabolism	0.3797
M5005_Spy0317	SpM1_ChORF0378_s_at	1.17	0.1643	*hlyX*	SPy0378	Putative hemolysin	Virulence	0.4745
M5005_Spy0544	SpM1_ChORF0715_at	1.29	0.1651	-	SPy0715	Transcriptional regulator, GntR family	Information processing	0.4558
M5005_Spy0932	SpM1_ChORF1219_s_at	1.26	0.1662	-	SPy1219	Luciferase-like monooxygenase (EC 1.14.-.-)	Unknown	0.6175
M5005_Spy0037	SpM12_ChORF296-1_s_at	-0.96	0.1668	-		Hypothetical membrane associated protein	Unknown	0.4482
M5005_Spy0448	SpM18_ChORF0607_s_at	-0.96	0.1671	-	spyM18_0607	Hypothetical protein	Unknown	0.6641
M5005_Spy0322	SpM1_ChORF0384_s_at	-1.03	0.168	*ftsA*	SPy0383	Ferrichrome transport system permease protein fhuB	Membrane transport	0.6442
M5005_Spy0199	SpM1_ChORF0235_s_at	-1.06	0.1686	-	SPy0235	Deoxyuridine 5'-triphosphate nucleotidohydrolase (EC 3.6.1.23)	Nucleotide metabolism	0.4451
M5005_Spy0516	SpM12_ChORF280-10_s_at	-0.93	0.1694	*pacL*		Calcium-transporting ATPase (EC 3.6.3.8)	Membrane transport	0.5280
M5005_Spy0001	SpM1_ChORF0002_s_at	1.01	0.1699	*dnaA*	SPy0002	Chromosomal replication initiator protein	Cellular processing	0.3817
M5005_Spy0363	SpM1_ChORF0444_s_at	1.03	0.1703	-	SPy0444	Phosphohydrolase (MutT/nudix family protein)	Unknown	0.6146
M5005_Spy1785	SpM1_ChORF2099_s_at	-0.86	0.1706	-	SPy2099	Trehalose operon transcriptional repressor	Information processing	0.4878
M5005_Spy0403	SpM1_ChORF0489_s_at	-0.94	0.1719	-	SPy0489	Hypothetical protein	Unknown	0.6562
M5005_Spy0957	SpM3_ChORF0884_s_at	-1.11	0.173	-	spyM3_0884	Myo-inositol-1(or 4)-monophosphatase (EC 3.1.3.25)	Carbohydrate metabolism	0.1787
M5005_Spy1124	SpM1_ChORF1378_s_at	1.06	0.173	*nrdF.2*	SPy1378	Ribonucleoside-diphosphate reductase beta chain (EC 1.17.4.1)	Nucleotide metabolism	0.1674

M5005_gene	RML Probeset	*T*-statistic *	Empirical *P*-value †	Gene	Synonym	Description	Function	Q-value (Strain) ‡
M5005_Spy1268	SpM1_ChORF1538_s_at	1.13	0.173	-	SPy1538	Methyltransferase (EC 2.1.1.-)	Unknown	0.3458
M5005_Spy1305	SpM1_ChORF1587_s_at	-1.29	0.1731	*lytR*	SPy1587	Two-component response regulator	Signal transduction	0.0991
M5005_Spy0642	SpM1_ChORF0833_s_at	-1.10	0.1735	*carA*	SPy0833	Carbamoyl-phosphate synthase small chain (EC 6.3.5.5)	Nucleotide metabolism	0.4334
M5005_Spy0739	SpM1_ChORF1012_s_at	1.06	0.1745	-	SPy1012	Tetratricopeptide repeat family protein	Unknown	0.4632
M5005_Spy1558	SpM1_ChORF1834_s_at	-0.93	0.1747	-	SPy1834	Transcriptional regulator	Information processing	0.5106
M5005_Spy0875	SpM1_ChORF1154_s_at	1.24	0.1749	*srtA*	SPy1154	Sortase	Cell wall metabolism	0.6555
M5005_Spy0863	SpM1_ChORF1141_s_at	-0.92	0.175	*prfA*	SPy1141	Bacterial Peptide Chain Release Factor 1 (RF-1)	Cellular processing	0.4337
M5005_Spy0094	SpM1_ChORF0109_s_at	0.86	0.1758	*ackA*	SPy0109	Acetate kinase (EC 2.7.2.1)	Carbohydrate metabolism	0.2853
M5005_Spy0134	SpM1_ChORF0158_s_at	-0.89	0.1762	-	SPy0158	Tellurite resistance protein	Unknown	0.5532
M5005_Spy1829	SpM1_ChORF2176_s_at	-0.92	0.1764	-	SPy2176	Phage infection protein	Phage	0.6565
M5005_Spy0688	SpM1_ChORF0882_s_at	1.03	0.1771	*thyA*	SPy0882	Thymidylate synthase (EC 2.1.1.45)	Unknown	0.3002
M5005_Spy1007	SpM49_ChORF7585-4_at	1.16	0.1775	-		Phage protein	Phage	0.2853
M5005_Spy0398	SpM18_ChORF0544_s_at	1.30	0.1784	-	spyM18_0544	Bacteriocin	Virulence	0.4859
M5005_Spy0961	SpM1_ChORF1251_s_at	1.06	0.1785	*truB*	SPy1251	tRNA pseudouridine synthase B (EC 4.2.1.70)	Protein synthesis	0.4776
M5005_Spy0498	SpM1_ChORF0599_s_at	-0.96	0.1786	-	SPy0599	Transcriptional regulator	Information processing	0.4728
M5005_Spy0901	SpM18_ChORF1133_s_at	-1.06	0.1796	-	spyM18_1133	Hypothetical protein	Unknown	0.5595
M5005_Spy0420	SpM1_ChORF0510_s_at	-0.91	0.1804	-	SPy0510	Glucosyltransferase (EC 2.4.1.-)	Carbohydrate metabolism	0.5120
M5005_Spy0796	SpM1_ChORF1073_s_at	-0.92	0.1808	*rplL*	SPy1073	LSU ribosomal protein L12P (L7/L12)	Protein synthesis	0.4999
M5005_Spy0687	SpM1_ChORF0881_s_at	-0.83	0.181	*mvaS.1*	SPy0881	Hydroxymethylglutaryl-CoA synthase (EC 4.1.3.5)	Lipid metabolism	0.6641
M5005_Spy0624	SpM1_ChORF0809_s_at	-0.91	0.1815	*aroD*	SPy0809	3-dehydroquinate dehydratase (EC 4.2.1.10)	Carbohydrate metabolism	0.4894
M5005_Spy0585	SpM1_ChORF0764_s_at	1.17	0.182	*epuA*	SPy0764	EpuA protein	Virulence	0.3851

M5005_gene	RML Probeset	*T* -statistic *	Empirical *P* -value †	Gene	Synonym	Description	Function	Q-value (Strain) ‡
M5005_Spy0126	SpM1_ChORF0148_s_at	-1.03	0.1822	*ntpI*	SPy0148	V-type sodium ATP synthase subunit I (EC 3.6.3.15)	Membrane transport	0.4779
M5005_Spy1306	SpM1_ChORF1588_s_at	-1.23	0.1822	*lytS*	SPy1588	Two-component sensor kinase	Signal transduction	0.1081
M5005_Spy0780	SpM1_ChORF1057_s_at	1.04	0.1839	-	SPy1057	PTS system, mannose/fructose family IIA component	Unknown	0.5248
M5005_Spy0429	SpM1_ChORF0519_s_at	-1.14	0.1845	-	SPy0519	Daunorubicin resistance transmembrane protein	Membrane transport	0.6145
M5005_Spy1749	SpM1_ChORF2055_s_at	0.91	0.185	-	SPy2055	Pyruvate formate-lyase activating enzyme (EC 1.97.1.4)	Unknown	0.1126
M5005_Spy0950	SpM1_ChORF1240_s_at	-1.02	0.1856	*phoU*	SPy1240	Phosphate transport system protein phoU	Membrane transport	0.2467
M5005_Spy0360	SpM1_ChORF0441_s_at	-1.20	0.1866	-	SPy0441	NAD-dependent oxidoreductase	Unknown	0.6493
M5005_Spy1040	SpM5_ChORF270b-7_at	-0.89	0.1867	-		Phage protein	Phage	0.6184
M5005_Spy1234	SpM1_ChORF1502_s_at	-0.86	0.1876	*folD*	SPy1502	Methylenetetrahydrofolate dehydrogenase (NADP+) (EC 1.5.1.5) / Methenyltetrahydrofolate cyclohydrolase (EC 3.5.4.9)	Coenzyme and cofactor metabolism	0.4110
M5005_Spy1845	SpM1_ChORF2194_s_at	-0.91	0.1879	*cbiO2*	SPy2194	ATP-binding protein involved in export of hyaluronan capsule	Membrane transport	0.5877
M5005_Spy0399	SpM1_ChORF0484_s_at	1.03	0.1883	-	SPy0484	Hypothetical membrane associated protein	Unknown	0.2541
M5005_Spy1760	SpyM3_1764_at	1.20	0.1886	-	-	Transcriptional regulator, MutR family	Unknown	0.3887
M5005_Spy0227	SpM1_ChORF0267_s_at	1.02	0.1896	*cbf*	SPy0267	CMP-binding factor	Virulence	0.5674
M5005_Spy0882	SpM1_ChORF1161_s_at	-0.79	0.1902	-	SPy1161	GTP-binding protein	Unknown	0.3618
M5005_Spy0437	SpM1_ChORF0530_s_at	-0.91	0.1906	*vicX*	SPy0530	Zn-dependent hydrolase (beta-lactamase superfamily)	Unknown	0.5176
M5005_Spy0356	SpM1_ChORF0436_at	-0.88	0.191	*speJ*	SPy0436	Pyrogenic toxin superantigen exotoxin type J precursor	Virulence	0.6525
M5005_Spy1456	SpyM3_1447_at	-1.00	0.1913	-	spyM3_1447	Phage protein	Phage	0.6466
M5005_Spy1242	SpM1_ChORF1511_s_at	1.21	0.1915	-	SPy1511	Hypothetical cytosolic protein	Unknown	0.5169
M5005_Spy0046	SpM1_ChORF0051_s_at	1.02	0.1916	*rplW*	SPy0051	LSU ribosomal protein L23P	Protein synthesis	0.6442
M5005_Spy1076	SpM1_ChORF1315_s_at	0.98	0.192	*glnH*	SPy1315	Transporter	Membrane transport	0.4776

M5005_gene	RML Probeset	*T*-statistic *	Empirical *P*-value †	Gene	Synonym	Description	Function	Q-value (Strain) ‡
M5005_Spy0271	SpM1_ChORF0319_s_at	1.11	0.1928	*atmB*	SPy0319	ABC transporter substrate-binding protein	Membrane transport	0.6466
M5005_Spy0871	SpM1_ChORF1149_s_at	0.93	0.1931	-	SPy1149	Multidrug resistance ABC transporter ATP-binding and permease protein	Membrane transport	0.5512
M5005_Spy0496	SpM1_ChORF0596_s_at	-0.95	0.1936	-	SPy0596	Hydrolase (HAD superfamily)	Unknown	0.5830
M5005_Spy0204	SpM1_ChORF0242_s_at	-0.82	0.1937	*fasB*	SPy0242	Sensory transduction protein kinase FasB (EC 2.7.3.-)	Signal transduction	0.5221
M5005_Spy0130	SpM18_ChORF0148_s_at	-0.92	0.1938	*msmRL*	spyM18_0148	V-type ATP synthase subunit F (EC 3.6.3.14)	Carbohydrate metabolism	0.4436
M5005_Spy0632	SpM1_ChORF0818_s_at	-0.88	0.1939	*capA*	SPy0818	Capsule biosynthesis protein capA	Unknown	0.4400
M5005_Spy1138	SpM1_ChORF1398_s_at	-1.12	0.194	-	SPy1398	Ribosomal small subunit pseudouridine synthase A (EC 4.2.1.70)	Protein synthesis	0.1908
M5005_Spy0547	SpM1_ChORF0720_s_at	0.91	0.1943	-	SPy0720	Phosphoesterase, DHH family protein	Unknown	0.6650
M5005_Spy1291	SpM1_ChORF1567_s_at	-1.16	0.1944	-	SPy1567	ATP-dependent RNA helicase	Stress adaptation	0.6918
M5005_Spy0687	SpM1_ChORF0880_s_at	-0.76	0.1957	*mvaS.1*	SPy0880	Hydroxymethylglutaryl-CoA synthase (EC 4.1.3.5)	Lipid metabolism	0.6690
M5005_Spy1771	SpM12_ChORF298-25_s_at	-0.90	0.198	*hutU*		Urocanate hydratase (EC 4.2.1.49)	Amino acid metabolism	0.6525
M5005_Spy0408	SpM1_ChORF0497_s_at	-1.20	0.1982	*fpg*	SPy0497	Formamidopyrimidine-DNA glycosylase (EC 3.2.2.23)	Information processing	0.6565
M5005_Spy0026	SpM1_ChORF0028_s_at	1.19	0.1984	*purN*	SPy0028	Phosphoribosylglycinamide formyltransferase (EC 2.1.2.2)	Nucleotide metabolism	0.4776
M5005_Spy0656	SpM1_ChORF0849_s_at	-1.03	0.2001	*trmD*	SPy0849	tRNA (Guanine-N(1)-)-methyltransferase (EC 2.1.1.31)	Protein synthesis	0.6469
M5005_Spy1175	SpM1_ChORF1443_s_at	1.19	0.2005	-	SPy1443	Phage protein	Phage	0.4390
M5005_Spy1751	SpM1_ChORF2058_s_at	-0.93	0.2012	*secE*	SPy2058	Protein translocase subunit secE	Secretion	0.5159
M5005_Spy1621	SpM1_ChORF1904_s_at	-0.84	0.2017	*hsdR*	SPy1904	Type I restriction-modification system restriction subunit (EC 3.1.21.3)	Information processing	0.6354
M5005_Spy1383	SpM1_ChORF1687_s_at	0.78	0.2023	-	SPy1687	Hypothetical cytosolic protein	Unknown	0.3083
M5005_Spy0634	SpM1_ChORF0821_s_at	1.01	0.2032	-	SPy0821	hypothetical ribosome-associated protein	Unknown	0.6501

M5005_gene	RML Probeset	*T* -statistic *	Empirical *P* -value †	Gene	Synonym	Description	Function	Q-value (Strain) ‡
M5005_Spy1061	SpM3_ChORF0986_x_at	-0.99	0.2033	*malT*	spyM3_0986	Transcriptional regulator, LacI family	Information processing	0.4441
M5005_Spy1249	SpM1_ChORF1520_s_at	1.16	0.2038	*ftsZ*	SPy1520	Cell division protein ftsZ	Cellular processing	0.4227
M5005_Spy0727	SpM1_ChORF0926_s_at	-0.91	0.2045	*recJ*	SPy0926	Single-stranded-DNA-specific exonuclease recJ (EC 3.1.-.-)	Information processing	0.5335
M5005_Spy0693	SpM1_ChORF0887_s_at	1.16	0.2048	-	SPy0887	Hypothetical protein	Unknown	0.4404
M5005_Spy0230	SpM1_ChORF0271_s_at	1.08	0.2053	*rpsL*	SPy0271	SSU ribosomal protein S12P	Protein synthesis	0.6081
M5005_Spy0416	SpM1_ChORF0505_s_at	0.86	0.2058	-	SPy0505	Glutaminyl-peptide cyclotransferase (EC 2.3.2.5)	Unknown	0.5410
M5005_Spy1727	SpM1_ChORF2031_s_at	1.13	0.2071	-	SPy2031	ABC transporter ATP-binding protein	Membrane transport	0.3149
M5005_Spy1228	SpM1_ChORF1495_s_at	-1.07	0.2077	*recN*	SPy1495	DNA repair protein recN	Cellular processing	0.1203
M5005_Spy0039	SpM18_ChORF0043_s_at	-0.98	0.208	*purK*	spyM18_0043	Alcohol dehydrogenase (EC 1.1.1.1) / Acetaldehyde dehydrogenase [acetylating] (EC 1.2.1.10)	Nucleotide metabolism	0.5962
M5005_Spy0816	SpM12_ChORF267 3_s_at	1.01	0.2087	-		DNA integration/recombination/invertion protein	Information processing	0.4088
M5005_Spy0201	SpM1_ChORF0237_s_at	-0.88	0.2091	-	SPy0237	Carbonic anhydrase (EC 4.2.1.1)	Unknown	0.5550
M5005_Spy0999	SpM49_ChORF7585-42_at	-0.88	0.2091	-		Phage protein	Phage	0.5443
M5005_Spy0195	SpM1_ChORF0227_s_at	-0.77	0.2105	-	SPy0227	Transcriptional regulator, MarR family	Information processing	0.3986
M5005_Spy1237	SpM1_ChORF1506_s_at	-0.92	0.2114	-	SPy1506	Arginine transport ATP-binding protein artP	Membrane transport	0.5763
M5005_Spy0733	SpM1_ChORF0932_s_at	0.96	0.2117	-	SPy0932	Glycine/D-amino acid oxidases family	Carbohydrate metabolism	0.2408
M5005_Spy1461	M12_1770_at	1.04	0.2118	-		Phage protein	Phage	0.4227
M5005_Spy0698	SpM1_ChORF0892_s_at	1.12	0.2129	*punA*	SPy0892	Purine nucleoside phosphorylase (EC 2.4.2.1)	Nucleotide metabolism	0.6512
M5005_Spy1642	SpM12_ChORF257 16_s_at	-0.83	0.2131	-		DNA integration/recombination/invertion protein	Information processing	0.5218
M5005_Spy0577	SpM1_ChORF0756_s_at	-0.78	0.2134	*atpF*	SPy0756	ATP synthase B chain (EC 3.6.3.14)	Carbohydrate metabolism	0.5176

M5005_gene	RML Probeset	*T* -statistic *	Empirical *P* -value †	Gene	Synonym	Description	Function	Q-value (Strain) ‡
M5005_Spy1719	SpM12_ChORF2484_s_at	1.24	0.2141	*emm1.0*	Spy2018	M protein	Virulence	0.4889
M5005_Spy0579	SpM1_ChORF0758_s_at	0.92	0.2145	*atpA*	SPy0758	ATP synthase alpha chain (EC 3.6.3.14)	Carbohydrate metabolism	0.6743
M5005_Spy0269	SpM1_ChORF0316_s_at	-0.90	0.215	-	SPy0316	Hypothetical cytosolic protein	Unknown	0.5698
M5005_Spy0316	SpM1_ChORF0377_s_at	0.98	0.2154	-	SPy0377	SAM-dependent methyltransferase (EC 2.1.-.-)	Unknown	0.4436
M5005_Spy0380	SpM1_ChORF0463_s_at	0.83	0.2155	*rrf*	SPy0463	Ribosome Recycling Factor (RRF)	Cellular processing	0.2979
M5005_Spy1519	SpM1_ChORF1785_s_at	0.98	0.2163	*recG*	SPy1785	ATP-dependent DNA helicase recG (EC 3.6.1.-)	Information processing	0.2773
M5005_Spy1184	SpM1_ChORF1455_s_at	1.07	0.2164	-	SPy1455	Phage protein	Phage	0.1982
M5005_Spy0147	SpM1_ChORF0173_s_at	-0.91	0.2174	*leuS*	SPy0173	Leucyl-tRNA synthetase (EC 6.1.1.4)	Protein synthesis	0.5176
M5005_Spy0655	SpM1_ChORF0847_s_at	1.20	0.2175	-	SPy0847	16S rRNA processing protein rimM	Cellular processing	0.4836
M5005_Spy0454	SpM1_ChORF0546_s_at	-0.89	0.2177	-	SPy0546	Hypothetical protein	Unknown	0.6933
M5005_Spy0600	SpM1_ChORF0782_s_at	0.95	0.2197	*rpoD*	SPy0782	RNA polymerase sigma factor rpoD	Information processing	0.4579
M5005_Spy1123	SpM1_ChORF1375_s_at	1.02	0.2197	*nrdE.2*	SPy1375	Ribonucleoside-diphosphate reductase alpha chain (EC 1.17.4.1)	Nucleotide metabolism	0.4278
M5005_Spy0189	SpM1_ChORF0219_x_at	1.08	0.2215	-	SPy0219	Hypothetical protein	Unknown	0.4854
M5005_Spy1522	SpM1_ChORF1787_s_at	1.04	0.2217	-	SPy1787	Cobalt transport protein cbiQ	Membrane transport	0.6904
M5005_Spy1789	SpM1_ChORF2105_s_at	0.90	0.2221	*nrdG*	SPy2105	Anaerobic ribonucleoside-triphosphate reductase activating protein (EC 1.97.1.4)	Cellular processing	0.3887
M5005_Spy0645	SpM1_ChORF0837_s_at	-0.80	0.2225	-	SPy0837	ABC transporter ATP-binding protein	Membrane transport	0.6525
M5005_Spy0353	SpM1_ChORF0432_x_at	-0.78	0.2229	-	SPy0432	Hypothetical membrane spanning protein	Unknown	0.6257
M5005_Spy1457	SpM12_ChORF29938_at	-0.98	0.2249	-		Phage protein	Phage	0.6838
M5005_Spy0411	SpM1_ChORF0501_s_at	0.92	0.2256	-	SPy0501	Multidrug resistance protein B	Membrane transport	0.4558
M5005_Spy1329	SpM1_ChORF1618_s_at	-0.80	0.227	*cysM*	SPy1618	Cysteine synthase (EC 4.2.99.8)	Amino acid metabolism	0.6623

M5005_gene	RML Probeset	*T* -statistic *	Empirical *P* -value †	Gene	Synonym	Description	Function	Q-value (Strain) ‡
M5005_Spy1863	SpM18_ChORF2254_s_at	-0.75	0.2272	-	spyM18_2254	Transposase	Mobile genetic element	0.4227
M5005_Spy1466	SpM12_ChORF299-14_at	-0.98	0.2274	-		Phage protein	Phage	0.5665
M5005_Spy0717	SpM1_ChORF0915_s_at	0.91	0.228	-	SPy0915	Rhodanese-related sulfurtransferases	Unknown	0.3002
M5005_Spy0447	SpM5_ChORFJ7578C-298_at	-0.90	0.2286	-		Glycosyltransferase involved in cell wall biogenesis (EC 2.4.-.-)	Cell wall metabolism	0.6772
M5005_Spy1724	SpM1_ChORF2026_s_at	1.12	0.2297	*ihk*	SPy2026	Two-component system histidine kinase	Signal transduction	0.4882
M5005_Spy1341	SpM1_ChORF1632_s_at	0.97	0.2343	*gmk*	SPy1632	Guanylate kinase (EC 2.7.4.8)	Nucleotide metabolism	0.5363
M5005_Spy0466	SpM18_ChORF0633_s_at	-0.80	0.2355	-	spyM18_0633	Hypothetical phage protein	Phage	0.5962
M5005_Spy0690	SpM1_ChORF0884_s_at	-1.02	0.2356	-	SPy0884	Hypothetical membrane associated protein	Unknown	0.2756
M5005_Spy0346	M12_0056_at	1.07	0.2359	-		Hypothetical protein	Unknown	0.4558
M5005_Spy1212	SpM1_ChORF1484_s_at	1.06	0.2378	*xis*	SPy1484	Excisionase	Phage	0.4836
M5005_Spy1521	SpM1_ChORF1788_s_at	-0.87	0.2378	-	SPy1788	Cobalt transport ATP-binding protein cbiO	Membrane transport	0.5962
M5005_Spy0098	SpM1_ChORF0116_at	1.11	0.2389	-	SPy0116	Hypothetical protein	Unknown	0.5494
M5005_Spy1361	SpM1_ChORF1656_s_at	-0.86	0.2389	*aapA*	SPy1654	Hypothetical membrane associated protein	Unknown	0.6650
M5005_Spy1692	SpM1_ChORF1986_s_at	-0.92	0.2396	-	SPy1986	PTS system, glucose-specific IIABC component (EC 2.7.1.69)	Carbohydrate metabolism	0.3149
M5005_Spy0518	SpM1_ChORF0628_s_at	-1.08	0.2402	-	SPy0628	Oligohyaluronate lyase (EC 4.2.2.-)	Unknown	0.6811
M5005_Spy0015	SpM5_ChORF223b-1_s_at	-0.86	0.2407	-		Hypothetical protein	Unknown	0.6000
M5005_Spy1730	SpM1_ChORF2034_s_at	-1.00	0.2416	-	SPy2034	Hypothetical protein	Unknown	0.5874
M5005_Spy0292	SpM1_ChORF0348_s_at	0.95	0.2417	-	SPy0348	Aminodeoxychorismate lyase family	Unknown	0.4745
M5005_Spy0735	SpM1_ChORF0935_s_at	-0.93	0.2423	*cpsFP*	SPy0935	dTDP-4-dehydrorhamnose 3,5-epimerase (EC 5.1.3.13)	Carbohydrate metabolism	0.2779
M5005_Spy1810	SpM1_ChORF2153_s_at	0.90	0.2442	-	SPy2153	Hypothetical membrane spanning protein	Unknown	0.3618
M5005_Spy1029	SpM18_ChORF1790_s_at	-0.78	0.2444	-	spyM18_1790	Phage protein	Phage	0.5443

M5005_gene	RML Probeset	*T*-statistic *	Empirical *P*-value †	Gene	Synonym	Description	Function	Q-value (Strain) ‡
M5005_Spy1135	SpM1_ChORF1392_s_at	1.04	0.2446	-	SPy1392	Oxalate/formate antiporter	Unknown	0.4981
M5005_Spy0079	SpM1_ChORF0094_s_at	1.01	0.2452	*adcB*	SPy0094	High-affinity zinc uptake system membrane protein znuB	Membrane transport	0.4888
M5005_Spy0744	SpM1_ChORF1017_x_at	-0.94	0.2455	-	SPy1017	Hypothetical protein	Unknown	0.2168
M5005_Spy1687	SpM1_ChORF1983_at	-0.98	0.2455	*sclA*	SPy1983	Collagen-like surface protein A	Virulence	0.3200
M5005_Spy0697	SpM1_ChORF0891_s_at	1.00	0.2473	*arsC*	SPy0891	Arsenate reductase family protein	Membrane transport	0.6641
M5005_Spy1011	SpM49_ChORF7585-28_at	-0.85	0.2476	-		Phage protein	Phage	0.6081
M5005_Spy0302	SpM1_ChORF0359_s_at	0.91	0.2483	-	SPy0359	Hypothetical exported protein	Unknown	0.4751
M5005_Spy1742	SpM1_ChORF2048_s_at	-0.85	0.2491	*mipB*	SPy2048	Transaldolase (EC 2.2.1.2)	Carbohydrate metabolism	0.6632
M5005_Spy0994	SpM1_ChORF1288_s_at	-0.89	0.2497	-	SPy1288	Putative membrane-associated alkaline phosphatase	Membrane transport	0.4776
M5005_Spy0312	SpM1_ChORF0371_s_at	-0.74	0.2515	-	SPy0371	23S rRNA methyltransferase (EC 2.1.1.-)	Information processing	0.5120
M5005_Spy0543	SpM1_ChORF0714_s_at	1.11	0.2517	*adcA*	SPy0714	High-affinity zinc uptake system protein znuA precursor	Membrane transport	0.4334
M5005_Spy0163	SpM1_ChORF0189_s_at	-0.98	0.2519	-	SPy0189	3'-phosphoadenosine 5'-phosphosulfate sulfotransferase (PAPS reductase)	Unknown	0.1901
M5005_Spy0036	SpM1_ChORF0039_s_at	-0.70	0.2525	-	SPy0039	Protein tyrosine phosphatase (EC 3.1.3.48)	Cellular processing	0.4929
M5005_Spy0228	SpM1_ChORF0268_s_at	0.98	0.2529	*purR*	SPy0268	Pur operon repressor	Information processing	0.6276
M5005_Spy0061	SpM1_ChORF0069_s_at	0.94	0.253	*rpsE*	SPy0069	SSU ribosomal protein S5P	Protein synthesis	0.6201
M5005_Spy1612	SpM1_ChORF1896_s_at	0.94	0.2535	*ropA*	SPy1896	Trigger factor, ppiase (EC 5.2.1.8)	Cellular processing	0.6036
M5005_Spy0261	SpM1_ChORF0306_s_at	-0.70	0.254	-	SPy0306	GTP-binding protein	Cellular processing	0.6517
M5005_Spy0022	SpM5_ChORF275f-5_s_at	0.82	0.2544	-		Phosphoribosylamino-imidazole-succinocarboxamide synthase (EC 6.3.2.6)	Cellular processing	0.2541
M5005_Spy0015	M12_0138_s_at	-0.81	0.2551	-		Hypothetical protein	Unknown	0.4227
M5005_Spy1600	SpM1_ChORF1882_s_at	0.93	0.2554	*lppC*	SPy1882	Acid phosphatase (EC 3.1.3.2)	Cellular processing	0.6366

M5005_gene	RML Probeset	*T*-statistic *	Empirical *P*-value †	Gene	Synonym	Description	Function	Q-value (Strain) ‡
M5005_Spy0296	SpM1_ChORF0352_s_at	0.87	0.2581	-	SPy0352	Acylphosphatase (EC 3.6.1.7)	Unknown	0.5875
M5005_Spy1029	SpM3_ChORF0954_s_at	-0.81	0.2582	-	spyM3_0954	Phage protein	Phage	0.6655
M5005_Spy1646	SpM1_ChORF1931_s_at	0.85	0.2587	*rpsI*	SPy1931	SSU ribosomal protein S9P	Protein synthesis	0.5698
M5005_Spy0071	SpM1_ChORF0080a_s_at	0.95	0.2601	*rplQ*	SPy0080a	LSU ribosomal protein L17P	Protein synthesis	0.4776
M5005_Spy0117	SpM18_ChORF0135_s_at	0.83	0.2607	-	spyM18_0135	Transcriptional regulators, LysR family	Information processing	0.4110
M5005_Spy1356	SpM1_ChORF1651_s_at	-1.01	0.261	*pepC*	SPy1651	Aminopeptidase C (EC 3.4.22.40)	Amino acid metabolism	0.2148
M5005_Spy0104	SpM1_ChORF0123_s_at	0.83	0.2613	-	SPy0123	tRNA-dihydrouridine synthase	Protein synthesis	0.4227
M5005_Spy1379	SpM1_ChORF1682_s_at	0.93	0.2615	*glpF*	SPy1682	Glycerol uptake facilitator protein	Carbohydrate metabolism	0.6139
M5005_Spy1428	SpM12_ChORF299 58_s_at	-0.89	0.2616	-		Phage protein	Phage	0.5532
M5005_Spy0110	SpM1_ChORF0129_at	0.87	0.2633	*eftLSL.B*	SPy0129	Hypothetical Exported Protein	Unknown	0.2538
M5005_Spy0020	SpM1_ChORF0022_s_at	-0.91	0.2647	*plsX*	SPy0022	Fatty acid/phospholipid synthesis protein plsX	Cellular processing	0.3002
M5005_Spy1435	SpM12_ChORF299 7_at	0.88	0.2647	-		Phage scaffold protein	Phage	0.3533
M5005_Spy0608	SpM1_ChORF0792_s_at	-0.76	0.2649	*rgpFc*	SPy0792	alpha-L-Rha alpha-1,2-L-rhamnosyltransferase (EC 2.4.1.-) / alpha-L-Rha alpha-1,3-L-rhamnosyltransferase (EC 2.4.1.-)	Cell wall metabolism	0.4059
M5005_Spy0418	SpM1_ChORF0507_s_at	0.85	0.2653	-	SPy0507	Permease	Unknown	0.4088
M5005_Spy0852	SpM3_ChORF0788_s_at	0.86	0.266	-	spyM3_0788	Short chain dehydrogenase	Unknown	0.1707
M5005_Spy1580	SpM1_ChORF1862_s_at	-0.74	0.2683	-	SPy1862	Hypothetical cytosolic protein	Unknown	0.4287
M5005_Spy0902	SpM1_ChORF1183_s_at	0.86	0.2687	-	SPy1183	Biotin carboxyl carrier protein of oxaloacetate decarboxylase (EC 4.1.1.3)	Carbohydrate metabolism	0.2756
M5005_Spy0848	SpM1_ChORF1126_s_at	0.77	0.2695	-	SPy1126	ATP-NAD kinase (EC 2.7.1.23)	Cellular processing	0.4269
M5005_Spy0176	SpM1_ChORF0205_s_at	-0.87	0.2704	-	SPy0205	Zinc finger protein	Unknown	0.5962

M5005_gene	RML Probeset	*T* -statistic *	Empirical *P* -value †	Gene	Synonym	Description	Function	Q-value (Strain) ‡
M5005_Spy0584	SpM1_ChORF0763_s_at	0.75	0.2705	*murA*	SPy0763	UDP-N-acetylglucosamine 1-carboxyvinyltransferase (EC 2.5.1.7)	Cellular processing	0.6368
M5005_Spy0345	SpM1_ChORF0422_s_at	-0.69	0.2723	*metS*	SPy0422	Methionyl-tRNA synthetase (EC 6.1.1.10)	Protein synthesis	0.4779
M5005_Spy0093	SpM1_ChORF0108_s_at	0.83	0.2729	-	SPy0108	Adenine-specific methyltransferase (EC 2.1.1.72)	Cellular processing	0.3002
M5005_Spy1831	SpM1_ChORF2178_s_at	-0.94	0.2732	*rpsD*	SPy2178	SSU ribosomal protein S4P	Protein synthesis	0.3037
M5005_Spy1346	SpM1_ChORF1639_s_at	-0.87	0.2734	*atoA*	SPy1639	Acetate CoA-transferase beta subunit (EC 2.8.3.8)	Cell wall metabolism	0.4227
M5005_Spy1442	SpM12_ChORF29947_s_at	0.80	0.2742	-		Phage transcriptional activator	Phage	0.1827
M5005_Spy1857	SpM1_ChORF2206_s_at	0.80	0.2746	*guaB*	SPy2206	Inosine-5'-monophosphate dehydrogenase (EC 1.1.1.205)	Nucleotide metabolism	0.4110
M5005_Spy1173	SpM1_ChORF0706_s_at	0.91	0.2747	-	SPy0706	Phage protein	Phage	0.4558
M5005_Spy0262	SpM1_ChORF0307_s_at	-0.78	0.275	-	SPy0307	Hypothetical RNA binding protein	Unknown	0.6667
M5005_Spy0200	SpM1_ChORF0236_s_at	0.88	0.2761	*sms*	SPy0236	DNA repair protein RadA	Stress adaptation	0.4278
M5005_Spy1506	SpM1_ChORF1770_s_at	1.00	0.2769	*gatB*	SPy1770	Aspartyl/glutamyl-tRNA(Asn/Gln) amidotransferase subunit B (EC 6.3.5.-)	Protein synthesis	0.5728
M5005_Spy1827	SpM1_ChORF2174_s_at	-0.71	0.2775	-	SPy2174	Hypothetical membrane associated protein	Phage	0.6051
M5005_Spy0654	SpM1_ChORF0846_s_at	-0.86	0.2779	-	SPy0846	Transcriptional regulator, TetR family	Information processing	0.5672
M5005_Spy1276	SpM1_ChORF1548_s_at	0.75	0.2785	-	SPy1548	Transcription regulator, Crp/Fnrfamily	Unknown	0.3936
M5005_Spy1804	SpM1_ChORF2121_s_at	0.78	0.2794	*mutL*	SPy2121	DNA mismatch repair protein mutL	Information processing	0.6046
M5005_Spy0946	SpM1_ChORF1234_s_at	0.87	0.2795	*rpsT*	SPy1234	SSU ribosomal protein S20P	Protein synthesis	0.4334
M5005_Spy1311	SpM1_ChORF1596_s_at	-0.82	0.2795	-	SPy1596	Glucokinase (EC 2.7.1.2) / transcription regulator	Information processing	0.4836
M5005_Spy1373	SpM1_ChORF1674_s_at	-0.84	0.2803	-	SPy1674	ABC transporter ATP-binding protein	Membrane transport	0.6563
M5005_Spy0476	SpM1_ChORF0574_s_at	-0.74	0.2808	*bglA*	SPy0574	6-phospho-beta-glucosidase (EC 3.2.1.86)	Carbohydrate metabolism	0.6499

M5005_gene	RML Probeset	*T* -statistic *	Empirical *P* -value †	Gene	Synonym	Description	Function	Q-value (Strain) ‡
M5005_Spy0621	SpM1_ChORF0806_s_at	-0.66	0.282	*rplT*	SPy0806	LSU ribosomal protein L20P	Protein synthesis	0.2717
M5005_Spy0762	SpM1_ChORF1037_s_at	-0.68	0.2827	-	SPy1037	Hypothetical membrane associated protein	Unknown	0.6466
M5005_Spy0977	SpM1_ChORF1267_s_at	0.76	0.2833	*pcrA*	SPy1267	DNA helicase II (EC 3.6.1.-)	Cellular processing	0.2912
M5005_Spy1472	SpM1_ChORF1730_s_at	0.79	0.2839	*hit*	SPy1730	Bis(5'-nucleosyl)-tetraphosphatase (asymmetrical) (EC 3.6.1.17)	Cellular processing	0.6874
M5005_Spy1192	SpM1_ChORF1463_s_at	-0.65	0.2841	-	SPy1463	Phage protein	Phage	0.6505
M5005_Spy1177	SpM1_ChORF1447_at	-0.88	0.2852	-	SPy1447	Phage protein	Phage	0.6294
M5005_Spy1610	SpM1_ChORF1894_s_at	0.87	0.2853	*pyrG*	SPy1894	CTP synthase (EC 6.3.4.2)	Nucleotide metabolism	0.6097
M5005_Spy0677	SpM1_ChORF0870_s_at	-0.67	0.2858	*fms*	SPy0870	Peptide deformylase (EC 3.5.1.88)	Information processing	0.3845
M5005_Spy0371	SpM1_ChORF0457_s_at	0.70	0.286	-	SPy0457	Peptidyl-prolyl cis-trans isomerase (EC 5.2.1.8)	Unknown	0.4968
M5005_Spy0307	SpM1_ChORF0365_s_at	0.72	0.2873	-	SPy0365	DNA integration/recombination/invertion protein	Phage	0.0566
M5005_Spy1807	SpM1_ChORF2150_s_at	0.90	0.2878	*ahrC*	SPy2150	Arginine repressor, argR	Information processing	0.3573
M5005_Spy0023	SpM49_ChORF8094-13_s_at	0.84	0.2897	-		Phosphoribosylformylglycinamidine synthase (EC 6.3.5.3)	Cellular processing	0.1481
M5005_Spy0460	SpM1_ChORF0556_s_at	0.76	0.291	-	SPy0556	Hypothetical protein	Unknown	0.2024
M5005_Spy1611	SpM1_ChORF1895_s_at	0.81	0.2918	*rpoE*	SPy1895	DNA-directed RNA polymerase delta chain (EC 2.7.7.6)	Cellular processing	0.6877
M5005_Spy1551	SpM1_ChORF1827_s_at	-0.68	0.2919	-	SPy1827	Magnesium and cobalt transport protein corA	Unknown	0.6918
M5005_Spy0291	SpM1_ChORF0346_s_at	-0.72	0.2929	-	SPy0346	Acetyltransferase (GNAT) family	Unknown	0.4798
M5005_Spy0221	SpM1_ChORF0261_s_at	-0.79	0.2938	-	SPy0261	Ribonuclease M5 (EC 3.1.26.8)	Cellular processing	0.3379
M5005_Spy1788	SpM1_ChORF2104_s_at	-0.92	0.2938	-	SPy2104	Protein yaaA	Cellular processing	0.6586
M5005_Spy1257	SpM1_ChORF1529_s_at	-0.75	0.2944	*glcK*	SPy1529	Glucokinase (EC 2.7.1.2)	Carbohydrate metabolism	0.4334
M5005_Spy1705	SpM1_ChORF2001_s_at	-0.83	0.2961	*dppB*	SPy2001	Dipeptide transport system permease protein dppB	Membrane transport	0.6793

M5005_gene	RML Probeset	*T* -statistic *	Empirical *P* -value †	Gene	Synonym	Description	Function	Q-value (Strain) ‡
M5005_Spy1800	SpM1_ChORF2117_s_at	-0.75	0.2962	*cinA*	SPy2117	Colligrin	Information processing	0.6612
M5005_Spy0351	SpM1_ChORF0428_s_at	-0.89	0.2963	*spyA*	SPy0428	C3 family ADP-ribosyltransferase (EC 2.4.2.-)	Virulence	0.1351
M5005_Spy1627	SpM1_ChORF1911_s_at	-0.70	0.2968	*salY*	SPy1911	ABC transporter permease protein	Membrane transport	0.6614
M5005_Spy0794	SpM1_ChORF1071_s_at	0.87	0.2977	*thdF*	SPy1071	tRNA (5-carboxymethylaminomethyl-2-thiouridylate) synthase	Protein synthesis	0.4473
M5005_Spy1046	SpM3_ChORF0972_at	-0.76	0.2982	-	spyM3_0972	Phage protein	Phage	0.5512
M5005_Spy1495	SpM1_ChORF1755_s_at	0.80	0.2989	-	SPy1755	Transcriptional regulator, MarR family	Information processing	0.4334
M5005_Spy1216	SpM1_ChORF0947_s_at	-0.67	0.2993	-	SPy0947	Phage protein	Phage	0.2767
M5005_Spy0445	SpM1_ChORF0538_s_at	-0.71	0.2999	*metK*	SPy0538	S-adenosylmethionine synthetase (EC 2.5.1.6)	Cellular processing	0.3149
M5005_Spy0989	SpM1_ChORF1283_s_at	0.88	0.2999	*pfk*	SPy1283	Non-allosteric 6-phosphofructokinase (EC 2.7.1.11)	Carbohydrate metabolism	0.6844
M5005_Spy0869	SpM1_ChORF1147_s_at	0.76	0.3003	-	SPy1147	Antigen	Unknown	0.4227
M5005_Spy0141	SpM1_ChORF0167_s_at	-0.84	0.3014	*slo*	SPy0167	Streptolysin O	Virulence	0.3817
M5005_Spy0643	SpM1_ChORF0835_s_at	-0.67	0.3016	*carB*	SPy0835	Carbamoyl-phosphate synthase large chain (EC 6.3.5.5)	Nucleotide metabolism	0.6091
M5005_Spy1820	SpM1_ChORF2165_s_at	0.98	0.3022	-	SPy2165	FtsK/SpoIIIE family	Phage	0.4177
M5005_Spy0680	SpM1_ChORF0874_s_at	-0.69	0.3023	*sptR*	SPy0874	Two-component response regulator	Signal transduction	0.6526
M5005_Spy1013	SpM49_ChORF7585-26_at	-0.85	0.303	-		Antigen B	Phage	0.4888
M5005_Spy0455	SpM3_ChORF0391_at	-0.74	0.3031	-	spyM3_0391	Hypothetical protein	Unknown	0.5596
M5005_Spy0885	SpM3_ChORF0820_s_at	-0.62	0.3036	-	spyM3_0820	DNA topoisomerase I (EC 5.99.1.2)	Cellular processing	0.5301
M5005_Spy1169	SpM1_ChORF1436_s_at	-0.95	0.3038	*spd3*	SPy1436	Streptodornase (EC 3.1.21.1)	Virulence	0.1982
M5005_Spy1655	SpM1_ChORF1941_s_at	-0.63	0.3062	*cysS*	SPy1941	Cysteinyl-tRNA synthetase (EC 6.1.1.16)	Protein synthesis	0.4806
M5005_Spy0788	SpM1_ChORF1065_at	-0.88	0.3066	-	SPy1065	Acetyltransferase (EC 2.3.1.-)	Cellular processing	0.6525

M5005_gene	RML Probeset	*T* -statistic *	Empirical *P* -value †	Gene	Synonym	Description	Function	Q-value (Strain) ‡
M5005_Spy0327	SpM1_ChORF0392_s_at	-0.71	0.3083	*upp*	SPy0392	Uracil phosphoribosyltransferase (EC 2.4.2.9)	Nucleotide metabolism	0.5615
M5005_Spy0685	SpM1_ChORF0879_s_at	-0.80	0.3085	-	SPy0879	Isopentenyl-diphosphate delta-isomerase (EC 5.3.3.2)	Lipid metabolism	0.1827
M5005_Spy0082	SpM1_ChORF0097_s_at	-0.83	0.3115	*pbp1b*	SPy0097	Multimodular transpeptidase-transglycosylase PBP 1B	Cell wall metabolism	0.4400
M5005_Spy1813	SpM1_ChORF2156_s_at	-0.69	0.3115	*aspS*	SPy2156	Aspartyl-tRNA synthetase (EC 6.1.1.12)	Protein synthesis	0.6512
M5005_Spy0899	SpM1_ChORF1178_s_at	-0.68	0.3123	*citG*	SPy1178	Transcriptional regulator, GntR family	Information processing	0.3573
M5005_Spy0349	SpM1_ChORF0427_s_at	-0.93	0.3124	*nrdE.1*	SPy0427	Ribonucleoside-diphosphate reductase alpha chain (EC 1.17.4.1)	Unknown	0.2918
M5005_Spy1582	SpM1_ChORF1864_s_at	0.80	0.3124	*dnaQ*	SPy1864	DNA polymerase III, epsilon chain (EC 2.7.7.7)	Cellular processing	0.2541
M5005_Spy1131	SpM1_ChORF1385_s_at	0.89	0.3128	-	SPy1385	Transcriptional regulator, Cro/CI family	Information processing	0.2743
M5005_Spy0865	SpM1_ChORF1143_s_at	0.73	0.3133	-	SPy1143	SUA5 protein	Information processing	0.3995
M5005_Spy0278	SpM1_ChORF0329_s_at	0.65	0.3134	*gidB*	SPy0329	Glucose inhibited division protein B	Cellular processing	0.1793
M5005_Spy1070	SpM1_ChORF1310_s_at	-0.83	0.3136	*dltC*	SPy1310	Putative D-alanyl carrier protein	Cell wall metabolism	0.2677
M5005_Spy1337	SpM1_ChORF1627_s_at	0.79	0.3146	*sunL*	SPy1627	16S rRNA m(5)C 967 methyltransferase (EC 2.1.1.-)	Information processing	0.4175
M5005_Spy0362	SpM1_ChORF0443_s_at	0.86	0.3155	*gcaD*	SPy0443	Glucosamine-1-phosphate acetyltransferase (EC 2.3.1.-) / UDP-N-acetylglucosamine pyrophosphorylase (EC 2.7.7.23)	Cellular processing	0.6512
M5005_Spy0718	SpM1_ChORF0916_s_at	-0.70	0.3156	-	SPy0916	Hypothetical protein	Unknown	0.6844
M5005_Spy1355	SpM1_ChORF1649_s_at	0.93	0.3157	*bp1A; pon*	SPy1649	Multimodular transpeptidase-transglycosylase PBP 1A	Cell wall metabolism	0.6613
M5005_Spy1583	SpM1_ChORF1865_s_at	0.67	0.3166	-	SPy1865	Hypothetical cytosolic protein	Unknown	0.5443
M5005_Spy1232	SpM1_ChORF1500_s_at	0.67	0.3173	*xseB*	SPy1500	Exodeoxyribonuclease VII small subunit (EC 3.1.11.6)	Information processing	0.6915
M5005_Spy0419	SpM1_ChORF0508_s_at	-0.65	0.3186	-	SPy0508	Permease	Unknown	0.5590

M5005_gene	RML Probeset	*T* -statistic *	Empirical *P* -value †	Gene	Synonym	Description	Function	Q-value (Strain) ‡
M5005_Spy1479	SpM1_ChORF1738_s_at	0.71	0.3186	*manL*	SPy1738	PTS system, mannose-specific IIAB component (EC 2.7.1.69)	Carbohydrate metabolism	0.5248
M5005_Spy0672	SpM1_ChORF0865_s_at	-0.72	0.3193	-	SPy0865	DegV family protein	Unknown	0.3283
M5005_Spy0857	SpM1_ChORF1135_s_at	0.76	0.3196	*guaC*	SPy1135	GMP reductase (EC 1.7.1.7)	Unknown	0.4184
M5005_Spy0067	SpM1_ChORF0076_x_at	0.91	0.3214	*rpmJ*	SPy0076	LSU ribosomal protein L36P	Protein synthesis	0.4792
M5005_Spy1799	SpM1_ChORF2116_s_at	0.90	0.3233	*recA*	SPy2116	RecA protein	Information processing	0.5120
M5005_Spy1345	SpM1_ChORF1638_s_at	-0.83	0.3262	*atoD.1*	SPy1638	Acetate CoA-transferase alpha subunit (EC 2.8.3.8)	Cell wall metabolism	0.6382
M5005_Spy1825	SpM1_ChORF2172_s_at	-0.71	0.3265	-	SPy2172	Transcriptional regulator, PadR family	Phage	0.6743
M5005_Spy0450	SpM1_ChORF0543_s_at	-0.71	0.3283	*mefE*	SPy0543	Macrolide-efflux protein	Membrane transport	0.6276
M5005_Spy1776	SpM12_ChORF298-21_at	-0.81	0.3295	-		putative cationic amino acid transporter protein	Membrane transport	0.4461
M5005_Spy1437	SpyM3_1432_at	0.82	0.3298	-	spyM3_1432	Hypothetical phage protein	Phage	0.3519
M5005_Spy0858	SpM12_ChORF256-17_at	-0.65	0.33	*xpt*		Xanthine phosphoribosyltransferase (EC 2.4.2.-)	Unknown	0.3078
M5005_Spy0347	SpM1_ChORF0425_s_at	0.80	0.3301	*nrdF.1*	SPy0425	Ribonucleoside-diphosphate reductase beta chain (EC 1.17.4.1)	Unknown	0.5995
M5005_Spy0041	SpM1_ChORF0045_s_at	-0.71	0.3305	-	SPy0045	Na+ driven multidrug efflux pump	Membrane transport	0.4751
M5005_Spy1114	SpM1_ChORF1366_s_at	-0.62	0.3316	-	SPy1366	Hypothetical membrane spanning protein	Unknown	0.5308
M5005_Spy0008	SpM1_ChORF0009_s_at	-0.65	0.3322	*divIC*	SPy0009	Cell division protein	Cellular processing	0.5295
M5005_Spy1543	SpM1_ChORF1816_s_at	-0.88	0.3323	*scrB*	SPy1816	Sucrose-6-phosphate hydrolase (EC 3.2.1.26)	Carbohydrate metabolism	0.4277
M5005_Spy1483	SpM1_ChORF1742_s_at	-0.66	0.333	*serS*	SPy1742	Seryl-tRNA synthetase (EC 6.1.1.11)	Protein synthesis	0.6058
M5005_Spy1655	SpM1_ChORF1940_s_at	-0.58	0.3335	*cysS*	SPy1940	Cysteinyl-tRNA synthetase (EC 6.1.1.16)	Protein synthesis	0.4334
M5005_Spy1413	SpM1_ChORF1725_s_at	-0.74	0.3353	-	SPy1725	Hypothetical cytosolic protein	Unknown	0.4589
M5005_Spy1253	SpM1_ChORF1525_s_at	-0.69	0.3355	*murD*	SPy1525	UDP-N-acetylmuramoylalanine--D-glutamate ligase (EC 6.3.2.9)	Cell wall metabolism	0.4222

M5005_gene	RML Probeset	*T* -statistic *	Empirical *P* -value †	Gene	Synonym	Description	Function	Q-value (Strain) ‡
M5005_Spy1845	SpM1_ChORF2193_s_at	-0.79	0.3356	*cbiO2*	SPy2193	ATP-binding protein involved in export of hyaluronan capsule	Membrane transport	0.4776
M5005_Spy0209	SpM1_ChORF0248_s_at	0.75	0.3357	-	SPy0248	Jag protein	Cellular processing	0.4776
M5005_Spy1014	SpM49_ChORF7585-24_at	-0.61	0.3363	-		Antigen C	Phage	0.4779
M5005_Spy0846	SpM1_ChORF1124_s_at	-0.62	0.3366	-	SPy1124	Putative adenylate cyclase family	Unknown	0.3978
M5005_Spy1656	SpM1_ChORF1942_s_at	0.73	0.3371	-	SPy1942	Hypothetical protein	Unknown	0.1908
M5005_Spy0002	SpM1_ChORF0003_s_at	-0.65	0.3409	*dnaN*	SPy0003	DNA polymerase III, beta chain (EC 2.7.7.7)	Cellular processing	0.6539
M5005_Spy0571	SpM1_ChORF0747_s_at	-0.88	0.3413	-	SPy0747	Endonuclease/Exonuclease/phosphatase family protein	Unknown	0.1126
M5005_Spy1084	SpM1_ChORF1326_s_at	0.74	0.3413	-	SPy1326	Outer surface protein	Unknown	0.3410
M5005_Spy1123	SpM5_ChORF270b-538_s_at	0.71	0.3416	-		Ribonucleoside-diphosphate reductase alpha chain (EC 1.17.4.1)	Nucleotide metabolism	0.3058
M5005_Spy0986	SpM1_ChORF1280_s_at	0.84	0.343	*glmS*	SPy1280	Glucosamine--fructose-6-phosphate aminotransferase [isomerizing] (EC 2.6.1.16)	Cell wall metabolism	0.6136
M5005_Spy1592	SpM1_ChORF1872_s_at	0.71	0.3447	-	SPy1872	Ribosomal-protein-alanine acetyltransferase (EC 2.3.1.128)	Protein synthesis	0.5532
M5005_Spy0983	SpM1_ChORF1275_s_at	-0.77	0.3449	-	SPy1275	Histidine transport ATP-binding protein hisP	Membrane transport	0.4088
M5005_Spy1062	SpM1_ChORF1298_at	0.89	0.3452	*malA*	SPy1298	Maltodextrose utilization protein malA	Carbohydrate metabolism	0.3546
M5005_Spy0285	SpM1_ChORF0339_s_at	0.82	0.3458	*dnaB*	SPy0339	Replicative DNA helicase (EC 3.6.1.-)	Unknown	0.6294
M5005_Spy0903	SpM1_ChORF1184_s_at	-0.62	0.3458	*oadB*	SPy1184	Oxaloacetate decarboxylase beta chain (EC 4.1.1.3)	Carbohydrate metabolism	0.6565
M5005_Spy1308	SpM1_ChORF1591_s_at	-0.89	0.3458	-	SPy1591	Sugar-binding protein	Membrane transport	0.1377
M5005_Spy1533	SpM1_ChORF1802_s_at	-0.61	0.3461	*alr*	SPy1802	Holo-[acyl-carrier protein] synthase (EC 2.7.8.7)	Cellular processing	0.6328
M5005_Spy1597	SpM1_ChORF1878_s_at	0.80	0.3486	-	SPy1878	Transcriptional regulator, MerR family	Information processing	0.6906
M5005_Spy0770	SpM1_ChORF1047_s_at	-0.73	0.3487	-	SPy1047	Hypothetical cytosolic protein	Unknown	0.6565
M5005_Spy1590	SpM1_ChORF1871_s_at	-0.92	0.3504	*rpsN2*	SPy1871	SSU ribosomal protein S14P	Protein synthesis	0.2190

M5005_gene	RML Probeset	*T* -statistic *	Empirical *P* -value †	Gene	Synonym	Description	Function	Q-value (Strain) ‡
M5005_Spy1623	SpM1_ChORF1906_s_at	0.84	0.3504	*hsdM*	SPy1906	Type I restriction-modification system methylation subunit	Information processing	0.3081
M5005_Spy0320	SpM1_ChORF0382_s_at	0.77	0.3509	-	SPy0382	Hypothetical cytosolic protein	Unknown	0.6850
M5005_Spy1523	SpM1_ChORF1789_s_at	-0.72	0.351	-	SPy1789	Permease	Unknown	0.3892
M5005_Spy0028	SpM1_ChORF0031_s_at	0.83	0.3524	-	SPy0031	Autolysin (EC 3.5.1.28)	Cellular processing	0.5453
M5005_Spy1834	SpM1_ChORF2181_s_at	0.67	0.3524	-	SPy2181	Hypothetical protein	Unknown	0.4110
M5005_Spy1205	SpM49_ChORF7585-11_s_at	-0.65	0.3528	-		Phage protein	Phage	0.5394
M5005_Spy1572	SpM1_ChORF1852_s_at	-0.54	0.3529	-	SPy1852	Hypothetical membrane spanning protein	Unknown	0.3058
M5005_Spy0459	SpM1_ChORF0555_s_at	0.83	0.3547	-	SPy0555	Portal protein	Phage	0.4885
M5005_Spy0276	SpM1_ChORF0326_s_at	-0.70	0.3551	-	SPy0326	Potassium uptake protein ktrA	Membrane transport	0.4765
M5005_Spy1206	SpM1_ChORF1479_s_at	0.87	0.3564	-	SPy1479	Phage protein	Phage	0.5874
M5005_Spy1364	SpM1_ChORF1659_s_at	0.77	0.3566	-	SPy1658	ATP-dependent RNA helicase	Stress adaptation	0.4947
M5005_Spy1155	SpM1_ChORF1416_s_at	0.72	0.358	*prfC*	SPy1416	Bacterial Peptide Chain Release Factor 3 (RF-3)	Cellular processing	0.5512
M5005_Spy1022	SpM49_ChORF7585-19_at	0.59	0.3584	-		Portal protein	Phage	0.1908
M5005_Spy1279	SpM1_ChORF1552_s_at	-0.68	0.3587	-	SPy1552	Hypothetical cytosolic protein	Unknown	0.4181
M5005_Spy0035	SpM12_ChORF2962_s_at	-0.82	0.3596	-		Holliday junction DNA helicase	Cellular processing	0.5231
M5005_Spy1294	SpM1_ChORF1569_s_at	-0.78	0.3608	-	SPy1569	Ribosomal-protein-serine acetyltransferase (EC 2.3.1.-)	Protein synthesis	0.4449
M5005_Spy1511	SpM1_ChORF1776_s_at	-0.55	0.3612	-	SPy1776	Pyrazinamidase (EC 3.5.1.-) / Nicotinamidase (EC 3.5.1.19)	Coenzyme and cofactor metabolism	0.5981
M5005_Spy1021	SpM49_ChORF7585-20_at	-0.59	0.3625	-		Phage protein	Phage	0.5348
M5005_Spy0004	SpM1_ChORF0006_s_at	-0.63	0.3637	-	SPy0006	GTP-binding protein	Unknown	0.6616
M5005_Spy1808	SpM1_ChORF2151_s_at	0.78	0.3647	*argS*	SPy2151	Arginyl-tRNA synthetase (EC 6.1.1.19)	Protein synthesis	0.5926

M5005_gene	RML Probeset	*T*-statistic *	Empirical *P*-value †	Gene	Synonym	Description	Function	Q-value (Strain) ‡
M5005_Spy0740	SpM1_ChORF1013_s_at	-0.59	0.3654	*fbp*	SPy1013	Fibronectin-binding protein / Fibrinogen-binding protein	Virulence	0.4888
M5005_Spy1296	SpM1_ChORF1572_s_at	-0.57	0.3658	-	SPy1572	Hypothetical protein	Unknown	0.5310
M5005_Spy0818	SpM1_ChORF1094_s_at	-0.63	0.3659	-	SPy1094	Polysaccharide deacetylase	Carbohydrate metabolism	0.3989
M5005_Spy0653	SpM1_ChORF0845_s_at	-0.68	0.3691	*czcD*	SPy0845	Cobalt-zinc-cadmium resistance protein czcD	Membrane transport	0.6690
M5005_Spy1726	SpM1_ChORF2029_s_at	0.81	0.37	-	SPy2029	ABC transporter permease protein	Membrane transport	0.3864
M5005_Spy0334	SpM1_ChORF0405_s_at	-0.66	0.3727	-	SPy0405	Hypothetical protein	Unknown	0.6061
M5005_Spy1196	SpM1_ChORF1468_s_at	-0.71	0.3727	-	SPy1468	HNH endonuclease family protein	Phage	0.6012
M5005_Spy1189	SpM5_ChORF270b-141_at	0.76	0.3737	-		Phage terminase	Phage	0.3242
M5005_Spy1663	SpM1_ChORF1952_s_at	-0.70	0.3741	-	SPy1952	PTS system, IIB component (EC 2.7.1.69)	Carbohydrate metabolism	0.6512
M5005_Spy0828	SpM5_ChORF270b-433_s_at	-0.71	0.3746	*potC*		Spermidine/putrescine transport system permease protein potC	Membrane transport	0.3590
M5005_Spy0222	SpM1_ChORF0262_s_at	-0.64	0.3748	*ksgA*	SPy0262	Dimethyladenosine transferase (EC 2.1.1.-)	Cellular processing	0.4888
M5005_Spy0895	SpM1_ChORF1175_s_at	-0.54	0.3766	-	SPy1175	Hypothetical membrane associated protein	Unknown	0.6061
M5005_Spy1805	SpM1_ChORF2148_s_at	-0.51	0.3768	*mutS*	SPy2148	DNA mismatch repair protein mutS	Information processing	0.3721
M5005_Spy0538	SpM12_ChORF263-13_s_at	-0.54	0.3787	*asnS*		Asparaginyl-tRNA synthetase (EC 6.1.1.22)	Protein synthesis	0.4929
M5005_Spy0215	SpM12_ChORF295-23_s_at	0.72	0.379	-		N-acetylneuraminate transport system permease protein	Membrane transport	0.4310
M5005_Spy0944	SpM1_ChORF1232_s_at	0.65	0.3822	-	SPy1232	16S rRNA m(2)G 1207 methyltransferase (EC 2.1.1.52)	Information processing	0.4541
M5005_Spy0449	SpM1_ChORF0542_s_at	-0.65	0.3845	-	SPy0542	UDP-glucose 6-dehydrogenase (EC 1.1.1.22)	Carbohydrate metabolism	0.4848
M5005_Spy1740	SpM1_ChORF2045_s_at	-0.60	0.3853	-	SPy2045	Low temperature requirement C protein	Unknown	0.5546
M5005_Spy0220	SpM1_ChORF0260_s_at	0.62	0.3865	-	SPy0260	Sec-independent protein translocase protein tatD (EC 3.1.21.-)	Secretion	0.5893
M5005_Spy1055	SpM1_ChORF1291_s_at	0.63	0.3882	*malP, glgP*	SPy1291	Maltodextrin (glycogen) phosphorylase (EC 2.4.1.1)	Carbohydrate metabolism	0.4266

M5005_gene	RML Probeset	*T* -statistic *	Empirical *P* -value †	Gene	Synonym	Description	Function	Q-value (Strain) ‡
M5005_Spy1324	SpM18_ChORF1621_s_at	0.85	0.3888	-	spyM18_1621	Hypothetical protein	Unknown	0.3892
M5005_Spy1563	SpM1_ChORF1840_s_at	-0.56	0.3905	-	SPy1840	Hypothetical cytosolic protein	Unknown	0.2502
M5005_Spy1173	SpM1_ChORF1441_s_at	0.70	0.3914	-	SPy1441	Phage protein	Phage	0.4755
M5005_Spy0660	SpM1_ChORF0853_s_at	-0.75	0.3917	*fruR*	SPy0853	Fructose repressor	Information processing	0.2629
M5005_Spy0245	SpM1_ChORF0289_s_at	0.67	0.3937	*nifU, yurV*	SPy0289	IscU protein	Coenzyme and cofactor metabolism	0.6565
M5005_Spy0089	SpM1_ChORF0104_s_at	-0.80	0.3949	-	SPy0104	ComG operon protein 4	Membrane transport	0.4884
M5005_Spy0457	SpM1_ChORF0552_s_at	0.65	0.3953	-	SPy0552	Plasmid stabilization system protein (putative toxin)	Unknown	0.4436
M5005_Spy1680	SpM1_ChORF1972_s_at	-0.67	0.398	*pulA*	SPy1972	Pullulanase/Amylopullulanase (EC 3.2.1.41)	Carbohydrate metabolism	0.5750
M5005_Spy1697	SpM5_ChORF125g-189_s_at	0.57	0.3985	-		Para-aminobenzoate synthetase component I (EC 4.1.3.-) /4-amino-4-deoxychorismate lyase (EC 4.-.-.-)	Unknown	0.1377
M5005_Spy0534	SpM18_ChORF0709_s_at	0.59	0.3989	*bsaA*	spyM18_0709	Acetoin(diacetyl) reductase (EC 1.1.1.5)	Carbohydrate metabolism	0.6563
M5005_Spy0638	SpM1_ChORF0827_s_at	0.68	0.4008	-	SPy0827	Ribosomal large subunit pseudouridine synthase D (EC 4.2.1.70)	Protein synthesis	0.6470
M5005_Spy1309	SpM1_ChORF1593_s_at	-0.78	0.4011	-	SPy1593	Sugar transport system permease protein	Unknown	0.1652
M5005_Spy1426	SpM12_ChORF299-60_at	0.76	0.4029	-		Phage protein	Phage	0.5231
M5005_Spy0259	SpM1_ChORF1806_s_at	0.74	0.4035	-	SPy1806	Hypothetical protein	Unknown	0.6481
M5005_Spy0472	SpM1_ChORF0569_s_at	-0.61	0.4084	*ftsY*	SPy0569	Cell division protein ftsY	Cellular processing	0.2467
M5005_Spy1560	SpM1_ChORF1836_s_at	-0.50	0.4093	-	SPy1836	Phosphatidylglycerophosphatase B (EC 3.1.3.27)	Unknown	0.6311
M5005_Spy0561	SpM1_ChORF0737_at	0.66	0.4103	*epf*	SPy0737	Putative extracellular matrix binding protein	Virulence	0.5421
M5005_Spy0764	SpM1_ChORF1039_s_at	-0.53	0.4108	-	SPy1039	Hypothetical protein	Unknown	0.1923
M5005_Spy1077	SpM1_ChORF1316_s_at	0.61	0.4108	*glnQ.2*	SPy1316	Glutamine transport ATP-binding protein glnQ	Membrane transport	0.4776

M5005_gene	RML Probeset	*T* -statistic *	Empirical *P* -value †	Gene	Synonym	Description	Function	Q-value (Strain) ‡
M5005_Spy1794	SpM1_ChORF2111_s_at	-0.66	0.4108	-	SPy2111	Hypothetical membrane spanning protein	Unknown	0.4166
M5005_Spy0523	SpM12_ChORF280 25_s_at	-0.62	0.4112	-		Hypothetical protein	Unknown	0.5893
M5005_Spy0596	SpM1_ChORF0778_s_at	-0.56	0.4118	-	SPy0778	Arginine-binding protein	Membrane transport	0.5698
M5005_Spy1427	SpM12_ChORF299 59_s_at	-0.59	0.412	-		Phage protein	Phage	0.5750
M5005_Spy1202	SpM18_ChORF1493_at	0.56	0.4129	-	spyM18_1493	Phage protein	Phage	0.3225
M5005_Spy0309	SpM1_ChORF0367_s_at	-0.52	0.4139	-	SPy0367	Hypothetical cytosolic protein	Unknown	0.4394
M5005_Spy0435	SpM1_ChORF0528_s_at	-0.63	0.4142	*vicR*	SPy0528	Two-component response regulator VicR	Signal transduction	0.3149
M5005_Spy0304	SpM1_ChORF0362_s_at	0.61	0.4153	-	SPy0362	Xanthosine triphosphate pyrophosphatase (EC 3.6.1.-)	Unknown	0.5176
M5005_Spy0984	SpM1_ChORF1276_s_at	0.66	0.4174	-	SPy1276	Histidine transport system permease protein hisM	Membrane transport	0.5804
M5005_Spy1274	SpM1_ChORF1546_s_at	0.84	0.422	-	SPy1546	Acetyltransferase (EC 2.3.1.-)	Cellular processing	0.5061
M5005_Spy1235	SpM1_ChORF1503_s_at	0.71	0.4247	-	SPy1503	Phosphglucomutase (EC 5.4.2.2) / Phosphomannomutase (EC 5.4.2.8)	Carbohydrate metabolism	0.2918
M5005_Spy0662	SpM1_ChORF0855_s_at	-0.67	0.4249	*fruA*	SPy0855	PTS system, fructose-specific IIABC component (EC 2.7.1.69)	Carbohydrate metabolism	0.4208
M5005_Spy0207	SpM1_ChORF0246_s_at	0.61	0.4281	*fasX*	SPy0246	Sensory transduction, Ribonuclease P protein component (EC 3.1.26.5)	Signal transduction	0.3801
M5005_Spy0580	SpM1_ChORF0759_s_at	-0.55	0.4284	*atpG*	SPy0759	ATP synthase gamma chain (EC 3.6.3.14)	Carbohydrate metabolism	0.6470
M5005_Spy0605	SpM1_ChORF0789_s_at	0.69	0.4305	*rgpCc*	SPy0789	Polysaccharide export ABC transporter permease protein	Cell wall metabolism	0.5695
M5005_Spy0029	SpM1_ChORF0032_s_at	0.62	0.4309	*purD*	SPy0032	Phosphoribosylamine--glycine ligase (EC 6.3.4.13)	Nucleotide metabolism	0.5151
M5005_Spy1513	SpM1_ChORF1779_s_at	0.62	0.4315	-	SPy1779	Aspartate aminotransferase (EC 2.6.1.1)	Carbohydrate metabolism	0.5218
M5005_Spy1682	SpM1_ChORF1976_s_at	-0.72	0.4332	*msmK*	SPy1976	Multiple sugar-binding ABC transporter protein	Membrane transport	0.2434
M5005_Spy0663	SpM1_ChORF0856_s_at	-0.67	0.4337	*mur1.1*	SPy0856	Autolysin (EC 3.5.1.28)	Cell wall metabolism	0.2853

M5005_gene	RML Probeset	*T*-statistic *	Empirical *P*-value †	Gene	Synonym	Description	Function	Q-value (Strain) ‡
M5005_Spy1118	SpM1_ChORF1370_s_at	-0.70	0.4341	-	SPy1370	Peptidoglycan N-acetylglucosamine deacetylase (EC 3.5.1.33)	Cell wall metabolism	0.2979
M5005_Spy1784	SpM1_ChORF2097_s_at	-0.59	0.4347	-	SPy2097	PTS system, trehalose-specific IIBC component (EC 2.7.1.69)	Carbohydrate metabolism	0.3353
M5005_Spy1165	SpM1_ChORF1432_s_at	-0.59	0.4383	*pyrD*	SPy1432	Dihydroorotate dehydrogenase (EC 1.3.3.1)	Nucleotide metabolism	0.5295
M5005_Spy1156	SpM1_ChORF1419_s_at	0.57	0.44	-	SPy1419	Hypothetical Membrane Spanning Protein	Unknown	0.6488
M5005_Spy1111	SpM1_ChORF1363_s_at	-0.48	0.4411	-	SPy1363	Hypothetical protein	Unknown	0.3149
M5005_Spy0422	SpM1_ChORF0512_s_at	-0.53	0.4414	-	SPy0512	NAD(P)H-dependent quinone reductase (EC 1.-.-.-)	Unknown	0.4227
M5005_Spy1686	SpM1_ChORF1981_s_at	-0.64	0.443	*relA*	SPy1981	GTP pyrophosphokinase (EC 2.7.6.5)	Stress adaptation	0.4166
M5005_Spy1745	SpM1_ChORF2051_s_at	-0.49	0.4446	-	SPy2051	PTS system, cellobiose-specific IIB component (EC 2.7.1.69)	Carbohydrate metabolism	0.4102
M5005_Spy1802	SpM1_ChORF2119_s_at	-0.66	0.4457	*ruvA*	SPy2119	Holliday junction DNA helicase ruvA	Information processing	0.4885
M5005_Spy1576	SpM1_ChORF1857_s_at	-0.50	0.4471	-	SPy1857	Transcription regulator, crp family	Information processing	0.5795
M5005_Spy1753	SpM1_ChORF2059_s_at	0.68	0.4477	*pbp2A*	SPy2059	Multimodular transpeptidase-transglycosylase PBP 2A	Cell wall metabolism	0.6254
M5005_Spy1098	SpM49_ChORF903-2_s_at	-0.45	0.4482	-		tRNA (Uracil-5-) -methyltransferase (EC 2.1.1.35)	Protein synthesis	0.6551
M5005_Spy1681	SpM1_ChORF1973_at	-0.76	0.4504	*dexB*	SPy1973	Dextran glucosidase/Glucan 1,6-alpha-glucosidase (EC 3.2.1.70)	Carbohydrate metabolism	0.4447
M5005_Spy0033	SpM1_ChORF0036_s_at	0.65	0.4524	*purB*	SPy0036	Adenylosuccinate lyase (EC 4.3.2.2)	Nucleotide metabolism	0.6512
M5005_Spy0306	SpM1_ChORF0364_s_at	0.51	0.4532	-	SPy0364	CBS domain containing protein	Unknown	0.1787
M5005_Spy0988	SpM1_ChORF1282_s_at	0.59	0.4545	*pyk, pykA*	SPy1282	Pyruvate kinase (EC 2.7.1.40)	Carbohydrate metabolism	0.4836
M5005_Spy1731	SpM18_ChORF2095_s_at	-0.60	0.4556	-	spyM18_2095	Hypothetical cytosolic protein	Unknown	0.6512
M5005_Spy1491	SpM1_ChORF1750_s_at	-0.46	0.4566	*fabD*	SPy1750	Malonyl-CoA-[acyl-carrier-protein] transacylase (EC 2.3.1.39)	Lipid metabolism	0.5430
M5005_Spy1284	SpM5_ChORF270b-69_s_at	0.56	0.4569	-		Cytochrome C-type biogenesis protein ccdA	Unknown	0.2552
M5005_Spy1050	SpM18_ChORF1306_at	-0.54	0.4585	-	spyM18_1306	Phage transcriptional repressor	Phage	0.6123

M5005_gene	RML Probeset	*T* -statistic *	Empirical *P* -value †	Gene	Synonym	Description	Function	Q-value (Strain) ‡
M5005_Spy0505	SpM1_ChORF0608_s_at	0.62	0.4588	*ppc*	SPy0608	Phosphoenolpyruvate carboxylase (EC 4.1.1.31)	Carbohydrate metabolism	0.6108
M5005_Spy1205	SpM1_ChORF0957_s_at	-0.50	0.4589	-	SPy0957	Phage protein	Phage	0.2467
M5005_Spy1672	SpM12_ChORF285-3_s_at	-0.55	0.4631	-		DNA polymerase III alpha subunit (EC 2.7.7.7)	Information processing	0.6155
M5005_Spy0960	SpM1_ChORF1250_s_at	-0.54	0.4632	*mreA*	SPy1250	Riboflavin kinase (EC 2.7.1.26) / FMN adenylyltransferase (EC 2.7.7.2)	Coenzyme and cofactor metabolism	0.5893
M5005_Spy1507	SpM1_ChORF1771_s_at	-0.54	0.4632	*gatA*	SPy1771	Aspartyl/glutamyl-tRNA(Asn/Gln) amidotransferase subunit A (EC 6.3.5.-)	Protein synthesis	0.3875
M5005_Spy1081	SpM1_ChORF1322_s_at	0.66	0.4633	-	SPy1322	PTS system, cellobiose-specific IIA component (EC 2.7.1.69)	Carbohydrate metabolism	0.6340
M5005_Spy1097	SpM1_ChORF1345_s_at	0.65	0.4646	-	SPy1345	Phosphorylase, Pnp/Udp family	Unknown	0.6662
M5005_Spy0541	SpM1_ChORF0654_s_at	-0.61	0.4649	-	SPy0654	Hypothetical cytosolic protein	Phage	0.4181
M5005_Spy1009	SpM49_ChORF7585-30_at	0.71	0.465	-		Phage protein	Phage	0.6483
M5005_Spy0286	SpM1_ChORF0340_s_at	0.63	0.4658	*dnaI*	SPy0340	Primosomal protein dnaI	Information processing	0.5512
M5005_Spy1492	SpM1_ChORF1751_s_at	0.64	0.466	*fabK*	SPy1751	Enoyl-[acyl-carrier protein] reductase (NADH) (EC 1.3.1.9)	Lipid metabolism	0.5287
M5005_Spy1675	SpM1_ChORF1964_s_at	0.51	0.4662	*cdsA*	SPy1964	Phosphatidate cytidylyltransferase (EC 2.7.7.41)	Lipid metabolism	0.5864
M5005_Spy0591	SpM1_ChORF0772_s_at	0.61	0.4669	-	SPy0772	ABC transporter permease protein	Membrane transport	0.6623
M5005_Spy1251	SpM1_ChORF1523_s_at	0.61	0.4669	*divIB*	SPy1523	Cell division protein ftsQ	Cellular processing	0.6368
M5005_Spy0919	SpM1_ChORF1204_s_at	0.48	0.4677	*guaA*	SPy1204	GMP synthase [glutamine-hydrolyzing] (EC 6.3.5.2)	Nucleotide metabolism	0.5801
M5005_Spy1121	SpM1_ChORF1373_s_at	0.67	0.468	*ptsH*	SPy1373	Phosphocarrier protein HPr	Carbohydrate metabolism	0.4779
M5005_Spy0005	SpM1_ChORF0007_s_at	-0.44	0.4684	*pth*	SPy0007	Peptidyl-tRNA hydrolase (EC 3.1.1.29)	Protein synthesis	0.3149
M5005_Spy0607	SpM1_ChORF0791_s_at	0.55	0.4695	*rgpEc*	SPy0791	Glycosyltransferase (EC 2.4.1.-)	Cell wall metabolism	0.5532
M5005_Spy0824	SpM1_ChORF1100_s_at	0.61	0.4704	*folK*	SPy1100	2-amino-4-hydroxy-6-hydroxymethyldihydropteridine pyrophosphokinase (EC 2.7.6.3)	Coenzyme and cofactor metabolism	0.6676

M5005_gene	RML Probeset	*T* -statistic *	Empirical *P* -value †	Gene	Synonym	Description	Function	Q-value (Strain) ‡
M5005_Spy0807	SpM1_ChORF1084_at	-0.51	0.4708	*srtT*	SPy1084	ABC transporter (ATP binding)-lantibiotic associated	Membrane transport	0.6205
M5005_Spy0390	SpM1_ChORF0476_s_at	0.51	0.4715	*era*	SPy0476	GTP-binding protein era homolog	Unknown	0.6068
M5005_Spy0589	SpM1_ChORF0770_s_at	-0.61	0.4715	-	SPy0770	Salt-stress induced protein	Unknown	0.4558
M5005_Spy0978	SpM1_ChORF1270_s_at	-0.56	0.4742	-	SPy1270	Na(+)-linked D-alanine glycine permease	Membrane transport	0.6690
M5005_Spy1336	SpM1_ChORF1626_s_at	0.54	0.4742	*pppL, stp1*	SPy1626	Protein phosphatase 2C (EC 3.1.3.16)	Cellular processing	0.6287
M5005_Spy1566	SpM1_ChORF1844_s_at	0.45	0.4755	*recD*	SPy1844	Exodeoxyribonuclease V alpha chain (EC 3.1.11.5)	Cellular processing	0.2767
M5005_Spy0473	SpM1_ChORF0570_s_at	0.61	0.4763	-	SPy0570	Multidrug resistance protein B	Membrane transport	0.5698
M5005_Spy1132	SpM18_ChORF1397_at	-0.51	0.4764	*alaS*	spyM18_1397	Alanyl-tRNA synthetase (EC 6.1.1.7)	Protein synthesis	0.4889
M5005_Spy1449	SpM12_ChORF299-10_at	0.60	0.4768	-		DNA primase	Phage	0.5403
M5005_Spy0393	SpM1_ChORF0479_at	0.61	0.4793	-	SPy0479	Hypothetical protein	Unknown	0.5330
M5005_Spy0440	SpM1_ChORF0533_s_at	-0.53	0.4807	-	SPy0533	Transcriptional regulator	Information processing	0.6091
M5005_Spy1281	SpM1_ChORF1556_s_at	-0.50	0.4819	*zmpS*	SPy1556	Two-component response regulator	Signal transduction	0.6931
M5005_Spy1850	SpM1_ChORF2199_s_at	-0.59	0.4821	-	SPy2199	Zinc protease (EC 3.4.99.-)	Cellular processing	0.5387
M5005_Spy0651	SpM12_ChORF291-7_s_at	0.47	0.4831	-		Cell surface protein	Unknown	0.2677
M5005_Spy1061	SpM1_ChORF1297_at	-0.46	0.4845	*malT*	SPy1297	Transcriptional regulator, LacI family	Information processing	0.6368
M5005_Spy1484	SpM1_ChORF1744_s_at	0.47	0.4846	*accD*	SPy1744	Acetyl-coenzyme A carboxylase carboxyl transferase subunit alpha (EC 6.4.1.2)	Lipid metabolism	0.3098
M5005_Spy1315	SpM1_ChORF1602_s_at	-0.51	0.489	-	SPy1602	Transcriptional regulator, GntR family / Transcriptional regulator, LacI family	Information processing	0.5172
M5005_Spy0681	SpM1_ChORF0875_s_at	0.53	0.4896	*sptS*	SPy0875	Two-component system histidine kinase	Signal transduction	0.6022
M5005_Spy1093	SpM1_ChORF1339_s_at	-0.56	0.4915	-	SPy1339	Hypothetical protein	Unknown	0.3563
M5005_Spy0358	SpM1_ChORF0439_s_at	-0.55	0.4917	-	SPy0439	Hypothetical protein	Unknown	0.6928

M5005_gene	RML Probeset	*T* -statistic *	Empirical *P* -value †	Gene	Synonym	Description	Function	Q-value (Strain) ‡
M5005_Spy1164	SpM1_ChORF1429_s_at	0.48	0.4921	*gpmA*	SPy1429	Phosphoglycerate mutase (EC 5.4.2.1)	Carbohydrate metabolism	0.6097
M5005_Spy1553	SpM1_ChORF1829_s_at	-0.50	0.4924	*rpsR*	SPy1829	SSU ribosomal protein S18P	Protein synthesis	0.4110
M5005_Spy1404	SpM1_ChORF1714_s_at	0.53	0.4925	*copZ*	SPy1714	Copper chaperone	Membrane transport	0.4854
M5005_Spy0401	SpM1_ChORF0486_s_at	0.65	0.4933	*silD*	SPy0486	Hypothetical protein	Virulence	0.6200
M5005_Spy0710	SpM1_ChORF0908_s_at	-0.41	0.4939	-	SPy0908	Hypothetical membrane spanning protein	Unknown	0.5231
M5005_Spy0249	SpM18_ChORF0281_s_at	0.57	0.4944	*oppA*	spyM18_0281	Oligopeptide-binding protein oppA	Membrane transport	0.3672
M5005_Spy0939	SpM1_ChORF1225_s_at	0.53	0.4947	-	SPy1225	Nucleoside transport system permease protein	Membrane transport	0.6495
M5005_Spy0361	SpM1_ChORF0442_s_at	0.59	0.4949	-	SPy0442	Phosphoglycerate transporter protein	Membrane transport	0.6200
M5005_Spy0370	SpM1_ChORF0456_s_at	0.49	0.4952	*mtsC*	SPy0456	Manganese transport system membrane protein mntB	Membrane transport	0.5394
M5005_Spy0375	SpM1_ChORF0461_s_at	-0.47	0.4953	*rplA*	SPy0461	LSU ribosomal protein L1P	Protein synthesis	0.6328
M5005_Spy0768	SpM1_ChORF1044_s_at	-0.43	0.4955	-	SPy1044	Hypothetical membrane spanning protein	Unknown	0.4066
M5005_Spy0432	SpM1_ChORF0524_s_at	-0.51	0.4959	-	SPy0524	Acetyl-CoA acetyltransferase (EC 2.3.1.9)	Lipid metabolism	0.6200
M5005_Spy1632	SpM1_ChORF1916_s_at	-0.53	0.4964	*lacG*	SPy1916	6-phospho-beta-galactosidase (EC 3.2.1.85)	Carbohydrate metabolism	0.4436
M5005_Spy0938	SpM1_ChORF1224_s_at	0.52	0.4974	*pgmA*	SPy1224	Phosphoglucomutase (EC 5.4.2.2) / Phosphomannomutase (EC 5.4.2.8)	Carbohydrate metabolism	0.6750
M5005_Spy0192	SpM1_ChORF0224_s_at	-0.58	0.498	*hasC.2*	SPy0224	UTP--glucose-1-phosphate uridylyltransferase (EC 2.7.7.9)	Carbohydrate metabolism	0.3002
M5005_Spy0879	SpM1_ChORF1158_s_at	0.57	0.4984	-	SPy1158	Hypothetical protein	Unknown	0.6775
M5005_Spy0177	SpM1_ChORF0207_s_at	-0.55	0.499	-	SPy0207	BioY protein	Unknown	0.4929
M5005_Spy0462	SpM1_ChORF0559_s_at	-0.49	0.4993	-	SPy0559	Hypothetical protein	Unknown	0.4502
M5005_Spy0314	SpM1_ChORF0374_s_at	0.50	0.4995	-	SPy0374	Phosphatidylglycerophosphatase B homolog	Unknown	0.4612
M5005_Spy0121	SpM1_ChORF0142_s_at	0.55	0.5003	-	SPy0142	Acetyl-CoA:acetoacetyl-CoA transferase beta subunit (EC 2.8.3.-)	Carbohydrate metabolism	0.5418

M5005_gene	RML Probeset	*T* -statistic *	Empirical *P* -value †	Gene	Synonym	Description	Function	Q-value (Strain) ‡
M5005_Spy0509	SpM1_ChORF0613_s_at	-0.53	0.502	*tpi*	SPy0613	Triosephosphate isomerase (EC 5.3.1.1)	Carbohydrate metabolism	0.5057
M5005_Spy0995	SpM18_ChORF0394_x_at	0.56	0.5032	-	spyM18_0394	Phage protein	Phage	0.5672
M5005_Spy0537	SpM1_ChORF0650_s_at	0.53	0.5034	*aspC*	SPy0650	Aspartate aminotransferase (EC 2.6.1.1)	Amino acid metabolism	0.6363
M5005_Spy0012	SpM18_ChORF0013_s_at	0.55	0.5039	*hpt*	spyM18_0013	Hypoxanthine-guanine phosphoribosyltransferase (EC 2.4.2.8)	Nucleotide metabolism	0.6184
M5005_Spy1476	SpM1_ChORF1735_s_at	-0.50	0.5044	-	SPy1735	ATP/GTP hydrolase	Cellular processing	0.5235
M5005_Spy0478	SpM1_ChORF0576_s_at	-0.45	0.5046	-	SPy0576	Hypothetical membrane spanning protein	Unknown	0.4177
M5005_Spy1458	M12_1767_at	-0.53	0.5046	-		Phage protein	Phage	0.6041
M5005_Spy1181	SpM1_ChORF1451_s_at	0.57	0.5051	-	SPy1451	Phage major tail protein	Phage	0.5443
M5005_Spy0138	SpM1_ChORF0164_s_at	-0.51	0.5055	*nusG*	SPy0164	Transcription antitermination protein nusG	Information processing	0.6104
M5005_Spy0037	SpM1_ChORF0040_s_at	0.53	0.5056	-	SPy0040	Hypothetical membrane associated protein	Unknown	0.5120
M5005_Spy1641	SpM1_ChORF1927_s_at	0.58	0.5058	-	SPy1927	Hypothetical cytosolic protein	Unknown	0.3076
M5005_Spy1415	SpM12_ChORF2516_at	-0.55	0.5061	*sdaD2*		Phage-encoded streptodornase (EC 3.1.21.1)	Virulence	0.3154
M5005_Spy0252	SpM1_ChORF0296_s_at	0.56	0.5062	*oppD*	SPy0296	Oligopeptide transport ATP-binding protein oppD	Membrane transport	0.6525
M5005_Spy1394	SpM1_ChORF1701_s_at	-0.53	0.5062	-	SPy1701	Hypothetical membrane spanning protein	Unknown	0.6525
M5005_Spy0873	SpM1_ChORF1151_s_at	-0.49	0.507	*ldh*	SPy1151	L-lactate dehydrogenase (EC 1.1.1.27)	Carbohydrate metabolism	0.4544
M5005_Spy0820	SpM1_ChORF1096_s_at	-0.56	0.5118	*folC.1*	SPy1096	Folylpolyglutamate synthase (EC 6.3.2.17) / dihydrofolate synthase (EC 6.3.2.12)	Coenzyme and cofactor metabolism	0.3116
M5005_Spy0414	SpM1_ChORF0503_s_at	0.57	0.5134	-	SPy0503	Exoribonuclease II (EC 3.1.13.1)	Information processing	0.4888
M5005_Spy0374	SpM1_ChORF0460_s_at	0.46	0.519	*rplK*	SPy0460	LSU ribosomal protein L11P	Protein synthesis	0.6201
M5005_Spy1133	SpM1_ChORF1390_s_at	0.58	0.5196	*surA, prsA*	SPy1390	Peptidyl-prolyl cis-trans isomerase (EC 5.2.1.8)	Unknown	0.5562
M5005_Spy1673	SpM5_ChORF125g177_at	-0.40	0.5211	*proS*		Prolyl-tRNA synthetase (EC 6.1.1.15)	Protein synthesis	0.4110

M5005_gene	RML Probeset	*T* -statistic *	Empirical *P* -value †	Gene	Synonym	Description	Function	Q-value (Strain) ‡
M5005_Spy1596	SpM1_ChORF1877_s_at	0.51	0.5229	*glnA*	SPy1877	Glutamine synthetase (EC 6.3.1.2)	Amino acid metabolism	0.6931
M5005_Spy0639	SpM5_ChORF4P31a-118_s_at	-0.60	0.5251	*pyrR*		PyrR bifunctional protein	Membrane transport	0.6322
M5005_Spy1473	SpM1_ChORF1731_s_at	0.51	0.5254	-	SPy1731	Hypothetical protein	Unknown	0.6231
M5005_Spy0724	SpM1_ChORF0923_s_at	0.40	0.5265	-	SPy0923	Cystathionine beta-lyase (EC 4.4.1.8) / Cystathionine gamma-lyase (EC 4.4.1.1)	Amino acid metabolism	0.4020
M5005_Spy0959	SpM1_ChORF1249_s_at	-0.51	0.5283	-	SPy1249	Arsenate reductase family protein	Unknown	0.4888
M5005_Spy1340	SpM1_ChORF1630_s_at	-0.55	0.5283	-	SPy1630	DNA-directed RNA polymerase omega chain (EC 2.7.7.6)	Unknown	0.3892
M5005_Spy0947	SpM1_ChORF1236_s_at	-0.49	0.5291	*ciaH*	SPy1236	Two-component sensor protein ciaH	Signal transduction	0.2979
M5005_Spy1167	SpM1_ChORF1434_s_at	0.56	0.5299	-	SPy1434	Lead, cadmium, zinc and mercury transporting ATPase (EC 3.6.3.-)	Membrane transport	0.6501
M5005_Spy1285	SpM1_ChORF1561_s_at	0.50	0.5305	-	SPy1561	Hypothetical cytosolic protein	Unknown	0.5804
M5005_Spy0759	SpM1_ChORF1034_s_at	-0.43	0.5308	-	SPy1034	Hypothetical membrane associated protein	Unknown	0.6236
M5005_Spy0280	SpM12_ChORF273-5_s_at	0.54	0.532	-		Heat shock protein HtpX	Stress adaptation	0.4208
M5005_Spy0572	SpM1_ChORF0749_s_at	-0.53	0.5325	-	SPy0749	Hypothetical membrane spanning protein	Unknown	0.2665
M5005_Spy1640	SpM1_ChORF1926_s_at	0.43	0.5344	-	SPy1926	DNA-damage-inducible protein J	Stress adaptation	0.2571
M5005_Spy0274	SpM1_ChORF0323_s_at	0.49	0.5347	*braB*	SPy0323	Branched-chain amino acid transport system carrier protein	Membrane transport	0.2393
M5005_Spy1555	SpM1_ChORF1831_s_at	0.59	0.5373	*rpsF*	SPy1831	SSU ribosomal protein S6P	Protein synthesis	0.1652
M5005_Spy1467	SpM12_ChORF299-15_at	-0.44	0.5375	*int.3*		DNA integration/recombination/invertion protein phi5005.3 int	Phage	0.4345
M5005_Spy1548	SpM1_ChORF1823_s_at	-0.44	0.5403	*comEB*	SPy1823	ComE operon protein 2	Membrane transport	0.5983
M5005_Spy1105	SpM1_ChORF1356_s_at	0.48	0.5412	-	SPy1356	Ribosomal-protein-alanine acetyltransferase (EC 2.3.1.128)	Protein synthesis	0.3672
M5005_Spy0556	SpM1_ChORF0731_s_at	0.55	0.5453	*eno*	SPy0731	Enolase (EC 4.2.1.11)	Carbohydrate metabolism	0.3814

M5005_gene	RML Probeset	*T* -statistic *	Empirical *P* -value †	Gene	Synonym	Description	Function	Q-value (Strain) ‡
M5005_Spy0396	SpM12_ChORF282-20_s_at	-0.42	0.5496	-		Transposase	Mobile genetic element	0.4502
M5005_Spy0588	SpM1_ChORF0769_s_at	0.51	0.5524	*pheT*	SPy0769	Phenylalanyl-tRNA synthetase beta chain (EC 6.1.1.20)	Protein synthesis	0.5169
M5005_Spy1252	SpM1_ChORF1524_s_at	0.44	0.5526	*murG*	SPy1524	UDP-N-acetylglucosamine--N-acetylmuramyl-(pentapeptide) pyrophosphoryl-undecaprenol N-acetylglucosamine transferase (EC 2.4.1.227)	Cellular processing	0.4798
M5005_Spy1426	SpM12_ChORF299-4_at	-0.47	0.5529	-		Phage protein	Phage	0.5951
M5005_Spy1199	SpM1_ChORF1471_x_at	-0.42	0.5548	-	SPy1471	Phage protein	Phage	0.3573
M5005_Spy1511	M12_1829_s_at	-0.54	0.5555	-		Pyrazinamidase (EC 3.5.1.-) / Nicotinamidase (EC 3.5.1.19)	Coenzyme and cofactor metabolism	0.6565
M5005_Spy1653	SpM1_ChORF1939_s_at	-0.39	0.5569	-	SPy1939	Hypothetical membrane associated protein	Unknown	0.6607
M5005_Spy1184	SpM1_ChORF1453_s_at	-0.46	0.5595	-	SPy1453	Phage protein	Phage	0.5443
M5005_Spy1608	SpM1_ChORF1892_s_at	0.50	0.5595	-	SPy1892	Alpha/beta hydrolase	Unknown	0.5829
M5005_Spy1446	SpyM3_1439_at	0.50	0.5608	-	spyM3_1439	Phage protein	Phage	0.5698
M5005_Spy1552	SpM1_ChORF1828_s_at	-0.45	0.5627	-	SPy1828	Hypothetical membrane spanning protein	Unknown	0.6743
M5005_Spy1573	SpM1_ChORF1854_s_at	0.48	0.5627	*glpF.2*	SPy1854	Aquaporin / Glycerol uptake facilitator protein	Membrane transport	0.5169
M5005_Spy0915	SpM1_ChORF1200_s_at	0.47	0.5629	*ffh*	SPy1200	Signal recognition particle, subunit FFH/SRP54	Secretion	0.5728
M5005_Spy1720	SpM1_ChORF2019_s_at	0.57	0.5632	*mga*	SPy2019	Multiple gene activator; Trans-acting positive regulator	Information processing	0.6294
M5005_Spy0897	SpM1_ChORF1177_s_at	0.44	0.564	-	SPy1177	Oxaloacetate decarboxylase beta chain (EC 4.1.1.3)	Carbohydrate metabolism	0.6200
M5005_Spy0511	SpM1_ChORF0615_s_at	0.43	0.5652	*murM*	SPy0615	UDP-N-acetylmuramoylpentapeptide-lysine N(6)-alanyltransferase (EC 2.3.2.10)	Cell wall metabolism	0.6704
M5005_Spy1337	SpM1_ChORF1628_s_at	0.46	0.5653	*sunL*	SPy1628	16S rRNA m(5)C 967 methyltransferase (EC 2.1.1.-)	Information processing	0.5695
M5005_Spy0993	SpM1_ChORF1287_s_at	0.43	0.5655	-	SPy1287	ABC transporter permease protein	Membrane transport	0.2979

M5005_gene	RML Probeset	*T*-statistic *	Empirical *P*-value †	Gene	Synonym	Description	Function	Q-value (Strain) ‡
M5005_Spy1716	SpM1_ChORF2013_s_at	0.45	0.5659	*tnp*	SPy2013	Transposase	Mobile genetic element	0.4778
M5005_Spy0544	SpM12_ChORF293-41_s_at	0.48	0.5674	-		Transcriptional regulator, GntR family	Information processing	0.3995
M5005_Spy0217	SpM1_ChORF0257_s_at	-0.45	0.5677	*nanH*	SPy0257	N-acetylneuraminate lyase (EC 4.1.3.3)	Cell wall metabolism	0.6759
M5005_Spy0766	SpM1_ChORF1042_s_at	0.51	0.5679	-	SPy1042	ACYL-ACYL CARRIER PROTEIN THIOESTERASE (EC 3.1.2.14)	Cell wall metabolism	0.6643
M5005_Spy0121	M12_0965_at	0.47	0.5721	-		Acetyl-CoA:acetoacetyl-CoA transferase beta subunit (EC 2.8.3.-)	Carbohydrate metabolism	0.6915
M5005_Spy0854	SpM1_ChORF1131_s_at	0.38	0.5731	-	SPy1131	Na+ driven multidrug efflux pump	Membrane transport	0.2634
M5005_Spy0661	SpM1_ChORF0854_s_at	-0.53	0.5735	*fruB*	SPy0854	1-phosphofructokinase (EC 2.7.1.56)	Carbohydrate metabolism	0.2918
M5005_Spy1713	M12_2021_x_at	0.40	0.5736	-		Hypothetical protein	Unknown	0.3379
M5005_Spy0626	SpM1_ChORF0811_s_at	-0.38	0.5751	-	SPy0811	Hypothetical cytosolic protein	Unknown	0.5263
M5005_Spy0597	SpM18_ChORF0838_x_at	0.45	0.5764	*rplU*	spyM18_0838	SSU ribosomal protein S21P	Protein synthesis	0.6184
M5005_Spy0787	SpM1_ChORF1064_at	0.44	0.5766	-	SPy1064	Hypothetical protein	Unknown	0.5590
M5005_Spy1782	SpM1_ChORF2095_s_at	-0.42	0.5774	*pepO*	SPy2095	Neutral endopeptidase (EC 3.4.24.-)	Cellular processing	0.4759
M5005_Spy1748	SpM5_ChORF125g-81_s_at	0.45	0.5777	-		Transcriptional regulator, DeoR family	Unknown	0.4227
M5005_Spy0237	SpM1_ChORF0278_s_at	0.42	0.5783	-	SPy0278	Hypothetical membrane spanning protein	Unknown	0.6704
M5005_Spy1168	SpM18_ChORF1444_x_at	-0.37	0.5801	-	spyM18_1444	Phage protein	Phage	0.4776
M5005_Spy1476	SpM1_ChORF1734_s_at	0.38	0.5804	-	SPy1734	ATP/GTP hydrolase	Cellular processing	0.2713
M5005_Spy0786	SpM1_ChORF1063_at	0.44	0.5808	-	SPy1063	Iron(III)-binding protein	Membrane transport	0.3730
M5005_Spy1024	SpM49_ChORF7585-17_at	-0.41	0.5819	-		Phage protein	Phage	0.5248
M5005_Spy0234	SpM18_ChORF0262_at	-0.42	0.583	-	spyM18_0262	Hypothetical protein	Unknown	0.6081
M5005_Spy1428	SpM12_ChORF299-6_s_at	-0.35	0.5833	-		Phage protein	Phage	0.3379

M5005_gene	RML Probeset	*T* -statistic *	Empirical *P* -value †	Gene	Synonym	Description	Function	Q-value (Strain) ‡
M5005_Spy1282	SpM1_ChORF1557_s_at	-0.41	0.5836	*msrA*	SPy1557	Peptide methionine sulfoxide reductase msrA/msrB (EC 1.8.4.6)	Cellular processing	0.6395
M5005_Spy0155	SpM1_ChORF0181_s_at	-0.46	0.5846	-	SPy0181	Transcription antiterminator, BglG family	Cellular processing	0.6555
M5005_Spy1444	SpM12_ChORF299-9_at	0.45	0.5864	-		Adenine-specific methyltransferase (EC 2.1.1.72)	Phage	0.5893
M5005_Spy1667	SpM1_ChORF1956_s_at	0.48	0.5874	-	SPy1956	Hypothetical protein	Unknown	0.6750
M5005_Spy0010	SpM12_ChORF239-12_s_at	-0.32	0.588	-		Predicted open reading frame	Unknown	0.1377
M5005_Spy1855	SpM1_ChORF2204_s_at	-0.41	0.5882	*recF*	SPy2204	DNA replication and repair protein recF	Information processing	0.5360
M5005_Spy1411	SpM1_ChORF1722_s_at	-0.38	0.5893	-	SPy1722	Hypothetical cytosolic protein	Unknown	0.4706
M5005_Spy0264	SpM1_ChORF0309_s_at	0.39	0.5895	-	SPy0309	Hydrolase (HAD superfamily)	Unknown	0.5653
M5005_Spy0539	SpM1_ChORF0652_s_at	-0.46	0.5902	-	SPy0652	ATP-binding protein (contains P-loop)	Membrane transport	0.2939
M5005_Spy0479	SpM1_ChORF0578_s_at	-0.47	0.591	-	SPy0578	Hypothetical membrane spanning protein	Unknown	0.6540
M5005_Spy0657	SpM1_ChORF0850_s_at	-0.38	0.5925	*trxB, yumC*	SPy0850	Thioredoxin reductase (EC 1.8.1.9)	Amino acid metabolism	0.5443
M5005_Spy0364	SpM1_ChORF0446_s_at	0.47	0.5943	-	SPy0446	Hypothetical membrane associated protein	Unknown	0.4653
M5005_Spy0180	SpM1_ChORF0210_s_at	-0.33	0.5967	-	SPy0210	Putative murein endopeptidase	Unknown	0.2521
M5005_Spy1384	SpM5_ChORF169a-196_at	0.41	0.5968	*glyS*		Glycyl-tRNA synthetase beta chain (EC 6.1.1.14)	Protein synthesis	0.3712
M5005_Spy0822	SpM1_ChORF1098_s_at	0.47	0.5982	*folP*	SPy1098	Dihydropteroate synthase (EC 2.5.1.15)	Coenzyme and cofactor metabolism	0.5538
M5005_Spy1729	SpM12_ChORF265-2_s_at	-0.39	0.5997	-		Hypothetical protein	Unknown	0.4999
M5005_Spy1039	SpM18_ChORF1798_at	-0.34	0.6001	-	spyM18_1798	Phage protein	Phage	0.3279
M5005_Spy0135	SpM1_ChORF0159_s_at	0.40	0.6009	-	SPy0159	Hypothetical membrane associated protein	Unknown	0.5463
M5005_Spy1771	SpM1_ChORF2082_at	0.50	0.6036	*hutU*	SPy2082	Urocanate hydratase (EC 4.2.1.49)	Amino acid metabolism	0.4933
M5005_Spy0679	SpM1_ChORF0873_s_at	-0.26	0.6046	-	SPy0873	GTP pyrophosphokinase (EC 2.7.6.5)	Stress adaptation	0.2521

M5005_gene	RML Probeset	*T* -statistic *	Empirical *P* -value †	Gene	Synonym	Description	Function	Q-value (Strain) ‡
M5005_Spy0622	SpM1_ChORF0807_s_at	-0.50	0.6051	-	SPy0807	Phosphoglycerol transferase	Unknown	0.4809
M5005_Spy0479	SpM1_ChORF0577_at	0.43	0.6063	-	SPy0577	Hypothetical membrane spanning protein	Unknown	0.6743
M5005_Spy1550	SpM1_ChORF1825_at	-0.36	0.6079	*uvrA*	SPy1825	Excinuclease ABC subunit A	Cellular processing	0.6539
M5005_Spy0006	SpM1_ChORF0008_s_at	-0.33	0.6106	*trcF*	SPy0008	Transcription-repair coupling factor	Cellular processing	0.4321
M5005_Spy1058	SpM1_ChORF1294_s_at	0.39	0.6126	*malE*	SPy1294	Maltose/maltodextrin (ABC transporter) substrate binding protein	Membrane transport	0.5880
M5005_Spy1645	SpM12_ChORF257 17_s_at	-0.31	0.6191	-		DNA integration/recombination/invertion protein	Information processing	0.2095
M5005_Spy1064	SpM1_ChORF1301_at	0.49	0.6205	*malC*	SPy1301	Maltodextrin/cyclodextrin ABC transport system (permease) protein	Membrane transport	0.2201
M5005_Spy1593	SpM1_ChORF1874_s_at	0.36	0.6237	-	SPy1874	Glycoprotease protein family	Amino acid metabolism	0.4702
M5005_Spy1778	SpM1_ChORF2090_s_at	-0.46	0.6249	*hutG*	SPy2090	Formiminoglutamase (EC 3.5.3.8)	Amino acid metabolism	0.3229
M5005_Spy0246	SpM1_ChORF0290_s_at	-0.35	0.6258	-	SPy0290	ABC transporter-associated protein	Membrane transport	0.6139
M5005_Spy1103	SpM1_ChORF1354_s_at	-0.35	0.6281	*map*	SPy1354	Methionine aminopeptidase (EC 3.4.11.18)	Unknown	0.3986
M5005_Spy0436	SpM1_ChORF0529_s_at	-0.33	0.6282	*vicK*	SPy0529	Two-component sensor histidine kinase VicK	Signal transduction	0.4706
M5005_Spy0160	SpM1_ChORF0186_s_at	0.43	0.6308	-	SPy0186	CoA binding protein	Unknown	0.3116
M5005_Spy0789	SpM1_ChORF1066_at	-0.39	0.6309	-	SPy1066	Hydrolase (HAD superfamily)	Unknown	0.6041
M5005_Spy0866	SpM1_ChORF1144_s_at	-0.32	0.6322	-	SPy1144	Phosphinothricin N-acetyltransferase (EC 2.3.1.-)	Unknown	0.6641
M5005_Spy0391	SpM1_ChORF0477_s_at	-0.41	0.6325	-	SPy0477	Phosphohydrolase (MutT/nudix family protein)	Unknown	0.6910
M5005_Spy1229	SpM1_ChORF1497_s_at	-0.38	0.6331	*argR*	SPy1497	Arginine repressor, argR	Information processing	0.3817
M5005_Spy0062	SpM1_ChORF0071_s_at	0.39	0.6338	*rpmD*	SPy0071	LSU ribosomal protein L30P	Protein synthesis	0.5504
M5005_Spy0315	SpM1_ChORF0376_s_at	-0.41	0.6353	-	SPy0376	Fe-S Oxidoreductase (1.8.-.-)	Unknown	0.3887

M5005_gene	RML Probeset	*T* -statistic *	Empirical *P* -value †	Gene	Synonym	Description	Function	Q-value (Strain) ‡
M5005_Spy1773	SpM1_ChORF2084_s_at	0.44	0.6353	-	SPy2084	Formiminotetrahydrofolate cyclodeaminase (EC 4.3.1.4)	Nucleotide metabolism	0.5094
M5005_Spy0729	SpM1_ChORF0928_s_at	0.34	0.6393	*dnaD*	SPy0928	DNA replication protein dnaD	Information processing	0.5411
M5005_Spy0243	SpM1_ChORF0287_s_at	0.37	0.64	-	SPy0287	ABC transporter-associated protein	Membrane transport	0.6649
M5005_Spy1024	SpM49_ChORF7585-18_at	-0.35	0.6407	-		Phage protein	Phage	0.5231
M5005_Spy0247	SpM18_ChORF0279_s_at	0.35	0.6411	-	spyM18_0279	D-alanyl-D-alanine carboxypeptidase (EC 3.4.16.4)	Cell wall metabolism	0.6419
M5005_Spy1565	SpM1_ChORF1842_s_at	-0.33	0.6413	*spi*	SPy1842	Signal peptidase I (EC 3.4.21.89)	Cellular processing	0.5749
M5005_Spy0136	SpM1_ChORF0160_s_at	0.31	0.6419	*purA*	SPy0160	Adenylosuccinate synthetase (EC 6.3.4.4)	Nucleotide metabolism	0.6442
M5005_Spy0790	SpM1_ChORF1067_s_at	0.35	0.6419	*gabD*	SPy1067	Succinate-semialdehyde dehydrogenase [NADP+] (EC 1.2.1.16)	Carbohydrate metabolism	0.6641
M5005_Spy1370	SpM1_ChORF1672_s_at	-0.33	0.6423	*proA*	SPy1670	Gamma-glutamyl phosphate reductase (EC 1.2.1.41)	Unknown	0.5310
M5005_Spy0018	SpM1_ChORF0020_s_at	0.32	0.6437	*prsA.2*	SPy0020	Ribose-phosphate pyrophosphokinase (EC 2.7.6.1)	Carbohydrate metabolism	0.6602
M5005_Spy1261	SpM1_ChORF1533_s_at	0.33	0.6438	-	SPy1533	Radical SAM family enzyme	Unknown	0.6743
M5005_Spy0692	SpM1_ChORF0886_s_at	-0.34	0.6445	-	SPy0886	GTP-binding protein	Unknown	0.6294
M5005_Spy0096	SpM1_ChORF0112_s_at	0.42	0.646	*proC*	SPy0112	Pyrroline-5-carboxylate reductase (EC 1.5.1.2)	Amino acid metabolism	0.4941
M5005_Spy0468	SpM18_ChORF0635_s_at	-0.39	0.6463	-	spyM18_0635	Transposase	Mobile genetic element	0.5923
M5005_Spy0270	SpM1_ChORF0317_s_at	0.45	0.6465	-	SPy0317	ABC transporter substrate-binding protein	Membrane transport	0.6106
M5005_Spy1047	SpM3_ChORF0973_at	-0.33	0.6469	-	spyM3_0973	Phage protein	Phage	0.4981
M5005_Spy0256	SpM1_ChORF0300_s_at	-0.33	0.6475	*comX1.1*	SPy0300	Competence-specific sigma factor ComX	Membrane transport	0.5120
M5005_Spy0513	SpM1_ChORF0619_s_at	-0.29	0.649	-	SPy0619	Hypothetical cytosolic protein	Unknown	0.3150
M5005_Spy0455	SpM1_ChORF0549_s_at	0.36	0.6491	-	SPy0549	Hypothetical protein	Unknown	0.6691
M5005_Spy0810	SpM1_ChORF1087_s_at	-0.30	0.6501	*srtG*	SPy1087	Lantibiotic transport permease protein	Membrane transport	0.3002

M5005_gene	RML Probeset	*T* -statistic *	Empirical *P* -value †	Gene	Synonym	Description	Function	Q-value (Strain) ‡
M5005_Spy1347	SpM12_ChORF289 13_s_at	-0.34	0.6502	-		D-beta-hydroxybutyrate dehydrogenase (EC 1.1.1.30)	Unknown	0.4227
M5005_Spy1538	SpM1_ChORF1810_s_at	-0.39	0.6502	*pmi*	SPy1810	Mannose-6-phosphate isomerase (EC 5.3.1.8)	Carbohydrate metabolism	0.4558
M5005_Spy1584	SpM1_ChORF1866_s_at	-0.33	0.6509	-	SPy1866	NAD(FAD)-utilizing dehydrogenases	Unknown	0.6750
M5005_Spy1474	SpM1_ChORF1733_s_at	-0.29	0.6515	*lytR*	SPy1733	Transcriptional regulator, LytR family	Information processing	0.6031
M5005_Spy0758	SpM1_ChORF1033_s_at	0.29	0.6527	*lplB*	SPy1033	Lipoate-protein ligase A (EC 6.-.-.-)	Coenzyme and cofactor metabolism	0.4779
M5005_Spy0552	SpM12_ChORF224 2_at	0.34	0.6531	-		DNA gyrase related protein (probably a hydrolase/phosphatase)	Unknown	0.3887
M5005_Spy0784	SpM12_ChORF284 30_s_at	0.36	0.654	*yesM*		Two-component sensor kinase yesM	Signal transduction	0.6184
M5005_Spy0823	SpM1_ChORF1099_s_at	-0.36	0.6553	*folQ*	SPy1099	Dihydroneopterin aldolase (EC 4.1.2.25)	Coenzyme and cofactor metabolism	0.2541
M5005_Spy1314	SpM1_ChORF1600_s_at	-0.34	0.6584	*hyl*	SPy1600	Hyaluronoglucosaminidase (EC 3.2.1.35)	Carbohydrate metabolism	0.4390
M5005_Spy1848	SpM1_ChORF2197_s_at	0.32	0.6587	-	SPy2197	Hypothetical membrane associated protein	Unknown	0.5833
M5005_Spy0410	SpM1_ChORF0500_s_at	-0.36	0.6596	-	SPy0500	ATPase	Unknown	0.4280
M5005_Spy1702	SpM12_ChORF291 40_s_at	-0.42	0.6603	*smeZ*		Streptococcal mitogenic exotoxin Z; Pyrogenic toxin superantigen exotoxin type Z	Virulence	0.6081
M5005_Spy0194	SpM1_ChORF0226_s_at	-0.37	0.6606	*gpsA*	SPy0226	Glycerol-3-phosphate dehydrogenase [NAD(P)+] (EC 1.1.1.94)	Cellular processing	0.3002
M5005_Spy1420	SpM12_ChORF299 66_at	0.32	0.6607	-		Phage protein	Phage	0.6081
M5005_Spy0635	SpM1_ChORF0822_s_at	-0.35	0.6613	*rpmA*	SPy0822	LSU ribosomal protein L27P	Protein synthesis	0.3225
M5005_Spy0949	SpM1_ChORF1239_s_at	-0.36	0.662	*pepN*	SPy1239	Lysyl aminopeptidase (EC 3.4.11.15) / alanine aminopeptidase (EC 3.4.11.2)	Amino acid metabolism	0.2840
M5005_Spy0101	SpM18_ChORF0118_s_at	-0.33	0.6632	*adhE*	spyM18_0118	tRNA binding domain protein	Protein synthesis	0.6743

M5005_gene	RML Probeset	*T* -statistic *	Empirical *P* -value †	Gene	Synonym	Description	Function	Q-value (Strain) ‡
M5005_Spy0920	SpM1_ChORF1205_s_at	0.37	0.6635	-	SPy1205	UDP-N-acetylmuramoylpentapeptide-lysine N(6)-alanyltransferase (EC 2.3.2.10) / UDP-N-acetylmuramoylpentapeptide-lysine N(6)-seryltransferase (EC 2.3.2.-)	Cell wall metabolism	0.6129
M5005_Spy0323	SpM1_ChORF0385_s_at	-0.37	0.6636	*ftsC*	SPy0385	Ferrichrome-binding protein	Membrane transport	0.4077
M5005_Spy1158	SpM12_ChORF247 14_s_at	0.28	0.6637	*ddlA*		D-alanine--D-alanine ligase (EC 6.3.2.4)	Cell wall metabolism	0.0442
M5005_Spy1559	SpM1_ChORF1835_s_at	0.31	0.6637	*trx*	SPy1835	Thioredoxin	Amino acid metabolism	0.5207
M5005_Spy0861	SpM1_ChORF1139_at	0.35	0.667	-	SPy1139	4-oxalocrotonate tautomerase (EC 5.3.2.-)	Unknown	0.5532
M5005_Spy0769	SpM1_ChORF1046_s_at	0.28	0.6675	-	SPy1046	Hypothetical cytosolic protein	Unknown	0.3672
M5005_Spy0736	SpM1_ChORF0936_s_at	0.32	0.668	*cpsFQ*	SPy0936	dTDP-glucose 4,6-dehydratase (EC 4.2.1.46)	Carbohydrate metabolism	0.6655
M5005_Spy0821	SpM1_ChORF1097_s_at	-0.35	0.669	*folE*	SPy1097	GTP cyclohydrolase I (EC 3.5.4.16)	Coenzyme and cofactor metabolism	0.4449
M5005_Spy0103	SpM1_ChORF0121_s_at	-0.35	0.6701	-	SPy0121	Deoxyadenosine kinase (EC 2.7.1.76) / Deoxyguanosine kinase (EC 2.7.1.113)	Nucleotide metabolism	0.6690
M5005_Spy0590	SpM1_ChORF0771_s_at	-0.29	0.6716	-	SPy0771	Hypothetical protein	Unknown	0.4436
M5005_Spy1858	SpM1_ChORF2207_s_at	-0.24	0.672	*trsA, trpA*	SPy2207	Tryptophanyl-tRNA synthetase (EC 6.1.1.2)	Protein synthesis	0.3993
M5005_Spy1440	SpM12_ChORF299 49_s_at	-0.31	0.6721	-		Terminase large subunit	Phage	0.6129
M5005_Spy1388	SpM1_ChORF1694_s_at	-0.36	0.6736	*nagA*	SPy1694	N-acetylglucosamine-6-phosphate deacetylase (EC 3.5.1.25)	Carbohydrate metabolism	0.2713
M5005_Spy1147	SpM1_ChORF1408_s_at	-0.31	0.6777	*comEC*	SPy1408	ComE operon protein 4	Unknown	0.6129
M5005_Spy0287	SpM1_ChORF0341_s_at	-0.35	0.679	*pgdA*	SPy0341	GTP-binding protein	Unknown	0.4048
M5005_Spy0052	SpM1_ChORF0059_s_at	0.31	0.6791	*rpmC*	SPy0059	LSU ribosomal protein L29P	Protein synthesis	0.5829
M5005_Spy1109	SpM1_ChORF1361_s_at	0.32	0.6809	*inlA*	SPy1361	Internalin protein	Virulence	0.5763

M5005_gene	RML Probeset	*T* -statistic *	Empirical *P* -value †	Gene	Synonym	Description	Function	Q-value (Strain) ‡
M5005_Spy0625	SpM1_ChORF0810_s_at	0.30	0.6817	*aroF*	SPy0810	Chorismate synthase (EC 4.2.3.5)	Amino acid metabolism	0.4981
M5005_Spy0279	SpM1_ChORF0330_s_at	-0.36	0.6829	*lemA*	SPy0330	Hypothetical protein LemA	Unknown	0.2229
M5005_Spy0493	SpM1_ChORF0593_s_at	-0.28	0.6864	-	SPy0593	Hypothetical cytosolic protein	Unknown	0.3002
M5005_Spy1638	SpM1_ChORF1923_s_at	-0.30	0.6875	*lacA.2*	SPy1923	Galactose-6-phosphate isomerase lacA subunit (EC 5.3.1.26)	Carbohydrate metabolism	0.6850
M5005_Spy1464	SpM12_ChORF299 12_at	0.27	0.6877	-		Phage transcriptional regulator, Cro/CI family	Phage	0.3033
M5005_Spy0778	SpM1_ChORF1055_s_at	0.31	0.689	*csrA*	SPy1055	Peptide methionine sulfoxide reductase msrB (EC 1.8.4.6)	Unknown	0.4537
M5005_Spy1777	SpM1_ChORF2089_s_at	-0.38	0.6902	*hutH*	SPy2089	Histidine ammonia-lyase (EC 4.3.1.3)	Amino acid metabolism	0.2665
M5005_Spy0985	SpM18_ChORF1226_s_at	0.30	0.6916	-	spyM18_122	PhnA protein	Unknown	0.4728
M5005_Spy1332	SpM1_ChORF1621_s_at	0.31	0.6922	*rr03*	SPy1621	Two-component response regulator yvqC	Signal transduction	0.5698
M5005_Spy1668	SpM1_ChORF1957_s_at	-0.27	0.6933	-	SPy1957	Putative transcriptional regulator	Unknown	0.5200
M5005_Spy1747	SpM1_ChORF2053_s_at	0.28	0.695	-	SPy2053	Sorbitol operon regulator	Information processing	0.3626
M5005_Spy0549	SpM1_ChORF0722_s_at	0.32	0.6962	-	SPy0722	Chorismate mutase (EC 5.4.99.5)	Amino acid metabolism	0.4473
M5005_Spy0104	SpM1_ChORF0122_s_at	-0.31	0.6965	-	SPy0122	tRNA-dihydrouridine synthase	Protein synthesis	0.4612
M5005_Spy1744	SpM1_ChORF2050_at	-0.32	0.6988	-	SPy2050	PTS system, cellobiose-specific IIC component	Carbohydrate metabolism	0.4908
M5005_Spy1272	SpM1_ChORF1543_s_at	-0.39	0.6989	-	SPy1543	Arginine/ornithine antiporter	Membrane transport	0.3279
M5005_Spy0161	SpM1_ChORF0187_s_at	-0.34	0.7004	*perR*	SPy0187	Ferric transport regulator protein/Ferric uptake regulation protein	Information processing	0.1479
M5005_Spy1003	SpM49_ChORF7585-38_at	0.26	0.7011	-		Phage protein	Phage	0.3410
M5005_Spy1239	SpM1_ChORF1508_s_at	-0.30	0.7016	-	SPy1508	Hypothetical cytosolic protein	Unknown	0.3853
M5005_Spy1803	SpM1_ChORF2120_s_at	-0.23	0.705	*lmrP*	SPy2120	Multidrug resistance protein B	Membrane transport	0.3489
M5005_Spy1715	SpM12_ChORF248 6_s_at	0.35	0.7058	*scpA*		C5A peptidase precursor (EC 3.4.21.-)	Virulence	0.3002

M5005_gene	RML Probeset	*T*-statistic *	Empirical *P*-value †	Gene	Synonym	Description	Function	Q-value (Strain) ‡
M5005_Spy1366	SpM1_ChORF1664_s_at	0.29	0.706	*mraY*	SPy1662	Division specific D,D-transpeptidase / Cell division protein ftsI	Cellular processing	0.6915
M5005_Spy0241	SpM1_ChORF0282_s_at	-0.28	0.7063	*rgpG*	SPy0282	Hypothetical cytosolic protein	Cellular processing	0.5763
M5005_Spy1546	SpM1_ChORF1820_s_at	0.27	0.7111	*nusB*	SPy1820	General stress protein, Gls24 family	Stress adaptation	0.6519
M5005_Spy1098	SpM1_ChORF1346_s_at	-0.30	0.7115	-	SPy1346	tRNA (Uracil-5-) -methyltransferase (EC 2.1.1.35)	Protein synthesis	0.5207
M5005_Spy0721	SpM1_ChORF0919_at	0.34	0.7116	-	SPy0919	Hypothetical protein	Unknown	0.3083
M5005_Spy0114	SpM12_ChORF300 50_s_at	0.26	0.7119	-		Sortase	Cell wall metabolism	0.6294
M5005_Spy1193	SpM1_ChORF1464_s_at	0.29	0.7119	-	SPy1464	Phage protein	Phage	0.4623
M5005_Spy0548	SpM1_ChORF0721_s_at	0.25	0.7162	-	SPy0721	Flavodoxin	Carbohydrate metabolism	0.4779
M5005_Spy1841	SpM1_ChORF2189_s_at	0.28	0.7163	*sdhB*	SPy2189	L-serine dehydratase (EC 4.2.1.13)	Amino acid metabolism	0.5963
M5005_Spy0402	SpM1_ChORF0488_s_at	-0.31	0.7167	-	SPy0488	Hypothetical protein	Unknown	0.5999
M5005_Spy1491	SpM1_ChORF1749_s_at	-0.25	0.7183	*fabD*	SPy1749	Malonyl-CoA-[acyl-carrier-protein] transacylase (EC 2.3.1.39)	Lipid metabolism	0.6013
M5005_Spy1775	SpM1_ChORF2087_s_at	0.34	0.7183	-	SPy2087	Hypothetical cytosolic protein	Unknown	0.4188
M5005_Spy1791	SpM1_ChORF2107_s_at	0.30	0.7197	-	SPy2107	Virulence factor mviM	Unknown	0.5726
M5005_Spy0652	SpM1_ChORF0844_s_at	-0.23	0.7206	-	SPy0844	Hypothetical cytosolic protein	Unknown	0.0952
M5005_Spy0444	SpM12_ChORF277 20_s_at	-0.27	0.7216	-		Hypothetical protein	Unknown	0.6270
M5005_Spy1690	SpM1_ChORF1984_s_at	0.29	0.723	*nrdI.1*	SPy1984	NrdI protein	Nucleotide metabolism	0.6081
M5005_Spy0263	SpM5_ChORFJ7578C-5_s_at	0.31	0.7233	*nadD*		Nicotinate-nucleotide adenylyltransferase (EC 2.7.7.18)	Coenzyme and cofactor metabolism	0.6254
M5005_Spy1415	SpM12_ChORF251 8_at	-0.33	0.7266	*sdaD2*		Phage-encoded streptodornase (EC 3.1.21.1)	Virulence	0.6548
M5005_Spy0728	SpM1_ChORF0927_s_at	-0.23	0.7271	*apt*	SPy0927	Adenine phosphoribosyltransferase (EC 2.4.2.7)	Cellular processing	0.5280

M5005_gene	RML Probeset	*T* -statistic *	Empirical *P* -value †	Gene	Synonym	Description	Function	Q-value (Strain) ‡
M5005_Spy1056	SpM1_ChORF1292_s_at	0.26	0.728	*malM*	SPy1292	Amylomaltase/4-alpha-glucanotransferase (EC 2.4.1.25)	Carbohydrate metabolism	0.4779
M5005_Spy0329	SpM1_ChORF0397_s_at	0.29	0.7281	-	SPy0397	Hypothetical cytosolic protein	Unknown	0.6388
M5005_Spy1157	SpM1_ChORF1420_s_at	-0.32	0.7293	*murF*	SPy1420	UDP-N-acetylmuramoylalanine-D-glutamyl-lysine--D-alanyl-D-alanine ligase (EC 6.3.2.10)	Cell wall metabolism	0.2713
M5005_Spy0173	SpM1_ChORF0201_s_at	-0.25	0.7324	-	SPy0201	Integral membrane protein	Unknown	0.6780
M5005_Spy0645	SpM1_ChORF0836_s_at	0.28	0.7324	-	SPy0836	ABC transporter ATP-binding protein	Membrane transport	0.6750
M5005_Spy1086	SpM1_ChORF1329_s_at	0.25	0.7362	-	SPy1329	Nicotinamide mononucleotide transporter	Membrane transport	0.4201
M5005_Spy1750	SpyM3_1756_s_at	0.28	0.7408	-	#N/A	Hypothetical protein	Unknown	0.5106
M5005_Spy1092	SpM1_ChORF1337_s_at	0.24	0.7411	*rsuA*	SPy1337	Ribosomal small subunit pseudouridine synthase A (EC 4.2.1.70)	Protein synthesis	0.3712
M5005_Spy1699	SpM1_ChORF1992_s_at	-0.27	0.7411	-	SPy1992	ATPase, AAA family	Unknown	0.5362
M5005_Spy1319	SpM49_ChORF7585-45_s_at	-0.31	0.7427	-		tRNA (Uracil-5-) -methyltransferase (EC 2.1.1.35)	Protein synthesis	0.6525
M5005_Spy0659	SpM1_ChORF0852_s_at	0.25	0.7438	*apbA*	SPy0852	2-dehydropantoate 2-reductase (EC 1.1.1.169)	Unknown	0.5269
M5005_Spy0966	SpM1_ChORF1255_s_at	0.27	0.7447	-	SPy1255	ABC transporter permease protein	Membrane transport	0.6472
M5005_Spy1246	SpM1_ChORF1516_s_at	0.21	0.7477	-	SPy1516	Integral membrane protein	Unknown	0.5390
M5005_Spy1772	SpM1_ChORF2083_s_at	-0.30	0.748	-	SPy2083	Glutamate formiminotransferase(EC 2.1.2.5)	Unknown	0.2541
M5005_Spy0186	SpM1_ChORF0216_s_at	-0.19	0.7483	-	SPy0216	Transcriptional regulator	Information processing	0.3228
M5005_Spy1702	SpM18_ChORF2063_at	-0.24	0.7486	*smeZ*	spyM18_2063	Streptococcal mitogenic exotoxin Z; Pyrogenic toxin superantigen exotoxin type Z	Virulence	0.4706
M5005_Spy0767	SpM1_ChORF1043_s_at	-0.20	0.7505	-	SPy1043	4-nitrophenylphosphatase (EC 3.1.3.41)	Unknown	0.3149
M5005_Spy0137	SpM1_ChORF0163_s_at	-0.26	0.7511	-	SPy0163	Nucleoside-binding protein	Unknown	0.6743

M5005_gene	RML Probeset	*T* -statistic *	Empirical *P* -value †	Gene	Synonym	Description	Function	Q-value (Strain) ‡
M5005_Spy1331	SpM18_ChORF1629_s_at	0.24	0.7515	-	spyM18_1629	Peptidyl-prolyl cis-trans isomerase (EC 5.2.1.8)	Unknown	0.6366
M5005_Spy0101	SpM18_ChORF0119_s_at	0.17	0.7519	*adhE*	spyM18_0119	tRNA binding domain protein	Protein synthesis	0.0952
M5005_Spy1426	SpM12_ChORF299-5_s_at	0.27	0.7519	-		Phage protein	Phage	0.4166
M5005_Spy0730	SpM1_ChORF0929_s_at	0.28	0.7542	*nth*	SPy0929	Endonuclease III (EC 4.2.99.18)	Information processing	0.6743
M5005_Spy1411	SpM1_ChORF1723_s_at	-0.25	0.7542	-	SPy1723	Hypothetical cytosolic protein	Unknown	0.5176
M5005_Spy0443	SpM1_ChORF0536_s_at	0.26	0.7549	-	SPy0536	Hypothetical protein	Unknown	0.6139
M5005_Spy0844	SpM1_ChORF1121_s_at	0.20	0.7561	*nifS, yrvO*	SPy1121	Cysteine desulfhydrase (EC 4.4.1.-) / Selenocysteine lyase (EC 4.4.1.16)	Coenzyme and cofactor metabolism	0.4806
M5005_Spy0868	SpM1_ChORF1146_s_at	0.25	0.7584	-	SPy1146	Hypothetical protein	Unknown	0.5695
M5005_Spy1697	SpM49_ChORF391-1_s_at	0.25	0.7631	-		Para-aminobenzoate synthetase component I (EC 4.1.3.-) /4-amino-4-deoxychorismate lyase (EC 4.-.-.-)	Unknown	0.4645
M5005_Spy1756	SpM1_ChORF2063_s_at	0.21	0.7636	-	SPy2063	Ribosomal large subunit pseudouridine synthase D (EC 4.2.1.70)	Protein synthesis	0.5698
M5005_Spy1478	SpM1_ChORF1737_s_at	0.22	0.7642	-	SPy1737	Hydrolase (HAD superfamily)	Unknown	0.4334
M5005_Spy0490	SpM1_ChORF0590_s_at	-0.20	0.7644	-	SPy0590	Peptidase family U32	Unknown	0.4702
M5005_Spy0691	SpM1_ChORF0885_s_at	-0.23	0.7654	*clpX*	SPy0885	ATP-dependent clp protease ATP-binding subunit clpX	Stress adaptation	0.4706
M5005_Spy1327	SpM1_ChORF1616_s_at	0.24	0.7666	*comFA*	SPy1616	ComF operon protein 1	Membrane transport	0.5147
M5005_Spy0838	SpM1_ChORF1115_s_at	-0.19	0.7683	-	SPy1115	Lipase/Acylhydrolase family protein	Unknown	0.5659
M5005_Spy1106	SpM5_ChORF270b-528_at	0.20	0.7707	*grab*		Protein G-related alpha 2M-binding protein	Virulence	0.2918
M5005_Spy0074	SpM12_ChORF300-26_s_at	0.24	0.7719	-		4-diphosphocytidyl-2-C-methyl-D-erythritol kinase (EC 2.7.1.148)	Unknown	0.6254
M5005_Spy0097	SpM1_ChORF0115_s_at	0.26	0.7726	*pepA*	SPy0115	Glutamyl aminopeptidase (EC 3.4.11.7)	Amino acid metabolism	0.5388
M5005_Spy0434	SpM1_ChORF0527_s_at	-0.19	0.7738	-	SPy0527	Hypothetical cytosolic protein	Unknown	0.3573

M5005_gene	RML Probeset	*T* -statistic *	Empirical *P* -value †	Gene	Synonym	Description	Function	Q-value (Strain) ‡
M5005_Spy0265	SpM1_ChORF0310_s_at	-0.24	0.7747	-	SPy0310	iojap protein family	Unknown	0.5698
M5005_Spy0803	SpM1_ChORF1080_s_at	0.21	0.7755	*srtI*	SPy1080	Protein involved in lantibiotic (srt) production	Virulence	0.3002
M5005_Spy0213	SpM1_ChORF0252_s_at	-0.22	0.7777	-	SPy0252	N-acetylneuraminate-binding protein	Membrane transport	0.4400
M5005_Spy1774	SpM1_ChORF2085_s_at	0.27	0.7785	*fhs.2*	SPy2085	Formate--tetrahydrofolate ligase (EC 6.3.4.3)	Carbohydrate metabolism	0.3998
M5005_Spy0674	SpM1_ChORF0867_s_at	-0.21	0.7787	-	SPy0867	ABC transporter ATP-binding protein uup	Membrane transport	0.3880
M5005_Spy1504	SpM1_ChORF1768_s_at	-0.20	0.7794	-	SPy1768	Hypothetical membrane spanning protein	Unknown	0.6525
M5005_Spy0463	SpM5_ChORFJ7578C-152_s_at	-0.27	0.7822	-		Hypothetical cytosolic protein	Phage	0.4473
M5005_Spy1453	SpM12_ChORF299-40_at	-0.20	0.7835	-		Phage protein	Phage	0.4255
M5005_Spy1755	SpM18_ChORF2122_s_at	0.21	0.7839	-	spyM18_2122	Hypothetical cytosolic protein	Unknown	0.3862
M5005_Spy0986	SpM12_ChORF272-9_s_at	0.24	0.7851	*glmS*		Glucosamine--fructose-6-phosphate aminotransferase [isomerizing] transamidination (EC 2.6.1.16)	Cell wall metabolism	0.3533
M5005_Spy0798	SpM1_ChORF1075_at	0.21	0.7858	-	SPy1075	IFN-response binding factor 1	Unknown	0.4702
M5005_Spy1085	SpM1_ChORF1328_s_at	-0.23	0.7864	*bglA.2*	SPy1328	Beta-glucosidase (EC 3.2.1.21)	Carbohydrate metabolism	0.6186
M5005_Spy1119	SpM1_ChORF1371_s_at	-0.24	0.7864	*gapN*	SPy1371	NADP-dependent glyceraldehyde-3-phosphate dehydrogenase (EC 1.2.1.9)	Carbohydrate metabolism	0.3626
M5005_Spy1515	SpM1_ChORF1781_s_at	0.18	0.7866	-	SPy1781	Hydrolase (HAD superfamily)	Unknown	0.3058
M5005_Spy1754	SpM1_ChORF2060_s_at	-0.21	0.7866	-	SPy2060	Translation initiation inhibitor	Unknown	0.3995
M5005_Spy1589	SpM12_ChORF217-10_s_at	-0.23	0.7873	*crgR*		Transcriptional regulator, GntR family	Information processing	0.6201
M5005_Spy1010	SpM49_ChORF7585-29_at	-0.23	0.7902	-		Phage protein	Phage	0.5118
M5005_Spy1481	SpM1_ChORF1740_s_at	-0.20	0.7905	*manN*	SPy1740	PTS system, mannose-specific IID component (EC 2.7.1.69)	Carbohydrate metabolism	0.5695
M5005_Spy1104	SpM1_ChORF1355_s_at	0.20	0.7906	-	SPy1355	Cytosolic protein containing multiple CBS domains	Unknown	0.5169

M5005_gene	RML Probeset	*T* -statistic *	Empirical *P* -value †	Gene	Synonym	Description	Function	Q-value (Strain) ‡
M5005_Spy1658	SpM1_ChORF1944_s_at	0.27	0.7917	*cysE*	SPy1944	Serine acetyltransferase (EC 2.3.1.30)	Amino acid metabolism	0.6632
M5005_Spy1527	SpM1_ChORF1794_s_at	-0.21	0.7924	-	SPy1794	Ferrichrome transport system permease protein fhuB	Membrane transport	0.6930
M5005_Spy0284	SpM1_ChORF0338_s_at	-0.16	0.7932	-	SPy0338	Putative regulatory protein	Unknown	0.6564
M5005_Spy0969	SpM18_ChORF1209_x_at	-0.18	0.7949	-	spyM18_1209	Hypothetical protein	Unknown	0.6347
M5005_Spy1029	SpM18_ChORF0740_x_at	0.18	0.7963	-	spyM18_0740	Phage protein	Phage	0.3993
M5005_Spy0785	SpM1_ChORF1062_s_at	0.18	0.7971	*yesN*	SPy1062	Two-component response regulator yesN	Signal transduction	0.6915
M5005_Spy0907	SpM1_ChORF1189_s_at	0.20	0.798	*citF*	SPy1189	Citrate lyase alpha chain (EC 4.1.3.6) / Citrate CoA-transferase (EC 2.8.3.10)	Carbohydrate metabolism	0.4836
M5005_Spy0339	SpM1_ChORF0412_s_at	0.17	0.7995	*exoA*	SPy0412	Exodeoxyribonuclease III (EC 3.1.11.2)	Information processing	0.3917
M5005_Spy1007	SpM49_ChORF7585-3_at	0.18	0.8005	-		Phage protein	Phage	0.4537
M5005_Spy0881	SpM1_ChORF1159_s_at	0.19	0.8009	-	SPy1159	Hypothetical cytosolic protein	Virulence	0.5807
M5005_Spy1811	SpM1_ChORF2155_s_at	-0.19	0.801	-	SPy2155	Hypothetical membrane spanning protein	Unknown	0.5316
M5005_Spy1030	SpM18_ChORF1789_s_at	-0.17	0.8027	-	spyM18_1789	Phage protein	Phage	0.0713
M5005_Spy0533	SpM1_ChORF0646_s_at	0.16	0.8045	-	SPy0646	Hydroxyacylglutathione hydrolase (EC 3.1.2.6)	Amino acid metabolism	0.6201
M5005_Spy0027	SpM18_ChORF0030_s_at	0.20	0.8071	-	spyM18_0030	Phosphoribosylaminoimidazolecarboxamide formyltransferase (EC 2.1.2.3) / IMP cyclohydrolase (EC 3.5.4.10)	Nucleotide metabolism	0.6008
M5005_Spy0573	SpM1_ChORF0751_s_at	-0.17	0.808	*lig*	SPy0751	NAD-dependent DNA ligase (EC 6.5.1.2)	Cellular processing	0.5766
M5005_Spy0216	SpM1_ChORF0256_s_at	0.17	0.8093	-	SPy0256	Hypothetical membrane spanning protein	Unknown	0.4266
M5005_Spy1335	SpM5_ChORF-b16C31-7_s_at	0.20	0.8097	-		Serine/threonine protein kinase (EC 2.7.1.37)	Unknown	0.5512
M5005_Spy1710	SpM1_ChORF2006_s_at	0.23	0.81	-	SPy2006	Streptococcal histidine triad protein	Unknown	0.6294
M5005_Spy1225	SpM1_ChORF1492_s_at	0.16	0.8107	-	SPy1492	Lipase/Acylhydrolase with GDSL-like motif	Unknown	0.6835

M5005_gene	RML Probeset	*T* -statistic *	Empirical *P* -value †	Gene	Synonym	Description	Function	Q-value (Strain) ‡
M5005_Spy0825	SpM1_ChORF1101_s_at	-0.16	0.8114	*murB*	SPy1101	UDP-N-acetylenolpyruvoylglucosamine reductase (EC 1.1.1.158)	Carbohydrate metabolism	0.4941
M5005_Spy0373	SpM1_ChORF0459_s_at	-0.15	0.8116	-	SPy0459	Integral membrane protein	Unknown	0.3225
M5005_Spy1313	SpM1_ChORF1599_s_at	0.19	0.8118	-	SPy1599	Beta-glucosidase (EC 3.2.1.21)	Carbohydrate metabolism	0.3986
M5005_Spy0065	SpM1_ChORF0074_s_at	-0.20	0.8126	*adk*	SPy0074	Adenylate kinase (EC 2.7.4.3)	Cellular processing	0.5006
M5005_Spy1786	SpM18_ChORF2160_s_at	0.18	0.8144	-	spyM18_2160	Transcriptional regulator, MarR family	Information processing	0.5148
M5005_Spy0277	SpM1_ChORF0327_s_at	-0.17	0.8171	*ntpJ*	SPy0327	Potassium uptake protein ktrB	Membrane transport	0.5874
M5005_Spy0581	SpM1_ChORF0760_s_at	0.15	0.8173	*atpD*	SPy0760	ATPase, beta subunit	Carbohydrate metabolism	0.6061
M5005_Spy1474	SpM12_ChORF29919_s_at	-0.22	0.818	*lytR*		Transcriptional regulator, LytR family	Information processing	0.4798
M5005_Spy1589	SpM12_ChORF2171_at	0.18	0.8196	*crgR*		Transcriptional regulator, GntR family	Information processing	0.3530
M5005_Spy0263	SpM1_ChORF0308_s_at	-0.17	0.8209	*nadD*	SPy0308	Nicotinate-nucleotide adenylyltransferase (EC 2.7.7.18)	Coenzyme and cofactor metabolism	0.6007
M5005_Spy1711	SpM1_ChORF2007_s_at	0.21	0.8212	*lbp, lmb*	SPy2007	Laminin binding protein	Virulence	0.5169
M5005_Spy1161	SpM1_ChORF1424_s_at	0.18	0.8215	-	SPy1424	Formate transporter	Membrane transport	0.5801
M5005_Spy0239	SpM1_ChORF0281_s_at	0.15	0.8224	*mecA*	SPy0281	Negative regulator of genetic competence mecA	Information processing	0.3989
M5005_Spy0649	SpM1_ChORF0841_s_at	-0.17	0.8231	-	SPy0841	RNA binding protein	Unknown	0.6850
M5005_Spy0844	SpM1_ChORF1123_s_at	0.16	0.8233	*nifS, yrvO*	SPy1123	Cysteine desulfhydrase (EC 4.4.1.-) / Selenocysteine lyase (EC 4.4.1.16)	Coenzyme and cofactor metabolism	0.6743
M5005_Spy0212	SpM1_ChORF0251_s_at	0.16	0.8238	-	SPy0251	N-acetylmannosamine-6-phosphate 2-epimerase (EC 5.1.3.9)	Carbohydrate metabolism	0.5348
M5005_Spy0990	SpM1_ChORF1284_s_at	-0.18	0.8258	*dnaE*	SPy1284	DNA polymerase III alpha subunit (EC 2.7.7.7)	Information processing	0.4889
M5005_Spy0335	SpM1_ChORF0406_s_at	-0.19	0.8259	-	SPy0406	Corrin/porphyrin methyltransferase (EC 2.1.1.-)	Unknown	0.3672

M5005_gene	RML Probeset	*T* -statistic *	Empirical *P* -value †	Gene	Synonym	Description	Function	Q-value (Strain) ‡
M5005_Spy0238	SpM1_ChORF0280_s_at	0.16	0.8268	*bacA*	SPy0280	Putative undecaprenol kinase (EC 2.7.1.66)	Lipid metabolism	0.5962
M5005_Spy0365	SpM1_ChORF0447_s_at	0.17	0.8273	*pfs*	SPy0447	5'-methylthioadenosine nucleosidase (EC 3.2.2.16) / S-adenosylhomocysteine nucleosidase (EC 3.2.2.9)	Carbohydrate metabolism	0.3665
M5005_Spy1159	SpM1_ChORF1422_s_at	-0.14	0.8284	*recR*	SPy1422	Recombination protein recR	Information processing	0.4798
M5005_Spy1422	SpM12_ChORF299-64_at	-0.18	0.8319	-		Phage protein	Phage	0.6565
M5005_Spy1262	SpM1_ChORF1534_s_at	-0.16	0.8336	-	SPy1534	Transcriptional regulator	Unknown	0.6907
M5005_Spy1225	SpM1_ChORF1491_s_at	-0.15	0.8346	-	SPy1491	Lipase/Acylhydrolase with GDSL-like motif	Unknown	0.5120
M5005_Spy0491	SpM1_ChORF0591_s_at	-0.15	0.839	-	SPy0591	Peptidase family U32	Information processing	0.6906
M5005_Spy0151	SpM1_ChORF0177_s_at	-0.17	0.8405	-	SPy0177	3-keto-L-gulonate-6-phosphate decarboxylase (EC 4.1.1.-)	Carbohydrate metabolism	0.5178
M5005_Spy1330	SpM1_ChORF1619_s_at	-0.17	0.8413	-	SPy1619	S1-type RNA-binding domain	Unknown	0.6775
M5005_Spy1572	SpM12_ChORF260-3_s_at	0.16	0.8424	-		Hypothetical membrane spanning protein	Unknown	0.6081
M5005_Spy1298	SpM1_ChORF1577_s_at	-0.13	0.8458	*aroB*	SPy1577	3-dehydroquinate synthase (EC 4.6.1.3)	Amino acid metabolism	0.5176
M5005_Spy0706	SpM1_ChORF0903_s_at	0.13	0.8461	-	SPy0903	Cystine-binding protein	Membrane transport	0.5962
M5005_Spy0708	SpM1_ChORF0905_s_at	-0.16	0.8472	*ung*	SPy0905	Uracil-DNA glycosylase (EC 3.2.2.-)	Information processing	0.6146
M5005_Spy1741	SpM1_ChORF2047_s_at	0.13	0.8496	*gldA*	SPy2047	Glycerol dehydrogenase (EC 1.1.1.6)	Carbohydrate metabolism	0.6525
M5005_Spy0273	SpM1_ChORF0321_s_at	-0.14	0.8498	-	SPy0321	ABC transporter permease protein	Membrane transport	0.2634
M5005_Spy1616	SpM1_ChORF1901_s_at	0.13	0.852	*thiD*	SPy1901	Phosphomethylpyrimidine kinase (EC 2.7.4.7) / Hydroxymethylpyrimidine kinase (EC 2.7.1.49)	Coenzyme and cofactor metabolism	0.4227
M5005_Spy1225	SpM1_ChORF1493_s_at	-0.17	0.8522	-	SPy1493	Lipase/Acylhydrolase with GDSL-like motif	Unknown	0.5169
M5005_Spy1639	SpM5_ChORF125g-147_at	0.16	0.854	*lacR.2*		Lactose phosphotransferase system repressor	Information processing	0.6565

M5005_gene	RML Probeset	*T* -statistic *	Empirical *P* -value †	Gene	Synonym	Description	Function	Q-value (Strain) ‡
M5005_Spy0415	SpM1_ChORF0504_s_at	-0.16	0.8541	-	SPy0504	SsrA-binding protein	Information processing	0.3072
M5005_Spy0631	SpM1_ChORF0817_s_at	0.10	0.8547	*thiI*	SPy0817	Thiamine biosynthesis protein thiI	Coenzyme and cofactor metabolism	0.2779
M5005_Spy0183	SpM18_ChORF0202_s_at	0.16	0.8555	-	spyM18_0202	Hypothetical membrane associated protein	Unknown	0.4436
M5005_Spy0992	SpM1_ChORF1286_s_at	0.11	0.8557	-	SPy1286	ABC transporter ATP-binding protein	Membrane transport	0.2300
M5005_Spy1069	SpM1_ChORF1308_s_at	-0.14	0.8569	*dltD*	SPy1308	Esterase (EC 3.1.1.-)	Cell wall metabolism	0.6065
M5005_Spy1129	SpM1_ChORF1384_s_at	0.12	0.8576	-	SPy1384	CAAX amino terminal protease family	Information processing	0.4836
M5005_Spy0640	SpM1_ChORF0831_s_at	-0.14	0.8581	*pyrP*	SPy0831	Uracil permease	Membrane transport	0.6081
M5005_Spy1006	SpM49_ChORF7585-35_at	-0.12	0.8616	-		Phage structural protein	Phage	0.1949
M5005_Spy1637	SpM1_ChORF1922_s_at	0.13	0.867	*lacB.2*	SPy1922	Galactose-6-phosphate isomerase lacB subunit (EC 5.3.1.26)	Carbohydrate metabolism	0.4544
M5005_Spy1616	SpM1_ChORF1900_s_at	-0.13	0.8675	*thiD*	SPy1900	Phosphomethylpyrimidine kinase (EC 2.7.4.7) / Hydroxymethylpyrimidine kinase (EC 2.7.1.49)	Coenzyme and cofactor metabolism	0.4577
M5005_Spy0486	SpM1_ChORF0587_s_at	-0.10	0.8676	-	SPy0587	Hypothetical protein	Unknown	0.4888
M5005_Spy0244	SpM1_ChORF0288_s_at	0.13	0.8685	*nifS, csd*	SPy0288	Cysteine desulfhydrase (EC 4.4.1.-) / Selenocysteine lyase (EC 4.4.1.16)	Amino acid metabolism	0.5926
M5005_Spy1408	SpM1_ChORF1719_s_at	0.13	0.8685	*rbfA*	SPy1719	Ribosome-binding factor A	Cellular processing	0.6200
M5005_Spy1822	SpM12_ChORF218-7_s_at	-0.15	0.8687	-		Transcriptional regulator	Information processing	0.6184
M5005_Spy1358	SpM1_ChORF1653_s_at	-0.13	0.8691	*nadE*	SPy1652	Nicotinate phosphoribosyltransferase (EC 2.4.2.11)	Phage	0.6019
M5005_Spy1025	SpM1_ChORF0677_s_at	0.11	0.8706	-	SPy0677	Phage encoded transcriptional regulator, ArpU family	Phage	0.3752
M5005_Spy1562	SpM1_ChORF1839_s_at	-0.11	0.8751	-	SPy1839	Colicin V production protein	Unknown	0.5176
M5005_Spy1434	SpM12_ChORF299-53_s_at	0.13	0.8786	-		Phage protein	Phage	0.6916

M5005_gene	RML Probeset	*T*-statistic *	Empirical *P*-value †	Gene	Synonym	Description	Function	Q-value (Strain) ‡
M5005_Spy1493	SpM1_ChORF1753_s_at	0.14	0.8794	*acpP*	SPy1753	Acyl carrier protein	Lipid metabolism	0.4222
M5005_Spy1665	SpM1_ChORF1955_s_at	-0.12	0.8802	-	SPy1955	Hypothetical protein	Unknown	0.6616
M5005_Spy1648	SpM1_ChORF1935_s_at	0.11	0.8805	-	SPy1935	Transcriptional regulator, Cro/CI family	Information processing	0.4888
M5005_Spy0725	SpM1_ChORF0924_s_at	-0.12	0.8807	*elaC*	SPy0924	Metal-dependent hydrolase (EC 3.-.-.-)	Unknown	0.3989
M5005_Spy0671	SpM1_ChORF0864_s_at	0.10	0.8813	-	SPy0864	Transposase	Mobile genetic element	0.5512
M5005_Spy1027	SpM18_ChORF1786_at	-0.13	0.8813	-	spyM18_1786	Phage protein	Phage	0.6512
M5005_Spy1280	SpM12_ChORF301-33_at	0.11	0.8815	*zmpR*		Two-component sensor kinase	Signal transduction	0.3186
M5005_Spy0475	SpM1_ChORF0572_s_at	0.10	0.8836	-	SPy0572	PTS system, beta-glucoside-specific IIABC component (EC 2.7.1.69)	Carbohydrate metabolism	0.3234
M5005_Spy1100	SpM1_ChORF1352_s_at	0.11	0.8839	*aroK*	SPy1352	Shikimate kinase (EC 2.7.1.71)	Amino acid metabolism	0.4436
M5005_Spy1561	SpM1_ChORF1837_s_at	-0.10	0.8874	*mutS2*	SPy1837	DNA mismatch repair protein mutS	Information processing	0.6419
M5005_Spy1205	SpM12_ChORF278-26_s_at	-0.11	0.8886	-		Phage protein	Phage	0.4227
M5005_Spy0480	SpM12_ChORF266-14_s_at	0.10	0.8893	-		Transcription accessory protein (S1 RNA binding domain)	Cellular processing	0.5176
M5005_Spy0465	SpM18_ChORF0631_s_at	-0.11	0.8894	-	spyM18_0631	Hypothetical protein	Unknown	0.6184
M5005_Spy0040	SpM1_ChORF0044_s_at	0.13	0.8902	*adhA*	SPy0044	Alcohol dehydrogenase (EC 1.1.1.1)	Carbohydrate metabolism	0.3989
M5005_Spy0598	SpM1_ChORF0780_s_at	0.12	0.8916	*mscL*	SPy0780	Large-conductance mechanosensitive channel	Membrane transport	0.4776
M5005_Spy1073	SpM1_ChORF1312_s_at	-0.11	0.893	*dltA*	SPy1312	Putative D-alanine-D-alanyl carrier protein ligase (EC 6.3.2.-); D-alanine-activating enzyme	Cell wall metabolism	0.4798
M5005_Spy0894	SpM1_ChORF1174_s_at	0.10	0.8931	*oadA*	SPy1174	Oxaloacetate decarboxylase alpha chain (EC 4.1.1.3)	Carbohydrate metabolism	0.5231
M5005_Spy1854	SpM1_ChORF2203_s_at	-0.10	0.8932	-	SPy2203	Hypothetical cytosolic protein	Cellular processing	0.5926
M5005_Spy1823	SpyM3_1824_at	-0.13	0.8943	-	#N/A	Integral membrane protein	Phage	0.6563
M5005_Spy0109	SpM1_ChORF0128_at	0.12	0.8947	-	SPy0128	Fibronectin-binding protein	Virulence	0.6081

M5005_gene	RML Probeset	*T* -statistic *	Empirical *P* -value †	Gene	Synonym	Description	Function	Q-value (Strain) ‡
M5005_Spy0148	SpM1_ChORF0174_s_at	0.09	0.8947	-	SPy0174	PTS system, 3-keto-L-gulonate specific IIC component (EC 2.7.1.69)	Membrane transport	0.6623
M5005_Spy0488	SpM1_ChORF0589_s_at	-0.09	0.8954	-	SPy0589	Hypothetical protein	Unknown	0.6184
M5005_Spy1107	SpM1_ChORF1358_s_at	-0.09	0.8963	*murZ*	SPy1358	UDP-N-acetylglucosamine 1-carboxyvinyltransferase (EC 2.5.1.7)	Cell wall metabolism	0.6512
M5005_Spy0633	SpM1_ChORF0819_s_at	0.12	0.8972	*rplU*	SPy0819	LSU ribosomal protein L21P	Protein synthesis	0.2867
M5005_Spy0400	SpM3_ChORF0341_s_at	-0.13	0.8996	*silD*	spyM3_0341	Hypothetical protein	Virulence	0.2905
M5005_Spy0749	SpM1_ChORF1024_s_at	0.08	0.9001	-	SPy1024	Hypothetical protein	Unknown	0.4745
M5005_Spy1514	SpM1_ChORF1780_s_at	0.08	0.9015	-	SPy1780	Universal stress protein family	Stress adaptation	0.3845
M5005_Spy1468	SpM1_ChORF1726_s_at	0.09	0.902	-	SPy1726	tRNA (m(7)G46) methyltransferase (EC 2.1.1.-)	Protein synthesis	0.6391
M5005_Spy1186	SpM1_ChORF1456_s_at	0.09	0.903	-	SPy1456	Phage protein	Phage	0.6065
M5005_Spy1409	SpM1_ChORF1721_s_at	-0.10	0.9039	*infB*	SPy1721	Bacterial Protein Translation Initiation Factor 2 (IF-2)	Cellular processing	0.2797
M5005_Spy1297	SpM1_ChORF1576_s_at	0.07	0.905	-	SPy1576	Phospho-2-dehydro-3-deoxyheptonate aldolase (EC 4.1.2.15)	Amino acid metabolism	0.3058
M5005_Spy1776	SpM1_ChORF2088_s_at	-0.11	0.9055	-	SPy2088	putative cationic amino acid transporter protein	Membrane transport	0.3379
M5005_Spy1146	SpM3_ChORF1072_s_at	-0.10	0.9071	-	spyM3_1072	DNA polymerase III, delta subunit (EC 2.7.7.7)	Information processing	0.6918
M5005_Spy0994	SpM1_ChORF1289_s_at	-0.08	0.9083	-	SPy1289	Putative membrane-associated alkaline phosphatase	Membrane transport	0.6750
M5005_Spy0906	SpM1_ChORF1188_s_at	-0.12	0.9101	*citE*	SPy1188	Citrate lyase beta chain (EC 4.1.3.6) / Citryl-CoA lyase subunit (EC 4.1.3.34)	Carbohydrate metabolism	0.3149
M5005_Spy0910	SpM1_ChORF1192_s_at	0.08	0.911	*citC*	SPy1192	[Citrate [pro-3S]-lyase] ligase (EC 6.2.1.22)	Carbohydrate metabolism	0.5672
M5005_Spy1529	SpM1_ChORF1795_s_at	0.09	0.9144	*htsA, siaA*	SPy1795	Putative heme binding protein	Membrane transport	0.5999
M5005_Spy0847	SpM1_ChORF1125_s_at	-0.07	0.9157	-	SPy1125	GTP pyrophosphokinase (EC 2.7.6.5)	Stress adaptation	0.3578
M5005_Spy1424	SpM12_ChORF299 2_x_at	-0.08	0.9198	-		Phage endopeptidase	Phage	0.4776

M5005_gene	RML Probeset	*T*-statistic *	Empirical *P*-value †	Gene	Synonym	Description	Function	Q-value (Strain) ‡
M5005_Spy1290	SpM1_ChORF1566_s_at	-0.07	0.9208	-	SPy1566	Hypothetical protein	Unknown	0.4779
M5005_Spy1215	SpM1_ChORF0948_s_at	-0.06	0.9228	-	SPy0948	Phage protein	Phage	0.3279
M5005_Spy1271	SpM1_ChORF1542_s_at	-0.09	0.9254	-	SPy1542	Xaa-His dipeptidase (EC 3.4.13.3)	Amino acid metabolism	0.3002
M5005_Spy1564	SpM1_ChORF1841_s_at	0.06	0.9299	-	SPy1841	Ribonuclease HIII (EC 3.1.26.4)	Cellular processing	0.6563
M5005_Spy0514	SpM1_ChORF0621_s_at	0.08	0.9305	-	SPy0621	dGTP triphosphohydrolase	Unknown	0.6305
M5005_Spy0368	SpM1_ChORF0453_s_at	0.08	0.9332	*mtsA*	SPy0453	Manganese-binding protein	Membrane transport	0.3296
M5005_Spy1275	SpM49_ChORF356-2_s_at	-0.07	0.9341	*arcA*		Arginine deiminase (EC 3.5.3.6)	Amino acid metabolism	0.6041
M5005_Spy0855	SpM1_ChORF1134_s_at	-0.05	0.9343	*proV*	SPy1134	Glycine betaine transport ATP-binding protein	Membrane transport	0.5874
M5005_Spy1432	SpyM3_1427_at	-0.05	0.936	-	spyM3_1427	Phage protein	Phage	0.4889
M5005_Spy1044	SpM18_ChORF1301_at	0.07	0.9369	-	spyM18_1301	Phage protein	Phage	0.6850
M5005_Spy0016	M12_0555_s_at	0.09	0.9379	-		Hypothetical protein	Unknown	0.5453
M5005_Spy0795	SpM1_ChORF1072_s_at	0.06	0.938	*rplJ*	SPy1072	LSU ribosomal protein L10P	Protein synthesis	0.5120
M5005_Spy1110	SpM1_ChORF1362_s_at	-0.05	0.9381	*birA*	SPy1362	Biotin operon repressor / Biotin--[acetyl-CoA-carboxylase] synthetase (EC 6.3.4.15)	Coenzyme and cofactor metabolism	0.5868
M5005_Spy1553	SpM5_ChORF169a-232_at	-0.06	0.9383	*rpsR*		SSU ribosomal protein S18P	Protein synthesis	0.2163
M5005_Spy0326	SpM1_ChORF0390_s_at	0.06	0.9384	-	SPy0390	Export protein for polysaccharides and teichoic acids	Unknown	0.5176
M5005_Spy0116	SpM1_ChORF0137_s_at	0.06	0.9393	*atoE*	SPy0137	Short-chain fatty acids transporter	Membrane transport	0.6512
M5005_Spy1557	SpM1_ChORF1833_s_at	-0.06	0.9402	*mutY*	SPy1833	A/G-specific adenine DNA glycosylase (EC 3.2.2.-)	Unknown	0.6609
M5005_Spy0980	SpM1_ChORF1272_s_at	-0.05	0.9405	-	SPy1272	Cobalt-zinc-cadmium resistance protein czcD	Membrane transport	0.5829
M5005_Spy1370	SpM1_ChORF1670_s_at	0.05	0.9434	-	SPy1666	Gamma-glutamyl phosphate reductase (EC 1.2.1.41)	Amino acid metabolism	0.5120
M5005_Spy0964	SpM1_ChORF1254_s_at	0.06	0.944	-	SPy1254	Type I restriction-modification system specificity subunit	Information processing	0.6651
M5005_Spy0043	SpM5_ChORF275f-245_at	0.06	0.945	*rpsJ*		SSU ribosomal protein S10P	Protein synthesis	0.4321

M5005_gene	RML Probeset	*T* -statistic *	Empirical *P* -value †	Gene	Synonym	Description	Function	Q-value (Strain) ‡
M5005_Spy1449	SpM12_ChORF299-44_at	-0.04	0.9467	-		DNA primase	Phage	0.0949
M5005_Spy1485	SpM1_ChORF1743_s_at	0.05	0.9483	*accA*	SPy1743	Acetyl-coenzyme A carboxylase carboxyl transferase subunit beta (EC 6.4.1.2)	Lipid metabolism	0.6512
M5005_Spy0179	SpM18_ChORF0196_s_at	-0.04	0.9486	-	spyM18_0196	tRNA-specific adenosine deaminase	Unknown	0.6262
M5005_Spy0936	SpM1_ChORF1222_s_at	0.05	0.9498	*dfp*	SPy1222	Phosphopantothenoylcysteine decarboxylase (EC 4.1.1.36)	Coenzyme and cofactor metabolism	0.5120
M5005_Spy1173	SpM1_ChORF1440_x_at	0.05	0.9516	-	SPy1440	Phage protein	Phage	0.6632
M5005_Spy0038	SpM1_ChORF0041_s_at	0.05	0.9519	-	SPy0041	Acyltransferase family	Unknown	0.4110
M5005_Spy0043	SpM1_ChORF0047_s_at	0.04	0.9541	*rpsJ*	SPy0047	SSU ribosomal protein S10P	Protein synthesis	0.5804
M5005_Spy0599	SpM1_ChORF0781_s_at	0.04	0.9543	*dnaG*	SPy0781	DNA primase (EC 2.7.7.-)	Cellular processing	0.4449
M5005_Spy0512	SpM1_ChORF0617_s_at	-0.05	0.955	-	SPy0617	Hydrolase (HAD superfamily)	Unknown	0.6146
M5005_Spy0901	SpM1_ChORF1181_s_at	-0.09	0.9555	-	SPy1181	Hypothetical protein	Unknown	0.6123
M5005_Spy1482	SpM1_ChORF1741_s_at	-0.04	0.9558	*manO*	SPy1741	Hypothetical cytosolic protein	Membrane transport	0.5280
M5005_Spy1270	SpM1_ChORF1541_s_at	-0.05	0.9573	*arcC*	SPy1541	Carbamate kinase (EC 2.7.2.2)	Carbohydrate metabolism	0.3712
M5005_Spy1303	SpM18_ChORF1591_s_at	-0.05	0.9581	*aroE*	spyM18_1591	Shikimate 5-dehydrogenase (EC 1.1.1.25)	Amino acid metabolism	0.5849
M5005_Spy1393	SpM1_ChORF1700_s_at	-0.04	0.9607	-	SPy1700	Hydrolase (HAD superfamily)	Unknown	0.4208
M5005_Spy1795	SpM1_ChORF2112_s_at	0.04	0.9616	-	SPy2112	Hypothetical cytosolic protein	Unknown	0.4400
M5005_Spy1005	SpM49_ChORF7585-37_at	-0.04	0.9631	-		Phage protein	Phage	0.6442
M5005_Spy0814	M12_0090_s_at	-0.03	0.9632	-		DNA integration/recombination/invertion protein	Information processing	0.6564
M5005_Spy1463	M12_1772_x_at	0.04	0.9633	-		Phage protein	Phage	0.5849
M5005_Spy1275	SpM1_ChORF1547_s_at	0.04	0.9636	*arcA*	SPy1547	Arginine deiminase (EC 3.5.3.6)	Amino acid metabolism	0.2541
M5005_Spy0133	SpM1_ChORF0157_s_at	0.03	0.9646	*ntpD*	SPy0157	V-type sodium ATP synthase subunit D (EC 3.6.3.15)	Membrane transport	0.6623

M5005_gene	RML Probeset	*T*-statistic *	Empirical *P*-value †	Gene	Synonym	Description	Function	Q-value (Strain) ‡
M5005_Spy1582	SpM12_ChORF217 7_s_at	0.03	0.9654	*dnaQ*		DNA polymerase III, epsilon chain (EC 2.7.7.7)	Cellular processing	0.6184
M5005_Spy0836	SpM1_ChORF1113_s_at	-0.04	0.9678	-	SPy1113	Class B acid phosphatase (EC 3.1.3.2)	Cellular processing	0.3887
M5005_Spy1357	SpM18_ChORF1663_s_at	-0.03	0.9684	-	spyM18_1663	NH(3)-dependent NAD(+) synthetase (EC 6.3.5.1)	Unknown	0.6850
M5005_Spy0417	SpM1_ChORF0506_s_at	0.03	0.9697	*pcp*	SPy0506	Pyrrolidone-carboxylate peptidase (EC 3.4.19.3)	Amino acid metabolism	0.5893
M5005_Spy0112	SpM1_ChORF0131_at	0.03	0.9698	-	SPy0131	Transposase	Mobile genetic element	0.5871
M5005_Spy1592	SpM1_ChORF1873_s_at	0.03	0.9715	-	SPy1873	Ribosomal-protein-alanine acetyltransferase (EC 2.3.1.128)	Protein synthesis	0.4400
M5005_Spy0428	SpM1_ChORF0518_s_at	-0.02	0.9727	-	SPy0518	Daunorubicin resistance ATP-binding protein drrA	Membrane transport	0.2979
M5005_Spy1297	SpM1_ChORF1575_s_at	0.02	0.9747	-	SPy1575	Phospho-2-dehydro-3-deoxyheptonate aldolase (EC 4.1.2.15)	Amino acid metabolism	0.6931
M5005_Spy0606	SpM1_ChORF0790_s_at	0.02	0.9754	*rgpDc*	SPy0790	Polysaccharide export ATP-binding protein	Cell wall metabolism	0.6750
M5005_Spy1150	SpM1_ChORF1411_s_at	-0.02	0.9763	-	SPy1411	Methyltransferase (EC 2.1.1.-)	Unknown	0.6743
M5005_Spy0982	SpM1_ChORF1274_s_at	-0.02	0.9772	-	SPy1274	Histidine-binding protein	Membrane transport	0.5159
M5005_Spy0024	SpM1_ChORF0026_s_at	0.02	0.9783	*purF*	SPy0026	Amidophosphoribosyltransferase (EC 2.4.2.14)	Nucleotide metabolism	0.6041
M5005_Spy0860	SpM1_ChORF1138_s_at	-0.02	0.9789	-	SPy1138	Thiamine biosynthesis lipoprotein apbE	Unknown	0.4776
M5005_Spy1798	SpM1_ChORF2115_s_at	0.03	0.9797	-	SPy2115	Arsenate reductase family protein	Unknown	0.2905
M5005_Spy1102	SpM1_ChORF1353_s_at	-0.02	0.9808	-	SPy1353	Ribonuclease BN (EC 3.1.-.-)	Cellular processing	0.5893
M5005_Spy1629	SpM1_ChORF1912_s_at	0.02	0.9815	*salX*	SPy1912	Lantibiotic transport ATP-binding protein	Membrane transport	0.6801
M5005_Spy0723	SpM1_ChORF0922_s_at	0.01	0.982	-	SPy0922	GTP-binding protein hflX	Information processing	0.4776
M5005_Spy0366	SpM5_ChORFJ7578C-81_s_at	-0.01	0.9833	-		Hypothetical protein	Unknown	0.5698
M5005_Spy1278	SpM12_ChORF301 71_s_at	-0.01	0.9868	-		Hypothetical protein	Unknown	0.6743
M5005_Spy0712	SpM1_ChORF0910_s_at	-0.01	0.9874	*parC*	SPy0910	Topoisomerase IV subunit A (EC 5.99.1.-)	Information processing	0.5977

M5005_gene	RML Probeset	*T* -statistic *	Empirical *P* -value †	Gene	Synonym	Description	Function	Q-value (Strain) ‡
M5005_Spy1787	SpM18_ChORF2161_s_at	0.01	0.9892	-	spyM18_2161	Glyoxalase family protein	Cellular processing	0.3368
M5005_Spy1695	SpM1_ChORF1988_s_at	-0.01	0.9894	-	SPy1988	Ribosomal protein L11 methyltransferase (EC 2.1.1.-)	Protein synthesis	0.6643
M5005_Spy1470	SpM1_ChORF1728_s_at	0.01	0.991	-	SPy1728	Protein ecsB	Membrane transport	0.4854
M5005_Spy1489	SpM1_ChORF1748_s_at	0.01	0.991	*fabF*	SPy1748	3-oxoacyl-[acyl-carrier-protein] synthase (EC 2.3.1.41)	Lipid metabolism	0.5874
M5005_Spy0732	SpM1_ChORF0931_s_at	0.01	0.9919	-	SPy0931	NIF3-related protein	Information processing	0.6382
M5005_Spy0480	SpM12_ChORF2201_s_at	-0.01	0.9928	-		Transcription accessory protein (S1 RNA binding domain)	Cellular processing	0.4544
M5005_Spy0308	SpM1_ChORF0366_s_at	0.00	0.9958	-	SPy0366	Hypothetical cytosolic protein	Unknown	0.5696
M5005_Spy0424	SpM1_ChORF0514_s_at	0.00	0.9959	*ccpA*	SPy0514	Catabolite control protein A	Information processing	0.3002
M5005_Spy0119	SpM1_ChORF0140_s_at	0.00	0.9973	-	SPy0140	Acetyl-CoA acetyltransferase (EC 2.3.1.9)	Cell wall metabolism	0.5176
M5005_Spy1471	SpM1_ChORF1729_s_at	0.00	0.9982	-	SPy1729	ABC-type transporter ATP-binding protein ecsA	Membrane transport	0.4077
M5005_Spy0369	SpM1_ChORF0454_s_at	0.00	0.9993	*mtsB*	SPy0454	Manganese transport system ATP-binding protein mntA	Membrane transport	0.6532
M5005_Spy0030	SpM1_ChORF0033_s_at	0.00	0.9996	*purE*	SPy0033	Phosphoribosylaminoimidazole carboxylase catalytic subunit (EC 4.1.1.21)	Nucleotide metabolism	0.6184
M5005_Spy0035	SpM1_ChORF0038_s_at	4.55	**<0.0001**	*ruvB*	SPy0038	Holliday junction DNA helicase	Cellular processing	0.1619
M5005_Spy0055	SpM1_ChORF0062_s_at	4.08	**<0.0001**	*rplX*	SPy0062	LSU ribosomal protein L24P	Protein synthesis	0.3154
M5005_Spy0092	SpM1_ChORF0107_s_at	-2.40	**<0.0001**	-	SPy0107	ComG operon protein 6	Unknown	0.4334
M5005_Spy0115	SpM1_ChORF0136_s_at	-7.57	**<0.0001**	-	SPy0136	Hypothetical protein	Unknown	6.6E-10
M5005_Spy0140	SpM1_ChORF0166_s_at	-2.76	**<0.0001**	-	SPy0166	Hypothetical protein	Unknown	0.0949
M5005_Spy0150	SpM1_ChORF0176_s_at	-3.65	**<0.0001**	-	SPy0176	PTS system, 3-keto-L-gulonate specific IIA component (EC 2.7.1.69)	Membrane transport	0.0006
M5005_Spy0168	SpM5_ChORF270b541_x_at	-2.64	**<0.0001**	-		Transposase	Mobile genetic element	0.1827
M5005_Spy0283	SpM1_ChORF0337_s_at	-6.41	**<0.0001**	*covS*	SPy0337	Two-component histidine kinase CovS (CsrS)	Signal transduction	5.6E-07

M5005_gene	RML Probeset	*T* -statistic *	Empirical *P* -value †	Gene	Synonym	Description	Function	Q-value (Strain) ‡
M5005_Spy0301	SpM1_ChORF0358_s_at	3.90	**<0.0001**	-	SPy0358	Integral membrane protein	Unknown	0.0713
M5005_Spy0524	SpM1_ChORF0636_s_at	-3.14	**<0.0001**	*idnO*	SPy0636	Gluconate 5-dehydrogenase (EC 1.1.1.69) Reaction: D-gluconate + NAD(P)+ = 5-dehydro-D-gluconate + NAD(P)H + H+	Carbohydrate metabolism	0.0048
M5005_Spy0525	SpM1_ChORF0637_s_at	-3.94	**<0.0001**	-	SPy0637	Galactose-6-phosphate isomerase LacB subunit (EC 5.3.1.26)	Carbohydrate metabolism	2.3E-05
M5005_Spy0526	SpM18_ChORF0701_s_at	-3.38	**<0.0001**	-	spyM18_0701	2-dehydro-3-deoxygluconokinase (EC 2.7.1.45) Reaction: ATP + 2-dehydro-3-deoxy-D-gluconate = ADP + 6-phospho-2-dehydro-3-deoxy-D-gluconate	Carbohydrate metabolism	0.0019
M5005_Spy0545	SpM1_ChORF0716_s_at	-4.30	**<0.0001**	*agaS*	SPy0716	Galactosamine-6-phosphate deaminase (isomerizing) (EC 3.5.99.-)	Carbohydrate metabolism	6.4E-06
M5005_Spy0557	SpM1_ChORF0732_at	-2.76	**<0.0001**	-	SPy0732	Transposase	Mobile genetic element	0.1619
M5005_Spy0559	SpM12_ChORF262 5_s_at	-5.23	**<0.0001**	-		Transcriptional regulator	Unknown	2.9E-06
M5005_Spy0562	SpM1_ChORF0738_at	-5.16	**<0.0001**	*sagA*	SPy0738	Streptolysin S precursor; pleiotropic effector locus	Virulence	5.5E-05
M5005_Spy0563	SpM1_ChORF0739_s_at	-4.07	**<0.0001**	*sagB*	SPy0739	Streptolysin S biosynthesis protein SagB	Protein synthesis	5.5E-05
M5005_Spy0564	SpM1_ChORF0740_s_at	-5.35	**<0.0001**	*sagC*	SPy0740	Streptolysin S biosynthesis protein SagC	Protein synthesis	1.2E-05
M5005_Spy0565	SpM1_ChORF0741_s_at	-4.81	**<0.0001**	*sagD*	SPy0741	Streptolysin S biosynthesis protein SagD	Protein synthesis	3.5E-05
M5005_Spy0566	SpM1_ChORF0742_s_at	-3.57	**<0.0001**	*sagE*	SPy0742	Streptolysin S putative self-immunity protein SagE	Protein synthesis	0.0006
M5005_Spy0567	SpM1_ChORF0743_s_at	-5.15	**<0.0001**	*sagF*	SPy0743	Streptolysin S biosynthesis protein SagF	Protein synthesis	1.9E-05
M5005_Spy0568	SpM1_ChORF0744_s_at	-5.08	**<0.0001**	*sagG*	SPy0744	Streptolysin S export ATP-binding protein SagG	Membrane transport	8.0E-06
M5005_Spy0568	SpM12_ChORF262 15_s_at	-4.11	**<0.0001**	*sagG*		Streptolysin S export ATP-binding protein SagG	Membrane transport	0.0003
M5005_Spy0569	SpM1_ChORF0745_s_at	-4.94	**<0.0001**	*sagH*	SPy0745	Streptolysin S export transmembrane protein SagH	Membrane transport	6.7E-06

M5005_gene	RML Probeset	*T* -statistic *	Empirical *P* -value †	Gene	Synonym	Description	Function	Q-value (Strain) ‡
M5005_Spy0570	SpM12_ChORF205·1_s_at	-4.91	**<0.0001**	*sagI*		Streptolysin S export transmembrane protein SagI	Membrane transport	1.3E-05
M5005_Spy0694	SpM1_ChORF0888_s_at	6.82	**<0.0001**	*clpL*	SPy0888	ATP-dependent protease ATP-binding subunit clpL	Stress adaptation	0.0004
M5005_Spy0970	SpM1_ChORF1259_s_at	3.31	**<0.0001**	-	SPy1259	NAD-dependent K+ or Na+ uptake system component / Transcriptional regulator, GntR family	Cellular processing	0.1005
M5005_Spy0975	SpM1_ChORF1264_s_at	5.21	**<0.0001**	-	SPy1264	Hypothetical protein	Unknown	0.2905
M5005_Spy1106	SpM1_ChORF1357_s_at	-5.24	**<0.0001**	*grab*	SPy1357	Protein G-related alpha 2M-binding protein	Virulence	3.1E-07
M5005_Spy1143	SpM1_ChORF1402_s_at	-5.90	**<0.0001**	-	SPy1402	Hypothetical protein	Unknown	6.8E-07
M5005_Spy1143	SpM1_ChORF1404_s_at	-5.32	**<0.0001**	-	SPy1404	Hypothetical protein	Unknown	1.6E-06
M5005_Spy1144	SpM3_ChORF1070_s_at	-6.05	**<0.0001**	-	spyM3_1070	Hypothetical protein	Unknown	3.1E-07
M5005_Spy1144	SpM1_ChORF1405_s_at	-5.89	**<0.0001**	-	SPy1405	Hypothetical protein	Unknown	1.6E-06
M5005_Spy1240	SpM1_ChORF1509_s_at	5.47	**<0.0001**	*clpE*	SPy1509	ATP-dependent clp protease ATP-binding subunit clpE	Stress adaptation	0.0465
M5005_Spy1289	SpM1_ChORF1565_s_at	-3.14	**<0.0001**	-	SPy1565	Hypothetical protein	Unknown	0.0132
M5005_Spy1497	SpM1_ChORF1759_s_at	4.43	**<0.0001**	*dnaJ*	SPy1759	Chaperone protein DnaJ	Stress adaptation	0.0803
M5005_Spy1498	SpM1_ChORF1760_s_at	8.54	**<0.0001**	*dnaK*	SPy1760	Chaperone protein DnaK	Stress adaptation	1.4E-05
M5005_Spy1499	SpM1_ChORF1761_s_at	8.57	**<0.0001**	*grpE*	SPy1761	Chaperone protein GrpE	Stress adaptation	4.2E-06
M5005_Spy1500	SpM1_ChORF1763_s_at	8.49	**<0.0001**	*hrcA*	SPy1763	Heat-inducible, Class I Heat shock transcriptional repressor	Information processing	1.4E-05
M5005_Spy1531	SpM1_ChORF1801_s_at	-8.03	**<0.0001**	*isp2*	SPy1801	Immunogenic secreted protein	Virulence	5.3E-11
M5005_Spy1569	SpM1_ChORF1849_s_at	4.94	**<0.0001**	*pfl*	SPy1849	Formate acetyltransferase (EC 2.3.1.54) acetyl-CoA + formate = CoA + pyruvate	Carbohydrate metabolism	0.1901
M5005_Spy1669	SpM1_ChORF1958_s_at	-2.32	**<0.0001**	*def*	SPy1958	Peptide deformylase (EC 3.5.1.88)	Cellular processing	0.1497
M5005_Spy1684	SpM1_ChORF1979_at	-4.64	**<0.0001**	*ska*	SPy1979	Streptokinase	Virulence	3.3E-06

M5005_gene	RML Probeset	*T* -statistic *	Empirical *P* -value †	Gene	Synonym	Description	Function	Q-value (Strain) ‡
M5005_Spy1732	SpM12_ChORF2654_s_at	-7.35	**<0.0001**	-		Protein export protein prsA precursor	Unknown	6.6E-10
M5005_Spy1733	SpM12_ChORF2213_s_at	-12.25	**<0.0001**	-		Hypothetical protein	Unknown	3.2E-15
M5005_Spy1734	SpM12_ChORF2212_s_at	-15.87	**<0.0001**	-		Streptopain precursor fragment	Unknown	4.5E-17
M5005_Spy1735	SpM1_ChORF2039_s_at	-16.23	**<0.0001**	*speB*	SPy2039	Pyrogenic toxin superantigen exotoxin B (EC 3.4.22.10)	Virulence	1.1E-17
M5005_Spy1736	SpM1_ChORF2040_at	-9.73	**<0.0001**	-	SPy2040	Hypothetical protein	Unknown	9.9E-14
M5005_Spy1738	SpM1_ChORF2043_s_at	-7.10	**<0.0001**	*sda*	SPy2043	Streptodornase (EC 3.1.21.1)	Virulence	2.5E-06
M5005_Spy1761	SpM1_ChORF2070_s_at	5.72	**<0.0001**	*groEL*	SPy2070	60 kDa chaperonin GroEL	Stress adaptation	0.0006
M5005_Spy1762	SpM1_ChORF2072_s_at	4.80	**<0.0001**	*groES*	SPy2072	10 kDa chaperonin GroES	Stress adaptation	0.0001
M5005_Spy1836	SpM1_ChORF2183_s_at	3.79	**<0.0001**	*rplI*	SPy2183	LSU ribosomal protein L9P	Protein synthesis	0.0256
M5005_Spy1851	SpM1_ChORF2200_s_at	-3.29	**<0.0001**	*hasA*	SPy2200	Hyaluronan synthase (EC 2.4.1.212)	Carbohydrate metabolism	0.0021

*Student's *t* -statistic calculated as local statistic measuring the association between expression estimate and treatment (strain).

†Bold text denotes genes with empirical P-value < 0.01 (derived from 10,000 permutations) and Benjamini-Yekutieli FDR < 0.05.

‡Bootstrapped Q-values assessing the treatment (strain) effect in RMLChip expression microarrays using ANOVA model (from Supplementary Table 3).

Supplementary Table 7. Qualitative assessment of immunohistochemical reactivity for mouse tissues with polyclonal antisera raised against Group A streptococcal antigens during GAS infection.

M5005_gene	Gene	Synonym[*]	Description	GAS Compartment [†]	Transcript Rank (WT) [‡]	Transcript Rank (Mutant) [‡]	Fold Change (Mutant : WT)[§]	IHC (WT)[**,††]	IHC Mutant[**,††]
-	-	-	Anti-Peptide X, (Isotype-matched Control Antibody)	N/A	N/A		N/A	–	–
M5005_Spy0271	-	*spy0319*	ABC transporter substrate-binding protein	Surface	366	425	1.11	–	–
M5005_Spy0342	*prtS*	*spy0416*	Putative cell envelope proteinase (*SPy*CEP) (EC 3.4.21.96)	Surface	97	129	0.72	–	–
M5005_Spy0368	*mtsA*	*spy0453*	Putative manganese-binding ABC transporter	Surface	88	111	1.36	–	–
M5005_Spy0668	*ideS, mac*	*spy0861*	Extracellular, IgG-degrading endoglycosidase	Extracellular	1780	1602	1.25	–	–
M5005_Spy0942	-	*spy1228*	Putative nucleoside-binding lipoprotein	Surface	189	150	1.08	–	+
M5005_Spy0955	*pstS*	*spy1245*	Putative phosphate-binding lipoprotein	Surface	411	339	2.93	–	–
M5005_Spy0996	*speA2*	N/A	Streptococcal Pyrogenic Toxin Superantigen (PTSAg) SpeA, A2 allele	Extracellular	1035	710	1.46	+	+
M5005_Spy1058	*malE*	*spy1294*	Putative maltodextrin-binding protein	Surface	561	405	1.18	+++	+++
M5005_Spy1133	*prsA*	*spy1390*	Proteinase maturation protein	Surface	121	104	1.16	+	++
M5005_Spy1308	-	*spy1592*	Putative oligosaccharide-binding protein	Surface	33	23	1.21	+	+
M5005_Spy1528	*htsA, siaA*	*spy1795*	Heme-binding lipoprotein	Surface	984	977	0.49	–	–
M5005_Spy1529	*shp*	*spy1796*	Heme-binding lipoprotein	Surface	1576	1575	0.98	–	±
M5005_Spy1704	*dppA*	*spy2000*	Dipeptide-binding protein	Surface	47	167	0.36	–	–

M5005_gene	Gene	Synonym*	Description	GAS Compartment †	Transcript Rank (WT) ‡	Transcript Rank (Mutant) ‡	Fold Change (Mutant : WT)§	IHC (WT)**,††	IHC Mutant**,††
M5005_Spy1711	*lmb*	*spy2007*	Laminin-binding protein	Surface	192	215	1.24	–	+
M5005_Spy1713	*fba*	*spy2009*	Putative surface protein	Surface	1022	1380	1.28	–	–
M5005_Spy1718	*sic 1.01*	*spy2016*	Streptococcal Inhibitor of Complement	Extracellular	1	3	1.46	++	+

*Synonym in M1 SF370, M3 MGAS315 or M18 MGAS8232 GAS strains.

†Predicted Cellular Localization according to psortb (available at: http://www.psort.org/genomes/genomes.pl)

‡Transcript rank for most abundant transcript is valued at 1. Rank increases arithmetically with decreasing transcript detection, according to the normalized expression estimates.

§Fold change calculated on the square of the normalized expression estimates.

**IHC results qualitatively assessed (-, no reactivity; ±, minimal reactivity; +, low-level reactivity; ++, mid-level reactivity; +++, high-level reactivity).

††Expression microarray (transcript) results obtained 53 hr postinoculation. IHC (protein) results obtained 48 h postinoculation.

Supplementary Table 8. GAS wild-type transcripts correlated with cutaneous lesion volume during soft-tissue infection expression profiling.

M5005_gene	RML Probeset	Gene	*P* -value (lesion volume) *	*Q* -value (lesion volume) †	Description	Function	Synonym ‡
M5005_Spy1507	SpM1_ChORF1771_s_at	*gatA*	1.2E-07	0.0003	Aspartyl/glutamyl-tRNA(Asn/Gln) amidotransferase subunit A (EC 6.3.5.-)	Protein synthesis	SPy1771
M5005_Spy0173	SpM1_ChORF0201_s_at	-	1.1E-06	0.0014	Integral membrane protein	Unknown	SPy0201
M5005_Spy1229	SpM1_ChORF1496_s_at	*argR1*	1.2E-05	0.0102	Arginine repressor, argR	Information processing	SPy1496
M5005_Spy0416	SpM1_ChORF0505_s_at	-	3.9E-05	0.0176	Glutaminyl-peptide cyclotransferase (EC 2.3.2.5)	Unknown	SPy0505
M5005_Spy0678	SpM1_ChORF0872_s_at	-	3.5E-05	0.0176	5'-nucleotidase (EC 3.1.3.5)	Unknown	SPy0872
M5005_Spy1720	SpM1_ChORF2019_s_at	*mga*	4.2E-05	0.0176	Multiple gene activator; Trans-acting positive transcriptional regulator	Information processing	SPy2019
M5005_Spy0073	SpM5_ChORF270b-605_s_at	-	0.0001	0.0185	Hypothetical protein	Unknown	
M5005_Spy1804	SpM1_ChORF2121_s_at	*mutL*	0.0001	0.0230	DNA mismatch repair protein mutL	Information processing	SPy2121
M5005_Spy1131	SpM1_ChORF1386_s_at	-	0.0001	0.0270	Transcriptional regulator, Cro/CI family	Information processing	SPy1386
M5005_Spy0621	SpM1_ChORF0806_s_at	*rplT*	0.0001	0.0338	LSU ribosomal protein L20P	Protein synthesis	SPy0806
M5005_Spy1474	SpM12_ChORF299-19_s_at	*lytR*	0.0001	0.0341	Transcriptional regulator, LytR family	Information processing	
M5005_Spy0387	SpM1_ChORF0472_s_at	-	0.0002	0.0415	Uracil DNA glycosylase superfamily protein	Information processing	SPy0472
M5005_Spy0993	SpM1_ChORF1287_s_at	-	0.0002	0.0415	ABC transporter permease protein	Membrane transport	SPy1287
M5005_Spy1225	SpM1_ChORF1493_s_at	-	0.0002	0.0415	Lipase/Acylhydrolase with GDSL-like motif	Unknown	SPy1493
M5005_Spy1665	SpM1_ChORF1955_s_at	-	0.0002	0.0415	Hypothetical protein	Cellular processing	SPy1955
M5005_Spy1136	SpM1_ChORF1393_s_at	*pepB*	0.0003	0.0491	Oligoendopeptidase F (EC 3.4.24.-)	Amino acid metabolism	SPy1393
M5005_Spy1474	SpM1_ChORF1733_s_at	*lytR*	0.0003	0.0491	Transcriptional regulator, LytR family	Information processing	SPy1733
M5005_Spy0034	SpM49_ChORF8094-24_s_at	-	0.0004	0.0499	Transcriptional regulator	Information processing	
M5005_Spy0461	SpM1_ChORF0558_s_at	-	0.0004	0.0499	Hypothetical cytosolic protein	Unknown	SPy0558

*Statistical assessment of correlation in RMLChip expression microarray dataset.

†Bootstrapped Q-values assessing correlation in RMLChip expression microarray dataset.
‡Synonym in M1 SF370, M3 MGAS315 or M18 MGAS8232 GAS strains.

Supplementary Table 9. Summary of Group A streptococcal pathogenicity-associated factors.

M5005 Spy#	Gene	Synonym	Description	Function	References*
0141	*slo*	Spy0167	Streptolysin O	Oxygen-labile cytolytic activity for many eukaryotic cells types	64-66
0351	*spyCEP*	Spy0428	*S. pyogenes* cell envelope proteinase	Human IL-8-cleavage, preventing translocation and recruitment of neutrophils	30
0351	*spyA*	Spy0428	C3 family ADP-ribosyltransferase	Loss of actin cytoskeletal structures	32
0562	*sagA, pel*	Spy0738	Streptolysin S	Potent oxygen-stable cytolysin; pleiotropic antisense RNA regulator (*pel*) of secreted and surface proteins	60-62,67-69
0996	*speA2*	N/A	Streptococcal pyrogenic toxin superantigen (PTSAg) type A	PTSAg: over stimulation of T cells resulting in proliferative cytokine response; induction of nitric oxide production	70,71
1106	*grab*	Spy1357	Protein G-related alpha 2M-binding protein, GRAB	Host α2-macroglobulin binding-mediated regulation of proteolysis; antimicrobial peptide resistance	56,72
1684	*ska*	SPy1979	Streptokinase	Activation of host blood clot-dissolving plasminogen	73,74
1711	*lbp*	SPy2007	Laminin-binding protein	Adhesion to host epithelial cells	31,75
1715	*scpA*	Spy2010	C5a peptidase	Cleavage of serum chemotaxin C5a; retards chemotaxis of PMNs	76
1718	*sic1.01*	Spy2016	Streptococcal Inhibitor of Complement	Inactivation of antimicrobial peptides (AMPs)	57,58,77
1719	*emm1.0*	Spy2018	Emm1 protein	Evasion of phagocytosis; inhibition of complement deposition; adherence to host cells; complexes with fibrinogen to promote vascular leakage	52,78-80
1735	*speB*	Spy2039	Streptococcal pyrogenic toxin superantigen (PTSAg) type B	Cysteine protease	19,52,54,55,81,82
1738	*spd, sda*	SPy2043	Streptodornase	Extracellular DNase; possible degradation of neutrophil extracellular traps (NET) that bind bacteria for localized killing by neutrophil granules contents	17,59,
1851-53	*hasABC*	Spy2200-02	Hyaluronic acid capsule	Oxygen and phagocytosis resistance; CD-44 mediated adherence to host cells	83,84

* See main article for complete references.