

TABLE S6 Fitness score of each gene in the M1 GAS genome after 48 hour saliva incubation.

locus_tag	gene_name	function	Fitness score*	q.value
M5005_Spy0004	M5005_Spy0004	GTP-binding protein	-0.80121639	0.026443415
M5005_Spy0009	M5005_Spy0009	hypothetical protein	-6.467121039	0.00052947
M5005_Spy0013	ftsH	cell division protein	-0.989293892	0.002280046
M5005_Spy0014	M5005_Spy0014	amino acid permease	-0.244946209	0.005182553
M5005_Spy0017	sibA	secreted protein	-6.628150267	3.95358E-05
M5005_Spy0019	recO	DNA repair protein	-0.810889535	0.060294579
M5005_Spy0022	M5005_Spy0022	phosphoribosylaminoimidazole-succinocarboxamide synthase	0.463506302	1.74504E-08
M5005_Spy0023	M5005_Spy0023	phosphoribosylformylglycinamide synthase	0.193846214	0.01281588
M5005_Spy0024	purF	amidophosphoribosyltransferase	0.696199804	3.81893E-22
M5005_Spy0025	purM	phosphoribosylformylglycinamide cyclo-ligase	0.320996766	0.000314478
M5005_Spy0033	purB	adenylosuccinate lyase	0.362710759	2.66928E-05
M5005_Spy0035	ruvB	holliday junction DNA helicase	-5.388536847	0.005013446
M5005_Spy0038	M5005_Spy0038	acyltransferase family	-5.077912819	0.034134532
M5005_Spy0040	adhA	alcohol dehydrogenase	0.487378041	0.000153791
M5005_Spy0041	M5005_Spy0041	Na ⁺ driven multidrug efflux pump	0.266866586	0.003751017
M5005_Spy0065	adk	adenylate kinase	-2.475594045	0.041836533
M5005_Spy0075	M5005_Spy0075	4-diphosphocytidyl-2-C-methyl-D-erythritol kinase	0.277208137	0.040827722
M5005_Spy0076	M5005_Spy0076	4-diphosphocytidyl-2-C-methyl-D-erythritol kinase	0.325246039	0.055392029
M5005_Spy0077	adcR	transcriptional regulator, MarR family	0.900675715	0.000103813
M5005_Spy0078	adcC	high-affinity zinc uptake system ATP-binding protein	0.282251128	0.000187604
M5005_Spy0079	adcB	high-affinity zinc uptake system membrane protein	0.263326621	0.00125906
M5005_Spy0084	rpoC	DNA-directed RNA polymerase beta' chain	0.457230017	0.095575452
M5005_Spy0085	M5005_Spy0085	putative DNA binding protein	-1.201021059	0.085926054
M5005_Spy0089	M5005_Spy0089	comG operon protein 4	-0.373618704	0.016956917
M5005_Spy0092	M5005_Spy0092	comG operon protein 6	0.210116192	0.079110579
M5005_Spy0097	pepA	glutamyl aminopeptidase	0.235203908	0.015581204
M5005_Spy0098	M5005_Spy0098	hypothetical protein	0.42939843	0.068725633
M5005_Spy0101	M5005_Spy0101	tRNA binding domain protein	0.373718916	2.65764E-05
M5005_Spy0102	M5005_Spy0102	single-strand DNA binding protein	0.212853957	0.073437748
M5005_Spy0103	M5005_Spy0103	deoxyadenosine kinase/deoxyguanosine kinase	0.408374505	0.000123443
M5005_Spy0104	M5005_Spy0104	tRNA-dihydrouridine synthase	-1.724483441	1.81124E-32
M5005_Spy0105	M5005_Spy0105	33 kDa chaperonin	-1.051651544	1.8081E-08
M5005_Spy0107	M5005_Spy0107	fibronectin-binding protein	0.280174385	0.000326299
M5005_Spy0109	M5005_Spy0109	fibronectin-binding protein	0.19814323	0.01281588
M5005_Spy0112	M5005_Spy0112	transposase	0.336676534	0.05576E-07
M5005_Spy0113	M5005_Spy0113	transposase	0.293925013	0.000829247
M5005_Spy0116	atoE	short-chain fatty acids transporter	0.22101831	0.002562473
M5005_Spy0119	M5005_Spy0119	acetyl-CoA acetyltransferase	0.370482102	4.89397E-06
M5005_Spy0121	M5005_Spy0121	acetyl-CoA:acetacetyl-CoA transferase beta subunit	0.393715791	0.011829084
M5005_Spy0122	M5005_Spy0122	putative DNA-binding protein	-1.227186208	7.96851E-14
M5005_Spy0124	sloR	transcriptional regulator	0.383862604	1.61404E-06
M5005_Spy0131	ntpA	V-type sodium ATP synthase subunit A	0.162451945	0.091708441
M5005_Spy0132	ntpB	V-type sodium ATP synthase subunit B	0.254761582	0.014345671
M5005_Spy0136	purA	adenylosuccinate synthetase	0.438147889	0.023036067
M5005_Spy0139	nga	NAD glycohydrolase	0.173657187	0.025149723
M5005_Spy0142	M5005_Spy0142	hypothetical protein	0.420822992	0.010120335
M5005_Spy0143	M5005_Spy0143	hypothetical protein	0.485076154	0.073437748
M5005_Spy0144	M5005_Spy0144	hypothetical protein	-0.559263662	0.000266666
M5005_Spy0147	leuS	leucyl-tRNA synthetase	-5.800450033	0.003807562
M5005_Spy0148	M5005_Spy0148	PTS system, 3-keto-L-gulonate specific IIC component	0.236265258	0.02858806
M5005_Spy0150	M5005_Spy0150	PTS system, 3-keto-L-gulonate specific IIA component	0.38901477	0.042981232
M5005_Spy0153	araD	L-ribulose-5-phosphate 4-epimerase	0.641949316	1.27144E-05
M5005_Spy0158	opuABC	glycine betaine-binding protein/glycine betaine transport system permease protein	0.258706707	0.031763716
M5005_Spy0160	M5005_Spy0160	CoA binding protein	0.598663149	0.076120107
M5005_Spy0161	perR	ferric uptake regulation protein	0.408142232	0.034134532
M5005_Spy0169	M5005_Spy0169	malonate permease	0.471727932	1.24953E-11
M5005_Spy0175	tgt	queuine tRNA-ribosyltransferase	0.262396654	0.023202172
M5005_Spy0176	M5005_Spy0176	zinc finger protein	0.294550917	0.011970461
M5005_Spy0177	M5005_Spy0177	bioY protein	0.182170037	0.073437748
M5005_Spy0178	M5005_Spy0178	metal-dependent hydrolase	0.411832661	0.000131456
M5005_Spy0180	M5005_Spy0180	S-layer homology domain	0.226477301	0.002553307
M5005_Spy0182	speG	exotoxin type G precursor	-0.306100467	0.003242166
M5005_Spy0183	M5005_Spy0183	putative membrane associated protein	0.475894873	1.63466E-05
M5005_Spy0196	M5005_Spy0196	multidrug resistance ABC transporter ATP-binding and permease protein	1.033497918	7.29201E-17
M5005_Spy0197	M5005_Spy0197	multidrug resistance ABC transporter ATP-binding and permease protein	0.722724919	6.83084E-10
M5005_Spy0198	M5005_Spy0198	putative cytosolic protein	0.363978533	0.027759554
M5005_Spy0199	M5005_Spy0199	deoxyuridine 5'-triphosphate nucleotidohydrolase	1.015124317	0.050478912
M5005_Spy0200	radA	DNA repair protein	0.293524189	0.020591145
M5005_Spy0201	M5005_Spy0201	carbonic anhydrase	0.884250218	2.11032E-06
M5005_Spy0205	fasC	sensory transduction protein kinase	-0.163852014	0.073437748
M5005_Spy0208	M5005_Spy0208	60 kDa inner membrane protein YIDC	0.492884799	0.001013129
M5005_Spy0209	M5005_Spy0209	jag protein	0.508362754	0.033839732
M5005_Spy0212	M5005_Spy0212	N-acetylmannosamine-6-phosphate 2-epimerase	0.455620545	0.009955499
M5005_Spy0213	M5005_Spy0213	N-acetylneuraminate-binding protein	0.397488606	4.46295E-05
M5005_Spy0214	M5005_Spy0214	N-acetylneuraminate transport system permease protein	0.322255752	9.78105E-05
M5005_Spy0217	nanH	N-acetylneuraminate lyase	0.504756214	0.000115354
M5005_Spy0218	M5005_Spy0218	N-acetylmannosamine kinase	0.601263302	0.001769122
M5005_Spy0224	rpe	ribulose-phosphate 3-epimerase	-2.083383598	6.64893E-05
M5005_Spy0225	M5005_Spy0225	thiamin pyrophosphokinase	-2.337037891	4.48623E-08
M5005_Spy0229	prgA	surface exclusion protein	0.347619408	0.005855709
M5005_Spy0240	M5005_Spy0240	undecaprenyl-phosphate alpha-N-acetylglucosaminophosphotransferase	-1.515247992	1.76367E-08
M5005_Spy0241	rgpG	putative cytosolic protein	-0.884096547	4.26258E-09

M5005_Spy0246	M5005_Spy0246	ABC transporter-associated protein	0.406650426	0.02192047
M5005_Spy0247	M5005_Spy0247	D-alanyl-D-alanine carboxypeptidase	0.778085762	5.14257E-26
M5005_Spy0249	oppA	oligopeptide-binding protein	-0.79729279	0.018141862
M5005_Spy0251	oppC	oligopeptide transport system permease protein	-1.003417326	0.001602549
M5005_Spy0253	oppF	oligopeptide transport ATP-binding protein	-0.701962833	0.0177399
M5005_Spy0267	M5005_Spy0267	putative cytosolic protein	0.27203195	0.000324183
M5005_Spy0268	M5005_Spy0268	hypothetical protein	-0.431157455	0.0336946
M5005_Spy0270	M5005_Spy0270	ABC transporter substrate-binding protein	-1.283741621	0.037893538
M5005_Spy0271	M5005_Spy0271	ABC transporter substrate-binding protein	0.708441769	1.69254E-27
M5005_Spy0272	M5005_Spy0272	ABC transporter ATP-binding protein	0.589353106	7.40574E-11
M5005_Spy0273	M5005_Spy0273	ABC transporter permease protein	0.610197338	3.01508E-16
M5005_Spy0274	braB	branched-chain amino acid transport system carrier protein	0.421796002	2.67003E-12
M5005_Spy0280	M5005_Spy0280	heat shock protein	0.4537848	0.030400319
M5005_Spy0284	M5005_Spy0284	putative regulatory protein	0.716586026	0.094935422
M5005_Spy0292	M5005_Spy0292	aminodeoxychorismate lyase family	-3.178649659	0.001602549
M5005_Spy0293	greA	transcription elongation factor	-3.671640444	0.000647673
M5005_Spy0300	M5005_Spy0300	hydrolase, HAD superfamily	1.219908623	4.68589E-08
M5005_Spy0301	M5005_Spy0301	integral membrane protein	-0.639476931	0.00292796
M5005_Spy0306	M5005_Spy0306	CBS domain containing protein	-0.4484368	0.099476807
M5005_Spy0308	M5005_Spy0308	putative cytosolic protein	-0.454277169	0.070987323
M5005_Spy0312	M5005_Spy0312	23S rRNA methyltransferase	0.458124661	0.001962543
M5005_Spy0314	M5005_Spy0314	phosphatidyglycerophosphatase B-like protein	-0.470570153	9.93959E-06
M5005_Spy0316	M5005_Spy0316	SAM-dependent methyltransferase	0.333100392	0.039741746
M5005_Spy0322	fluB	ferrichrome transport system permease protein	0.217962872	0.046276251
M5005_Spy0326	M5005_Spy0326	export protein for polysaccharides and teichoic acids	-0.789552653	0.001909207
M5005_Spy0327	upp	uracil phosphoribosyltransferase	-3.760793283	3.56E-47
M5005_Spy0330	tmk	thymidylate kinase	-5.474524159	0.005126851
M5005_Spy0336	M5005_Spy0336	putative membrane associated protein	0.227719554	0.066639105
M5005_Spy0339	exoA	exodeoxyribonuclease III	-0.521764974	0.001201726
M5005_Spy0347	nrdF1	ribonucleoside-diphosphate reductase beta chain	0.414548993	0.01183171
M5005_Spy0349	nrdE1	ribonucleoside-diphosphate reductase alpha chain	0.239585762	0.00231244
M5005_Spy0355	M5005_Spy0355	hypothetical protein	-0.413641052	0.033509226
M5005_Spy0356	speJ	exotoxin type J precursor	-0.531416664	8.08557E-06
M5005_Spy0360	M5005_Spy0360	NAD-dependent oxidoreductase	0.560109837	0.073777816
M5005_Spy0362	gcaD	glucosamine-1-phosphate acetyltransferase/UDP-N-acetylglucosamine pyrophosphorylase	-2.819901279	0.027283575
M5005_Spy0382	mrsA2	peptide methionine sulfoxide reductase	-0.450389941	0.063082975
M5005_Spy0386	phoH	phoH protein	0.251675584	0.008742256
M5005_Spy0392	M5005_Spy0392	hypothetical protein	-0.275849052	0.097700924
M5005_Spy0401	M5005_Spy0401	putative cytosolic protein	-0.745819735	0.023429239
M5005_Spy0402	M5005_Spy0402	hypothetical protein	0.212113026	0.045483892
M5005_Spy0403	M5005_Spy0403	hypothetical protein	0.345460377	0.011247255
M5005_Spy0404	M5005_Spy0404	hypothetical protein	0.333799383	0.015896016
M5005_Spy0408	fpg	formamidopyrimidine-DNA glycosylase	0.77133238	0.000104062
M5005_Spy0410	M5005_Spy0410	ATPase	0.371146259	0.005101339
M5005_Spy0413	secG	protein translocase subunit	-5.454139643	0.010122892
M5005_Spy0414	M5005_Spy0414	exoribonuclease II	0.658883991	0.07552E-10
M5005_Spy0416	M5005_Spy0416	glutaminyl-peptide cyclotransferase	0.146665752	0.087758496
M5005_Spy0418	M5005_Spy0418	permease	1.195384928	0.012376206
M5005_Spy0421	gloA	lactoylglutathione lyase	-0.348835937	0.055819524
M5005_Spy0422	M5005_Spy0422	NAD(P)H-dependent quinone reductase	0.318253322	0.089536422
M5005_Spy0424	ccpA	catabolite control protein A	5.44809319	0.085908597
M5005_Spy0427	thrS	threonyl-tRNA synthetase	0.743032579	0.059036931
M5005_Spy0430	M5005_Spy0430	ABC transporter permease protein	0.324537781	0.038329821
M5005_Spy0436	vickK	two-component sensor histidine kinase	-0.409116947	0.097553316
M5005_Spy0441	aroE2	shikimate 5-dehydrogenase	-0.240832379	0.00420541
M5005_Spy0442	M5005_Spy0442	putative cytosolic protein	-0.503253364	0.000112234
M5005_Spy0447	M5005_Spy0447	glycosyltransferase involved in cell wall biogenesis	-0.18654923	0.050478912
M5005_Spy0448	M5005_Spy0448	hypothetical protein	-0.864731121	0.002763543
M5005_Spy0449	M5005_Spy0449	UDP-glucose 6-dehydrogenase	-0.251396648	0.02086061
M5005_Spy0450	mefE	macrolide-efflux protein	-0.246618577	0.00473631
M5005_Spy0459	M5005_Spy0459	portal protein	0.199630433	0.042981232
M5005_Spy0460	M5005_Spy0460	hypothetical protein	0.359757774	0.008286162
M5005_Spy0462	M5005_Spy0462	hypothetical protein	-0.3496676	0.011235629
M5005_Spy0463	M5005_Spy0463	putative cytosolic protein	-0.319129954	0.016477617
M5005_Spy0465	M5005_Spy0465	hypothetical protein	-0.350703968	0.055819524
M5005_Spy0466	M5005_Spy0466	hypothetical protein	-0.559105426	1.95809E-08
M5005_Spy0476	bglA	6-phospho-beta-glucosidase	0.139432888	0.074138854
M5005_Spy0480	M5005_Spy0480	transcription accessory protein	0.254495367	0.003921628
M5005_Spy0485	lgt	prolipoprotein diacylglycerol transferase	-1.514213018	2.90969E-13
M5005_Spy0486	M5005_Spy0486	hypothetical protein	-1.335010684	1.60421E-48
M5005_Spy0491	M5005_Spy0491	peptidase family U32	0.195959898	0.035799135
M5005_Spy0495	lysS	lysyl-tRNA synthetase	5.566998795	0.075621278
M5005_Spy0497	M5005_Spy0497	phosphoglycerate mutase	0.24300318	0.042251224
M5005_Spy0500	M5005_Spy0500	N-acetylmuramoyl-L-alanine amidase	2.009170538	0.003074125
M5005_Spy0504	pepF	oligoendopeptidase F	0.231640968	0.012708056
M5005_Spy0513	M5005_Spy0513	putative cytosolic protein	-0.399169698	3.83489E-05
M5005_Spy0517	regR	transcriptional regulator, LacI family	0.150030807	0.09943065
M5005_Spy0518	M5005_Spy0518	oligohyaluronate lyase	0.173131629	0.013228998
M5005_Spy0520	M5005_Spy0520	PTS system, N-acetylgalactosamine-specific IIC component	0.204210298	0.036622746
M5005_Spy0522	M5005_Spy0522	unsaturated glucuronyl hydrolase	0.150878671	0.095827026
M5005_Spy0524	idnO	gluconate 5-dehydrogenase	-0.248533492	0.037022899
M5005_Spy0525	M5005_Spy0525	galactose-6-phosphate isomerase LacB subunit	-0.486542277	0.004543723
M5005_Spy0536	dinG	ATP-dependent helicase	0.860612947	1.64063E-51
M5005_Spy0539	M5005_Spy0539	ATP-binding protein	1.216549546	0.000218713
M5005_Spy0542	pepD	dipeptidase	0.17046382	0.066246537

M5005_Spy0545	agaS	galactosamine-6-phosphate deaminase (isomerizing)	0.187969276	0.045050329
M5005_Spy0547	M5005_Spy0547	phosphoesterase, DHH family protein	-3.021810625	0.083049626
M5005_Spy0554	M5005_Spy0554	separation ring formation regulator	1.590734331	0.009463789
M5005_Spy0560	M5005_Spy0560	transcriptional regulator	-0.16372523	0.055481599
M5005_Spy0561	epf	putative extracellular matrix binding protein	-0.130974269	0.052587559
M5005_Spy0566	sagE	streptolysin S putative self-immunity protein	-0.886178576	5.0364E-08
M5005_Spy0567	sagF	streptolysin S biosynthesis protein	-0.646069417	1.02794E-09
M5005_Spy0568	sagG	streptolysin S export ATP-binding protein	-3.591807255	1.01347E-10
M5005_Spy0569	sagH	streptolysin S export transmembrane protein	-9.550753286	3.97519E-45
M5005_Spy0570	sagI	streptolysin S export transmembrane protein	-3.535902059	0.000896931
M5005_Spy0582	atpC	ATP synthase epsilon chain	-3.619434894	0.035600914
M5005_Spy0583	M5005_Spy0583	putative membrane associated protein	-0.482292413	0.008864751
M5005_Spy0585	epuA	epuA protein	-3.431252691	0.010310805
M5005_Spy0588	pheT	phenylalanyl-tRNA synthetase beta chain	3.374952552	0.048432699
M5005_Spy0591	M5005_Spy0591	ABC transporter permease protein	-0.356290488	0.000625482
M5005_Spy0601	M5005_Spy0601	putative cytosolic protein	0.450310749	0.018874614
M5005_Spy0606	rgpDc	polysaccharide export ATP-binding protein	-2.056855802	0.020685526
M5005_Spy0609	M5005_Spy0609	phosphoglycerol transferase	-0.208803679	0.006397367
M5005_Spy0611	M5005_Spy0611	hypothetical protein	-0.741203306	1.43172E-08
M5005_Spy0623	M5005_Spy0623	methyltransferase	-0.337974689	0.062642017
M5005_Spy0627	gor	glutathione reductase	-0.140512191	0.042358766
M5005_Spy0628	folC2	folylpolyglutamate synthase/dihydrofolate synthase	0.258789027	0.061712435
M5005_Spy0630	nifS1	cysteine desulfhydrase	-4.486916794	4.85637E-16
M5005_Spy0631	thil	thiamine biosynthesis protein	-4.590172489	1.08352E-65
M5005_Spy0632	capA	capsule biosynthesis protein	0.184018221	0.051535364
M5005_Spy0641	pyrB	aspartate carbamoyltransferase	-0.288579385	0.015988407
M5005_Spy0642	carA	carbamoyl-phosphate synthase small chain	-0.631877871	9.22589E-08
M5005_Spy0643	carB	carbamoyl-phosphate synthase large chain	-0.706332579	1.17224E-30
M5005_Spy0644	M5005_Spy0644	periplasmic component of efflux system	-1.541440308	4.1128E-99
M5005_Spy0645	M5005_Spy0645	ABC transporter ATP-binding protein	-1.44457496	8.63787E-42
M5005_Spy0646	M5005_Spy0646	ABC transporter permease protein	-1.584508519	1.48656E-95
M5005_Spy0647	M5005_Spy0647	glycerophosphoryl diester phosphodiesterase	-0.185580246	0.017530482
M5005_Spy0650	M5005_Spy0650	hypothetical protein	-1.15478348	4.72271E-06
M5005_Spy0651	M5005_Spy0651	cell surface protein	-0.17118654	0.013345994
M5005_Spy0656	trmD	tRNA (guanine-N(1)-)-methyltransferase	-1.153304497	0.043052855
M5005_Spy0659	apbA	2-dehydropanoate 2-reductase	-0.240377318	0.062493676
M5005_Spy0662	fruA	PTS system, fructose-specific IIBC component	0.491315856	0.001298911
M5005_Spy0665	M5005_Spy0665	transposase	-0.658091204	2.65764E-05
M5005_Spy0667	M5005_Spy0667	exotoxin type C precursor	-0.513485414	0.008731135
M5005_Spy0668	mac	IgG-degrading protease	-0.138720984	0.086878004
M5005_Spy0678	M5005_Spy0678	5'-nucleotidase	-0.158651615	0.022373836
M5005_Spy0681	M5005_Spy0681	two-component system histidine kinase	0.497114507	2.31717E-14
M5005_Spy0693	M5005_Spy0693	hypothetical protein	-0.682978656	7.96851E-14
M5005_Spy0694	cipl	ATP-dependent protease ATP-binding subunit	-0.203670826	0.012695731
M5005_Spy0697	arsC	arsenate reductase family protein	-1.103526379	0.039499256
M5005_Spy0701	cpsY	transcriptional regulator, LysR family	0.451992162	0.000726224
M5005_Spy0702	M5005_Spy0702	hypothetical protein	-0.537928537	0.00578271
M5005_Spy0703	pyrF	orotidine 5'-phosphate decarboxylase	0.227778564	0.032126133
M5005_Spy0715	M5005_Spy0715	SSU ribosomal protein S1P	2.815455688	0.029015736
M5005_Spy0717	M5005_Spy0717	rhodanese-related sulfurtransferase	-0.193034028	0.03428942
M5005_Spy0718	M5005_Spy0718	hypothetical protein	-0.66768531	0.015455493
M5005_Spy0719	M5005_Spy0719	glutathione S-transferase	0.326122642	0.001070897
M5005_Spy0720	M5005_Spy0720	putative exfoliative toxin	0.374509326	0.000854963
M5005_Spy0722	miaA	tRNA delta(2)-isopentenylpyrophosphate transferase	-0.897445585	1.79528E-06
M5005_Spy0723	hfIX	GTP-binding protein	0.282690168	0.083792854
M5005_Spy0728	apt	adenine phosphoribosyltransferase	-1.269625217	0.011695203
M5005_Spy0732	M5005_Spy0732	NIF3-related protein	0.47300846	0.007023517
M5005_Spy0736	cpsFQ	dTDP-glucose 4,6-dehydratase	-1.388990268	0.050082517
M5005_Spy0739	M5005_Spy0739	tetratricopeptide repeat family protein	-0.220365503	0.01052467
M5005_Spy0743	M5005_Spy0743	ABC transporter substrate-binding protein	0.19731534	0.079479868
M5005_Spy0745	M5005_Spy0745	ABC transporter permease protein	0.428030981	0.023036067
M5005_Spy0757	hylA	hyaluronate lyase precursor	-0.184658465	0.018862339
M5005_Spy0759	M5005_Spy0759	putative membrane associated protein	-2.577094924	0.007148767
M5005_Spy0767	M5005_Spy0767	4-nitrophenylphosphatase	0.308412199	0.004047161
M5005_Spy0769	M5005_Spy0769	putative cytosolic protein	-0.274591418	3.75238E-05
M5005_Spy0770	M5005_Spy0770	putative cytosolic protein	-0.23246321	0.015180111
M5005_Spy0772	M5005_Spy0772	hypothetical protein	-0.436729708	3.75238E-05
M5005_Spy0775	M5005_Spy0775	nucleoside diphosphate kinase	-0.552164962	0.00646147
M5005_Spy0777	M5005_Spy0777	collagen-like surface protein	-0.458186186	0.001668183
M5005_Spy0779	M5005_Spy0779	putative membrane spanning protein	-0.163138512	0.041869067
M5005_Spy0780	M5005_Spy0780	PTS system, mannose/fructose family IIA component	0.454006654	0.037326927
M5005_Spy0781	ptsB	PTS system, mannose/fructose family IIB component	0.611672318	7.63204E-06
M5005_Spy0782	ptsC	PTS system, mannose/fructose family IIC component	0.376551959	0.000569725
M5005_Spy0783	ptsD	PTS system, mannose/fructose family IID component	0.331255596	0.019975057
M5005_Spy0790	gabD	succinate-semialdehyde dehydrogenase [NADP+]	-0.284347021	0.02086061
M5005_Spy0791	uvrC	excinuclease ABC subunit C	-0.445433229	2.20381E-05
M5005_Spy0793	M5005_Spy0793	Xaa-His dipeptidase	0.560703965	0.000100943
M5005_Spy0802	M5005_Spy0802	relaxase	-0.381411232	0.06865672
M5005_Spy0803	srtI	protein involved in lantibiotic production	-0.319651566	4.02023E-06
M5005_Spy0804	srtR	nisin biosynthesis two-component response regulator	-0.509964755	9.90401E-11
M5005_Spy0805	srtK	nisin biosynthesis sensor protein	-0.593047294	3.99619E-12
M5005_Spy0806	srtA	lantibiotic precursor	-0.302245633	0.031801553
M5005_Spy0807	srtT	ABC transporter (ATP binding)-lantibiotic associated	-0.287940337	0.001915724
M5005_Spy0808	srtF	lantibiotic transport ATP-binding protein	-0.217577442	0.009049016
M5005_Spy0809	srtE	lantibiotic transport permease protein	-0.310343937	0.00050868

M5005_Spy0810	srtG	lantibiotic transport permease protein	-0.732801902	1.81742E-10
M5005_Spy0817	dacA1	D-alanyl-D-alanine carboxypeptidase	-0.646428424	2.21266E-11
M5005_Spy0826	potA	spermidine/putrescine transport system ATP-binding protein	-1.626790119	0.001197982
M5005_Spy0829	M5005_Spy0829	spermidine/putrescine-binding protein	-0.961070303	0.002665322
M5005_Spy0830	dpiA	transcriptional regulatory protein	-0.20632639	0.024495548
M5005_Spy0834	M5005_Spy0834	Zn-dependent alcohol dehydrogenase	-0.212902628	0.006286012
M5005_Spy0835	M5005_Spy0835	class B acid phosphatase	-0.201184949	0.009524881
M5005_Spy0837	M5005_Spy0837	chloride channel protein	-0.185223605	0.039954176
M5005_Spy0838	M5005_Spy0838	lipase/acylhydrolase family protein	-0.55727827	4.33802E-06
M5005_Spy0840	radC	DNA repair protein	-0.227820748	0.005101339
M5005_Spy0841	M5005_Spy0841	glutamine amidotransferase, class I	-0.707558395	0.000125584
M5005_Spy0852	M5005_Spy0852	short chain dehydrogenase	-0.256792483	0.090248662
M5005_Spy0858	xpt	xanthine phosphoribosyltransferase	-0.268954242	0.018862339
M5005_Spy0872	nox	NADH oxidase H ₂ O-forming	-0.59864277	7.62002E-09
M5005_Spy0873	ldh	L-lactate dehydrogenase	-0.477887123	0.019613879
M5005_Spy0874	gyrA	DNA gyrase subunit A	-0.977681224	0.029248331
M5005_Spy0876	M5005_Spy0876	lactoylglutathione lyase	-0.25003312	0.038977515
M5005_Spy0877	M5005_Spy0877	hypothetical protein	-0.473604404	0.031736637
M5005_Spy0878	M5005_Spy0878	hypothetical protein	-0.234939345	0.080297955
M5005_Spy0879	M5005_Spy0879	hypothetical protein	-0.261789326	0.019374036
M5005_Spy0891	satD	SatD	0.617325194	0.045483892
M5005_Spy0893	gid	glucose inhibited division protein A	-0.259273813	0.048432699
M5005_Spy0895	M5005_Spy0895	putative membrane associated protein	-0.389309652	0.064991662
M5005_Spy0898	M5005_Spy0898	2-(5"-triphosphoribosyl)-3'-dephosphocoenzyme-A synthase	-0.188588206	0.043052855
M5005_Spy0899	citG	transcriptional regulator, GntR family	-0.337749688	1.58332E-05
M5005_Spy0902	M5005_Spy0902	biotin carboxyl carrier protein of oxaloacetate decarboxylase	0.366176653	0.012105096
M5005_Spy0903	oadB	oxaloacetate decarboxylase beta chain	0.307217067	0.011247255
M5005_Spy0907	citF	citrate lyase alpha chain/citrate CoA-transferase	0.171550105	0.050478912
M5005_Spy0909	oadA1	oxaloacetate decarboxylase alpha chain	0.216740059	0.00420541
M5005_Spy0910	citC	(citrate [pro-3S]-lyase)-ligase	-0.333546645	2.57351E-05
M5005_Spy0911	M5005_Spy0911	hypothetical protein	-0.277163007	0.003043587
M5005_Spy0912	M5005_Spy0912	hypothetical protein	-0.856426057	0.079110579
M5005_Spy0914	M5005_Spy0914	phage transcriptional repressor	-0.346738044	9.02856E-06
M5005_Spy0917	M5005_Spy0917	transcriptional regulator, GntR family	-3.369771849	0.00210549
M5005_Spy0918	M5005_Spy0918	hypothetical protein	-0.397583243	0.000129472
M5005_Spy0919	guaA	GMP synthase (glutamine-hydrolyzing)	-2.644873012	0.079479868
M5005_Spy0921	M5005_Spy0921	ABC transporter ATP-binding protein	-0.177911404	0.025445763
M5005_Spy0922	pdxK	putative membrane spanning protein	-0.204543515	0.064346731
M5005_Spy0923	M5005_Spy0923	pyridoxine kinase	-0.255226652	0.005013446
M5005_Spy0924	M5005_Spy0924	transcriptional regulator, GntR family	-0.206589577	0.003163037
M5005_Spy0925	rhbB	anaerobic ribonucleoside-triphosphate reductase	-0.367195648	0.015540508
M5005_Spy0926	M5005_Spy0926	cardiolipin synthetase	-4.518570737	1.87905E-05
M5005_Spy0933	M5005_Spy0933	putative NADH-dependent flavin oxidoreductase	-0.269177519	0.018819632
M5005_Spy0934	M5005_Spy0934	lipoate-protein ligase A	0.172382542	0.091852654
M5005_Spy0937	M5005_Spy0937	transporter	-1.497022595	0.03428942
M5005_Spy0938	pgmA	phosphoglucomutase/phosphomannomutase	-0.704754428	0.020334567
M5005_Spy0939	M5005_Spy0939	nucleoside transport system permease protein	1.423525894	4.01779E-91
M5005_Spy0940	M5005_Spy0940	nucleoside transport system permease protein	1.522236924	7.0464E-117
M5005_Spy0941	M5005_Spy0941	nucleoside transport ATP-binding protein	1.466779159	9.4611E-102
M5005_Spy0942	M5005_Spy0942	nucleoside-binding protein	1.113322223	7.93514E-49
M5005_Spy0943	cdd	cytidine deaminase	1.143622623	1.06445E-31
M5005_Spy0944	M5005_Spy0944	16S rRNA m(2)G 1207 methyltransferase	-0.620482362	7.22081E-11
M5005_Spy0945	coaA	pantothenate kinase	-5.221473982	0.022902762
M5005_Spy0947	ciaH	sensor protein	-0.474748144	3.00238E-06
M5005_Spy0951	pstB	phosphate transport ATP-binding protein	-2.978192892	2.6596E-117
M5005_Spy0952	pstB2	phosphate transport ATP-binding protein	-3.039122372	8.19558E-91
M5005_Spy0953	pstA	phosphate transport system permease protein	-3.66352396	3.76273E-82
M5005_Spy0954	pstC	phosphate transport system permease protein	-3.731565246	2.41396E-27
M5005_Spy0955	pstS	phosphate-binding protein	-3.418296477	1.20833E-65
M5005_Spy0961	truB	tRNA pseudouridine synthase B	-2.988818399	0.008611858
M5005_Spy0962	M5005_Spy0962	hypothetical protein	-0.334517118	0.009641165
M5005_Spy0970	M5005_Spy0970	NAD-dependent K ⁺ or Na ⁺ uptake system component	-2.489910656	0.003229991
M5005_Spy0971	M5005_Spy0971	general stress protein, Gls24 family	-1.314912395	7.44134E-07
M5005_Spy0972	M5005_Spy0972	hypothetical protein	-1.147445632	0.025445763
M5005_Spy0973	M5005_Spy0973	general stress protein, Gls24 family	-0.928622544	1.00356E-06
M5005_Spy0975	M5005_Spy0975	hypothetical protein	-1.850186941	2.2057E-06
M5005_Spy0977	pcrA	DNA helicase II	-6.171575411	0.000202935
M5005_Spy0980	M5005_Spy0980	cobalt-zinc-cadmium resistance protein	-0.484768716	5.37384E-06
M5005_Spy0981	cfa	cAMP factor	-0.490437364	6.58601E-08
M5005_Spy0982	M5005_Spy0982	histidine-binding protein	-0.197637301	0.052582081
M5005_Spy0987	sipC	signal peptidase I	-1.84149263	1.3023E-51
M5005_Spy0992	M5005_Spy0992	ABC transporter ATP-binding protein	-1.509443047	6.36708E-09
M5005_Spy0993	M5005_Spy0993	ABC transporter permease protein	-1.477594628	7.95215E-08
M5005_Spy0995	M5005_Spy0995	phage protein	-0.377219036	0.050065503
M5005_Spy0998	M5005_Spy0998	phage protein	-0.262429119	0.074605928
M5005_Spy1000	M5005_Spy1000	phage protein	-0.274441447	0.001201726
M5005_Spy1001	M5005_Spy1001	phage-associated cell wall hydrolase	0.424829892	0.000451039
M5005_Spy1002	M5005_Spy1002	N-acetylmuramoyl-L-alanine amidase	-0.305979042	0.062600297
M5005_Spy1021	M5005_Spy1021	phage protein	-0.624056329	2.90969E-13
M5005_Spy1022	M5005_Spy1022	portal protein	-0.473504708	9.63722E-09
M5005_Spy1023	M5005_Spy1023	terminase large subunit	-0.635879032	2.22189E-16
M5005_Spy1044	M5005_Spy1044	phage protein	-0.319188699	0.085908597
M5005_Spy1050	M5005_Spy1050	phage transcriptional repressor	-1.354754083	3.5842E-05
M5005_Spy1051	M5005_Spy1051	phage protein	-0.280017355	0.001109135
M5005_Spy1055	glgP	glycogen phosphorylase	-0.163806986	0.022373836

M5005_Spy1056	malM	4-alpha-glucanotransferase	0.936798644	4.06672E-54
M5005_Spy1057	malR	transcriptional regulator, LacI family	0.278212091	0.000168493
M5005_Spy1058	malE	maltose/maltodextrin-binding protein	0.313247685	6.64893E-05
M5005_Spy1059	malF	maltose transport system permease protein	0.367270557	1.46348E-07
M5005_Spy1060	malG	maltose transport system permease protein	0.258151957	0.004640916
M5005_Spy1061	M5005_Spy1061	transcriptional regulator, LacI family	0.618085185	1.3616E-21
M5005_Spy1065	amyA	alpha-amylase	-0.274386065	2.62039E-05
M5005_Spy1066	amyB	neopullulanase/cyclomaltodextrinase/maltogenic alpha-amylase	-0.579233429	4.25792E-15
M5005_Spy1067	malX	maltose/maltodextrin-binding protein	-0.923463181	2.79824E-34
M5005_Spy1068	M5005_Spy1068	transposase	-0.915354586	1.02556E-10
M5005_Spy1069	M5005_Spy1069	esterase	-0.236876084	0.018862339
M5005_Spy1075	uvrB	excinuclease ABC subunit B	-0.578960835	6.39446E-09
M5005_Spy1076	glnH	transporter	4.977975137	0.034134532
M5005_Spy1078	M5005_Spy1078	hypothetical protein	-2.257774081	0.039513967
M5005_Spy1081	M5005_Spy1081	PTS system, cellobiose-specific IIA component	0.359129573	0.022636552
M5005_Spy1083	M5005_Spy1083	transcription antiterminator, BglG family	0.161968481	0.015915663
M5005_Spy1084	M5005_Spy1084	outer surface protein	0.21339749	0.013905271
M5005_Spy1085	bgIA2	beta-glucosidase	0.480840127	2.64073E-08
M5005_Spy1086	M5005_Spy1086	nicotinamide mononucleotide transporter	0.56485107	8.0465E-15
M5005_Spy1087	M5005_Spy1087	putative cytosolic protein	0.884612135	0.068385305
M5005_Spy1094	M5005_Spy1094	transporter, MFS superfamily	0.259696899	0.008742256
M5005_Spy1095	M5005_Spy1095	putative cytosolic protein	-0.20114759	0.088303192
M5005_Spy1097	M5005_Spy1097	phosphorylase, Pnp/Udp family	0.235713751	0.050203386
M5005_Spy1099	M5005_Spy1099	transcriptional regulator, LytR family	-0.584428981	1.33375E-18
M5005_Spy1102	M5005_Spy1102	ribonuclease BN	-0.447898576	0.03208786
M5005_Spy1108	metK2	S-adenosylmethionine synthetase	-2.665666795	0.000187604
M5005_Spy1110	birA	biotin operon repressor/biotin-[acetyl-CoA-carboxylase] synthetase	-1.40299824	0.003061224
M5005_Spy1115	M5005_Spy1115	putative membrane spanning protein	-0.386317245	0.001229649
M5005_Spy1119	gapN	NADP-dependent glyceraldehyde-3-phosphate dehydrogenase	6.441865579	0.025186074
M5005_Spy1129	M5005_Spy1129	CAAX amino terminal protease family	-0.220385518	0.01058867
M5005_Spy1130	M5005_Spy1130	putative membrane spanning protein	-0.183858675	0.05984632
M5005_Spy1133	surA	peptidyl-prolyl cis-trans isomerase	-0.551867045	0.000192463
M5005_Spy1137	M5005_Spy1137	putative competence protein/transcription factor	-0.267886336	0.071907398
M5005_Spy1139	nagB	glucosamine-6-phosphate isomerase	-4.193665393	1.07975E-14
M5005_Spy1147	comEC	COME operon protein 3	0.217555709	0.001629878
M5005_Spy1151	M5005_Spy1151	hypothetical protein with endo/excinuclease domain	-0.354245713	0.000873811
M5005_Spy1157	murF	UDP-N-acetylmuramoylalanine-D-glutamyl-lysine-- D-alanyl-D-alanine ligase	5.556998795	0.075621278
M5005_Spy1165	pyrD	dihydroorotate dehydrogenase	-0.281950298	0.006286012
M5005_Spy1167	M5005_Spy1167	lead, cadmium, zinc and mercury transporting ATPase	0.276071356	0.011358486
M5005_Spy1170	M5005_Spy1170	putative membrane associated protein	-0.494774633	2.98226E-06
M5005_Spy1171	M5005_Spy1171	phage-associated cell wall hydrolase	0.210612451	0.024969828
M5005_Spy1174	M5005_Spy1174	phage protein	0.385565848	0.020320816
M5005_Spy1182	M5005_Spy1182	phage protein	-0.731757122	0.008286162
M5005_Spy1188	M5005_Spy1188	phage protein	0.290216255	0.045335182
M5005_Spy1197	M5005_Spy1197	phage protein	-0.456008396	0.003538408
M5005_Spy1203	M5005_Spy1203	phage protein	0.389134188	0.001668183
M5005_Spy1215	M5005_Spy1215	phage protein	0.495964939	0.002686892
M5005_Spy1220	M5005_Spy1220	phage protein	-0.226785558	0.005190239
M5005_Spy1222	int2	integrase	-0.148565939	0.041659261
M5005_Spy1223	M5005_Spy1223	DNA-binding protein HU	-2.174913445	0.048130396
M5005_Spy1226	M5005_Spy1226	degV family protein	-0.630511253	1.32692E-07
M5005_Spy1235	M5005_Spy1235	phosphoglucomutase	0.225470105	0.023982661
M5005_Spy1236	phr	deoxyribodipyrimidine photolyase	-0.16361355	0.07534827
M5005_Spy1237	artP	arginine transport ATP-binding protein	-0.190283184	0.065660389
M5005_Spy1238	artQ	arginine transport system permease protein	0.259577814	0.027982524
M5005_Spy1240	clpE	ATP-dependent clp protease ATP-binding subunit	-0.323440964	0.000274659
M5005_Spy1242	M5005_Spy1242	putative cytosolic protein	-7.608444821	1.51381E-33
M5005_Spy1255	typA	GTP-binding protein	-4.575433519	0.000830429
M5005_Spy1269	asnA	aspartate--ammonia ligase	-0.251033505	0.020141515
M5005_Spy1270	arcC	carbamate kinase	-0.482305522	0.039741746
M5005_Spy1271	M5005_Spy1271	Xaa-His dipeptidase	0.502225237	4.92346E-07
M5005_Spy1272	M5005_Spy1272	arginine/ornithine antiporter	0.161242981	0.054643931
M5005_Spy1273	arcB	ornithine carbamoyltransferase	-1.319030567	1.8134E-11
M5005_Spy1279	M5005_Spy1279	putative cytosolic protein	0.429928638	7.50195E-07
M5005_Spy1280	M5005_Spy1280	two-component sensor kinase	0.224361638	0.008122161
M5005_Spy1287	M5005_Spy1287	hypothetical protein	0.472912603	0.000537535
M5005_Spy1293	M5005_Spy1293	hypothetical protein	-0.334049905	0.049929831
M5005_Spy1297	M5005_Spy1297	phospho-2-dehydro-3-deoxyheptonate aldolase	-0.540603823	0.084059288
M5005_Spy1301	M5005_Spy1301	putative cytosolic protein	0.378482422	0.000125584
M5005_Spy1304	lacZ	beta-galactosidase	0.408229233	5.58481E-08
M5005_Spy1305	M5005_Spy1305	two-component response regulator	0.4667239	0.000112969
M5005_Spy1306	M5005_Spy1306	two-component sensor kinase	0.488308793	2.92151E-09
M5005_Spy1307	M5005_Spy1307	putative membrane spanning protein	0.840468479	3.92899E-08
M5005_Spy1308	M5005_Spy1308	sugar-binding protein	0.361881858	1.17645E-05
M5005_Spy1309	M5005_Spy1309	sugar transport system permease protein	0.546001949	0.000169225
M5005_Spy1310	M5005_Spy1310	sugar transport system permease protein	0.553540433	5.52214E-07
M5005_Spy1317	M5005_Spy1317	alpha-mannosidase	-0.301693882	9.69997E-05
M5005_Spy1318	rocA	sensory transduction protein kinase	1.398347665	0.084124674
M5005_Spy1319	M5005_Spy1319	tRNA (uracil-5-)-methyltransferase	-0.132432433	0.099630691
M5005_Spy1320	recX	regulatory protein	-0.194478815	0.022641037
M5005_Spy1325	M5005_Spy1325	ribosome-associated factor Y	-1.099584576	4.04882E-23
M5005_Spy1326	comFC	COMF operon protein 3	-0.405790057	4.83685E-06
M5005_Spy1328	M5005_Spy1328	Xaa-Pro dipeptidase	-0.231903753	0.070341295
M5005_Spy1329	cysM	cysteine synthase	0.288006618	0.000647673
M5005_Spy1333	yvqE	two-component sensor protein	0.366821548	0.013230485

M5005_Spy1344	atoB	acetyl-CoA acetyltransferase	-0.444354546	0.015527665
M5005_Spy1348	M5005_Spy1348	D-beta-hydroxybutyrate permease	0.218834135	0.015540508
M5005_Spy1349	luxS	autoinducer-2 production protein	0.29427768	0.018862339
M5005_Spy1355	pbp1A	multimodular transpeptidase-transglycosylase	-0.561682942	0.013925526
M5005_Spy1356	pepC	aminopeptidase C	0.169469573	0.064346731
M5005_Spy1359	M5005_Spy1359	amino acid permease	-0.561029009	0.002763543
M5005_Spy1366	M5005_Spy1366	division specific D,D-transpeptidase/cell division protein ftsI	3.371976055	0.097918619
M5005_Spy1372	proB	ABC transporter permease protein	0.233415478	0.002429291
M5005_Spy1373	M5005_Spy1373	ABC transporter ATP-binding protein	-0.202126916	0.093583862
M5005_Spy1375	tkt	transketolase	-3.962639533	6.29298E-36
M5005_Spy1377	M5005_Spy1377	trans-acting positive regulator	-0.477973153	0.000888004
M5005_Spy1380	glpO	alpha-glycerophosphate oxidase	0.240273589	0.035634592
M5005_Spy1381	glpK	glycerol kinase	-0.433757478	0.002733999
M5005_Spy1382	M5005_Spy1382	putative membrane associated protein	-0.344693195	0.080866813
M5005_Spy1388	nagA	N-acetylglucosamine-6-phosphate deacetylase	-7.212465674	5.2677E-157
M5005_Spy1389	M5005_Spy1389	sodium-dependent phosphate transporter	-0.148806118	0.066687474
M5005_Spy1391	M5005_Spy1391	degV family protein	1.736095736	0.052582081
M5005_Spy1399	M5005_Spy1399	PTS system, galactose-specific IIC component	0.784935252	7.88432E-18
M5005_Spy1400	M5005_Spy1400	PTS system, galactose-specific IIB component	0.490815896	1.04592E-13
M5005_Spy1401	M5005_Spy1401	PTS system, galactose-specific IIA component	0.383376922	0.003497479
M5005_Spy1402	lacR1	lactose phosphotransferase system repressor	-1.366480206	7.25676E-31
M5005_Spy1407	M5005_Spy1407	esterase	0.226700319	0.001668183
M5005_Spy1415	sdaD2	phage-encoded streptodornase	-0.253198709	0.009657764
M5005_Spy1418	M5005_Spy1418	phage protein	-0.497771868	0.000246481
M5005_Spy1419	M5005_Spy1419	phage protein	0.424467921	0.018862339
M5005_Spy1420	M5005_Spy1420	phage protein	-0.846504521	0.005417691
M5005_Spy1423	M5005_Spy1423	hyaluronoglucosaminidase	0.275804483	0.001902523
M5005_Spy1431	M5005_Spy1431	phage protein	0.67520532	0.018862339
M5005_Spy1438	M5005_Spy1438	phage protein	-0.281395691	0.00229437
M5005_Spy1439	M5005_Spy1439	portal protein	-1.439983846	8.4564E-127
M5005_Spy1440	M5005_Spy1440	terminase large subunit	-0.412153157	0.006194723
M5005_Spy1444	M5005_Spy1444	adenine-specific methyltransferase	-0.311112327	0.039954176
M5005_Spy1445	M5005_Spy1445	phage protein	-4.664231618	0.001085592
M5005_Spy1449	M5005_Spy1449	DNA primase	0.217251909	0.085116271
M5005_Spy1456	M5005_Spy1456	phage protein	-4.990186237	0.042209046
M5005_Spy1462	M5005_Spy1462	phage protein	-5.267644344	1.66913E-05
M5005_Spy1465	M5005_Spy1465	phage protein	-0.424735962	0.001915724
M5005_Spy1467	int3	integrase	0.180163013	0.06865672
M5005_Spy1468	M5005_Spy1468	tRNA (m(7)G46) methyltransferase	-13.00104577	3.2463E-165
M5005_Spy1472	hit	bis(5'-nucleosyl)-tetraphosphatase (asymmetrical)	-1.211067462	1.12156E-35
M5005_Spy1473	M5005_Spy1473	hypothetical protein	-0.974893093	1.96627E-05
M5005_Spy1479	manL	PTS system, mannose-specific IIAB component	-0.702215056	1.36384E-08
M5005_Spy1480	manM	PTS system, mannose-specific IIC component	-0.937929851	2.97938E-06
M5005_Spy1481	manN	PTS system, mannose-specific IID component	-0.83889263	1.93122E-17
M5005_Spy1498	dnaK	chaperone protein	-5.236670412	0.022641037
M5005_Spy1500	hrcA	heat-inducible transcription repressor	-3.599239831	0.005039853
M5005_Spy1504	M5005_Spy1504	putative membrane spanning protein	0.366307101	0.02192047
M5005_Spy1509	M5005_Spy1509	pyruvate, phosphate dikinase	0.817043773	0.027317056
M5005_Spy1512	codY	transcription pleiotropic repressor	-2.959789517	0.039513967
M5005_Spy1513	M5005_Spy1513	aspartate aminotransferase	-0.368993456	0.000189285
M5005_Spy1515	M5005_Spy1515	hydrolase, HAD superfamily	0.172917017	0.060336408
M5005_Spy1516	asnB	L-asparaginase	0.455509504	0.000307381
M5005_Spy1519	recG	ATP-dependent DNA helicase	-1.11657301	6.08348E-11
M5005_Spy1527	M5005_Spy1527	ferrichrome transport system permease protein	0.618036991	5.33413E-05
M5005_Spy1538	pmi	mannose-6-phosphate isomerase	0.628777823	0.00138895
M5005_Spy1539	scrK	fructokinase	0.414684224	0.010664926
M5005_Spy1550	uvrA	excinuclease ABC subunit A	-0.236775662	0.06826675
M5005_Spy1558	M5005_Spy1558	transcriptional regulator	-0.301444678	0.001966332
M5005_Spy1560	M5005_Spy1560	phosphatidyglycerophosphate B	-1.2080037	5.63962E-24
M5005_Spy1561	mutS2	DNA mismatch repair protein	-0.584722062	3.65797E-09
M5005_Spy1567	M5005_Spy1567	hypothetical protein	-0.286061264	0.090397294
M5005_Spy1568	dinP	DNA polymerase IV	0.202610587	0.030632061
M5005_Spy1573	glpF2	aquaporin	1.611622487	0.050478912
M5005_Spy1577	pepXP	Xaa-Pro dipeptidyl-peptidase	0.340952	0.004979884
M5005_Spy1582	dnaQ	DNA polymerase III, epsilon chain	0.307848822	0.009955499
M5005_Spy1584	M5005_Spy1584	NAD(FAD)-utilizing dehydrogenase	0.441960562	0.000317167
M5005_Spy1585	deoC	deoxyribose-phosphate aldolase	-0.233869603	0.02175804
M5005_Spy1586	nupC	nucleoside permease	0.223529451	0.009561789
M5005_Spy1587	udp	uridine phosphorylase	0.270827675	0.012740525
M5005_Spy1595	M5005_Spy1595	Zn-dependent hydrolase	5.022470538	0.064532535
M5005_Spy1602	M5005_Spy1602	putative kinase related to hydroxyacetone kinase	-2.352861447	0.080939509
M5005_Spy1608	M5005_Spy1608	alpha/beta hydrolase	-0.580446044	0.003265802
M5005_Spy1610	pyrG	CTP synthase	-0.142100121	0.052582081
M5005_Spy1611	ropE	DNA-directed RNA polymerase delta chain	-1.41963475	2.98726E-16
M5005_Spy1612	ropA	trigger factor, ppiase	0.70095093	0.002163563
M5005_Spy1616	thiD	phosphomethylpyrimidine kinase/hydroxymethylpyrimidine kinase	-2.492894758	0.095126277
M5005_Spy1617	M5005_Spy1617	tRNA pseudouridine synthase A	-2.283340962	0.0177399
M5005_Spy1625	salR	transcriptional regulatory protein	-0.20136515	0.02883937
M5005_Spy1626	M5005_Spy1626	sensory transduction protein kinase	-0.194677778	0.054116435
M5005_Spy1632	lacG	6-phospho-beta-galactosidase	0.258338563	0.000218513
M5005_Spy1636	lacC2	tagatose-6-phosphate kinase	-0.404226621	0.000283646
M5005_Spy1638	lacA2	galactose-6-phosphate isomerase lacA subunit	-0.328668168	0.012289529
M5005_Spy1639	lacR2	lactose phosphotransferase system repressor	0.494478436	1.25242E-14
M5005_Spy1640	M5005_Spy1640	DNA-damage-inducible protein J	0.283527932	0.015794251
M5005_Spy1649	M5005_Spy1649	putative membrane spanning protein	0.355707135	0.00206804

M5005_Spy1651	M5005_Spy1651	putative cytosolic protein	0.259398798	0.081912993
M5005_Spy1659	M5005_Spy1659	hypothetical protein	0.453523068	0.073437748
M5005_Spy1660	M5005_Spy1660	polyribonucleotide nucleotidyltransferase	1.245338181	0.020348967
M5005_Spy1664	M5005_Spy1664	transcription antiterminator, BglG family	0.362199458	5.73456E-06
M5005_Spy1669	def	peptide deformylase	3.26014419	0.051298786
M5005_Spy1680	pulA	pullulanase	0.224386848	0.013551182
M5005_Spy1682	msmK	multiple sugar transport ATP-binding protein	0.797553942	2.07391E-22
M5005_Spy1683	lrp	leucine rich protein	0.737409202	1.98177E-09
M5005_Spy1685	M5005_Spy1685	D-tyrosyl-tRNA(Tyr) deacylase	0.53485458	0.005929472
M5005_Spy1692	M5005_Spy1692	PTS system, glucose-specific IIBC component	0.597116861	2.77651E-07
M5005_Spy1695	M5005_Spy1695	ribosomal protein L11 methyltransferase	0.559880437	0.022636552
M5005_Spy1697	M5005_Spy1697	para-aminobenzoate synthetase component I/4-amino-4-deoxychorismate lyase	0.239293096	0.012376206
M5005_Spy1699	M5005_Spy1699	ATPase, AAA family	0.683634362	4.99451E-13
M5005_Spy1700	M5005_Spy1700	acetyltransferase	0.278100883	0.070666156
M5005_Spy1701	flaR	DNA topology modulation protein flar-related protein	0.309190756	0.000449019
M5005_Spy1702	smeZ	mitogenic exotoxin Z	-0.256644386	0.01183171
M5005_Spy1704	dppA	dipeptide-binding protein	0.177291251	0.084144004
M5005_Spy1705	dppB	dipeptide transport system permease protein	0.295792923	0.001602549
M5005_Spy1706	dppC	dipeptide transport system permease protein	0.416414853	0.000248447
M5005_Spy1707	dppD	dipeptide transport ATP-binding protein	0.326891016	0.000693831
M5005_Spy1708	dppE	dipeptide transport ATP-binding protein	0.264083142	0.020320816
M5005_Spy1710	M5005_Spy1710	streptococcal histidine triad protein	0.185034073	0.029788019
M5005_Spy1716	M5005_Spy1716	transposase	0.393492466	3.31866E-05
M5005_Spy1719	emm10	M protein	-0.607432361	1.24953E-11
M5005_Spy1720	mga	trans-acting positive regulator	-0.416490412	1.91766E-11
M5005_Spy1723	isp	immunogenic secreted protein	0.2862176	0.002852784
M5005_Spy1726	M5005_Spy1726	ABC transporter permease protein	0.696430374	1.04083E-20
M5005_Spy1727	M5005_Spy1727	ABC transporter ATP-binding protein	0.594670157	7.12678E-14
M5005_Spy1728	M5005_Spy1728	periplasmic component of efflux system	0.830880895	4.61118E-26
M5005_Spy1730	M5005_Spy1730	hypothetical protein	0.331111849	0.001354501
M5005_Spy1733	M5005_Spy1733	hypothetical protein	-0.571358682	0.001602549
M5005_Spy1735	speB	streptococcal pyrogenic exotoxin B	-0.448614901	1.46348E-07
M5005_Spy1737	rgg	transcriptional regulator	-0.60803916	1.01158E-12
M5005_Spy1741	gidA	glycerol dehydrogenase	0.477242048	0.001350488
M5005_Spy1744	M5005_Spy1744	PTS system, cellobiose-specific IIC component	0.332225662	3.53777E-05
M5005_Spy1749	M5005_Spy1749	pyruvate formate-lyase activating enzyme	0.273188698	0.036267549
M5005_Spy1753	pbp2A	multimodular transpeptidase-transglycosylase	-1.701073932	1.21918E-38
M5005_Spy1754	M5005_Spy1754	translation initiation inhibitor	0.578133079	8.59764E-09
M5005_Spy1758	M5005_Spy1758	putative dipeptidase B	0.224893912	0.012922985
M5005_Spy1763	clpC	negative regulator of genetic competence	0.527358057	0.002822606
M5005_Spy1764	ctsR	transcriptional regulator	-2.112263538	0.017323405
M5005_Spy1769	ahpF	peroxiredoxin reductase (NAD(P)H)	-1.608013058	4.78705E-08
M5005_Spy1770	hutI	imidazolonepropionase	-0.658878789	7.49962E-08
M5005_Spy1771	hutU	urocanate hydratase	0.223761645	0.025186074
M5005_Spy1772	M5005_Spy1772	glutamate formiminotransferase	0.535045256	1.59808E-11
M5005_Spy1773	M5005_Spy1773	formiminotetrahydrofolate cyclodeaminase	0.452499942	0.000502414
M5005_Spy1774	fts2	formate-tetrahydrofolate ligase	0.293682962	0.092294308
M5005_Spy1776	M5005_Spy1776	amino acid permease	0.287974874	0.054082194
M5005_Spy1778	hutG	formiminoglutamase	0.311724949	0.056344786
M5005_Spy1779	M5005_Spy1779	transcriptional regulator, LuxR family	0.36470297	8.17407E-06
M5005_Spy1781	M5005_Spy1781	protein translation elongation factor Ts	-5.108954746	0.012376206
M5005_Spy1782	pepO	neutral endopeptidase	-0.229625995	0.05278458
M5005_Spy1783	dexS	trehalose-6-phosphate hydrolase	-1.191324288	1.63034E-05
M5005_Spy1787	M5005_Spy1787	glyoxalase family protein	0.160235378	0.1079360043
M5005_Spy1788	yaaA	protein yaaA	0.255043352	0.01895794
M5005_Spy1790	M5005_Spy1790	acetyltransferase	0.449027849	0.047012372
M5005_Spy1795	M5005_Spy1795	putative cytosolic protein	-1.386113921	0.015769961
M5005_Spy1797	M5005_Spy1797	putative cytosolic protein	0.729447051	0.079431343
M5005_Spy1807	argR2	arginine repressor	0.732316047	5.52603E-05
M5005_Spy1808	argS	arginyl-tRNA synthetase	-0.673288887	0.001422107
M5005_Spy1809	uviB	bacteriocin	-0.291216386	0.016747596
M5005_Spy1810	M5005_Spy1810	putative membrane spanning protein	-1.971145625	5.58352E-60
M5005_Spy1811	M5005_Spy1811	putative membrane spanning protein	-0.472299452	0.062886601
M5005_Spy1817	cadD	cadmium resistance protein	0.249493028	0.041999538
M5005_Spy1820	M5005_Spy1820	ftsK/SpoIIIE family	0.386963026	0.001421108
M5005_Spy1823	M5005_Spy1823	integral membrane protein	-0.916375635	0.019816437
M5005_Spy1828	M5005_Spy1828	phage infection protein	0.268573588	0.020320816
M5005_Spy1834	M5005_Spy1834	hypothetical protein	-5.17957345	0.018862339
M5005_Spy1837	M5005_Spy1837	phosphoesterase, DHH family protein	-7.356812768	3.8605E-29
M5005_Spy1840	trmU	tRNA (5-methylaminomethyl-2-thiouridylate)-methyltransferase	-5.815019933	0.010094839
M5005_Spy1842	sdhA	L-serine dehydratase	0.557134673	3.0844E-06
M5005_Spy1843	M5005_Spy1843	transglycosylase SLT domain family protein	0.434316506	0.000318608
M5005_Spy1848	M5005_Spy1848	putative membrane associated protein	4.837011797	0.065629818
M5005_Spy1851	hasA	hyaluronan synthase	0.214319893	0.001422107
M5005_Spy1852	hasB	UDP-glucose 6-dehydrogenase	-0.233693097	0.001201726
M5005_Spy1853	hasC	UTP--glucose-1-phosphate uridylyltransferase	0.324775405	5.05641E-05
M5005_Spy1856	M5005_Spy1856	glucose uptake protein-like protein	-0.22040789	0.015259435
M5005_Spy1857	guaB	inosine-5'-monophosphate dehydrogenase	0.882414252	2.46744E-24
M5005_Spy1862	M5005_Spy1862	ABC transporter, permease protein	-0.5200987	2.46798E-09
M5005_Spy1864	M5005_Spy1864	putative cytosolic protein	-0.253255289	0.027283575
M5005_Spy1866	parB	chromosome partitioning protein	-0.305944422	0.006097699

* fitness score is defined as log2 fold changes in sequence read counts between input and output pools. Only genes with statistically significant change (q value < 0.1) are listed.