TABLE S5 Fitness score of each gene in the M1 GAS genome after 24 hour saliva incubation.

loous ton	aana nama	function	Eitness seers*	a value
locus_tag	gene_name		Fitness score*	q.value 0.010657001
		GTP-binding protein	-0.665004783	
M5005_Spy0013		cell division protein	-0.540255124	0.012515326
		amino acid permease	-0.373112573	1.99782E-12
M5005_Spy0017		secreted protein	-4.058691305	0.000996406
		phosphoribosylaminoimidazole-succinocarboxamide synthase	0.244397101	0.004571132
M5005_Spy0024		amidophosphoribosyltransferase	0.628808878	2.94011E-28
M5005_Spy0025	•	phosphoribosylformylglycinamidine cyclo-ligase	0.315246875	6.01592E-06
M5005_Spy0029		phosphoribosylamineglycine ligase	0.15681278	0.057010926
M5005_Spy0031		phosphoribosylaminoimidazole carboxylase ATPase subunit	0.184328333	0.070302886
M5005_Spy0033	purB	adenylosuccinate lyase	0.245133331	0.002537863
M5005_Spy0036	M5005_Spy0036	protein tyrosine phosphatase	1.156193535	0.041533509
M5005_Spy0040	adhA	alcohol dehydrogenase	0.315290017	0.00226187
M5005 Spy0041	M5005 Spy0041	Na+ driven multidrug efflux pump	0.185403687	0.006648581
		4-diphosphocytidyl-2-C-methyl-D-erythritol kinase	0.307908538	0.000726122
M5005 Spy0077		transcriptional regulator, MarR family	0.493200724	0.006974333
M5005 Spy0084		DNA-directed RNA polymerase beta' chain	0.487830148	0.029023215
M5005 Spy0086	•	comG operon protein 1	-0.135116642	0.059947646
		adenine-specific methyltransferase	0.16477377	0.009073766
M5005_Spy0093		acetate kinase	-2.887494997	0.053003495
M5005_Spy0096		pyrroline-5-carboxylate reductase	0.153119358	0.092715344
M5005_Spy0097		glutamyl aminopeptidase	0.156641254	0.028037604
		tRNA binding domain protein	0.205864916	0.008029168
		deoxyadenosine kinase/deoxyguanosine kinase	0.336216853	0.001389716
M5005_Spy0106		transcriptional regulator	-0.183928077	0.003940136
M5005_Spy0107	M5005_Spy0107	fibronectin-binding protein	0.186548615	0.005085303
M5005_Spy0110	eftLSLB	putative exported protein	-0.254260236	0.004130506
M5005_Spy0112	M5005_Spy0112	transposase	0.158869452	0.006853968
	M5005 Spy0114		0.133647982	0.081416785
M5005 Spy0116		short-chain fatty acids transporter	0.163778128	0.015300755
		transcriptional regulator, LysR family	0.143517086	0.021644626
		acetyl-CoA acetyltransferase	0.302136411	5.58187E-06
M5005_Spy0113	,	acetate CoA-transferase alpha subunit	0.253294588	0.012515326
		•		
		acetyl-CoA:acetoacetyl-CoA transferase beta subunit	0.376502453	0.000945219
		putative DNA-binding protein	-0.351892926	0.000946492
		translation initiation inhibitor	0.42702981	0.030011302
M5005_Spy0124		transcriptional regulator	0.242733466	0.000420179
M5005_Spy0127	ntpK	V-type sodium ATP synthase subunit K	0.327164728	0.012515326
M5005_Spy0128	ntpE	V-type sodium ATP synthase subunit E	-0.122698651	0.079707588
M5005_Spy0132	ntpB	V-type sodium ATP synthase subunit B	0.225740798	0.003190623
M5005_Spy0143	M5005_Spy0143	hypothetical protein	0.461319239	0.0257664
M5005 Spy0144	M5005 Spy0144	hypothetical protein	-0.341250295	0.073122383
		PTS system, 3-keto-L-gulonate specific IIC component	0.196173265	0.033706494
		3-keto-L-gulonate-6-phosphate decarboxylase	-0.217634407	0.039844253
M5005_Spy0153		L-ribulose-5-phosphate 4-epimerase	0.448641474	0.00226187
M5005 Spy0158		glycine betaine-binding protein/glycine betaine transport system permease protein	0.24073878	0.013081521
M5005_Spy0161		ferric uptake regulation protein	0.358291756	0.016923119
		parB-like nuclease	-0.236067844	0.003656682
	M5005_Spy0166		-0.213852034	0.098801441
	M5005_Spy0168		-0.36264416	0.002961694
		malonate permease	0.254525406	0.00011877
M5005_Spy0170		nicotinate-nucleotide pyrophosphorylase (carboxylating)	0.155264141	0.068987033
M5005_Spy0175		queuine tRNA-ribosyltransferase	0.188055286	0.051073256
M5005_Spy0178	M5005_Spy0178	metal-dependent hydrolase	0.239175921	0.01251374
M5005_Spy0180	M5005_Spy0180	S-layer homology domain	0.143875572	0.053003495
M5005_Spy0182	speG	exotoxin type G precursor	-0.207507899	0.020074681
M5005_Spy0183	M5005_Spy0183	putative membrane associated protein	0.288963975	0.030627964
		multidrug resistance ABC transporter ATP-binding and permease protein	0.731356011	7.21887E-21
		multidrug resistance ABC transporter ATP-binding and permease protein	0.586289653	4.70347E-08
		carbonic anhydrase	0.604146494	0.000777963
		60 kDa inner membrane protein YIDC	0.378482402	0.003755128
		N-acetylneuraminate-binding protein	0.247023752	0.007658404
M5005_Spy0217		N-acetylneuraminate lyase	0.379657729	0.0070337974
		N-acetylmannosamine kinase	0.45662322	0.003280108
M5005_Spy0224		ribulose-phosphate 3-epimerase	-1.297249405	7.60141E-06
		thiamin pyrophosphokinase	-1.155154563	9.11318E-08
M5005_Spy0229		surface exclusion protein	0.409144878	9.0459E-08
		putative membrane spanning protein	0.14223694	0.017600519
M5005_Spy0238		putative undecaprenol kinase	0.374255847	0.000436339
		undecaprenyl-phosphate alpha-N-acetylglucosaminephosphotransferase	-0.933389105	1.471E-11
M5005_Spy0241	rgpG	putative cytosolic protein	-0.479394132	0.001048597
		D-alanyl-D-alanine carboxypeptidase	0.549705123	5.26841E-16
M5005 Spy0248		D-alanyl-D-alanine carboxypeptidase	-0.235561863	0.001549324
M5005 Spy0249		oligopeptide-binding protein	0.58721773	0.012623158
M5005_Spy0250		oligopeptide transport system permease protein	0.583755139	0.000420179
M5005_Spy0251		oligopeptide transport system permease protein	0.540206486	0.044729181
M5005_Spy0251		oligopeptide transport ATP-binding protein	0.699645769	0.000160727
M5005_Spy0252 M5005_Spy0253		oligopeptide transport ATP-binding protein	0.445960022	0.035734291
		methyltransferase	-0.193157971	0.015461712
		putative cytosolic protein	0.239579573	0.000479484
www.apyu268	www.phyuzb8	hypothetical protein	-0.330037686	0.015976035

M5005 Spy0271	M5005 Spy0271	ABC transporter substrate-binding protein	0.398367517	3.80984E-13
		ABC transporter ATP-binding protein	0.341832509	6.20946E-09
M5005_Spy0273	M5005_Spy0273	ABC transporter permease protein	0.307664351	1.4867E-06
M5005_Spy0274	braB	branched-chain amino acid transport system carrier protein	0.284865561	4.57064E-07
M5005_Spy0278		glucose inhibited division protein B	-0.253396474	0.055279479
M5005_Spy0279		LemA	0.650278118	0.053003495
		heat shock protein	0.307480851	0.059241498
M5005_Spy0288		SWF/SNF family helicase	-0.385826857	1.37911E-07
		aminodeoxychorismate lyase family hydrolase, HAD superfamily	-2.934037901 0.563197772	0.026263958 0.007630395
		CBS domain containing protein	-0.40801628	0.007030393
		putative cytosolic protein	-0.37270861	0.045937634
		23S rRNA methyltransferase	0.187842942	0.073238915
		riboflavin transporter	-1.078108144	0.00396604
M5005_Spy0321		ferrichrome transport system permease protein	0.139219058	0.053029593
M5005_Spy0322	fhuB	ferrichrome transport system permease protein	0.225532045	0.009103104
M5005_Spy0326	M5005_Spy0326	export protein for polysaccharides and teichoic acids	-0.599705726	0.001387193
M5005_Spy0327	• •	uracil phosphoribosyltransferase	-0.801230988	1.329E-07
M5005_Spy0330		thymidylate kinase	-6.322129727	0.000518282
		corrin/porphyrin methyltransferase	0.315595694	0.080103876
		putative membrane associated protein	-0.161633945	0.076731256
M5005_Spy0339 M5005_Spy0340		exodeoxyribonuclease III L-lactate oxidase	-0.352901389 -0.176318206	0.015461712 0.03022142
M5005_Spy0340		ribonucleoside-diphosphate reductase alpha chain	0.157979372	0.021035449
		hypothetical protein	-0.523338202	0.019221914
		hypothetical protein	-0.243266706	0.018478687
		hypothetical protein	-0.341615166	0.025342832
M5005_Spy0356		exotoxin type J precursor	-0.326584202	0.003845103
		hypothetical protein	-0.205475642	0.067724702
M5005 Spy0367		iron-dependent repressor	-0.372659988	0.008985218
		integral membrane protein	-1.168078319	0.006902019
M5005_Spy0374	rplK	LSU ribosomal protein L11P	4.968094849	0.060683246
M5005_Spy0382	msrA2	peptide methionine sulfoxide reductase	-0.761459896	5.49792E-13
M5005_Spy0383	M5005_Spy0383	D-alanyl-D-alanine carboxypeptidase	-0.219921483	0.053029593
M5005_Spy0386		phoH protein	0.132041334	0.092715344
		hypothetical protein	-0.265215692	0.084768133
		putative cytosolic protein	-0.599019706	0.022101334
		hypothetical protein	0.216724338	0.080364615
M5005_Spy0408		formamidopyrimidine-DNA glycosylase	0.494796502	0.001830271
	M5005_Spy0410		0.243982751	0.000702035
		multidrug resistance protein B	0.210506606	0.010945467
		exoribonuclease II	0.274822071	0.004737113
	M5005_Spy0418		0.728287151	0.028561733
M5005_Spy0420		glucosyltransferase lactoylglutathione lyase	-0.322616694	0.000965194
M5005_Spy0427	•	threonyl-tRNA synthetase	-0.25417388 0.730878554	0.055886711 0.010952329
		ABC transporter permease protein	0.415981979	0.000502737
		dihydroxyacetone kinase	-0.365752544	0.092922588
		acetyl-CoA acetyltransferase	0.361952329	0.007609484
		long-chain-fatty-acidCoA ligase	0.196125091	0.045247482
M5005_Spy0436		two-component sensor histidine kinase	-0.752220911	3.56529E-06
M5005 Spy0439		chromosome partition protein	-0.169939454	0.006974333
M5005_Spy0442	M5005_Spy0442	putative cytosolic protein	-0.2822698	0.03026461
M5005_Spy0447	M5005_Spy0447	glycosyltransferase involved in cell wall biogenesis	-0.15902536	0.080103876
M5005_Spy0460	M5005_Spy0460	hypothetical protein	0.229072648	0.048354292
		hypothetical protein	-0.269348546	0.009526976
		putative cytosolic protein	-0.229154019	0.038014411
M5005_Spy0466	M5005 Spv0466			
			-0.418950118	5.16552E-06
	M5005_Spy0471	hydrolase, HAD superfamily	0.191271445	0.047828105
M5005_Spy0472	M5005_Spy0471 ftsY	hydrolase, HAD superfamily cell division protein	0.191271445 -0.369328675	0.047828105 0.009752698
M5005_Spy0472 M5005_Spy0478	M5005_Spy0471 ftsY M5005_Spy0478	hydrolase, HAD superfamily cell division protein putative membrane spanning protein	0.191271445 -0.369328675 -0.18644643	0.047828105 0.009752698 0.012654748
M5005_Spy0472 M5005_Spy0478 M5005_Spy0480	M5005_Spy0471 ftsY M5005_Spy0478 M5005_Spy0480	hydrolase, HAD superfamily cell division protein putative membrane spanning protein transcription accessory protein	0.191271445 -0.369328675 -0.18644643 0.170608423	0.047828105 0.009752698 0.012654748 0.022216871
M5005_Spy0472 M5005_Spy0478 M5005_Spy0480 M5005_Spy0483	M5005_Spy0471 ftsY M5005_Spy0478 M5005_Spy0480 M5005_Spy0483	hydrolase, HAD superfamily cell division protein putative membrane spanning protein transcription accessory protein stress-responsive transcriptional regulator	0.191271445 -0.369328675 -0.18644643 0.170608423 1.767840586	0.047828105 0.009752698 0.012654748 0.022216871 0.032316602
M5005_Spy0472 M5005_Spy0478 M5005_Spy0480 M5005_Spy0483 M5005_Spy0485	M5005_Spy0471 ftsY M5005_Spy0478 M5005_Spy0480 M5005_Spy0483 lgt	hydrolase, HAD superfamily cell division protein putative membrane spanning protein transcription accessory protein stress-responsive transcriptional regulator prolipoprotein diacylglyceryl transferase	0.191271445 -0.369328675 -0.18644643 0.170608423 1.767840586 -0.333569372	0.047828105 0.009752698 0.012654748 0.022216871 0.032316602 0.049555241
M5005_Spy0472 M5005_Spy0478 M5005_Spy0480 M5005_Spy0483 M5005_Spy0485 M5005_Spy0486	M5005_Spy0471 ftsY M5005_Spy0478 M5005_Spy0480 M5005_Spy0483 lgt M5005_Spy0486	hydrolase, HAD superfamily cell division protein putative membrane spanning protein transcription accessory protein stress-responsive transcriptional regulator prolipoprotein diacylglyceryl transferase hypothetical protein	0.191271445 -0.369328675 -0.18644643 0.170608423 1.767840586 -0.333569372 -0.688506625	0.047828105 0.009752698 0.012654748 0.022216871 0.032316602 0.049555241 7.42415E-25
M5005_Spy0472 M5005_Spy0478 M5005_Spy0480 M5005_Spy0483 M5005_Spy0485 M5005_Spy0486 M5005_Spy0491	M5005_Spy0471 ftsY M5005_Spy0478 M5005_Spy0480 M5005_Spy0483 lgt M5005_Spy0486 M5005_Spy0491	hydrolase, HAD superfamily cell division protein putative membrane spanning protein transcription accessory protein stress-responsive transcriptional regulator prolipoprotein diacylglyceryl transferase hypothetical protein peptidase family U32	0.191271445 -0.369328675 -0.18644643 0.170608423 1.767840586 -0.333569372 -0.688506625 0.204144541	0.047828105 0.009752698 0.012654748 0.022216871 0.032316602 0.049555241 7.42415E-25 0.002362146
M5005_Spy0472 M5005_Spy0478 M5005_Spy0480 M5005_Spy0483 M5005_Spy0485 M5005_Spy0486 M5005_Spy0491 M5005_Spy0491	M5005_Spy0471 ftsY M5005_Spy0478 M5005_Spy0480 M5005_Spy0483 lgt M5005_Spy0486 M5005_Spy0491 M5005_Spy0499	hydrolase, HAD superfamily cell division protein putative membrane spanning protein transcription accessory protein stress-responsive transcriptional regulator prolipoprotein diacylglyceryl transferase hypothetical protein peptidase family U32 transcriptional regulator	0.191271445 -0.369328675 -0.18644643 0.170608423 1.767840586 -0.333569372 -0.688506625 0.204144541 0.250906561	0.047828105 0.009752698 0.012654748 0.022216871 0.032316602 0.049555241 7.42415E-25 0.002362146 0.030466932
M5005_Spy0472 M5005_Spy0478 M5005_Spy0480 M5005_Spy0483 M5005_Spy0485 M5005_Spy0486 M5005_Spy0491 M5005_Spy0491	M5005_Spy0471 ftsY M5005_Spy0478 M5005_Spy0480 M5005_Spy0483 lgt M5005_Spy0486 M5005_Spy0491 M5005_Spy0498 M5005_Spy0513	hydrolase, HAD superfamily cell division protein putative membrane spanning protein transcription accessory protein stress-responsive transcriptional regulator prolipoprotein diacylglyceryl transferase hypothetical protein peptidase family U32 transcriptional regulator putative cytosolic protein	0.191271445 -0.369328675 -0.18644643 0.170608423 1.767840586 -0.333569372 -0.688506625 0.204144541 0.250906561 -0.481820775	0.047828105 0.009752698 0.012654748 0.022216871 0.032316602 0.049555241 7.42415E-25 0.002362146
M5005_Spy0472 M5005_Spy0478 M5005_Spy0480 M5005_Spy0483 M5005_Spy0485 M5005_Spy0491 M5005_Spy0491 M5005_Spy0498 M5005_Spy0513	M5005_Spy0471 ftsY M5005_Spy0478 M5005_Spy0480 M5005_Spy0483 lgt M5005_Spy0486 M5005_Spy0491 M5005_Spy0498 M5005_Spy0513 regR	hydrolase, HAD superfamily cell division protein putative membrane spanning protein transcription accessory protein stress-responsive transcriptional regulator prolipoprotein diacylglyceryl transferase hypothetical protein peptidase family U32 transcriptional regulator	0.191271445 -0.369328675 -0.18644643 0.170608423 1.767840586 -0.333569372 -0.688506625 0.204144541 0.250906561	0.047828105 0.009752698 0.012654748 0.022216871 0.032316602 0.049555241 7.42415E-25 0.002362146 0.030466932 1.26156E-09
M5005_Spy0472 M5005_Spy0478 M5005_Spy0480 M5005_Spy0483 M5005_Spy0485 M5005_Spy0491 M5005_Spy0491 M5005_Spy0491 M5005_Spy0513 M5005_Spy0513	M5005_Spy0471 ftsY M5005_Spy0478 M5005_Spy0480 M5005_Spy0483 lgt M5005_Spy0486 M5005_Spy0491 M5005_Spy0498 M5005_Spy0513 regR ftsX	hydrolase, HAD superfamily cell division protein putative membrane spanning protein transcription accessory protein stress-responsive transcriptional regulator prolipoprotein diacylglyceryl transferase hypothetical protein peptidase family U32 transcriptional regulator putative cytosolic protein transcriptional regulator, Lacl family	0.191271445 -0.369328675 -0.18644643 0.170608423 1.767840586 -0.333569372 -0.688506625 0.204144541 0.250906561 -0.481820775 -0.313439269	0.047828105 0.009752698 0.012654748 0.022216871 0.032316602 0.049555241 7.42415E-25 0.002362146 0.030466932 1.26156E-09 6.30121E-06
M5005_Spy0472 M5005_Spy0478 M5005_Spy0480 M5005_Spy0483 M5005_Spy0485 M5005_Spy0491 M5005_Spy0491 M5005_Spy0491 M5005_Spy0517 M5005_Spy0517 M5005_Spy0532 M5005_Spy0536	M5005_Spy0471 ftsY M5005_Spy0478 M5005_Spy0480 M5005_Spy0483 lgt M5005_Spy0481 M5005_Spy0491 M5005_Spy0491 M5005_Spy0513 regR ftsX dinG	hydrolase, HAD superfamily cell division protein putative membrane spanning protein transcription accessory protein stress-responsive transcriptional regulator prolipoprotein diacylglyceryl transferase hypothetical protein peptidase family U32 transcriptional regulator putative cytosolic protein transcriptional regulator putative cytosolic protein transcriptional regulator, Lacl family cell division protein	0.191271445 -0.369328675 -0.18644643 0.170608423 1.767840586 -0.333569372 -0.688506625 0.204144541 0.250906561 -0.481820775 -0.313439269 -1.810786977	0.047828105 0.009752698 0.012654748 0.022216871 0.032316602 0.049555241 7.42415E-25 0.002362146 0.030466932 1.26156E-09 6.30121E-06 0.03511752
M5005_Spy0472 M5005_Spy0478 M5005_Spy0480 M5005_Spy0483 M5005_Spy0485 M5005_Spy0491 M5005_Spy0491 M5005_Spy0491 M5005_Spy0517 M5005_Spy0517 M5005_Spy0532 M5005_Spy0536	M5005_Spy0471 ftsY M5005_Spy0478 M5005_Spy0480 M5005_Spy0483 lgt M5005_Spy0491 M5005_Spy0491 M5005_Spy0513 regR ftsX dinG M5005_Spy0539	hydrolase, HAD superfamily cell division protein putative membrane spanning protein transcription accessory protein stress-responsive transcriptional regulator prolipoprotein diacylglyceryl transferase hypothetical protein peptidase family U32 transcriptional regulator putative cytosolic protein transcriptional regulator, Lacl family cell division protein ATP-dependent helicase	0.191271445 -0.369328675 -0.18644643 0.170608423 1.767840586 -0.333569372 -0.688506625 0.204144541 0.250906561 -0.481820775 -0.313439269 -1.810786977 0.345617357	0.047828105 0.009752698 0.012654748 0.022216871 0.032316602 0.049555241 7.42415E-25 0.002362146 0.030466932 1.26156E-09 6.30121E-06 0.03511752 2.82347E-12
M5005_Spy0472 M5005_Spy0478 M5005_Spy0480 M5005_Spy0483 M5005_Spy0485 M5005_Spy0491 M5005_Spy0491 M5005_Spy0513 M5005_Spy0517 M5005_Spy0517 M5005_Spy0532 M5005_Spy0538 M5005_Spy0538	M5005_Spy0471 ftsY M5005_Spy0478 M5005_Spy0480 M5005_Spy0483 lgt M5005_Spy0486 M5005_Spy0498 M5005_Spy0513 regR ftsX dinG M5005_Spy0539 pepD	hydrolase, HAD superfamily cell division protein putative membrane spanning protein transcription accessory protein stress-responsive transcriptional regulator prolipoprotein diacylglyceryl transferase hypothetical protein peptidase family U32 transcriptional regulator putative cytosolic protein transcriptional regulator, Lacl family cell division protein ATP-dependent helicase ATP-binding protein	0.191271445 -0.369328675 -0.18644643 0.170608423 1.767840586 -0.333569372 -0.688506625 0.204144541 0.250906561 -0.481820775 -0.313439269 -1.810786977 0.345617357 0.692569383	0.047828105 0.009752698 0.012654748 0.022216871 0.032316602 0.049555241 7.42415E-25 0.002362146 0.030466932 1.26156E-09 6.30121E-06 0.03511752 2.82347E-12 0.00966813
M5005_Spy0472 M5005_Spy0478 M5005_Spy0480 M5005_Spy0483 M5005_Spy0485 M5005_Spy0491 M5005_Spy0491 M5005_Spy0513 M5005_Spy0517 M5005_Spy0532 M5005_Spy0539 M5005_Spy0539 M5005_Spy0534 M5005_Spy0542 M5005_Spy0545 M5005_Spy0545 M5005_Spy0553	M5005_Spy0471 ftsY M5005_Spy0478 M5005_Spy0480 M5005_Spy0480 M5005_Spy0481 M5005_Spy0491 M5005_Spy0491 M5005_Spy0513 regR ftsX dinG M5005_Spy0539 pepD agaS gyrB	hydrolase, HAD superfamily cell division protein putative membrane spanning protein transcription accessory protein stress-responsive transcriptional regulator prolipoprotein diacylglyceryl transferase hypothetical protein peptidase family U32 transcriptional regulator putative cytosolic protein transcriptional regulator, Lacl family cell division protein ATP-dependent helicase ATP-binding protein dipeptidase galactosamine-6-phosphate deaminase (isomerizing) DNA gyrase subunit B	0.191271445 -0.369328675 -0.18644643 0.170608423 1.767840586 -0.333569372 -0.688506625 0.204144541 0.250906561 -0.481820775 -0.313439269 -1.810786977 0.345617357 0.692569383 0.123574802	0.047828105 0.009752698 0.012654748 0.022216871 0.032316602 0.049555241 7.42415E-25 0.002362146 0.030466932 1.26156E-09 6.30121E-06 0.03511752 2.82347E-12 0.00966813 0.078176188
M5005_Spy0472 M5005_Spy0478 M5005_Spy0480 M5005_Spy0483 M5005_Spy0485 M5005_Spy0491 M5005_Spy0513 M5005_Spy0517 M5005_Spy0517 M5005_Spy0532 M5005_Spy0532 M5005_Spy0538 M5005_Spy0533 M5005_Spy0533 M5005_Spy0542 M5005_Spy0545 M5005_Spy0545 M5005_Spy0554	M5005_Spy0471 ftsY M5005_Spy0478 M5005_Spy0480 M5005_Spy0480 M5005_Spy0481 M5005_Spy0491 M5005_Spy0491 M5005_Spy0513 regR ftsX dinG M5005_Spy0539 pepD agaS gyrB M5005_Spy0554	hydrolase, HAD superfamily cell division protein putative membrane spanning protein transcription accessory protein stress-responsive transcriptional regulator prolipoprotein diacylglyceryl transferase hypothetical protein peptidase family U32 transcriptional regulator putative cytosolic protein transcriptional regulator, Lacl family cell division protein ATP-dependent helicase ATP-binding protein dipeptidase galactosamine-6-phosphate deaminase (isomerizing) DNA gyrase subunit B septation ring formation regulator	0.191271445 -0.369328675 -0.18644643 0.170608423 1.767840586 -0.333569372 -0.688506625 0.204144541 0.250906561 -0.481820775 -0.313439269 -1.810786977 0.345617357 0.692569383 0.123574802 0.198373773 5.490126719 0.917687423	0.047828105 0.009752698 0.012654748 0.022216871 0.032316602 0.049555241 7.42415E-25 0.002362146 0.030466932 1.26156E-09 6.30121E-06 0.03511752 2.82347E-12 0.00966813 0.078176188 0.003561777 0.03292876 0.089936639
M5005_Spy0472 M5005_Spy0478 M5005_Spy0480 M5005_Spy0485 M5005_Spy0486 M5005_Spy0491 M5005_Spy0491 M5005_Spy0513 M5005_Spy0513 M5005_Spy0532 M5005_Spy0532 M5005_Spy0539 M5005_Spy0545 M5005_Spy0545 M5005_Spy0545 M5005_Spy0554 M5005_Spy0554 M5005_Spy0554 M5005_Spy0554 M5005_Spy0554 M5005_Spy0556	M5005_Spy0471 ftsY M5005_Spy0478 M5005_Spy0480 M5005_Spy0480 M5005_Spy0486 M5005_Spy0491 M5005_Spy0491 M5005_Spy0513 regR ftsX dinG M5005_Spy0539 pepD agaS gyrB M5005_Spy0554 M5005_Spy05560	hydrolase, HAD superfamily cell division protein putative membrane spanning protein transcription accessory protein stress-responsive transcriptional regulator prolipoprotein diacylglyceryl transferase hypothetical protein peptidase family U32 transcriptional regulator putative cytosolic protein transcriptional regulator, Lacl family cell division protein ATP-dependent helicase ATP-binding protein dipeptidase galactosamine-6-phosphate deaminase (isomerizing) DNA gyrase subunit B septation ring formation regulator transcriptional regulator	0.191271445 -0.369328675 -0.18644643 0.170608423 1.767840586 -0.333569372 -0.688506625 0.204144541 0.250906561 -0.481820775 -0.313439269 -1.810786977 0.345617357 0.692569383 0.123574802 0.198373773 5.490126719 0.917687423 -0.168989421	0.047828105 0.009752698 0.012654748 0.022216871 0.032316602 0.049555241 7.42415E-25 0.002362146 0.030466932 1.26156E-09 6.30121E-06 0.03511752 2.82347E-12 0.00966813 0.078176188 0.003561777 0.03292876 0.089936639 0.013959393
M5005_Spy0472 M5005_Spy0478 M5005_Spy0480 M5005_Spy0485 M5005_Spy0486 M5005_Spy0491 M5005_Spy0513 M5005_Spy0513 M5005_Spy0513 M5005_Spy0532 M5005_Spy0536 M5005_Spy0536 M5005_Spy0536 M5005_Spy0542 M5005_Spy0545 M5005_Spy0553 M5005_Spy0553 M5005_Spy0554 M5005_Spy0556 M5005_Spy0556	M5005_Spy0471 ftsY M5005_Spy0478 M5005_Spy0480 M5005_Spy0480 M5005_Spy0486 M5005_Spy0491 M5005_Spy0491 M5005_Spy0513 regR ftsX dinG M5005_Spy0539 pepD agaS gyrB M5005_Spy0554 M5005_Spy05560 sagB	hydrolase, HAD superfamily cell division protein putative membrane spanning protein transcription accessory protein stress-responsive transcriptional regulator prolipoprotein diacylglyceryl transferase hypothetical protein peptidase family U32 transcriptional regulator putative cytosolic protein transcriptional regulator, Lacl family cell division protein ATP-dependent helicase ATP-binding protein dipeptidase galactosamine-6-phosphate deaminase (isomerizing) DNA gyrase subunit B septation ring formation regulator transcriptional regulator streptolysin S biosynthesis protein	0.191271445 -0.369328675 -0.18644643 0.170608423 1.767840586 -0.333569372 -0.688506625 0.204144541 0.250906561 -0.481820775 -0.313439269 -1.810786977 0.345617357 0.692569383 0.123574802 0.198373773 5.490126719 0.917687423 -0.168989421 -0.233676538	0.047828105 0.009752698 0.012654748 0.022216871 0.032316602 0.049555241 7.42415E-25 0.002362146 0.030466932 1.26156E-09 6.30121E-06 0.03511752 2.82347E-12 0.00966813 0.078176188 0.003561777 0.03292876 0.089936639 0.013959393 0.001549324
M5005_Spy0472 M5005_Spy0478 M5005_Spy0480 M5005_Spy0483 M5005_Spy0485 M5005_Spy0491 M5005_Spy0491 M5005_Spy0513 M5005_Spy0517 M5005_Spy0532 M5005_Spy0532 M5005_Spy0539 M5005_Spy0542 M5005_Spy0545 M5005_Spy0554 M5005_Spy0554 M5005_Spy0554 M5005_Spy0554 M5005_Spy0554 M5005_Spy0554 M5005_Spy0563 M5005_Spy0563 M5005_Spy0563	M5005_Spy0471 ftsY M5005_Spy0478 M5005_Spy0480 M5005_Spy0480 M5005_Spy0481 M5005_Spy0491 M5005_Spy0491 M5005_Spy0513 regR ftsX dinG M5005_Spy0539 pepD agaS gyrB M5005_Spy0554 M5005_Spy0554 M5005_Spy0554 M5005_Spy0560 sagB sagF	hydrolase, HAD superfamily cell division protein putative membrane spanning protein transcription accessory protein stress-responsive transcriptional regulator prolipoprotein diacylglyceryl transferase hypothetical protein peptidase family U32 transcriptional regulator putative cytosolic protein transcriptional regulator, Lacl family cell division protein ATP-dependent helicase ATP-binding protein dipeptidase galactosamine-6-phosphate deaminase (isomerizing) DNA gyrase subunit B septation ring formation regulator transcriptional regulator transcriptional regulator streptolysin S biosynthesis protein streptolysin S biosynthesis protein	0.191271445 -0.369328675 -0.18644643 0.170608423 1.767840586 -0.333569372 -0.688506625 0.204144541 0.250906561 -0.481820775 -0.313439269 -1.810786977 0.345617357 0.692569383 0.123574802 0.198373773 5.490126719 0.917687423 -0.168989421 -0.2336766538 -0.292561784	0.047828105 0.009752698 0.012654748 0.022216871 0.032316602 0.049555241 7.42415E-25 0.002362146 0.030466932 1.26156E-09 6.30121E-06 0.03511752 2.82347E-12 0.00966813 0.078176188 0.003561777 0.03292876 0.089936639 0.013959393 0.001549324 0.00022828
M5005_Spy0472 M5005_Spy0478 M5005_Spy0480 M5005_Spy0483 M5005_Spy0485 M5005_Spy0491 M5005_Spy0513 M5005_Spy0517 M5005_Spy0513 M5005_Spy0532 M5005_Spy0532 M5005_Spy0538 M5005_Spy0539 M5005_Spy0542 M5005_Spy0545 M5005_Spy0554 M5005_Spy0554 M5005_Spy0566 M5005_Spy0566 M5005_Spy0566 M5005_Spy0566	M5005_Spy0471 ftsY M5005_Spy0478 M5005_Spy0480 M5005_Spy0480 M5005_Spy0481 M5005_Spy0491 M5005_Spy0491 M5005_Spy0513 regR ftsX dinG M5005_Spy0539 pepD agaS gyrB M5005_Spy0554 M5005_Spy05560 sagB sagF sagG	hydrolase, HAD superfamily cell division protein putative membrane spanning protein stress-responsive transcriptional regulator prolipoprotein diacylglyceryl transferase hypothetical protein peptidase family U32 transcriptional regulator putative cytosolic protein transcriptional regulator, Lacl family cell division protein ATP-dependent helicase ATP-binding protein dipeptidase galactosamine-6-phosphate deaminase (isomerizing) DNA gyrase subunit B septation ring formation regulator streptolysin S biosynthesis protein streptolysin S biosynthesis protein streptolysin S export ATP-binding protein	0.191271445 -0.369328675 -0.18644643 0.170608423 1.767840586 -0.333569372 -0.688506625 0.204144541 0.250906561 -0.481820775 -0.313439269 -1.810786977 0.345617357 0.692569383 0.123574802 0.198373773 5.490126719 0.917687423 -0.168989421 -0.233676538 -0.292561784 -2.996793078	0.047828105 0.009752698 0.012654748 0.022216871 0.032316602 0.049555241 7.42415E-25 0.002362146 0.030466932 1.26156E-09 6.30121E-06 0.03511752 2.82347E-12 0.00966813 0.078176188 0.003561777 0.03292876 0.089936639 0.013599393 0.001549324 0.00022828 2.80862E-12
M5005_Spy0472 M5005_Spy0478 M5005_Spy0480 M5005_Spy0485 M5005_Spy0486 M5005_Spy0491 M5005_Spy0513 M5005_Spy0513 M5005_Spy0517 M5005_Spy0532 M5005_Spy0532 M5005_Spy0539 M5005_Spy0542 M5005_Spy0545 M5005_Spy0553 M5005_Spy0553 M5005_Spy0554 M5005_Spy0563 M5005_Spy0563 M5005_Spy0568 M5005_Spy0568 M5005_Spy0568 M5005_Spy0568 M5005_Spy0568 M5005_Spy0568	M5005_Spy0471 ftsY M5005_Spy0478 M5005_Spy0480 M5005_Spy0480 M5005_Spy0480 M5005_Spy0491 M5005_Spy0491 M5005_Spy0513 regR ftsX dinG M5005_Spy0539 pepD agas gyrB M5005_Spy0554 M5005_Spy0560 sagB sagF sagG sagH	hydrolase, HAD superfamily cell division protein putative membrane spanning protein stress-responsive transcriptional regulator prolipoprotein diacylglyceryl transferase hypothetical protein peptidase family U32 transcriptional regulator putative cytosolic protein transcriptional regulator, Lacl family cell division protein ATP-dependent helicase ATP-binding protein dipeptidase galactosamine-6-phosphate deaminase (isomerizing) DNA gyrase subunit B septation ring formation regulator transcriptional regulator streptolysin S biosynthesis protein streptolysin S sexport ATP-binding protein streptolysin S export transmembrane protein	0.191271445 -0.369328675 -0.18644643 0.170608423 1.767840586 -0.333569372 -0.688506625 0.204144541 0.250906561 -0.481820775 -0.313439269 -1.810786977 0.345617357 0.692569383 0.123574802 0.198373773 5.490126719 0.917687423 -0.168989421 -0.233676538 -0.292561784 -2.996793078 -3.755023247	0.047828105 0.009752698 0.012654748 0.022216871 0.032316602 0.049555241 7.42415E-25 0.002362146 0.030466932 1.26156E-09 6.30121E-06 0.03511752 2.82347E-12 0.00966813 0.078176188 0.003561777 0.03292876 0.089936639 0.013959393 0.001549324 0.00022828 2.80862E-12 2.38518E-19
M5005_Spy0472 M5005_Spy0478 M5005_Spy0480 M5005_Spy0483 M5005_Spy0485 M5005_Spy0491 M5005_Spy0513 M5005_Spy0517 M5005_Spy0513 M5005_Spy0532 M5005_Spy0532 M5005_Spy0538 M5005_Spy0539 M5005_Spy0542 M5005_Spy0545 M5005_Spy0554 M5005_Spy0554 M5005_Spy0566 M5005_Spy0566 M5005_Spy0566 M5005_Spy0566	M5005_Spy0471 ftsY M5005_Spy0478 M5005_Spy0480 M5005_Spy0480 M5005_Spy0486 M5005_Spy0491 M5005_Spy0491 M5005_Spy0513 regR ftsX dinG M5005_Spy0539 pepD agaS gyrB M5005_Spy0554 M5005_Spy0554 M5005_Spy05560 sagB sagF sagG sagH sagI	hydrolase, HAD superfamily cell division protein putative membrane spanning protein stress-responsive transcriptional regulator prolipoprotein diacylglyceryl transferase hypothetical protein peptidase family U32 transcriptional regulator putative cytosolic protein transcriptional regulator, Lacl family cell division protein ATP-dependent helicase ATP-binding protein dipeptidase galactosamine-6-phosphate deaminase (isomerizing) DNA gyrase subunit B septation ring formation regulator streptolysin S biosynthesis protein streptolysin S biosynthesis protein streptolysin S export ATP-binding protein	0.191271445 -0.369328675 -0.18644643 0.170608423 1.767840586 -0.333569372 -0.688506625 0.204144541 0.250906561 -0.481820775 -0.313439269 -1.810786977 0.345617357 0.692569383 0.123574802 0.198373773 5.490126719 0.917687423 -0.168989421 -0.233676538 -0.292561784 -2.996793078	0.047828105 0.009752698 0.012654748 0.022216871 0.032316602 0.049555241 7.42415E-25 0.002362146 0.030466932 1.26156E-09 6.30121E-06 0.03511752 2.82347E-12 0.00966813 0.078176188 0.003561777 0.03292876 0.089936639 0.013599393 0.001549324 0.00022828 2.80862E-12

M5005 Spy05	91 M5005 Spy0591	ABC transporter permease protein	-0.271919708	0.000118696
		ABC transporter ATP-binding protein	0.223107764	0.080103876
M5005_Spy06		alpha-L-Rha alpha-1,2-L-rhamnosyltransferase/alpha-L-Rha alpha-1,3-L-rhamnosyltransferase	0.76685673	0.050214614
		phosphoglycerol transferase	-0.330537792	2.92346E-08
	10 M5005_Spy0610		-0.260047575	0.001332251
,	- ' '	hypothetical protein	-0.413316355	0.000118696
	23 M5005_Spy0623	·	-0.270538786	0.057240245
M5005_Spy06		3-dehydroquinate dehydratase	-0.790123126	0.069301282
M5005_Spy06	25 aroF	chorismate synthase	0.164763093	0.06552743
M5005_Spy06	28 folC2	folylpolyglutamate synthase/dihydrofolate synthase	0.302915937	0.004863907
M5005_Spy06	30 nifS1	cysteine desulfhydrase	-0.785746308	8.07078E-16
M5005_Spy06	31 thil	thiamine biosynthesis protein	-0.891808276	5.69544E-27
M5005 Spy06		capsule biosynthesis protein	0.248789323	0.00199065
M5005 Spy06		pyrR bifunctional protein	0.288980515	0.080364615
M5005_Spy06		aspartate carbamoyltransferase	-0.34417952	3.8062E-06
M5005_Spy06		carbamoyl-phosphate synthase small chain	-0.482512662	9.85233E-10
M5005_Spy06		carbamoyl-phosphate synthase large chain	-0.504546485	3.92332E-27
- ' '	- ' '	periplasmic component of efflux system	-1.199493265	2.2698E-119
		ABC transporter ATP-binding protein	-1.003725727	5.66253E-50
M5005_Spy06	16 M5005_Spy0646	ABC transporter permease protein	-1.080793964	1.13135E-58
M5005_Spy06	50 M5005_Spy0650	hypothetical protein	-0.568062657	0.019077018
M5005 Spy06	51 M5005 Spy0651	cell surface protein	-0.146485771	0.018288297
M5005 Spv06	54 M5005 Spv0654	transcriptional regulator, TetR family	-0.158974186	0.081707288
	58 M5005_Spy0658		0.250587274	0.003835445
M5005 Spy06		2-dehydropantoate 2-reductase	-0.200916289	0.054447704
- ' '	•		-0.348845785	
M5005_Spy06		fructose repressor		0.0019036
M5005_Spy06		autolysin	-0.294166996	0.015606729
M5005_Spy06		autolysin	-0.179426866	0.00226187
M5005_Spy06	35 M5005_Spy0665	transposase	-0.54208821	9.04652E-05
M5005 Spy06	37 M5005 Spy0667	exotoxin type C precursor	-0.317119474	0.03787804
		hypothetical protein	-0.2935379	0.054896731
	78 M5005 Spy0678		-0.126810121	0.076743411
M5005_Spy0681	M5005_Spy0681	two-component system histidine kinase	0.287256033	5.34132E-06
		hypothetical protein	-0.278946483	4.92321E-08
M5005_Spy06		arsenate reductase family protein	-0.886984646	0.015161945
M5005_Spy07	00 cpsX	attenuator of transcription, LytR family regulator	0.19235965	0.080103876
M5005_Spy07	01 cpsY	transcriptional regulator, LysR family	0.632360713	1.37813E-09
M5005_Spy07	03 pyrF	orotidine 5'-phosphate decarboxylase	0.223381483	0.012394136
		hypothetical protein	-0.249001769	0.054833279
	19 M5005 Spy0719		0.189793287	0.02035695
		putative exfoliative toxin	0.231721192	0.00226187
		hypothetical protein	-0.490745007	0.00838298
M5005_Spy07		tRNA delta(2)-isopentenylpyrophosphate transferase	-0.558768581	8.84514E-07
M5005_Spy07	28 apt	adenine phosphoribosyltransferase	1.254715727	7.31515E-08
M5005_Spy07	30 nth	endonuclease III	0.456694225	0.009967812
M5005 Spy07	32 M5005 Spy0732	NIF3-related protein	0.300362579	0.064528984
M5005_Spy07		dTDP-glucose 4,6-dehydratase	-0.882496835	0.093633876
		hypothetical protein	-0.315158479	0.067323966
		ABC transporter substrate-binding protein	0.184722158	0.039844253
		ABC transporter permease protein	0.222893679	0.073831208
		hypothetical protein	-0.281725548	0.019110027
M5005_Spy07		pyruvate dehydrogenase E1 component alpha subunit	1.346770979	8.82618E-12
M5005_Spy07		pyruvate dehydrogenase E1 component beta subunit	1.30046369	2.18003E-05
M5005_Spy07	33 femD	phosphoglucosamine mutase	0.434777412	0.035989381
M5005 Spy07	37 M5005 Spy0767	4-nitrophenylphosphatase	0.311027581	0.000362317
		hypothetical protein	-0.199714385	0.097893876
M5005_Spy07		GTP-binding protein	0.218927122	0.059896994
		putative membrane spanning protein	-0.116513698	0.051658108
		PTS system, mannose/fructose family IIA component	0.365181175	0.012493001
			0.238802692	
M5005_Spy07		PTS system, mannose/fructose family IIB component		0.038826054
M5005_Spy07	•	PTS system, mannose/fructose family IID component	0.318703918	0.004175881
		two-component sensor kinase	-0.165988277	0.010618701
M5005_Spy07	35 M5005_Spy0785	two-component response regulator	0.176926985	0.089936639
M5005_Spy07	90 gabD	succinate-semialdehyde dehydrogenase [NADP+]	-0.277852605	0.009302731
M5005_Spy07		excinuclease ABC subunit C	-0.490818006	9.94957E-15
M5005 Spv07	92 M5005 Spv0792	NAD(P)H-dependent quinone reductase	-4.591449118	0.000403352
		Xaa-His dipeptidase	0.49924245	1.44978E-05
		hypothetical protein	-0.472591467	0.038826054
		··· ·		
M5005_Spy08		protein involved in lantibiotic production	-0.113585198	0.062580786
M5005_Spy08		nisin biosynthesis two-component response regulator	-0.364818885	7.43452E-07
M5005_Spy08		nisin biosynthesis sensor protein	-0.409132164	1.19398E-05
M5005_Spy08	06 srtA	lantibiotic precursor	-0.30336635	0.005448808
M5005_Spy08	7 srtT	ABC transporter (ATP binding)-lantibiotic associated	-0.172830249	0.028614514
M5005_Spy08		lantibiotic transport ATP-binding protein	-0.147961448	0.034461155
M5005 Spy08		lantibiotic transport permease protein	-0.195167556	0.035288119
M5005_Spy08		lantibiotic transport permease protein	-0.419005932	
				0.000241508
M5005_Spy08		D-alanyl-D-alanine carboxypeptidase	-0.287211373	0.001332251
M5005_Spy08		folylpolyglutamate synthase/dihydrofolate synthase	-4.717898063	0.003090914
		spermidine/putrescine-binding protein	-0.477750882	0.053029593
M5005_Spy08	30 dpiA	transcriptional regulatory protein	-0.165461731	0.023340543
M5005_Spy08	32 malP	malate-sodium symport	0.129759918	0.047608087
		class B acid phosphatase	-0.149166912	0.02332191
		lipase/acylhydrolase family protein	-0.251130081	0.001983269
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M5005 Spy0840				
	radC	DNA repair protein	-0.156673248	0.031269306
M5005_Spy0841	M5005_Spy0841	glutamine amidotransferase, class I	-0.317951282	0.028997701
M5005_Spy0847	M5005_Spy0847	GTP pyrophosphokinase	-0.638723899	0.03903346
M5005_Spy0852	M5005_Spy0852	short chain dehydrogenase	-0.30914668	0.008138086
M5005_Spy0858		xanthine phosphoribosyltransferase	-0.201371271	0.012493001
M5005_Spy0860		thiamine biosynthesis lipoprotein	-1.001686198	0.023885916
M5005_Spy0872		NADH oxidase H2O-forming	0.174444631	0.015461712
M5005_Spy0874		DNA gyrase subunit A	-0.987238492	0.021907198
		lactoylglutathione lyase hypothetical protein	-0.248641795 -0.191887855	0.00183013 0.045937634
M5005_Spy0876		Smf	-0.161746767	0.043837925
		transcriptional regulator, LysR family	-0.156037626	0.024270271
		transcriptional regulator, LysR family	-0.344860984	0.000273569
M5005 Spy0892		SatE	0.158971492	0.073831208
M5005_Spy0893		glucose inhibited division protein A	0.191298547	0.023340543
M5005_Spy0894	oadA2	oxaloacetate decarboxylase alpha chain	0.136770458	0.068694134
,	- ' '	putative membrane associated protein	-0.267701647	0.021926363
M5005_Spy0899		transcriptional regulator, GntR family	-0.155940452	0.016254912
		Mg2+/citrate complex secondary transporter	-0.112199025	0.086037306
		biotin carboxyl carrier protein of oxaloacetate decarboxylase	0.204535818	0.065627356
M5005_Spy0903		oxaloacetate decarboxylase beta chain	0.306661003	0.001004456
M5005_Spy0906 M5005_Spy0907		citrate lyase beta chain/citryl-CoA lyase subunit citrate lyase alpha chain/citrate CoA-transferase	0.152234138 0.291146128	0.021283451 2.75204E-06
M5005_Spy0907		apo-citrate lyase phosphoribosyl-dephospho-CoA transferase	0.144659069	0.034413833
M5005_Spy0909		oxaloacetate decarboxylase alpha chain	0.169435659	0.006628769
		hypothetical protein	-0.141584281	0.078601573
		phage transcriptional repressor	-0.177700247	0.009103104
		hypothetical protein	-0.243234013	0.000729209
		ABC transporter ATP-binding protein	-0.121444385	0.056554657
	M5005 Spy0923		-0.216548825	0.001150693
M5005_Spy0925	rnhB	anaerobic ribonucleoside-triphosphate reductase	-0.354341446	0.003599192
M5005_Spy0926	M5005_Spy0926	cardiolipin synthetase	-2.584797561	4.41145E-12
M5005_Spy0929	M5005_Spy0929	SIR2 family protein	0.1953777	0.029218989
M5005_Spy0931	M5005_Spy0931	glycine cleavage system H protein	0.300217169	0.069753844
M5005_Spy0934	M5005_Spy0934	lipoate-protein ligase A	0.205622966	0.012216566
	M5005_Spy0937	•	-1.570665731	0.001714623
M5005_Spy0938		phosphoglucomutase/phosphomannomutase	-0.495373701	0.005765678
		nucleoside transport system permease protein	0.762944266	1.16149E-24
		nucleoside transport system permease protein	0.808308031	5.71726E-26
		nucleoside transport ATP-binding protein	0.740973987	5.71726E-26
		nucleoside-binding protein	0.517779639	1.17283E-11
M5005_Spy0943		cytidine deaminase	0.606962135	9.0459E-08
		16S rRNA m(2)G 1207 methyltransferase	-0.46763997	3.28147E-13
M5005_Spy0947 M5005_Spy0949		sensor protein	-0.289342227 0.189947281	0.000723319
M5005_Spy0949		lysyl aminopeptidase/alanine aminopeptidase phosphate transport ATP-binding protein		0.006829623 7.7655E-100
M5005_Spy0951	•			
			-1.599727177 -1.85889123	
		phosphate transport ATP-binding protein	-1.85889123	5.07094E-53
M5005_Spy0953	pstA	phosphate transport system permease protein	-1.85889123 -1.893478286	5.07094E-53 1.7075E-162
M5005_Spy0953 M5005_Spy0954	pstA pstC	phosphate transport system permease protein phosphate transport system permease protein	-1.85889123 -1.893478286 -1.934505396	5.07094E-53 1.7075E-162 1.37154E-65
M5005_Spy0953 M5005_Spy0954 M5005_Spy0955	pstA pstC pstS	phosphate transport system permease protein phosphate transport system permease protein phosphate-binding protein	-1.85889123 -1.893478286 -1.934505396 -2.028958081	5.07094E-53 1.7075E-162 1.37154E-65 2.6174E-112
M5005_Spy0953 M5005_Spy0954 M5005_Spy0955 M5005_Spy0961	pstA pstC pstS truB	phosphate transport system permease protein phosphate transport system permease protein	-1.85889123 -1.893478286 -1.934505396	5.07094E-53 1.7075E-162 1.37154E-65
M5005_Spy0953 M5005_Spy0954 M5005_Spy0955 M5005_Spy0961 M5005_Spy0970	pstA pstC pstS truB M5005_Spy0970	phosphate transport system permease protein phosphate transport system permease protein phosphate-binding protein tRNA pseudouridine synthase B	-1.85889123 -1.893478286 -1.934505396 -2.028958081 -1.471604692	5.07094E-53 1.7075E-162 1.37154E-65 2.6174E-112 0.003736548
M5005_Spy0953 M5005_Spy0954 M5005_Spy0955 M5005_Spy0961 M5005_Spy0970 M5005_Spy0971	pstA pstC pstS truB M5005_Spy0970 M5005_Spy0971	phosphate transport system permease protein phosphate transport system permease protein phosphate-binding protein tRNA pseudouridine synthase B NAD-dependent K+ or Na+ uptake system component	-1.85889123 -1.893478286 -1.934505396 -2.028958081 -1.471604692 -1.421419043	5.07094E-53 1.7075E-162 1.37154E-65 2.6174E-112 0.003736548 0.002161896
M5005_Spy0953 M5005_Spy0954 M5005_Spy0955 M5005_Spy0961 M5005_Spy0970 M5005_Spy0971 M5005_Spy0972 M5005_Spy0973	pstA pstC pstS truB M5005_Spy0970 M5005_Spy0971 M5005_Spy0972 M5005_Spy0973	phosphate transport system permease protein phosphate transport system permease protein phosphate-binding protein tRNA pseudouridine synthase B NAD-dependent K+ or Na+ uptake system component general stress protein, Gls24 family hypothetical protein general stress protein, Gls24 family	-1.85889123 -1.893478286 -1.934505396 -2.028958081 -1.471604692 -1.421419043 -0.729582942	5.07094E-53 1.7075E-162 1.37154E-65 2.6174E-112 0.003736548 0.002161896 9.50436E-05
M5005_Spy0953 M5005_Spy0954 M5005_Spy0955 M5005_Spy0961 M5005_Spy0970 M5005_Spy0971 M5005_Spy0973 M5005_Spy0973 M5005_Spy0973	pstA pstC pstS truB M5005_Spy0970 M5005_Spy0971 M5005_Spy0972 M5005_Spy0973 M5005_Spy0975	phosphate transport system permease protein phosphate transport system permease protein phosphate-binding protein tRNA pseudouridine synthase B NAD-dependent K+ or Na+ uptake system component general stress protein, Gls24 family hypothetical protein general stress protein, Gls24 family hypothetical protein	-1.85889123 -1.893478286 -1.934505396 -2.028958081 -1.471604692 -1.421419043 -0.729582942 -0.74247025 -0.796444899 -0.929213758	5.07094E-53 1.7075E-162 1.37154E-65 2.6174E-112 0.003736548 0.002161896 9.50436E-05 0.051969253
M5005_Spy0953 M5005_Spy0954 M5005_Spy0955 M5005_Spy0961 M5005_Spy0970 M5005_Spy0971 M5005_Spy0972 M5005_Spy0973 M5005_Spy0973 M5005_Spy0975 M5005_Spy0980	pstA pstC pstS truB M5005_Spy0970 M5005_Spy0972 M5005_Spy0972 M5005_Spy0978 M5005_Spy0978	phosphate transport system permease protein phosphate transport system permease protein phosphate-binding protein tRNA pseudouridine synthase B NAD-dependent K+ or Na+ uptake system component general stress protein, Gls24 family hypothetical protein general stress protein, Gls24 family hypothetical protein cobalt-zinc-cadmium resistance protein	-1.85889123 -1.893478286 -1.934505396 -2.028958081 -1.471604692 -1.421419043 -0.729582942 -0.74247025 -0.796444899 -0.929213758 -0.213823413	5.07094E-53 1.7075E-162 1.37154E-65 2.6174E-112 0.003736548 0.002161896 9.50436E-05 0.051969253 1.99619E-07 4.86128E-06 0.038826054
M5005_Spy0953 M5005_Spy0954 M5005_Spy0955 M5005_Spy0961 M5005_Spy0970 M5005_Spy0972 M5005_Spy0973 M5005_Spy0973 M5005_Spy0975 M5005_Spy0978 M5005_Spy0980 M5005_Spy0981	pstA pstC pstS M5005_Spy0970 M5005_Spy0971 M5005_Spy0972 M5005_Spy0973 M5005_Spy0975 M5005_Spy0980 cfa	phosphate transport system permease protein phosphate transport system permease protein phosphate-binding protein tRNA pseudouridine synthase B NAD-dependent K+ or Na+ uptake system component general stress protein, Gls24 family hypothetical protein general stress protein, Gls24 family hypothetical protein cobalt-zinc-cadmium resistance protein cAMP factor	-1.85889123 -1.893478286 -1.934505396 -2.028958081 -1.471604692 -1.421419043 -0.729582942 -0.796444899 -0.929213758 -0.213823413 -0.248755992	5.07094E-53 1.7075E-162 1.37154E-65 2.6174E-112 0.003736548 0.002161896 9.50436E-05 0.051969253 1.99619E-07 4.86128E-06 0.038826054 0.000414249
M5005_Spy0953 M5005_Spy0954 M5005_Spy0956 M5005_Spy0961 M5005_Spy0970 M5005_Spy0972 M5005_Spy0972 M5005_Spy0973 M5005_Spy0980 M5005_Spy0980 M5005_Spy0981	pstA pstC pstS truB M5005_Spy0970 M5005_Spy0971 M5005_Spy0973 M5005_Spy0973 M5005_Spy0980 cfa M5005_Spy0980	phosphate transport system permease protein phosphate transport system permease protein phosphate-binding protein tRNA pseudouridine synthase B NAD-dependent K+ or Na+ uptake system component general stress protein, Gls24 family hypothetical protein general stress protein, Gls24 family hypothetical protein cobalt-zinc-cadmium resistance protein cobalt-zinc-cadmium resistance protein cAMP factor histidine-binding protein	-1.85889123 -1.893478286 -1.934505396 -2.028958081 -1.471604692 -1.421419043 -0.729582942 -0.74247025 -0.796444899 -0.929213758 -0.213823413 -0.248755992 -0.186238825	5.07094E-53 1.7075E-162 1.37154E-65 2.6174E-112 0.003736548 0.002161896 9.50436E-05 0.051969253 1.99619E-07 4.86128E-06 0.038826054 0.000414249 0.023885916
M5005_Spy0953 M5005_Spy0954 M5005_Spy0955 M5005_Spy0961 M5005_Spy0970 M5005_Spy0971 M5005_Spy0973 M5005_Spy0973 M5005_Spy0975 M5005_Spy0980 M5005_Spy0980 M5005_Spy0982 M5005_Spy0982 M5005_Spy0982 M5005_Spy0986	pstA pstC pstS truB M5005_Spy0970 M5005_Spy0971 M5005_Spy0973 M5005_Spy0973 M5005_Spy0975 M5005_Spy0980 cfa M5005_Spy0982 glmS	phosphate transport system permease protein phosphate transport system permease protein phosphate-binding protein tRNA pseudouridine synthase B NAD-dependent K+ or Na+ uptake system component general stress protein, Gls24 family hypothetical protein general stress protein, Gls24 family hypothetical protein cobalt-zinc-cadmium resistance protein cAMP factor histidine-binding protein glucosaminefructose-6-phosphate aminotransferase (isomerizing)	-1.85889123 -1.893478286 -1.934505396 -2.028958081 -1.471604692 -1.421419043 -0.729582942 -0.74247025 -0.796444899 -0.929213758 -0.213823413 -0.248755992 -0.186238825 5.006626723	5.07094E-53 1.7075E-162 1.37154E-65 2.6174E-112 0.003736548 0.002161896 9.50436E-05 0.051969253 1.99619E-07 4.86128E-06 0.038826054 0.000414249 0.023885916 0.058546555
M5005_Spy0953 M5005_Spy0954 M5005_Spy0956 M5005_Spy0970 M5005_Spy0971 M5005_Spy0972 M5005_Spy0972 M5005_Spy0975 M5005_Spy0975 M5005_Spy0980 M5005_Spy0981 M5005_Spy0982 M5005_Spy0986 M5005_Spy0987	pstA pstC pstS truB M5005_Spy0970 M5005_Spy0971 M5005_Spy0973 M5005_Spy0973 M5005_Spy0975 M5005_Spy0980 cfa M5005_Spy0982 glmS sipC	phosphate transport system permease protein phosphate transport system permease protein phosphate-binding protein tRNA pseudouridine synthase B NAD-dependent K+ or Na+ uptake system component general stress protein, Gls24 family hypothetical protein general stress protein, Gls24 family hypothetical protein cobalt-zinc-cadmium resistance protein cAMP factor histidine-binding protein glucosamine—fructose-6-phosphate aminotransferase (isomerizing) signal peptidase I	-1.85889123 -1.893478286 -1.934505396 -2.028958081 -1.471604692 -1.421419043 -0.729582942 -0.74247025 -0.295823413 -0.248755992 -0.186238825 5.006626723 -0.739674013	5.07094E-53 1.7075E-162 1.37154E-65 2.6174E-112 0.003736548 0.002161896 9.50436E-05 0.051969253 1.99619E-07 4.86128E-06 0.038826054 0.000414249 0.023885916 0.0588546555 1.81062E-27
M5005_Spy0953 M5005_Spy0954 M5005_Spy0956 M5005_Spy0961 M5005_Spy0970 M5005_Spy0972 M5005_Spy0973 M5005_Spy0975 M5005_Spy0980 M5005_Spy0980 M5005_Spy0981 M5005_Spy0982 M5005_Spy0982 M5005_Spy0988 M5005_Spy0987 M5005_Spy0987 M5005_Spy0987	pstA pstC pstS truB M5005_Spy0970 M5005_Spy0972 M5005_Spy0972 M5005_Spy0978 M5005_Spy0980 cfa M5005_Spy0980 glmS sipC M5005_Spy0992	phosphate transport system permease protein phosphate transport system permease protein phosphate-binding protein tRNA pseudouridine synthase B NAD-dependent K+ or Na+ uptake system component general stress protein, Gls24 family hypothetical protein general stress protein, Gls24 family hypothetical protein cobalt-zinc-cadmium resistance protein cAMP factor histidine-binding protein glucosaminefructose-6-phosphate aminotransferase (isomerizing) signal peptidase I ABC transporter ATP-binding protein	-1.85889123 -1.893478286 -1.934505396 -2.028958081 -1.471604692 -1.421419043 -0.729582942 -0.796444899 -0.929213758 -0.218823413 -0.248755992 -0.186238825 5.006626723 -0.739674013 -1.0011065	5.07094E-53 1.7075E-162 1.37154E-65 2.6174E-112 0.003736548 0.002161896 9.50436E-05 0.051969253 1.99619E-07 4.86128E-06 0.038826054 0.000414249 0.023885916 0.058546555 1.81062E-27 4.48554E-11
M5005_Spy0953 M5005_Spy0954 M5005_Spy0956 M5005_Spy0961 M5005_Spy0970 M5005_Spy0972 M5005_Spy0973 M5005_Spy0973 M5005_Spy0981 M5005_Spy0981 M5005_Spy0981 M5005_Spy0988 M5005_Spy0982 M5005_Spy0987 M5005_Spy0987 M5005_Spy0987	pstA pstC pstS truB M5005_Spy0970 M5005_Spy0971 M5005_Spy0972 M5005_Spy0973 M5005_Spy0980 cfa M5005_Spy0982 glmS sipC M5005_Spy0982 M5005_Spy0992 M5005_Spy0999999999999999999999999999999999999	phosphate transport system permease protein phosphate transport system permease protein phosphate-binding protein tRNA pseudouridine synthase B NAD-dependent K+ or Na+ uptake system component general stress protein, Gls24 family hypothetical protein general stress protein, Gls24 family hypothetical protein general stress protein, Gls24 family hypothetical protein cobalt-zinc-cadmium resistance protein cobalt-zinc-cadmium resistance protein cAMP factor histidine-binding protein glucosaminefructose-6-phosphate aminotransferase (isomerizing) signal peptidase I ABC transporter ATP-binding protein ABC transporter permease protein	-1.85889123 -1.893478286 -1.934505396 -2.028958081 -1.471604692 -1.421419043 -0.729582942 -0.74247025 -0.796444899 -0.929213758 -0.213823413 -0.248755992 -0.186238825 5.006626723 -0.79674013 -1.0011065 -1.100487928	5.07094E-53 1.7075E-162 1.37154E-65 2.6174E-112 0.003736548 0.002161896 9.50436E-05 0.051969253 1.99619E-07 4.86128E-06 0.038826054 0.000414249 0.023885916 0.058546555 1.81062E-27 4.48554E-11 1.66809E-09
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M5005_Spy0953 M5005_Spy0954 M5005_Spy0956 M5005_Spy0961 M5005_Spy0970 M5005_Spy0973 M5005_Spy0973 M5005_Spy0973 M5005_Spy0973 M5005_Spy0980 M5005_Spy0981 M5005_Spy0982 M5005_Spy0982 M5005_Spy0982 M5005_Spy0998 M5005_Spy0999 M5005_Spy1000 M5005_Spy1001 M5005_Spy1001 M5005_Spy1003 M5005_Spy1003 M5005_Spy1004 M5005_Spy1022 M5005_Spy1022 M5005_Spy1044 M5005_Spy1044 M5005_Spy1044 M5005_Spy1050 M5005_Spy1055 M5005_Spy1055	pstA pstC pstS truB M5005_Spy0970 M5005_Spy0971 M5005_Spy0972 M5005_Spy0973 M5005_Spy0973 M5005_Spy0980 cfa M5005_Spy0982 glmS sipC M5005_Spy0982 M5005_Spy0993 M5005_Spy0993 M5005_Spy0993 M5005_Spy1093 M5005_Spy1003 M5005_Spy1001 M5005_Spy1003 M5005_Spy1003 M5005_Spy1003 M5005_Spy1003 M5005_Spy1003 M5005_Spy1021 M5005_Spy1044 M5005_Spy1044 M5005_Spy1051 M3005_Spy1051 M3005_Spy1051 M3005_Spy1051 M3005_Spy1051 M3005_Spy1051 M3005_Spy1051 M3005_Spy1051 M3005_Spy1051	phosphate transport system permease protein phosphate transport system permease protein phosphate-binding protein tRNA pseudouridine synthase B NAD-dependent K+ or Na+ uptake system component general stress protein, Gls24 family hypothetical protein general stress protein, Gls24 family hypothetical protein cobalt-zinc-cadmium resistance protein cobalt-zinc-cadmium resistance protein cobalt-zinc-binding protein glucosaminefructose-6-phosphate aminotransferase (isomerizing) signal peptidase I ABC transporter ATP-binding protein ABC transporter permease protein phage protein phage protein phage protein phage protein phage protein phage structural protein phage structural protein phage protein portal protein terminase large subunit phage protein	-1.85889123 -1.893478286 -1.934505396 -2.028958081 -1.471604692 -1.421419043 -0.729582942 -0.74247025 -0.796444899 -0.929213758 -0.213823413 -0.248755992 -0.186238825 5.006626723 -0.739674013 -1.0011065 -1.100487928 -0.369379627 -0.192884927 -0.220096914 0.290821588 -0.388171259 -0.153974239 -0.254826936 -0.163801909 -0.241228951 -0.352452909 -0.184063525 -0.871526387 -0.200203681 -0.390985413 0.546280281 0.470840295	5.07094E-53 1.7075E-162 1.37154E-65 2.6174E-112 0.003736548 0.002161896 9.50436E-05 0.051969253 1.99619E-07 4.86128E-06 0.038826054 0.000414249 0.023885916 0.058546555 1.81062E-27 4.48554E-11 1.66809E-09 0.023340543 0.020757093 0.020757093 0.001418424 0.006171991 8.61926E-05 0.027782755 0.0001313 0.021926363 0.000337722 0.011597364 0.093573571 0.001036328 0.019927209 3.2408E-15 1.79676E-29 8.3561E-12
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M5005_Spy0953 M5005_Spy0954 M5005_Spy0956 M5005_Spy0970 M5005_Spy0971 M5005_Spy0971 M5005_Spy0973 M5005_Spy0973 M5005_Spy0975 M5005_Spy0980 M5005_Spy0982 M5005_Spy0982 M5005_Spy0982 M5005_Spy0988 M5005_Spy0998 M5005_Spy0999 M5005_Spy0999 M5005_Spy0999 M5005_Spy1000 M5005_Spy1000 M5005_Spy1000 M5005_Spy1001 M5005_Spy1002 M5005_Spy1021 M5005_Spy1022 M5005_Spy1023 M5005_Spy1023 M5005_Spy1024 M5005_Spy1024 M5005_Spy1055 M5005_Spy1056 M5005_Spy1056 M5005_Spy1058	pstA pstC pstS pytO970 M5005_Spy0971 M5005_Spy0975 M5005_Spy0982 glmS sipC M5005_Spy0993 M5005_Spy0993 M5005_Spy0995 M5005_Spy0999 M5005_Spy1001 M5005_Spy1001 M5005_Spy1001 M5005_Spy1001 M5005_Spy1001 M5005_Spy1001 M5005_Spy1003 M5005_Spy1003 M5005_Spy1004 M5005_Spy1023 M5005_Spy1023 M5005_Spy1023 M5005_Spy1021 M5005_Spy1021 M5005_Spy1021 M5005_Spy1021 M5005_Spy1021 M5005_Spy1021 M5005_Spy1021 M5005_Spy1044 M5005_Spy1051 glgP malM malR malE M5005_Spy1061	phosphate transport system permease protein phosphate transport system permease protein phosphate-binding protein tRNA pseudouridine synthase B NAD-dependent K+ or Na+ uptake system component general stress protein, Gls24 family hypothetical protein general stress protein, Gls24 family hypothetical protein cobalt-zinc-cadmium resistance protein cAMP factor histidine-binding protein glucosaminefructose-6-phosphate aminotransferase (isomerizing) signal peptidase I ABC transporter ATP-binding protein phage structural protein phage protein	-1.85889123 -1.893478286 -1.934505396 -2.028958081 -1.471604692 -1.421419043 -0.729582942 -0.74247025 -0.796444899 -0.929213758 -0.213823413 -0.248755992 -0.186238825 5.006626723 -0.739674013 -1.0011065 -1.100487928 -0.369379627 -0.192884927 -0.220096914 -0.290821588 -0.388171259 -0.153974239 -0.254826936 -0.163801909 -0.184063525 -0.871526387 -0.200203681 -0.390985413 -0.40840295 -0.125967292 -0.433144416	5.07094E-53 1.7075E-162 1.37154E-65 2.6174E-112 0.003736548 0.002161896 9.50436E-05 0.051969253 1.99619E-07 4.86128E-06 0.038826054 0.000414249 0.023885916 0.058546555 1.81062E-27 4.48554E-11 1.66809E-09 0.023340543 0.020757093 0.001418424 0.006171991 8.61926E-05 0.02782755 0.0001313 0.021926363 0.00037722 0.011597364 0.093573571 0.001036328 0.019927209 3.2408E-15 1.79676E-29 8.3561E-12 0.03903346 1.47207E-16
M5005_Spy0953 M5005_Spy0954 M5005_Spy0956 M5005_Spy0970 M5005_Spy0971 M5005_Spy0973 M5005_Spy0973 M5005_Spy0973 M5005_Spy0975 M5005_Spy0980 M5005_Spy0980 M5005_Spy0982 M5005_Spy0982 M5005_Spy0988 M5005_Spy0999 M5005_Spy0999 M5005_Spy0999 M5005_Spy1000 M5005_Spy1050 M5005_Spy1050 M5005_Spy1050 M5005_Spy1055 M5005_Spy1055 M5005_Spy1056 M5005_Spy1056	pstA pstC pstS truB M5005_Spy0970 M5005_Spy0971 M5005_Spy0973 M5005_Spy0973 M5005_Spy0980 cfa M5005_Spy0982 glmS sipC M5005_Spy0982 M5005_Spy0998 M5005_Spy0998 M5005_Spy0999 M5005_Spy0993 M5005_Spy1003 M5005_Spy1001 M5005_Spy1001 M5005_Spy1001 M5005_Spy1001 M5005_Spy1002 M5005_Spy1021 M5005_Spy1021 M5005_Spy1021 M5005_Spy1021 M5005_Spy1021 M5005_Spy1021 M5005_Spy1021 M5005_Spy1021 M5005_Spy1021 M5005_Spy1044 M5005_Spy1050 M5005_Spy1050 M5005_Spy1050 M5005_Spy1051 m3IM maIR maIR maIE M5005_Spy1061 maID	phosphate transport system permease protein phosphate transport system permease protein phosphate-binding protein tRNA pseudouridine synthase B NAD-dependent K+ or Na+ uptake system component general stress protein, Gls24 family hypothetical protein general stress protein, Gls24 family hypothetical protein cobalt-zinc-cadmium resistance protein cAMP factor histidine-binding protein glucosaminefructose-6-phosphate aminotransferase (isomerizing) signal peptidase I ABC transporter ATP-binding protein ABC transporter permease protein phage protein phage protein phage protein phage associated cell wall hydrolase phage protein phage structural protein terminase large subunit phage protein	-1.85889123 -1.893478286 -1.934505396 -2.028958081 -1.471604692 -1.421419043 -0.729582942 -0.74247025 -0.796444899 -0.929213758 -0.213823413 -0.248755992 -0.186238825 5.006626723 -0.739674013 -1.0011065 -1.100487928 -0.369379627 -0.192884927 -0.192884927 -0.153974239 -0.153974239 -0.153974239 -0.153974239 -0.153974239 -0.153974239 -0.153974239 -0.153974239 -0.153974239 -0.153974239 -0.153974239 -0.153974239 -0.153974239 -0.153974239 -0.154806355 -0.371526387 -0.200203681 -0.390985413 -0.546280281 -0.470840295 -0.125967292	5.07094E-53 1.7075E-162 1.37154E-65 2.6174E-112 0.003736548 0.002161896 9.50436E-05 0.051969253 1.99619E-07 4.86128E-06 0.038826054 0.000414249 0.023885916 0.058546555 1.81062E-27 4.48554E-11 1.66809E-09 0.023340543 0.020757093 0.001418424 0.006177991 8.61926E-05 0.027782755 0.0001313 0.021926363 0.000337722 0.011597364 0.093573571 0.001036328 0.019927209 3.2408E-15 1.79676E-29 8.3561E-12 0.03903346

M5005_Spy1065	amyA	alpha-amylase	-0.150486893	0.020663041
M5005_Spy1066		neopullulanase/cyclomaltodextrinase/maltogenic alpha-amylase	-0.270234517	3.92313E-06
M5005_Spy1067		maltose/maltodextrin-binding protein	-0.419161272	9.7197E-15
	M5005_Spy1068 M5005_Spy1069		-0.595992535 -0.185810681	2.14565E-09 0.004770442
M5005_Spy1009		protein precursor	-2.754178196	0.0004770442
M5005 Spy1075		excinuclease ABC subunit B	-0.614268961	8.46179E-13
- ' '		PTS system, cellobiose-specific IIA component	0.211330964	0.062755564
M5005_Spy1085		beta-glucosidase	0.225321267	0.001714623
		nicotinamide mononucleotide transporter	0.12560052	0.075730336
		transporter, MFS superfamily phosphorylase, Pnp/Udp family	0.26784177 0.241880353	0.003823032 0.020179413
		transcriptional regulator, LytR family	-0.371112968	7.64254E-11
,	M5005_Spy1102		-0.29608233	0.039666652
M5005_Spy1108		S-adenosylmethionine synthetase	-1.470981694	0.003090914
M5005_Spy1110		biotin operon repressor/biotin[acetyl-CoA-carboxylase] synthetase	-0.595948793	0.030466932
		putative membrane spanning protein	-0.252840367	0.028614514
M5005_Spy1116 M5005_Spy1119		uridine kinase NADP-dependent glyceraldehyde-3-phosphate dehydrogenase	-0.286922827 5.807651869	0.012623158 0.020074681
M5005_Spy1120		phosphoenolpyruvate-protein phosphotransferase	-3.011272175	0.006719284
M5005 Spy1133	•	peptidyl-prolyl cis-trans isomerase	-0.39763532	0.000388025
M5005_Spy1139		glucosamine-6-phosphate isomerase	-2.093827111	2.88467E-45
M5005_Spy1147		COME operon protein 3	0.148873576	0.01593488
		hypothetical protein with endo/excinuclease domain	-0.261493392	0.00193561
M5005_Spy1152 M5005_Spy1155		kup system potassium uptake protein	0.128619751	0.028614514
M5005_Spy1157		bacterial peptide chain release factor 3 (RF-3) UDP-N-acetylmuramoylalanine-D-glutamyl-lysine D-alanyl-D-alanine ligase	0.357879816 6.719714196	0.009073766 0.013461377
M5005_Spy1159		recombination protein	-1.280897205	0.096045264
		lead, cadmium, zinc and mercury transporting ATPase	0.199057926	0.022427384
M5005_Spy1170	M5005_Spy1170	putative membrane associated protein	-0.340661019	8.2749E-05
	M5005_Spy1173		-0.510577256	0.04034404
	M5005_Spy1184		-0.297235957	0.065806857
			0.207693425	0.070456533
	M5005_Spy1193 M5005_Spy1198		-0.139853802 -0.2460794	0.020393212 0.042029066
	M5005_Spy1205		-0.530447481	0.031023338
M5005 Spy1212		excisionase	-0.283754226	0.001323835
M5005_Spy1215	M5005_Spy1215	phage protein	0.240319288	0.081897455
	M5005_Spy1220		-0.217194686	0.001032325
M5005_Spy1222		integrase	-0.145201209	0.020774348
		DNA-binding protein HU	-0.786453801	0.048158486
M5005_Spy1229		degV family protein arginine repressor	-0.166376836 -0.287412646	0.083125274 0.070161556
M5005_Spy1238	-	arginine transport system permease protein	0.335345657	7.87538E-05
		putative cytosolic protein	-5.991188884	8.52842E-06
M5005_Spy1240		ATP-dependent clp protease ATP-binding subunit	-0.311334502	2.68547E-05
M5005_Spy1241		mutator protein (7,8-dihydro-8-oxoguanine-triphosphatase)	0.306965042	1.40526E-06
		putative cytosolic protein	-3.825808456	3.99866E-18
M5005_Spy1257	-	glucokinase/Xylose repressor	0.463168135	0.000616995
M5005_Spy1259 M5005_Spy1261		non-specific DNA-binding protein/iron-binding ferritin-like antioxidant protein radical SAM family enzyme	0.54163315 -0.277455862	0.026754736 0.000143065
M5005_Spy1269		aspartateammonia ligase	-0.324396241	0.00022588
		Xaa-His dipeptidase	0.355033327	6.96162E-06
M5005_Spy1272	M5005_Spy1272	arginine/ornithine antiporter	0.34567922	2.73948E-10
		acetyltransferase	0.352489823	0.062755564
M5005_Spy1275		arginine deiminase	0.432105002	4.41244E-11
		transcription regulator, crp family	0.242779764	0.001036328
M5005_Spy1277 M5005_Spy1278		arginine repressor hypothetical protein	0.384121152 0.405186181	0.001365761 0.000362317
		putative cytosolic protein	0.303346171	0.000263411
		two-component sensor kinase	0.119234668	0.086037306
		hypothetical protein	0.381899297	0.00033272
M5005_Spy1292		valyl-tRNA synthetase	3.391011069	0.074713922
		hypothetical protein	0.908935502	0.060043898
M5005_Spy1304		beta-galactosidase two-component response regulator	0.137980874 0.205269508	0.048679478 0.040222719
		two-component sensor kinase	0.132984775	0.059241498
		putative membrane spanning protein	0.368399167	0.046731974
M5005_Spy1308	M5005_Spy1308	sugar-binding protein	0.145471244	0.053891616
,		sugar transport system permease protein	0.354242186	0.000513027
M5005_Spy1314		hyaluronoglucosaminidase	-0.227328213	0.014696612
		hypothetical protein	-0.128551022	0.085160895
		alpha-mannosidase ribosome-associated factor Y	-0.245505003 -0.221347596	0.001387193 0.041573651
M5005_Spy1326		COMF operon protein 3	-0.372110262	2.10923E-06
		S1-type RNA-binding domain	-0.74692518	0.075490492
		serine/threonine protein kinase	-6.585073438	0.006793532
M5005_Spy1337		16S rRNA m(5)C 967 methyltransferase	0.239694789	0.053003495
		D-beta-hydroxybutyrate permease	0.14496096	0.047084545
M5005_Spy1349		autoinducer-2 production protein	0.343853044	0.004009047
M5005_Spy1355 M5005_Spy1359		multimodular transpeptidase-transglycosylase amino acid permease	-0.357965209 -0.304658981	0.017686211 0.01702493
M5005_Spy1367		cell division protein	-4.551689394	0.000108524
- 17		•		

M5005_Spy1368 mraW	S-adenosyl-methyltransferase	1.67930909	0.090073585
M5005_Spy1372 proB	ABC transporter permease protein	0.133261314	0.058546555
,,	ABC transporter ATP-binding protein	-0.356746012	3.41443E-06
M5005_Spy1375_tkt	transketolase	-2.51859695	3.09045E-34
M5005_Spy1380_glpO	alpha-glycerophosphate oxidase	0.291621409	0.001966032
M5005_Spy1381_glpK	glycerol kinase	-0.387105112	0.000176667
M5005_Spy1388 nagA	N-acetylglucosamine-6-phosphate deacetylase	-2.967080193	9.81928E-67
M5005_Spy1399 M5005_Spy1399	PTS system, galactose-specific IIC component	0.966600808	9.68348E-46
M5005_Spy1400 M5005_Spy1400	PTS system, galactose-specific IIB component	0.766318977	6.56928E-56
M5005_Spy1401 M5005_Spy1401	PTS system, galactose-specific IIA component	0.748829764	7.90408E-17
M5005_Spy1402_lacR1	lactose phosphotransferase system repressor	-0.553815332	4.66666E-15
M5005_Spy1407 M5005_Spy1407	esterase	0.19769693	0.000922219
M5005 Spy1415 sdaD2	phage-encoded streptodornase	-0.465311301	1.02888E-19
M5005 Spy1418 M5005 Spy1418		-0.586820285	1.06578E-08
M5005_Spy1424 M5005_Spy1424		-0.24846314	0.005541929
M5005 Spy1429 M5005 Spy1429		0.723358181	0.037713588
M5005_Spy1432 M5005_Spy1432		-0.242009298	0.067313007
M5005_Spy1434 M5005_Spy1434		-0.134451994	0.064042121
M5005_Spy1439 M5005_Spy1439		-1.046023558	2.75952E-94
		-0.26903225	
M5005_Spy1440 M5005_Spy1440			0.01702493
M5005_Spy1444 M5005_Spy1444		-0.483602884	1.22193E-05
M5005_Spy1445 M5005_Spy1445		-3.11670764	0.0019036
M5005_Spy1447 M5005_Spy1447		-0.36668461	0.001549324
M5005_Spy1450 M5005_Spy1450		-0.392703831	0.001036328
M5005_Spy1452 M5005_Spy1452		-1.357985539	0.002521384
M5005_Spy1453 M5005_Spy1453		-0.52535912	0.000867075
M5005_Spy1456 M5005_Spy1456		-5.865683189	0.007275635
M5005_Spy1459 M5005_Spy1459	phage protein	4.948664617	0.070190509
M5005_Spy1462 M5005_Spy1462	phage protein	-3.37461592	0.002345239
M5005_Spy1467 int3	integrase	0.162128269	0.028614514
M5005 Spy1468 M5005 Spy1468	tRNA (m(7)G46) methyltransferase	-4.531276109	2.1863E-104
M5005 Spy1472 hit	bis(5'-nucleosyl)-tetraphosphatase (asymmetrical)	-0.749819225	3.43726E-29
M5005_Spy1473 M5005_Spy1473	hypothetical protein	-0.416631681	0.093032464
M5005 Spy1479 manL	PTS system, mannose-specific IIAB component	-0.297216685	0.003410052
M5005_Spy1481 manN	PTS system, mannose-specific IID component	-0.23871645	0.003859713
M5005_Spy1485_accA	acetyl-coenzyme A carboxylase carboxyl transferase subunit beta	5.150732112	0.053003495
M5005 Spy1498 dnaK	chaperone protein	-2.761056382	0.073631479
M5005_Spy1505 M5005_Spy1505		0.231450181	0.019244545
M5005_Spy1505 M5005_Spy1505	transcription pleiotropic repressor	-2.430113697	
M5005_Spy1512 Cod1 M5005_Spy1513 M5005_Spy1513			0.046340261
		-0.291579792	5.6449E-05
M5005_Spy1515 M5005_Spy1515		0.151260986	0.035734291
M5005_Spy1516_asnB	L-asparaginase	0.266714114	0.047444226
M5005_Spy1519 recG	ATP-dependent DNA helicase	-1.196217506	7.00861E-22
	ferrichrome transport system permease protein	0.362243739	0.007434617
M5005_Spy1528 M5005_Spy1528	÷.	0.225701691	0.035989381
M5005_Spy1531 isp2	immunogenic secreted protein	0.147449983	0.042690936
M5005_Spy1538 pmi	mannose-6-phosphate isomerase	0.549596975	0.000337974
M5005_Spy1543 scrB	sucrose-6-phosphate hydrolase	0.58307602	0.008441112
M5005_Spy1544 scrR	sucrose operon repressor	0.424628928	1.48977E-09
M5005_Spy1546 M5005_Spy1546	general stress protein, Gls24 family	4.610387445	0.096298826
M5005_Spy1554 ssb3	phage single-strand DNA binding protein	-2.883450906	0.016433127
M5005_Spy1556 M5005_Spy1556	hypothetical protein	-0.295605182	0.078666556
M5005_Spy1558 M5005_Spy1558		-0.183045694	0.055279479
	phosphatidylglycerophosphatase B	-0.601488049	4.68211E-12
M5005_Spy1561 mutS2	DNA mismatch repair protein	-0.318372284	1.31956E-06
M5005 Spy1566 recD	exodeoxyribonuclease V alpha chain	-0.198012638	0.003992761
M5005_Spy1569 pfl	formate acetyltransferase	0.219644111	0.051658108
M5005_Spy1571 M5005_Spy1571		0.158398807	0.012028133
M5005_Spy1571 MS005_Spy1571	quinolone resistance protein	0.288128283	0.070372434
M5005_Spy1583 M5005 Spy1583		-0.689740143	0.06131078
M5005_Spy1585_deoC	deoxyribose-phosphate aldolase	-0.176406289	0.008518949
M5005_Spy1586_nupC	nucleoside permease	0.210194156	0.006516949
M5005_Spy1595 M5005_Spy1595			
		4.136269425	0.046803536
M5005_Spy1607_fba	fructose-bisphosphate aldolase	3.187168475	0.068861964
M5005_Spy1608 M5005_Spy1608		-0.305972667	0.025041831
M5005_Spy1611 rpoE	DNA-directed RNA polymerase delta chain	-1.062584944	8.28587E-39
M5005_Spy1612 ropA	trigger factor, ppiase	0.537905124	0.005470417
M5005_Spy1617 M5005_Spy1617		-1.687984388	0.000853296
M5005_Spy1620 M5005_Spy1620		0.186255087	0.074439808
M5005_Spy1625_salR	transcriptional regulatory protein	-0.213017119	0.004571132
	sensory transduction protein kinase	-0.201910317	0.025361034
	ABC transporter ATP-binding protein	-0.155640457	0.068694134
M5005_Spy1636 lacC2	tagatose-6-phosphate kinase	-0.235748911	0.001214377
M5005_Spy1637 lacB2	galactose-6-phosphate isomerase lacB subunit	-0.184879789	0.0884185
M5005_Spy1638 lacA2	galactose-6-phosphate isomerase lacA subunit	-0.466057228	1.1464E-09
M5005_Spy1639_lacR2	lactose phosphotransferase system repressor	0.442227619	3.26984E-16
M5005_Spy1641 M5005_Spy1641	putative cytosolic protein	-0.193258928	0.030466932
	putative membrane associated protein	-0.178210109	0.056205149
M5005_Spy1654 M5005_Spy1654		0.218946555	0.027782755
M5005 Spy1658 cysE	serine acetyltransferase	0.284746722	0.021035449
	polyribonucleotide nucleotidyltransferase	1.21659417	0.007300065
M5005 Spy1661 M5005 Spy1661		0.320638041	0.012028133
	transcription antiterminator, BgIG family	0.129232287	0.033876806
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MEOOF Courtees N	45005 Cm, 1666	SSU ribosomal protein S15P	1.26756869	0.044442389
			0.532943513	0.044442369
M5005_Spy1678 M M5005 Spy1683 Ir		leucine rich protein	0.26514934	0.054447704
M5005_Spy1684 s		streptokinase	-0.167414356	0.00396604
		PTS system, glucose-specific IIABC component	0.22754629	0.00390004
		ribosomal protein L11 methyltransferase	0.378942638	0.039960084
		ATPase, AAA family	0.438937934	3.33963E-07
M5005_Spy1701 fl		DNA topology modulation protein flar-related protein	0.219567905	0.002521455
M5005_Spy1704 d		dipeptide-binding protein	0.169272735	0.016433127
M5005_Spy1704_d		dipeptide transport system permease protein	0.311227603	0.000724689
		hypothetical protein	0.609290595	0.076397832
M5005 Spy1716 N			0.285978288	0.000215362
M5005_Spy1723 is		immunogenic secreted protein	0.187114534	0.014814538
		ABC transporter permease protein	0.41960124	1.14975E-10
		ABC transporter ATP-binding protein	0.456661447	3.48731E-11
M5005 Spy1728 N	M5005 Spy1728	periplasmic component of efflux system	0.597386975	1.89224E-25
M5005_Spy1733 N	M5005_Spy1733	hypothetical protein	-0.327011341	0.00396604
M5005_Spy1734 s	spi	streptopain protease inhibitor	-1.306111591	0.055924712
M5005_Spy1737 rg	gg	transcriptional regulator	-0.287939227	5.13485E-05
M5005_Spy1741 g	gldA	glycerol dehydrogenase	0.301455488	0.006304499
M5005_Spy1744 N	M5005_Spy1744	PTS system, cellobiose-specific IIC component	0.318130964	5.43431E-06
M5005_Spy1747 N	M5005_Spy1747	sorbitol operon regulator	0.173643909	0.04604258
		transcriptional regulator, DeoR family	-0.229936107	0.003190623
		pyruvate formate-lyase activating enzyme	0.184752698	0.081288026
M5005_Spy1753 p		multimodular transpeptidase-transglycosylase	-1.489990102	1.67134E-39
		translation initiation inhibitor	0.679504841	1.75313E-20
		putative dipeptidase B	0.166753885	0.020774348
M5005_Spy1770 h		imidazolonepropionase	-0.394015218	1.09926E-06
M5005_Spy1771 h		urocanate hydratase	0.265960905	0.000724689
		glutamate formiminotransferase	0.276809073	4.05381E-06
		transcriptional regulator, LuxR family	0.261823917	8.61926E-05
M5005_Spy1783 d		trehalose-6-phosphate hydrolase	-0.412219696	0.031653124
		PTS system, trehalose-specific IIBC component	0.199426863	0.012515326
		glyoxalase family protein	0.184634433	0.004600307
M5005_Spy1788 y		protein yaaA	0.271256921	0.001549324
		putative membrane spanning protein	-0.249876842	0.011433773
		putative cytosolic protein	-1.000465879	0.01862386
M5005_Spy1799 re		RecA	-0.69730192	0.089030926
M5005_Spy1802 rt M5005_Spy1805_n		holliday junction DNA helicase DNA mismatch repair protein	-2.752251314 -0.172856862	0.02362407 0.016835327
M5005_Spy1807 a		arginine repressor	0.540279525	0.001549324
M5005_Spy1808 a		arginyl-tRNA synthetase	-0.434441451	0.001349324
		putative membrane spanning protein	-0.57868553	5.24865E-20
		putative membrane spanning protein	-0.37349165	0.053447917
M5005 Spy1813 a		aspartyl-tRNA synthetase	-4.834405166	0.059571138
M5005 Spy1815 rg		LSU ribosomal protein L32P	-6.916976722	0.001147592
M5005 Spy1817 c		cadmium resistance protein	0.199311254	0.023764653
M5005 Spy1818 c		cadmium efflux system accessory protein	0.586704766	6.96365E-09
M5005 Spy1820 N			0.308328803	0.002005886
		phage infection protein	0.386702347	1.36339E-05
		hypothetical protein	-4.003417166	0.015006992
M5005 Spy1837 N	M5005 Spy1837	phosphoesterase, DHH family protein	-4.225291276	6.28895E-17
M5005_Spy1842 s	sdhA	L-serine dehydratase	0.371627958	4.40495E-09
M5005_Spy1843 N	M5005_Spy1843	transglycosylase SLT domain family protein	0.177933795	0.060683246
M5005_Spy1849 N	M5005_Spy1849	zinc protease	0.186953924	0.042739332
M5005_Spy1850 N	M5005_Spy1850	zinc protease	0.206005312	0.028349113
M5005_Spy1851 h		hyaluronan synthase	0.173996812	0.005514679
		putative cytosolic protein	0.426090392	0.05897268
		glucose uptake protein-like protein	0.137265613	0.079117191
M5005_Spy1857 g		inosine-5'-monophosphate dehydrogenase	0.414805974	0.000169353
		ABC transporter, permease protein	-0.254089421	0.004770442
M5005_Spy1863 N			0.394988955	0.027103422
M5005_Spy1866 p	oarB	chromosome partitioning protein	-0.179182668	0.03784202

^{*} 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.