Supplementary Table 1. Transcriptional response to relaxation by novobiocin, genes listed by chromosomal location

R6 locus	**Protein**[a]	**Cluster**	**Relative fold variation at**[b]					
			0,5 x MIC			**40 x MIC**		
			5’	**15’**	**30’**	**5’**	**15’**	**30’**
spr0002	DNA polymerase III beta-subunit	**1**	2.05	2.19	2.01	2.32	3.02	3.00
spr0003	Hypothetical protein	**1**	2.37	2.85		2.38	3.53	3.72
spr0004	Conserved hypothetical protein	**1**		2.02			2.83	3.04
spr0005	Peptidyl-tRNA hydrolase	**1**	2.40	2.80		2.38	5.36	6.06
spr0006	Transcription-repair coupling factor	**1**					2.33	2.30
spr0007	Conserved hypothetical protein	**1**	2.06	2.28		2.01	4.07	4.17
spr0008	Hypothetical protein	**1**					3.13	3.35
spr0009	Conserved hypothetical protein	**1**				2.03	3.34	3.46
spr0010	Conserved hypothetical protein	**1**	2.66	2.81		2.88	6.53	6.96
spr0011	Hypoxanthine guanine P-ribosyltransferase	**1**	2.45	2.73	2.06	2.41	5.52	5.69
spr0012	Cell-division protein /general stress protein	**1**	2.16	2.39			3.12	3.26
spr0013	Competence-specific transcription modulator	**1**	2.31	2.77	2.13		2.00	
spr0017	Degenerate transposase (orf2)	**1**					2.67	2.92
spr0018	Degenerate transposase (orf2)	**1**		2.04			3.33	4.01
spr0019	Degenerate transposase (orf1)	**1**		2.04			3.27	3.92
spr0028	P-ribosylpyrophosphate synthase	**2**	-3.13	-2.76				
spr0029	Degenerate transposase (orf1)	**2**	-2.95	-2.87		-3.43	-2.83	
spr0030	Hypothetical protein	**2**	-3.01	-4.05		-3.09	-5.27	-4.08
spr0031	Hypothetical protein	**2**	-2.99	-4.23		-2.45	-3.71	-2.29
spr0032	DNA polymerase I	**2**	-5.27	-5.61				
spr0033	Conserved hypothetical protein	**2**	-5.35	-4.64				
spr0034	Conserved hypothetical protein	**2**	-3.37	-2.21				
spr0035	Aspartate aminotransferase	**2**	-3.08	-2.72				
spr0036	Conserved hypothetical protein	**2**	-2.74	-2.56				
spr0037	Involved in fatty acid/phospholipid synthesis	**2**	-2.40	-2.54				
spr0038	Acyl carrier protein	**2**	-2.13	-2.37				
spr0039	Degenerate transposase (orf2)	**2**					2.30	2.17
spr0040	Amphipathic pore-forming peptide precursor	**2**	-2.22	-2.06				
spr0041	Transposase (orf2)	**2**	-3.68	-3.92				
spr0044	Transport protein ComB	**2**	-2.25	-2.04				
spr0045	P-ribosylaminoimidazole-succinocarboxamide synthetase				6.41			
spr0046	P-ribosylformylglycinamide synthetase				7.62			2.52
spr0047	Amido-P-ribosyl transferase				3.88			2.14
spr0048	P-ribosylaminoimidazole synthetase				3.15			2.00
spr0049	5-P-ribosylglycinamide transformylase 1				4.75			2.28
spr0050	Teicoplanin resistance protein				5.90		3.06	2.89
spr0051	P-ribosylaminoimidazolecarboxamide formyltransferase				4.80		2.09	2.14
spr0052	P-ribosylglycinamide synthetase				5.24	3.86	3.98	3.33
spr0053	P-ribosylaminoimidazole carboxylase				2.71	3.09	3.05	2.82
spr0054	P-ribosyl glucinamide formyltransferase				3.11	3.07	3.20	2.84
spr0067	Conserved hypothetical protein					-2.09	-2.68	-2.64
spr0068	Conserved hypothetical protein		-2.71	-2.07			-2.73	-2.40
spr0069	Hypothetical protein		-2.97	-2.76				
spr0070	Trk transporter membrane-spanning protein - K+		-2.70	-2.24				
spr0071	Trk transporter NAD+ binding protein - K+		-2.13					
spr0072	Conserved hypothetical protein		-2.18					
spr0073	Hypothetical protein			-2.04				
spr0074	Hypothetical protein			-2.05				
spr0081	ABCT membrane-spanning permease - sugar						4.77	6.92
spr0082	ABCT membrane spanning permease - sugar						3.74	6.52
spr0083	ABCT solute binding protein - sugar							2.35
spr0089	Conserved hypothetical protein		-2.11					
spr0090	Conserved hypothetical protein		-2.69	-2.47				

spr0092	CapD protein, biosynthesis of type 1 capsule		-2.09	-2.21				
spr0102	Argininosuccinate synthase			-2.35				
spr0103	Arginine succinate lyase		-2.04	-2.38				
spr0115	Hypothetical protein						2.27	2.05
spr0117	Hypothetical protein						2.36	2.19
spr0118	Hypothetical protein						2.40	2.22
spr0119	Hypothetical protein						2.31	2.02
spr0129	Conserved hypothetical protein	**3**		2.26			2.74	2.32
spr0130	Ribosomal protein alanine acetyltransferase	**3**					2.48	2.46
spr0132	Degenerate transposase (orf2)	**3**		2.09		2.45	3.56	4.04
spr0133	Degenerate transposase (orf2)	**3**		2.32		2.13	2.84	3.46
spr0134	Degenerative transposase	**3**					3.16	3.27
spr0135	Glycosyltransferase, exopolysaccharide synthesis	**3**					2.89	2.70
spr0136	Glycosyl transferase	**3**					3.81	3.31
spr0137	ABCT ATP-binding/membrane spanning permease	**3**		2.01		2.16	4.12	4.04
spr0139	UDP-glucose DH	**3**					2.77	2.67
spr0140	Positive transcriptional regulator of mutA	**3**					2.49	2.56
spr0141	Hypothetical protein	**3**						2.03
spr0142	Hypothetical protein	**3**					3.04	3.13
spr0143	Hypothetical protein	**3**					2.26	2.43
spr0144	Conserved hypothetical protein	**3**		2.07		2.43	3.63	4.63
spr0145	Hypothetical protein	**3**	2.60	3.21		2.80	5.02	7.25
spr0146	ABCT, substrate-binding protein - amino acid	**3**		2.41			3.32	3.31
spr0147	ABCT, solute-binding protein	**3**	2.43	2.86		2.49	4.86	5.15
spr0148	Succinyl-diaminopimelic descuccinlyase	**3**		2.16			2.47	2.60
spr0149	ABCT, ATP-binding protein	**3**		2.20			2.82	2.94
spr0150	ABCT, membrane-spanning permease	**3**		2.59			3.04	3.30
spr0151	Hypothetical protein	**3**	2.30	2.99		2.22	4.51	5.16
spr0152	Conserved hypothetical protein	**3**	2.19	2.46		2.69	4.28	4.44
spr0153	Histidine kinase	**3**				2.59	3.21	3.39
spr0154	Response regulator	**3**	2.42	2.46		3.19	4.51	4.39
spr0155	Hypothetical protein	**3**				2.75	3.34	3.09
spr0156	Conserved hypothetical protein	**3**	2.98	2.97	2.23	4.25	6.26	5.08
spr0157	Conserved hypothetical protein	**3**	2.94	2.87		4.09	4.92	3.88
spr0158	Hypothetical protein	**3**	2.98	3.03		4.49	5.63	4.34
spr0159	Conserved hypothetical protein	**3**	2.84	2.53		4.10	5.41	4.02
spr0161	Riboflavin synthase beta chain	**3**	2.06			2.31	2.64	
spr0168	Conserved hypothetical protein	**3**	2.49	2.12		3.05	3.89	3.14
spr0170	Magnesium and cobalt transporter	**3**					2.30	2.17
spr0172	Aminopeptidase P	**3**					2.02	
spr0173	Arsenate reductase, putative	**3**					2.15	2.04
spr0174	Hypothetical protein	**3**					2.08	
spr0179	Hypothetical protein	**3**					2.33	2.27
spr0180	Cardiolipin synthase	**3**	2.21	2.64		2.37	3.43	3.55
spr0181	Orf47	**3**					2.05	
spr0208	50S Ribosomal protein L15				-2.05			
spr0210	Adenylate kinase					2.24	2.86	
spr0218	Conserved hypothetical protein						-2.09	-2.25
spr0232	Formate acetyltransferase 3	**4**	-2.15	-2.11				
spr0235	Leucyl-tRNA synthetase	**4**	-2.21				-2.07	-2.01
spr0236	Conserved hypothetical protein	**4**	-2.98	-2.49		-3.27	-2.60	-2.14
spr0237	Conserved hypothetical protein	**4**	-2.83	-2.41		-2.64	-2.22	
spr0238	Branch migration of Holliday structures	**4**	-2.48					
spr0239	Hypothetical protein	**4**	-2.16					
spr0240	Undecaprenyl diphosphate synthase	**4**	-2.03					
spr0244	6-P-beta-glucosidase	**4**					-2.16	-2.09
spr0245	L-glutamine-D-fructose-6-P amidotransferase	**4**	-5.56	-4.90		-5.65	-5.92	-4.14
spr0246	Conserved hypothetical protein	**4**	-2.56	-2.17		-3.05	-3.12	-3.01
spr0247	Alkaline amylopullulanase	**4**	-3.32	-3.21		-4.30	-4.68	-3.27
spr0251	DNA polymerase III, alpha subunit	**4**	-2.42	-2.19		-2.42	-3.38	-2.73
spr0252	Hypothetical protein	**4**	-3.01	-2.67		-3.54	-3.57	-3.63
spr0253	Conserved hypothetical protein	**4**	-3.83	-3.73		-4.46	-4.35	-3.49
spr0254	Aminopeptidase	**4**	-3.97	-4.43	-2.19		-5.51	-4.24
spr0255	Conserved hypothetical protein	**4**	-3.40	-3.27		-4.69	-4.78	-3.96

spr0256	Ribosomal small subunit pseudouridine synthase A	**4**	-2.02			-2.09	-2.47	-2.68
spr0257	Hypothetical protein	**4**		-2.07				
spr0258	Aminopeptidase C	**4**		-3.11			-2.89	-3.20
spr0259	PTS, mannose-specific EIID	**4**		-3.88	-2.32			-2.08
spr0260	PTS, mannose-specific EIIC	**4**	-2.12	-5.33	-2.39			-2.92
spr0261	PTS, mannose-specific EIIAB	**4**	-2.55	-3.72		-2.55	-3.83	-3.18
spr0262	Alcohol DH, propanol-preferring	**4**	-3.00	-2.94		-4.66	-4.02	-2.86
spr0263	Conserved hypothetical protein	**4**	-7.26	-4.31		-8.46	-8.13	-5.79
spr0264	Conserved hypothetical protein	**4**				-3.32	-4.18	-3.51
spr0265	Conserved hypothetical protein	**4**				-3.06	-4.07	-3.61
spr0266	Dihydropteroate synthase	**4**	-2.17	-4.11		-5.40	-7.37	-6.44
spr0267	Dihydrofolate synthetase	**4**	-2.78	-4.70		-4.03	-6.47	-6.03
spr0268	GTP cyclohydrolase	**4**	-2.51	-4.15		-3.44	-5.79	-5.76
spr0269	Aldolase-pyro-P-kinase	**4**	-2.31	-3.09		-3.40	-3.98	-4.64
spr0270	Hypothetical protein	**4**				-4.94	-3.91	-4.00
spr0271	50S Ribosomal protein L13	**4**						-2.76
spr0272	30S Ribosomal protein S9	**4**						-3.03
spr0284	Alpha-xylosidase		-2.20			-2.04	-2.45	-2.34
spr0309	Hypothetical protein		-2.23			-2.13	-2.28	-2.01
spr0318	Type 2 capsule		-2.40	-2.54	-2.07		-2.26	-2.21
spr0319	Type 2 capsule		-2.41	-2.69	-2.21		-2.50	-2.58
spr0320	Type 2 capsule		-2.87	-3.42	-2.67		-3.31	-3.02
spr0321	Type 2 capsule		-3.00	-3.48	-2.86		-3.04	-2.96
spr0322	dTDP-glucose-4,6-dehydratase		-2.95	-3.37	-2.72		-3.03	-3.12
spr0323	dTDP-L-rhamnose synthase			-2.26				-2.15
spr0327	ABCT, substrate-binding protein – oligopeptide		-2.30	-2.47	-2.42		-4.20	-3.97
spr0337	Choline-binding protein F						2.18	
spr0392	Elongation factor P						2.26	2.18
spr0397	Conserved hypothetical protein						2.43	2.05
spr0398	50S Ribosomal protein L28						2.60	
spr0401	Acetolactate synthase large subunit			-2.06			-2.08	-2.48
spr0402	Acetolactate synthase small subunit			-2.30				-2.38
spr0416	Hypothetical protein	**5**				2.06	3.87	2.76
spr0417	Conserved hypothetical protein	**5**				2.16	4.02	3.23
spr0418	Hypothetical protein	**5**				2.20	4.11	2.55
spr0419	Hypothetical protein	**5**				2.39	3.64	3.21
spr0420	Xylose repressor protein	**5**				2.00	2.96	2.35
spr0421	PTS, sugar-specific EII component	**5**				2.33	4.38	3.87
spr0422	Hypothetical protein	**5**				2.35	3.62	3.19
spr0423	PTS, sugar-specific EII component	**5**				2.15	3.49	3.17
spr0424	P-beta-D-galactosidase	**5**					3.05	2.70
spr0425	PTS, sugar-specific EII component	**5**					2.11	
spr0428	Conserved hypothetical protein	**5**					2.56	2.46
spr0429	Conserved hypothetical protein	**5**					2.87	2.79
spr0430	ABCT, ATP-binding protein – cobalt	**5**					2.02	2.00
spr0431	ABCT, membrane-spanning permease	**5**		2.31		2.18	3.99	4.07
spr0432	rRNA methylase	**5**	3.47	3.58		4.51	10.86	10.75
spr0437	RNA polymerase delta subunit	**5**				2.05	2.48	2.30
spr0440	Hypothetical protein	**5**					2.64	2.72
spr0442	Hypothetical protein	**5**		2.08			2.51	2.23
spr0445	Type I restriction enzyme	**5**	2.05	2.09		3.10	4.67	2.87
spr0446	Type I restriction enzyme EcoKI specificity protein	**5**	2.17	2.24		3.22	4.42	3.10
spr0447	Integrase/recombinase	**5**	2.40			3.38	4.78	4.09
spr0448	Type I site-specific deoxyribonuclease chain S	**5**				2.23	2.72	2.29
spr0449	EcoE type I restriction-modification, M subunit	**5**				2.08	2.27	2.21
spr0450	EcoA type I restriction-modification, R subunit	**5**				2.10	2.33	2.24
spr0451	Hypothetical protein	**5**					2.69	2.60
spr0452	Hypothetical protein	**5**				2.64	4.60	4.65
spr0456	Heat-shock protein	**5**					2.12	2.00
spr0457	Hypothetical protein	**5**		2.15		2.49	3.13	4.19
spr0458	Conserved hypothetical protein	**5**	2.47	2.86	3.05	3.30	4.74	7.47
spr0459	ABCT, ATP-binding protein	**5**		2.13	2.26	2.19	2.69	3.69
spr0461	Hypothetical protein	**5**		2.09	2.63		2.78	3.46
spr0465	Bacteriocin-like peptide	**5**	2.33	2.40	2.06			

spr0469	Conserved hypothetical protein	**5**			2.36		3.04	3.70
spr0470	Hypothetical protein	**5**		2.26			3.20	3.14
spr0471	Hypothetical protein	**5**					2.75	2.55
spr0474	ABCT, ATP binding protein	**5**					2.14	2.16
spr0475	Conserved hypothetical protein	**5**					2.11	2.28
spr0476	Conserved hypothetical protein	**5**	2.74	3.83	3.07	3.11	5.51	7.49
spr0477	Conserved hypothetical protein	**5**	2.16	2.51	2.13	2.87	4.08	4.55
spr0481	Initiation factor IF2	**5**					2.17	2.30
spr0482	Ribosome binding factor A	**5**	2.82	3.56		4.72	7.27	8.25
spr0483	Conserved hypothetical protein	**5**						2.61
spr0484	Hypothetical protein	**5**					2.19	2.34
spr0489	Hypothetical protein						-2.60	-3.16
spr0490	Conserved hypothetical protein			-2.06			-2.95	-3.90
spr0491	Hypothetical protein						-2.28	-3.06
spr0492	Valyl-tRNA synthetase							-2.36
spr0494	Hypothetical protein							-2.14
spr0507	Phe-tRNA synthetase alpha chain						-2.13	-2.92
spr0508	Conserved hypothetical protein							-2.54
spr0509	Phe-tRNA synthetase beta chain							-2.45
spr0511	Degenerate transposase						-2.06	-2.07
spr0514	Tetrahydropteroyl triGlu methyltransferase						-2.48	-2.73
spr0515	5,10-methylenetetrahydrofolate reductase				-2.10		-2.12	-2.54
spr0525	ABCT, ATP-binding protein - peptide					2.47	2.16	
spr0526	ABCT, membrane-spanning permease - peptide					2.63	2.33	2.12
spr0527	Peptide which is the signal sensed by VncR/S		2.00			3.43	3.98	2.80
spr0528	VncR, response regulator					2.20	2.05	
spr0531	Hypothetical protein		2.40	2.90	2.09	2.63	3.43	4.06
spr0532	ABCT, membrane-spanning permease – Gln			2.28				2.04
spr0537	Single-stranded DNA-specific exonuclease						-2.27	-2.31
spr0542	Hypothetical protein				2.01			
spr0562	PTS, sugar-specific EII component						2.87	3.01
spr0563	Hypothetical protein						2.61	3.16
spr0594	Conserved hypothetical protein						2.79	2.46
spr0599	Hypothetical protein				-2.00			
spr0607	Hypothetical protein					2.26	2.95	
spr0608	Hypothetical protein					2.63	3.62	2.38
spr0610	ABCT, ATP-binding protein					2.36	2.73	2.31
spr0611	Hypothetical protein					2.92	3.05	
spr0613	Orotidine-5-decarboxylase			-2.02	-2.23			
spr0614	Orotate P-ribosyltransferase			-2.14	-2.23			
spr0623	ABCT, membrane-spanning permease – Gln							2.61
spr0624	ABCT, membrane-spanning permease –Gln							2.28
spr0625	Lactate oxidase							2.49
spr0644	Degenerate transposase	**6**	2.38	2.30		2.54	2.82	2.84
spr0645	Hypothetical protein	**6**	2.05			2.56	2.90	2.71
spr0647	Mannose-6-P isomerise	**6**		2.48				
spr0655	Uracil P-ribosyltransferase	**6**	2.16	2.58		2.59	2.51	2.07
spr0656	ATP-dependent Clp protease proteolytic subunit	**6**	2.43	2.56		2.95	2.80	2.48
spr0663	ABCT, ATP-binding protein - branched chain AA	**6**	2.16					
spr0664	Conserved hypothetical protein	**6**	2.26	2.12		3.71	3.14	2.47
spr0667	Cell division protein FtsX	**6**	2.17			2.51	2.36	
spr0669	Hypothetical protein	**6**	2.24	2.06		2.75	2.45	2.31
spr0679	Peptidyl-prolyl cis-trans isomerise	**6**		2.40				
spr0683	Conserved hypothetical protein	**6**			-2.28			
spr0688	Hypothetical protein	**6**	2.18			2.58	3.07	2.61
spr0689	Hypothetical protein	**6**	2.08	2.27		2.32	2.46	2.30
spr0690	Conserved hypothetical protein	**6**		2.51				
spr0699	Conserved hypothetical protein	**6**		2.00				
spr0700	Hypothetical protein	**6**		2.50			2.34	2.18
spr0703	Hypothetical protein	**6**					2.07	
spr0707	Response regulator, transcriptional regulation	**6**				2.14	2.47	2.08
spr0709	Hypothetical protein	**6**	4.28	4.68	2.93	7.63	8.56	8.62
spr0710	Conserved hypothetical protein	**6**		2.22		2.62	2.99	2.91
spr0711	ATP-dependent DNA helicase	**6**				2.12	2.56	2.37

spr0712	Rod shape determining protein	**6**				2.12	2.18	2.10
spr0713	4-methyl-5-thiazole mono-P biosynthesis	**6**	2.15	2.06		2.79	2.98	2.78
spr0714	Phosphoglycolate phosphatase	**6**				2.40	2.66	2.48
spr0717	Transposase	**6**	2.12			2.64	3.01	2.86
spr0718	Transposase	**6**	2.32	2.24		2.52	2.81	2.77
spr0720	Hypothetical protein	**6**		2.01		2.34	2.85	2.69
spr0721	Conserved hypothetical protein	**6**	3.22	3.22		4.07	4.94	4.51
spr0738	Purine nucleoside phosphorylase		2.08					
spr0739	Modulates DNA topology			2.36	2.23			
spr0740	30S Ribosomal protein subunit S20				2.17			
spr0742	Hypothetical protein		2.25	2.38				
spr0756	Topoisomerase IV subunit B						-2.89	-2.58
spr0757	Topoisomerase IV subunit A						-2.98	-2.45
spr0758	Branched-chain-AA transaminase						-3.29	-2.81
spr0759	ABCT, substrate-binding protein - oligopeptide						-2.73	-2.42
spr0760	Conserved hypothetical protein						-2.76	-2.85
spr0761	Conserved hypothetical protein							-2.13
spr0776	D-Ala-D-Ala carboxypeptidase						-2.14	-2.24
spr0778	Transcriptional repressor of the fructose operon					-5.13	-2.57	-2.10
spr0782	Hypothetical protein					-2.47	-2.46	-2.14
spr0783	Probable pyridoxal-P dependent aminotransferase						-2.70	-2.67
spr0784	Thiamin biosynthesis protein					-2.02	-2.60	-2.62
spr0787	Hypothetical protein							-2.00
spr0794	Xaa-pro dipeptidyl-peptidase							-2.22
spr0815	Degenerate transposase						-2.46	-2.23
spr0816	Lysine decarboxylase					-2.06	-2.88	
spr0818	Degenerate transposase					-2.07	-2.60	-2.10
spr0825	Hypothetical protein				3.94			
spr0826	Hypothetical protein				4.03			
spr0841	Tranposase (orf2)						2.40	
spr0856	Competence protein	**7**	-2.48			-2.20	-3.40	-3.92
spr0857	Competence protein	**7**					-2.02	-2.19
spr0858	Hypothetical protein	**7**					-2.38	-2.94
spr0859	Hypothetical protein	**7**	-2.24				-2.75	-3.42
spr0860	Hypothetical protein	**7**					-2.29	-2.49
spr0863	50S Ribosomal protein L20	**7**			-2.25			
spr0864	Lactoylglutathione lyase	**7**			-2.20			
spr0865	Dihydroorotate DH	**7**						-3.79
spr0866	Dihydroorotate DH	**7**					-2.32	
spr0868	Fibronectin-binding protein-like protein A	**7**	-2.27				-2.42	-2.60
spr0869	Conserved hypothetical protein	**7**				-3.36	-2.69	-2.31
spr0870	Diacylglycerol kinase	**7**	-2.53	-2.25		-5.20	-3.96	-3.01
spr0871	GTPase/GTP-binding protein	**7**	-2.19			-4.22	-3.29	-2.52
spr0872	Formamidopyrimidine-DNA glycosylase	**7**	-2.11	-2.16		-3.40	-3.46	-2.70
spr0873	Conserved hypothetical protein	**7**	-2.07			-3.48	-3.23	-2.68
spr0874	Hypothetical protein	**7**	-2.00			-3.34	-3.18	-2.43
spr0875	Multi-drug resistance efflux pump	**7**				-3.38	-3.15	-2.54
spr0876	50S Ribosomal protein L33	**7**				-2.66	-2.33	-2.24
spr0877	Protein-export membrane protein secG	**7**	-2.09			-3.54	-2.81	-2.34
spr0878	Exoribonuclease R	**7**				-3.99	-2.48	
spr0879	Small protein B	**7**				-4.94	-2.68	-2.46
spr0880	Tellurite resistance	**7**				-5.20	-2.97	-2.61
spr0881	Competence protein	**7**				-3.08	-2.56	-2.55
spr0888	Regulatory protein	**7**	-2.37			-2.17	-2.16	
spr0889	Conserved hypothetical protein	**7**	-2.46			-3.65	-2.40	-2.11
spr0903	Cytochrome c-type biogenesis protein	**7**	-2.06			-4.23	-2.78	-2.24
spr0904	Conserved hypothetical protein	**7**				-3.37	-2.43	-2.15
spr0905	Cationic amino acid transporter	**7**	-2.37	-2.50	-2.70	-4.29	-3.67	-3.40
spr0906	Lipoprotein	**7**	-2.13	-2.40	-3.05	-4.02	-3.61	-4.28
spr0907	His triad protein D precursor	**7**			-2.58		-2.17	-2.96
spr0908	His triad protein E precursor	**7**			-3.46	-2.63	-2.63	-3.39
spr0913	Aminotripeptidase; tripeptidase	**7**					-2.51	-2.28
spr0914	Ferrochelatase	**7**				-3.00	-2.11	-2.48
spr0921	4-oxalocrotonate tautomerase	**7**			2.09			

spr0925	HemK protein	**7**				-3.03	-2.52	-2.21
spr0929	Hypothetical protein	**7**				-2.36	-2.23	
spr0930	Conserved hypothetical protein	**7**				-2.54	-2.25	
spr0931	Conserved hypothetical protein	**7**	-2.95	-2.31		-6.02	-4.57	-4.50
spr0932	Conserved hypothetical protein	**7**	-2.14			-4.75	-3.54	-2.83
spr0945	Hypothetical protein				2.57			
spr0946	Conserved hypothetical protein				2.35			
spr0977	ABCT, ATP-binding protein				-2.01			
spr0980	Conserved hypothetical protein				-2.01			
spr0989	UDP-N-acetylglucosamine 1-carboxyvinyl transferase	**8**	-3.91	-3.09	-2.00	-5.82	-4.15	-3.50
spr0990	Conserved hypothetical protein	**8**	-3.77	-3.63	-2.54	-2.69	-3.81	-3.95
spr0991	Conserved hypothetical protein	**8**	-2.72	-2.88			-2.73	-2.32
spr0992	Methionine aminopeptidase	**8**	-2.92	-2.85	-2.12	-2.31	-3.21	-2.65
spr0993	Degenerate transposase (orf1)	**8**				-2.18	-2.00	
spr0994	Tranposase (orf2)	**8**					2.14	2.01
spr0995	ATP-dependent DNA helicase	**8**				-2.64	-2.57	
spr0996	DNA repair protein	**8**	-2.47			-3.88	-3.62	-3.28
spr0997	Conserved hypothetical protein	**8**				-3.03	-2.90	-2.33
spr1007	Phosphate acetyltransferase	**8**				-2.92	-2.35	
spr1011	Conserved hypothetical protein	**8**				-2.56		
spr1020	Histone-like DNA-binding protein	**8**				-3.12	-3.09	-2.80
spr1021	ABCT, ATP-binding protein	**8**	-3.04	-2.08		-4.64	-3.91	-2.45
spr1022	Transcriptional regulator	**8**	-2.70	-2.00		-3.72	-3.48	-2.77
spr1023	ABCT, membrane-spanning permease - macrolides	**8**				-2.20	-2.00	
spr1024	DNA ligase	**8**	-2.35			-3.53	-2.60	-2.02
spr1028	NADP-dependent glyceraldehyde-3-P DH	**8**	-2.70	-4.76	-4.00		-2.90	-3.78
spr1029	1,4-alpha-glucan branching enzyme	**8**					2.90	3.55
spr1034	Glycerate kinase	**8**	-2.15	-2.02		-3.00	-2.73	-2.48
spr1036	Enolase	**8**					-2.83	-2.49
spr1039	Second subunit of major exonuclease	**8**	-3.80	-3.61	-2.95	-2.06	-3.13	-3.31
spr1040	First subunit of major exonuclease	**8**	-3.39	-3.95	-3.46	-2.15	-3.17	-3.59
spr1041	Hypothetical protein	**8**	-3.33	-3.04	-2.63		-2.63	-3.08
spr1042	Immunoglobulin A1 protease	**8**	-2.16	-2.43	-2.00	-2.02	-2.16	-2.07
spr1043	Conserved hypothetical protein	**8**	-4.67	-4.20	-2.78	-5.48	-5.42	-5.32
spr1044	Ribonuclease H	**8**	-4.73	-4.62	-3.01	-5.14	-5.55	-5.11
spr1045	Conserved hypothetical protein	**8**	-3.32	-3.47	-3.05	-2.88	-3.71	-3.98
spr1050	TPP-dependent acetoin DH beta chain	**8**	-2.20			-3.31	-2.79	-2.05
spr1051	TPP-dependent acetoin DH alpha chain	**8**				-3.69	-2.66	
spr1060	Histidine motif-containing protein	**8**						-2.29
spr1061	His triad protein A precursor	**8**					-2.32	-2.33
spr1078	Degenerate transposase						2.14	
spr1080	Hypothetical protein						2.62	3.15
spr1109	Formate-tetrahydrofolate ligase		2.42					
spr1110	Similar to C-terminus of the Dfp protein		2.07	3.05	2.51			
spr1112	Conserved hypothetical protein			3.42	2.31	2.78	4.25	2.55
spr1119	Conserved hypothetical protein			2.18				
spr1122	Glucose-6-P 1-DH			2.00				
spr1128	GMP reductase				-2.40			
spr1132	Hypothetical protein	**9**				-2.33	-2.16	-2.11
spr1133	3-isopropylmalate dehydratase small subunit	**9**	-2.24		-2.27	-3.29	-3.11	-2.80
spr1134	Conserved hypothetical protein	**9**	-2.38	-2.49	-2.59	-3.42	-3.14	-3.11
spr1135	3-isopropylmalate DH	**9**	-2.52	-2.61	-2.45	-3.78	-4.31	-3.87
spr1136	2-isopropylmalate synthase	**9**	-2.96	-3.36	-2.94	-4.58	-6.00	-4.68
spr1137	2-isopropylmalate synthase	**9**	-3.01	-3.23	-2.74	-4.64	-5.43	-4.41
spr1138	Hypothetical protein	**9**	-3.02	-3.19	-2.65	-4.61	-5.49	-4.37
spr1139	Copper sensitivity	**9**	-3.04	-3.24	-2.56	-5.81	-6.28	-5.18
spr1140	Conserved hypothetical protein	**9**	-2.81	-2.66	-2.30	-4.90	-4.54	-4.29
spr1141	DNA topoisomerase I	**9**	-3.91	-4.36	-3.46	-4.73	-6.28	-5.26
spr1142	Conserved hypothetical protein	**9**	-2.73	-2.76		-6.01	-4.96	-3.43
spr1143	Hypothetical protein	**9**				-2.19		
spr1144	DNA processing Smf protein	**9**	-2.32	-2.02		-5.73	-4.33	-2.93
spr1149	Conserved hypothetical protein	**9**				-6.62	-3.14	-2.38
spr1157	Endonuclease III			-2.04	-2.08			-4.59

spr1170	Conserved hypothetical protein						-2.17	
spr1176	Conserved hypothetical protein					-2.78	-2.47	-2.46
spr1180	Degenerate transposase						2.11	2.12
spr1183	ABCT, ATP-binding protein - possibly multidrug				-2.11			
spr1186	N-acetylneuraminate lyase subunit							2.02
spr1187	N-acetylneuraminate lyase subunit		2.04	2.56			2.00	3.36
spr1196	N-acetylmannosamine-6-P epimerase						2.53	2.37
spr1197	Degenerate transposase (orf2)						2.12	2.04
spr1202	ABCT, ATP-binding protein - unknown substrate			-2.09				-2.04
spr1204	Protease II (oligopeptidase B)			-2.13				-2.01
spr1205	Conserved hypothetical protein			-2.42		-2.20	-2.49	-2.46
spr1214	N-ethylammeline chlorohydrolase		-2.41	-3.36		-2.26	-3.97	-3.58
spr1215	ABCT, ATP-binding/membrane-spanning protein		-2.18	-3.42	-2.04		-2.91	-2.39
spr1216	ABCT, ATP-binding/membrane-spanning protein		-2.35	-3.16			-2.50	-2.12
spr1217	Peptide Met sulfoxide reductase		-2.36	-2.79		-2.29	-2.90	-2.57
spr1218	Homoserine kinase		-3.08	-4.05	-2.14	-2.91	-4.40	-3.86
spr1219	Homoserine DH		-2.91	-3.66	-2.02	-2.78	-3.95	-3.66
spr1237	Hypothetical protein		-3.21	-2.16		-4.87	-2.73	-2.14
spr1238	ABCT, ATP-binding protein		-2.30	-2.11				
spr1240	Alanyl-tRNA synthetase						-2.09	-2.45
spr1248	Conserved hypothetical protein						-2.02	
spr1249	Alpha-acetolactate decarboxylase						-2.67	-3.14
spr1266	Coproporphyrinogen III oxidase					2.20	2.12	2.10
spr1271	30S Ribosomal protein S21		2.28	2.38		2.56	3.52	2.92
spr1300	Gln amidotransferase	**10**						-2.74
spr1310	Peptide deformylase	**10**	-2.58			-4.21	-4.64	-4.18
spr1311	tRNA (guanosine-2-O-)-methyltransferase	**10**	-2.50			-3.32	-3.34	-3.14
spr1313	Hypothetical protein	**10**	-2.17	-2.30		-2.41	-2.42	-2.66
spr1314	ABCT, ATP-binding protein - Asp/Glu	**10**	-3.72	-4.54	-2.52	-3.46	-5.70	-5.65
spr1315	ABCT membrane-spanning permease - Asp/Glu	**10**	-3.74	-4.40	-2.14	-3.30	-5.84	-5.61
spr1316	Conserved hypothetical protein	**10**	-3.63	-4.26	-2.53	-3.72	-5.51	-6.24
spr1317	O6-methylguanine-DNA methyltransferase	**10**	-3.45	-3.60	-2.35	-3.79	-5.70	-6.40
spr1318	Hypothetical protein	**10**	-3.41	-3.04	-2.05	-4.17	-5.59	-6.06
spr1319	Hypothetical protein	**10**	-4.57	-3.54	-2.25	-3.05	-3.67	-4.45
spr1320	Conserved hypothetical protein	**10**	-3.44	-3.19	-2.25	-2.13	-2.87	-3.39
spr1321	Conserved hypothetical protein	**10**	-4.12	-4.02	-2.42	-3.73	-6.08	-6.21
spr1322	Pyridoxine biosynthesis protein	**10**	-3.97	-3.63	-2.09	-3.64	-5.42	-5.12
spr1324	Thiamine biosynthesis lipoprotein	**10**				-2.01	-2.61	-3.08
spr1325	Conserved hypothetical protein	**10**					-3.13	-3.32
spr1329	Gly-tRNA synthetase alpha chain	**10**						-2.05
spr1333	Peptidoglycan GlcNAc deacetylase	**10**						-2.30
spr1334	Hypothetical protein	**10**					-2.10	-2.59
spr1336	DEAD RNA helicase	**10**						-2.46
spr1338	Degenerate transposase		2.23	2.07		2.26	2.77	2.31
spr1342	Degenerate transposase		2.01			2.28	2.63	2.49
spr1353	ABCT, substrate-binding protein – Gln	**11**	-2.37			-2.79	-2.88	-2.56
spr1354	ABCT, ATP-binding protein – Gln	**11**	-2.61	-2.28		-3.30	-3.41	-3.07
spr1355	ABCT, membrane-spanning permease – Gln	**11**	-2.04			-2.21	-2.27	
spr1359	Proton-translocating ATPase, F1, epsilon subunit	**11**					-2.62	-3.62
spr1361	Proton-translocating ATPase, F1, gamma subunit	**11**					-2.32	-2.24
spr1362	Proton-translocating ATPase, F1, alpha subunit	**11**		-2.42			-2.40	-2.29
spr1363	Proton-translocating ATPase, F1, delta subunit	**11**	-2.74	-5.44		-2.04	-5.11	-5.81
spr1364	Proton-translocating ATPase, F0, b subunit	**11**	-2.73	-4.96		-2.02	-4.46	-5.12
spr1365	Proton-translocating ATPase, F0, a subunit	**11**	-2.34	-3.07			-2.96	-3.11
spr1366	Proton-translocating ATPase, F0, c subunit	**11**	-2.68	-2.91		-2.33	-3.56	-3.54
spr1367	Transposase	**11**					-2.47	-2.28
spr1368	Hypothetical protein	**11**					-2.08	-2.14
spr1377	Cystathionine gamma-synthase	**11**		-2.77			-3.48	-3.96
spr1379	ABCT	**11**					-2.30	-2.78
spr1380	ABCT	**11**					-2.04	-3.03
spr1381	ABCT	**11**					-2.06	-2.66
spr1382	ABCT, substrate-binding protein – oligopeptide	**11**					-3.77	-4.63
spr1383	Polysaccharide transporter	**11**		-2.50				-2.07
spr1384	UDP-N-acetylmuramoyl-L-Ala-D-Glu-L-Lys	**11**	-3.05	-2.89		-2.82	-4.97	-4.90

	ligase							
spr1387	Hypothetical protein	**11**					-2.18	-2.18
spr1388	Hypothetical protein	**11**					-2.19	-2.11
spr1397	Asn-tRNA synthetase	**11**	-2.40	-2.94		-2.13	-3.50	-3.29
spr1398	Conserved hypothetical protein	**11**	-2.20	-2.02		-2.65	-3.30	-3.02
spr1399	Asp aminotransferase	**11**	-2.45	-2.38		-2.74	-3.57	-2.67
spr1400	Conserved hypothetical protein	**11**	-3.98	-3.28		-4.86	-4.96	-4.45
spr1402	Hypothetical protein	**11**					-3.07	-3.44
spr1403	Hypothetical protein	**11**		-2.06				
spr1405	Conserved hypothetical protein	**11**					-2.13	-2.44
spr1407	Hypothetical protein	**11**	-2.11	-2.30			-3.03	-3.16
spr1408	Formylmethionine deformylase	**11**					-3.33	-2.47
spr1411	Conserved hypothetical protein	**11**	-2.42	-2.31		-2.53	-3.62	-3.04
spr1436	Conserved hypothetical protein					2.17	2.94	3.16
spr1437	ABCT, ATP-binding protein - multiple sugar					2.02	3.24	3.85
spr1441	Major facilitator:oxalate/formate antiporter		4.70	2.45	3.63	5.46	3.64	4.55
spr1442	Oxidoreductase (Mercury (II) reductase)				2.05			
spr1470	Hypothetical protein	**12**	-3.10			-2.92	-2.91	-2.23
spr1471	Hypothetical protein	**12**	-3.12			-2.80	-2.66	
spr1472	Thr-tRNA synthetase	**12**	-2.61			-2.49	-3.13	
spr1485	Hypothetical protein	**12**	-2.67	-2.50		-2.14	-2.30	
spr1486	Conserved hypothetical protein	**12**	-2.74	-3.15				-2.13
spr1487	GTP pyrophosphokinase	**12**	-4.27	-4.62		-2.05	-2.72	-2.79
spr1490	Conserved hypothetical protein	**12**	-4.37	-3.42		-4.49	-4.09	-3.46
spr1491	Endopeptidase O	**12**	-3.15	-4.77	-2.15		-3.79	-3.47
spr1492	ABCT, ATP-binding protein – Mn	**12**	-4.98	-7.40	-2.86	-3.48	-8.75	-9.34
spr1493	ABCT, membrane-spanning permease – Mn	**12**	-2.26	-3.63			-3.60	-2.94
spr1494	ABCT, substrate-binding protein – Mn	**12**	-2.77	-6.04	-2.75		-5.03	-5.45
spr1495	Thioredoxin-linked thiol peroxidase	**12**		-2.30		-2.02	-4.05	-3.73
spr1496	Hypothetical protein	**12**	-2.53	-3.55	-2.51	-2.38	-4.44	-3.90
spr1497	ABCT, ATP-binding protein - unknown substrate	**12**	-2.81	-3.77	-2.37	-2.61	-4.33	-3.64
spr1498	Conserved hypothetical protein	**12**	-2.75	-2.87		-2.49	-3.24	-2.61
spr1502	Ile-tRNA synthetase	**13**	2.04					
spr1513	Mutator protein	**13**	2.02	2.33				
spr1515	D-Ala-D-Ala ligase	**13**		2.21				
spr1516	Recombination protein RecR	**13**	2.20					
spr1519	Glucokinase	**13**		2.11				
spr1520	N-acetylneuraminate lyase subunit	**13**		2.22				
spr1522	Hypothetical protein	**13**		2.44		2.16		3.13
spr1523	Hypothetical protein	**13**	2.04	2.38		2.32	2.25	3.16
spr1524	Conserved hypothetical protein	**13**	2.24	2.32		2.25	2.20	3.14
spr1525	ABCT, membrane-spanning permease – sugar	**13**		2.04				2.05
spr1526	ABCT, membrane-spanning permease – sugar	**13**		2.07				2.49
spr1527	ABCT, substrate-binding protein – sugar	**13**		2.19				2.66
spr1528	PTS, sugar-specific EII component	**13**		2.19		2.00	2.44	2.99
spr1529	N-acetylmannosamine-6-P epimerase	**13**						2.73
spr1530	Conserved hypothetical protein	**13**	2.27	2.60		2.32	2.68	3.71
spr1531	Sialidase B precursor (neuraminidase B)	**13**		2.11			2.20	2.65
spr1532	ABCT, membrane-spanning permease – sugar	**13**		2.12			2.16	2.81
spr1533	ABCT, membrane-spanning permease – sugar	**13**		2.15			2.01	2.44
spr1536	Sialidase A precursor (neuraminidase A)	**13**	2.11	2.19		2.55	2.07	2.02
spr1547	Hypothetical protein	**13**	2.36	2.41		3.31	3.93	3.49
spr1548	Hypothetical protein	**13**	2.33	2.68		3.03	3.46	3.44
spr1549	Hypothetical protein	**13**	2.14	2.39		2.53	3.57	2.78
spr1550	Conserved hypothetical protein	**13**	2.09	2.40		2.46	2.89	
spr1551	Hypothetical protein	**13**	2.16	2.14				
spr1552	Hypothetical protein	**13**	2.04					
spr1557	Conserved hypothetical protein	**13**				2.65	2.64	2.49
spr1563	Degenerate transposase	**13**		2.00			3.04	3.50
spr1564	Hypothetical protein	**13**						2.30
spr1565	Fructokinase	**13**					2.38	2.08
spr1566	PTS, enzyme II	**13**					2.66	2.51
spr1568	Sucrose-6-P hydrolase	**13**				2.24	2.66	2.38
spr1569	Sucrose regulon regulatory protein	**13**					2.12	

spr1570	3-hydroxy-3-methylglutaryl-coenzyme a reductase	**13**				2.01	2.16	2.06
spr1601	Hypothetical protein						2.42	
spr1602	Thioredoxin reductase			2.51			2.62	2.36
spr1603	Conserved hypothetical protein		2.07	3.16			3.19	4.58
spr1604	Aquaporin Z - water channel protein						2.38	2.27
spr1605	Hypothetical protein						2.33	2.40
spr1611	Hypothetical protein						2.19	2.48
spr1616	Chromosome segregation helicase				2.03			
spr1617	Sucrose-6-P hydrolase			2.74			2.27	2.79
spr1618	ABCT, membrane-spanning permease – sugar						2.10	2.54
spr1619	ABCT, membrane-spanning permease – sugar							2.29
spr1627	Conserved hypothetical protein			2.32		2.13	3.30	3.46
spr1632	Trp synthetase beta chain						-2.22	-2.98
spr1633	P-ribosylanthranilate isomerase.						-2.19	-2.55
spr1634	Indole-3-glycerol-P synthase.					-2.17	-2.46	-2.76
spr1635	Anthranilate P-ribosyltransferase					-2.13	-2.12	-2.73
spr1636	Anthranilate synthase component II					-2.20	-2.28	-2.66
spr1637	Anthranilate synthase component I					-2.32	-2.06	-2.49
spr1652	Hypothetical protein	**14**	-2.16	-2.32				
spr1654	Conserved hypothetical protein	**14**		-2.77				
spr1655	Conserved hypothetical protein	**14**		-2.64		-2.58	-2.05	-2.22
spr1656	ABCT, ATP-binding/membrane spanning protein	**14**		-2.18				
spr1657	ABCT, ATP-binding/membrane spanning protein	**14**		-2.06				
spr1658	Conserved hypothetical protein	**14**		-2.56				
spr1659	Hypothetical protein	**14**	-2.42	-3.24				
spr1661	Hypothetical protein	**14**			2.33			
spr1662	Xanthine P-ribosyltransferase	**14**			2.02			
spr1668	Galactokinase	**14**			-2.47			
spr1669	GalR, regulator of gal operon	**14**	-3.37	-3.87	-3.27	-3.84	-3.82	-4.47
spr1670	Alcohol DH	**14**	-2.87	-3.78	-3.93	-2.84	-2.88	-2.45
spr1671	Conserved hypothetical protein	**14**	-2.76	-3.85	-3.52			
spr1672	Cation diffusion facilitator - heavy metal	**14**	-2.25	-3.02				
spr1674	Conserved hypothetical protein	**14**	-2.51	-2.21				
spr1677	ABCT, membrane-spanning permease - choline	**14**	-2.73	-2.92				
spr1678	ABCT, ATP-binding protein – choline	**14**	-3.25	-3.16			-2.18	
spr1679	Hypothetical protein	**14**	-3.41	-3.08		-2.02	-2.33	
spr1680	Hypothetical protein	**14**	-2.96	-2.56		-2.15	-2.43	-2.45
spr1681	Hypothetical protein	**14**		-2.20				
spr1682	Glu aminopeptidase	**14**	-2.98	-3.10			-2.41	-2.94
spr1684	ABCT, membrane-spanning permease - ferric iron	**14**				-2.20	-2.19	-2.58
spr1685	ABCT, membrane-spanning permease - ferric iron	**14**				-2.17	-2.25	-2.56
spr1686	ABCT, ATP-binding protein - ferric iron	**14**						-2.00
spr1687	ABCT, substrate-binding protein - ferric iron	**14**					-2.50	-2.15
spr1694	Conserved hypothetical protein	**14**	-2.10	-2.25				
spr1695	Hypothetical protein	**14**	-2.05	-2.01				
spr1696	Glutamate racemase	**14**	-2.10					
spr1697	Hypothetical protein	**14**	-2.25		-2.23			
spr1698	Dextran glucosidase	**14**	-2.82	-3.35				
spr1708	Hypothetical protein		-2.36	-3.01	-2.20		-2.05	-2.24
spr1709	Dextransucrase (sucrose 6-glucosyltransferase)			-3.20			-2.07	
spr1710	ABCT, membrane spanning permease - sugars			-2.18				
spr1718	Conserved hypothetical protein							2.48
spr1721	Degenerate transposase (fusion of orf1 and orf2)						2.33	3.15
spr1734	ABCT, ATP-binding protein							2.01
spr1735	ABCT, ATP-binding protein						2.01	2.76
spr1736	ABCT, ATP-binding protein							2.25
spr1749	Hypothetical protein						2.15	2.20
spr1750	Hypothetical protein						2.35	2.00
spr1751	Hypothetical protein						2.02	2.30
spr1752	Hypothetical protein						2.21	
spr1761	Conserved hypothetical protein				2.07			
spr1762	Hypothetical protein			2.57			2.28	2.78
spr1763	Transcriptional activator						2.97	3.43
spr1765	Hypothetical protein					2.25	3.03	3.60

spr1766	Hypothetical protein			2.03		2.85	3.80	4.62
spr1767	CylM protein, cytolytic toxin system		2.08	2.02		2.64	3.32	3.92
spr1768	Conserved hypothetical protein					2.50	3.25	3.37
spr1770	ABCT, ATP-binding/membrane-spanning – hemolysin					2.23	2.55	2.63
spr1771	Subtilisin-like serine protease		2.03			2.60	2.91	3.07
spr1772	Hypothetical protein					2.09		2.43
spr1773	ABCT, ATP-binding protein							2.06
spr1775	Nucleoside di-P kinase		2.34	2.66				
spr1808	Potential aminotransferase						-2.02	-2.30
spr1815	Histidine kinase		2.00			2.25		2.14
spr1816	Conserved hypothetical protein					2.93	2.62	2.93
spr1817	ABCT, ATP binding protein		2.09	2.08		2.95	2.65	2.90
spr1818	Hypothetical protein		2.41	2.64		3.24	3.47	3.33
spr1820	Transcription antitermination factor		2.43	2.31				
spr1821	Preprotein translocase secE component		2.30	2.35		2.15	2.10	
spr1822	50S Ribosomal protein L33					2.00		
spr1826	Conserved hypothetical protein					2.37		2.21
spr1832	Conserved hypothetical protein				-2.04			
spr1833	Beta-glucosidase				-2.21		-2.68	-2.43
spr1834	PTS, cellobiose-specific IIC component				-2.05		-2.29	-2.12
spr1836	PTS, cellobiose-specific IIA component				-3.23			
spr1837	Alcohol-acetaldehyde DH						-2.97	-2.55
spr1867	N-acetylglucosamine-6-P deacetylase						-2.51	-3.10
spr1878	Threonine synthase	**15**				2.19	2.47	2.30
spr1879	Hypothetical protein	**15**				2.18	2.64	2.41
spr1880	Conserved hypothetical protein	**15**	2.31	2.43		2.52	3.49	3.21
spr1881	Glu-tRNA synthetase	**15**					2.15	2.20
spr1882	Glucose-6-P isomerase	**15**						2.15
spr1883	Hypothetical protein	**15**	2.94	3.46	3.29	3.06	6.26	6.55
spr1884	Glutamine amidotransferase	**15**	4.13	5.76		5.73	9.69	12.15
spr1885	ABCT, ATP-binding/membrane spanning protein	**15**		2.10		2.47	3.06	3.13
spr1887	ABCT, ATP-binding/membrane spanning protein	**15**					2.15	2.16
spr1891	Tranposase (orf2)	**15**					2.16	2.06
spr1895	ABCT, substrate-binding protein – phosphate	**15**	2.48	2.54		3.61	7.82	10.12
spr1896	ABCT, membrane-spanning permease – phosphate	**15**	2.47	2.45		3.34	8.11	10.72
spr1897	ABCT, membrane-spanning permease – phosphate	**15**	2.37	2.28		3.18	6.40	8.39
spr1898	ABCT, ATP-binding protein – phosphate	**15**	2.32	2.31		2.92	6.27	7.76
spr1899	Negative regulator of pho regulon for phosphate	**15**	2.20	2.34		2.85	5.87	7.94
spr1900	Transposase, IS1380-Spn1 related	**15**				2.21	4.41	5.71
spr1901	Hypothetical protein	**15**				2.22	4.28	4.85
spr1902	Glycerol-3-P DH	**15**					2.21	2.15
spr1908	Conserved hypothetical protein	**15**				2.73	3.40	3.31
spr1909	Penicillin-binding protein 1b	**15**				2.11	2.75	2.54
spr1910	Tyrosyl-tRNA synthetase 1	**15**	2.00			2.25	2.48	2.40
spr1916	Maltodextrin phosphorylase	**15**				2.80	2.38	2.19
spr1918	ABCT, substrate-binding protein – maltose	**15**					2.49	2.34
spr1919	ABCT, membrane-spanning permease – maltose	**15**					2.55	2.86
spr1920	ABCT, membrane-spanning permease – maltose	**15**						2.17
spr1925	Hypothetical protein	**15**					2.97	2.81
spr1926	Hypothetical protein	**15**				2.03	3.21	3.08
spr1927	Hypothetical protein	**15**					3.15	3.17
spr1928	Hypothetical protein	**15**					2.97	2.39
spr1929	Conserved hypothetical protein	**15**					3.07	2.39
spr1941	Hypothetical protein				2.11			
spr1947	Tranposase (orf2)						2.14	2.01
spr1948	Hypothetical protein							2.48
spr1952	Conserved hypothetical protein							3.09
spr1955	Arg deiminase						2.44	2.61
spr1956	Arg deiminase						2.18	2.40
spr1959	Conserved hypothetical protein							2.14
spr1960	Conserved hypothetical protein					2.94	3.04	3.14
spr1975	ABCT, substrate-binding protein –Zinc		-2.11	-2.71				
spr1976	ABCT, membrane-spanning permease – Zinc		-2.18	-2.67			-2.15	

spr1977	ABCT, ATP-binding domain - Zinc permease		-2.29	-2.66		-2.14	-2.22	
spr1978	Transcriptional repressor for Zinc-responsive expression		-2.20	-2.47				
spr1979	D-Ala transfer from undecaprenol-P to poly (glycero-P)			-2.95			-2.36	-2.61
spr1980	D-Ala carrier protein			-2.36				
spr1981	D-Ala transfer from Dcp to undecaprenol-P			-2.78				
spr1982	D-Ala-D-Ala carrier protein ligase		-2.05	-2.81				
spr1984	Transposase			-2.07				
spr1985	Transposase						3.26	2.94
spr2003	Conserved hypothetical protein							2.02
spr2004	ABCT, membrane-spanning permease				2.76			
spr2005	Conserved hypothetical protein						2.26	
spr2012	Involved in transformation		-2.10			-2.28	-2.07	
spr2013	Involved in transformation		-2.53			-3.08	-2.56	
spr2018	Degenerate transposase				-2.30			
spr2021	General stress protein GSP-781					-3.43		
spr2022	Cell-shape determining protein MreD	**1**	2.66	2.54		3.01	4.93	4.42
spr2023	Cell shape determining protein MreC	**1**					2.27	2.24
spr2024	ABCT, membrane-spanning permease	**1**					2.14	2.07
spr2027	Phosphotidylglycero-P synthase	**1**					2.32	2.26
spr2028	Conserved hypothetical protein	**1**	2.01			2.57	3.99	3.51
spr2029	Conserved hypothetical protein	**1**				2.02	2.95	2.85
spr2030	Conserved hypothetical protein	**1**				2.13	3.59	3.47
spr2031	Conserved hypothetical protein	**1**	2.12	2.67			4.24	4.01
spr2032	Recombination protein RecF	**1**					2.81	2.88
spr2033	Inosine-5-mono-P DH	**1**					2.09	2.23
spr2034	Trp-tRNA synthetase	**1**					3.08	2.69
spr2035	ABCT, ATP-binding protein	**1**					2.85	2.58
spr2036	Conserved hypothetical protein	**1**					3.67	3.29
spr2037	Conserved hypothetical protein	**1**					2.95	2.20
spr2038	Conserved hypothetical protein	**1**					2.87	2.17
spr2039	Conserved hypothetical protein	**1**			2.56		2.49	2.21
spr2040	Conserved hypothetical protein	**1**	2.05	2.77		2.46	4.59	4.08
spr2041	Response regulator	**1**					2.12	2.10
spr2042	His protein kinase	**1**					2.10	2.07
spr2043	Competence stimulating peptide precursor	**1**					3.71	
spr2044	Conserved hypothetical protein	**1**					2.90	2.08

[a] ABCT, ATP-binding cassette transporter; DH, dehydrogenase; P, phospho; PTS, phosphotransferase system; AA, amino acid.

[b] Only genes whose transcript level showed significant fold variations with respect to time 0 min (≥2.0-fold and $p<0.01$) are shown.

Supplementary Table 2. Validation of microarray data by real-time RT-PCR

R6 locus (gene)	PCR			Relative expresión level analysis at[a]:			
				0.5 × MIC		40 × MIC	
	Primers (5'→3')[b]	Product (bp)	Time (min)	RT-PCR	Array	RT-PCR	Array
spr0444	GGATCCAATGGCGAACCCTTAC +	134	5	1,00	1,09	-1,40	1,17
(*glnA*)	CCTTGCGCTCTTCTGCTGTCAT –		15	2,10	1,08	1,49	1,24
spr0715	TGAAATAGTTGGAGATACGGA +	149	5	1,83	1,58	1,84	1,79
(*gyrB*)	GAAATTTGAAGACCGCGATTT –		15	2,44	1,44	2,95	1,93
spr0756	AAGCGAACAGATGAAGCGATTGAG +	205	5	-2,86	-1,46	-4,76	-1,26
(*parE*)	TCCTTGGTGCGAACGTTATTGACA –		15	-1,56	-1,25	-11,11	-2,89
spr1099	TGATAAACGCCGTACAGAGTT +	158	5	-1,22	1,23	-1,47	1,28
(*gyrA*)	CCACGACCCCCACGTTTTGAGC –		15	1,56	1,22	1,12	1,34
spr1122	CGGAGCGCTTGGGTGTAGAA +	107	5	1,14	1,63	-1,75	1,61
(*zwf*)	CATGGCGAGGAGCGAAAGAA –		15	2,52	2,00	-1,02	1,62
spr1141	TCACCAAGGATGCAGTCAAAAATG +	118	5	-7,86	-3,91	-22,37	-4,73
(*topA*)	GGCGAAATCGAATACCCTACCA –		15	-5,42	-4,36	-20,69	-6,28
spr1366	GCTTATGTATTGCCTGTA +	177	5	-19,55	-2,68	-20,88	-2,33
(*atpC*)	TTGATAATAAATGAGAAGAC –		15	-14,08	-2,91	-31,80	-3,56
spr1538	TGTTTCCACGCTTCCATCCT +	113	5	1,11	1,76	-1,26	1,55
	TGCGTGCATAGACCTTTCCTT –		15	1,55	1,66	-1,59	1,37
spr1552	TGAAAAGGCCAACAGAAATA +	197	5	1,20	2,04	1,07	2,53
	CAATAGCTAGCAGAATAAAAAGAA –		15	2,06	1,87	-1,03	2,46
spr1625	AACTAAAGAACAGCATGAAGCAGA +	129	5	-1,84	1,02	-2,65	1,06
	GAGAAACCAGATCCAAGACCAG –		15	-1,29	1,05	-1,62	1,16
spr1680	TGCTAGCCCATCATATTCGTTTGT +	138	5	-14,06	-2,96	-16,56	-2,15
	CAGTTGCGCAGCCAGTTTCA –		15	-8,62	-2,56	-14,19	-2,43
spr1794	AAGATGATAGTGGCGAGATTGATG +	134	5	-1,55	1,37	-1,41	1,83
(*cbf1*)	TTGATTGACTTGAGGGGTATTGTT –		15	-1,86	-1,10	-2,40	1,15
spr1863	ATGCACGTGAATGGGGGAATA +	116	5	-2,81	1,01	-2,40	1,04
(*cglB*)	TTGAGCCAGATCTTGACCGACTT –		15	-1,72	-1,08	-2,47	1,09
spr2001	GCCTACATCAAGGCGATTTT +	123	5	-3,15	-1,13	-5,06	-1,19
(*ctsR*)	TTCCGTAAAGCGTGTCTTGA –		15	-1,47	1,21	-2,27	1,28

[a] RT-PCR fluorescente values were normalizad with those obtained from the amplification of 16 SrDNA and *rpoB*.

[b] +, forward primer, –, reverse primer.