Supplemental Table 1: Primers used in the study

Name	Sequence (5' to 3')
AB57_0091+	GGGTTTATCGGCGCTTTAATTG
AB57_0091-	GGAACGAGGTACTGTTGCATAG
AB57_1479+	GGCTAAGAGAGAAAGCGTACAA
AB57_1479-	CTTTCGCTTCTTTCGCATCAC
AB57_1527+	TCTGTGTGCATCGGGTTTAG
AB57_1527-	AACGCTTCGGTCGGTTTAG
AB57_16S+	CAGCTCGTGTCGTGAGATGT
AB57_16S-	CGTAAGGGCCATGATGACTT
AB57_2007+	GGTGCTCAAGCTAACTCTCAA
AB57_2007-	CAGCAGTAGAAGCACCAGTT
AB57_2570+	GCTGCACGTACAAACCTTTATG
AB57_2570-	TTGGTGTACCTGTGTTTGGAG

Supplemental Table 2: Complete table of transcript data from *P. gingivalis* and *A. baumannii*

PGN	Gene	Product	log2 Fold Change	p-value	q-value
PGN_0001	dnaA	chromosomal replication initiator protein DnaA	-0.31276	0.3026	0.419359
PGN_0002		conserved hypothetical protein	-0.206714	0.46085	0.575792
PGN_0003		conserved hypothetical protein	0.577411	0.06255	0.117226
PGN_0004		putative nicotinate mononucleotide:5,6-dimethylbenzimidazole phosphorib	-1.70588	5.00E-05	0.00026
PGN_0005		conserved hypothetical protein	1.20939	5.00E-05	0.00026
PGN_0006		putative Na+driven multidrug efflux pump	0.587552	0.03535	0.07321
PGN_0007		hypothetical protein	-0.799151	0.0542	0.103398
PGN_0008	clpC	ATP-dependent Clp protease ATP-binding subunit ClpC	-2.15603	5.00E-05	0.00026
PGN_0009		glycosyl hydrolase family 3	-0.90838	0.00255	0.007891
PGN_0010		probable L-threonine-O-3-phosphate decarboxylase	0.081122	0.77955	0.848932
PGN_0011		conserved hypothetical protein	0.455126	0.0976	0.167034
PGN_0012		two-component system response regulator	0.523943	0.06555	0.121657
PGN_0013		putative two-component system sensor histidine kinase	1.25406	5.00E-05	0.00026
PGN_0014		conserved hypothetical protein	1.58567	5.00E-05	0.00026
PGN_0015		probable transcriptional regulator	-0.90761	0.07175	0.130672
PGN_0016		putative TIM-barrel protein	-0.228265	0.70835	0.796239
PGN_0017		sulfate transporter permease	0.177185	0.7379	0.817427
PGN_0018		hypothetical protein	1.69181	0.09645	0.165465
PGN_0019		hypothetical protein	0.311715	0.8001	0.862924
PGN_0020		probable DNA-binding protein	-0.635194	0.0304	0.065244
PGN_0021		probable hydrolase	0.48924	0.0937	0.162185
PGN_0022	porU	Por secretion system protein porU	1.22292	0.00025	0.00108
PGN_0023	porV	Por secretion system protein porV (pg27, lptO)	1.72454	5.00E-05	0.00026
PGN_0024	ispF	putative 2C-methyl-D-erythritol 2,4-cyclodiphosphate synthase	1.35228	5.00E-05	0.00026
PGN_0025		probable SpoU rRNA methylase family protein	-0.56049	0.05395	0.103106
PGN_0026		putative cytidine deaminase	-1.39022	5.00E-05	0.00026
PGN_0027		transposase in ISPg1	-2.36099	5.00E-05	0.00026
PGN_0028		hypothetical protein	-1.34358	0.0015	0.004944
PGN_0029		conserved hypothetical protein	-0.300144	0.30275	0.419359
PGN_0030		beta-mannosidase	-0.196418	0.4656	0.580025
PGN_0031		conserved hypothetical protein with RmuC domain	-0.0314477	0.9048	0.938295
PGN_0032		conserved hypothetical protein	-0.250104	0.6238	0.725325
PGN_0033		thioredoxin	-1.22917	0.00115	0.003911
PGN_0034		DNA polymerase III alpha subunit	-0.56406	0.0613	0.115391
PGN_0035	rplS	50S ribosomal protein L19	2.58517	5.00E-05	0.00026
PGN_0036		hypothetical protein	-1.06125	0.0009	0.003178
PGN_0037		conserved hypothetical protein	0.00254296	0.98945	0.991312
PGN_0038	glyA	serine hydroxymethyltransferase	0.632302	0.0344	0.071661
PGN_0039		beta-hexosaminidase	0.0765989	0.79015	0.856969
PGN_0040		hypothetical protein	-0.867723	0.05815	0.110144
PGN_0041	htpG	heat shock protein 90	-0.0921516	0.75165	0.828293
PGN_0042		probable phosphatidate cytidylyltransferase	-1.17536	0.00065	0.00239
PGN_0043		putative transmembrane AAA-metalloprotease FtsH	-1.6019	5.00E-05	0.00026
PGN_0044		GTP-binding protein	-0.168025	0.55635	0.666181
PGN_0045		conserved hypothetical protein	1.39085	0.0115	0.028602
PGN_0046		hypothetical protein	0.437533	0.429	0.545278
PGN_0047		conserved hypothetical protein	-1.07898	0.10075	0.171735
PGN_0048		conserved hypothetical protein	-0.0339944	0.93385	0.956208
PGN_0049		probable anti-restriction protein	-0.995034	0.0797	0.14235
PGN_0050		conserved hypothetical protein	-0.921216	0.02075	0.047298
PGN_0051		conserved hypothetical protein	-2.19231	0.00125	0.004224
PGN_0052		hypothetical protein	-0.899609	0.034	0.070967
PGN_0053		conserved hypothetical protein	-0.51947	0.0986	0.168475
PGN_0054		hypothetical protein	-1.97665	5.00E-05	0.00026
PGN_0055		probable lysozyme	-2.18931	5.00E-05	0.00026
PGN_0056		probable conserved protein found in conjugate transposon	-0.663437	0.41905	0.536475
PGN_0057	traP_1	probable conserved protein found in conjugate transposon TraP	-1.25834	0.00025	0.00108
PGN_0058		probable conserved protein found in conjugate transposon	-1.09091	0.03995	0.081081
PGN_0059	traN_1	conserved protein found in conjugate transposon TraN	-1.32619	5.00E-05	0.00026
PGN_0060	traM_1	conserved protein found in conjugate transposon TraM	-1.27226	5.00E-05	0.00026
PGN_0061		hypothetical protein	-0.918222	0.48055	0.59344

PGN_0062	traK_1	putative conserved protein found in conjugate transposon TraK	-0.921548	0.18895	0.28899
PGN_0063	traJ_1	conserved transmembrane protein found in conjugate transposon TraJ	-0.851446	0.0026	0.008022
PGN_0064	traI_1	putative conserved protein found in conjugate transposon TraI	-0.702813	0.01935	0.04444
PGN_0065	traG	conserved protein found in conjugate transposon TraG	-1.23245	0.0001	0.000483
PGN_0066	traF_1	probable conserved transmembrane protein found in conjugate transposon	0.0502714	0.8614	0.906535
PGN_0068		hypothetical protein	-1.54075	5.00E-05	0.00026
PGN_0069	traA_1	probable conserved protein found in conjugate transposon TraA	-1.01945	0.01125	0.028112
PGN_0070		hypothetical protein	-0.759222	0.05655	0.107495
PGN_0071		hypothetical protein	-0.837239	0.0908	0.158194
PGN_0072		hypothetical protein	-1.22684	0.01265	0.03085
PGN_0074		conserved hypothetical protein	-0.639529	0.25375	0.365764
PGN_0075		conserved hypothetical protein	-0.308339	0.38145	0.499582
PGN_0076		putative mobilization protein TraG family	-0.102126	0.7123	0.798319
PGN_0077		hypothetical protein	-1.16895	5.00E-05	0.00026
PGN_0078		hypothetical protein	-1.02059	0.00105	0.003606
PGN_0079		conserved hypothetical protein with DUF1016 domain	-1.26466	0.00045	0.001764
PGN_0080		probable tetracycline resistance element mobilization regulatory protein Rte	-0.521884	0.0664	0.123034
PGN_0081		putative Na driven multidrug efflux pump	0.266416	0.36015	0.479225
PGN_0082		probable transcriptional regulator AraC family	-0.331875	0.2783	0.393378
PGN_0083		conserved hypothetical protein	-0.645539	0.0212	0.048067
PGN_0084		DNA topoisomerase I	-1.08413	0.00015	0.000685
PGN_0085		hypothetical protein	-0.712641	0.6311	0.731416
PGN_0086		putative DNA methylase	-0.601366	0.03335	0.07016
PGN_0087		conserved hypothetical protein	-1.18529	0.00055	0.002076
PGN_0088		putative transcriptional regulator	-1.36922	0.1984	0.301279
PGN_0089		hypothetical protein	-0.138609	0.79485	0.858132
PGN_0090		hypothetical protein	0.0696362	0.8796	0.920683
PGN_0091		hypothetical protein	-0.939875	0.00065	0.00239
PGN_0092		conserved hypothetical protein	-1.12442	0.0001	0.000483
PGN_0093		conserved hypothetical protein	0.221169	0.4421	0.558326
PGN_0094		putative bacteriophage integrase	-0.197166	0.48675	0.598666
PGN_0095		hypothetical protein	-0.0291627	0.93035	0.953642
PGN_0096		aspartate kinase	-0.544003	0.06125	0.115391
PGN_0097		putative cell-division ATP-binding protein	-1.17366	0.00025	0.00108
PGN_0098		hypothetical protein	-2.69714	0.0098	0.024987
PGN_0099		probable peptidase	1.48918	5.00E-05	0.00026
PGN_0100		diaminopimelate decarboxylase	-1.31074	5.00E-05	0.00026
PGN_0101		putative 1,4-dihydroxy-2-naphthoate octaprenyltransferase	-0.781509	0.44115	0.558056
PGN_0102		conserved hypothetical protein	-1.67431	5.00E-05	0.00026
PGN_0103		putative TonB	-1.26353	0.0001	0.000483
PGN_0104		transposase in ISPg1	-2.32402	5.00E-05	0.00026
PGN_0105		conserved hypothetical protein	-0.536697	0.36175	0.480652
PGN_0106		partial transposase in ISPg3	-0.388515	0.19085	0.291478
PGN_0107		partial transposase in ISPg3	-1.31066	0.16055	0.252819
PGN_0108		partial transposase in ISPg1	-2.36929	0.0006	0.002241
PGN_0109		conserved hypothetical protein	1.55052	0.1051	0.177727
PGN_0110		hypothetical protein	1.1618	0.0008	0.002848
PGN_0111		partial transposase in ISPg6	0.170235	0.7004	0.791062
PGN_0112		partial transposase Orf1 in ISPg5	-1.2998	0.00025	0.00108
PGN_0113		hypothetical protein	-0.898508	0.0516	0.099508
PGN_0114		Na translocating NADH-quinone reductase subunit A	0.168165	0.5593	0.668585
PGN_0115		Na translocating NADH-quinone reductase subunit B	0.0307391	0.9169	0.946234
PGN_0116		probable Na translocating NADH-quinone reductase subunit C	0.668024	0.0185	0.042672
PGN_0117		putative Na translocating NADH-quinone reductase subunit D	0.711593	0.0105	0.026581
PGN_0118		putative Na translocating NADH-quinone reductase subunit E	1.09904	5.00E-05	0.00026
PGN_0119		Na translocating NADH-quinone reductase subunit F	1.19023	0.00025	0.00108
PGN_0120		conserved hypothetical protein	1.13242	0.00025	0.00108
PGN_0121		conserved hypothetical protein	1.14528	0.0004	0.001607
PGN_0122		28 kDa outer membrane protein Omp28	0.382616	0.5588	0.668362
PGN_0123		conserved hypothetical protein	-1.16504	0.003	0.009047
PGN_0124		hypothetical protein	-0.370021	0.25985	0.373545
PGN_0125		D-isomer specific 2-hydroxyacid dehydrogenase family protein	-0.578723	0.04895	0.095522

PGN_0126		putative transmembrane glucose/galactose transporter	0.753331	0.0129	0.031316
PGN_0127		hypothetical protein	0.269208	0.5188	0.632966
PGN_0128		immunoreactive 53 kDa antigen	0.0577569	0.8493	0.898688
PGN_0129		conserved hypothetical protein	0.249152	0.389	0.507153
PGN_0130		partial transposase in ISPg1	-2.33488	5.00E-05	0.00026
PGN_0131		partial transposase in ISPg1	-2.73925	5.00E-05	0.00026
PGN_0132		conserved hypothetical protein	0.358653	0.34105	0.459845
PGN_0133		adenosylmethionine--8-amino-7-oxononanoate aminotransferase	0.204695	0.60945	0.711359
PGN_0134		putative biotin synthetase	0.556734	0.1856	0.285172
PGN_0135		putative H+/peptide symporter	1.31621	0.0002	0.000895
PGN_0136		conserved hypothetical protein	0.513125	0.0768	0.138097
PGN_0137		putative tryptophanyl-tRNA synthetase	0.628133	0.0389	0.07948
PGN_0138		conserved hypothetical protein	0.396382	0.29595	0.412895
PGN_0139		conserved hypothetical protein	0.422582	0.3937	0.51109
PGN_0140		peptide methionine sulfoxide reductase	1.13709	0.00025	0.00108
PGN_0141		conserved hypothetical protein	1.17963	5.00E-05	0.00026
PGN_0142		putative cation efflux protein	1.73572	5.00E-05	0.00026
PGN_0143		probable dihydroneopterin aldolase	0.593978	0.0344	0.071661
PGN_0144		hypothetical protein	-0.689759	0.0186	0.042857
PGN_0145		conserved hypothetical protein	0.434336	0.1379	0.222753
PGN_0146		hypothetical protein	1.83645	0.0098	0.024987
PGN_0147		conserved hypothetical protein	0.623313	0.02405	0.053005
PGN_0148		conserved hypothetical protein	0.587415	0.0434	0.086678
PGN_0149		ribose-phosphate pyrophosphokinase	0.919991	0.00185	0.00595
PGN_0150		putative ATP-dependent RNA helicase	0.417496	0.1416	0.227866
PGN_0151		conserved hypothetical protein	-1.83591	5.00E-05	0.00026
PGN_0152		immunoreactive 61 kDa antigen	-2.02252	5.00E-05	0.00026
PGN_0153		conserved hypothetical protein	-2.58374	5.00E-05	0.00026
PGN_0154		conserved hypothetical protein	2.88584	5.00E-05	0.00026
PGN_0155		hypothetical protein	0.825313	0.0264	0.057411
PGN_0156		conserved hypothetical protein	-0.042848	0.8901	0.929089
PGN_0157	thiH	putative thiamine biosynthesis protein ThiH	-1.45769	5.00E-05	0.00026
PGN_0158	thiG	putative thiazole biosynthesis protein ThiG	-2.47931	5.00E-05	0.00026
PGN_0159		probable thiamin-phosphate pyrophosphorylase	-1.57236	0.00275	0.008448
PGN_0160		thiamine biosynthesis protein	-1.52294	0.00035	0.001436
PGN_0161		putative thiamine biosynthesis protein ThiS	0.362545	0.3286	0.447949
PGN_0162		conserved hypothetical protein	-0.51578	0.11795	0.195573
PGN_0163		hypothetical protein	-1.8145	5.00E-05	0.00026
PGN_0164		conserved hypothetical protein	1.79925	0.0055	0.015307
PGN_0165		conserved hypothetical protein	2.44857	0.0029	0.008858
PGN_0166		conserved hypothetical protein	2.7094	0.00015	0.000685
PGN_0167	rpsP	30S ribosomal protein S16	2.38962	5.00E-05	0.00026
PGN_0168		lipopolysaccharide biosynthesis protein WbpB	-0.268405	0.3402	0.459394
PGN_0169		probable metallo-beta-lactamase superfamily protein	1.353	5.00E-05	0.00026
PGN_0170		L-asparaginase	1.29102	5.00E-05	0.00026
PGN_0171		partial transposase in ISPg2	1.15133	0.0523	0.100584
PGN_0172		conserved hypothetical protein	-0.72962	0.02925	0.062966
PGN_0173		glyceraldehyde 3-phosphate dehydrogenase type I	-0.781482	0.01595	0.037689
PGN_0174		probable transcriptional regulator AraC family	1.4165	5.00E-05	0.00026
PGN_0175		conserved hypothetical protein	0.961485	0.01335	0.032188
PGN_0176		conserved hypothetical protein	0.937963	0.0394	0.080194
PGN_0177		hypothetical protein	-0.91062	0.04145	0.083965
PGN_0178		conserved hypothetical protein	-3.40036	5.00E-05	0.00026
PGN_0179		60 kDa protein	-3.61951	5.00E-05	0.00026
PGN_0180	fimA	FimA type I fimbrilin	-4.41145	5.00E-05	0.00026
PGN_0181		conserved hypothetical protein	-3.5532	5.00E-05	0.00026
PGN_0182		conserved hypothetical protein	-1.77212	0.03075	0.065928
PGN_0183	fimC	minor component FimC	-1.83071	5.00E-05	0.00026
PGN_0184	fimD	minor component FimD	-1.79448	0.00025	0.00108
PGN_0185	fimE	minor component FimE	-1.2907	0.00145	0.004794
PGN_0186		hypothetical protein	-1.7883	0.00485	0.013786
PGN_0187		conserved hypothetical protein	1.23709	0.0002	0.000895

PGN_0188	rpmF	50S ribosomal protein L32	1.23731	5.00E-05	0.00026
PGN_0189		beta-ketoacyl-acyl-carrier-protein synthase III	1.26476	0.0002	0.000895
PGN_0190	era	putative GTP-binding protein	1.46095	5.00E-05	0.00026
PGN_0191	engA	GTP-binding protein EngA	1.65962	5.00E-05	0.00026
PGN_0192		conserved hypothetical protein	1.88712	5.00E-05	0.00026
PGN_0193		putative polysaccharide deacetylase	2.33549	5.00E-05	0.00026
PGN_0194		conserved hypothetical protein	1.6138	5.00E-05	0.00026
PGN_0195		putative xanthine phosphoribosyltransferase	1.81218	5.00E-05	0.00026
PGN_0196		xanthine/uracil permease	1.13646	5.00E-05	0.00026
PGN_0197		conserved hypothetical protein	0.407552	0.14575	0.233821
PGN_0198		conserved hypothetical protein	0.880483	0.003	0.009047
PGN_0199		hypothetical protein	-0.777256	0.00635	0.01731
PGN_0200		conserved hypothetical protein	-0.795351	0.0075	0.020009
PGN_0201		conserved hypothetical protein with DUF558 domain	-1.32677	5.00E-05	0.00026
PGN_0202		probable leucine aminopeptidase precursor	1.08659	0.00035	0.001436
PGN_0203		probable SufE Fe/S-cluster-related protein	1.13829	0.00015	0.000685
PGN_0204		protoporphyrinogen oxidase	0.958795	0.0008	0.002848
PGN_0205		conserved hypothetical protein	1.80144	0.03195	0.067954
PGN_0206		putative lipid A disaccharide synthase	1.72407	5.00E-05	0.00026
PGN_0207	surE	probable stationary-phase survival protein	0.981522	0.16175	0.254332
PGN_0208		conserved hypothetical protein	0.875888	0.22835	0.335744
PGN_0209		glycyl-tRNA synthetase	0.692008	0.0777	0.139245
PGN_0210		transposase in ISPg1	-2.47664	5.00E-05	0.00026
PGN_0211		conserved hypothetical protein	-1.73465	5.00E-05	0.00026
PGN_0212		transposase in ISPg1	-2.39537	5.00E-05	0.00026
PGN_0213		conserved hypothetical protein	-2.50482	5.00E-05	0.00026
PGN_0214		conserved hypothetical protein	0.913636	0.29655	0.41319
PGN_0215		conserved hypothetical protein	0.572931	0.3995	0.515918
PGN_0216		conserved hypothetical protein	-1.39592	5.00E-05	0.00026
PGN_0217		conserved hypothetical protein	0.786233	0.00825	0.021711
PGN_0218		transposase in ISPg1	-2.46572	5.00E-05	0.00026
PGN_0219		partial transposase in ISPg1	-2.86189	5.00E-05	0.00026
PGN_0220		partial transposase in ISPg1	-2.80863	5.00E-05	0.00026
PGN_0221		DNA topoisomerase III	-1.22845	0.0003	0.00126
PGN_0222		conserved hypothetical protein	0.0673572	0.88565	0.925754
PGN_0223		glycosyl transferase family 4	0.569133	0.06375	0.119149
PGN_0224		UDP-N-acetyl-D-mannosaminuronic acid dehydrogenase	0.84651	0.00585	0.016091
PGN_0225		probable glycosyltransferase	1.29059	5.00E-05	0.00026
PGN_0226		conserved hypothetical protein	1.87092	5.00E-05	0.00026
PGN_0227		probable glycosyl transferase family 1	1.39732	5.00E-05	0.00026
PGN_0228		probable coenzyme F390 synthetase	1.14764	0.0001	0.000483
PGN_0229		putative DNA-binding protein histone-like family	0.0760551	0.7787	0.84844
PGN_0230		probable serine acetyltransferase	0.451441	0.34645	0.464771
PGN_0231		probable delta-aminolevulinic acid dehydratase	0.477881	0.16215	0.254742
PGN_0232		probable glycosyl transferase family 2	0.492466	0.0914	0.158979
PGN_0233		conserved hypothetical protein with glycosyl transferase WecB/TagA/CpsF f	0.581188	0.0467	0.091974
PGN_0234		UDP-N-acetylglucosamine 2-epimerase	0.388517	0.154	0.244027
PGN_0235		DNA-binding protein HU	-0.850525	0.00795	0.021104
PGN_0236		conserved hypothetical protein	0.431132	0.12735	0.20808
PGN_0237		conserved hypothetical protein	0.0324633	0.9057	0.938771
PGN_0238		conserved hypothetical protein	0.697651	0.28405	0.39917
PGN_0239		putative type I phosphodiesterase-nucleotide pyrophosphatase	0.662442	0.0395	0.08032
PGN_0240		putative ferrochelatase	0.298536	0.2765	0.391142
PGN_0241		conserved hypothetical protein	0.195698	0.48545	0.597758
PGN_0242		probable glycosyl transferase family 1	-0.185727	0.49435	0.606612
PGN_0243	gpmA	phosphoglycerate mutase	2.00091	5.00E-05	0.00026
PGN_0244		hypothetical protein	0.701827	0.2102	0.315747
PGN_0245		hypothetical protein	0.275158	0.5018	0.614691
PGN_0246		conserved hypothetical protein	0.0824873	0.8322	0.885647
PGN_0247		putative magnesium transporter	-0.4324	0.12885	0.210208
PGN_0248	ksgA	putative dimethyladenosine transferase	-0.234385	0.41545	0.532827
PGN_0249		conserved hypothetical protein	-0.0528937	0.85165	0.899938

PGN_0250		aminoacyl-histidine dipeptidase	-0.127535	0.6545	0.749786
PGN_0251		malonyl CoA-acyl carrier protein transacylase	-0.42096	0.1436	0.230735
PGN_0252		putative membrane-bound lytic murein transglycosylase D	1.78222	5.00E-05	0.00026
PGN_0253		conserved hypothetical protein	0.682186	0.0155	0.036748
PGN_0254		putative ParB chromosome partitioning protein	0.629285	0.02425	0.05339
PGN_0255		putative ParA chromosome partitioning protein	1.05695	0.00045	0.001764
PGN_0256		hydrolase	-0.691375	0.0209	0.047488
PGN_0257		putative arginine deiminase	0.0989272	0.73095	0.813058
PGN_0258	secG	hypothetical protein	-0.388365	0.1977	0.300431
PGN_0259		conserved hypothetical protein	-0.12548	0.65	0.748432
PGN_0260		conserved hypothetical protein	-0.188807	0.79245	0.857878
PGN_0261		sigma-54-dependent transcriptional regulator	-0.09133	0.77045	0.842469
PGN_0262		conserved hypothetical protein	-0.320826	0.2618	0.375335
PGN_0263		putative Fe-S oxidoreductase	-0.846934	0.04425	0.087963
PGN_0264		signal recognition particle-docking protein	-0.938966	0.0273	0.059187
PGN_0265		carboxynorspermidine decarboxylase	-1.14143	0.00015	0.000685
PGN_0266	aspS	aspartyl-tRNA synthetase	-0.960774	0.00165	0.005388
PGN_0267		putative riboflavin biosynthesis protein	-0.36185	0.2011	0.304511
PGN_0268		protoporphyrinogen oxidase	-0.621361	0.09585	0.164834
PGN_0269		putative transcriptional regulatory protein	-0.676471	0.29225	0.408268
PGN_0270		probable amidophosphoribosyl-transferase	0.170852	0.81465	0.873136
PGN_0271		endopeptidase PepO	0.219669	0.45555	0.572043
PGN_0272		conserved hypothetical protein	-0.0137047	0.9612	0.972159
PGN_0273		conserved hypothetical protein	0.382981	0.19615	0.29844
PGN_0274		putative RNA polymerase sigma-70 factor ECF subfamily	0.869147	0.00825	0.021711
PGN_0275		phosphofructokinase	-0.483304	0.09405	0.162658
PGN_0276		hypothetical protein	0.449252	0.3655	0.483623
PGN_0277	hslR	putative heat shock protein 15	0.707507	0.03675	0.075815
PGN_0278		putative peptidyl-tRNA hydrolase	1.48677	5.00E-05	0.00026
PGN_0279	rplY	putative 50S ribosomal protein L25	2.07858	5.00E-05	0.00026
PGN_0280		hypothetical protein	-1.58604	0.00615	0.016873
PGN_0281	metG	methionyl-tRNA synthetase	0.0752886	0.79085	0.857291
PGN_0282		2',3'-cyclic-nucleotide 2'-phosphodiesterase precursor	0.00914116	0.98085	0.986195
PGN_0283		probable exonuclease	0.0992377	0.8352	0.886411
PGN_0284		probable transcriptional regulator	-0.407408	0.14685	0.23507
PGN_0285		pyridine nucleotide-disulphide oxidoreductase	0.0686918	0.80095	0.863404
PGN_0286		hypothetical protein frame-shifted with PGN0285	0.656853	0.39325	0.510817
PGN_0287	mfa1	Mfa1fimbrilin	0.157022	0.63905	0.738219
PGN_0288	mfa2	conserved hypothetical protein	0.847863	0.0037	0.010971
PGN_0289	mfa3	conserved hypothetical protein	1.34748	5.00E-05	0.00026
PGN_0290	mfa4	immunoreactive 32 kDa antigen	1.29728	5.00E-05	0.00026
PGN_0291	mfa5	conserved hypothetical protein	1.43414	5.00E-05	0.00026
PGN_0292		hypothetical protein	-0.534509	0.4123	0.529425
PGN_0293	ragA	receptor antigen A	0.263097	0.4761	0.589498
PGN_0294	ragB	receptor antigen B	0.0915214	0.7868	0.854641
PGN_0295		C-terminal domain of Arg- and Lys-gingipain proteinase	-1.24493	0.0021	0.006663
PGN_0296		conserved hypothetical protein	0.15662	0.58925	0.692336
PGN_0297		conserved hypothetical protein	0.256639	0.36965	0.487297
PGN_0298		putative undecaprenyl diphosphate synthase	0.820753	0.00565	0.015683
PGN_0299		putative outer membrane protein	1.09977	0.0005	0.001921
PGN_0300		conserved hypothetical protein	0.00840409	0.9769	0.984297
PGN_0301		conserved hypothetical protein	0.927541	0.00255	0.007891
PGN_0302		rubrerythrin	-2.4839	5.00E-05	0.00026
PGN_0303		putative zinc protease	0.186445	0.5331	0.64597
PGN_0304		conserved hypothetical protein	-0.201898	0.7948	0.858132
PGN_0305		conserved hypothetical protein	0.156188	0.8302	0.885076
PGN_0306		conserved hypothetical protein	0.531022	0.26105	0.374764
PGN_0307		conserved hypothetical protein	0.681124	0.0797	0.14235
PGN_0308		conserved hypothetical protein	1.47751	0.17575	0.27272
PGN_0309	rnpA	probable ribonuclease P protein component	1.56231	0.05135	0.099386
PGN_0310		putative uroporphyrinogen-III synthase	1.37449	0.0001	0.000483
PGN_0311		conserved hypothetical protein	1.61706	0.15225	0.242076

PGN_0312		hypothetical protein	1.16139	0.00055	0.002076
PGN_0313		peptide chain release factor 3	1.57079	5.00E-05	0.00026
PGN_0314		probable formate/nitrite transporter	0.456819	0.1007	0.171735
PGN_0315		precorrin-6x reductase/cobalamin biosynthetic protein CbiD	0.307805	0.46815	0.5815
PGN_0316		precorrin-4 C11-methyltransferase	0.251518	0.53835	0.650112
PGN_0317		decarboxylating precorrin-6Y C5,15-methyltransferase	0.271101	0.62315	0.724965
PGN_0318		precorrin-3B C17-methyltransferase	-0.288112	0.4057	0.52221
PGN_0319		probable RNA polymerase sigma-70 factor ECF subfamily	0.306296	0.3695	0.487297
PGN_0320		conserved hypothetical protein	-0.0573941	0.9019	0.937341
PGN_0321		conserved hypothetical protein	0.0054463	0.9846	0.988314
PGN_0322		conserved hypothetical protein	-0.0608739	0.82795	0.883562
PGN_0323		conserved hypothetical protein	0.390374	0.1658	0.258599
PGN_0324		transposase in ISPg1	-2.35151	5.00E-05	0.00026
PGN_0325		hypothetical protein	-1.07474	0.0112	0.02802
PGN_0326		DNA-binding protein histone-like family	-1.3148	0.00125	0.004224
PGN_0327		putative DNA polymerase III epsilon chain	-0.160772	0.5837	0.688475
PGN_0328		conserved hypothetical protein	-0.127499	0.65395	0.749786
PGN_0329		conserved hypothetical protein	0.311925	0.2907	0.407044
PGN_0330		DNA repair protein	0.111729	0.69915	0.790069
PGN_0331		conserved hypothetical protein	-0.226601	0.4332	0.549632
PGN_0332		conserved hypothetical protein	-0.18535	0.6536	0.749786
PGN_0333		putative transaldolase	0.124512	0.73835	0.817445
PGN_0334		conserved hypothetical protein with DUF1343 domain	-0.538915	0.3244	0.443007
PGN_0335		conserved hypothetical protein with Zinc carboxypeptidase domain	0.500973	0.1017	0.172939
PGN_0336		immunoreactive 23 kDa antigen	1.64842	5.00E-05	0.00026
PGN_0337		conserved hypothetical protein	1.16224	0.3222	0.441134
PGN_0338		hypothetical protein	-0.315382	1	1
PGN_0339		hypothetical protein	0.43697	0.65425	0.749786
PGN_0340		carboxyl-terminal processing protease	1.63635	5.00E-05	0.00026
PGN_0341		conserved hypothetical protein	0.580947	0.04655	0.091764
PGN_0342		putative uracil-DNA glycosylase	1.05462	0.00045	0.001764
PGN_0343		hypothetical protein	1.64412	0.00295	0.008947
PGN_0344		probable haloacid dehalogenase-like hydrolase	2.43639	5.00E-05	0.00026
PGN_0345		conserved hypothetical protein	0.470335	0.1476	0.235916
PGN_0346		putative methyltransferase	-0.0311522	0.91845	0.946915
PGN_0347		conserved hypothetical protein	0.10106	0.73325	0.813915
PGN_0348	uspA	putative universal stress protein UspA	-2.7189	5.00E-05	0.00026
PGN_0349	ustA	upregulated in stationary phase protein A	-2.67263	5.00E-05	0.00026
PGN_0350		probable translation initation factor SUI1	-0.904605	0.00395	0.011552
PGN_0351		pyruvate carboxylase subunit B	-0.683335	0.0331	0.069772
PGN_0352		conserved hypothetical protein	-1.52287	0.00175	0.005688
PGN_0353		conserved hypothetical protein	0.271293	0.363	0.481345
PGN_0354	nusA	putative nitrogen utilization substance protein A	0.30706	0.317	0.435696
PGN_0355	infB	translation initiation factor IF-2	0.184853	0.54525	0.656211
PGN_0356		conserved hypothetical protein	0.584567	0.04625	0.091342
PGN_0357		ABC transporter membrane protein	-0.516701	0.0947	0.163517
PGN_0358		putative ABC transporter ATP-binding protein	-0.328143	0.27325	0.387716
PGN_0359		putative ABC transporter permease protein	-0.246514	0.42665	0.543589
PGN_0360		tyrosyl-tRNA synthetase	0.293509	0.3244	0.443007
PGN_0361		putative glycosyl transferase family 2	0.927308	0.00145	0.004794
PGN_0362		hypothetical protein	0.150476	0.8817	0.922427
PGN_0363		conserved hypothetical protein	1.09123	0.23705	0.346383
PGN_0364		arginyl-tRNA synthetase	-1.47865	5.00E-05	0.00026
PGN_0364	argS	hypothetical protein	-0.754568	0.1819	0.280018
PGN_0366	mnmA	putative tRNA 5-methylaminomethyl-2-thiouridylate 5-methyltransferase	-1.06052	0.00055	0.002076
PGN_0367		exodeoxyribonuclease III	-0.337174	0.2191	0.325289
PGN_0368	oxyR	redox-sensitive transcriptional activator OxyR	-0.161541	0.55335	0.663335
PGN_0369		probable single-stranded binding protein	0.559175	0.04325	0.086541
PGN_0370		conserved hypothetical protein	1.01801	0.0005	0.001921
PGN_0371		conserved hypothetical protein	0.212181	0.47295	0.586095
PGN_0372		hypothetical protein	-0.276108	0.46205	0.576953
PGN_0373		putative thioredoxin	-1.33874	0.0009	0.003178

PGN_0374		conserved hypothetical protein	-0.666384	0.0289	0.062339
PGN_0375		phosphoribulose/uridine kinase	-1.47002	5.00E-05	0.00026
PGN_0376		2-dehydro-3-deoxyphosphooctonate aldolase	-0.447761	0.1063	0.179471
PGN_0377	aspA	aspartate ammonia-lyase	-0.0236181	0.9381	0.956979
PGN_0378		putative exopolyphosphatase	0.354602	0.204	0.307807
PGN_0379		conserved hypothetical protein	0.818251	0.0055	0.015307
PGN_0380		partial ROK family transcriptional repressor with glucose kinase domain	-0.225859	0.5505	0.661035
PGN_0381		partial ROK family transcriptional repressor with glucose kinase domain	-0.533366	0.38155	0.499582
PGN_0382		conserved hypothetical protein	-0.354212	0.7494	0.82667
PGN_0383		probable transporter	1.50535	0.42945	0.545524
PGN_0384		conserved hypothetical protein	0.755683	0.6605	0.753997
PGN_0385		putative integrase/recombinase XerD	-0.622939	0.0221	0.049684
PGN_0386		probable 3-dehydroquinate dehydratase type II	-0.722497	0.00965	0.024753
PGN_0387		putative O-methyltransferase	-0.340555	0.22295	0.330084
PGN_0388		putative thiol peroxidase	-2.2156	5.00E-05	0.00026
PGN_0389		putative cytidine/deoxycytidylate deaminase	0.542833	0.0606	0.114479
PGN_0390		conserved hypothetical protein	1.16693	0.0001	0.000483
PGN_0391		conserved hypothetical protein	0.449945	0.12345	0.202797
PGN_0392		conserved hypothetical protein with competence-damaged protein domain	0.836131	0.22725	0.334357
PGN_0393		putative O-sialoglycoprotein endopeptidase	0.382204	0.21555	0.321212
PGN_0394	rpsT	probable 30S ribosomal protein S20	1.37038	5.00E-05	0.00026
PGN_0395		conserved hypothetical protein	0.73698	0.0351	0.072834
PGN_0396		ribonuclease R	0.0593897	0.8335	0.886198
PGN_0397		putative auxin-regulated protein	0.263886	0.3476	0.46602
PGN_0398		ABC transporter ATP-binding protein MsbA family	0.123164	0.6679	0.760512
PGN_0399		conserved hypothetical protein	1.62296	0.0299	0.064235
PGN_0400		conserved hypothetical protein	0.683094	0.0332	0.069914
PGN_0401		conserved hypothetical protein	-0.638118	0.23905	0.348826
PGN_0402		hypothetical protein	-1.42942	0.04755	0.093303
PGN_0403		putative pyridoxamine-phosphate oxidase	-0.00797731	0.9767	0.984297
PGN_0404		conserved hypothetical protein	0.267942	0.33545	0.454309
PGN_0405		alpha-1,2-mannosidase family protein	0.762174	0.00905	0.023355
PGN_0406		conserved hypothetical protein with glycosyl hydrolase family 92 domain	0.953781	0.0008	0.002848
PGN_0407		hypothetical protein	0.733273	0.0769	0.13816
PGN_0408		conserved hypothetical protein	1.03386	0.0006	0.002241
PGN_0409		conserved hypothetical protein	0.721051	0.01145	0.028578
PGN_0410		probable RNA pseudouridylate synthase	0.936953	0.00145	0.004794
PGN_0411		thiol-disulfide interchange protein	1.42424	5.00E-05	0.00026
PGN_0412	mazG	conserved hypothetical protein	0.952143	0.00135	0.004519
PGN_0413	gyrB	DNA gyrase B subunit	0.0560514	0.87475	0.916959
PGN_0414		probable membrane-bound dipeptidase	-0.499041	0.45	0.566558
PGN_0415		restriction endonuclease	-0.909493	0.00225	0.007076
PGN_0416		putative type II DNA modification methyltransferase	-1.32564	5.00E-05	0.00026
PGN_0417		conserved hypothetical protein	-0.627544	0.05305	0.101751
PGN_0418		conserved hypothetical protein with aminodeoxychorismate lyase domain	-0.706828	0.0878	0.153975
PGN_0419		putative dinucleotide-utilizing enzyme involved in molybdopterin and thiam	-0.674699	0.2155	0.321212
PGN_0420		putative lipoprotein releasing system ATP-binding protein	-0.184441	0.79695	0.859963
PGN_0421		conserved hypothetical protein	-0.698225	0.0161	0.038001
PGN_0422		conserved hypothetical protein	0.417915	0.13965	0.225239
PGN_0423		putative transcription elongation factor	2.06013	5.00E-05	0.00026
PGN_0424		putative HIT family protein	2.11132	5.00E-05	0.00026
PGN_0425		partial transposase in ISPg3	-0.351242	0.3281	0.447772
PGN_0426		conserved hypothetical protein	-1.59191	0.0755	0.136567
PGN_0427		putative glycosyl hydrolase	-1.60105	0.1581	0.249514
PGN_0428		putative glycosyl transferase family 1	-1.5652	0.17825	0.275795
PGN_0429		putative 4-alpha-glucanotransferase	-2.002	0.0036	0.010705
PGN_0430		putative ATP-binding component of ABC transporter protein	0.765233	0.03445	0.071695
PGN_0431		conserved hypothetical protein	0.146412	0.65325	0.749786
PGN_0432		conserved hypothetical protein	-0.161294	0.8605	0.906535
PGN_0433	pgk	phosphoglycerate kinase	0.506911	0.07185	0.130742
PGN_0434		phosphoenolpyruvate carboxykinase	0.0368356	0.90245	0.937341
PGN_0435		probable partial hemagglutinin-related protein	-1.68964	0.0935	0.16197

PGN_0436		probable partial hemagglutinin-related protein	-1.10433	0.0758	0.136851
PGN_0437		conserved hypothetical protein	0.855197	0.33255	0.451818
PGN_0438		conserved hypothetical protein	0.540998	0.42125	0.53832
PGN_0439		conserved hypothetical protein	-1.34513	5.00E-05	0.00026
PGN_0440		conserved hypothetical protein	0.731778	0.01515	0.036038
PGN_0441		hypothetical protein	-0.575521	0.5802	0.685106
PGN_0442		transposase in ISPg3	-0.400286	0.17645	0.273408
PGN_0443		hypothetical protein	1.01761	0.04985	0.096923
PGN_0444		probable outer membrane efflux protein	0.128321	0.72325	0.807446
PGN_0445		membrane fusion efflux protein	-0.0982218	0.83135	0.885647
PGN_0446		putative ABC transporter ATP-binding protein	-0.0368573	0.89515	0.932831
PGN_0447		putative ABC transporter permease protein	-0.20928	0.45855	0.573255
PGN_0448		putative ABC transporter ATP-binding protein	-0.030326	0.91645	0.946228
PGN_0449		conserved hypothetical protein	0.0498106	0.8657	0.90963
PGN_0450		putative RNA polymerase sigma-70 factor ECF subfamily	-1.24973	0.00125	0.004224
PGN_0451		conserved hypothetical protein	-0.461733	0.3505	0.469022
PGN_0453		partial transposase Orf1 in ISPg5	-0.340241	0.39325	0.510817
PGN_0454		transposase in ISPg3	-0.293091	0.31915	0.438085
PGN_0455		partial transposase Orf1 in ISPg5	-0.441753	0.2327	0.341197
PGN_0456		methylmalonyl-CoA mutase large subunit	-1.14472	0.0003	0.00126
PGN_0457		methylmalonyl-CoA mutase small subunit	-1.14193	0.0003	0.00126
PGN_0458		hypothetical protein	0.0334129	0.9066	0.93879
PGN_0459		transposase in ISPg3	-0.278155	0.33915	0.458736
PGN_0460		DNA-binding protein histone-like family	-1.41381	0.00065	0.00239
PGN_0461		probable D-alanyl-D-alanine dipeptidase	0.079371	0.77425	0.844889
PGN_0462		probable haloacid dehalogenase-like hydrolase	-0.963814	0.0013	0.004379
PGN_0463		conserved hypothetical protein	-0.661541	0.02345	0.051951
PGN_0464		conserved hypothetical protein	-0.983133	0.00215	0.006791
PGN_0465		GTP pyrophosphokinase	-1.29426	5.00E-05	0.00026
PGN_0466		putative cardiolipin synthetase	-1.05015	0.0002	0.000895
PGN_0467		conserved hypothetical protein	-1.13305	0.6519	0.749786
PGN_0468		conserved hypothetical protein with DUF452 domain	1.76236	0.00055	0.002076
PGN_0469		probable biotin synthesis protein	0.981604	0.0266	0.057787
PGN_0470		conserved hypothetical protein	-0.200728	0.82085	0.877304
PGN_0471		conserved hypothetical protein	0.0144998	0.99015	0.991547
PGN_0472		DNA topoisomerase IV A subunit	-1.09496	0.0021	0.006663
PGN_0473		conserved hypothetical protein	-1.07531	0.0005	0.001921
PGN_0474		hypothetical protein	-0.861655	0.3984	0.514993
PGN_0475		hypothetical protein	0.224765	0.65505	0.749786
PGN_0476		conserved hypothetical protein	-0.657473	0.0396	0.080447
PGN_0477		conserved hypothetical protein	-0.626545	0.0515	0.099495
PGN_0478		partial transposase in ISPg4	2.18427	5.00E-05	0.00026
PGN_0479		hypothetical protein	0.543967	0.34035	0.459394
PGN_0480		partial transposase in ISPg4	0.382082	0.3365	0.455441
PGN_0481		hypothetical protein	1.47091	5.00E-05	0.00026
PGN_0482		probable immunoreactive 23 kDa antigen	1.72469	5.00E-05	0.00026
PGN_0483		putative aldose 1-epimerase	0.0327616	0.903	0.937341
PGN_0484		putative galactokinase	0.506835	0.0767	0.138034
PGN_0485		conserved hypothetical protein	1.12045	0.00025	0.00108
PGN_0486		conserved hypothetical protein	0.503859	0.0694	0.127593
PGN_0487		FtsK/SpoIIIE family cell division protein	0.628255	0.03275	0.06924
PGN_0488		conserved hypothetical protein	1.07413	0.00045	0.001764
PGN_0489		conserved hypothetical protein	0.767007	0.5345	0.64693
PGN_0490		putative DNA-damage-inducible protein F	-0.315472	0.304	0.420612
PGN_0491		probable phosphotyrosine protein phosphatase	-0.829598	0.0085	0.022204
PGN_0492		cation-transporting ATPase	-1.18037	0.00315	0.009459
PGN_0493		hypothetical protein	-2.01802	5.00E-05	0.00026
PGN_0494		hypothetical protein	1.27228	1	1
PGN_0495		conserved hypothetical protein	-1.09132	0.0005	0.001921
PGN_0496		putative cytochrome B subunit	-0.894611	0.00385	0.011337
PGN_0497	sdhA	fumarate reductase flavoprotein subunit	-0.793443	0.0125	0.030589
PGN_0498		fumarate reductase iron-sulfur protein	-0.773807	0.01525	0.036236

PGN_0499		conserved hypothetical protein	-0.590048	0.04425	0.087963
PGN_0500		methylmalonyl-CoA decarboxylase alpha subunit	0.141871	0.64435	0.743534
PGN_0501		conserved hypothetical protein	0.0770825	0.81045	0.870496
PGN_0502		conserved hypothetical protein	0.0290094	0.9746	0.983376
PGN_0503		putative biotin carboxyl carrier protein	0.235465	0.41985	0.536917
PGN_0504		methylmalonyl-CoA decarboxylase beta subunit	0.1402	0.64185	0.741051
PGN_0505		hypothetical protein	-0.322752	0.84115	0.890949
PGN_0506		hypothetical protein	0.671559	0.12985	0.211515
PGN_0507		putative ion transporter	-0.0307933	0.92085	0.94893
PGN_0508		putative aminopeptidase	2.44013	5.00E-05	0.00026
PGN_0509		immunoreactive 84 kDa antigen	0.778044	0.01075	0.027021
PGN_0510		probable xanthosine triphosphate pyrophosphatase	0.680962	0.02185	0.049174
PGN_0511		conserved hypothetical protein	-0.306465	0.4038	0.520272
PGN_0512		probable biotin--acetyl-CoA-carboxylase ligase	0.757443	0.1197	0.198023
PGN_0513		conserved hypothetical protein	1.96326	5.00E-05	0.00026
PGN_0514		conserved hypothetical protein	1.60446	0.0007	0.002543
PGN_0515		probable lipoprotein signal peptidase	1.6067	5.00E-05	0.00026
PGN_0516		putative DnaK suppressor protein	0.659279	0.0216	0.048663
PGN_0517	ileS	isoleucyl-tRNA synthetase	1.20056	0.0001	0.000483
PGN_0518		putative ribulose-phosphate 3-epimerase	-0.728646	0.01505	0.035881
PGN_0519		probable competence protein	1.1915	0.00705	0.018951
PGN_0520		probable shikimate kinase	0.620613	0.1602	0.252454
PGN_0521		conserved hypothetical protein	0.698614	0.0212	0.048067
PGN_0522		putative dihydropteroate synthase	0.460874	0.10105	0.172108
PGN_0523		conserved hypothetical protein	0.878498	0.00305	0.009172
PGN_0524		lipid A 4'-phosphatase	1.63893	5.00E-05	0.00026
PGN_0525	batE	probable aerotolerance-related exported protein BatE	1.69542	0.00095	0.003316
PGN_0526	batD	aerotolerance-related exported protein BatD	2.01967	5.00E-05	0.00026
PGN_0527	batC	probable aerotolerance-related exported protein BatC	1.92968	0.0037	0.010971
PGN_0528	batB	putative aerotolerance-related exported protein BatB	1.49842	5.00E-05	0.00026
PGN_0529	batA	aerotolerance-related membrane protein BatA	1.11344	0.03925	0.079965
PGN_0530		conserved hypothetical protein	1.06581	0.0854	0.150635
PGN_0531		putative von Willebrand factor type A	0.503518	0.2863	0.401537
PGN_0532		magnesium chelatase subunit I	0.493024	0.09215	0.159892
PGN_0533		putative quinolinate synthetase complex subunit A	1.77522	5.00E-05	0.00026
PGN_0534		putative nicotinate-nucleotide pyrophosphorylase	1.48703	5.00E-05	0.00026
PGN_0535		L-aspartate oxidase	0.954195	0.0011	0.003753
PGN_0536		conserved hypothetical protein	0.542366	0.38515	0.503367
PGN_0537		probable transcriptional regulator Crp family	-1.44267	5.00E-05	0.00026
PGN_0538		conserved hypothetical protein	-0.333958	0.3189	0.438025
PGN_0539		metallo-beta-lactamase superfamily protein	0.173737	0.64475	0.743536
PGN_0540		conserved hypothetical protein	-0.251567	0.67665	0.768314
PGN_0541		hypothetical protein	0.108595	0.94525	0.960233
PGN_0542		partial transposase in ISPg2	0.403033	0.2749	0.389137
PGN_0543	gltX	glutamyl-tRNA synthetase	0.446201	0.1118	0.186977
PGN_0544		3-deoxy-D-manno-octulosonic-acid transferase	0.999265	0.0005	0.001921
PGN_0545		putative sulfatase	1.94074	5.00E-05	0.00026
PGN_0546		glucose-1-phosphate thymidylyltransferase	0.405194	0.1672	0.260592
PGN_0547		dTDP-4-dehydrorhamnose 3,5-epimerase	1.56331	0.00015	0.000685
PGN_0548		putative dTDP-4-dehydrorhamnose reductase	1.75945	0.00035	0.001436
PGN_0549		dTDP-glucose 4,6-dehydratase	2.06162	5.00E-05	0.00026
PGN_0550	gcvT	aminomethyltransferase	1.04942	0.0007	0.002543
PGN_0551		conserved hypothetical protein	0.94185	0.5195	0.633457
PGN_0552		hypothetical protein	2.94524	0.20185	0.305212
PGN_0553	hmuV	conserved hypothetical protein	3.38663	5.00E-05	0.00026
PGN_0554	hmuU	conserved hypothetical protein	3.76953	5.00E-05	0.00026
PGN_0555	hmuT	conserved hypothetical protein	3.60573	0.1174	0.194965
PGN_0556	hmuS	putative cobalamin biosynthesis-related protein	1.98106	5.00E-05	0.00026
PGN_0557	hmuR	TonB-dependent receptor HmuR	3.24018	5.00E-05	0.00026
PGN_0558	hmuY	conserved hypothetical protein	4.7244	5.00E-05	0.00026
PGN_0559		conserved hypothetical protein	-0.0437987	0.92275	0.949509
PGN_0560		hypothetical protein	-0.794423	0.7602	0.835122

PGN_0561	prtT	trypsin like proteinase PrtT	1.46929	5.00E-05	0.00026
PGN_0562		conserved hypothetical protein	-2.62179	5.00E-05	0.00026
PGN_0563		conserved hypothetical protein	-2.06691	0.00045	0.001764
PGN_0564	sod	superoxide dismutase Fe-Mn	-1.53121	0.00105	0.003606
PGN_0565		conserved hypothetical protein	-0.0295915	0.92525	0.951622
PGN_0566		probable thioesterase protein	0.333737	0.28655	0.401623
PGN_0567	prtC	collagenase	-0.305406	0.3308	0.450015
PGN_0568		2-amino-4-hydroxy-6- hydroxymethyldihydropteridine pyrophosphokinase	-0.94481	0.00295	0.008947
PGN_0569	queA	S-adenosylmethionine:tRNA ribosyltransferase-isomerase	-1.28462	0.00055	0.002076
PGN_0570		putative tRNA pseudouridine synthase B	0.181161	0.514	0.627829
PGN_0571		putative undecaprenol kinase	1.30799	5.00E-05	0.00026
PGN_0572		conserved hypothetical protein	-0.242848	0.38645	0.504446
PGN_0573		putative cell division protein FtsX	0.338625	0.2461	0.356912
PGN_0574		conserved hypothetical protein	-1.72591	0.00105	0.003606
PGN_0575		transposase in ISPg1	-2.4107	5.00E-05	0.00026
PGN_0576		hypothetical protein	#NAME?	1	1
PGN_0577		transposase in ISPg1	-2.36923	5.00E-05	0.00026
PGN_0578		conserved hypothetical protein found in conjugate transposon	-1.68786	0.0005	0.001921
PGN_0579		conserved hypothetical protein	-0.496428	0.16835	0.262001
PGN_0580		conserved hypothetical protein	-2.11134	5.00E-05	0.00026
PGN_0581		conserved hypothetical protein	-0.290534	0.4403	0.557375
PGN_0582		DNA topoisomerase I	-0.802444	0.01355	0.032633
PGN_0583		conserved hypothetical protein	-1.24235	0.00015	0.000685
PGN_0584		conserved hypothetical protein	1.40228	5.00E-05	0.00026
PGN_0585		transposase in ISPg3	-0.371724	0.2005	0.304035
PGN_0586		conserved hypothetical protein	-0.170119	0.7624	0.836675
PGN_0587		transposase in ISPg1	-2.39681	5.00E-05	0.00026
PGN_0588		conserved hypothetical protein	-1.40551	0.0003	0.00126
PGN_0589		conserved hypothetical protein	-1.8301	0.00065	0.00239
PGN_0590		putative Fic family protein	-1.02745	0.00195	0.006262
PGN_0591		conserved hypothetical protein	-0.815518	0.00445	0.012838
PGN_0592	traQ_1	putative conserved protein found in conjugate transposon TraQ	-1.76921	0.0001	0.000483
PGN_0593	traO_1	putative conserved protein found in conjugate transposon TraO	-1.63411	0.0007	0.002543
PGN_0596		conserved hypothetical protein found in conjugate transposon	-0.252226	0.8108	0.870496
PGN_0600		conserved hypothetical protein	-0.477041	0.3558	0.474326
PGN_0601		conserved hypothetical protein	-2.11668	0.00015	0.000685
PGN_0602		transposase in ISPg1	-2.36492	5.00E-05	0.00026
PGN_0603		hypothetical protein	-0.138996	0.75695	0.833271
PGN_0604		ferritin	-2.07196	0.0001	0.000483
PGN_0605		transposase in ISPg1	-2.31118	5.00E-05	0.00026
PGN_0606		glucosamine-6-phosphate isomerase	-0.997726	0.0004	0.001607
PGN_0607		dipeptidyl peptidase 11	0.562294	0.05275	0.101267
PGN_0608		conserved hypothetical protein	-0.753096	0.00735	0.019634
PGN_0609		probable DNA mismatch repair protein	-0.892585	0.00205	0.006553
PGN_0610		conserved hypothetical protein with DUF1015 domain	1.05589	0.0004	0.001607
PGN_0611		D-3-phosphoglycerate dehydrogenase	1.07244	0.00035	0.001436
PGN_0612		phosphoserine aminotransferase	0.639798	0.0354	0.073243
PGN_0613		UDP-glucose 6-dehydrogenase	-0.640071	0.0245	0.053774
PGN_0614		DNA-binding protein histone-like family	-0.494056	0.07585	0.136851
PGN_0615		hypothetical protein	-0.596006	0.11135	0.186371
PGN_0616		probable elongation factor P	1.21019	5.00E-05	0.00026
PGN_0617		conserved hypothetical protein	0.0495808	0.86125	0.906535
PGN_0618		aspartate-semialdehyde dehydrogenase	-0.311589	0.29135	0.407278
PGN_0619		conserved hypothetical protein	-0.096502	0.9662	0.975464
PGN_0620	mraW	putative S-adenosyl-methyltransferase MraW	-1.17532	0.00035	0.001436
PGN_0621		conserved hypothetical protein	-0.726912	0.32365	0.442755
PGN_0622		penicillin-binding protein	-0.207521	0.47035	0.583552
PGN_0623	murE	UDP-N-acetylmuramoylalanyl-D-glutamyl-2, 6-diaminopimelate ligase	0.06748	0.8149	0.873136
PGN_0624	mraY	phospho-N-acetylmuramoyl-pentapeptide- transferase	-0.176206	0.52695	0.639975
PGN_0625		UDP-N-acetylmuramoylalanine--D-glutamate ligase	-0.135034	0.62585	0.726518
PGN_0626		putative rod shape-determining protein RodA	0.721579	0.2609	0.374764
PGN_0627	murG	N-acetylglucosaminyl transferase	-0.0635702	0.90475	0.938295

PGN_0628	murC	UDP-N-acetylmuramate-alanine ligase	0.374686	0.52265	0.635841
PGN_0629		putative cell division protein FtsQ	0.164726	0.8055	0.867869
PGN_0630		probable cell division protein FtsA	-0.75875	0.01285	0.03123
PGN_0631		putative cell division protein FtsZ	-1.27146	0.0001	0.000483
PGN_0632		conserved hypothetical protein	-0.631681	0.02225	0.049916
PGN_0633		conserved hypothetical protein	1.92398	5.00E-05	0.00026
PGN_0634	panB	3-methyl-2-oxobutanoate hydroxymethyltransferase	1.25486	5.00E-05	0.00026
PGN_0635	guaA	glutamine-hydrolyzing GMP synthase	0.557515	0.05705	0.108349
PGN_0636	rpmE2	50S ribosomal protein L31	1.21542	0.00025	0.00108
PGN_0637	htrA	putative heat shock-related protease htrA protein	-0.126277	0.66925	0.761007
PGN_0638	rpoD	RNA polymerase sigma factor RpoD	0.374401	0.2194	0.325507
PGN_0639	rpsF	30S ribosomal protein S6	1.46637	5.00E-05	0.00026
PGN_0640	rpsR	30S ribosomal protein S18	1.37144	5.00E-05	0.00026
PGN_0641	rplI	50S ribosomal protein L9	1.2119	0.00025	0.00108
PGN_0642		conserved hypothetical protein	-0.424954	0.1363	0.220336
PGN_0643		3,4-dihydroxy-2-butanone 4-phosphate synthase	-0.779502	0.0097	0.024821
PGN_0644		transposase in ISPg1	-2.42908	5.00E-05	0.00026
PGN_0645		Por secretion system protein porQ	0.457662	0.10865	0.182426
PGN_0646	cmk	probable cytidylate kinase	0.185177	0.80885	0.870041
PGN_0647	ispH	hydroxymethylbutenyl pyrophosphate reductase	-0.104427	0.8568	0.904376
PGN_0648		conserved hypothetical protein	-1.22943	0.0048	0.013662
PGN_0649		conserved hypothetical protein	0.261035	0.3631	0.481345
PGN_0650		conserved hypothetical protein	0.309832	0.3405	0.459394
PGN_0651		conserved hypothetical protein	-0.199156	0.7047	0.792974
PGN_0652		conserved hypothetical protein	-0.36026	0.4836	0.596169
PGN_0653		conserved hypothetical protein	-3.09398	5.00E-05	0.00026
PGN_0654		conserved hypothetical protein	-2.8665	5.00E-05	0.00026
PGN_0655		conserved hypothetical protein	-2.29985	0.07795	0.139576
PGN_0656		conserved hypothetical protein	-2.56003	5.00E-05	0.00026
PGN_0657		conserved hypothetical protein	-3.02141	5.00E-05	0.00026
PGN_0658		GTP-binding elongation factor family protein TypA/BipA	1.09959	0.0002	0.000895
PGN_0659		35 kDa hemin binding protein	0.947194	0.00405	0.011763
PGN_0660		putative alkyl hydroperoxide reductase C subunit	-2.7331	5.00E-05	0.00026
PGN_0661		alkyl hydroperoxide reductase F subunit	-1.41407	0.0001	0.000483
PGN_0662		ATP-dependent protease La	0.489482	0.19	0.290388
PGN_0663		conserved hypothetical protein	0.366692	0.719	0.803966
PGN_0664		conserved hypothetical protein	0.919131	0.21405	0.320023
PGN_0665	tpiA	putative triosephosphate isomerase	0.948069	0.0016	0.005241
PGN_0666		conserved hypothetical protein	1.05616	0.00045	0.001764
PGN_0667	folE	putative GTP cyclohydrolase I	1.0248	0.00055	0.002076
PGN_0668		RNA-binding protein	2.70212	5.00E-05	0.00026
PGN_0669		ABC transporter ATP-binding protein	1.27725	5.00E-05	0.00026
PGN_0670	ppnK	probable inorganic polyphosphate/ATP-NAD kinase	0.926252	0.00135	0.004519
PGN_0671		putative pyridoxal phosphate biosynthetic protein	1.05062	0.00035	0.001436
PGN_0672		probable biopolymer transport protein	1.26701	0.00045	0.001764
PGN_0673		probable biopolymer transport protein	1.41246	0.0047	0.013395
PGN_0674		conserved hypothetical protein	1.05642	0.0004	0.001607
PGN_0675		conserved hypothetical protein	1.12536	0.0001	0.000483
PGN_0676	prmA	putative ribosomal protein L11 methyltransferase	1.65352	0.0115	0.028602
PGN_0677		putative multi antimicrobial extrusion protein MatE	1.16679	0.03155	0.067372
PGN_0678		thiamine monophosphate kinase	0.264001	0.53345	0.646027
PGN_0679		putative tetraacyldisaccharide 4'-kinase	-0.156972	0.5857	0.690069
PGN_0680		signal peptide peptidase SppA 67K type	-0.445362	0.13075	0.212819
PGN_0681		hypothetical protein	1.38877	0.2738	0.387838
PGN_0682		hypothetical protein	-0.922035	0.71725	0.802852
PGN_0683		TonB-linked receptor Tlr	-1.29541	5.00E-05	0.00026
PGN_0684		conserved hypothetical protein with adenosylcobinamide amidohydrolase d	-1.32007	5.00E-05	0.00026
PGN_0685		putative iron compound ABC transporter ATP-binding protein	-1.22345	5.00E-05	0.00026
PGN_0686		putative iron compound ABC transporter permease protein	-1.22094	0.01205	0.029693
PGN_0687		putative iron compound ABC transporter periplasmic iron compound-bindin	-1.14108	0.00295	0.008947
PGN_0688		conserved hypothetical protein	1.16497	0.0003	0.00126
PGN_0689		conserved hypothetical protein	1.16483	0.00045	0.001764

PGN_0690		conserved hypothetical protein	0.959206	0.0006	0.002241
PGN_0691		conserved hypothetical protein	0.669793	0.0182	0.042117
PGN_0692		phosphoserine phosphatase	0.606633	0.0415	0.083986
PGN_0693		conserved hypothetical protein	0.544244	0.0686	0.126231
PGN_0694	rpmH	50S ribosomal protein L34	1.22279	0.00015	0.000685
PGN_0695		probable septum formation protein Maf	-0.120769	0.6564	0.750524
PGN_0696		probable hydrolase	-0.505721	0.0656	0.121657
PGN_0697		conserved hypothetical protein	-1.07672	0.0574	0.108917
PGN_0698		probable nitroreductase	-1.35003	0.001	0.003462
PGN_0699		conserved hypothetical protein	1.85392	5.00E-05	0.00026
PGN_0700		putative oxidoreductase Gfo/Idh/MocA family	-0.102494	0.7092	0.79641
PGN_0701	lacZI	beta-galactosidase	0.818574	0.0039	0.011468
PGN_0702		conserved hypothetical protein	0.883385	0.0054	0.015087
PGN_0703		hypothetical protein	1.44386	0.0001	0.000483
PGN_0704	ihtA	putative tonB-linked outer membrane receptor	0.427146	0.1542	0.244083
PGN_0705	ihtB	heme-binding protein FetB	0.0173827	0.9575	0.969338
PGN_0706	ihtC	putative exported periplasmic protein	0.712751	0.1142	0.190692
PGN_0707	ihtD	putative iron compound ABC transporter permease protein	0.434304	0.25165	0.363373
PGN_0708	ihtE	putative iron compound ABC transporter ATP-binding protein	0.648173	0.0246	0.053882
PGN_0709		putative indolepyruvate ferredoxin oxidoreductase beta subunit	-0.359049	0.21315	0.319125
PGN_0710		indolepyruvate ferredoxin oxidoreductase alpha subunit	-0.0766343	0.79465	0.858132
PGN_0711		putative oxidoreductase short chain dehydrogenase/reductase family	-0.655238	0.0214	0.048366
PGN_0712		conserved hypothetical protein	-0.868572	0.33405	0.453567
PGN_0713		saccharopine dehydrogenase	-0.579559	0.0431	0.086503
PGN_0714		probable pyrazinamidase/nicotinamidase	-0.405245	0.14725	0.235534
PGN_0715		outer membrane efflux protein	-1.06297	0.001	0.003462
PGN_0716		ABC transporter permease	-0.679352	0.0468	0.092086
PGN_0717		conserved hypothetical protein	-2.02997	5.00E-05	0.00026
PGN_0718		putative ABC transporter permease protein	-0.0994058	0.7684	0.841524
PGN_0719		probable ABC transporter permease protein	-0.396558	0.19905	0.302051
PGN_0720		putative ABC transporter permease protein	-1.75601	5.00E-05	0.00026
PGN_0721		putative ABC transporter ATP-binding protein	-2.60154	5.00E-05	0.00026
PGN_0722		conserved hypothetical protein	-1.90287	5.00E-05	0.00026
PGN_0723		succinate-semialdehyde dehydrogenase	1.72124	5.00E-05	0.00026
PGN_0724		NAD-dependent 4-hydroxybutyrate dehydrogenase	0.121705	0.68615	0.77827
PGN_0725		4-hydroxybutyrate CoA-transferase	0.16561	0.56375	0.672416
PGN_0726		conserved hypothetical protein	-0.179057	0.51625	0.630216
PGN_0727		4-hydroxybutyryl-CoA dehydratase	-0.39531	0.2411	0.351096
PGN_0728		outer membrane protein 40 precursor	-0.938723	0.0249	0.054483
PGN_0729		outer membrane protein 41 precursor	-0.919581	0.02295	0.051109
PGN_0730		hypothetical protein	0.214584	0.58285	0.687853
PGN_0731		hypothetical protein	-0.502821	0.1266	0.207013
PGN_0732		conserved hypothetical protein	-0.0998733	0.7179	0.803158
PGN_0733		alpha-glucan phosphorylase	-0.427988	0.14335	0.230508
PGN_0734		conserved hypothetical protein	-1.49142	0.00825	0.021711
PGN_0735		putative bifunctional cobalamin biosynthesis protein	-0.793036	0.00585	0.016091
PGN_0736		putative nicotinate-nucleotide-dimethylbenzimidazole phosphoribosyltransf	-0.687808	0.0169	0.039452
PGN_0737		probable cobalamin-5'-phosphate synthase	-0.74811	0.01025	0.026072
PGN_0738		putative phosphoglycerate mutase	-0.755382	0.0067	0.018171
PGN_0739		glutamate racemase	-0.743301	0.01235	0.030292
PGN_0740		conserved hypothetical protein	-0.861876	0.00395	0.011552
PGN_0741		TonB-dependent receptor	-1.04899	0.0021	0.006663
PGN_0742		probable FKBP-type peptidyl-prolyl cis-trans isomerase	1.61268	5.00E-05	0.00026
PGN_0743		probable FKBP-type peptidyl-prolyl cis-trans isomerase FkpA	-0.0188845	0.94735	0.96089
PGN_0744		probable FKBP-type peptidyl-prolyl cis-trans isomerase	0.968931	0.0008	0.002848
PGN_0745		hypothetical protein	-0.408271	0.39515	0.512036
PGN_0746		conserved hypothetical protein	1.93596	5.00E-05	0.00026
PGN_0747		probable anthranilate synthase component II	0.505567	0.06975	0.128015
PGN_0748		gingipain-sensitive ligand A	-2.28975	5.00E-05	0.00026
PGN_0749		transposase in ISPg1	-2.48543	5.00E-05	0.00026
PGN_0750		putative copper homeostasis protein CutC	0.160025	0.58555	0.690069
PGN_0751		putative cationic transporter	0.806273	0.0047	0.013395

PGN_0752		hypothetical protein	-1.79924	0.05005	0.097223
PGN_0753		probable two component system response regulator	-1.59375	5.00E-05	0.00026
PGN_0754		conserved hypothetical protein	1.12869	0.00065	0.00239
PGN_0755		hypothetical protein	0.324381	0.50265	0.615378
PGN_0756		prolyl oligopeptidase	0.0195176	0.9458	0.960233
PGN_0757		conserved hypothetical protein	0.417261	0.15475	0.244772
PGN_0758		conserved hypothetical protein	2.44064	5.00E-05	0.00026
PGN_0759		conserved hypothetical protein	1.04505	0.00025	0.00108
PGN_0760	ddl	putative D-alanine--D-alanine ligase	1.02701	0.00025	0.00108
PGN_0761		ribosomal large subunit pseudouridine synthase	-0.230476	0.4168	0.534237
PGN_0762		conserved hypothetical protein	-0.595503	0.0434	0.086678
PGN_0763		conserved hypothetical protein	-0.691164	0.8132	0.872632
PGN_0764		putative riboflavin synthase alpha subunit	1.23954	0.00045	0.001764
PGN_0765		probable nitroreductase	0.765671	0.1798	0.27779
PGN_0766		aminotransferase class V	1.39364	5.00E-05	0.00026
PGN_0767	rnhB	putative ribonuclease HII	1.98281	0.01515	0.036038
PGN_0768		conserved hypothetical protein	0.844304	0.0878	0.153975
PGN_0769		putative cytosine/adenosine deaminase	0.68143	0.08535	0.150635
PGN_0770		conserved hypothetical protein	0.255927	0.41305	0.530068
PGN_0771		conserved hypothetical protein	0.936498	0.1223	0.201145
PGN_0772		probable tRNA/rRNA methyltransferase	0.626481	0.02035	0.046536
PGN_0773		putative lactoylglutathione lyase	1.02824	0.00055	0.002076
PGN_0774		two-component system sensor histidine kinase	0.698319	0.013	0.031487
PGN_0775		two-component system response regulator	0.140758	0.60295	0.705377
PGN_0776		conserved hypothetical protein	0.815526	0.17325	0.269233
PGN_0777		probable glycosyl transferase	1.30112	5.00E-05	0.00026
PGN_0778	porT	Por secretion system protein porT/sprT	0.577577	0.04745	0.093193
PGN_0779	upp	probable uracil phosphoribosyltransferase	0.933502	0.0543	0.103496
PGN_0780	prtQ	PrtQ, protease	0.809517	0.02775	0.06004
PGN_0781		DNA topoisomerase I	1.3813	5.00E-05	0.00026
PGN_0782	truA	putative tRNA pseudouridine synthase A	0.890123	0.0051	0.014324
PGN_0783		putative DNA-binding protein histone-like family	-0.309383	0.335	0.454309
PGN_0784		hypothetical protein	0.278964	0.3209	0.440204
PGN_0785		hypothetical protein	0.202664	0.5322	0.645615
PGN_0786		conserved hypothetical protein	1.17506	0.0001	0.000483
PGN_0787		conserved hypothetical protein	0.338387	0.25175	0.363373
PGN_0788		peptidyl-dipeptidase	0.30759	0.2818	0.397056
PGN_0789		conserved hypothetical protein	0.0771929	0.7852	0.853339
PGN_0790		transposase in ISPg3	-0.501941	0.0902	0.157536
PGN_0791		putative cell division trigger factor	2.72591	5.00E-05	0.00026
PGN_0792		polyribonucleotide nucleotidyltransferase	0.364088	0.22975	0.337569
PGN_0793		4-alpha-glucanotransferase	-0.0470892	0.86535	0.90963
PGN_0794		conserved hypothetical protein	-0.116662	0.6712	0.762532
PGN_0795		conserved hypothetical protein	0.572559	0.04085	0.082828
PGN_0796		hypothetical protein	-0.190202	1	1
PGN_0797		conserved hypothetical protein	0	1	1
PGN_0798		conserved hypothetical protein	-0.761131	0.0083	0.021816
PGN_0799		putative acyl-CoA dehydrogenase	-0.174963	0.57925	0.684777
PGN_0800		putative electron transfer flavoprotein alpha subunit	-0.33748	0.26205	0.37544
PGN_0801		probable electron transfer flavoprotein beta subunit	-0.470383	0.11975	0.198023
PGN_0802		probable glycoprotease	-0.804242	0.00705	0.018951
PGN_0803		conserved hypothetical protein	1.00064	0.0014	0.004672
PGN_0804		conserved hypothetical protein	0.915843	0.00465	0.013306
PGN_0805		conserved hypothetical protein	0.901811	0.00425	0.012311
PGN_0806		putative MotA/TolQ/ExbB proton channel protein	0.879017	0.0057	0.015781
PGN_0807		putative DNAse related protein	0.857174	0.00395	0.011552
PGN_0808		probable isoprenyl synthetase	0.243812	0.38215	0.50006
PGN_0809		putative TonB protein	-1.21127	0.0001	0.000483
PGN_0810		conserved hypothetical protein	2.35642	0.0018	0.005833
PGN_0811		conserved hypothetical protein	2.02568	5.00E-05	0.00026
PGN_0812		conserved hypothetical protein	0.915876	0.23685	0.346328
PGN_0813	obgE	GTP-binding protein	0.579376	0.0676	0.124823

PGN_0814	adk	probable adenylate kinase	0.821219	0.0045	0.012947
PGN_0815		putative hypoxanthine phosphoribosyltransferase	0.954004	0.00075	0.002697
PGN_0816		fructose-1,6-bisphosphatase	-0.619151	0.0448	0.08889
PGN_0817		penicillin-binding protein 1A	-0.254951	0.3815	0.499582
PGN_0818		conserved hypothetical protein	0.331734	0.2424	0.352507
PGN_0819	leuS	leucyl-tRNA synthetase	0.63633	0.02595	0.056606
PGN_0820		hypothetical protein	0.386291	0.34255	0.460992
PGN_0821		hypothetical protein	-0.75921	0.4675	0.581433
PGN_0822		conserved hypothetical protein	0.600592	0.4273	0.543767
PGN_0823		NAD-utilizing dehydrogenases	0.167579	0.65485	0.749786
PGN_0824		tRNA nucleotidyltransferase	0.404181	0.33995	0.459394
PGN_0825		conserved hypothetical protein	1.29459	0.0132	0.031899
PGN_0826		dihydrolipoamide dehydrogenase	1.76894	5.00E-05	0.00026
PGN_0827	nagB	glucosamine-6-phosphate isomerase	1.75643	5.00E-05	0.00026
PGN_0828		flavoprotein	1.18163	5.00E-05	0.00026
PGN_0829		putative prolipoprotein diacylglyceryl transferase	1.83426	5.00E-05	0.00026
PGN_0830		meso-diaminopimelate D-dehydrogenase	1.69139	5.00E-05	0.00026
PGN_0831		probable nitrogen utilization substance protein	1.52526	5.00E-05	0.00026
PGN_0832		Por secretion system protein sov/gliding motility protein SprA	1.30212	0.0001	0.000483
PGN_0833	ruvA	probable Holliday junction DNA helicase RuvA	1.06629	0.0005	0.001921
PGN_0834		transposase in ISPg1	-2.39159	5.00E-05	0.00026
PGN_0835		conserved hypothetical protein	0.26866	0.5768	0.682842
PGN_0836		conserved hypothetical protein	-1.14121	0.00035	0.001436
PGN_0837		conserved hypothetical protein	-1.26064	0.00015	0.000685
PGN_0838		conserved hypothetical protein	-1.89767	5.00E-05	0.00026
PGN_0839		transposase in ISPg2	1.15806	0.00045	0.001764
PGN_0840		conserved hypothetical protein	-0.873196	0.11705	0.194535
PGN_0841	ispD	putative 4-diphosphocytidyl-2C-methyl-D-erythritol synthase	-0.196534	0.56595	0.673886
PGN_0842		transposase in ISPg1	-2.403	5.00E-05	0.00026
PGN_0843		conserved hypothetical protein	-1.1909	0.009	0.023254
PGN_0844		conserved hypothetical protein	-0.993291	0.0119	0.029425
PGN_0845		conserved hypothetical protein	-1.77809	0.0863	0.151845
PGN_0846		conserved hypothetical protein	-1.56851	0.0239	0.052729
PGN_0847		conserved hypothetical protein	-0.992455	0.0477	0.093511
PGN_0848		conserved hypothetical protein	-1.12772	0.0149	0.035603
PGN_0849		conserved hypothetical protein	-0.519318	0.36965	0.487297
PGN_0850		conserved hypothetical protein	-0.991682	0.2568	0.36941
PGN_0851		conserved hypothetical protein	-1.07529	0.0645	0.120246
PGN_0852		immunoreactive 47 kDa antigen	2.86831	5.00E-05	0.00026
PGN_0853		conserved hypothetical protein	1.95227	0.0004	0.001607
PGN_0854		hypothetical protein	0.238538	0.6247	0.725579
PGN_0855		hypothetical protein	-0.715211	0.163	0.255543
PGN_0856		putative A/G-specific adenine glycosylase	-0.792166	0.005	0.014118
PGN_0857		conserved hypothetical protein	0.474728	0.08825	0.154598
PGN_0858		probable ABC transporter ATP-binding protein	0.150097	0.6695	0.761007
PGN_0859		probable ABC transporter permease protein	0.781869	0.10475	0.177276
PGN_0860		conserved hypothetical protein	1.79604	5.00E-05	0.00026
PGN_0861		conserved hypothetical protein	0.58151	0.0389	0.07948
PGN_0862		Type III restriction enzyme, res subunit	0.386654	0.25585	0.368293
PGN_0863		DNA methylase N-4/N-6	0.980014	0.0497	0.09672
PGN_0864		transposase in ISPg3	-0.494054	0.0971	0.166446
PGN_0865	purH	bifunctional phosphoribosylaminoimidazolecarboxamide formyltransferase/	-0.665488	0.03735	0.076755
PGN_0866		cell shape-determining protein MreB	-0.0505298	0.8594	0.906222
PGN_0867		probable cell shape-determining protein MreC	1.18728	0.06515	0.121232
PGN_0868		conserved hypothetical protein	1.32286	0.26615	0.380036
PGN_0869		penicillin-binding protein 2	1.45157	0.0082	0.02166
PGN_0870		putative rod shape-determining protein RodA	0.654077	0.23315	0.341622
PGN_0871		conserved hypothetical protein	-0.452894	0.10665	0.179919
PGN_0872		DNA-binding protein histone-like family	-0.658762	0.0259	0.056555
PGN_0873		conserved hypothetical protein	0.182638	0.52035	0.63413
PGN_0874		conserved hypothetical protein	0.242004	0.3981	0.514918
PGN_0875	gyrA	DNA gyrase A subunit	0.591097	0.0576	0.109199

PGN_0876		TPR domain protein	0.931781	0.00295	0.008947
PGN_0877		SNF2-related helicase	0.808512	0.00505	0.014222
PGN_0878		hypothetical protein	1.09959	0.0009	0.003178
PGN_0879		transposase in ISPg3	-0.336543	0.2507	0.362595
PGN_0880	tnaA	tyrosine phenol-lyase	1.0181	0.00075	0.002697
PGN_0881		conserved hypothetical protein	1.63255	5.00E-05	0.00026
PGN_0882		conserved hypothetical protein	1.78743	5.00E-05	0.00026
PGN_0883		conserved hypothetical protein	1.59081	5.00E-05	0.00026
PGN_0884		organic solvent tolerance protein OstA	1.55885	5.00E-05	0.00026
PGN_0885		probable nitroimidazole resistance protein	0.444695	0.18685	0.285984
PGN_0886		putative cation efflux protein	-0.201514	0.5104	0.62379
PGN_0887		conserved hypothetical protein	0.822273	0.34615	0.464662
PGN_0888		conserved hypothetical protein	1.14494	0.0094	0.02417
PGN_0889		potassium uptake protein TrkA	1.00826	0.0007	0.002543
PGN_0890		putative TonB-dependent outer membrane receptor protein	-0.904961	0.0023	0.007212
PGN_0891		dioxygenase	0.521515	0.0609	0.114943
PGN_0892		hypothetical protein	-0.306206	0.4323	0.548817
PGN_0893		fumarate hydratase class I anaerobic	0.828502	0.00495	0.013995
PGN_0894		DNA polymerase III, gamma and tau subunits	-0.764122	0.0103	0.026137
PGN_0895		ferredoxin 4Fe-4S	-2.14764	5.00E-05	0.00026
PGN_0896		probable D-alanyl-D-alanine carboxypeptidase	-0.258841	0.3693	0.487297
PGN_0897		conserved hypothetical protein	-0.0713344	0.94045	0.958917
PGN_0898		probable peptidylarginine deiminase	1.00888	0.00205	0.006553
PGN_0899		conserved hypothetical protein	#NAME?	5.00E-05	0.00026
PGN_0900		thiol protease	2.57956	5.00E-05	0.00026
PGN_0901	ribH	putative riboflavin synthase beta subunit	2.94772	5.00E-05	0.00026
PGN_0902		conserved hypothetical protein	1.68133	5.00E-05	0.00026
PGN_0903	fimR	two-component system response regulator FimR	0.132809	0.63625	0.735841
PGN_0904	fimS	two-component system sensor histidine kinase FimS	-0.00795374	0.97795	0.984889
PGN_0905		putative dihydroorotate dehydrogenase	-0.607985	0.02935	0.063117
PGN_0906		probable dihydroorotate dehydrogenase electron transfer subunit	-0.614044	0.03265	0.069235
PGN_0907		conserved hypothetical protein	-0.376558	0.1914	0.292108
PGN_0908		hypothetical protein	0.280479	1	1
PGN_0909		transposase in ISPg3	-0.522801	0.08435	0.149154
PGN_0910		conserved hypothetical protein	0.34612	0.25135	0.363289
PGN_0911		putative ribonuclease H	-0.673325	0.01725	0.040137
PGN_0912		conserved hypothetical protein	-0.46287	0.0963	0.165465
PGN_0913		putative acetyltransferase	-0.788849	0.0047	0.013395
PGN_0914		peptidase M24 family	-0.722722	0.01555	0.036784
PGN_0915		conserved hypothetical protein	-1.92986	5.00E-05	0.00026
PGN_0916	dnaK	molecular chaperone DnaK	-0.910561	0.00855	0.02228
PGN_0917		tyrosine type site-specific recombinase	-0.804486	0.00585	0.016091
PGN_0918		transposase in ISPg1	-2.48737	5.00E-05	0.00026
PGN_0919		hypothetical protein	0.518386	0.1342	0.217602
PGN_0920		putative partial excisionase	-0.00155837	0.92225	0.949454
PGN_0921		hypothetical protein	-2.91817	0.1069	0.180055
PGN_0922		conserved hypothetical protein	-1.33784	0.00975	0.024919
PGN_0923		putative DNA primase	-0.635139	0.2126	0.318526
PGN_0924		mobilization protein	-1.32887	0.22485	0.332665
PGN_0925		putative mobilization protein	-0.893715	0.14585	0.233821
PGN_0926		conserved hypothetical protein	-0.882221	0.05125	0.099282
PGN_0927		conserved hypothetical protein	-1.73307	5.00E-05	0.00026
PGN_0928		conserved hypothetical protein	-1.24794	0.0183	0.042303
PGN_0929		conserved hypothetical protein	-1.7577	5.00E-05	0.00026
PGN_0930		hypothetical protein	-1.5069	5.00E-05	0.00026
PGN_0931		conserved hypothetical protein	-1.73454	5.00E-05	0.00026
PGN_0932		probable GCN5-related N-acetyltransferase	-1.39223	5.00E-05	0.00026
PGN_0933		probable transcriptional regulator	-0.641709	0.0208	0.047362
PGN_0934		transposase in ISPg3	-0.398127	0.18105	0.27919
PGN_0935		conserved hypothetical protein	-0.394907	0.21865	0.325223
PGN_0936		putative glycerate dehydrogenase	-1.82595	5.00E-05	0.00026
PGN_0937		hypothetical protein	-0.546173	0.1564	0.247198

PGN_0938		8-amino-7-oxononanoate synthase	-0.0296977	0.9263	0.951988
PGN_0939		conserved hypothetical protein	-0.153544	0.8257	0.881923
PGN_0940		partial transposase in ISPg2	0.463878	0.2008	0.304273
PGN_0941		conserved hypothetical protein	0.20091	0.4796	0.592955
PGN_0942		conserved hypothetical protein	0.282783	0.32135	0.440322
PGN_0943		alginate O-acetyltransferase	0.825348	0.00445	0.012838
PGN_0944		transposase in ISPg3	-0.463326	0.1025	0.17416
PGN_0945		putative TetR family transcriptional regulator	1.56209	5.00E-05	0.00026
PGN_0946		conserved hypothetical protein	1.06513	0.0003	0.00126
PGN_0947		conserved hypothetical protein	0.951215	0.00145	0.004794
PGN_0948		conserved hypothetical protein	0.520632	0.07065	0.129182
PGN_0949		ABC transporter ATP-binding protein	0.859473	0.00275	0.008448
PGN_0950		ABC transporter ATP-binding protein	0.638243	0.02045	0.046715
PGN_0951		conserved hypothetical protein	-0.544398	0.08765	0.153966
PGN_0952		carboxyl-terminal processing protease	0.477928	0.1202	0.198377
PGN_0953		transposase in ISPg3	-0.286624	0.32965	0.448737
PGN_0954		partial transposase in ISPg6	0.370783	0.37995	0.498406
PGN_0955		transposase in ISPg3	-0.682695	0.0193	0.044373
PGN_0956		hypothetical protein	-0.546067	0.10775	0.1812
PGN_0957		conserved hypothetical protein	-1.31023	0.00015	0.000685
PGN_0958		conserved hypothetical protein	-2.73918	0.0331	0.069772
PGN_0959		probable transcriptional regulator	-2.51179	5.00E-05	0.00026
PGN_0960		conserved hypothetical protein	-1.44521	5.00E-05	0.00026
PGN_0961		conserved hypothetical protein	0.0434317	1	1
PGN_0962	thrS	threonyl-tRNA synthetase	1.34908	5.00E-05	0.00026
PGN_0963	infC	translation initiation factor IF-3	2.23303	5.00E-05	0.00026
PGN_0964	rpmI	probable 50S ribosomal protein L35	1.81472	5.00E-05	0.00026
PGN_0965	rplT	putative 50S ribosomal protein L20	1.80925	5.00E-05	0.00026
PGN_0966		partial transposase in ISPg1	-2.90815	5.00E-05	0.00026
PGN_0967		partial transposase in ISPg1	-2.76091	5.00E-05	0.00026
PGN_0968		conserved hypothetical protein	-0.32141	0.2705	0.384956
PGN_0969		conserved hypothetical protein	-1.62325	0.00465	0.013306
PGN_0970		putative RNA polymerase sigma-70 factor ECF subfamily	-0.513006	0.16405	0.256245
PGN_0971		transposase in ISPg1	-2.40758	5.00E-05	0.00026
PGN_0972		TPR domain protein	-1.26081	0.00015	0.000685
PGN_0973		conserved hypothetical protein	0.926916	0.00105	0.003606
PGN_0974		putative shikimate 5-dehydrogenase	0.721306	0.07415	0.134353
PGN_0975	ubiE	putative ubiquinone/menaquinone biosynthesis methyltransferase	0.966623	0.01555	0.036784
PGN_0976		phosphoribosylaminoimidazole-succinocarboxamide synthase	1.09607	0.00015	0.000685
PGN_0977		phosphate starvation-inducible PhoH-like protein	0.953396	0.001	0.003462
PGN_0978		hypothetical protein	0.703421	0.33545	0.454309
PGN_0979		hypothetical protein	0.876928	0.46365	0.578272
PGN_0980		putative alpha-1,2-mannosidase family protein	-0.251379	0.36055	0.479457
PGN_0981		S-adenosylmethionine:tRNA ribosyltransferase-isomerase	0.14297	0.61715	0.71877
PGN_0982		putative Mrr restriction system protein	-0.081929	0.77365	0.844667
PGN_0983		hypothetical protein	4.2373	5.00E-05	0.00026
PGN_0984		probable phosphatidylserine decarboxylase proenzyme	-0.596272	0.03695	0.07608
PGN_0985		probable phosphatidylserine synthase	0.278051	0.3291	0.448275
PGN_0986		hypothetical protein	1.17902	0.00135	0.004519
PGN_0987		prolyl-tRNA synthetase	0.50227	0.0904	0.157713
PGN_0988		hypothetical protein	-0.216744	0.4288	0.545278
PGN_0989	trmB	putative methyltransferase	0.391831	0.18565	0.285172
PGN_0990		ATP-binding protein Mrp/Nbp35 family	0.698279	0.01665	0.039083
PGN_0991		putative ribonuclease BN	0.932342	0.0013	0.004379
PGN_0992		putative riboflavin biosynthesis protein	0.218109	0.654	0.749786
PGN_0993		putative peptidase M23/M37 family	0.109919	0.7588	0.834445
PGN_0994		conserved hypothetical protein	-0.0668754	0.86915	0.912436
PGN_0995		TPR domain protein	-0.827107	0.07075	0.129182
PGN_0996		TPR domain protein	1.22371	5.00E-05	0.00026
PGN_0997	dut	putative deoxyuridine 5'-triphosphate nucleotidohydrolase	1.12425	0.00075	0.002697
PGN_0998		4-hydroxy-3-methylbut-2-en-1-yl diphosphate synthase	0.630276	0.0336	0.070339
PGN_0999		putative phosphoribosylaminoimidazole carboxylase	-0.102171	0.72805	0.810255

PGN_1000		putative glycine cleavage system H protein	-0.451544	0.12485	0.204623
PGN_1001		conserved hypothetical protein	0.303064	0.27845	0.393378
PGN_1002		AMP nucleosidase	-0.039896	0.88845	0.928121
PGN_1003		conserved hypothetical protein	0.305382	0.27365	0.387838
PGN_1004		putative ABC transporter ATP-binding protein	-0.0201488	0.9425	0.960233
PGN_1005		probable ABC transporter permease protein	0.108849	0.70385	0.792661
PGN_1006		transposase in ISPg3	-0.501066	0.0883	0.154598
PGN_1007		conserved hypothetical protein	0.834482	0.10905	0.182953
PGN_1008		partial transposase in ISPg1	-2.01051	5.00E-05	0.00026
PGN_1009		calcium-transporting ATPase	-0.727521	0.03135	0.06708
PGN_1010		conserved hypothetical protein	0.680235	0.2644	0.378298
PGN_1011		xanthine/uracil/vitamin C permease	0.659515	0.0167	0.039157
PGN_1012		putative 4-diphosphocytidyl-2C-methyl-D-erythritol kinase	0.818222	0.0667	0.123375
PGN_1013		putative Fe-S oxidoreductase	0.788871	0.0391	0.079812
PGN_1014		elongation factor G	-1.24542	0.00035	0.001436
PGN_1015		putative DNA polymerase III delta prime subunit	-0.972701	0.0016	0.005241
PGN_1016		conserved hypothetical protein	0.545178	0.07565	0.136722
PGN_1017		conserved hypothetical protein	0.412506	0.26885	0.38312
PGN_1018		conserved hypothetical protein	-1.37717	5.00E-05	0.00026
PGN_1019		Por secretion system response regulatr protein porX	-0.50665	0.0862	0.151845
PGN_1020		probable ATP/GTP-binding transmembrane protein	0.000652139	0.99865	0.99865
PGN_1021		hypothetical protein	0.950376	0.2265	0.333715
PGN_1022		putative thymidine kinase	-0.106691	0.7736	0.844667
PGN_1023		acid phosphatase OlpA	-0.0355282	0.93465	0.956208
PGN_1024		putative ribosome-binding factor A	0.159454	0.577	0.682842
PGN_1025		conserved hypothetical protein	0.780553	0.00525	0.014707
PGN_1026		glycosyl transferase family 2	-0.903772	0.00295	0.008947
PGN_1027		dihydroorotase	-0.686632	0.0199	0.045605
PGN_1028		conserved hypothetical protein	0.0950739	0.7666	0.839985
PGN_1029		conserved hypothetical protein	0.420678	0.45705	0.572725
PGN_1030		hypothetical protein	0.790993	0.12365	0.202969
PGN_1031		conserved hypothetical protein	0.0353417	0.9445	0.960233
PGN_1032		conserved hypothetical protein	-4.09866	5.00E-05	0.00026
PGN_1033		O-antigen flippase	-0.0909811	0.7534	0.829792
PGN_1034		conserved hypothetical protein	0.564565	0.0518	0.099803
PGN_1035		conserved hypothetical protein with DUF1063 domain	0.836154	0.00395	0.011552
PGN_1036		putative G/U mismatch-specific DNA glycosylase	0.699835	0.0136	0.032717
PGN_1037		conserved hypothetical protein	-0.405444	0.2304	0.338291
PGN_1038		conserved hypothetical protein	-1.15569	0.00015	0.000685
PGN_1039		putative alpha-1,2-mannosidase precursor	0.0910982	0.74795	0.825498
PGN_1040		conserved hypothetical protein	-2.14266	5.00E-05	0.00026
PGN_1041		cytochrome d ubiquinol oxidase subunit I	-1.55907	5.00E-05	0.00026
PGN_1042		cytochrome d ubiquinol oxidase subunit II	-1.66187	5.00E-05	0.00026
PGN_1043		conserved hypothetical protein	-0.906275	0.055	0.104736
PGN_1044		alpha-amylase	-0.959435	0.01305	0.031572
PGN_1045	lacZII	beta-galactosidase	0.622255	0.02325	0.051562
PGN_1046		putative DNA repair protein	1.32681	0.0004	0.001607
PGN_1047		hydroxylamine reductase	0.392508	0.2103	0.315747
PGN_1048		hypothetical protein	-0.977787	0.0424	0.085564
PGN_1049		putative alkaline phosphatase	0.580463	0.06145	0.115572
PGN_1050		conserved hypothetical protein	0.332185	0.24065	0.35068
PGN_1051		hypothetical protein	0.166855	0.6193	0.72088
PGN_1052		conserved hypothetical protein	-0.5642	0.11955	0.198023
PGN_1053		putative phospho-2-dehydro-3-deoxyheptonate aldolase/chorismate mutas	0.0834273	0.87075	0.913665
PGN_1054	vimF	virulence modulating gene F	-0.0893688	0.9007	0.937239
PGN_1055	vimE	virulence modulating gene E	-0.50719	0.35395	0.473015
PGN_1056	vimA	virulence modulating gene A	-1.23992	0.00575	0.015898
PGN_1057	recA	recombinase A	-1.89944	5.00E-05	0.00026
PGN_1058	bcp	putative bacterioferritin comigratory protein	-1.70217	5.00E-05	0.00026
PGN_1059		conserved hypothetical protein	-0.656322	0.7261	0.809354
PGN_1060		transposase in ISPg3	-0.690743	0.02385	0.052673
PGN_1061		conserved hypothetical protein	-0.0580671	0.83375	0.886198

PGN_1062	trmE	tRNA modification GTPase	1.12974	0.0001	0.000483
PGN_1063		partial transposase Orf2 in ISPg5	0.251785	0.51	0.623659
PGN_1064		transposase in ISPg3	-0.303441	0.3064	0.423313
PGN_1065		transposase in ISPg3	-0.53561	0.07345	0.133312
PGN_1066		transposase in ISPg3	-0.532925	0.07595	0.136916
PGN_1067		hypothetical protein	-0.96533	0.0018	0.005833
PGN_1068		conserved hypothetical protein	-0.766875	0.15945	0.251459
PGN_1069		hypothetical protein	-1.51608	0.0358	0.073998
PGN_1070		hypothetical protein	-1.38827	0.09415	0.162699
PGN_1071		hypothetical protein	-1.25052	0.0821	0.146146
PGN_1072		hypothetical protein	-1.29075	0.04635	0.091454
PGN_1073		hypothetical protein	-1.44417	5.00E-05	0.00026
PGN_1074		hypothetical protein	-1.17414	5.00E-05	0.00026
PGN_1075		hypothetical protein	-1.25837	0.12075	0.19913
PGN_1076		putative DNA methylase	-1.06929	0.0003	0.00126
PGN_1077		transposase in ISPg1	-2.40901	5.00E-05	0.00026
PGN_1078		GDP-mannose 4,6-dehydratase	0.267992	0.46985	0.583272
PGN_1079		GDP-fucose synthetase	-0.179841	0.7123	0.798319
PGN_1080		branched-chain amino acid aminotransferase	0.953671	0.00375	0.011073
PGN_1081		conserved hypothetical protein	-1.57568	5.00E-05	0.00026
PGN_1082		hypothetical protein	0.559427	0.2822	0.397357
PGN_1083		hypothetical protein	1.08884	0.14075	0.226669
PGN_1084		hypothetical protein	0.393955	0.5681	0.676026
PGN_1085	feoB	ferrous iron transport protein B	0.0982291	0.7276	0.810178
PGN_1086		hypothetical protein	0.842771	0.0236	0.052229
PGN_1087		conserved hypothetical protein	1.31512	0.00025	0.00108
PGN_1088	rpsA	30S ribosomal protein S1	1.73005	5.00E-05	0.00026
PGN_1089		probable methyltransferase	2.14438	5.00E-05	0.00026
PGN_1090		conserved hypothetical protein	1.05518	0.0004	0.001607
PGN_1091		conserved hypothetical protein	0.625233	0.04315	0.086503
PGN_1092		ATP-dependent exoDNAse alpha subunit	0.330667	0.2252	0.332721
PGN_1093		conserved hypothetical protein	0.0338366	0.90285	0.937341
PGN_1094		glycine dehydrogenase	0.252595	0.40105	0.517476
PGN_1095		probable metallo-beta-lactamase	-0.0821152	0.87165	0.914159
PGN_1096	gidB	glucose-inhibited division protein B	-0.388311	0.28255	0.397587
PGN_1097		conserved hypothetical protein	-0.625622	0.03185	0.067809
PGN_1098		probable succinoglycan biosynthesis regulator ExsB protein	0.487449	0.08335	0.147754
PGN_1099		probable phosphoesterase	0.360434	0.23455	0.343201
PGN_1100		putative capsule biosynthesis protein CapA	0.838069	0.00405	0.011763
PGN_1101		conserved hypothetical protein	1.71019	0.003	0.009047
PGN_1102		hypothetical protein	0.917803	0.1141	0.190674
PGN_1103		dipeptidase	0.167126	0.5751	0.68173
PGN_1104		chorismate synthase	-0.681426	0.03275	0.06924
PGN_1105		probable FKBP-type peptidyl-prolyl cis-trans isomerase	0.0170226	0.954	0.966714
PGN_1106		conserved hypothetical protein	-0.263054	0.603	0.705377
PGN_1107		conserved hypothetical protein	-0.758177	0.0534	0.10233
PGN_1108		putative RNA polymerase ECF-type sigma factor	-0.900029	0.003	0.009047
PGN_1109		hypothetical protein	1.48844	0.01335	0.032188
PGN_1110		partial transposase in ISPg1	-2.37873	5.00E-05	0.00026
PGN_1111		formate-tetrahydrofolate ligase	-0.155321	0.60715	0.709452
PGN_1112		PhoH-like protein	-0.934176	0.00215	0.006791
PGN_1113	ruvC	putative crossover junction endodeoxyribonuclease RuvC	-0.928778	0.0016	0.005241
PGN_1114		conserved hypothetical protein	-0.595114	0.0326	0.069198
PGN_1115		putative hemagglutinin	-2.64142	5.00E-05	0.00026
PGN_1116		putative aminotransferase	0.552599	0.0623	0.116964
PGN_1117		acetyl-CoA synthetase	0.76311	0.00795	0.021104
PGN_1118		transposase in ISPg1	-2.42819	5.00E-05	0.00026
PGN_1119		probable large conductance mechanosensitive channel protein	-1.67819	5.00E-05	0.00026
PGN_1120		putative NADPH-NAD transhydrogenase	0.783174	0.00885	0.022922
PGN_1121		probable NADPH-NAD transhydrogenase alpha subunit	0.998603	0.47275	0.586095
PGN_1122		NADPH-NAD transhydrogenase beta subunit	1.20935	0.0003	0.00126
PGN_1123		conserved hypothetical protein	1.00725	0.15405	0.244027

PGN_1124		Band 7 protein	-0.139219	0.6783	0.769776
PGN_1125		conserved hypothetical protein	-0.626671	0.02305	0.051278
PGN_1126		putative error-prone repair: SOS-response transcriptional repressor UmuD h	-0.704425	0.01255	0.030641
PGN_1127		putative SOS mutagenesis and repair protein UmuC homolog	-0.230892	0.40615	0.522473
PGN_1128		L-lactate permease	0.173598	0.55205	0.662149
PGN_1129		conserved hypothetical protein	-0.699136	0.09205	0.159849
PGN_1130	murB	putative UDP-N-acetylenolpyruvoylglucosamine reductase	-0.42136	0.6244	0.725579
PGN_1131		conserved hypothetical protein	-0.552229	0.0639	0.119231
PGN_1132		transposase in ISPg1	-2.57717	5.00E-05	0.00026
PGN_1133		hypothetical protein	-0.693987	0.31285	0.430826
PGN_1134		conserved hypothetical protein	-0.00534496	0.9879	0.990226
PGN_1135		putative glycosyltransferase	0.566516	0.2615	0.375157
PGN_1136		probable GTP-cyclohydrolase protein	-0.159494	0.56855	0.676026
PGN_1137		conserved hypothetical protein	-0.0493206	0.85175	0.899938
PGN_1138		conserved hypothetical protein	-1.36935	5.00E-05	0.00026
PGN_1139		conserved hypothetical protein	-0.636878	0.0232	0.051558
PGN_1140	pyrE	putative orotate phosphoribosyltransferase	-0.656108	0.0243	0.05339
PGN_1141		putative amidohydrolase	-0.920708	0.0523	0.100584
PGN_1142		probable acetyltransferase	-0.909057	0.0169	0.039452
PGN_1143		conserved hypothetical protein	-1.81525	5.00E-05	0.00026
PGN_1144		hypothetical protein	0.132433	0.7466	0.824601
PGN_1145		conserved hypothetical protein	0.611671	0.2156	0.321212
PGN_1146		conserved hypothetical protein	-0.233794	0.39455	0.511881
PGN_1147		conserved hypothetical protein	-0.798804	0.00465	0.013306
PGN_1148		phosphoribosylamine-glycine ligase	-1.11859	0.01455	0.034845
PGN_1149		prolyl tripeptidase A	-0.944621	0.03805	0.078043
PGN_1150		putative N6-adenine-specific DNA methylase	-1.27869	0.00015	0.000685
PGN_1151		1-deoxy-D-xylulose-5-phosphate reductoisomerase	0.450144	0.3354	0.454309
PGN_1152	rimM	probable 16S rRNA processing protein	-0.583138	0.14935	0.237821
PGN_1153		UDP-N-acetylglucosamine 1-carboxyvinyltransferase	-0.543913	0.0696	0.12785
PGN_1154		conserved hypothetical protein	-0.150954	0.5878	0.691014
PGN_1155	pgi	glucose-6-phosphate isomerase	-0.630361	0.0334	0.070196
PGN_1156		glycerol-3-phosphate dehydrogenase	-1.01816	0.00125	0.004224
PGN_1157	lysS	lysyl-tRNA synthetase	-0.902505	0.00415	0.012037
PGN_1158		putative purine nucleoside phosphorylase	-1.17653	0.0004	0.001607
PGN_1159		conserved hypothetical protein	-0.981792	0.00155	0.0051
PGN_1160		transposase in ISPg2	1.03182	0.0008	0.002848
PGN_1161		transposase in ISPg1	-2.28234	5.00E-05	0.00026
PGN_1162		putative CoA transferase subunit A	-0.00793261	0.97655	0.984297
PGN_1163		conserved hypothetical protein	0.0294981	0.91445	0.944776
PGN_1164		conserved hypothetical protein with prokaryotic DUF849 domain	0.373711	0.16745	0.260791
PGN_1165		conserved hypothetical protein	0.124981	0.66835	0.760512
PGN_1166		L-lysine 2,3-aminomutase	0.433726	0.13165	0.21412
PGN_1167		conserved hypothetical protein	0.80768	0.0448	0.08889
PGN_1168		probable DNA mismatch repair protein MutS	0.940104	0.02615	0.056984
PGN_1169		D-lysine 5,6-aminomutase alpha subunit	1.14274	0.00305	0.009172
PGN_1170		D-lysine 5,6-aminomutase beta subunit	0.0568421	0.91235	0.943367
PGN_1171		coenzyme A transferase beta subunit	0.0957522	0.72755	0.810178
PGN_1172		acyl-CoA dehydrogenase short-chain specific	1.09766	0.00045	0.001764
PGN_1173		putative electron transfer flavoprotein beta subunit	1.04818	0.0003	0.00126
PGN_1174		electron transfer flavoprotein alpha subunit	0.187471	0.54265	0.654562
PGN_1175		putative enoyl-CoA hydratase	0.0763727	0.78355	0.852416
PGN_1176		putative 3-hydroxybutyryl-CoA dehydrogenase	-0.108169	0.6907	0.782597
PGN_1177		transposase in ISPg1	-2.29272	5.00E-05	0.00026
PGN_1178		acetate kinase	0.207355	0.4874	0.599081
PGN_1179		phosphotransacetylase	0.257015	0.3841	0.502303
PGN_1180		conserved hypothetical protein	-1.02314	0.0003	0.00126
PGN_1181		probable thiol:disulfide oxidoreductase	-0.296078	0.3214	0.440322
PGN_1182		conserved hypothetical protein	-2.42501	5.00E-05	0.00026
PGN_1183		hypothetical protein	-1.46217	0.0005	0.001921
PGN_1184		conserved hypothetical protein	-1.26656	5.00E-05	0.00026
PGN_1185		conserved hypothetical protein	-0.654233	0.02085	0.047425

PGN_1186	rprY	putative DNA-binding response regulator RprY	-1.2723	0.0005	0.001921
PGN_1187		conserved hypothetical protein	-0.355033	0.21505	0.321212
PGN_1188		conserved hypothetical protein	-0.287907	0.2987	0.415371
PGN_1189		phosphoglucomutase/phosphomannomutase	0.201332	0.47625	0.589498
PGN_1190		RNA methyltransferase	0.123127	0.66155	0.754791
PGN_1191		transposase in ISPg1	-2.41014	5.00E-05	0.00026
PGN_1192		DNA-binding protein histone-like family	-3.31914	5.00E-05	0.00026
PGN_1193		conserved hypothetical protein	-0.063048	0.81675	0.874239
PGN_1194		alanine racemase	0.484548	0.077	0.138223
PGN_1195		conserved hypothetical protein	1.34864	5.00E-05	0.00026
PGN_1196	murQ	putative sugar phosphate isomerase	-0.342787	0.52345	0.636451
PGN_1197		conserved hypothetical protein	-0.405549	0.45315	0.56985
PGN_1198		putative sodium-solute transporter	-0.146229	0.74035	0.818808
PGN_1199		DNA-binding protein histone-like family	-0.309776	0.3912	0.509086
PGN_1200		ATPase AAA family	-0.461145	0.0956	0.164537
PGN_1201		conserved hypothetical protein	-0.830506	0.5079	0.621448
PGN_1202	rpoN	RNA polymerase sigma-54 factor	-0.346076	0.44295	0.559004
PGN_1203		UDP-N-acetylmuramoylalanyl-D-glutamyl-2, 6-diaminopimelate--D-alanyl-D-	-0.603975	0.15705	0.248041
PGN_1204		probable aspartate-1-decarboxylase	0.874423	0.0017	0.005534
PGN_1205		signal recognition particle protein	1.12218	0.0002	0.000895
PGN_1206		putative methylenetetrahydrofolate dehydrogenase/methenyltetrahydrofol	-1.71837	5.00E-05	0.00026
PGN_1207		putative transport multidrug efflux protein	0.376389	0.22095	0.32735
PGN_1208	clpB	ClpB protein	-1.01691	0.0011	0.003753
PGN_1209		probable flavodoxin	-0.487788	0.08885	0.155305
PGN_1210		hypothetical protein	-1.25382	5.00E-05	0.00026
PGN_1211		hypothetical protein	-1.02106	0.0014	0.004672
PGN_1212		hypothetical protein	-1.02649	0.1319	0.214363
PGN_1213		putative ATP-binding protein	-0.423676	0.16535	0.258087
PGN_1214		hypothetical protein	-0.528863	0.0885	0.15482
PGN_1215		hypothetical protein	-0.801169	0.0214	0.048366
PGN_1216		transposase in ISPg1	-2.44293	5.00E-05	0.00026
PGN_1217		hypothetical protein	0.386723	0.46755	0.581433
PGN_1218	asnC	asparaginyl-tRNA synthetase	0.80826	0.01055	0.026644
PGN_1219		ribosomal large subunit pseudouridine synthase B	0.339575	0.2787	0.39347
PGN_1220		adenylosuccinate lyase	-0.168721	0.59975	0.702734
PGN_1221		probable ATP:corrinoid adenosyltransferase	-1.58164	5.00E-05	0.00026
PGN_1222		conserved hypothetical protein	1.34704	0.0002	0.000895
PGN_1223		uracil permease	1.27057	0.0001	0.000483
PGN_1224		probable transcriptional regulator	-0.285043	0.29695	0.413477
PGN_1225	xseA	probable exodeoxyribonuclease VII large subunit	-0.655587	0.0243	0.05339
PGN_1226		ribonucleotide reductase	-0.965784	0.00285	0.008718
PGN_1227		TPR domain protein	-0.457344	0.10575	0.178684
PGN_1228		hypothetical protein	-0.797113	1	1
PGN_1229	valS	valyl-tRNA synthetase	0.55171	0.0625	0.117226
PGN_1230		conserved hypothetical protein	0.647743	0.03355	0.070339
PGN_1231		hypothetical protein	-0.983764	0.00215	0.006791
PGN_1232		thioredoxin reductase	-1.09459	0.00225	0.007076
PGN_1233		conserved hypothetical protein	0.667444	0.02285	0.05094
PGN_1234		conserved hypothetical protein	1.13395	0.0067	0.018171
PGN_1235	porS	membrane protein PorS	0.919771	0.1176	0.195145
PGN_1236	porR	regulator PorR	1.40536	0.0118	0.02928
PGN_1237		hypothetical protein	#NAME?	0.02135	0.048356
PGN_1238		conserved hypothetical protein	1.34563	5.00E-05	0.00026
PGN_1239		probable lipopolysaccharide biosynthesis glycosyltransferase	1.40712	5.00E-05	0.00026
PGN_1240		conserved hypothetical protein	1.7283	5.00E-05	0.00026
PGN_1241		hypothetical protein	1.40267	0.0001	0.000483
PGN_1242		putative O-antigen polymerase Wzy	0.375191	0.17955	0.277605
PGN_1243		UDP-glucose 6-dehydrogenase	-0.116173	0.6915	0.783087
PGN_1244		putative peptide chain release factor RF-2	1.36878	5.00E-05	0.00026
PGN_1245		long-chain-fatty-acid-CoA ligase	-0.00532352	0.98585	0.988636
PGN_1246		hypothetical protein	-1.76592	5.00E-05	0.00026
PGN_1247		hypothetical protein	-0.405996	0.2649	0.378759

PGN_1248	hypothetical protein	0.493944	1	1
PGN_1249	conserved hypothetical protein	0.716089	0.4928	0.605058
PGN_1250	hypothetical protein	-0.685418	1	1
PGN_1251	probable glycosyltransferase	-0.697002	0.01365	0.0328
PGN_1252	iron-containing alcohol dehydrogenase	-1.76814	5.00E-05	0.00026
PGN_1253	hypothetical protein	0.925069	0.01085	0.027208
PGN_1254	hypothetical protein	1.03842	0.00065	0.00239
PGN_1255	putative heptosyltransferase	1.79554	5.00E-05	0.00026
PGN_1256	conserved hypothetical protein	2.26135	0.00035	0.001436
PGN_1257	hypothetical protein	0.996694	0.22575	0.333071
PGN_1258	cobalamin biosynthesis protein	0.194885	0.4842	0.596564
PGN_1259	probable histidinol-phosphate aminotransferase	0.0646789	0.9265	0.951988
PGN_1260	cobyric acid synthase	-0.563769	0.20565	0.310077
PGN_1261	probable cobalamin adenosyltransferase	-0.687516	0.1292	0.210618
PGN_1262	cobyrinic acid a,c-diamide synthase	-0.41257	0.15295	0.242827
PGN_1263	conserved hypothetical protein	-0.763731	0.02155	0.048602
PGN_1264	conserved hypothetical protein	-0.453407	0.53625	0.648311
PGN_1265	hypothetical protein	0.78478	0.2503	0.362408
PGN_1266	conserved hypothetical protein	0.232766	0.73265	0.813915
PGN_1267	conserved hypothetical protein	-0.0963185	0.7254	0.808998
PGN_1268	putative oxidoreductase	-1.12057	0.01645	0.038698
PGN_1269	putative electron transport protein	-0.896135	0.0416	0.084109
PGN_1270	conserved hypothetical protein	-0.850567	0.00385	0.011337
PGN_1271	probable thioesterase superfamily protein	0.441839	0.11555	0.192493
PGN_1272	putative diaminopimelate decarboxylase	-1.28777	0.0001	0.000483
PGN_1273	probable 1,4-dihydroxy-2-naphthoate octaprenyltransferase	-1.1777	0.1488	0.237459
PGN_1274	conserved hypothetical protein	-1.5073	5.00E-05	0.00026
PGN_1275	conserved hypothetical protein	-1.1686	0.00015	0.000685
PGN_1276	transposase in ISPg1	-2.40109	5.00E-05	0.00026
PGN_1277	conserved hypothetical protein	-0.15196	0.7925	0.857878
PGN_1278	partial transposase in ISPg3	-0.481742	0.11065	0.185345
PGN_1279	partial transposase in ISPg3	-1.11291	0.1093	0.183228
PGN_1280	partial transposase in ISPg1	-2.37956	5.00E-05	0.00026
PGN_1286	probable lysozyme	-2.23586	5.00E-05	0.00026
PGN_1287	conserved hypothetical protein	-1.98999	5.00E-05	0.00026
PGN_1288	conserved hypothetical protein	-0.541292	0.0829	0.147324
PGN_1289	conserved hypothetical protein	-1.09958	0.0104	0.026359
PGN_1290	conserved hypothetical protein	-1.27589	0.01185	0.02937
PGN_1291	conserved hypothetical protein related to phage	-0.916244	0.01725	0.040137
PGN_1292	probable anti-restriction protein	-0.562679	0.2854	0.400803
PGN_1293	conserved hypothetical protein	-0.569711	0.21545	0.321212
PGN_1294	conserved hypothetical protein	-0.716647	0.22635	0.333715
PGN_1295	hypothetical protein	-0.107552	0.8608	0.906535
PGN_1296	putative OmpA family protein	-0.469283	0.10675	0.179945
PGN_1297	conserved hypothetical protein	-0.749576	0.0115	0.028602
PGN_1298	conserved hypothetical protein	-1.4846	0.0001	0.000483
PGN_1299	hypothetical protein	0.573827	0.78725	0.854694
PGN_1300	probable transcriptional regulator	0.24629	0.3759	0.493398
PGN_1301	probable transcriptional regulator	0.0498913	0.85665	0.904376
PGN_1302	O-antigen ligase waaL	1.53608	5.00E-05	0.00026
PGN_1303	hypothetical protein	-0.272439	0.3619	0.480652
PGN_1304	conserved hypothetical protein	-0.553566	0.0727	0.132176
PGN_1305	putative N-acetylmuramoyl-L-alanine amidase	-0.420183	0.1489	0.237459
PGN_1306	hypothetical protein	1.53861	0.00335	0.009989
PGN_1307	hypothetical protein	-0.974609	0.01675	0.039231
PGN_1308	probable iron dependent repressor	0.0612356	0.83	0.885076
PGN_1309	ferrous iron transport protein B	0.0943979	0.73325	0.813915
PGN_1310	glycogen synthase	-0.122299	0.65745	0.751321
PGN_1311	putative K+dependent Na+exchanger related-protein	1.05488	0.00015	0.000685
PGN_1312	probable transcriptional regulator	0.48397	0.1198	0.198023
PGN_1313	conserved hypothetical protein	1.46383	5.00E-05	0.00026
PGN_1314	ATP-dependent DNA helicase	0.930154	0.4336	0.549812

PGN_1315		conserved hypothetical protein	0.192197	0.60285	0.705377
PGN_1316	uvrAI	excinuclease ABC A subunit	-0.609826	0.0738	0.133833
PGN_1317		conserved hypothetical protein	0.859205	0.0494	0.096312
PGN_1318		putative ABC transporter ATP-binding protein	0.559688	0.1933	0.294796
PGN_1319		transposase in ISPg1	-2.46789	5.00E-05	0.00026
PGN_1320		conserved hypothetical protein	0.93914	0.00145	0.004794
PGN_1321		conserved hypothetical protein	-2.15763	5.00E-05	0.00026
PGN_1322		conserved hypothetical protein	-1.19238	0.03855	0.078992
PGN_1323		TPR domain protein	0.962577	0.0023	0.007212
PGN_1324		probable ABC transporter membrane protein	-0.662526	0.08155	0.14541
PGN_1325		probable ABC transporter membrane protein	-0.696485	0.08315	0.147611
PGN_1326		hypothetical protein	-0.455056	0.0964	0.165465
PGN_1327		hypothetical protein	-0.0290693	0.9469	0.96089
PGN_1328		hypothetical protein	-0.426351	0.3109	0.428696
PGN_1329		hypothetical protein	-0.911553	0.44675	0.563132
PGN_1330		probable branched chain amino acid ABC transporter ATP-binding protein	-0.771352	0.00735	0.019634
PGN_1331		conserved hypothetical protein	-0.562685	0.34515	0.463904
PGN_1332		putative para-aminobenzoate synthase component I	0.419982	0.14395	0.231123
PGN_1333		probable para-aminobenzoate synthase component I	1.47372	0.0006	0.002241
PGN_1334		conserved hypothetical protein	1.30022	0.0003	0.00126
PGN_1335		conserved hypothetical protein	1.79035	5.00E-05	0.00026
PGN_1336		conserved hypothetical protein	1.18168	5.00E-05	0.00026
PGN_1337		conserved hypothetical protein	0.00291521	0.98255	0.987187
PGN_1338		pyruvate phosphate dikinase	-0.030916	0.92815	0.952922
PGN_1339		conserved hypothetical protein	-0.284601	0.34955	0.46834
PGN_1340		conserved hypothetical protein	-0.724643	0.01495	0.035682
PGN_1341		putative CoA transferase	0.0241309	0.93585	0.956517
PGN_1342		putative SAM/TRAM family methylase protein	0.866047	0.0028	0.00859
PGN_1343		probable ABC transporter ATP-binding protein	-0.234101	0.40395	0.520272
PGN_1344		conserved hypothetical protein	-0.29638	0.48005	0.593167
PGN_1345		conserved hypothetical protein	0.25062	0.57385	0.680628
PGN_1346		putative transcriptional regulator	0.040062	0.9548	0.967064
PGN_1347		putative TonB-dependent receptor exported protein	-1.10625	0.00035	0.001436
PGN_1348		conserved hypothetical protein	-0.26881	0.3708	0.488511
PGN_1349		probable dipeptidyl anminopeptidase	0.687718	0.0168	0.039305
PGN_1350		conserved hypothetical protein	-0.158988	0.5642	0.672416
PGN_1351		conserved hypothetical protein	0.0264585	0.93455	0.956208
PGN_1352		conserved hypothetical protein with DUF1706 domain	0.0955543	0.7498	0.826683
PGN_1353		conserved hypothetical protein	-0.322544	0.291	0.407056
PGN_1354		conserved hypothetical protein	0.563146	0.10795	0.181393
PGN_1355		conserved hypothetical protein	0.450773	0.7012	0.791545
PGN_1356		conserved hypothetical protein	0.966242	0.1491	0.2376
PGN_1357		conserved hypothetical protein	1.28156	5.00E-05	0.00026
PGN_1358		conserved hypothetical protein	-1.07666	0.00045	0.001764
PGN_1359		putative erythronate-4-phosphate dehydrogenase	-0.623961	0.03175	0.067731
PGN_1360		probable oxidoreductase	0.237957	0.38545	0.50345
PGN_1361		conserved hypothetical protein	-0.105243	0.71035	0.797225
PGN_1362		probable exported transglycosylase protein	-0.00640405	0.9811	0.986195
PGN_1363		ABC transporter ATP-binding protein	-0.168408	0.5548	0.664698
PGN_1364		probable peptidyl-prolyl cis-trans isomerase cyclophilin-type	-0.107477	0.7077	0.795929
PGN_1365		conserved hypothetical protein	0.383497	0.35415	0.473015
PGN_1366		conserved hypothetical protein	-1.6502	5.00E-05	0.00026
PGN_1367		NAD-specific glutamate dehydrogenase	0.207538	0.548	0.658776
PGN_1368		conserved hypothetical protein	0.508717	0.3905	0.508616
PGN_1369		conserved hypothetical protein	0.469309	0.2672	0.381279
PGN_1370		NAD-dependent nucleotide-diphosphate-sugar epimerase	0.730421	0.01255	0.030641
PGN_1371		hypothetical protein	0.225464	0.69365	0.784687
PGN_1372		conserved hypothetical protein	-0.0417184	0.9082	0.939989
PGN_1373		probable transcriptional regulator	0.121298	0.8177	0.874816
PGN_1374		putative ribosomal large subunit pseudouridine synthase D	-0.821199	0.0063	0.01724
PGN_1375		putative beta-ketoacyl-acyl carrier protein reductase	-0.877599	0.008	0.021184
PGN_1376		putative transcriptional regulator	-1.13813	0.0004	0.001607

PGN_1377		GTP-binding protein LepA	0.307992	0.30115	0.417686
PGN_1378		replicative DNA helicase	0.346444	0.2251	0.332721
PGN_1379		hypothetical protein	0.0297992	0.91745	0.946343
PGN_1380		hypothetical protein	-0.45868	0.15355	0.243598
PGN_1381	alaS	alanyl-tRNA synthetase	0.470273	0.11685	0.194354
PGN_1382		putative 3-dehydroquinate synthase	0.633679	0.0318	0.06777
PGN_1383		conserved hypothetical protein	-0.174959	0.5242	0.636999
PGN_1384		probable 1-acyl-sn-glycerol-3-phosphate acetyltransferase	-0.93998	0.001	0.003462
PGN_1385		hypothetical protein	-0.588811	0.043	0.086503
PGN_1386		conserved hypothetical protein	1.24382	0.0057	0.015781
PGN_1387		putative ABC transporter permease protein	1.86098	5.00E-05	0.00026
PGN_1388		DNA ligase	1.9553	5.00E-05	0.00026
PGN_1389		probable acetyltransferase	1.85627	0.0049	0.013873
PGN_1390	recR	putative recombination protein RecR	1.67891	0.1956	0.297877
PGN_1391		putative ribonuclease E	1.55414	5.00E-05	0.00026
PGN_1392		conserved hypothetical protein	1.08116	0.00025	0.00108
PGN_1393		putative DNA-binding protein HU	1.18029	0.00015	0.000685
PGN_1394		transposase in ISPg2	1.23203	5.00E-05	0.00026
PGN_1395		putative anaerobic ribonucleoside-triphosphate reductase activating proteir	0.203391	0.47875	0.592248
PGN_1396		anaerobic ribonucleoside-triphosphate reductase	-1.29045	0.0017	0.005534
PGN_1397		transposase in ISPg1	-2.41622	5.00E-05	0.00026
PGN_1398		conserved hypothetical protein	0.762262	0.0118	0.02928
PGN_1399		conserved hypothetical protein	-1.27266	5.00E-05	0.00026
PGN_1400		conserved hypothetical protein	0.288638	0.29715	0.413485
PGN_1401		delta-1-pyrroline-5-carboxylate dehydrogenase	-0.960049	0.00245	0.007615
PGN_1402		putative amidinotransferase	-1.15718	0.00045	0.001764
PGN_1403		ornithine aminotransferase	-1.12876	0.00095	0.003316
PGN_1404		conserved hypothetical protein	0.646887	0.66755	0.760512
PGN_1405		elongation factor P	1.19663	5.00E-05	0.00026
PGN_1406		hypothetical protein	-0.555077	0.12635	0.206922
PGN_1407		DNA-binding protein histone-like family	-0.533436	0.0541	0.103299
PGN_1408		conserved hypothetical protein with predicted permease membrane region	-1.23093	5.00E-05	0.00026
PGN_1409		putative peptidase	-0.958726	0.01105	0.027677
PGN_1410		conserved hypothetical protein	-1.01041	0.69655	0.787549
PGN_1411		putative N-ethylammeline chlorohydrolase	-0.848164	0.21185	0.31785
PGN_1412		putative purine nucleoside phosphorylase I	-0.727017	0.0121	0.029781
PGN_1413		conserved hypothetical protein	0.490452	0.0743	0.134511
PGN_1414		hypothetical protein	-1.09297	0.08155	0.14541
PGN_1415		DNA-binding protein histone-like family	0.207119	0.45665	0.572561
PGN_1416		probable lysyl endopeptidase precursor	-0.597378	0.0484	0.094535
PGN_1417		hypothetical protein	1.13295	0.01755	0.04079
PGN_1418		pyruvate-flavodoxin oxidoreductase	-0.885569	0.0527	0.101262
PGN_1419		conserved hypothetical protein	-0.868834	0.0325	0.069054
PGN_1420		transposase in ISPg1	-2.38809	5.00E-05	0.00026
PGN_1421		hypothetical protein	-0.762297	0.18415	0.283277
PGN_1422		putative partial DNA-binding protein histone-like family	-1.26209	0.0001	0.000483
PGN_1423		putative partial DNA-binding protein histone-like family	-1.1603	0.0001	0.000483
PGN_1424		putative partial Type II restriction enzyme	-1.50595	5.00E-05	0.00026
PGN_1425		putative partial Type II restriction enzyme	-1.32912	5.00E-05	0.00026
PGN_1426		adenine-specific methyltransferase	-0.702562	0.013	0.031487
PGN_1427		hypothetical protein	0.537941	0.2937	0.410024
PGN_1428		transposase in ISPg3	-0.490984	0.09555	0.164537
PGN_1429		conserved hypothetical protein	-0.191265	0.84825	0.898023
PGN_1430		putative transmembrane Acr-type transport protein	-0.269569	0.42575	0.543093
PGN_1431		putative cation efflux system protein	-0.193859	0.78515	0.853339
PGN_1432		probable outer membrane efflux protein	-0.515461	0.06	0.113446
PGN_1433		transposase in ISPg1	-2.4003	5.00E-05	0.00026
PGN_1434		aminoacyl-histidine dipeptidase	-1.76132	5.00E-05	0.00026
PGN_1435		hypothetical protein	-0.577716	0.04795	0.093829
PGN_1436		conserved hypothetical protein	0.079909	0.77625	0.846637
PGN_1437		conserved hypothetical protein	-0.411201	0.1708	0.26562
PGN_1438		hypothetical protein	0.673408	0.227	0.334221

PGN_1439		hypothetical protein	0.655265	0.1341	0.217602
PGN_1440		putative vancomycin B-type resistance protein VanW	0.597133	0.03875	0.079326
PGN_1441	nadE	glutamine-dependent NAD synthetase	-0.0193567	0.94455	0.960233
PGN_1442		transposase in ISPg1	-2.37718	5.00E-05	0.00026
PGN_1443		carbamoyl-phosphate synthase large subunit	0.224462	0.44395	0.559935
PGN_1444		carbamoyl-phosphate synthase small subunit	0.0221818	0.9351	0.956209
PGN_1445		putative amidophosphoribosyltransferase	0.135581	0.6363	0.735841
PGN_1446		conserved hypothetical protein	0.777931	0.0092	0.023684
PGN_1447	pyrG	CTP synthase	0.218583	0.4582	0.573255
PGN_1448		conserved hypothetical protein	-1.14246	0.044	0.087712
PGN_1449		inosine-5'-monophosphate dehydrogenase	-0.239548	0.4584	0.573255
PGN_1450	miaA_1	putative tRNA isopentenyltransferase	0.172705	0.81655	0.874239
PGN_1451	groES	chaperonin GroES	-0.450675	0.1216	0.200222
PGN_1452	groEL	chaperonin GroEL	-0.590971	0.08435	0.149154
PGN_1453		conserved hypothetical protein	2.30759	0.53505	0.647228
PGN_1454		probable abortive infection protein	-0.181644	0.77255	0.844332
PGN_1455		conserved hypothetical protein	0.0145512	0.9663	0.975464
PGN_1456		conserved hypothetical protein	-0.131961	0.83505	0.886411
PGN_1457		probable alkaline phosphatase	0.113446	0.73965	0.818459
PGN_1458	secA	preprotein translocase SecA subunit	0.69624	0.02285	0.05094
PGN_1459		conserved hypothetical protein	-0.163432	0.5719	0.678693
PGN_1460	gmk	putative guanylate kinase	0.343935	0.26875	0.38312
PGN_1461		putative spore maturation protein A/B	0.273932	0.35005	0.468715
PGN_1462		conserved hypothetical protein	-0.331127	0.27265	0.387716
PGN_1463		probable UbiA prenyltransferase	1.26198	0.0044	0.012728
PGN_1464		probable HAD-superfamily subfamily IB hydrolase	0.784734	0.07075	0.129182
PGN_1465		hypothetical protein	0.419552	0.3238	0.442755
PGN_1466	rgpB	arginine-specific cysteine proteinase RgpB	1.02398	0.00275	0.008448
PGN_1467		conserved hypothetical protein	1.27961	5.00E-05	0.00026
PGN_1468		putative lipoic acid synthase	1.17737	5.00E-05	0.00026
PGN_1469	dpp	dipeptidyl peptidase IV	1.74434	5.00E-05	0.00026
PGN_1470	smpB	putative SsrA-binding protein	1.56178	5.00E-05	0.00026
PGN_1471		conserved hypothetical protein	1.41634	5.00E-05	0.00026
PGN_1472		queuine tRNA-ribosyltransferase	1.18397	0.0003	0.00126
PGN_1473		hypothetical protein	1.15133	0.02235	0.050035
PGN_1474		putative autoinducer-2 production protein LuxS	1.14966	0.0007	0.002543
PGN_1475		probable 5'-methylthioadenosine/S-adenosylhomocysteine nucleosidase	1.02153	0.0006	0.002241
PGN_1476		conserved hypothetical protein	2.46329	5.00E-05	0.00026
PGN_1477		conserved hypothetical protein	-0.753369	0.13435	0.21768
PGN_1478		conserved hypothetical protein	0.22517	0.7206	0.804909
PGN_1479		dipeptidyl peptidase 7	0.179363	0.5587	0.668362
PGN_1480		conserved hypothetical protein with DUF389 domain	0.159653	0.5862	0.690276
PGN_1481		putative polysaccharide biosynthesis protein	-0.058917	0.8319	0.885647
PGN_1482	ruvB	holliday junction DNA helicase RuvB	-0.553498	0.05045	0.097911
PGN_1483		conserved hypothetical protein	1.20528	0.0337	0.070479
PGN_1484		putative methylated-DNA-protein-cysteine methyltransferase	-1.17861	5.00E-05	0.00026
PGN_1485		conserved hypothetical protein	-0.54683	0.0638	0.119149
PGN_1486		conserved hypothetical protein	0.910846	0.0024	0.007481
PGN_1487		probable dephospho-CoA kinase	0.474932	0.09505	0.163988
PGN_1488		conserved hypothetical protein	0.980101	0.00075	0.002697
PGN_1489		2-amino-3-ketobutyrate CoA ligase	0.70125	0.01655	0.038891
PGN_1490		probable precorrin-2 C20-methyltransferase	-0.115221	0.72465	0.808585
PGN_1491		conserved hypothetical protein	-0.593596	0.04585	0.09072
PGN_1492	panC	putative pantoate-beta-alanine ligase	0.141927	0.74675	0.824601
PGN_1493		conserved hypothetical protein	0.295409	0.4864	0.598581
PGN_1494		putative oxygen-independent coproporphyrinogen III oxidase	0.985766	0.2856	0.400819
PGN_1495		putative low-specificity L-threonine aldolase	1.69395	5.00E-05	0.00026
PGN_1496		hypothetical protein	0.723361	0.0128	0.031144
PGN_1497		putative iron-sulfur cluster binding protein	-0.626548	0.0281	0.060736
PGN_1498		conserved hypothetical protein	-1.11998	0.00055	0.002076
PGN_1499		conserved hypothetical protein	0.0971892	0.92185	0.949454
PGN_1500		conserved hypothetical protein	-1.24181	5.00E-05	0.00026

PGN_1501		putative mannose-6-phosphate isomerase	-1.44102	5.00E-05	0.00026
PGN_1502		conserved hypothetical protein	-0.711031	0.01275	0.031058
PGN_1503		probable ferric uptake transcriptional regulator	0.17412	0.52895	0.642038
PGN_1504		adenylosuccinate synthetase	0.882004	0.02025	0.046357
PGN_1505		putative folylpolyglutamate synthase	0.980018	0.0336	0.070339
PGN_1506		putative transporter	1.92454	5.00E-05	0.00026
PGN_1507		hypothetical protein	-1.80501	5.00E-05	0.00026
PGN_1508		hypothetical protein	0.346356	0.53285	0.64597
PGN_1509		conserved hypothetical protein	-1.62392	5.00E-05	0.00026
PGN_1510		putative peptidyl-prolyl cis-trans isomerase	0.647778	0.0392	0.07994
PGN_1511		probable hemolysin	1.00032	0.0064	0.017424
PGN_1512		conserved hypothetical protein	0.733359	0.11995	0.198118
PGN_1513		conserved hypothetical protein	0.331162	0.26985	0.384288
PGN_1514		conserved hypothetical protein	0.710688	0.0178	0.041326
PGN_1515		conserved hypothetical protein	0.496687	0.7926	0.857878
PGN_1516		probable molybdopterin biosynthesis MoeB protein	0.0569843	0.85105	0.899938
PGN_1517	pepT	peptidase T	0.126619	0.65555	0.749955
PGN_1518		putative oligopeptide transporter	-0.153881	0.59115	0.69392
PGN_1519		hemagglutinin-related protein	0.202457	0.48295	0.595713
PGN_1520		conserved hypothetical protein	-2.07897	5.00E-05	0.00026
PGN_1521		conserved hypothetical protein	-1.75603	0.00015	0.000685
PGN_1522		conserved hypothetical protein	-1.77278	5.00E-05	0.00026
PGN_1523		putative polysaccharide export outer membrane protein	-0.036374	0.89765	0.934979
PGN_1524		conserved hypothetical protein	0.220642	0.4557	0.572043
PGN_1525		probable capsular polysaccharide biosynthesis protein	0.314993	0.2504	0.362408
PGN_1526		conserved hypothetical protein	-0.556887	0.09725	0.166569
PGN_1527		conserved hypothetical protein	-0.201009	0.5214	0.635046
PGN_1528		conserved hypothetical protein	0.0370036	0.9091	0.940464
PGN_1529		putative oxidoreductase	1.63212	5.00E-05	0.00026
PGN_1530		putative 2-oxoglutarate ferredoxin oxidoreductase subunit	1.58551	5.00E-05	0.00026
PGN_1531		hypothetical protein	0.293958	0.83745	0.888356
PGN_1532		conserved hypothetical protein	-1.01776	0.1632	0.255668
PGN_1533		putative carbonic anhydrase	-1.20634	0.00015	0.000685
PGN_1534		hypothetical protein	1.00297	0.00095	0.003316
PGN_1535		hypothetical protein	0.873646	0.00255	0.007891
PGN_1536		hypothetical protein	-1.70974	5.00E-05	0.00026
PGN_1537		probable cation efflux system protein	-1.90092	5.00E-05	0.00026
PGN_1538		putative cation efflux system	-1.4241	0.0001	0.000483
PGN_1539		putative ABC transport system exported protein	-1.30427	0.04795	0.093829
PGN_1540		putative ABC transport membrane protein	-1.02012	0.0005	0.001921
PGN_1541		hypothetical protein	0.585734	0.8404	0.890598
PGN_1542		putative esterase	-0.721058	0.01085	0.027208
PGN_1543		conserved hypothetical protein	-1.2282	0.0535	0.102429
PGN_1544		conserved hypothetical protein	-1.56239	5.00E-05	0.00026
PGN_1545		hypothetical protein	-1.32024	0.02145	0.048427
PGN_1546		hypothetical protein	-2.73209	5.00E-05	0.00026
PGN_1547	rplA	conserved hypothetical protein	0.955061	0.00405	0.011763
PGN_1547		conserved hypothetical protein	-2.67883	5.00E-05	0.00026
PGN_1548		putative ATP-dependent Clp protease proteolytic subunit	-0.722661	0.01215	0.02987
PGN_1549	clpP	ATP-dependent Clp protease ATP-binding subunit ClpX	0.179623	0.541	0.652942
PGN_1550	clpX	ATP-dependent DNA helicase RecQ	0.30331	0.3138	0.431855
PGN_1551	recQI	putative peptidyl-prolyl cis-trans isomerase	0.427222	0.1624	0.25479
PGN_1552		conserved hypothetical protein	0.607362	0.0424	0.085564
PGN_1553		conserved hypothetical protein	0.0212798	0.96205	0.972557
PGN_1554		DNA mismatch repair protein MutL	-0.245274	0.80595	0.867915
PGN_1555		putative hemagglutinin	-0.704255	0.13355	0.216879
PGN_1556		conserved hypothetical protein	-2.03039	5.00E-05	0.00026
PGN_1557		conserved hypothetical protein	-1.69317	5.00E-05	0.00026
PGN_1558		hypothetical protein	-1.63713	5.00E-05	0.00026
PGN_1559		conserved hypothetical protein	0.35749	0.39505	0.512035
PGN_1560		conserved hypothetical protein	0.228731	0.70405	0.792661
PGN_1561		conserved hypothetical protein	-1.85606	5.00E-05	0.00026

PGN_1562		hypothetical protein	-1.71235	5.00E-05	0.00026
PGN_1563		conserved hypothetical protein	-1.36407	5.00E-05	0.00026
PGN_1564		conserved hypothetical protein with PSP1 C-terminal conserved region	-1.10866	0.00095	0.003316
PGN_1565		conserved hypothetical protein	-1.09883	0.00055	0.002076
PGN_1566		putative DNA replication and repair protein RecF	-1.03605	0.06115	0.115313
PGN_1567		conserved hypothetical protein	-1.29884	0.00065	0.00239
PGN_1568		probable transcriptional regulator Crp/Fnr family	-2.03969	5.00E-05	0.00026
PGN_1569		DNA-directed RNA polymerase beta' subunit	-0.634322	0.02325	0.051562
PGN_1570	rpoC	DNA-directed RNA polymerase beta subunit	1.21295	0.0003	0.00126
PGN_1571	rpoB	putative 50S ribosomal protein L7/L12	1.09115	0.0007	0.002543
PGN_1572	rplL	putative 50S ribosomal protein L10	0.161693	0.60825	0.710348
PGN_1573	rplJ	50S ribosomal protein L1	0.80993	0.00855	0.02228
PGN_1575	rplK	50S ribosomal protein L11	1.03436	0.00185	0.00595
PGN_1576		putative transcription antitermination protein	1.09791	0.00165	0.005388
PGN_1577		putative preprotein translocase SecE subunit	1.21874	0.00015	0.000685
PGN_1578		translation elongation factor Tu	0.36811	0.32865	0.447949
PGN_1579		putative site-specific recombinase	-1.82197	5.00E-05	0.00026
PGN_1580	rpsU	putative 30S ribosomal protein S21	1.37647	5.00E-05	0.00026
PGN_1581		DNA mismatch repair protein MutS	0.486839	0.0986	0.168475
PGN_1582		membrane-associated zinc metalloprotease	-0.26024	0.37165	0.489025
PGN_1583		hypothetical protein	-0.73381	0.18025	0.278283
PGN_1584		putative sodium/hydrogen antiporter	0.45692	0.37565	0.493374
PGN_1585	uvrB	excinuclease ABC B subunit	-1.15561	0.00685	0.018484
PGN_1586		hypothetical protein	0.159172	0.7932	0.858091
PGN_1587	tsf	putative translation elongation factor Ts	2.36353	5.00E-05	0.00026
PGN_1588	rpsB	putative 30S ribosomal protein S2	1.85811	5.00E-05	0.00026
PGN_1589	rpsI	putative 30S ribosomal protein S9	1.72397	5.00E-05	0.00026
PGN_1590	rplM	putative 50S ribosomal protein L13	2.10712	5.00E-05	0.00026
PGN_1591		conserved hypothetical protein	0.0206286	0.9375	0.956825
PGN_1592		conserved hypothetical protein	-1.13181	0.42385	0.540993
PGN_1593	coaD	putative phosphopantetheine adenylyltransferase	1.06411	0.00085	0.003021
PGN_1594		DNA topoisomerase IV B subunit	0.746084	0.0089	0.023023
PGN_1595		conserved hypothetical protein	-0.909798	0.00185	0.00595
PGN_1596		probable 3'-5' exonuclease	-0.328593	0.537	0.64885
PGN_1597		conserved hypothetical protein	-0.261694	0.4416	0.558294
PGN_1598		probable glutamine ABC transporter	-0.610561	0.03515	0.072867
PGN_1599		conserved hypothetical protein	0.286604	0.5444	0.65593
PGN_1600		conserved hypothetical protein	-0.404568	0.2997	0.416489
PGN_1601		conserved hypothetical protein with lemA family domain	-0.228101	0.42705	0.543767
PGN_1602		putative flavoredoxin	-0.586243	0.0336	0.070339
PGN_1603		aspartate carbamoyltransferase regulatory subunit	-0.250941	0.3569	0.475494
PGN_1604	pyrB	aspartate carbamoyltransferase catalytic subunit	-0.0807751	0.7703	0.842469
PGN_1605		conserved hypothetical protein	-0.487546	0.08685	0.152687
PGN_1606		conserved hypothetical protein	-0.633105	0.03105	0.066505
PGN_1607		hypothetical protein	-1.05032	0.073	0.132608
PGN_1608		neuraminidase	-0.342534	0.21355	0.3195
PGN_1609		hypothetical protein	-0.467896	0.60405	0.706218
PGN_1610		conserved hypothetical protein	-0.386187	0.1954	0.297786
PGN_1611	inlJ	conserved hypothetical protein	0.0975961	0.7339	0.814212
PGN_1612		probable beta-phosphoglucomutase	-0.775225	0.00635	0.01731
PGN_1613		ATP-dependent DNA helicase RecG	-0.839597	0.0032	0.009595
PGN_1614		UDP-glucose 4-epimerase	-1.55126	5.00E-05	0.00026
PGN_1615	engB	putative GTP-binding protein	-1.69781	5.00E-05	0.00026
PGN_1616		conserved hypothetical protein	-1.47649	5.00E-05	0.00026
PGN_1617		probable metallophosphoesterase	-1.49877	5.00E-05	0.00026
PGN_1618		methionine gamma-lyase	-1.03434	0.00055	0.002076
PGN_1619		transposase in ISPg1	-2.56714	5.00E-05	0.00026
PGN_1620		hypothetical protein	-0.834246	0.0119	0.029425
PGN_1621		conserved hypothetical protein	-2.32829	5.00E-05	0.00026
PGN_1622		conserved hypothetical protein	-1.76516	5.00E-05	0.00026
PGN_1623		conserved hypothetical protein	-1.45041	5.00E-05	0.00026
PGN_1624		conserved hypothetical protein	-1.15452	0.3743	0.491904

PGN_1625		conserved hypothetical protein	-0.724538	0.0147	0.035164
PGN_1627		probable 4-amino-4-deoxy-L-arabinose transferase	-0.766205	0.00715	0.019196
PGN_1628		putative glycosyltransferases	-0.796231	0.0045	0.012947
PGN_1629		conserved hypothetical protein with integral membrane domain DUF6	0.623951	0.02915	0.062814
PGN_1630	rho	transcription termination factor Rho	0.621659	0.0372	0.076521
PGN_1631		piutative DNA-binding protein histone-like family	2.30006	5.00E-05	0.00026
PGN_1632		hypothetical protein	1.57356	5.00E-05	0.00026
PGN_1633		formiminotransferase-cyclodeaminase	-0.356372	0.2422	0.352456
PGN_1634		imidazolonepropionase	-0.137308	0.63435	0.734783
PGN_1635		conserved hypothetical protein with nucleoside recognition domain	-0.582695	0.0452	0.0896
PGN_1636		conserved hypothetical protein	1.54011	5.00E-05	0.00026
PGN_1637		putative methenyltetrahydrofolate cyclohydrolase	1.91137	5.00E-05	0.00026
PGN_1638		histidine ammonia-lyase	1.13991	5.00E-05	0.00026
PGN_1639		conserved hypothetical protein	1.6212	5.00E-05	0.00026
PGN_1640		serine/threonine transporter	0.76464	0.0084	0.021997
PGN_1641		arginine/ornithine transport system ATPase	-0.0964903	0.73795	0.817427
PGN_1642		conserved hypothetical protein	-0.611541	0.0435	0.086796
PGN_1643		conserved hypothetical protein	-1.25907	0.0001	0.000483
PGN_1644		transposase in ISPg1	-2.34034	5.00E-05	0.00026
PGN_1645		putative dipeptidyl peptidase III	0.378194	0.17735	0.274602
PGN_1646		seryl-tRNA synthetase	1.20882	0.0001	0.000483
PGN_1647	rpmA	putative 50S ribosomal protein L27	2.15757	5.00E-05	0.00026
PGN_1648	rplU	putative 50S ribosomal protein L21	2.26294	5.00E-05	0.00026
PGN_1649		conserved hypothetical protein	-0.550564	0.20295	0.306658
PGN_1650		conserved hypothetical protein	0.0843684	0.8942	0.932754
PGN_1651		putative glycosyltransferase	-0.122884	0.78805	0.855127
PGN_1652		probable nitroreductase	0.331243	0.61675	0.718698
PGN_1653		putative thiamine biosynthesis lipoprotein ApbE	0.473777	0.562	0.671059
PGN_1654		putative electron transport complex RnfABCDGE type A subunit	0.592901	0.043	0.086503
PGN_1655		putative electron transport complex RnfABCDGE type E subunit	0.461384	0.44215	0.558326
PGN_1656		putative electron transport complex RnfABCDGE type G subunit	0.0962991	0.8577	0.904878
PGN_1657		electron transport complex RnfABCDGE type D subunit	0.273993	0.59125	0.69392
PGN_1658		electron transport complex RnfABCDGE type C subunit	0.141189	0.64505	0.743536
PGN_1659		putative electron transport complex RnfABCDGE type B subunit	0.109822	0.71245	0.798319
PGN_1660		conserved hypothetical protein	-0.315814	0.2805	0.395486
PGN_1661		conserved hypothetical protein	-0.935807	0.00095	0.003316
PGN_1662		partial transposase in ISPg3	-0.231307	0.5984	0.701831
PGN_1663		hypothetical protein	-0.892649	0.0656	0.121657
PGN_1664		conserved hypothetical protein	-2.14945	5.00E-05	0.00026
PGN_1665		hypothetical protein	1.15315	0.08435	0.149154
PGN_1666		phosphoribosylformylglycinamidine synthase	-0.882283	0.0085	0.022204
PGN_1667		putative DNA processing Smf-like protein	0.390506	0.7038	0.792661
PGN_1668		conserved hypothetical protein	0.504071	0.0679	0.125051
PGN_1669		transposase in ISPg1	-2.48894	5.00E-05	0.00026
PGN_1670		conserved hypothetical protein with predicted lysozyme domain	-1.98416	5.00E-05	0.00026
PGN_1671		probable chromate transport protein	-1.23489	0.00015	0.000685
PGN_1672		probable chromate transport protein	-0.022105	0.9372	0.956825
PGN_1673		Por secretion system protein porN/gldN	1.96986	5.00E-05	0.00026
PGN_1674		Por secretion system protein porM/gldM	1.98866	5.00E-05	0.00026
PGN_1675		Por secretion system protein porL/gldL	1.58494	5.00E-05	0.00026
PGN_1676		Por secretion system protein porK/gldK	1.49036	5.00E-05	0.00026
PGN_1677		Por secretion system protein porP	1.87914	5.00E-05	0.00026
PGN_1678		conserved hypothetical protein	2.38073	5.00E-05	0.00026
PGN_1679		conserved hypothetical protein	-1.41496	0.0004	0.001607
PGN_1680		putative ABC transporter permease protein	-0.549292	0.1149	0.19171
PGN_1681		putative ABC transporter ATP-binding protein	-0.709319	0.0821	0.146146
PGN_1682		probable ABC transporter permease protein	-0.490453	0.16225	0.254742
PGN_1683		probable ABC transporter permease protein	-0.572487	0.11555	0.192493
PGN_1684		hypothetical protein	0.0609839	0.944	0.960233
PGN_1685		NADP-dependent malate dehydrogenase	-0.0651727	0.8194	0.876194
PGN_1686		hypothetical protein	-1.19896	0.00815	0.021555
PGN_1687		conserved hypothetical protein	-0.885034	0.00335	0.009989

PGN_1688		putative ribose 5-phosphate isomerase B	-0.993668	0.00185	0.00595
PGN_1689		transketolase	-0.417192	0.16115	0.253576
PGN_1690		putative exported fucosidase	-1.6516	5.00E-05	0.00026
PGN_1691		putative cysteine desulfurase	0.225297	0.49855	0.611413
PGN_1692		conserved hypothetical protein	1.2096	0.56165	0.671017
PGN_1693		selenide water dikinase	0.63815	0.3595	0.478659
PGN_1694		putative alanyl dipeptidyl peptidase	0.897555	0.0021	0.006663
PGN_1695		putative fructose-bisphosphate aldolase class I	-1.07565	0.002	0.006413
PGN_1696		conserved hypothetical protein	-1.74872	0.00025	0.00108
PGN_1697		conserved hypothetical protein	0.75112	0.0063	0.01724
PGN_1698	rpsO	putative 30S ribosomal protein S15	2.1627	5.00E-05	0.00026
PGN_1699		probable zinc ABC transporter zinc-binding protein	-0.644993	0.02635	0.057361
PGN_1700		probable metal uptake system ABC transporter ATP-binding protein	-0.72915	0.05505	0.104738
PGN_1701		conserved hypothetical protein	-0.743191	0.10275	0.174446
PGN_1702		protein-export membrane protein SecD/SecF	0.791958	0.0185	0.042672
PGN_1703		putative ribonuclease III	-0.167387	0.56995	0.677134
PGN_1704		beta-ketoacyl-acyl-carrier-protein synthase II	-0.587781	0.23435	0.343144
PGN_1705	acpP	putative acyl carrier protein	-0.594682	0.09955	0.169961
PGN_1706		probable phosphoribosylglycinamide formyltransferase	0.68389	0.0774	0.138824
PGN_1707		conserved hypothetical protein	1.01652	0.0172	0.040108
PGN_1708		magnesium chelatase subunit ChlI	0.239475	0.3975	0.514454
PGN_1709		conserved hypothetical protein	0.243804	0.4019	0.518259
PGN_1710		conserved hypothetical protein	-0.879212	0.00345	0.010273
PGN_1711	pheS	phenylalanyl-tRNA synthetase alpha subunit	0.719539	0.01395	0.033483
PGN_1712		putative endonuclease III	0.0812867	0.7695	0.842296
PGN_1713		conserved hypothetical protein	0.2487	0.65235	0.749786
PGN_1714		transcription-repair coupling factor	-0.61708	0.0832	0.147611
PGN_1715	grpE	putative chaperone protein GrpE	-0.772442	0.0076	0.020251
PGN_1716	dnaJ	chaperone protein DnaJ	-0.712733	0.018	0.0417
PGN_1717		conserved hypothetical protein	-0.71371	0.0106	0.026739
PGN_1718		probable UDP-2,3-diacylglucosamine hydrolase	-0.42956	0.12645	0.206927
PGN_1719		conserved hypothetical protein with appr-1-p processing enzyme domain	-0.0482882	0.8649	0.90963
PGN_1720		hypothetical protein	0.340139	0.42635	0.543532
PGN_1721		8-amino-7-oxononanoate synthase	-0.0473623	0.87635	0.918184
PGN_1722		putative uridine kinase	0.019284	0.945	0.960233
PGN_1723		conserved hypothetical protein	0.992782	0.0011	0.003753
PGN_1724		conserved hypothetical protein	0.846083	0.1865	0.285807
PGN_1725		probable polysaccharide deacetylase	-1.0952	0.02695	0.058488
PGN_1726		transposase in ISPg3	-0.311341	0.2908	0.407044
PGN_1727		transposase in ISPg1	-2.42416	5.00E-05	0.00026
PGN_1728	kgp	lysine-specific cysteine proteinase Kgp	0.00429063	0.9909	0.991816
PGN_1729		probable acetyltransferase	-0.00724004	0.98005	0.986071
PGN_1730		conserved hypothetical protein	-0.133423	0.6595	0.753259
PGN_1731		conserved hypothetical protein	-1.15582	0.06215	0.116785
PGN_1732		hypothetical protein	-1.6927	0.00705	0.018951
PGN_1733	hagA	hemagglutinin protein HagA	-3.09185	5.00E-05	0.00026
PGN_1734		nucleoside permease NupG	1.00719	0.00065	0.00239
PGN_1735		conserved hypothetical protein	0.813404	0.008	0.021184
PGN_1736		putative glycogen synthase	-0.434267	0.16335	0.255715
PGN_1737	recQII	ATP-dependent DNA helicase RecQ	-1.18635	0.0002	0.000895
PGN_1738		putative long-chain-fatty-acid-CoA ligase	-0.529852	0.09535	0.164373
PGN_1739		conserved hypothetical protein	0.865471	0.0055	0.015307
PGN_1740		putative RNA polymerase ECF-type sigma factor	-1.19075	0.001	0.003462
PGN_1741		conserved hypothetical protein	-0.848247	0.00865	0.022486
PGN_1742		conserved hypothetical protein	-0.558897	0.3906	0.508616
PGN_1743	eno	phosphopyruvate hydratase	0.853185	0.00375	0.011073
PGN_1744		conserved hypothetical protein	-0.44133	0.16395	0.256245
PGN_1745		putative NapC/NirT cytochrome c-type protein	-1.51774	5.00E-05	0.00026
PGN_1746		cytochrome c nitrite reductase catalytic subunit NrfA	-1.99696	5.00E-05	0.00026
PGN_1747		conserved hypothetical protein	-0.987877	0.0026	0.008022
PGN_1748		putative cytochrome c biogenesis protein CcsA	-0.893304	0.13875	0.223957
PGN_1749		probable NADPH-quinone reductase	0.145719	0.73245	0.813915

PGN_1750		putative 3-deoxy-D-manno-octulosonate cytidylyltransferase	0.0532439	0.89025	0.929089
PGN_1751		DNA primase	0.0792143	0.7814	0.850512
PGN_1752		putative ferredoxin 4Fe-4S	-1.24345	0.0001	0.000483
PGN_1753		putative 2-oxoglutarate oxidoreductase alpha subunit	-1.05616	0.00135	0.004519
PGN_1754		hypothetical protein	-1.48571	5.00E-05	0.00026
PGN_1755		putative 2-oxoglutarate oxidoreductase beta subunit	-0.935061	0.00225	0.007076
PGN_1756		putative 2-oxoglutarate oxidoreductase gamma subunit	-0.765567	0.01235	0.030292
PGN_1757		GTP pyrophosphokinase	-1.22559	0.0002	0.000895
PGN_1758		putative v-type ATPase subunit K	2.42124	5.00E-05	0.00026
PGN_1759		putative v-type ATPase subunit I	1.54896	5.00E-05	0.00026
PGN_1760		putative v-type ATPase subunit D	0.813375	0.3055	0.422344
PGN_1761		v-type ATPase subunit B	0.993603	0.0003	0.00126
PGN_1762		v-type ATPase subunit A	2.24128	5.00E-05	0.00026
PGN_1763		conserved hypothetical protein	1.66545	5.00E-05	0.00026
PGN_1764		putative v-type ATPase subunit E	2.61345	5.00E-05	0.00026
PGN_1765		hypothetical protein	-0.652967	0.5644	0.672416
PGN_1766		conserved hypothetical protein	-0.214886	0.7634	0.837341
PGN_1767		immunoreactive 46 kDa antigen	-2.0675	5.00E-05	0.00026
PGN_1768	gppX	putative DNA-binding response regulator/sensor histidine kinase	0.385191	0.1815	0.279605
PGN_1769		hypothetical protein	-0.131068	0.65495	0.749786
PGN_1770		conserved hypothetical protein	0.268876	0.3996	0.515918
PGN_1771		DNA polymerase I	-0.535261	0.0651	0.121232
PGN_1772		1,4-alpha-glucan branching enzyme	-1.26852	0.0162	0.038195
PGN_1773		sodium/hydrogen antiporter	-1.1426	0.0056	0.015565
PGN_1774		conserved hypothetical protein	-0.250367	0.7433	0.821644
PGN_1775		conserved hypothetical protein	-0.340504	0.2793	0.394055
PGN_1776		peptidyl-dipeptidase	1.08595	0.00015	0.000685
PGN_1777		bleomycin hydrolase	1.95568	5.00E-05	0.00026
PGN_1778		hypothetical protein	-0.46788	0.5877	0.691014
PGN_1779		conserved hypothetical protein	2.74276	1	1
PGN_1780		putative YjgF-like protein	0.324771	0.2637	0.37755
PGN_1781		putative tRNA:rRNA methyltransferase	0.665371	0.30935	0.426835
PGN_1782		DNA repair protein RecN	0.29934	0.3647	0.482865
PGN_1783		conserved hypothetical protein	-0.0322891	0.95315	0.966313
PGN_1784		DNA/pantothenate metabolism flavoprotein	-0.300334	0.39205	0.509881
PGN_1785		putative DNA polymerase III epsilon chain	-0.607553	0.0347	0.072074
PGN_1786		putative DNA polymerase III beta chain	-0.887121	0.00375	0.011073
PGN_1787		probable 5-formyltetrahydrofolate cyclo-ligase	0.289402	0.30785	0.425041
PGN_1788		carboxyl-terminal processing protease	1.1565	0.00015	0.000685
PGN_1789		putative deoxycytidylate deaminase	0.220208	0.45625	0.572396
PGN_1790		conserved hypothetical protein	2.64664	5.00E-05	0.00026
PGN_1791		putative flavodoxin	3.18349	5.00E-05	0.00026
PGN_1792		glycerate kinase	-0.942409	0.00115	0.003911
PGN_1793		conserved hypothetical protein	-0.654447	0.02385	0.052673
PGN_1794		conserved hypothetical protein	-1.77764	5.00E-05	0.00026
PGN_1795		conserved hypothetical protein	-1.93059	0.00865	0.022486
PGN_1796		conserved hypothetical protein	-1.38094	0.0001	0.000483
PGN_1797		conserved hypothetical protein	-0.501438	0.0829	0.147324
PGN_1798		conserved hypothetical protein	0.0812974	0.77745	0.847512
PGN_1799		hypothetical protein	0.304136	0.4551	0.571965
PGN_1800		urocanate hydratase	0.794663	0.01075	0.027021
PGN_1801		conserved hypothetical protein	-0.462078	0.4199	0.536917
PGN_1802		hemolysin	0.761785	0.033	0.069699
PGN_1803		conserved hypothetical protein	0.214245	0.45285	0.569809
PGN_1804		Na+/H+ antiporter	-0.121902	0.6898	0.781994
PGN_1805	cysS	cysteinyl-tRNA synthetase	-0.525272	0.07005	0.128345
PGN_1806		conserved hypothetical protein	-0.157676	0.57555	0.681884
PGN_1807		putative glycosyltransferase	-0.0249709	0.9292	0.952922
PGN_1808		conserved hypothetical protein	0.334016	0.24595	0.356912
PGN_1809		hypothetical protein	-0.247137	0.4584	0.573255
PGN_1810		hypothetical protein	0.343336	0.2536	0.365764
PGN_1811		putative alpha-L-fucosidase	-0.592669	0.048	0.09384

PGN_1812		polyphosphate kinase	-0.892065	0.00325	0.009732
PGN_1813		GTP-binding protein	-0.905131	0.0021	0.006663
PGN_1814		conserved hypothetical protein	0.3613	0.2402	0.350264
PGN_1815		conserved hypothetical protein	0.460519	0.52235	0.635839
PGN_1816		conserved hypothetical protein	1.17655	5.00E-05	0.00026
PGN_1817		conserved hypothetical protein	-0.202382	0.4664	0.580682
PGN_1818		conserved hypothetical protein	0.274636	0.3742	0.491904
PGN_1819		hypothetical protein	0.0252183	0.9796	0.986071
PGN_1820		conserved hypothetical protein	0.399737	0.1864	0.285807
PGN_1821		conserved hypothetical protein	0.314446	0.2834	0.39852
PGN_1822		hypothetical protein	0.550421	0.3713	0.488867
PGN_1823		conserved hypothetical protein	1.1532	0.0051	0.014324
PGN_1824		hypothetical protein	0.0365191	0.9289	0.952922
PGN_1825		hypothetical protein	-0.760371	0.0677	0.124899
PGN_1826		conserved hypothetical protein	-0.145191	0.8103	0.870496
PGN_1827		S-adenosylmethionine synthase	-2.39382	5.00E-05	0.00026
PGN_1828		conserved hypothetical protein	-0.361978	0.31265	0.430826
PGN_1829		probable nicotinamide mononucleotide transporter	0.203371	0.6659	0.759347
PGN_1830		putative TonB-dependent receptor	0.00496681	0.98525	0.9885
PGN_1831		putative GTPase	-0.109774	0.69195	0.78318
PGN_1832	frr	putative ribosome recycling factor	-0.582291	0.04535	0.089814
PGN_1833	pyrH	putative uridylate kinase	-0.780026	0.00885	0.022922
PGN_1834		conserved hypothetical protein	-0.727643	0.01205	0.029693
PGN_1835		conserved hypothetical protein	0.227511	0.63045	0.731061
PGN_1836		transposase in ISPg3	-0.539785	0.0706	0.129182
PGN_1837		conserved hypothetical protein	-2.49482	5.00E-05	0.00026
PGN_1838		partial transposase in ISPg1	-2.36636	5.00E-05	0.00026
PGN_1839		partial transposase in ISPg1	-2.83725	5.00E-05	0.00026
PGN_1840	rplQ	50S ribosomal protein L17	1.36145	0.0001	0.000483
PGN_1841	rpoA	DNA-directed RNA polymerase alpha subunit	1.2693	0.0001	0.000483
PGN_1842	rpsD	30S ribosomal protein S4	1.86171	5.00E-05	0.00026
PGN_1843	rpsK	30S ribosomal protein S11	1.84036	5.00E-05	0.00026
PGN_1844	rpsM	30S ribosomal protein S13	1.56528	5.00E-05	0.00026
PGN_1845	rpmJ	50S ribosomal protein L36	1.70243	5.00E-05	0.00026
PGN_1846	infA	translation initiation factor IF-1	1.49355	5.00E-05	0.00026
PGN_1847		putative methionine aminopeptidase type I	1.16393	0.0631	0.118049
PGN_1848	secY	preprotein translocase SecY subunit	1.22835	0.0015	0.004944
PGN_1849	rplO	50S ribosomal protein L15	0.78595	0.0068	0.018395
PGN_1850	rpmD	50S ribosomal protein L30	1.26033	5.00E-05	0.00026
PGN_1851	rpsE	30S ribosomal protein S5	1.08363	0.00015	0.000685
PGN_1852	rplR	50S ribosomal protein L18	1.35795	5.00E-05	0.00026
PGN_1853	rplF	50S ribosomal protein L6	1.36503	5.00E-05	0.00026
PGN_1854	rpsH	30S ribosomal protein S8	1.47836	5.00E-05	0.00026
PGN_1855	rpsN	30S ribosomal protein S14	1.67644	5.00E-05	0.00026
PGN_1856	rplE	50S ribosomal protein L5	1.41067	5.00E-05	0.00026
PGN_1857	rplX	50S ribosomal protein L24	1.44283	0.02505	0.054755
PGN_1858	rplN	50S ribosomal protein L14	1.35971	5.00E-05	0.00026
PGN_1859	rpsQ	30S ribosomal protein S17	1.46918	5.00E-05	0.00026
PGN_1860	rpmC	50S ribosomal protein L29	1.50863	5.00E-05	0.00026
PGN_1861	rplP	50S ribosomal protein L16	1.5161	5.00E-05	0.00026
PGN_1862	rpsC	30S ribosomal protein S3	1.38443	5.00E-05	0.00026
PGN_1863	rplV	50S ribosomal protein L22	1.57908	5.00E-05	0.00026
PGN_1864	rpsS	30S ribosomal protein S19	1.6038	5.00E-05	0.00026
PGN_1865	rplB	50S ribosomal protein L2	1.59935	5.00E-05	0.00026
PGN_1866	rplW	50S ribosomal protein L23	1.80594	5.00E-05	0.00026
PGN_1867	rplD	50S ribosomal protein L4	1.52848	0.0005	0.001921
PGN_1868	rplC	50S ribosomal protein L3	1.93212	5.00E-05	0.00026
PGN_1869	rpsJ	30S ribosomal protein S10	2.0155	5.00E-05	0.00026
PGN_1870		translation elongation factor G	1.45628	5.00E-05	0.00026
PGN_1871	rpsG	30S ribosomal protein S7	2.14457	5.00E-05	0.00026
PGN_1872	rpsL	30S ribosomal protein S12	1.9181	5.00E-05	0.00026
PGN_1873		conserved hypothetical protein	-0.653403	0.0226	0.050541

PGN_1874		putative 3-phosphoshikimate 1-carboxyvinyltransferase	-0.898094	0.004	0.011666
PGN_1875		conserved hypothetical protein	-0.898631	0.2654	0.379219
PGN_1876		putative ABC transporter membrane protein	-0.315193	0.703	0.792661
PGN_1877		Por secretion system protein porW/sprE	-0.180856	0.6162	0.71845
PGN_1878		conserved hypothetical protein	-0.208276	0.4625	0.577176
PGN_1879		hypothetical protein	-0.0907616	0.8069	0.868499
PGN_1880		malate dehydrogenase	-1.11093	0.00105	0.003606
PGN_1881		conserved hypothetical protein	-1.89068	5.00E-05	0.00026
PGN_1882		probable permease	-0.795697	0.00685	0.018484
PGN_1883		glutaminyl-tRNA synthetase	-0.505593	0.09045	0.157713
PGN_1884		probable alkaline phosphatase	0.0246523	0.9291	0.952922
PGN_1885		conserved hypothetical protein	0.291852	0.31545	0.433846
PGN_1886		putative NAD dependent epimerase	0.74926	0.0073	0.019549
PGN_1887		hypothetical protein	-0.0979642	0.80915	0.870041
PGN_1888		4-hydroxybutyrate CoA-transferase	0.973332	0.0011	0.003753
PGN_1889		conserved hypothetical protein	2.0584	5.00E-05	0.00026
PGN_1890	rpmG	50S ribosomal protein L33	2.24414	5.00E-05	0.00026
PGN_1891	rpmB	50S ribosomal protein L28	2.07858	5.00E-05	0.00026
PGN_1892		conserved hypothetical protein	0.154628	0.615	0.717444
PGN_1893		hypothetical protein	-0.38217	0.1763	0.273374
PGN_1894		conserved hypothetical protein	-1.33673	0.1036	0.175609
PGN_1895		conserved hypothetical protein	-0.180773	0.73675	0.816948
PGN_1896		galactose-1-phosphate transferase	0.191873	0.75845	0.834445
PGN_1897		putative transport related membrane protein	0.481747	0.38835	0.506616
PGN_1898		probable transport protein	0.552239	0.435	0.551259
PGN_1899		conserved hypothetical protein	-1.21132	5.00E-05	0.00026
PGN_1900		hypothetical protein	-0.619565	0.14075	0.226669
PGN_1901		transposase in ISPg1	-2.36026	5.00E-05	0.00026
PGN_1902		conserved hypothetical protein	-0.968148	0.05375	0.102816
PGN_1903		putative adenine-specific DNA methyltransferase	-0.83662	0.02235	0.050035
PGN_1904	hagB	hemagglutinin protein HagB	-0.356457	0.20655	0.311214
PGN_1905		conserved hypothetical protein	1.95369	5.00E-05	0.00026
PGN_1906	hagC	hemagglutinin protein HagC	-0.380751	0.1811	0.27919
PGN_1907		conserved hypothetical protein	0.996574	0.00065	0.00239
PGN_1908		hypothetical protein	2.85114	0.3418	0.460408
PGN_1909		conserved hypothetical protein	0.61457	0.23755	0.346875
PGN_1910		conserved hypothetical protein	0.643437	0.0915	0.159023
PGN_1911		transposase in ISPg3	-0.598349	0.0431	0.086503
PGN_1912		partial transposase in ISPg6	0.0670502	0.87835	0.919826
PGN_1913		transposase in ISPg3	-0.275317	0.35325	0.472405
PGN_1914		carboxyl-terminal processing protease	0.469948	0.12235	0.201145
PGN_1915		conserved hypothetical protein	-0.694477	0.03155	0.067372
PGN_1916		putative ABC transporter ATP-binding protein	0.604531	0.0286	0.061754
PGN_1917		putative ABC transporter ATP-binding protein	0.965317	0.0008	0.002848
PGN_1918		conserved hypothetical protein	0.499308	0.07815	0.139816
PGN_1919		conserved hypothetical protein	0.968256	0.00095	0.003316
PGN_1920		conserved hypothetical protein	1.01113	0.00075	0.002697
PGN_1921		probable transcriptional regulator	1.63324	5.00E-05	0.00026
PGN_1922		transposase in ISPg3	-0.368711	0.19625	0.29844
PGN_1923		hypothetical protein	-0.66993	0.17485	0.271521
PGN_1924		conserved hypothetical protein	-0.537439	0.1527	0.242611
PGN_1925		conserved hypothetical protein	-1.2525	5.00E-05	0.00026
PGN_1926		transposase in ISPg1	-2.43203	5.00E-05	0.00026
PGN_1927		conserved hypothetical protein	-1.0902	0.0001	0.000483
PGN_1928		conserved hypothetical protein	-0.797546	0.1238	0.203059
PGN_1929		conserved hypothetical protein	-0.987785	0.10725	0.180502
PGN_1930		conserved hypothetical protein	-1.1558	0.0049	0.013873
PGN_1931		conserved hypothetical protein	-0.933887	0.00145	0.004794
PGN_1932		conserved hypothetical protein	-0.78834	0.00505	0.014222
PGN_1933		conserved hypothetical protein	-0.558392	0.04945	0.096321
PGN_1934		conserved hypothetical protein	-0.947004	0.0103	0.026137
PGN_1935		hypothetical protein	-0.574071	0.03765	0.077297

PGN_1936		conserved hypothetical protein	-0.730693	0.21875	0.325223
PGN_1937		glucose-inhibited division protein A	-1.16407	0.00035	0.001436
PGN_1938	uvrC	excinuclease ABC C subunit	-0.725245	0.01075	0.027021
PGN_1939		putative D-tyrosyl-tRNA deacylase	-0.787797	0.0097	0.024821
PGN_1940		conserved hypothetical protein	-0.721586	0.481	0.593652
PGN_1941		putative deoxyribose-phosphate aldolase	-0.156635	0.59865	0.701831
PGN_1942		hypothetical protein	-0.158149	0.6297	0.730589
PGN_1943		putative polyprenyl synthetase	-0.233076	0.4187	0.536349
PGN_1944		conserved hypothetical protein	0.18269	0.54375	0.655517
PGN_1945		probable signal peptidase-related protein	-0.0617217	0.89465	0.932767
PGN_1946		signal peptidase I	-0.198476	0.5876	0.691014
PGN_1947	dapB	putative dihydrodipicolinate reductase	-0.296926	0.29645	0.41319
PGN_1948		deoxyguanosinetriphosphate triphosphohydrolase	-1.7196	5.00E-05	0.00026
PGN_1949		conserved hypothetical protein	-0.472718	0.1012	0.172226
PGN_1950		hypothetical protein	0.240203	0.7661	0.83987
PGN_1951		conserved hypothetical protein	-0.0317815	0.9146	0.944776
PGN_1952		hypothetical protein	0.185735	0.7157	0.801539
PGN_1953		TonB-dependent outer membrane receptor	0.760519	0.00725	0.01944
PGN_1954		probable DNA repair protein RecO	-0.509055	0.06785	0.125051
PGN_1955		phosphomannomutase	-0.240836	0.4073	0.523449
PGN_1956		hypothetical protein	-0.850223	0.02215	0.049744
PGN_1957		transposase in ISPg1	-2.44489	5.00E-05	0.00026
PGN_1959		CRISPR-associated protein Cas2	-1.08132	0.20675	0.311295
PGN_1960		CRISPR-associated protein Cas1	-1.34734	0.0009	0.003178
PGN_1961		CRISPR-associated protein Cas4	-1.42493	0.0087	0.022588
PGN_1962		conserved hypothetical protein	-1.84941	5.00E-05	0.00026
PGN_1963		conserved hypothetical protein	-1.68431	5.00E-05	0.00026
PGN_1964		probable CRISPR-associated helicase Cas3 core	-1.61869	5.00E-05	0.00026
PGN_1965		hypothetical protein	-2.06696	5.00E-05	0.00026
PGN_1966		conserved hypothetical protein	-1.73913	5.00E-05	0.00026
PGN_1967		putative sulfatase	1.29426	5.00E-05	0.00026
PGN_1968		conserved hypothetical protein	0.808245	0.0052	0.014586
PGN_1969	fmt	putative methionyl-tRNA formyltransferase	-1.40354	5.00E-05	0.00026
PGN_1970	rgpA	arginine-specific cysteine proteinase RgpA	-0.45801	0.22065	0.327134
PGN_1971		hypothetical protein	-0.779249	0.3419	0.460408
PGN_1972		conserved hypothetical protein	-1.01746	0.39745	0.514454
PGN_1973		probable phosphoglycerate mutase	-0.498605	0.08515	0.150443
PGN_1974		conserved hypothetical protein	-0.538576	0.07005	0.128345
PGN_1975		putative regulatory protein	-0.428611	0.1351	0.218643
PGN_1976		conserved hypothetical protein	0.414154	0.1465	0.234687
PGN_1977		conserved hypothetical protein	-1.32444	5.00E-05	0.00026
PGN_1978		conserved hypothetical protein	-1.89069	5.00E-05	0.00026
PGN_1979		primosomal protein N	-1.04494	0.0007	0.002543
PGN_1980		putative NADPH-dependent glutamate synthase	0.683976	0.01795	0.041629
PGN_1981		conserved hypothetical protein	0.968752	0.00185	0.00595
PGN_1982	trmD	putative tRNA guanine 1-methyltransferase	-0.310121	0.2554	0.367894
PGN_1983		putative ion transporter	0.262207	0.3558	0.474326
PGN_1984		hypothetical protein	-0.522747	0.30405	0.420612
PGN_1985		probable N-acetylmuramoyl-L-alanine amidase	-0.402639	0.34595	0.464662
PGN_1986		DNA-binding protein, histone-like family	-1.31094	5.00E-05	0.00026
PGN_1987		conserved hypothetical protein	-0.197888	0.468	0.5815
PGN_1988		conserved hypothetical protein	-1.13706	0.0004	0.001607
PGN_1989		conserved hypothetical protein with NIF3 domain	-1.12891	0.00035	0.001436
PGN_1990		conserved hypothetical protein	0.827243	0.0066	0.017946
PGN_1991		putative cell-cycle protein	0.284481	0.54845	0.658945
PGN_1992		putative helicase	-0.61867	0.12115	0.199635
PGN_1993		conserved hypothetical protein	-1.25456	5.00E-05	0.00026
PGN_1994		conserved hypothetical protein	-1.60403	5.00E-05	0.00026
PGN_1995		conserved hypothetical protein	-1.97251	5.00E-05	0.00026
PGN_1996	dapA	putative dihydrodipicolinate synthase	-0.754581	0.01055	0.026644
PGN_1997	bioD	putative dethiobiotin synthase	-0.489092	0.07145	0.130349
PGN_1998		immunoreactive 23 kDa antigen	-0.12948	0.668	0.760512

PGN_1999		putative dihydroorotate dehydrogenase	-0.622155	0.04595	0.090833
PGN_2000		hypothetical protein	-0.373781	0.301	0.417686
PGN_2001		Por secretion system protein porY/putative sensor histidine kinase	-0.259544	0.35555	0.474326
PGN_2002		conserved hypothetical protein	-0.83768	0.0084	0.021997
PGN_2003		single-stranded-DNA-specific exonuclease	-0.434934	0.21205	0.317926
PGN_2004		conserved hypothetical protein	-0.347379	0.54785	0.658776
PGN_2005		conserved hypothetical protein	-0.615881	0.04715	0.092689
PGN_2006		nicotinate phosphoribosyltransferase	-0.829945	0.00985	0.025085
PGN_2007	nadD	probable nicotinamide-nucleotide adenylyltransferase	-0.105597	0.90045	0.937239
PGN_2008		conserved hypothetical protein	-1.09958	0.0002	0.000895
PGN_2009		conserved hypothetical protein	0.914594	0.02075	0.047298
PGN_2010		putative secreted protein	1.18682	5.00E-05	0.00026
PGN_2011		putative helicase	0.659049	0.0198	0.045425
PGN_2012		outer membrane efflux protein	0.0880876	0.76	0.835122
PGN_2013		cation efflux system protein	0.0365201	0.90225	0.937341
PGN_2014		cation efflux system protein	0.345434	0.27335	0.387716
PGN_2015		conserved hypothetical protein	0.471559	0.5714	0.678478
PGN_2016		hypothetical protein	-0.512641	0.06665	0.123375
PGN_2017		conserved hypothetical protein	0.370581	0.2018	0.305212
PGN_2018		putative UDP-N-acetylglucosamine acyltransferase	-0.234756	0.6488	0.747454
PGN_2019		UDP-3-O-[3-hydroxymyristoyl] N-acetylglucosamine deacetylase	0.0277393	0.9454	0.960233
PGN_2020	lpxD	UDP-3-O-[3-hydroxymyristoyl] glucosamine N-acyltransferase	-0.46729	0.48765	0.599081
PGN_2021		orotidine 5'-phosphate decarboxylase	-0.34472	0.21725	0.323444
PGN_2022	prfA	peptide chain release factor 1	-0.613176	0.0347	0.072074
PGN_2023		putative phosphoribosylformylglycinamidine cyclo-ligase	-0.552844	0.0584	0.110519
PGN_2024		putative hemagglutinin	-0.404992	0.16395	0.256245
PGN_2025		conserved hypothetical protein	-0.782075	0.14875	0.237459
PGN_2026		putative abortive infection protein	-0.701638	0.0505	0.097919
PGN_2027		conserved hypothetical protein	0.18618	0.70925	0.79641
PGN_2028		conserved hypothetical protein	-0.374757	0.1866	0.285807
PGN_2029		conserved hypothetical protein	0.300082	0.273	0.387716
PGN_2030		conserved hypothetical protein	-0.0321576	0.90635	0.93879
PGN_2031		L-serine dehydratase	-0.138273	0.72035	0.804909
PGN_2032		putative alpha-galactosidase	0.435266	0.3312	0.450271
PGN_2033		ATP-dependent RNA helicase	1.78809	5.00E-05	0.00026
PGN_2034		probable sugar isomerase	1.36179	5.00E-05	0.00026
PGN_2035		putative peptidase	-0.258775	0.34345	0.461911
PGN_2036		hypothetical protein	-0.876201	0.1282	0.209308
PGN_2037	dps	DNA-binding protein from starved cells Dps	-3.72725	0.0024	0.007481
PGN_2038		conserved hypothetical protein	-0.0211341	0.94285	0.960233
PGN_2039		conserved hypothetical protein	0.045693	0.86605	0.90963
PGN_2040		conserved hypothetical protein	-0.513639	0.0652	0.121232
PGN_2041		putative alkaline protease AprF	-0.137671	0.63545	0.735657
PGN_2042		DNA mismatch repair protein MutS	0.769795	0.0084	0.021997
PGN_2043		conserved hypothetical protein	-0.11298	0.8324	0.885647
PGN_2044		conserved hypothetical protein	-0.193645	0.95885	0.970243
PGN_2045	pheT	phenylalanyl-tRNA synthetase beta subunit	0.220831	0.564	0.672416
PGN_2046		conserved hypothetical protein	0.793242	0.36575	0.483653
PGN_2047		conserved hypothetical protein	0.521522	0.44035	0.557375
PGN_2048		conserved hypothetical protein	-1.42869	5.00E-05	0.00026
PGN_2049		conserved hypothetical protein	0.759273	0.01195	0.029515
PGN_2050		ATP-dependent helicase	0.986927	0.03385	0.070723
PGN_2051		conserved hypothetical protein	1.11769	0.04315	0.086503
PGN_2052		conserved hypothetical protein	1.32372	0.03275	0.06924
PGN_2053		conserved hypothetical protein	-0.158701	0.5687	0.676026
PGN_2054		putative glycerol-3-phosphate cytidylyltransferase	0.60064	0.04405	0.087729
PGN_2055		putative 4-hydroxythreonine-4-phosphate dehydrogenase	-0.0406799	0.88575	0.925754
PGN_2056		conserved hypothetical protein	0.369013	0.2094	0.314839
PGN_2057		conserved hypothetical protein	-1.17402	0.0001	0.000483
PGN_2058		conserved hypothetical protein	-0.529792	0.13515	0.218643
PGN_2059		conserved hypothetical protein	1.39783	0.00915	0.023584
PGN_2060	hisS	histidyl-tRNA synthetase	1.56199	5.00E-05	0.00026

PGN_2061		probable dihydrofolate reductase	1.20507	5.00E-05	0.00026
PGN_2062	thyA	thymidylate synthase	-0.347984	0.2254	0.332785
PGN_2063		hypothetical protein	#NAME?	1	1
PGN_2064		putative peptidase M48 family	-0.911341	0.00235	0.007347
PGN_2065		putative Lys- and Rgp- gingipain domain protein	-2.72732	5.00E-05	0.00026
PGN_2066		putative ABC transporter ATP-binding protein	0.859249	0.0863	0.151845
PGN_2067		TPR domain protein	0.591056	0.10465	0.177247
PGN_2068	def	putative peptide deformylase	0.395285	0.14985	0.238438
PGN_2069		probable endonuclease	-0.6597	0.01875	0.043155
PGN_2070		conserved hypothetical protein	-1.90256	5.00E-05	0.00026
PGN_2071		probable ketopantoate reductase ApbA/PanE	-0.522922	0.07625	0.13734
PGN_2072		ABC transporter ATP-binding protein	0.835645	0.0049	0.013873
PGN_2073		conserved hypothetical protein	-0.523137	0.10325	0.175155
PGN_2074		conserved hypothetical protein	-1.90547	5.00E-05	0.00026
PGN_2075	uvrAII	excinuclease ABC A subunit	-0.263999	0.3663	0.48408
PGN_2076		conserved hypothetical protein	-1.47924	5.00E-05	0.00026
PGN_2077		conserved hypothetical protein	-1.27607	0.00015	0.000685
PGN_2078		conserved hypothetical protein	-0.904871	0.00285	0.008718
PGN_2079		mannose-1-phosphate guanylyltransferase	-1.48373	5.00E-05	0.00026
PGN_2080		conserved hypothetical protein	1.6173	5.00E-05	0.00026
PGN_2081		1-deoxy-D-xylulose 5-phosphate synthase	-0.854683	0.0058	0.016016
PGN_2082	trkA	putative potassium uptake protein TrkA	-0.876887	0.00335	0.009989
PGN_2083		potassium uptake protein TrkH	-0.36181	0.20835	0.313482
PGN_2084		conserved hypothetical protein	0.283163	0.5796	0.684777
PGN_2085		putative Fe-S oxidoreductases	0.195042	0.50125	0.61437
PGN_2086		probable acetyltransferase	0.590962	0.03685	0.075947
PGN_2087		glycosyltransferase	-0.537377	0.05145	0.099489
PGN_2088		conserved hypothetical protein	-0.89121	0.00955	0.024526
PGN_2089		conserved hypothetical protein	-1.45412	0.00795	0.021104
PGN_2090	husB	conserved hypothetical protein	-0.87859	0.03645	0.075269
PGN_2091	husA	conserved hypothetical protein	-1.17726	0.00635	0.01731
PGN_r0001			-0.108765	0.81385	0.87289
PGN_r0002			-0.0690001	0.8346	0.886411
PGN_r0003			-2.29177	0.02455	0.053828
PGN_r0004			-0.100589	0.826	0.881923
PGN_r0005			-0.0040235	0.99135	0.991816
PGN_r0006			-1.7307	0.04315	0.086503
PGN_r0007			-2.39873	0.01635	0.038506
PGN_r0008			0.0066057	0.98455	0.988314
PGN_r0009			-0.566805	0.07155	0.130419
PGN_r0010			-0.120924	0.794	0.858132
PGN_r0011			-0.0250106	0.93715	0.956825
PGN_r0012			-3.20771	0.0432	0.086522
PGN_t0001			-1.86596	0.0911	0.158587
PGN_t0002			-2.1311	5.00E-05	0.00026
PGN_t0003			-0.788691	0.4074	0.523449
PGN_t0004			-0.147257	0.6371	0.736366
PGN_t0005			-0.374893	0.2315	0.339672
PGN_t0006			-0.43351	0.4234	0.540743
PGN_t0007			-2.43928	0.24845	0.360075
PGN_t0008			1.48797	0.067	0.123822
PGN_t0009			1.45239	5.00E-05	0.00026
PGN_t0010			1.10293	0.004	0.011666
PGN_t0011			1.14343	0.0124	0.030379
PGN_t0012			-0.0195976	0.96465	0.974722
PGN_t0013			1.57891	5.00E-05	0.00026
PGN_t0014			1.34284	0.00075	0.002697
PGN_t0015			2.44261	0.0228	0.050935
PGN_t0016			1.39007	0.00535	0.014967
PGN_t0017			-3.16436	5.00E-05	0.00026
PGN_t0018			0.914993	0.0059	0.016208
PGN_t0019			0.405231	0.44865	0.565193

PGN_t0020		0.405688	0.5448	0.65604
PGN_t0021		-0.640235	0.0516	0.099508
PGN_t0022		0.137482	0.8396	0.890193
PGN_t0023		-2.34459	5.00E-05	0.00026
PGN_t0024		-1.3195	0.0932	0.161582
PGN_t0025		-1.14187	0.11585	0.192842
PGN_t0026		1.34273	0.18585	0.285274
PGN_t0027		1.05158	0.24375	0.354228
PGN_t0028		0.0343399	0.9327	0.955591
PGN_t0029		-0.133127	0.7022	0.792254
PGN_t0030		-0.103179	0.7616	0.836228
PGN_t0031	inf		0.3628	0.481345
PGN_t0032		-0.69549	0.01435	0.034404
PGN_t0033		1.03817	0.27315	0.387716
PGN_t0034		1.22578	0.02745	0.059452
PGN_t0035		1.37489	0.0006	0.002241
PGN_t0036		1.57244	5.00E-05	0.00026
PGN_t0037		-0.858642	0.2034	0.30712
PGN_t0038		0.326414	0.5793	0.684777
PGN_t0039		0.336563	0.24595	0.356912
PGN_t0040		-0.162555	0.55195	0.662149
PGN_t0041		-1.7043	0.00095	0.003316
PGN_t0042		-0.241236	0.464	0.57837
PGN_t0043		-0.36834	0.219	0.325289
PGN_t0044		-0.283399	0.30005	0.416703
PGN_t0045		-0.975927	0.01535	0.036433
PGN_t0046		-1.74059	0.00025	0.00108
PGN_t0047		2.59636	0.00235	0.007347
PGN_t0048		1.5537	5.00E-05	0.00026
PGN_t0049		1.1889	0.00245	0.007615
PGN_t0050		-0.602885	0.063	0.117966
PGN_t0051		-0.785538	0.00675	0.018283
PGN_t0052		-0.851205	0.0046	0.013217
PGN_t0053		0.803697	0.3641	0.48237

Gene ID	Gene Name	Product	log2 Fold Change	p-value	q-value
AB57_0001	tyrS	tyrosyl-tRNA synthetase	1.134754213	3.82E-12	3.25E-11
AB57_0002	anmK	anhydro-N-acetylmuramic acid kinase	-0.506366168	3.35E-05	8.68E-05
AB57_0003		hydrolase	-0.620770596	5.26E-09	2.50E-08
AB57_0004		iron-sulfur cluster insertion protein ErpA	-0.169365265	0.15027	0.191526
AB57_0005		RND type efflux pump	-1.154301227	2.76E-17	5.89E-16
AB57_0006		RND type efflux pump	-0.917931555	9.98E-09	4.56E-08
AB57_0007		transposase subunit	-0.721165651	3.24E-06	1.00E-05
AB57_0008		transposase 1	-0.369727499	0.009139	0.015109
AB57_0009		beta-lactamase	1.779682641	3.10E-13	3.11E-12
AB57_0010		hypothetical protein	0.176823102	0.116001	0.151608
AB57_0011		transposase subunit	-0.805782769	4.69E-07	1.67E-06
AB57_0012		transposase 1	-0.358434474	0.013102	0.02095
AB57_0013		RND type efflux pump	-0.219990112	0.075295	0.102878
AB57_0014		ABC transporter, ATP-binding protein	1.301876895	7.07E-17	1.41E-15
AB57_0015		DedA family protein	-0.054192635	0.623667	0.672172
AB57_0016		cytochrome b562	-0.039908672	0.756418	0.792846
AB57_0017	gyrB	DNA gyrase, B subunit	0.390735789	0.034284	0.050197
AB57_0018	recF	recombination protein F	0.086388794	0.479127	0.539492
AB57_0019	dnaN	DNA polymerase III, beta subunit	0.830612846	1.79E-08	7.86E-08
AB57_0020	dnaA	chromosomal replication initiation protein	0.596231753	8.31E-06	2.39E-05
AB57_0021	rpmH	50S ribosomal protein L34	0.826582549	1.68E-06	5.51E-06
AB57_0022	rnpA	ribonuclease P protein component	1.368610705	5.91E-11	3.98E-10
AB57_0023		hypothetical protein	1.886098027	4.85E-17	9.87E-16
AB57_0024		putative inner membrane protein translocase component YidC	1.458295782	2.71E-11	1.95E-10
AB57_0025		probable tRNA modification GTPase TrmE	1.416752971	3.58E-15	5.16E-14
AB57_0026	trmE	tRNA modification GTPase TrmE	1.038053657	1.09E-12	1.02E-11
AB57_0027		hypothetical protein	-0.318944927	0.00666	0.011339
AB57_0028		cation diffusion facilitator family transporter	0.117193264	0.39885	0.459447
AB57_0029		thiol:disulfide interchange protein DsbC	-0.583631911	1.63E-08	7.22E-08
AB57_0030		transglycosylase-associated protein	-1.128605061	3.56E-12	3.04E-11
AB57_0031	hpt	hypoxanthine phosphoribosyltransferase	0.916708235	2.07E-10	1.27E-09
AB57_0032		hypothetical protein	0.46718453	0.011905	0.019211
AB57_0033	guaD	guanine deaminase	0.648911436	1.63E-07	6.19E-07
AB57_0034		rieske protein	-0.357595963	0.022979	0.034917
AB57_0035		glutathionylspermidine synthase	0.72792576	6.41E-08	2.60E-07
AB57_0036		lipoprotein, putative	0.169210229	0.352018	0.411652
AB57_0037		integral membrane protein TerC	0.29525729	0.010169	0.016619
AB57_0038		PAP2 superfamily protein	0.133752234	0.266728	0.323359
AB57_0039	ltrA	low temperature requirement protein LtrA	-0.568631447	6.20E-08	2.52E-07
AB57_0040	mpl	UDP-N-acetylmuramate:L-alanyl-gamma-D-glutamyl-meso-diam	0.703738499	2.08E-09	1.08E-08
AB57_0041		transmembrane signal peptide protein	-0.171732201	0.124195	0.161462
AB57_0042	purE	phosphoribosylaminoimidazole carboxylase, catalytic subunit	1.566439118	1.25E-16	2.38E-15
AB57_0043	purK	phosphoribosylaminoimidazole carboxylase, ATPase subunit	1.477993236	1.75E-10	1.09E-09
AB57_0044		transglycolase	0.104083923	0.395748	0.456159
AB57_0045		hypothetical protein	-0.333066186	0.009757	0.016045
AB57_0046		matrixin superfamily	0.427294174	0.005164	0.009009
AB57_0047		matrixin superfamily	-0.265632608	0.033186	0.048783
AB57_0048	dnaK	molecular chaperone DnaK	0.307398574	0.092038	0.123246
AB57_0049	grpE	co-chaperone GrpE	-0.31781467	0.03188	0.047086
AB57_0050		putative transcriptional regulator	-0.108475126	0.553323	0.610359
AB57_0051		metallo-beta-lactamase family protein	-0.727775654	1.63E-09	8.65E-09
AB57_0052		lipoprotein, putative	-0.514472202	0.000204	0.000459
AB57_0053		lipoprotein, putative	-1.058470967	1.31E-20	4.80E-19
AB57_0054		esterase	-0.73132608	6.87E-10	3.89E-09
AB57_0055		peptidyl-prolyl cis-trans isomerase	-0.095907746	0.413272	0.474289
AB57_0057		hypothetical protein	-0.671615691	4.74E-11	3.26E-10
AB57_0058		putative flavoprotein	-0.35152073	0.008006	0.013427

AB57_0059		peptidylprolyl isomerase, fkbp-type	1.01288012	2.44E-17	5.28E-16
AB57_0060	lspA	lipoprotein signal peptidase	0.690624951	1.07E-07	4.21E-07
AB57_0061	ileS	isoleucyl-tRNA synthetase	0.898299984	3.04E-06	9.46E-06
AB57_0062	ribF	riboflavin biosynthesis protein RibF	0.292097451	0.008688	0.014466
AB57_0063		C4-dicarboxylate transporter/malic acid transport protein	-0.439112318	6.05E-05	0.000149
AB57_0064		putative MTA/SAH nucleosidase	-0.540504252	5.68E-07	1.99E-06
AB57_0065		transcriptional regulator, TetR family	-0.001786068	0.986606	0.988476
AB57_0066		aliphatic sulfonates import ATP-binding protein SsuB	0.929777341	3.41E-11	2.42E-10
AB57_0067		aliphatic sulfonates transport permease protein SsuC	0.110128466	0.455166	0.51565
AB57_0068		alkanesulfonate monooxygenase	-0.706795177	6.29E-06	1.85E-05
AB57_0069		aliphatic sulfonates-binding protein	-1.490849575	0.000259	0.000571
AB57_0070		aliphatic sulfonates-binding protein	-1.784574643	7.42E-06	2.16E-05
AB57_0071	argA	N-acetylglutamate synthase	-0.178208077	0.083335	0.11278
AB57_0072		hypothetical protein	-1.48611507	4.15E-35	1.18E-32
AB57_0073		hypothetical protein	-0.586810812	1.03E-08	4.68E-08
AB57_0074		short chain dehydrogenase	-0.650723032	5.22E-07	1.84E-06
AB57_0075		phosphoglycolate phosphatase 2	0.164757168	0.105031	0.13884
AB57_0076	ubiG	3-demethylubiquinone-9 3-methyltransferase	0.103235967	0.319405	0.378297
AB57_0077		thiol:disulfide interchange protein DsbA	0.069677824	0.578594	0.632997
AB57_0078		transcriptional regulator, TetR family	-0.463913899	3.42E-05	8.85E-05
AB57_0079		transcriptional regulator, TetR family	0.265996352	0.013963	0.022169
AB57_0080		putative oxidoreductase	1.533176254	2.06E-40	9.53E-38
AB57_0081		fatty acid desaturase	0.802544252	1.96E-11	1.45E-10
AB57_0082	rph	ribonuclease PH	1.411958774	1.05E-20	3.92E-19
AB57_0084		phospholipase C, phosphocholine-specific	-0.358349351	0.004018	0.00714
AB57_0085	nadC	nicotinate-nucleotide diphosphorylase	1.216136387	7.42E-24	4.57E-22
AB57_0086		hypothetical protein	0.085596148	0.609911	0.660425
AB57_0087		N-acetyl-anhydromuranmyl-L-alanine amidase	-0.21227742	0.106303	0.140317
AB57_0088	mviN	integral membrane protein MviN	0.95492806	4.41E-11	3.06E-10
AB57_0089	fklB	immunoreactive 21 kD antigen PG10	-0.224631394	0.042483	0.060997
AB57_0090		peptidyl-prolyl cis-trans isomerase Mip	0.081337436	0.485739	0.545609
AB57_0091		tyrosine-protein kinase ptk	0.909877266	8.23E-07	2.82E-06
AB57_0092		protein-tyrosine-phosphatase ptp	0.719250208	4.50E-09	2.19E-08
AB57_0093		polysaccharide export protein	0.543584357	0.000253	0.000559
AB57_0094		VI polysaccharide biosynthesis protein VipA/tviB	1.358791243	3.83E-14	4.48E-13
AB57_0095		VI polysaccharide biosynthesis protein VipB/tviC	1.349661255	1.55E-11	1.17E-10
AB57_0096		polysaccharide biosynthesis protein	0.084785797	0.575477	0.629774
AB57_0097		hypothetical protein	0.542644084	0.001659	0.003173
AB57_0098		hypothetical protein	-0.194975984	0.153753	0.195695
AB57_0099		glycosyl transferase, group 1	-0.354191708	0.030943	0.045905
AB57_0100		hypothetical protein	-0.316337565	0.014224	0.022529
AB57_0101		hypothetical protein	-0.476855072	8.88E-05	0.000213
AB57_0102		putative glycosyl transferase family 1	0.327795918	0.005545	0.0096
AB57_0103		glycosyl transferase, group 1	-0.069224548	0.639686	0.68676
AB57_0104		UDP-glucose 4-epimerase	0.524308684	1.66E-05	4.53E-05
AB57_0105		polyprenol phosphate:N-acetyl-hexosamine 1-phosphate transf	0.951933252	8.44E-10	4.70E-09
AB57_0106		acetyltransferase	0.34510268	0.002985	0.005426
AB57_0107		nucleotide sugar epimerase/dehydratase	0.460675346	0.00264	0.004847
AB57_0108	galE	UDP-glucose 4-epimerase	0.721101154	2.25E-09	1.16E-08
AB57_0109		hypothetical protein	-0.454567973	1.06E-05	2.98E-05
AB57_0110		acyltransferase	-0.271856448	0.061728	0.085894
AB57_0111	galU	UTP-glucose-1-phosphate uridylyltransferase	-0.149833442	0.223146	0.275306
AB57_0112		NDP-sugar dehydrogenase	-0.139511969	0.404906	0.4657
AB57_0113	pgi	glucose-6-phosphate isomerase	0.181159698	0.098188	0.1304
AB57_0114	galE	UDP-glucose 4-epimerase	0.149769961	0.206212	0.256207
AB57_0115		phosphomannomutase	0.415703552	0.000306	0.000663
AB57_0116		L-lactate permease	0.6755914	9.25E-11	6.03E-10
AB57_0117		DNA-binding transcriptional repressor LldR	0.522537814	1.34E-05	3.71E-05

AB57_0118		L-lactate dehydrogenase	0.443701647	6.50E-05	0.000159
AB57_0119		D-lactate dehydrogenase	0.315380525	0.004944	0.008641
AB57_0120	araT	aromatic amino acid aminotransferase	0.587047151	0.00032	0.000692
AB57_0121		transcriptional regulator, GntR family	0.992581887	5.15E-06	1.54E-05
AB57_0122	prpB	2-methylisocitrate lyase	1.648610564	4.26E-48	3.94E-45
AB57_0123		methylcitrate synthase	0.940815947	2.63E-13	2.70E-12
AB57_0124	acnD	aconitate hydratase	0.645291069	1.70E-05	4.62E-05
AB57_0125		hypothetical protein	-0.633997366	3.62E-07	1.31E-06
AB57_0126		hypothetical protein	-0.368787342	0.001184	0.00232
AB57_0127		probable transposase (ISN1)	-0.558663834	0.000512	0.001069
AB57_0128		hypothetical protein	-0.457360938	0.031891	0.047086
AB57_0129		transposase, Mutator family	-0.298099668	0.016448	0.02569
AB57_0130		short-chain dehydrogenase/reductase SDR	-0.299031409	0.03133	0.046394
AB57_0131		hypothetical protein	-0.847293213	1.46E-07	5.57E-07
AB57_0132		dual specificity pseudouridine synthase	0.947309557	6.14E-11	4.12E-10
AB57_0133		hypothetical protein	-0.753555201	2.32E-10	1.40E-09
AB57_0134		hypothetical protein	-0.411965579	0.000149	0.000343
AB57_0135		TonB-dependent siderophore receptor	-0.200008422	0.073709	0.100785
AB57_0136		hypothetical protein	-0.322057744	0.024908	0.037616
AB57_0137		leucine-responsive regulatory protein	0.051742489	0.766994	0.80234
AB57_0138		D-amino acid dehydrogenase small subunit	0.485647683	0.000142	0.000329
AB57_0139	dadX	alanine racemase	0.014195574	0.889498	0.909909
AB57_0140		endoribonuclease L-PSP family protein	-0.185315632	0.148	0.188892
AB57_0141		D-serine/D-alanine/glycine transporter	-0.283661197	0.064395	0.089169
AB57_0142		D-serine/D-alanine/glycine transporter	-0.134290589	0.368293	0.428113
AB57_0143		transcriptional regulator, LysR family	-0.63711057	8.56E-05	0.000206
AB57_0144	mmsA	methylmalonate-semialdehyde dehydrogenase	-0.225073382	0.098243	0.130427
AB57_0145	mmsB	3-hydroxyisobutyrate dehydrogenase	-0.015420239	0.889444	0.909909
AB57_0146		acetyl-coenzyme A synthetase	-0.023013591	0.848409	0.875137
AB57_0147		acyl-CoA dehydrogenase	0.494277057	1.76E-05	4.75E-05
AB57_0148		short-chain enoyl-CoA hydratase	0.816398997	1.60E-12	1.44E-11
AB57_0149		enoyl-CoA hydratase/isomerase family protein	0.534048264	1.29E-07	4.97E-07
AB57_0150		shikimate transporter	0.005810404	0.955127	0.964692
AB57_0151		homoserine lactone synthase	-0.461615336	0.059002	0.082412
AB57_0152		hypothetical protein	-0.609977226	0.021113	0.032387
AB57_0153		eR transcriptional regulator	-0.463224342	0.024379	0.036888
AB57_0154		acyl-CoA synthetase/AMP-acid ligase	-0.172703272	0.258273	0.314449
AB57_0155		acyl-CoA dehydrogenase	-0.114123103	0.475781	0.53605
AB57_0156		acyl carrier protein	-0.63614359	0.008923	0.014805
AB57_0157		amino acid adenylation	-0.047407664	0.687579	0.730417
AB57_0158		polyketide cyclase/dehydrase family	-0.134636233	0.2674	0.323962
AB57_0159		hypothetical protein	-0.330026062	0.006317	0.010821
AB57_0160		NAD dependent epimerase/dehydratase family	-0.276177568	0.01088	0.017679
AB57_0161		phosphopantethiene-protein transferase	-0.49628954	7.25E-05	0.000176
AB57_0162		BolA family protein	0.057400264	0.655254	0.700908
AB57_0163		hypothetical protein	-0.071966241	0.536523	0.593997
AB57_0164		ParA family protein	0.11223997	0.256089	0.312304
AB57_0165		hypothetical protein	-0.57791667	2.55E-08	1.10E-07
AB57_0166		hypothetical protein	-0.723344085	5.76E-09	2.73E-08
AB57_0167		protein DedA	-0.884150541	9.48E-11	6.17E-10
AB57_0168		DoxX family protein	-0.629849303	1.43E-06	4.76E-06
AB57_0169		hypothetical protein	0.263771688	0.028639	0.042749
AB57_0170		GMP synthase	2.081226659	1.07E-17	2.47E-16
AB57_0171		putative adenylyltransferase	-1.125255074	4.79E-19	1.36E-17
AB57_0172		putative transcriptional regulator	0.130624075	0.596804	0.648891
AB57_0173		hypothetical protein	0.336330299	0.085839	0.115577
AB57_0174		pirin domain protein	-0.248355849	0.092153	0.123315
AB57_0175		OsmC family protein	0.273269618	0.024056	0.036449

AB57_0176		glutathione S-transferase	-0.56304975	0.000155	0.000356
AB57_0177		hypothetical protein	0.467332267	7.49E-06	2.18E-05
AB57_0178	argS	arginyl-tRNA synthetase	0.771747976	1.54E-05	4.21E-05
AB57_0179		malate dehydrogenase	0.108381384	0.481159	0.541286
AB57_0180		melanin biosynthesis protein TyrA	0.367651019	0.000623	0.001281
AB57_0181		homoserine/homoserine lactone efflux protein	-0.514551348	1.20E-06	4.02E-06
AB57_0182		high affinity Zn transport protein	0.730264996	2.03E-09	1.06E-08
AB57_0183		zinc import ATP-binding protein ZnuC	0.168628158	0.132472	0.171081
AB57_0184		transcriptional regulator, Fur family	-0.065430196	0.528141	0.585943
AB57_0185		high affinity Zn transport protein	0.642666378	3.07E-08	1.30E-07
AB57_0186	atpI	ATP synthase F0, I subunit	0.700974297	1.77E-07	6.67E-07
AB57_0187	atpB	F0F1 ATP synthase subunit A	1.667335204	6.40E-15	8.94E-14
AB57_0188	atpE	ATP synthase F0, C subunit	1.614933495	1.04E-11	8.12E-11
AB57_0189	atpF	F0F1 ATP synthase subunit B	1.854800068	2.14E-15	3.25E-14
AB57_0190	atpH	F0F1 ATP synthase subunit delta	1.942890025	7.26E-17	1.44E-15
AB57_0191	atpA	F0F1 ATP synthase subunit alpha	0.963547686	1.64E-06	5.38E-06
AB57_0192	atpG	F0F1 ATP synthase subunit gamma	0.79397996	2.46E-05	6.53E-05
AB57_0193	atpD	F0F1 ATP synthase subunit beta	0.50330372	0.005253	0.009142
AB57_0194	atpC	F0F1 ATP synthase subunit epsilon	0.610414076	0.001104	0.002177
AB57_0195		lipoprotein, putative	-0.169254038	0.119303	0.15562
AB57_0196		glutathione peroxidase	0.350106691	0.001121	0.002207
AB57_0197		transcriptional regulator AraC family	-0.638652147	1.37E-07	5.25E-07
AB57_0198		major facilitator superfamily MFS_1	-0.52626606	3.20E-05	8.34E-05
AB57_0199		transcriptional regulator, TetR family	-0.752395159	3.68E-06	1.13E-05
AB57_0200		transporter, drug/metabolite exporter family	0.033588241	0.749761	0.787202
AB57_0201		protein YrdC	-0.10795814	0.380139	0.440174
AB57_0202		DNA protecting protein DprA	-0.052365937	0.717067	0.758042
AB57_0203		peptidoglycan-binding LysM	0.068761004	0.612389	0.662139
AB57_0204	def	peptide deformylase	0.115632151	0.456885	0.517282
AB57_0205		hypothetical protein	1.266528696	3.13E-12	2.71E-11
AB57_0206		TonB-dependent copper receptor	1.845451244	1.21E-13	1.29E-12
AB57_0207		hypothetical protein	0.470634427	0.001793	0.003415
AB57_0208		hypothetical protein	-0.07790362	0.619142	0.668074
AB57_0209		putative transcription regulator protein	-0.690957244	0.00551	0.009553
AB57_0212		putative acetyltransferase	0.736391793	2.53E-09	1.29E-08
AB57_0213	cysK	cysteine synthase A	0.367009342	0.008017	0.013441
AB57_0214		transglycosylase SLT domain protein	-0.252840168	0.024501	0.037047
AB57_0215		NADPH-dependent fmn reductase	-0.16095675	0.182726	0.229962
AB57_0216		hypothetical protein	-0.273191003	0.045191	0.064385
AB57_0217		transcriptional regulator SoxR-family	-0.243206349	0.065495	0.090625
AB57_0218		glycerophosphoryl diester phosphodiesterase	0.056496293	0.660062	0.705235
AB57_0219		hypothetical protein	-0.619219596	0.000696	0.001422
AB57_0220		hypothetical protein	1.641539101	8.32E-12	6.66E-11
AB57_0221		hypothetical protein	-1.445784932	8.72E-18	2.05E-16
AB57_0222		hypothetical protein	-0.165929944	0.286784	0.344625
AB57_0223		DNA polymerase IV	-0.101999247	0.383777	0.444019
AB57_0226		inner membrane transport protein YieO	-0.608764758	1.68E-08	7.42E-08
AB57_0227		hypothetical protein	-0.573205177	4.45E-06	1.35E-05
AB57_0228		protein YegH	-0.327806495	0.019436	0.029976
AB57_0229		hypothetical protein	0.351851105	0.015013	0.023628
AB57_0230		hypothetical protein	-0.268951516	0.015589	0.024399
AB57_0231		major facilitator superfamily MFS_1	-0.510476032	3.36E-07	1.21E-06
AB57_0232	parC	DNA topoisomerase IV subunit A	0.313482487	0.009794	0.016092
AB57_0233		long-chain-fatty-acid--CoA ligase	0.831900337	3.22E-06	9.99E-06
AB57_0234		hypothetical protein	0.004765427	0.965838	0.972673
AB57_0235		hypothetical protein	0.131322486	0.26576	0.322398
AB57_0236	ppa	inorganic pyrophosphatase	1.628363649	2.45E-25	2.06E-23
AB57_0237		outer membrane protein OprE3	-0.089791994	0.584105	0.637314

AB57_0239		hypothetical protein	-0.741109457	6.80E-08	2.75E-07
AB57_0240		putative dihydrodipicolinate synthase	-0.200849593	0.195637	0.244382
AB57_0241		class II aldolase/adducin domain protein	-0.64752669	9.87E-06	2.79E-05
AB57_0242		transcriptional regulator, GntR family	-0.268474592	0.044505	0.063506
AB57_0243		competence protein ComM	-0.11025855	0.487431	0.547113
AB57_0244		transposase protein A	-0.074189695	0.52085	0.579418
AB57_0245		transposition protein B	0.072738804	0.522547	0.581131
AB57_0246		transposition helper protein C	-0.102559315	0.37589	0.436045
AB57_0247		hypothetical protein	-0.4008538	0.002563	0.004721
AB57_0248		hypothetical protein	-0.72214077	1.30E-07	5.00E-07
AB57_0249		FAD-dependent pyridine nucleotide-disulphide oxidoreductase	-0.344265236	0.001145	0.002251
AB57_0250	trxB	thioredoxin-disulfide reductase	0.255845517	0.019494	0.030053
AB57_0251	arsH	arsenical resistance protein ArsH	0.090211883	0.483394	0.543469
AB57_0252	arsB	arsenical-resistance protein	0.017194214	0.883898	0.905433
AB57_0253		arsenate reductase	0.492254978	0.003245	0.005871
AB57_0254		arsenical resistance operon repressor	0.834938527	0.004491	0.007928
AB57_0255	arsC	arsenate reductase	0.922647273	0.001442	0.002778
AB57_0256		universal stress protein	-0.022220045	0.892245	0.912215
AB57_0257		ISPpu12 hypothetical protein	-0.233805098	0.025937	0.038995
AB57_0258		ISPpu12 hypothetical protein	-0.166217352	0.367878	0.427765
AB57_0259	lspA	lipoprotein signal peptidase	-0.133328884	0.214392	0.265301
AB57_0260		ISPpu12 transposase	0.021065985	0.841376	0.86885
AB57_0261		hypothetical protein	0.16078835	0.156584	0.199115
AB57_0262	topA	DNA topoisomerase I	0.553575741	2.32E-06	7.36E-06
AB57_0263		Ssb protein	0.503207905	0.010413	0.016973
AB57_0264		hypothetical protein	-0.148195902	0.343978	0.404307
AB57_0265	folP	dihydropteroate synthase	-0.072349209	0.633748	0.680658
AB57_0266		NTP-binding protein	0.364340109	0.014322	0.022646
AB57_0267		hypothetical protein	0.156222546	0.310831	0.369467
AB57_0268		insertion sequence IS6100	0.565907983	0.00069	0.00141
AB57_0269		hypothetical protein	0.56350379	9.16E-06	2.61E-05
AB57_0270		hypothetical protein	1.076365244	6.71E-14	7.41E-13
AB57_0271	merA	putative mercuric reductase	0.931672846	2.89E-09	1.46E-08
AB57_0272		putative mercury transport protein MerC	0.754504835	3.24E-11	2.31E-10
AB57_0273	tetR	tetracycline repressor protein, class A	-0.215745558	0.088993	0.119519
AB57_0274		hypothetical protein	0.636662962	0.000157	0.00036
AB57_0275	tetA	tetracycline resistance protein, class A	0.577228283	3.49E-08	1.47E-07
AB57_0276		regulator protein PecM	0.580641521	8.51E-07	2.90E-06
AB57_0277		hypothetical protein	0.560443429	0.00053	0.001103
AB57_0278		isochorismatase hydrolase	0.797656573	4.22E-08	1.75E-07
AB57_0279		transposase ISSod9	0.180761558	0.24722	0.302449
AB57_0280	cat	chloramphenicol acetyltransferase	-0.307517132	0.032482	0.047844
AB57_0281		transposase Tn3	0.012973362	0.913692	0.929775
AB57_0282		transposon Tn3 resolvase	0.08717361	0.425638	0.48697
AB57_0283		beta-lactamase TEM	0.068086242	0.676073	0.719847
AB57_0284		transposase InsB3 for insertion sequence IS26	0.133086089	0.23839	0.292842
AB57_0285		transposase IS26	0.40148112	0.000956	0.001907
AB57_0286		resolvase IS26	-0.395224153	0.024973	0.037668
AB57_0287		transposase S26	0.109617305	0.282812	0.340405
AB57_0288		aminoglycoside 3'-phosphotransferase aphA1	-0.475578942	0.001866	0.003547
AB57_0289		transposase InsB3 for insertion sequence IS26	0.114337238	0.288705	0.346483
AB57_0290		IntI1 integrase	-0.38072282	0.007352	0.012416
AB57_0291		aminoglycoside N(3')-acetyltransferase I aacC1	-0.342375622	0.032054	0.047307
AB57_0292		acetyltransferase, gnat family	0.003021093	0.984429	0.987062
AB57_0293		aminoglycoside resistance protein	0.61310553	1.38E-05	3.80E-05
AB57_0294	folP	dihydropteroate synthase	-0.064090516	0.680593	0.723411
AB57_0295		acetyltransferase, gnat family	0.205959559	0.183407	0.230739
AB57_0296		hypothetical protein	0.539246033	2.01E-05	5.39E-05

AB57_0297		invertase/recombinase protein	0.875582785	1.21E-11	9.29E-11
AB57_0298		transcriptional regulator	0.57884374	4.53E-05	0.000114
AB57_0299		hypothetical protein ISPpu12	0.053176132	0.629705	0.677199
AB57_0300		hypothetical protein ISPpu12	-0.012058492	0.931619	0.944381
AB57_0301		heavy metal detoxification protein	-0.200198405	0.099614	0.132152
AB57_0302	lspA	lipoprotein signal peptidase	-0.063129531	0.559825	0.615923
AB57_0303		ISPpu12 transposase	0.047806749	0.642309	0.689052
AB57_0304		universal stress protein	-0.079095679	0.510041	0.569168
AB57_0305		sulfate permease	0.347304725	0.007181	0.012166
AB57_0306		hypothetical protein	-0.408846662	0.00275	0.005034
AB57_0307		Mg chelatase-related protein	-0.177407302	0.193922	0.242649
AB57_0308		hypothetical protein	-0.651691404	3.16E-10	1.88E-09
AB57_0309		nitrogen regulatory protein P-II	-0.595400792	4.50E-06	1.37E-05
AB57_0310	amt	ammonium transporter	-0.350307277	0.008151	0.01364
AB57_0311	nrdR	transcriptional regulator NrdR	0.060301279	0.560777	0.616789
AB57_0312	ribD	riboflavin biosynthesis protein RibD	0.333139687	0.002038	0.003838
AB57_0313		site-specific DNA-methyltransferase	0.394170403	0.012013	0.019358
AB57_0314	ribE	riboflavin synthase subunit alpha	0.107497181	0.396414	0.456784
AB57_0315		hypothetical protein	0.429223522	0.00265	0.004864
AB57_0316		hypothetical protein	0.004558115	0.968348	0.974405
AB57_0317		DNA polymerase III, chi subunit	0.097781894	0.35199	0.411652
AB57_0318	pepA	leucyl aminopeptidase	0.218644502	0.128239	0.166369
AB57_0319		permease YjgP/YjgQ family protein	0.404207833	0.001236	0.002412
AB57_0320		permease YjgP/YjgQ family protein	0.799747625	6.10E-08	2.49E-07
AB57_0321	gpmI	phosphoglyceromutase	1.278575042	6.60E-11	4.40E-10
AB57_0322		putative periplasmic carboxyl-terminal protease	0.473106959	4.31E-05	0.000109
AB57_0323		type 4 fimbriae expression regulatory protein PilR	-0.381866252	0.001421	0.002741
AB57_0324		sensor protein histidine kinase	-0.392486954	0.000231	0.000514
AB57_0325		response regulator	-0.475038098	0.000144	0.000333
AB57_0326		D-alanyl-D-alanine carboxypeptidase family protein	-0.629590095	0.000775	0.001573
AB57_0327	thrC	threonine synthase	1.599092229	2.37E-15	3.55E-14
AB57_0328		homoserine dehydrogenase	0.827518823	4.20E-08	1.75E-07
AB57_0329		thiol:disulfide interchange protein	-0.114201667	0.253341	0.309156
AB57_0330	xerD	tyrosine recombinase XerD	0.063334248	0.671115	0.715435
AB57_0331	feoA	putative ferrous iron transport protein A	-0.634841317	2.74E-07	1.00E-06
AB57_0332	feoB	ferrous iron transport protein B	0.646032305	0.000111	0.000261
AB57_0333		hypothetical protein	0.172424034	0.285612	0.343439
AB57_0334	murD	UDP-N-acetylmuramoyl-L-alanyl-D-glutamate synthetase	0.693915053	7.89E-08	3.16E-07
AB57_0335	ftsW	cell division protein FtsW	0.240326753	0.095657	0.127131
AB57_0336		glutamyl-tRNA synthetase	0.730744671	1.55E-11	1.17E-10
AB57_0337		DnaK suppressor protein	0.52161525	0.001328	0.002575
AB57_0338		cyclic AMP phosphodiesterase	-0.050156152	0.671155	0.715435
AB57_0339		ADP-ribose pyrophosphatase	-0.480308616	4.58E-05	0.000116
AB57_0340	thiC	thiamine biosynthesis protein ThiC	-0.254896405	0.035082	0.051245
AB57_0341		hypothetical protein	-0.423633377	0.002037	0.003838
AB57_0342		transcriptional regulator	-0.481396101	1.67E-06	5.48E-06
AB57_0343		permease	-0.649372861	1.38E-08	6.20E-08
AB57_0344		type I secretion outer membrane protein	0.062791045	0.582345	0.636348
AB57_0345	phoU	phosphate transport system regulatory protein PhoU	0.853881226	4.67E-09	2.26E-08
AB57_0346		hypothetical protein	1.774290392	6.66E-25	5.13E-23
AB57_0347	argH	argininosuccinate lyase	1.14403795	3.67E-11	2.60E-10
AB57_0348		alginate biosynthesis protein	-0.739733182	8.61E-11	5.64E-10
AB57_0349		alginate biosynthesis regulatory protein	-1.044230536	1.88E-07	7.08E-07
AB57_0350	hemC	porphobilinogen deaminase	0.241942106	0.024386	0.036888
AB57_0351	hemD	uroporphyrinogen-III synthase	0.482837705	1.25E-05	3.47E-05
AB57_0352		hypothetical protein	0.759374037	2.07E-11	1.52E-10
AB57_0353		hypothetical protein	0.973175909	1.33E-14	1.69E-13
AB57_0354		thioesterase superfamily protein	0.57577461	1.48E-07	5.64E-07

AB57_0355		DNA-binding protein H-NS	-0.688072386	7.40E-06	2.16E-05
AB57_0356		putative general secretion pathway protein	0.212643992	0.040345	0.058289
AB57_0357		putative general secretion pathway protein	0.584419615	1.30E-08	5.87E-08
AB57_0358	gspD	general secretion pathway protein D	0.51982433	0.000223	0.000499
AB57_0359		FHA domain protein	0.356734846	0.001318	0.002558
AB57_0360	gph	phosphoglycolate phosphatase	0.290998672	0.006139	0.010537
AB57_0361	trpE	anthranilate synthase component I	0.365649918	0.001938	0.003673
AB57_0362	tuf	elongation factor Tu	0.793099398	8.09E-06	2.33E-05
AB57_0363	secE	preprotein translocase subunit SecE	1.215942769	4.68E-12	3.90E-11
AB57_0364	nusG	transcription termination/antitermination factor NusG	1.404569221	1.71E-10	1.06E-09
AB57_0365	rplK	50S ribosomal protein L11	1.38567338	4.26E-10	2.47E-09
AB57_0366	rplA	50S ribosomal protein L1	1.303895353	8.07E-10	4.52E-09
AB57_0367		50S ribosomal protein L10	1.350456249	1.17E-11	9.04E-11
AB57_0368	rplL	50S ribosomal protein L7/L12	1.093255759	1.53E-08	6.84E-08
AB57_0369	rpoB	DNA-directed RNA polymerase subunit beta	1.146689742	1.68E-08	7.39E-08
AB57_0370	rpoC	DNA-directed RNA polymerase subunit beta'	-0.036029679	0.820405	0.850757
AB57_0371		lipoprotein, putative	-0.286675802	0.010016	0.01639
AB57_0372		hypothetical protein	-1.106051455	2.55E-18	6.55E-17
AB57_0373		hypothetical protein	-0.832274921	3.01E-10	1.79E-09
AB57_0374		short chain dehydrogenase	-0.140420022	0.168387	0.213148
AB57_0375		Na+/H+ antiporter NhaC	2.426049184	4.63E-19	1.34E-17
AB57_0376		putative outer membrane protein W	-0.765646403	9.76E-11	6.33E-10
AB57_0377		hypothetical protein	-0.445756801	1.56E-05	4.26E-05
AB57_0378		heat shock protein 90	-0.185254337	0.128825	0.167012
AB57_0379		hypothetical protein	-0.60766591	0.000325	0.000701
AB57_0380		hypothetical protein	-0.482993591	3.66E-05	9.43E-05
AB57_0381		DSBA oxidoreductase	-0.183808662	0.113679	0.148942
AB57_0382		hypothetical protein	-0.709001814	5.16E-10	2.96E-09
AB57_0383		transcriptional regulator MerR family	-0.319228636	0.069355	0.095395
AB57_0384		hypothetical protein	-1.203722564	1.94E-21	8.43E-20
AB57_0385		hypothetical protein	-0.857834513	2.69E-15	4.00E-14
AB57_0386	fadA	3-ketoacyl-CoA thiolase	0.372866951	0.056962	0.079713
AB57_0387	fadB	multifunctional fatty acid oxidation complex subunit alpha	0.641863929	0.000197	0.000444
AB57_0388		lipoprotein, putative	0.299392271	0.019844	0.030555
AB57_0389		beta-hydroxylase	0.700985538	5.89E-11	3.97E-10
AB57_0390		hypothetical protein	0.451681018	0.000276	0.000605
AB57_0391	uvrC	excinuclease ABC subunit C	-0.528831577	2.57E-07	9.44E-07
AB57_0392		acyl-CoA thioesterase II	-0.706026237	2.36E-10	1.42E-09
AB57_0393	pgsA	CDP-diacylglycerol--glycerol-3-phosphate 3-phosphatidyltransfe	-0.395103333	0.001819	0.00346
AB57_0394		methylated-DNA--protein-cysteine methyltransferase transcript	-0.636727049	2.19E-08	9.54E-08
AB57_0395		DNA repair system	-1.067004812	3.39E-17	7.17E-16
AB57_0396		transcriptional regulator, IclR family	-0.301879937	0.007231	0.01224
AB57_0397		putative fusaric acid resistance protein	0.060287589	0.618186	0.667237
AB57_0398		hypothetical protein	0.064470665	0.738328	0.776525
AB57_0399		HlyD family secretion protein	0.445559563	2.93E-05	7.68E-05
AB57_0400		Holliday junction resolvase-like protein	0.466004342	1.82E-06	5.94E-06
AB57_0401		hypothetical protein	0.264271457	0.031708	0.046852
AB57_0402	recN	DNA repair protein RecN	0.114873824	0.316564	0.375533
AB57_0403		tetratricopeptide repeat domain protein	-0.421578212	0.00053	0.001103
AB57_0404		protein Nfa15710	-0.053277494	0.597237	0.64917
AB57_0405		RNA methyltransferase, TrmH family, group 3	1.210941251	9.42E-14	1.03E-12
AB57_0406	coaE	dephospho-CoA kinase	-0.041249453	0.723845	0.763898
AB57_0407		integral membrane protein DUF6	0.300714456	0.016667	0.025998
AB57_0408	pilD	type IV pilus prepilin peptidase PilD	-0.070842847	0.557702	0.614319
AB57_0409		pilin biogenesis protein	0.084688991	0.584349	0.637314
AB57_0410	pilB	type IV-A pilus assembly ATPase PilB	-0.133952882	0.243455	0.298175
AB57_0411	tpiA	triosephosphate isomerase	1.897978551	1.64E-21	7.32E-20
AB57_0412		preprotein translocase subunit SecG	0.817786337	2.66E-06	8.32E-06

AB57_0413		hypothetical protein	1.534722657	2.64E-17	5.68E-16
AB57_0414		transcription elongation factor NusA	1.121731872	5.82E-08	2.37E-07
AB57_0415		translation initiation factor IF-2	0.416532837	0.014043	0.022277
AB57_0416	rbfA	ribosome-binding factor A	0.296358718	0.104381	0.13813
AB57_0417		putative monovalent cation/H+ antiporter subunit G	-0.26497631	0.008789	0.014615
AB57_0418		pH adaptation potassium efflux system protein F	0.254756354	0.034957	0.051103
AB57_0419		pH adaptation potassium efflux system transmembrane protein	0.411771446	0.000843	0.0017
AB57_0420		putative monovalent cation/H+ antiporter subunit D	0.588438352	4.26E-05	0.000108
AB57_0421		putative monovalent cation/H+ antiporter subunit C	0.725006405	0.000117	0.000275
AB57_0422		putative monovalent cation/H+ antiporter subunit A	0.644711993	0.0008	0.001621
AB57_0423		putative ATP binding site	-0.909672485	1.42E-11	1.08E-10
AB57_0424		putative DNA helicase	0.642523077	2.44E-06	7.71E-06
AB57_0425		phosphoribosyl (-ATP, -AMP) pyrophosphohydrolase/cyclohydrc	0.084759023	0.489658	0.549177
AB57_0426		putative oxidoreductase; putative flavoprotein monooxygenase	-0.605826789	9.20E-06	2.62E-05
AB57_0427		2-octaprenylphenol hydroxylase of ubiquinone biosynthetic patl	0.611457418	0.000179	0.000407
AB57_0428		hypothetical protein	0.726549744	1.85E-09	9.66E-09
AB57_0429		ubiquinone/menaquinone biosynthesis methyltransferase UbiE	0.127949155	0.339581	0.400015
AB57_0430		hypothetical protein	-0.264788121	0.028449	0.042496
AB57_0433		hypothetical protein	-0.878366952	1.24E-10	7.87E-10
AB57_0434		exonuclease V gamma chain	0.04581091	0.695956	0.738468
AB57_0435		exonuclease V beta chain	-0.275280893	0.024658	0.037269
AB57_0436	recD	exonuclease V alpha subunit	0.034639656	0.723551	0.763805
AB57_0437		beta-lactamase	-0.541688815	2.76E-07	1.01E-06
AB57_0438	rpsO	30S ribosomal protein S15	-0.343822638	0.027623	0.041361
AB57_0439		polynucleotide phosphorylase/polyadenylase	0.841019303	8.69E-06	2.49E-05
AB57_0440		magnesium Mg(2+)/cobalt Co(2+) transport protein	-1.016247849	3.04E-12	2.64E-11
AB57_0441		hypothetical protein	-1.068027767	3.11E-23	1.69E-21
AB57_0442		curved DNA-binding protein	-1.148177101	3.70E-25	2.91E-23
AB57_0443		transporter, LysE family	-0.684152882	1.01E-10	6.51E-10
AB57_0444	hslO	heat shock protein 33	-0.224138041	0.088163	0.11849
AB57_0445		glutathione-regulated potassium-efflux system protein KefB	-0.24203191	0.015132	0.023784
AB57_0446	priA	primosomal protein N`	-0.029050881	0.768433	0.803618
AB57_0447	gspF	general secretion pathway protein F	0.164866849	0.1205	0.156934
AB57_0448		general secretion pathway protein G	0.058129342	0.580474	0.634679
AB57_0449		hypothetical protein	0.189927205	0.351185	0.411067
AB57_0450		secretion chaperone	-0.283064742	0.007991	0.013409
AB57_0451	lnt	apolipoprotein N-acyltransferase	0.276530165	0.02235	0.034113
AB57_0452		magnesium and cobalt efflux protein CorC	-0.084063041	0.430685	0.491528
AB57_0453		sulfurtransferase TusA	-0.622458268	2.27E-09	1.17E-08
AB57_0454		hypothetical protein	-0.346546044	0.002505	0.004622
AB57_0455		electron transfer flavoprotein-ubiquinone oxidoreductase (EsvG	0.727120742	0.000102	0.000241
AB57_0456		hypothetical protein	0.185967937	0.08383	0.113203
AB57_0457	murI	glutamate racemase	-0.769797645	3.60E-11	2.55E-10
AB57_0459		hypothetical protein	-0.091164121	0.48767	0.547113
AB57_0460	hemH	ferrochelatase	-0.059384761	0.559593	0.615852
AB57_0461		hypothetical protein	-0.129011686	0.292386	0.350447
AB57_0462		beta-lactamase domain protein	-0.067043205	0.593646	0.646026
AB57_0463		methyltransferase superfamily	1.267151745	9.72E-20	3.07E-18
AB57_0464		hypothetical protein	0.985396957	6.43E-11	4.31E-10
AB57_0465		hypothetical protein	0.071777367	0.499195	0.558688
AB57_0466	crcB	camphor resistance protein CrcB	-0.305901447	0.004721	0.008278
AB57_0467		type III effector HopPmaJ	0.416901036	0.000538	0.00112
AB57_0468	rpmE	50S ribosomal protein L31 type B	0.466411212	0.005637	0.009746
AB57_0469		hypothetical protein	-0.921233981	3.52E-08	1.48E-07
AB57_0470		acyl-CoA dehydrogenase-family protein	-2.087031159	1.01E-08	4.62E-08
AB57_0471		acyl-CoA dehydrogenase-family protein	-1.68668074	4.48E-20	1.45E-18
AB57_0472	abeM	multidrug efflux pump	0.197068839	0.042211	0.060676
AB57_0473		hypothetical protein	-1.321748784	4.21E-16	7.38E-15

AB57_0474		putative oxygen-independent coproporphyrinogen III oxidase	0.401883467	0.000444	0.000942
AB57_0475		short chain dehydrogenase	0.031732283	0.829408	0.858408
AB57_0476		transcriptional regulator, HTH-type	-0.452267507	0.000126	0.000294
AB57_0477		long-chain-acyl-CoA synthetase	0.149653909	0.273476	0.330242
AB57_0478		ribonuclease E	0.336912834	0.052459	0.073943
AB57_0480		hypothetical protein	0.011962126	0.904819	0.922521
AB57_0481	rluC	ribosomal large subunit pseudouridine synthase C	0.611983535	1.97E-07	7.35E-07
AB57_0482		HAD-superfamily hydrolase	0.498592637	9.32E-05	0.000223
AB57_0483		transcriptional regulator, DeoR family	0.146795264	0.199526	0.248987
AB57_0484		glutathione S-transferase	-0.045476449	0.658966	0.704267
AB57_0485		hypothetical protein	-0.379739301	0.005377	0.009345
AB57_0486		DNA-binding transcriptional regulator HcaR	-0.579843564	1.42E-05	3.91E-05
AB57_0487		hypothetical protein	-0.290036577	0.032708	0.04812
AB57_0488	katG	catalase/peroxidase HPI	-0.356174882	0.010826	0.0176
AB57_0489	ptsP	phosphoenolpyruvate-protein phosphotransferase	-0.1234576	0.293763	0.351795
AB57_0490		dinucleoside polyphosphate hydrolase	-0.382627912	0.001382	0.002671
AB57_0491		HAD-superfamily subfamily IB hydrolase	-0.018113769	0.87225	0.895485
AB57_0492		transcriptional regulator, LysR family	0.046283203	0.707761	0.749489
AB57_0493		hypothetical protein	0.026651854	0.872793	0.895793
AB57_0494	leuC	isopropylmalate isomerase large subunit	0.531164774	2.39E-07	8.85E-07
AB57_0495	leuD	isopropylmalate isomerase small subunit	0.245747981	0.023605	0.035794
AB57_0496		hypothetical protein	-0.413486692	0.00021	0.000473
AB57_0497	leuB	3-isopropylmalate dehydrogenase	0.042779903	0.777693	0.812154
AB57_0499		hypothetical protein	-0.814910115	3.57E-14	4.19E-13
AB57_0500	infA	translation initiation factor IF-1	0.734734672	0.000136	0.000316
AB57_0501		helix-turn-helix- domain containing protein, AraC type	-0.364516171	0.007316	0.012361
AB57_0502	truA	tRNA pseudouridine synthase A	0.134437058	0.205115	0.255016
AB57_0503		putative L-asparaginase I	0.202420612	0.042093	0.060531
AB57_0504		hypothetical protein	-0.053528686	0.674071	0.718129
AB57_0505		hypothetical protein	-0.000269852	0.998809	0.999079
AB57_0506		hypothetical protein	-0.380115748	0.000642	0.001316
AB57_0507	asd	aspartate-semialdehyde dehydrogenase	1.207088685	5.99E-12	4.90E-11
AB57_0508		endonuclease/exonuclease/phosphatase	-0.26738697	0.02429	0.036781
AB57_0509	dctA	glutamate/aspartate:proton symporter	2.341219249	5.16E-18	1.26E-16
AB57_0510		glycosyl transferase, group 1	0.389731437	0.000205	0.000461
AB57_0511		lipid A biosynthesis acyltransferase	0.129427348	0.195602	0.244382
AB57_0512		RhtB family transporter	-0.559910368	1.45E-06	4.79E-06
AB57_0513		ABC transporter ATP-binding protein uup	-0.708202549	9.84E-06	2.78E-05
AB57_0514		transposase subunit	-0.667026863	1.92E-05	5.17E-05
AB57_0515		transposase 1	-0.476942997	0.006369	0.010895
AB57_0516		ABC transporter ATP-binding protein uup	0.55186947	2.02E-05	5.43E-05
AB57_0517		SlyX superfamily	0.06460039	0.552247	0.609398
AB57_0518		alcohol dehydrogenase, zinc-binding	-0.054527353	0.622477	0.671281
AB57_0519		transcriptional regulatory protein	-0.50552647	0.000903	0.001814
AB57_0520		hypothetical protein	-0.335403459	0.002238	0.004166
AB57_0521	topA	DNA topoisomerase I	0.55593899	0.000971	0.001936
AB57_0522		hypothetical protein	-0.188923915	0.119365	0.15562
AB57_0523		hypothetical protein	-1.037020487	3.37E-11	2.39E-10
AB57_0524		putative ATP-dependent DNA helicase	0.10498428	0.344661	0.404968
AB57_0525		hypothetical protein	0.21632941	0.085132	0.114822
AB57_0526		hypothetical protein	0.054812661	0.62809	0.675758
AB57_0527		hypothetical protein	-0.59252179	8.22E-06	2.37E-05
AB57_0528		hypothetical protein	-0.878641209	8.34E-09	3.85E-08
AB57_0529		monovalent cation transporter	-0.124051269	0.358107	0.418112
AB57_0530	rpmG	50S ribosomal protein L33	1.008598924	1.23E-09	6.63E-09
AB57_0531	rpmB	50S ribosomal protein L28	1.016317563	2.42E-08	1.05E-07
AB57_0532		aldehyde dehydrogenase	-0.22865977	0.047929	0.067972
AB57_0533		transcriptional regulator, TetR family	0.410913645	0.000156	0.000357

AB57_0534	purU	formyltetrahydrofolate deformylase	1.579636964	9.57E-21	3.61E-19
AB57_0535		TonB protein	0.537815256	1.91E-07	7.16E-07
AB57_0536		MotA/TolQ/ExbB proton channel	0.943853031	1.21E-06	4.05E-06
AB57_0537		biopolymer transport protein ExbD/TolR	0.98492032	4.30E-09	2.11E-08
AB57_0538	msrA	methionine-S-sulfoxide reductase	0.491145271	5.77E-05	0.000143
AB57_0539		hypothetical protein	0.516300808	2.35E-07	8.72E-07
AB57_0540	folA	dihydrofolate reductase	1.323823704	7.68E-16	1.27E-14
AB57_0541	thyA	thymidylate synthase	1.365370591	1.23E-17	2.80E-16
AB57_0542		hypothetical protein	-0.592718683	2.45E-07	9.04E-07
AB57_0543		hypothetical protein	-0.725656673	1.25E-10	7.91E-10
AB57_0544	lgt	prolipoprotein diacylglyceryl transferase	0.024709396	0.811743	0.843665
AB57_0545		hypothetical protein	-0.121448955	0.445508	0.506103
AB57_0546		putative phosphatase	-0.430552574	0.022197	0.03391
AB57_0547		hypothetical protein	-0.20595882	0.384051	0.444197
AB57_0548		hypothetical protein	-0.242742934	0.203224	0.253089
AB57_0549		transposase subunit	-0.816701724	2.62E-06	8.23E-06
AB57_0550		transposase 1	-0.467073297	0.00087	0.001751
AB57_0551		beta-lactamase OXA-23	0.619642537	0.000146	0.000337
AB57_0552		AAA ATPase superfamily	0.112888722	0.342622	0.403085
AB57_0553		hypothetical protein	-0.055097593	0.588778	0.641673
AB57_0554		YeeA	0.033087077	0.756296	0.792846
AB57_0555		transposase 1	-0.315222255	0.0141	0.022353
AB57_0556		transposase subunit	-0.741915072	3.39E-08	1.43E-07
AB57_0557		sulfate permease	-0.114328353	0.400573	0.461145
AB57_0558		universal stress protein	0.064725831	0.548161	0.605793
AB57_0559		hypothetical protein	0.015484761	0.896839	0.9159
AB57_0560		hypothetical protein	-0.362919531	0.005848	0.010078
AB57_0561		hypothetical protein	-0.836291267	2.41E-15	3.60E-14
AB57_0562		hypothetical protein	-0.408976277	0.000266	0.000586
AB57_0563		transposition helper protein C	-0.151960187	0.200918	0.250387
AB57_0564		transposition protein B	0.193202014	0.204561	0.254413
AB57_0565		transposase protein A	0.007894541	0.939799	0.951369
AB57_0567		alkaline phosphatase	0.569154386	3.54E-06	1.09E-05
AB57_0568	tatC	twin arginine-targeting protein translocase TatC	-0.568520637	9.27E-06	2.64E-05
AB57_0569		Sec-independent protein translocase protein	0.240751363	0.164139	0.208127
AB57_0570		Sec-independent protein translocase protein	0.384743491	0.084051	0.113458
AB57_0571		hypothetical protein	0.413663468	0.00029	0.000633
AB57_0572	rdgB	putative deoxyribonucleotide triphosphate pyrophosphatase	0.826128915	7.11E-15	9.64E-14
AB57_0573		Sel1 domain protein	-0.132323027	0.304268	0.363042
AB57_0574	metW	methionine biosynthesis protein MetW	0.287915792	0.014294	0.022611
AB57_0575	metX	homoserine O-acetyltransferase	0.641571164	7.23E-06	2.12E-05
AB57_0576	leuA	2-isopropylmalate synthase	0.299336964	0.067559	0.093272
AB57_0577		putative hydroxylase	0.264189698	0.021154	0.032435
AB57_0578		TonB-dependent receptor	2.069088132	1.60E-14	1.98E-13
AB57_0579	tig	trigger factor	1.681858163	5.32E-14	5.96E-13
AB57_0580	clpP	ATP-dependent Clp protease proteolytic subunit	-0.07427049	0.601963	0.653156
AB57_0581	clpX	ATP-dependent protease ATP-binding subunit ClpX	0.091389845	0.561091	0.61695
AB57_0582		hypothetical protein	-0.708257304	2.17E-09	1.12E-08
AB57_0583		hypothetical protein	-0.805248765	1.34E-10	8.47E-10
AB57_0584		fumarate hydratase	1.422704565	2.88E-12	2.52E-11
AB57_0585		phosphate acetyltransferase	0.56690284	8.90E-05	0.000213
AB57_0586	ackA	acetate kinase	0.122684684	0.349465	0.409452
AB57_0587	edd	phosphogluconate dehydratase	0.494944613	0.003074	0.005578
AB57_0588		khg/kdpg aldolase	0.437061007	0.005288	0.009199
AB57_0589		high affinity gluconate permease	0.443475961	0.008594	0.014323
AB57_0590		shikimate kinase	0.244453609	0.053166	0.074825
AB57_0591		aldehyde dehydrogenase	-0.034500457	0.797923	0.831872
AB57_0592	proA	gamma-glutamyl phosphate reductase	-0.023935654	0.859066	0.884157

AB57_0593		putative hydrolase	-0.26698706	0.041717	0.060059
AB57_0594		hypothetical protein	-0.525818474	5.64E-06	1.67E-05
AB57_0595		beta-hexosaminidase	0.330899997	0.000928	0.001859
AB57_0596		carboxy- protease	-0.257675701	0.078516	0.106806
AB57_0597		glycosyl transferase, group 1 family protein	-1.24415256	2.25E-26	2.25E-24
AB57_0598		putative phosphatidylglycerophosphatase B	-1.155751832	4.40E-16	7.61E-15
AB57_0599		hypothetical protein	1.401294377	1.12E-25	1.07E-23
AB57_0600		nucleoside diphosphate kinase	2.139374584	5.38E-23	2.84E-21
AB57_0601		radical SAM enzyme, Cfr family	0.604596803	0.000955	0.001907
AB57_0602	pilF	type IV pilus biogenesis/stability protein PilW	0.268865365	0.020714	0.031815
AB57_0603		hypothetical protein	0.830851876	4.67E-09	2.26E-08
AB57_0604	ispG	4-hydroxy-3-methylbut-2-en-1-yl diphosphate synthase	0.562341367	0.000333	0.000717
AB57_0605	hisS	histidyl-tRNA synthetase	0.918280301	1.81E-07	6.84E-07
AB57_0606		hypothetical protein	1.078074831	1.35E-13	1.44E-12
AB57_0607	yfgL	outer membrane assembly lipoprotein YfgL	0.261471806	0.098322	0.130485
AB57_0608		GTP-binding protein EngA	1.526224699	2.79E-13	2.84E-12
AB57_0609		4'-phosphopantetheinyl transferase	-0.099152007	0.380016	0.440174
AB57_0610	secB	preprotein translocase subunit SecB	1.359895645	4.31E-12	3.62E-11
AB57_0611	grxC	glutaredoxin 3	0.618942179	7.93E-05	0.000191
AB57_0612		rhodanese domain protein	0.161094876	0.310852	0.369467
AB57_0613	engC	probable GTPase	0.946750333	1.45E-12	1.31E-11
AB57_0614	orn	oligoribonuclease	0.331635369	0.006396	0.010931
AB57_0615		hypothetical protein	-0.330683553	0.023051	0.035011
AB57_0616		NADH-dependent enoyl-ACP reductase	2.053734077	6.62E-39	2.72E-36
AB57_0617		RND efflux system, outer membrane lipoprotein, NodT family	0.353009715	0.009004	0.014912
AB57_0618		macrolide export ATP-binding/permease protein MacB	0.116482529	0.46954	0.529987
AB57_0619		efflux transporter, RND family, MFP subunit	0.236803057	0.122655	0.159573
AB57_0620	holA	DNA polymerase III, delta subunit	0.243011531	0.016264	0.025413
AB57_0621		hypothetical protein	-0.091563016	0.456458	0.516956
AB57_0622	leuS	leucyl-tRNA synthetase	0.804594273	5.73E-06	1.69E-05
AB57_0623		hypothetical protein	-0.501893203	0.0032	0.005798
AB57_0624	ilvB	acetolactate synthase 3 catalytic subunit	0.309793217	0.036402	0.053089
AB57_0625	ilvN	acetolactate synthase 3 regulatory subunit	0.635497634	4.93E-06	1.48E-05
AB57_0626	ilvC	ketol-acid reductoisomerase	1.491655199	7.55E-15	1.02E-13
AB57_0627		ggdef domain/eal domain protein	-0.892553624	4.39E-06	1.33E-05
AB57_0628		putative transcriptional regulator	-0.138079595	0.592013	0.644439
AB57_0629		putative transcriptional regulator	-0.491630221	1.47E-05	4.03E-05
AB57_0630		hypothetical protein	-0.108671792	0.296026	0.354236
AB57_0631	prfC	peptide chain release factor 3	2.161473823	8.94E-19	2.42E-17
AB57_0632		hypothetical protein	1.449704383	4.09E-22	1.94E-20
AB57_0633		hypothetical protein	0.739935952	6.08E-09	2.87E-08
AB57_0634		hypothetical protein	-0.336539034	0.003851	0.006871
AB57_0635		hydrolase, TatD family	-0.340006115	0.016507	0.025771
AB57_0636	acnA	aconitate hydratase 1	-0.40127617	0.008956	0.014846
AB57_0637		ThiF family protein	0.906595734	4.61E-12	3.85E-11
AB57_0639		transcriptional Regulator, LysR family	0.749559274	1.02E-12	9.64E-12
AB57_0640		hypothetical protein	1.527370301	1.56E-38	5.78E-36
AB57_0641	dusA	tRNA-dihydrouridine synthase A	1.139989699	2.90E-25	2.38E-23
AB57_0642		hypothetical protein	-0.125193736	0.503739	0.563262
AB57_0643		hypothetical protein	-0.526083189	0.000275	0.000604
AB57_0644		chorismate mutase family protein	-0.175027583	0.103118	0.136555
AB57_0645		hypothetical protein	-0.446902427	0.000118	0.000278
AB57_0646		hypothetical protein	-0.295195149	0.028942	0.043128
AB57_0647		hypothetical protein	-0.480282959	2.70E-05	7.13E-05
AB57_0648		hypothetical protein	-0.884425368	3.08E-14	3.64E-13
AB57_0649		hypothetical protein	0.306010307	0.108499	0.142711
AB57_0650		hypothetical protein	0.455330224	0.072102	0.098843
AB57_0651		hypothetical protein	0.57308992	5.93E-05	0.000146

AB57_0653		hypothetical protein	-0.181725556	0.195529	0.244382
AB57_0654		hypothetical protein	0.019683621	0.912957	0.929282
AB57_0655		hypothetical protein	-0.041260899	0.832967	0.861128
AB57_0656		phage/plasmid-related protein	0.22311537	0.139469	0.179117
AB57_0657		copper resistance D	-0.484226845	0.004007	0.007125
AB57_0658		copper resistance protein CopC	-0.462473535	0.014268	0.022581
AB57_0659		copper-translocating P-type ATPase	-0.644502581	1.26E-10	7.95E-10
AB57_0660		sensor kinase CusS	0.053115192	0.617018	0.666433
AB57_0661		transcriptional activator protein CusR	-0.244318192	0.040816	0.058922
AB57_0662		hypothetical protein	-0.217210744	0.186313	0.234077
AB57_0663		copper resistance protein A	-0.319200081	0.001349	0.002612
AB57_0664		copper resistance protein B	-0.145490868	0.200146	0.249592
AB57_0665		transcriptional regulator, HTH_3 family	0.476016644	0.001875	0.003564
AB57_0666		hypothetical protein	0.01547137	0.895369	0.914651
AB57_0667		major facilitator superfamily MFS_1	0.205372922	0.042416	0.060924
AB57_0668		ribonuclease	-0.147984261	0.447199	0.507401
AB57_0669		integral membrane protein, DUF6	-0.542468283	6.63E-06	1.95E-05
AB57_0670		NAD(P) transhydrogenase subunit alpha	0.104850392	0.393001	0.453415
AB57_0671		NAD(P) transhydrogenase subunit alpha	0.464751947	0.009568	0.015755
AB57_0672		NAD(P) transhydrogenase subunit beta	0.45293362	0.003361	0.006054
AB57_0673		short chain dehydrogenase	-0.387693929	0.000549	0.00114
AB57_0674		hypothetical protein	0.310193083	0.044824	0.063911
AB57_0675		hydroxypyruvate isomerase	-0.929102558	3.21E-16	5.75E-15
AB57_0676		3-hydroxyisobutyrate dehydrogenase	0.262818665	0.018092	0.028032
AB57_0677		enoyl-CoA hydratase	-0.142786281	0.307918	0.366806
AB57_0678		multi-sensor hybrid histidine kinase	-0.472072457	2.90E-06	9.05E-06
AB57_0679		hamp domain protein	-0.303057648	0.018623	0.028793
AB57_0680	cysM	cysteine synthase B	0.92550377	4.97E-12	4.11E-11
AB57_0681		hypothetical protein	0.886096331	4.95E-10	2.84E-09
AB57_0682	rumA	23S rRNA 5-methyluridine methyltransferase	0.293917348	0.013035	0.020851
AB57_0683		GTP pyrophosphokinase (ppGpp synthetase I)	-0.170154951	0.273906	0.330654
AB57_0684		short chain dehydrogenase	-0.815330201	7.90E-11	5.20E-10
AB57_0685		nucleoside triphosphate pyrophosphohydrolase	-0.426255355	0.00025	0.000553
AB57_0686		putative DNA uptake protein ComEA	0.093602207	0.537044	0.594395
AB57_0687		poly(A) polymerase	0.232938436	0.05453	0.076628
AB57_0688	folK	2-amino-4-hydroxy-6-hydroxymethyldihydropteridine pyrophos	0.865545066	4.46E-11	3.09E-10
AB57_0689	panB	3-methyl-2-oxobutanoate hydroxymethyltransferase	0.980330045	8.30E-12	6.66E-11
AB57_0690	panC	pantoate--beta-alanine ligase	0.492617272	0.000724	0.001475
AB57_0691		hypothetical protein	-0.363520584	0.006706	0.011409
AB57_0692		phosphocarrier protein HPr	-0.318130231	0.00196	0.003711
AB57_0693		hypothetical protein	0.525166125	4.41E-07	1.57E-06
AB57_0694		acyl-CoA synthetase	-0.445474659	0.00045	0.00095
AB57_0695	thrS	threonyl-tRNA synthetase	1.043592573	6.49E-08	2.63E-07
AB57_0696		translation initiation factor IF-3	1.07245771	3.16E-09	1.59E-08
AB57_0697		glutathione S-transferase	-0.211815384	0.078115	0.106299
AB57_0698		hypothetical protein	-0.573977306	4.56E-06	1.38E-05
AB57_0699		major facilitator superfamily MFS_1	0.099181306	0.436554	0.497766
AB57_0700	rpmI	50S ribosomal protein L35	0.248818772	0.189936	0.238144
AB57_0701	rplT	50S ribosomal protein L20	0.249999101	0.183556	0.230849
AB57_0703		hypothetical protein	0.020314046	0.842601	0.869872
AB57_0704	pheS	phenylalanyl-tRNA synthetase subunit alpha	1.323007337	2.95E-16	5.32E-15
AB57_0705	pheT	phenylalanyl-tRNA synthetase subunit beta	0.750921256	0.000112	0.000264
AB57_0706	ihfA	integration host factor subunit alpha	0.025443612	0.84522	0.87209
AB57_0707		hypothetical protein	-0.127105738	0.447048	0.507386
AB57_0708	rho	transcription termination factor Rho	1.248778505	2.60E-09	1.33E-08
AB57_0709	trx	thioredoxin	0.607966143	4.99E-06	1.50E-05
AB57_0710		exopolyphosphatase	0.570404513	1.28E-07	4.95E-07
AB57_0711	accA	acetyl-CoA carboxylase, carboxyl transferase, alpha subunit	0.873708838	1.81E-10	1.12E-09

AB57_0712		tRNA(Ile)-lysidine synthase	-0.145208992	0.186992	0.23485
AB57_0713	proC	pyrroline-5-carboxylate reductase	0.609407604	3.09E-06	9.62E-06
AB57_0714		hypothetical protein	0.726547894	1.64E-08	7.25E-08
AB57_0715		DNA polymerase I	1.061919803	1.60E-08	7.10E-08
AB57_0716		MscS Mechanosensitive ion channel	-0.131206064	0.282675	0.340351
AB57_0717		hypothetical protein	-0.912770027	3.52E-10	2.07E-09
AB57_0718		hypothetical protein	0.010562447	0.917759	0.933657
AB57_0719	gspE	general secretory pathway protein E	-0.379063012	0.000848	0.001708
AB57_0720		hypothetical protein	0.492083243	0.000147	0.000339
AB57_0721		transcriptional regulator OhrR	-0.783070083	7.64E-08	3.07E-07
AB57_0722		hypothetical protein	-0.333492624	0.007734	0.013024
AB57_0723		hypothetical protein	-0.599652173	1.14E-09	6.18E-09
AB57_0724		carbon-nitrogen hydrolase	0.39841595	0.001568	0.003007
AB57_0725		putative anti-anti-sigma factor	-0.002509198	0.984578	0.987062
AB57_0726		putative two-component response regulator	-0.283898884	0.023352	0.03544
AB57_0727		VacJ family lipoprotein	-0.071921887	0.54373	0.601075
AB57_0729	rpoN	RNA polymerase factor sigma-54	-0.57733677	4.63E-06	1.40E-05
AB57_0730	raiA	ribosomal subunit interface protein	-1.586829379	3.89E-17	8.14E-16
AB57_0731		hypothetical protein	0.533866713	6.58E-06	1.94E-05
AB57_0732	murA	UDP-N-acetylglucosamine 1-carboxyvinyltransferase	1.354743353	2.97E-12	2.58E-11
AB57_0733	hisG	ATP phosphoribosyltransferase catalytic subunit	0.896888011	1.69E-07	6.39E-07
AB57_0737	hisC	histidinol-phosphate aminotransferase	1.253496636	1.01E-16	1.96E-15
AB57_0738		P-aminobenzoate synthetase	0.239529891	0.051375	0.072497
AB57_0739		FilA	-0.416538385	0.008077	0.013529
AB57_0740		FilB	-0.67044999	0.000619	0.001274
AB57_0741		FilC	-0.05912403	0.599229	0.650762
AB57_0742		FilD	-0.065125327	0.549678	0.606745
AB57_0743		FilE	-0.704464547	9.63E-12	7.58E-11
AB57_0744		FilF	-0.725557777	9.31E-09	4.28E-08
AB57_0745		nudix hydrolase	-0.59625052	6.41E-07	2.23E-06
AB57_0746		nudix hydrolase	-0.885469584	7.34E-09	3.44E-08
AB57_0747		transferase hexapeptide repeat protein	-0.402156321	0.000446	0.000945
AB57_0748		glycoprotease	0.871347888	5.59E-14	6.25E-13
AB57_0749		hypothetical protein	0.708692321	3.37E-09	1.69E-08
AB57_0750		hypothetical protein	-0.187834807	0.131368	0.169833
AB57_0751	fghA	S-formylglutathione hydrolase	-0.194442675	0.069033	0.094987
AB57_0752		hypothetical protein	-0.070851894	0.594894	0.647194
AB57_0753	rpe	ribulose-phosphate 3-epimerase	0.629331644	6.55E-05	0.00016
AB57_0754		hypothetical protein	0.329617365	0.002266	0.004214
AB57_0755		hypothetical protein	-0.220407306	0.04683	0.066515
AB57_0756		copper resistance protein A	-0.227154001	0.035811	0.052247
AB57_0757		copper resistance protein B	0.039912359	0.7145	0.755761
AB57_0758		Co/Zn/Cd efflux system component	-0.881242543	3.22E-15	4.73E-14
AB57_0759		suppressor of gro	-0.547902853	3.19E-05	8.31E-05
AB57_0760		6-O-methylguanine-DNA methyltransferase	-0.385130229	0.003298	0.005953
AB57_0761	argJ	bifunctional ornithine acetyltransferase/N-acetylglutamate synt	0.089245984	0.420147	0.481432
AB57_0762	nadA	quinolinate synthetase	0.349673747	0.00727	0.012294
AB57_0763	add	adenosine deaminase	-1.088978398	6.16E-19	1.73E-17
AB57_0764		zinc-binding dehydrogenase	-1.045389619	9.61E-14	1.05E-12
AB57_0765		transcriptional regulator, LysR family	-0.371782966	0.004125	0.00732
AB57_0766		glutaryl-CoA dehydrogenase	0.300193478	0.009221	0.015237
AB57_0767		cis,cis-muconate transport protein	-0.157103351	0.253273	0.309156
AB57_0768		L-carnitine dehydrogenase	-0.329394697	0.006158	0.010562
AB57_0769		citrate utilization protein B	-0.253186601	0.107751	0.141879
AB57_0770		tricarballylate dehydrogenase	-0.340000136	0.053906	0.075809
AB57_0771		LysR-family transcriptional regulator	-0.716639644	2.68E-07	9.81E-07
AB57_0772		extracellular solute-binding protein, family 1	-1.094749149	1.13E-11	8.76E-11
AB57_0773		citrate-proton symporter	-0.373229197	0.013966	0.022169

AB57_0774		transcriptional regulator, LysR family	-0.820795546	2.62E-09	1.34E-08
AB57_0775		long-chain fatty acid transport protein	-0.741338516	2.47E-06	7.79E-06
AB57_0776		amidohydrolase	0.234476095	0.027336	0.040965
AB57_0777		transcriptional regulator, AraC family	-0.886592343	1.06E-12	1.00E-11
AB57_0778		fatty acid desaturase	-0.637938147	0.000181	0.00041
AB57_0779		transporter	-0.493927448	0.050197	0.071025
AB57_0780		transcriptional regulator	-1.009651671	5.10E-09	2.43E-08
AB57_0781		hypothetical protein	-1.325203927	1.10E-16	2.12E-15
AB57_0782		5-methyltetrahydropteroyltriglutamate--homocysteine methylt	-0.823649318	1.17E-06	3.93E-06
AB57_0783		4-hydroxyphenylacetate 3-monooxygenase reductase compone	-0.70230374	1.02E-09	5.61E-09
AB57_0784		transcriptional regulator, TetR family	-0.664497168	0.007415	0.01251
AB57_0785		hypothetical protein	-0.531667005	3.06E-07	1.11E-06
AB57_0786		hypothetical protein	-0.442629876	0.000153	0.000351
AB57_0787		hypothetical protein	-0.146723159	0.247273	0.302449
AB57_0788		hypothetical protein	-0.579272251	2.46E-07	9.09E-07
AB57_0789		transcriptional regulator, LysR family	-1.083985985	5.34E-16	9.06E-15
AB57_0790		hypothetical protein	-0.557947862	0.000127	0.000297
AB57_0791		hypothetical protein	-1.221994462	2.02E-11	1.49E-10
AB57_0792		ribonucleotide-diphosphate reductase subunit beta	0.644222801	0.00048	0.001008
AB57_0793		hypothetical protein	0.675015355	5.83E-06	1.72E-05
AB57_0794		ribonucleotide-diphosphate reductase subunit alpha	1.060644822	4.45E-08	1.84E-07
AB57_0796		two-component system response regulator protein	-0.26876174	0.052068	0.073419
AB57_0797		two-component system sensor kinase protein	0.010716431	0.934446	0.946468
AB57_0798		hypothetical protein	-0.835755807	6.04E-09	2.85E-08
AB57_0799		diguanylate cyclase	-0.648462453	4.19E-08	1.74E-07
AB57_0800	nuoA	NADH dehydrogenase I chain A	0.613968283	9.10E-05	0.000218
AB57_0801	nuoB	NADH dehydrogenase subunit B	0.830260203	7.22E-07	2.49E-06
AB57_0802	nuoCD	bifunctional NADH:ubiquinone oxidoreductase subunit C/D	0.97908246	1.27E-06	4.22E-06
AB57_0803	nuoE	NADH dehydrogenase subunit E	0.797541797	1.65E-05	4.49E-05
AB57_0804	nuoF	NADH dehydrogenase I chain F	0.662944133	0.000288	0.000629
AB57_0805	nuoG	NADH dehydrogenase subunit G	0.322868443	0.064334	0.089119
AB57_0806	nuoH	NADH dehydrogenase subunit H	0.435706128	0.012128	0.019537
AB57_0807	nuoI	NADH dehydrogenase subunit I	0.455079416	0.006303	0.010802
AB57_0808	nuoJ	NADH dehydrogenase I chain J	0.404232258	0.016855	0.026237
AB57_0809	nuoK	NADH dehydrogenase I chain K	0.50780203	0.000819	0.001654
AB57_0810	nuoL	NADH dehydrogenase subunit L	0.452731426	0.013884	0.022076
AB57_0811	nuoM	NADH dehydrogenase subunit M	0.266299785	0.124818	0.162158
AB57_0812	nuoN	NADH dehydrogenase I chain N	0.14519787	0.389703	0.450031
AB57_0813	upp	uracil phosphoribosyltransferase	0.067387969	0.642904	0.689292
AB57_0814		putative cold shock protein	0.519323586	1.45E-05	3.98E-05
AB57_0815		putative cold shock protein	-0.240628456	0.055558	0.077954
AB57_0816		transcriptional regulator, LysR family	0.109176655	0.272819	0.329664
AB57_0817		ferredoxin-NADP reductase	0.038263413	0.727172	0.766864
AB57_0818		hypothetical protein	1.079205872	5.14E-17	1.04E-15
AB57_0819		hypothetical protein	-0.646432051	5.00E-05	0.000125
AB57_0820		hypothetical protein	-0.449308715	0.004625	0.008118
AB57_0821		hypothetical protein	-1.12298972	1.79E-20	6.31E-19
AB57_0822		hypothetical protein	0.13717167	0.268489	0.324962
AB57_0823		1-aminocyclopropane-1-carboxylate deaminase	-0.433562827	0.000796	0.001615
AB57_0824		secretion protein HlyD	-0.455502109	8.61E-06	2.47E-05
AB57_0825		major facilitator superfamily	-0.511394729	0.000816	0.001649
AB57_0826		transcriptional regulator TetR/AcrR family	-0.314381019	0.03708	0.05395
AB57_0827		lysine exporter protein	-0.395240953	0.001189	0.002328
AB57_0828		hypothetical protein	-0.524746358	0.000322	0.000696
AB57_0829	metG	methionyl-tRNA synthetase	1.936647044	2.19E-15	3.31E-14
AB57_0830		hypothetical protein	-0.755179418	2.21E-07	8.20E-07
AB57_0831		putative ATP-binding protein	0.077992876	0.48761	0.547113
AB57_0832	mtnN	5'-methylthioadenosine/S-adenosylhomocysteine nucleosidase	0.135234485	0.34528	0.405439

AB57_0833		hypothetical protein	-0.387230784	0.001059	0.002096
AB57_0834		amino acid efflux pump, RhtB family	-1.012039437	5.58E-11	3.80E-10
AB57_0835	dcd	deoxycytidine triphosphate deaminase	0.662517164	8.04E-07	2.76E-06
AB57_0836		hypothetical protein	-0.683111815	5.66E-07	1.99E-06
AB57_0837		hypothetical protein	-0.681850671	7.73E-06	2.24E-05
AB57_0838		hypothetical protein	-0.752102032	3.95E-10	2.31E-09
AB57_0839		hypothetical protein	-0.579717297	1.72E-07	6.50E-07
AB57_0840		hypothetical protein	-0.310056484	0.017776	0.027578
AB57_0841		hypothetical protein	-1.123741868	9.15E-17	1.79E-15
AB57_0842		tRNA-dihydrouridine synthase C	1.085732849	1.42E-15	2.20E-14
AB57_0843		cytochrome c assembly protein	-1.479796597	1.32E-21	6.09E-20
AB57_0844	ffh	signal recognition particle protein	0.818016481	8.49E-07	2.90E-06
AB57_0845		pantothenate kinase	0.026301868	0.803403	0.836643
AB57_0846		biotin-[acetyl-CoA-carboxylase] ligase	-0.302999939	0.011147	0.018074
AB57_0847		hypothetical protein	-0.344403758	0.000456	0.000962
AB57_0848		transcriptional regulator, GntR family	-0.752766485	4.87E-09	2.35E-08
AB57_0849	smc	chromosome segregation protein SMC	-0.090462021	0.437656	0.498869
AB57_0850	zipA	cell division protein ZipA	-0.41354162	0.003574	0.00642
AB57_0851	ligA	DNA ligase, NAD-dependent	0.818536454	8.38E-08	3.34E-07
AB57_0852	bfr	bacterioferritin	0.35521714	0.017419	0.027081
AB57_0853		major facilitator superfamily MFS_1	1.112771568	1.26E-05	3.51E-05
AB57_0854		trehalose-6-phosphate synthase	-0.646283662	1.41E-06	4.70E-06
AB57_0855	otsB	trehalose-phosphatase	-1.383341213	1.52E-23	8.92E-22
AB57_0856		biotin biosynthesis protein BioH	-0.269816108	0.025419	0.038248
AB57_0857	bioA	adenosylmethionine-8-amino-7-oxononanoate transaminase	0.516940615	2.15E-06	6.86E-06
AB57_0860	bioC	biotin biosynthesis protein BioC	0.903543707	2.62E-09	1.33E-08
AB57_0861	bioD	dithiobiotin synthetase	1.136301512	7.32E-16	1.22E-14
AB57_0862		ribosomal large subunit pseudouridine synthase B	0.706381102	2.51E-05	6.66E-05
AB57_0863	scpB	chromosome segregation and condensation protein ScpB	0.523926104	4.52E-05	0.000114
AB57_0864	scpA	chromosome segregation and condensation protein ScpA	0.414095746	0.000225	0.000502
AB57_0865		Sua5/YciO/YrdC/YwlC family protein	-0.253286779	0.012636	0.020308
AB57_0866		hypothetical protein	-0.554166153	7.49E-05	0.000181
AB57_0869	rpmF	50S ribosomal protein L32	0.603478055	0.000254	0.00056
AB57_0870	fabD	malonyl CoA-acyl carrier protein transacylase	1.510080507	2.14E-21	9.19E-20
AB57_0871	fabG	3-oxoacyl-(acyl-carrier-protein) reductase	1.537459865	3.89E-20	1.27E-18
AB57_0872	acpP	acyl carrier protein	0.784014214	1.22E-06	4.07E-06
AB57_0873		peptidoglycan-binding LysM	-0.849052439	1.41E-08	6.30E-08
AB57_0874		putative phosphomethylpyrimidine kinase	0.485754075	0.000149	0.000343
AB57_0875		5'-nucleotidase	0.07942231	0.523099	0.581396
AB57_0876	ribB	3,4-dihydroxy-2-butanone 4-phosphate synthase	0.134721253	0.430287	0.491377
AB57_0877		hypothetical protein	-0.588931237	7.10E-06	2.08E-05
AB57_0878		hypothetical protein	-0.683241575	9.95E-11	6.41E-10
AB57_0879	panD	aspartate alpha-decarboxylase	0.936515841	7.15E-12	5.77E-11
AB57_0880	pth	peptidyl-tRNA hydrolase	1.308946059	1.37E-12	1.26E-11
AB57_0881		50S ribosomal protein L25	0.82118569	7.05E-05	0.000171
AB57_0882		ribose-phosphate pyrophosphokinase	1.649444048	4.26E-14	4.91E-13
AB57_0883	ispE	4-diphosphocytidyl-2-C-methyl-D-erythritol kinase	1.107747104	2.83E-11	2.03E-10
AB57_0884	lolB	outer membrane lipoprotein LolB	0.13023942	0.245764	0.300902
AB57_0885		hypothetical protein	-0.776612835	3.71E-08	1.55E-07
AB57_0886	dnaG	DNA primase	-0.250788671	0.022589	0.034409
AB57_0887	hemA	glutamyl-tRNA reductase	0.040729155	0.716012	0.757144
AB57_0888		putative competence protein	0.713148593	5.53E-06	1.64E-05
AB57_0889		ribosomal large subunit pseudouridine synthase D	0.510132133	0.000161	0.000367
AB57_0890		hypothetical protein	0.258498821	0.029974	0.044594
AB57_0891		NADPH-dependent fmn reductase	-0.053765811	0.620039	0.668847
AB57_0892	smpB	SsrA-binding protein	0.049172762	0.645922	0.691725
AB57_0893	coaD	pantetheine-phosphate adenylyltransferase	-0.311165358	0.00339	0.006103
AB57_0894		ferredoxin	-0.398502287	0.000169	0.000385

AB57_0895		hypothetical protein	-0.221820935	0.067749	0.0935
AB57_0896		transcriptional regulator, LysR family	-0.361287864	0.022358	0.034113
AB57_0897		tartrate dehydrogenase	-0.606409631	3.49E-05	9.01E-05
AB57_0898		putative transporter	-0.397384217	0.000719	0.001468
AB57_0899		lipolytic enzyme	-0.263234754	0.011661	0.018841
AB57_0900		dioxygenase alpha subunit	0.058528776	0.627569	0.675632
AB57_0901		succinate-semialdehyde dehydrogenase (NADP+)	0.183108203	0.108316	0.142521
AB57_0904		hypothetical protein	-0.866448133	9.01E-10	4.99E-09
AB57_0905	nadE	glutamine-dependent NAD+ synthetase	0.406024734	0.006045	0.010393
AB57_0906		hypothetical protein	-0.716006255	2.02E-07	7.53E-07
AB57_0907		pirin domain protein	-1.035587975	4.16E-14	4.81E-13
AB57_0908		hypothetical protein	0.555604186	8.87E-06	2.54E-05
AB57_0909		3-oxoacyl-[acyl-carrier-protein] synthase 1	0.801705719	1.63E-06	5.37E-06
AB57_0910		hypothetical protein	-0.923601197	1.61E-08	7.15E-08
AB57_0911	rpsL	30S ribosomal protein S12	1.357396349	3.74E-12	3.19E-11
AB57_0912	rpsG	30S ribosomal protein S7	1.011673396	8.97E-08	3.57E-07
AB57_0913	fusA	elongation factor G	1.092090964	1.32E-09	7.11E-09
AB57_0914	tuf	elongation factor Tu	0.784079465	9.04E-06	2.58E-05
AB57_0915		hypothetical protein	0.079434462	0.49504	0.554541
AB57_0916		transposase subunit	-0.827373058	5.59E-07	1.97E-06
AB57_0917		transposase 1	-0.467759043	0.002166	0.004045
AB57_0918		putative metal-dependent hydrolase	-0.340472249	0.002023	0.003814
AB57_0919	rimI	ribosomal-protein-alanine acetyltransferase	0.114277973	0.312783	0.371524
AB57_0920		arginyl-tRNA-protein transferase	-0.998572691	6.26E-12	5.09E-11
AB57_0921	aat	leucyl/phenylalanyl-tRNA--protein transferase	-0.623512826	8.72E-10	4.84E-09
AB57_0922	trxB	thioredoxin-disulfide reductase	0.604364616	2.39E-05	6.37E-05
AB57_0923		putative cell division protein	-0.133633052	0.321986	0.381231
AB57_0924	ftsK	DNA translocase FtsK	-0.002485506	0.987455	0.989059
AB57_0925		threonine efflux system	-0.577829992	2.37E-05	6.33E-05
AB57_0926		hypothetical protein	1.202659929	2.34E-18	6.10E-17
AB57_0927	minE	cell division topological specificity factor MinE	0.798010743	1.83E-06	5.96E-06
AB57_0928	minD	septum site-determining protein MinD	0.82877526	1.30E-06	4.32E-06
AB57_0929	minC	septum site-determining protein MinC	0.984507014	4.13E-17	8.59E-16
AB57_0930		hypothetical protein	0.403215617	0.00021	0.000472
AB57_0931		putative acyltransferase	0.636314333	7.17E-10	4.04E-09
AB57_0932		OmpA/MotB domain protein	-0.387563251	0.011309	0.018304
AB57_0933		ATP-dependent DNA helicase	1.622134408	4.80E-15	6.86E-14
AB57_0934		deoxyuridine 5'-triphosphate nucleotidohydrolase	1.960852709	2.16E-30	3.99E-28
AB57_0935		phosphomannomutase	-0.098317426	0.392909	0.453415
AB57_0936	argB	acetylglutamate kinase	0.457971229	0.00045	0.000951
AB57_0937		hypothetical protein	-0.206520557	0.140342	0.179988
AB57_0938		glutamine amidotransferase, class-II	-0.656350087	1.04E-06	3.52E-06
AB57_0939		hypothetical protein	-0.474567766	0.001791	0.003412
AB57_0940		hypothetical protein	0.258178769	0.078099	0.106299
AB57_0941		hypothetical protein	-0.330854922	0.25839	0.314488
AB57_0942		outer membrane lipoprotein	-0.162478002	0.138556	0.178148
AB57_0943		ferric uptake regulation protein	0.149870481	0.267696	0.324215
AB57_0944		twitching motility protein	0.003133829	0.983386	0.986585
AB57_0945		twitching mobility protein	-0.332777059	0.01552	0.024312
AB57_0946		hypothetical protein	0.001266814	0.990896	0.992236
AB57_0947		ATP-dependent dsDNA exonuclease	-0.220343984	0.061486	0.085622
AB57_0948		ATP-dependent dsDNA exonuclease	-0.333237355	0.00519	0.009043
AB57_0949		hypothetical protein	-0.594660608	0.000224	0.000501
AB57_0950		glyoxalase	-1.013047237	1.21E-12	1.12E-11
AB57_0951		hypothetical protein	-0.052141206	0.613262	0.662889
AB57_0952		FAD dependent oxidoreductase	0.243805731	0.014046	0.022277
AB57_0953		hypothetical protein	-0.235547027	0.028173	0.042117
AB57_0954	hemB	delta-aminolevulinic acid dehydratase	-0.13454075	0.276998	0.334059

AB57_0955		hypothetical protein	-0.664858112	2.07E-06	6.62E-06
AB57_0956		RND family multidrug resistance secretion protein	0.270121272	0.081198	0.11021
AB57_0957		multidrug resistance protein B	0.374262757	0.012173	0.019592
AB57_0958	ggt	gamma-glutamyltransferase	-0.411990756	3.33E-05	8.65E-05
AB57_0959		integrase	-0.629917816	2.88E-07	1.05E-06
AB57_0960		hypothetical protein	-0.730530762	2.04E-09	1.06E-08
AB57_0963		gp54 protein	-0.196178602	0.427032	0.488238
AB57_0964		hypothetical protein	-0.413197174	0.09445	0.125887
AB57_0966		hypothetical protein	1.056947324	2.01E-06	6.45E-06
AB57_0967		inner membrane protein	0.166743345	0.139416	0.179111
AB57_0968		single-strand binding protein	-0.866093604	5.09E-05	0.000127
AB57_0969		hypothetical protein	-0.783203538	3.38E-10	2.00E-09
AB57_0970		nucleoid-associated protein	0.047219531	0.644116	0.690391
AB57_0971		hypothetical protein	-0.660798316	4.62E-08	1.90E-07
AB57_0972		hypothetical protein	-0.595012979	0.005674	0.009806
AB57_0973		hypothetical protein	-0.838834644	1.80E-06	5.86E-06
AB57_0974		KAP P-loop domain protein	-0.361185571	0.013116	0.020963
AB57_0975		hypothetical protein	-0.331831151	0.001974	0.003733
AB57_0976		hypothetical protein	-0.370773872	0.000978	0.001945
AB57_0977		hypothetical protein	-0.681186252	5.09E-09	2.43E-08
AB57_0978		hypothetical protein	-0.535733601	9.91E-06	2.80E-05
AB57_0979		hypothetical protein	-0.104121902	0.51215	0.571114
AB57_0980		putative benzoate transport porin	-0.474770656	0.038234	0.055477
AB57_0981		hypothetical protein	-0.135505614	0.520545	0.579253
AB57_0982		major facilitator superfamily MFS_1	-0.210979852	0.135707	0.174831
AB57_0983		dihydrodipicolinate synthetase	-0.177465874	0.331687	0.391589
AB57_0984		transcriptional regulator, LysR family	-0.273757062	0.070597	0.09696
AB57_0985		RNA polymerase sigma factor FecI	-0.127646982	0.419568	0.480917
AB57_0986		putative transmembrane sensor protein FecR	0.152267093	0.310468	0.369249
AB57_0987		hypothetical protein	-0.464575212	0.003756	0.00672
AB57_0988		hypothetical protein	-0.646852259	0.000112	0.000264
AB57_0989		hypothetical protein	-0.57719434	0.000282	0.000618
AB57_0990		TonB family protein	-0.533094869	0.003417	0.00615
AB57_0991		heme oxygenase	-0.429574285	0.0151	0.023745
AB57_0992		hypothetical protein	-0.287197324	0.260777	0.31708
AB57_0994		hypothetical protein	-0.811269082	3.88E-09	1.92E-08
AB57_0995		hypothetical protein	-0.842125971	1.01E-07	3.96E-07
AB57_0996		hypothetical protein	-0.649730758	1.18E-05	3.29E-05
AB57_0997		hypothetical protein	-0.559813885	2.13E-06	6.82E-06
AB57_0998		arginine/ornithine antiporter	-1.347789566	8.83E-15	1.17E-13
AB57_0999		homocysteine S-methyltransferase family protein	0.253971886	0.023576	0.035765
AB57_1000		hypothetical protein	-0.447438275	0.00036	0.000769
AB57_1001	mqo	malate:quinone oxidoreductase	0.882466059	2.63E-05	6.95E-05
AB57_1002	betA	choline dehydrogenase	0.646510628	5.57E-05	0.000138
AB57_1003	betB	betaine aldehyde dehydrogenase	1.408033569	3.87E-14	4.51E-13
AB57_1004	betI	transcriptional regulator BetI	1.122216573	1.30E-12	1.20E-11
AB57_1005		high-affinity choline transport protein	-0.332390191	0.00986	0.016193
AB57_1006		choline transport protein BetT	1.05405983	1.61E-07	6.10E-07
AB57_1007		MarC family integral membrane protein	0.516261565	0.003055	0.005546
AB57_1008		thioesterase superfamily protein	0.470884207	6.44E-06	1.90E-05
AB57_1009		hypothetical protein	-0.926899974	8.84E-09	4.07E-08
AB57_1010		putative cobalamin synthesis protein	-0.035793019	0.8074	0.839859
AB57_1011		aerobic C4-dicarboxylate transport protein	-0.329129767	0.026046	0.039143
AB57_1012		YaeQ protein	1.656927583	1.88E-19	5.74E-18
AB57_1013		peptidyl-prolyl cis-trans isomerase	0.135192743	0.213578	0.26447
AB57_1014		polysaccharide deacetylase	0.254928092	0.017853	0.027673
AB57_1015		N-glycosyltransferase	0.574392056	7.03E-07	2.43E-06
AB57_1016		hypothetical protein	0.570082248	1.52E-05	4.17E-05

AB57_1017		enoyl-CoA hydratase	-0.724693474	9.57E-08	3.78E-07
AB57_1018		nicotinamide mononucleotide transporter PnuC	0.290402449	0.010378	0.016931
AB57_1019		hypothetical protein	-0.360722921	0.0446	0.063616
AB57_1020		putative transcriptional regulator	-0.003702395	0.972074	0.977888
AB57_1021		rieske (2Fe-2S) protein	0.534295994	0.003882	0.006919
AB57_1022		hypothetical protein	0.515294202	0.010015	0.01639
AB57_1023		rieske (2Fe-2S) protein	0.671820059	0.000434	0.000921
AB57_1024		short chain dehydrogenase	0.763768447	4.00E-05	0.000102
AB57_1025		glyoxalase/bleomycin resistance protein/dioxygenase	0.2708196	0.032447	0.047811
AB57_1026		FAD-dependent pyridine nucleotide-disulphide oxidoreductase	0.090368432	0.432238	0.493149
AB57_1027		major facilitator superfamily MFS_1	0.248215402	0.016229	0.025369
AB57_1028		hypothetical protein	0.322610141	0.00427	0.007559
AB57_1029		putative hydrolase	0.598028584	1.27E-07	4.91E-07
AB57_1030		short chain dehydrogenase	0.745511646	4.38E-10	2.54E-09
AB57_1031		L-aspartate dehydrogenase	0.828764874	1.49E-12	1.35E-11
AB57_1032		betaine aldehyde dehydrogenase	0.795118747	4.74E-11	3.26E-10
AB57_1033		hypothetical protein	0.317409536	0.02003	0.030815
AB57_1034		hypothetical protein	-0.508628247	2.20E-05	5.90E-05
AB57_1035		major facilitator family transporter	-0.559909278	6.96E-06	2.04E-05
AB57_1037	def	peptide deformylase	-0.506640138	0.000206	0.000463
AB57_1038		glutaminase	0.409938086	4.24E-05	0.000108
AB57_1039		transcriptional Regulator, AraC family	0.212011151	0.095349	0.126932
AB57_1040	fsr	fosmidomycin resistance protein	0.410186007	0.00653	0.011145
AB57_1041		aldose 1-epimerase	-0.402635925	4.34E-05	0.00011
AB57_1042		hypothetical protein	-0.57056595	6.68E-05	0.000163
AB57_1043		transcriptional regulatory protein	-0.552246581	7.28E-05	0.000176
AB57_1044		3-oxoacyl-[acyl-carrier-protein] reductase	-0.280102834	0.037361	0.05432
AB57_1045		major facilitator superfamily MFS_1	-0.020328011	0.871304	0.895009
AB57_1046		transketolase, alpha subunit	0.216216375	0.093009	0.124371
AB57_1047		transketolase, beta subunit	0.198720209	0.151253	0.192713
AB57_1048	metH	B12-dependent methionine synthase	1.436779633	1.83E-10	1.13E-09
AB57_1050		phosphate transporter	1.064936752	1.36E-07	5.22E-07
AB57_1052	dsdA	D-serine dehydratase	0.659139016	7.28E-06	2.13E-05
AB57_1053		hypothetical protein	0.561631377	1.61E-05	4.40E-05
AB57_1054		hypothetical protein	-1.370655196	4.27E-21	1.74E-19
AB57_1055		hypothetical protein	-0.52025795	0.00282	0.005149
AB57_1056		arylsulfatase	-0.77969167	0.009906	0.016261
AB57_1057		rhomboid family protein	-1.111374867	1.77E-20	6.30E-19
AB57_1058	yhgI	IscR-regulated protein YhgI	-0.211106362	0.061073	0.085144
AB57_1059		outer membrane receptor FepA	-0.469684931	1.56E-05	4.26E-05
AB57_1060		hypothetical protein	0.163767579	0.129151	0.167318
AB57_1063		carbonate dehydratase	0.425245633	4.21E-05	0.000107
AB57_1064		acyl-CoA thioesterase	-0.597250763	0.000557	0.001155
AB57_1065		lipoprotein-releasing system ATP-binding protein LolD	-0.239576688	0.193068	0.241662
AB57_1066		efflux ABC transporter, permease protein	-0.533988347	3.07E-07	1.11E-06
AB57_1067		rhomboid family protein	-0.256687293	0.028798	0.04293
AB57_1068	mtgA	monofunctional biosynthetic peptidoglycan transglycosylase	0.46995528	2.19E-05	5.87E-05
AB57_1069	ppk	polyphosphate kinase	0.500448063	0.00035	0.000751
AB57_1070		hypothetical protein	-0.602000049	3.71E-07	1.33E-06
AB57_1071	estR	transcriptional regulator EstR, HTH-type	0.067659857	0.617671	0.666876
AB57_1072	estB	alpha/beta hydrolase fold protein EstB	-0.17260858	0.093328	0.124752
AB57_1073		rubredoxin reductase	-0.132598505	0.235535	0.289432
AB57_1074		rubredoxin	-0.278289023	0.034577	0.050568
AB57_1075		hypothetical protein	-1.13008377	1.42E-13	1.49E-12
AB57_1076		hypothetical protein	-0.887440102	4.62E-09	2.25E-08
AB57_1077	lysS	lysyl-tRNA synthetase	2.002970779	1.80E-14	2.21E-13
AB57_1078		hypothetical protein	0.996452789	1.75E-11	1.31E-10
AB57_1080		sulfate adenylyltransferase subunit 2	-0.137267274	0.425135	0.486544

AB57_1081		sulfate adenylyltransferase subunit 1	0.500808	0.001795	0.003416
AB57_1082		hypothetical protein	0.324563036	0.008138	0.013625
AB57_1083		hypothetical protein	-0.012222983	0.919815	0.934695
AB57_1084		citrate transporter	0.146975141	0.372533	0.432498
AB57_1085		hypothetical protein	-0.238921042	0.026912	0.040378
AB57_1086		transcriptional regulator, LysR family	0.244791836	0.06892	0.094902
AB57_1087		isocitrate lyase	-0.186076512	0.247413	0.302521
AB57_1088		lipoprotein	-0.956913844	8.50E-10	4.72E-09
AB57_1089		hypothetical protein	-0.087637869	0.427017	0.488238
AB57_1091	ureD	urease accessory protein UreD	-0.408616088	0.030389	0.045139
AB57_1092	ureA	urease subunit gamma	-0.252194921	0.195342	0.24426
AB57_1093	ureB	urease, beta subunit	-0.272598509	0.261841	0.318136
AB57_1094	ureC	urease subunit alpha	-0.141722556	0.201336	0.250823
AB57_1095	ureE	urease accessory protein UreE	0.044344235	0.717846	0.758649
AB57_1096	ureF	urease accessory protein F	0.577877433	5.34E-06	1.59E-05
AB57_1097	ureG	urease accessory protein G	0.456148571	0.000495	0.001037
AB57_1098	ureJ	urease accessory protein J	0.311989283	0.022954	0.034893
AB57_1099		putative methyltransferase	-0.241268802	0.034299	0.050201
AB57_1100	mrdA	penicillin-binding protein 2	0.911062935	3.81E-07	1.37E-06
AB57_1101		hypothetical protein	-0.374799491	0.002199	0.004096
AB57_1102		hypothetical protein	0.388694211	0.003602	0.006463
AB57_1103		adenylate kinase	0.82736056	2.54E-09	1.30E-08
AB57_1104		hypothetical protein	1.166035822	2.65E-13	2.70E-12
AB57_1105	nth	endonuclease III	0.363884858	0.004338	0.007672
AB57_1106		electron transport complex, rnfaBcdge type, B subunit	0.536117977	2.00E-05	5.38E-05
AB57_1107		glutamate dehydrogenase	1.938864143	1.06E-24	7.54E-23
AB57_1108		hypothetical protein	0.791695223	6.66E-08	2.70E-07
AB57_1109		extradiol ring-cleavage dioxygenase, class III enzyme, subunit B	-0.146390438	0.307799	0.366781
AB57_1110		hypothetical protein	-0.349018543	0.007804	0.013125
AB57_1111	lon	ATP-dependent protease La	-0.436852367	0.00613	0.01053
AB57_1112		5-formyltetrahydrofolate cyclo-ligase	-0.756123962	2.77E-10	1.66E-09
AB57_1113		hypothetical protein	-0.757612413	1.01E-06	3.43E-06
AB57_1115		hypothetical protein	-0.831439851	3.25E-09	1.63E-08
AB57_1116		hypothetical protein	-0.321138041	0.005047	0.008812
AB57_1117		hypothetical protein	0.017467984	0.899208	0.917559
AB57_1118		YecA family protein	1.02907072	1.05E-14	1.37E-13
AB57_1119		X-Pro aminopeptidase	0.319569496	0.027247	0.040848
AB57_1120		2-octaprenyl-6-methoxyphynol hydroxylase, FAD/NAD UbiH	0.539546739	4.59E-05	0.000116
AB57_1121		ubiquinone biosynthesis hydroxylase, UbiH/UbiF/VisC/COQ6 far	0.592444836	3.20E-05	8.33E-05
AB57_1123		hypothetical protein	-0.229862596	0.022702	0.034566
AB57_1124		transcriptional regulator, MerR family	-0.029289974	0.823002	0.852971
AB57_1125		Co/Zn/Cd efflux system	-0.4932889	7.30E-06	2.13E-05
AB57_1126		lysine exporter protein ArgO	0.328867857	0.009606	0.015811
AB57_1127		chromosome replication initiation inhibitor protein	-0.376970365	0.016949	0.026371
AB57_1128		hypothetical protein	-0.281960699	0.14307	0.183106
AB57_1129		hypothetical protein	0.611017755	3.16E-07	1.14E-06
AB57_1130		hypothetical protein	-0.503425153	0.004569	0.008028
AB57_1131		hypothetical protein	0.111571622	0.356171	0.415982
AB57_1132		esterase	0.378456333	0.000366	0.000782
AB57_1133		NADH pyrophosphatase	0.492292903	6.97E-06	2.05E-05
AB57_1134		hypothetical protein	-0.284834913	0.005982	0.010291
AB57_1135		DNA polymerase III ,epsilon subunit	0.680606521	3.30E-08	1.40E-07
AB57_1136		lytic transglycosylase	0.631590148	0.000342	0.000736
AB57_1137		extracellular solute-binding protein, family 5	0.368161371	0.000922	0.001847
AB57_1138		peptide ABC transporter, permease protein	-0.22507226	0.062036	0.086259
AB57_1139		peptide ABC transporter, permease protein	-0.39805677	0.000455	0.000959
AB57_1140		glutathione import ATP-binding protein GsiA	-0.339285186	0.004543	0.007994
AB57_1141		oxidoreductase, FAD/FMN-binding	-0.476399488	0.001033	0.002048

AB57_1142		hypothetical protein	-0.8309791	1.30E-07	5.00E-07
AB57_1143		hypothetical protein	-0.674422	1.98E-06	6.38E-06
AB57_1144		hypothetical protein	-0.678537617	1.69E-05	4.59E-05
AB57_1145		hypothetical protein	-0.324896655	0.007255	0.012274
AB57_1146		hypothetical protein	-0.53400837	0.00064	0.001313
AB57_1147		hypothetical protein	-0.615495876	4.87E-07	1.72E-06
AB57_1148		TonB-dependent siderophore receptor	0.911453247	3.37E-06	1.04E-05
AB57_1149	rnt	ribonuclease T	-0.269484432	0.013292	0.021226
AB57_1150	pyrC	dihydroorotase	0.423721128	0.001696	0.003242
AB57_1151		hypothetical protein	-0.758874962	3.41E-12	2.93E-11
AB57_1152	argG	argininosuccinate synthase	2.415834482	1.81E-21	7.97E-20
AB57_1153		2,4-dienoyl-CoA reductase	-1.10949277	6.37E-13	6.14E-12
AB57_1154		hypothetical protein	-0.038577892	0.743773	0.781363
AB57_1155		hypothetical protein	-0.550874428	0.008934	0.014816
AB57_1157		transcriptional regulator, TetR family	-0.868528114	7.81E-05	0.000189
AB57_1158		Rhs element Vgr protein, putative	0.362724407	0.011506	0.018599
AB57_1159		YD repeat protein	-0.05101309	0.750654	0.787474
AB57_1160		hypothetical protein	-1.0937907	1.08E-19	3.36E-18
AB57_1161		hypothetical protein	-0.233139669	0.128378	0.166491
AB57_1162		hypothetical protein	-0.104162926	0.302062	0.360758
AB57_1163		hypothetical protein	-0.437656265	0.000285	0.000624
AB57_1164		hypothetical protein	-0.013421292	0.904086	0.922028
AB57_1165		aromatic amino acid transport protein AroP	0.117446569	0.360689	0.420729
AB57_1166		FAD dependent oxidoreductase	1.049404591	1.52E-09	8.07E-09
AB57_1167		putrescine importer	0.751410934	2.26E-05	6.04E-05
AB57_1168		hypothetical protein	-0.50001544	2.35E-06	7.46E-06
AB57_1169		transcriptional regulator, GntR family	0.19228892	0.060616	0.084602
AB57_1170		hypothetical protein	-0.575161733	2.03E-07	7.58E-07
AB57_1171		betaine aldehyde dehydrogenase	-0.488712882	1.70E-06	5.55E-06
AB57_1172		transcriptional regulator, AsnC family	0.016021586	0.911294	0.928101
AB57_1173		bifunctional succinylornithine transaminase/acetylornithine tran	0.135424999	0.256699	0.312944
AB57_1174	astA	arginine N-succinyltransferase	-0.797240126	5.88E-12	4.83E-11
AB57_1175		D-serine/D-alanine/glycine transporter	-0.730446839	1.76E-09	9.22E-09
AB57_1176		hypothetical protein	-0.29982439	0.042658	0.0612
AB57_1177		hypothetical protein	-0.503338473	1.13E-05	3.16E-05
AB57_1178		aldehyde dehydrogenase	-0.63379567	4.82E-10	2.77E-09
AB57_1179		transcriptional regulator, AraC family	-0.705959041	2.15E-06	6.87E-06
AB57_1180		hypothetical protein	-0.460118215	5.30E-06	1.58E-05
AB57_1181	garD	galactarate dehydratase	0.430362431	0.009463	0.015589
AB57_1182		glucarate transporter	0.010824167	0.947056	0.957406
AB57_1183	gudD	glucarate dehydratase	0.062460167	0.631993	0.679168
AB57_1185	kdgD	5-dehydro-4-deoxyglucarate dehydratase	0.138503601	0.375942	0.436045
AB57_1186		NADP-dependent fatty aldehyde dehydrogenase	-0.227496737	0.035773	0.052214
AB57_1187		transcriptional regulator, GntR family	-0.177125316	0.120724	0.157171
AB57_1188		tannase/feruloyl esterase family protein	-0.035866987	0.75752	0.793552
AB57_1190		hypothetical protein	-0.174680106	0.540257	0.597415
AB57_1191		porin	-0.182406959	0.16281	0.206513
AB57_1192		long-chain specific acyl-coa dehydrogenase	0.105971699	0.490134	0.549377
AB57_1193		feruloyl-CoA synthase	-0.515777492	1.15E-06	3.87E-06
AB57_1194		aldehyde dehydrogenase	-0.027268251	0.818154	0.848898
AB57_1195		p-hydroxycinnamoyl CoA hydratase/lyase	0.197686542	0.078745	0.107038
AB57_1196		putative 3-hydroxyphenylpropionic transporter MhpT	0.109894599	0.617081	0.666433
AB57_1197		transcriptional regulator, MarR-family	-0.106128853	0.584304	0.637314
AB57_1198		transcriptional regulator, GntR family	-0.124771703	0.372042	0.432335
AB57_1199		2Fe-2S iron-sulfur cluster binding domain protein	-0.44520316	0.000934	0.00187
AB57_1200		vanillate O-demethylase oxygenase subunit	-0.460162375	0.000237	0.000527
AB57_1201		vanillate transporter	-0.946955555	2.47E-07	9.10E-07
AB57_1202		porin	-0.590083744	2.33E-06	7.40E-06

AB57_1203		GMC oxidoreductase	-0.326495874	0.001543	0.002963
AB57_1204		acetyl-hydrolase	1.770288939	7.85E-09	3.66E-08
AB57_1205		short chain dehydrogenase	3.226955765	1.68E-13	1.75E-12
AB57_1206		monooxygenase	3.685675055	8.70E-19	2.38E-17
AB57_1207		transcriptional regulator, AraC family	-0.191445656	0.149153	0.190299
AB57_1208		putative transferase	-0.232004369	0.176341	0.222532
AB57_1209		monooxygenase, flavin-binding family	-0.011747155	0.918635	0.934034
AB57_1210		oxidoreductase short chain dehydrogenase/reductase family	0.378048583	0.037363	0.05432
AB57_1211		hypothetical protein	0.129005695	0.362204	0.422229
AB57_1212		transcriptional regulator	-0.73690914	1.90E-07	7.15E-07
AB57_1213		pirin domain protein	-0.274826612	0.041617	0.059939
AB57_1214		hypothetical protein	-0.540873025	0.009093	0.015041
AB57_1215		oxidoreductase short chain dehydrogenase/reductase family	-0.47930474	0.010048	0.016436
AB57_1216		monooxygenase, flavin-binding family	-0.194899333	0.153503	0.195444
AB57_1217		hypothetical protein	-0.433209876	0.002162	0.004039
AB57_1218		xanthine/uracil permease	1.578456963	4.76E-13	4.67E-12
AB57_1219	add	adenosine deaminase	2.019392601	2.17E-24	1.46E-22
AB57_1220		cytochrome B561	-0.881712728	1.24E-15	1.97E-14
AB57_1221		hypothetical protein	0.610207017	5.19E-05	0.000129
AB57_1222	rnhB	ribonuclease HII	0.970337961	4.96E-12	4.11E-11
AB57_1223	csrA	carbon storage regulator	-0.627367835	5.50E-05	0.000137
AB57_1224		aspartate kinase	2.256291423	2.99E-20	9.98E-19
AB57_1225		hypothetical protein	-0.010361619	0.95834	0.966965
AB57_1226		hypothetical protein	-0.398770748	0.031281	0.046351
AB57_1227		hypothetical protein	-0.654950076	3.44E-06	1.06E-05
AB57_1228		hypothetical protein	-0.383006176	0.112317	0.147418
AB57_1231		hypothetical protein	-0.362848044	0.016681	0.026009
AB57_1232		exodeoxyribonuclease X	-0.830401578	4.98E-07	1.76E-06
AB57_1233		hypothetical protein	-0.682479569	0.007773	0.013085
AB57_1234		hypothetical protein	-0.8061936	0.000975	0.001942
AB57_1235		hypothetical protein	0.293929964	0.03785	0.054962
AB57_1236		hypothetical protein	0.20908283	0.341201	0.401668
AB57_1237		prophage LambdaSo, transcriptional regulator, Cro/CI family	0.446777743	9.75E-05	0.000232
AB57_1241		hypothetical protein	-0.436507278	0.12027	0.15669
AB57_1242		hypothetical protein	-0.337048317	0.239617	0.294057
AB57_1243		hypothetical protein	-0.478437221	0.034977	0.051112
AB57_1244		phosphoadenosine phosphosulfate reductase	-0.444549342	0.012521	0.020133
AB57_1245		hypothetical protein	-0.65325248	0.001466	0.00282
AB57_1246		C-5 cytosine-specific DNA methylase	-0.416644471	0.001728	0.003301
AB57_1247		hypothetical protein	-0.098554741	0.561965	0.617728
AB57_1248		phage replication protein, putative	-0.206946201	0.296296	0.354443
AB57_1249		hypothetical protein	-0.511834262	0.06086	0.084879
AB57_1250		hypothetical protein	-0.611849212	1.30E-05	3.61E-05
AB57_1251		hypothetical protein	0.408501225	0.063651	0.088371
AB57_1252		hypothetical protein	0.726940082	1.93E-06	6.23E-06
AB57_1253		hypothetical protein	-0.640485212	2.30E-06	7.31E-06
AB57_1254		hypothetical protein	-0.364194726	0.00062	0.001276
AB57_1255		hypothetical protein	-0.806753367	1.05E-09	5.74E-09
AB57_1256		hypothetical protein	-0.824196413	6.50E-09	3.06E-08
AB57_1257		hypothetical protein	-0.01980504	0.871228	0.895009
AB57_1258		antirepressor protein	-0.494226049	0.000216	0.000484
AB57_1259		hypothetical protein	-0.820059504	9.40E-12	7.43E-11
AB57_1260		hypothetical protein	-0.257032506	0.090542	0.121423
AB57_1261		hypothetical protein	-0.734035158	0.001175	0.002305
AB57_1262		hypothetical protein	-0.323651021	0.050703	0.071659
AB57_1263		hypothetical protein	-0.409541322	0.03023	0.044956
AB57_1266		hypothetical protein	-0.964674015	6.05E-05	0.000149
AB57_1269		hypothetical protein	-0.531819167	0.041823	0.060188

AB57_1270		phage terminase	-0.682819993	2.00E-05	5.36E-05
AB57_1271		hypothetical protein	-0.699074578	1.45E-06	4.81E-06
AB57_1272		hypothetical protein	-1.085798959	6.11E-07	2.13E-06
AB57_1273		hypothetical protein	-0.640614174	0.008271	0.013816
AB57_1274		hypothetical protein	-0.353667131	0.109486	0.143958
AB57_1275		hypothetical protein	-0.580313084	6.34E-05	0.000155
AB57_1276		hypothetical protein	-0.377051428	0.045298	0.064512
AB57_1277		hypothetical protein	-0.086529855	0.708747	0.750319
AB57_1278		hypothetical protein	-0.632452329	0.00553	0.009579
AB57_1280		hypothetical protein	0.645314367	0.00219	0.004083
AB57_1282		hypothetical protein	-0.008270808	0.966107	0.972679
AB57_1283		hypothetical protein	-0.626890817	0.000103	0.000243
AB57_1284		hypothetical protein	-0.708368936	0.000147	0.000339
AB57_1285		hypothetical protein	-0.566560363	0.037744	0.054852
AB57_1286		carbohydrate binding domain protein	-0.598873423	5.43E-06	1.61E-05
AB57_1287		hypothetical protein	-0.518266559	0.013353	0.021304
AB57_1288		hypothetical protein	-0.913903789	4.47E-16	7.65E-15
AB57_1289		hypothetical protein	-0.571957118	0.018435	0.028528
AB57_1290		hypothetical protein	-0.799398465	1.11E-07	4.33E-07
AB57_1291		hypothetical protein	-0.79987345	0.000413	0.000879
AB57_1292		hypothetical protein	-0.512735009	0.003228	0.005846
AB57_1293		hypothetical protein	-0.40597009	0.011031	0.017908
AB57_1294		type III restriction enzyme, res subunit family	-0.528870898	0.000297	0.000645
AB57_1295		hypothetical protein	-0.608102387	9.13E-05	0.000218
AB57_1296		hypothetical protein	-0.697313731	0.001143	0.002247
AB57_1297		hypothetical protein	-0.233816934	0.192301	0.240782
AB57_1300		hypothetical protein	-0.352846654	0.021623	0.033088
AB57_1301		hypothetical protein	-0.0392143	0.703625	0.745963
AB57_1302		hypothetical protein	0.06122317	0.548414	0.605892
AB57_1303		paar motif family	-0.300334828	0.005949	0.010247
AB57_1304		hypothetical protein	0.187996532	0.234284	0.288155
AB57_1305		DNA-directed DNA polymerase UmuC	-0.710178684	5.65E-05	0.00014
AB57_1306		DNA polymerase V component	-0.762280636	9.06E-06	2.58E-05
AB57_1307		hypothetical protein	-0.60750477	8.85E-05	0.000212
AB57_1308		hypothetical protein	1.752423741	2.30E-21	9.80E-20
AB57_1309		hypothetical protein	1.059794911	1.13E-09	6.14E-09
AB57_1310		phage integrase	1.175237344	9.89E-15	1.30E-13
AB57_1311	alaS	alanyl-tRNA synthetase	1.461196298	2.15E-10	1.31E-09
AB57_1312		glyceraldehyde 3-phosphate dehydrogenase	0.378194488	0.000511	0.001069
AB57_1314		ATP phosphoribosyltransferase regulatory subunit	1.312068507	4.85E-13	4.74E-12
AB57_1315	purA	adenylosuccinate synthetase	1.910968148	3.90E-14	4.53E-13
AB57_1316		peptidase M48 family protein	0.397256	0.003293	0.005947
AB57_1317		aldo/keto reductase	-0.22807397	0.02495	0.037665
AB57_1318		cAMP-regulatory protein	0.535051686	1.67E-05	4.55E-05
AB57_1319		OsmC-like protein	0.32456029	0.002458	0.00454
AB57_1320		peptidase M23/M37 family	-0.3570891	0.005111	0.00892
AB57_1321		acetyltransferase, GNAT family	-1.055414832	3.25E-12	2.80E-11
AB57_1322	clpB	ATP-dependent chaperone ClpB	-0.161583846	0.332061	0.39179
AB57_1323	cinA	competence/damage-inducible protein CinA	-0.414841656	0.001088	0.002146
AB57_1324		hypothetical protein	-0.59083622	7.12E-07	2.46E-06
AB57_1325		23S rRNA m(2)G2445 methyltransferase	1.538438403	3.34E-13	3.33E-12
AB57_1326		hypothetical protein	-0.739948837	0.000392	0.000836
AB57_1327	pyrB	aspartate carbamoyltransferase catalytic subunit	1.900204985	2.15E-26	2.21E-24
AB57_1328		dihydroorotase	1.364016432	2.21E-13	2.27E-12
AB57_1331		hypothetical protein	-0.379419034	0.000356	0.000762
AB57_1332		glutathione S-transferase family protein	-0.563922351	0.001413	0.002729
AB57_1333	trmB	tRNA (guanine-N(7)-)-methyltransferase	2.131992354	5.84E-23	3.05E-21
AB57_1334		endonuclease/exonuclease/phosphatase	-0.196178871	0.100216	0.132832

AB57_1335	gst	glutathione S-transferase	-1.015891027	5.25E-11	3.59E-10
AB57_1336		hypothetical protein	-0.702951168	3.77E-07	1.35E-06
AB57_1337	ahpF	alkyl hydroperoxide reductase, F subunit	0.3938609	0.000921	0.001846
AB57_1338		hypothetical protein	-0.218453462	0.066671	0.092114
AB57_1339		O-methyl transferase	-0.681029348	2.71E-08	1.16E-07
AB57_1340		hypothetical protein	-1.407278938	9.97E-28	1.23E-25
AB57_1341	ahpC	peroxiredoxin	1.037417474	1.40E-09	7.49E-09
AB57_1342	hrpA	ATP-dependent helicase HrpA	0.305597285	0.03657	0.053314
AB57_1343		3-oxoacyl-(acyl carrier protein) synthase III	0.531273036	4.90E-05	0.000123
AB57_1344		benzoate transport porin BenP	-1.556842632	1.49E-21	6.78E-20
AB57_1345		major facilitator superfamily MFS_1	-2.270430642	4.16E-29	6.70E-27
AB57_1346		benzoate transporter	-0.068299836	0.559191	0.615775
AB57_1347		1,6-dihydroxycyclohexa-2,4-diene-1-carboxylate dehydrogenase	-0.491966711	0.004518	0.007961
AB57_1348		benzoate 1,2-dioxygenase, electron transfer component	-0.570866181	0.008993	0.014901
AB57_1349	benB	benzoate 1,2-dioxygenase, small subunit	-1.234787476	1.13E-05	3.16E-05
AB57_1350	benA	benzoate 1,2-dioxygenase, large subunit	-2.028178202	4.16E-12	3.51E-11
AB57_1351	benM	ben operon transcriptional regulator BenM	-0.66032561	6.91E-07	2.39E-06
AB57_1352		Heavy metal transport/detoxification protein	-0.855692631	1.33E-11	1.01E-10
AB57_1353		copper-translocating P-type ATPase	-0.720182968	1.15E-10	7.35E-10
AB57_1354	cueR	Cu(I)-responsive transcriptional regulator	-0.708813154	7.57E-10	4.26E-09
AB57_1355		hypothetical protein	-0.399667222	0.003631	0.006509
AB57_1356		hypothetical protein	-0.554706119	8.08E-06	2.33E-05
AB57_1357		hypothetical protein	-1.274744598	3.22E-28	4.11E-26
AB57_1358		amino acid efflux pump, RhtB family	-0.114520163	0.51363	0.572418
AB57_1359		hypothetical protein	-0.446776122	0.000141	0.000327
AB57_1360		hypothetical protein	-0.216621986	0.171963	0.217377
AB57_1361		exodeoxyribonuclease VII large subunit	-0.658690287	1.94E-06	6.26E-06
AB57_1362		hypothetical protein	-0.343040183	0.038606	0.05595
AB57_1363		peptidase S24 S26A and S26B	-0.2204793	0.076486	0.104311
AB57_1364		hypothetical protein	-0.002830381	0.984661	0.987062
AB57_1365		hypothetical protein	0.09017997	0.483654	0.543596
AB57_1366		transporter LysE family	-0.319123364	0.0033	0.005953
AB57_1367		cold-shock DNA-binding domain protein	-0.708844405	3.03E-06	9.43E-06
AB57_1368		hypothetical protein	-0.142665663	0.339782	0.400125
AB57_1369		pyrroline-5-carboxylate reductase	-0.208313988	0.085495	0.115197
AB57_1370		hypothetical protein	-0.36358749	0.026254	0.03944
AB57_1371		hypothetical protein	-1.045589014	2.57E-10	1.54E-09
AB57_1372		hypothetical protein	-0.558333452	1.13E-05	3.16E-05
AB57_1373		transporter, major facilitator family	-0.321202742	0.044018	0.062932
AB57_1374		phage putative head morphogenesis protein	-0.496370587	0.000159	0.000363
AB57_1375		transcriptional regulator, MarR-family	0.000208249	0.99924	0.99924
AB57_1376		hypothetical protein	0.575430796	2.21E-06	7.04E-06
AB57_1377		hypothetical protein	-0.900700354	1.67E-09	8.79E-09
AB57_1378		17 kDa surface antigen	-0.955841428	1.91E-20	6.68E-19
AB57_1379		hypothetical protein	-0.616937979	3.57E-06	1.10E-05
AB57_1380		hypothetical protein	-0.607207438	1.65E-07	6.26E-07
AB57_1381		hypothetical protein	-0.953072367	1.08E-09	5.92E-09
AB57_1382		hypothetical protein	-0.818379293	4.86E-12	4.04E-11
AB57_1383		hypothetical protein	-1.051649341	3.76E-16	6.70E-15
AB57_1384		hypothetical protein	-0.453131666	2.48E-05	6.57E-05
AB57_1385		hypothetical protein	-0.776553493	0.002261	0.004207
AB57_1386		hypothetical protein	-0.178207287	0.443485	0.50458
AB57_1387		phage protein	-0.49326515	0.12251	0.159439
AB57_1388		putative helicase	0.121567707	0.566958	0.622094
AB57_1389		phage-associated protein, family	-0.046092466	0.77685	0.811503
AB57_1390		putative bacteriophage protein	-0.497693344	0.028642	0.042749
AB57_1391		hypothetical protein	0.207045334	0.339426	0.39996
AB57_1392		hypothetical protein	0.135418418	0.283997	0.341608

AB57_1393		putative phage-related protein	-0.025283655	0.885038	0.90635
AB57_1394		hypothetical protein	-0.046094137	0.836718	0.864281
AB57_1395		hypothetical protein	-0.218496101	0.306622	0.365497
AB57_1396		fibronectin type III domain protein	-0.532589324	4.80E-06	1.45E-05
AB57_1397		hypothetical protein	-0.886833694	2.54E-11	1.84E-10
AB57_1398		hypothetical protein	-1.24593086	2.30E-08	9.98E-08
AB57_1399		hypothetical protein	-0.837437277	1.79E-13	1.85E-12
AB57_1403		lipoprotein, putative	-0.721230202	9.03E-08	3.58E-07
AB57_1404		hypothetical protein	-0.596269869	3.36E-07	1.21E-06
AB57_1405		lipoprotein, putative	-0.723314404	4.35E-08	1.80E-07
AB57_1408	cysS	cysteinyl-tRNA synthetase	1.045972703	6.25E-10	3.56E-09
AB57_1409		arabinose 5-phosphate isomerase	0.409077055	0.002602	0.004782
AB57_1410		3-deoxy-D-manno-octulosonate 8-phosphate phosphatase	0.573296261	5.28E-06	1.58E-05
AB57_1411		hypothetical protein	-0.049270573	0.642666	0.689236
AB57_1412	lptA	lipopolysaccharide transport periplasmic protein LptA	0.271629847	0.007635	0.012869
AB57_1413		ABC transporter, ATP-binding protein	0.357491653	0.001592	0.00305
AB57_1414		putative RND family drug transporter	0.300442162	0.004401	0.007776
AB57_1415		protein secretion ABC efflux system, permease and ATP-binding	0.204330471	0.117638	0.153585
AB57_1416		membrane spanning export protein	0.23977787	0.055396	0.077757
AB57_1417		thymidylate synthase	-0.088806373	0.587521	0.640491
AB57_1418		acetyltransferase	-0.291136703	0.08909	0.119606
AB57_1419		universal stress protein family	-1.055067603	1.05E-15	1.70E-14
AB57_1420		O-methyltransferase	0.386450271	0.000513	0.001071
AB57_1421		hypothetical protein	0.580261762	1.02E-05	2.88E-05
AB57_1422		ferredoxin-1	1.849906323	2.88E-54	3.56E-51
AB57_1423		GCN5-related N-acetyltransferase	0.54232265	6.86E-07	2.38E-06
AB57_1424	mutS	DNA mismatch repair protein MutS	0.670161595	9.58E-06	2.72E-05
AB57_1425		hypothetical protein	-0.372566704	0.007051	0.011967
AB57_1426		transcriptional regulator	-0.150436636	0.443671	0.504637
AB57_1427		inner membrane transport protein YbiF	-0.558348797	2.01E-06	6.45E-06
AB57_1428		hypothetical protein	-0.607476691	3.81E-07	1.37E-06
AB57_1429		diguanylate cyclase/phosphodiesterase	-0.560065907	0.00188	0.003571
AB57_1430		lipid A biosynthesis lauroyl acyltransferase	-0.063047142	0.623018	0.671669
AB57_1431		transcriptional regulator, TetR family	-0.111953047	0.624541	0.672918
AB57_1432	pcaK	4-hydroxybenzoate transporter	-1.705407491	1.01E-30	1.97E-28
AB57_1433		hypothetical protein	-0.196898016	0.257072	0.313193
AB57_1434		hypothetical protein	-0.21894404	0.051142	0.072223
AB57_1436		hypothetical protein	-0.090998311	0.467805	0.528352
AB57_1437		3-hydroxyacyl-CoA dehydrogenase	-1.040899165	3.71E-17	7.81E-16
AB57_1438		hypothetical protein	-0.246075833	0.303183	0.36198
AB57_1439		hypothetical protein	-0.083935641	0.464698	0.525323
AB57_1440		GCN5-related N-acetyltransferase	-0.453252609	0.084285	0.113732
AB57_1441		putative class A beta-lactamase	-0.360662327	0.010974	0.017824
AB57_1442		putative VGR-related protein	0.186301172	0.178649	0.225291
AB57_1443		RHS family protein	0.194298467	0.221833	0.273868
AB57_1444		hypothetical protein	0.674275297	3.19E-08	1.35E-07
AB57_1445		hypothetical protein	-0.428954627	0.001044	0.002067
AB57_1446		hypothetical protein	-0.422565348	0.000273	0.000601
AB57_1447		RHS family protein	-0.014591503	0.92472	0.938158
AB57_1448		hypothetical protein	-0.046025481	0.679837	0.722815
AB57_1449		hypothetical protein	-0.266394994	0.009781	0.016077
AB57_1450		hypothetical protein	-0.543274948	3.80E-06	1.16E-05
AB57_1451		transcriptional regulator, LysR-type	-0.208983964	0.093688	0.125143
AB57_1452		hypothetical protein	-0.843724557	3.32E-05	8.64E-05
AB57_1453		LamB/YcsF family protein	-0.285207061	0.056885	0.079634
AB57_1454		hypothetical protein	0.240330091	0.058603	0.081916
AB57_1455		allophanate hydrolase	0.654791268	7.94E-06	2.30E-05
AB57_1456		carbamoyl-phosphate synthase	1.223181779	1.75E-13	1.82E-12

AB57_1457		voltage-gated chloride channel	0.877903157	2.92E-06	9.10E-06
AB57_1458		Sel1 repeat family	-0.100197337	0.337768	0.398134
AB57_1459		hypothetical protein	-0.317125601	0.005773	0.009968
AB57_1460		hypothetical protein	-0.149075718	0.314784	0.373541
AB57_1461		transcriptional regulator, TetR family	-0.486247301	0.025381	0.038206
AB57_1462		hypothetical protein	-0.916543481	5.86E-10	3.35E-09
AB57_1463		glutathione-dependent formaldehyde dehydrogenase	-1.305545411	1.68E-26	1.83E-24
AB57_1466		urea amidolyase	-0.288594573	0.033922	0.049727
AB57_1467		urea amidolyase	-0.186541363	0.263073	0.319347
AB57_1468		NADPH oxidoreductase	-0.682156295	0.001599	0.003061
AB57_1469		transcriptional regulator, DUF24 family	-0.370651792	0.016651	0.025984
AB57_1471		transcriptional regulator, CopG family	-0.16145904	0.534953	0.592612
AB57_1472		allophanate hydrolase	-0.554131822	0.007652	0.012893
AB57_1473		ABC transport system substrate-binding protein	-0.636690909	0.000138	0.00032
AB57_1474		nitrate transport ATP-binding protein NrtC	-0.361457753	0.020101	0.030907
AB57_1475		binding-protein-dependent transport systems inner membrane	0.043320795	0.749288	0.786934
AB57_1477		hypothetical protein	0.378500407	0.000872	0.001754
AB57_1478		hypothetical protein	-0.41383935	0.012735	0.020442
AB57_1479		type VI secretion protein, family	1.430908043	1.92E-25	1.65E-23
AB57_1480		type VI secretion protein, EvpB/family	1.191922354	5.13E-09	2.44E-08
AB57_1481		type VI secretion system effector, Hcp1 family	0.796721367	1.55E-06	5.11E-06
AB57_1482		type VI secretion system lysozyme-related protein	0.948822145	2.98E-18	7.56E-17
AB57_1483	vasA	type VI secretion protein, family	0.339108435	0.002766	0.00506
AB57_1484		type VI secretion protein, family	-0.286881688	0.006384	0.010915
AB57_1485		hypothetical protein	-0.695777134	4.19E-10	2.45E-09
AB57_1486	icmF	type VI secretion protein IcmF	0.316561375	0.01533	0.024034
AB57_1487		type VI secretion-associated protein, family	0.393005828	0.000611	0.001262
AB57_1488		OmpA/MotB domain protein	0.315158034	0.006339	0.010849
AB57_1489		hypothetical protein	-0.12307874	0.411571	0.472483
AB57_1490	clpV	type VI secretion ATPase, ClpV1 family	0.45938664	0.000949	0.001897
AB57_1491		type VI secretion-associated protein, ImpA family	1.004990314	6.62E-15	9.11E-14
AB57_1492		type VI secretion protein, family	0.948661025	2.65E-08	1.14E-07
AB57_1493		type IV / VI secretion system protein, DotU family	0.525834915	9.54E-05	0.000227
AB57_1494		hypothetical protein	0.728733391	8.00E-08	3.19E-07
AB57_1495		D-alanyl-D-alanine carboxypeptidase family	0.531199125	1.72E-05	4.66E-05
AB57_1496		regulatory protein LysR:LysR, substrate-binding	-0.425662095	0.001778	0.003392
AB57_1497		ankyrin repeat protein	-0.394891881	0.032164	0.047413
AB57_1498		guanine deaminase	-0.071381156	0.626403	0.674728
AB57_1499		cyanate transport protein CynX	-0.395365591	0.000383	0.000818
AB57_1500		hypothetical protein	-0.198713604	0.064328	0.089119
AB57_1501		acetyltransferase, gnat family	-0.524299646	3.29E-06	1.02E-05
AB57_1502		hypothetical protein	-0.639211177	5.52E-09	2.62E-08
AB57_1503	soxR	redox-sensitive transcriptional activator SoxR	-0.150057603	0.492203	0.551529
AB57_1504		putative hemolysin	-0.486744995	1.68E-05	4.56E-05
AB57_1505		dihydrodipicolinate synthetase	-0.156546428	0.290393	0.348359
AB57_1506		hypothetical protein	-0.347071873	0.003695	0.006618
AB57_1509		proline racemase	-0.096787597	0.528016	0.585943
AB57_1510		FAD dependent oxidoreductase	-0.129678439	0.487227	0.547113
AB57_1512		pyridine nucleotide-disulphide oxidoreductase	-0.464690112	0.002597	0.004778
AB57_1513		transcriptional regulator, AraC family	-0.58497478	0.00967	0.015909
AB57_1514		shikimate transporter	-0.77406287	1.99E-11	1.47E-10
AB57_1515		aldehyde dehydrogenase	0.133132181	0.231902	0.285346
AB57_1516		amino acid transporter	-0.269901957	0.038625	0.055957
AB57_1517		L-serine dehydratase	-0.21114275	0.042964	0.061567
AB57_1518	paaZ	bifunctional aldehyde dehydrogenase/enoyl-CoA hydratase	0.548116534	0.00332	0.005986
AB57_1519	paaA	phenylacetate-CoA oxygenase subunit PaaA	0.318644501	0.092068	0.123246
AB57_1520	paaB	phenylacetate-CoA oxygenase subunit PaaB	0.238650376	0.131161	0.169624
AB57_1521	paaC	phenylacetate-CoA oxygenase, PaaI subunit	0.232136183	0.180034	0.226805

AB57_1522	paaD	phenylacetate-CoA oxygenase, PaaJ subunit	0.185356609	0.204515	0.254413
AB57_1523	paaE	phenylacetate-CoA oxygenase/reductase, PaaK subunit	0.178957167	0.251617	0.307255
AB57_1524	paaF	enoyl-coA hydratase	0.258020138	0.077086	0.105053
AB57_1525	paaG	phenylacetate degradation probable enoyl-CoA hydratase PaaB	0.51571397	0.001021	0.002026
AB57_1526	paaH	3-hydroxyacyl-CoA dehydrogenase	0.652551243	0.000283	0.000619
AB57_1527	paaJ	beta-ketoadipyl CoA thiolase	0.555218466	0.000717	0.001463
AB57_1528	paaK	phenylacetate-CoA ligase	0.086335426	0.608847	0.659466
AB57_1529	paaX	phenylacetic acid degradation operon negative regulatory prote	0.314907129	0.030889	0.045844
AB57_1530	paaY	phenylacetic acide degration protein PaaY	0.491573914	2.81E-05	7.39E-05
AB57_1531		thioesterase domain protein	1.303880804	3.90E-32	8.02E-30
AB57_1532		putative exonuclease	-0.124794226	0.308352	0.367204
AB57_1533		UvrD/REP helicase	-0.69786111	4.24E-10	2.46E-09
AB57_1534		transcriptional regulator, TetR family	-0.672962784	2.81E-06	8.78E-06
AB57_1535		hypothetical protein	-0.863768611	4.19E-12	3.53E-11
AB57_1536		putative aminotransferase	-0.927000161	3.09E-05	8.08E-05
AB57_1538		hypothetical protein	-0.848301959	7.73E-06	2.24E-05
AB57_1539		cold-shock DNA-binding domain protein	-1.04768262	1.81E-14	2.22E-13
AB57_1540		hypothetical protein	-2.380602589	3.97E-44	2.45E-41
AB57_1541		hypothetical protein	-1.465905792	6.59E-15	9.11E-14
AB57_1542		hypothetical protein	-1.329544715	1.06E-05	2.99E-05
AB57_1543		hypothetical protein	-1.341371149	1.50E-14	1.88E-13
AB57_1544		transcriptional regulator, TetR family	-1.401334933	9.12E-15	1.21E-13
AB57_1545		transcriptional regulator, LysR family	-0.951073405	9.62E-09	4.41E-08
AB57_1546		L-carnitine dehydratase/bile acid-inducible protein F	-0.088896206	0.527347	0.585414
AB57_1547		3-hydroxy-3-methylglutaryl-CoA lyase	-0.511803859	1.06E-05	2.98E-05
AB57_1548		major facilitator superfamily MFS_1	-0.026452911	0.849529	0.876047
AB57_1549		catalase	-0.545196801	1.22E-05	3.41E-05
AB57_1550		cytochrome B561	-0.462594915	3.92E-05	0.0001
AB57_1551		hypothetical protein	0.39871949	0.001219	0.002382
AB57_1552		transcriptional regulator, GntR family	0.483848988	4.75E-06	1.43E-05
AB57_1553		hypothetical protein	0.50993719	0.004695	0.008237
AB57_1554		hydrolase	0.495008749	0.000223	0.000499
AB57_1555		flavoprotein oxidoreductase	0.536753013	0.000793	0.001609
AB57_1556		monooxygenase	0.524289885	3.06E-05	8.01E-05
AB57_1557		aldehyde dehydrogenase	0.057793801	0.589436	0.642012
AB57_1558		hypothetical protein	-0.206561136	0.446255	0.506797
AB57_1559		permease, cytosine/purines, uracil, thiamine, allantoin permeas	0.129559271	0.277207	0.334202
AB57_1560		hypothetical protein	0.029668611	0.851863	0.87821
AB57_1561		succinate-semialdehyde dehydrogenase (NADP+)	-0.467484721	2.43E-05	6.46E-05
AB57_1562		4-carboxymuconolactone decarboxylase	0.023396159	0.864903	0.88967
AB57_1563		transcriptional regulator, LysR family	-0.595410048	0.001451	0.002793
AB57_1564		acyl carrier protein phosphodiesterase	-0.437056093	0.03362	0.049343
AB57_1565		P-hydroxybenzoate hydroxylase transcriptional activator	0.289048574	0.019618	0.030232
AB57_1566	pobA	4-hydroxybenzoate 3-monooxygenase	1.091941295	3.73E-06	1.14E-05
AB57_1567		transcriptional regulator, GntR family	-0.023236024	0.868998	0.893385
AB57_1568		2-aminoethylphosphonate ABC transport system, 1-aminoethyl	-0.260118071	0.218161	0.269604
AB57_1569		ABC transporter, ATP-binding protein	-0.434506296	0.112955	0.148098
AB57_1570		ABC transporter, permease	-0.306533047	0.095633	0.127131
AB57_1571		FAD dependent oxidoreductase	-0.655542031	0.00452	0.007961
AB57_1572	phnW	2-aminoethylphosphonate--pyruvate transaminase	0.483705804	0.000157	0.00036
AB57_1573	phnX	phosphonoacetaldehyde hydrolase	0.080945925	0.567283	0.622094
AB57_1574		cis-muconate transport protein	0.056756776	0.669026	0.713782
AB57_1575		acyl-CoA dehydrogenase	0.557650117	0.000243	0.000539
AB57_1576		L-carnitine dehydrogenase	-0.501564852	0.000584	0.001207
AB57_1577		transcriptional regulator, IclR family	0.390205445	0.000513	0.001072
AB57_1578		enoyl-CoA hydratase/isomerase	-0.442432016	0.001435	0.002766
AB57_1579		2-nitropropane dioxygenase	-1.01784001	1.66E-09	8.74E-09
AB57_1580		major facilitator superfamily MFS_1	-0.311440408	0.015562	0.024367

AB57_1581		transcriptional regulator, IclR family	-0.212129629	0.078595	0.106873
AB57_1582		acetyl-CoA acetyltransferase	0.176698895	0.138556	0.178148
AB57_1583		3-hydroxy-acyl-CoA dehydrogenase	-0.168068903	0.139607	0.179232
AB57_1584		3-ketoacyl-(acyl-carrier-protein) reductase	-0.287362003	0.083553	0.112986
AB57_1585		enoyl-CoA hydratase	0.218264676	0.190918	0.239294
AB57_1586		acyl-CoA dehydrogenase	-0.043394644	0.706911	0.748803
AB57_1587		MFS short chain dicaboxylate:H+ symporter	-0.241137944	0.017717	0.027509
AB57_1588		3-oxoadipate CoA-transferase subunit A	-0.163782023	0.167822	0.212506
AB57_1589		3-oxoadipate CoA-transferase subunit B	-0.026906806	0.82029	0.850757
AB57_1590		hypothetical protein	0.175145929	0.214921	0.265867
AB57_1591		major facilitator superfamily MFS_1	-0.302580152	0.007892	0.013255
AB57_1592		thioesterase superfamily protein	-0.257060204	0.056793	0.079567
AB57_1593		acyl-CoA dehydrogenase	-0.183290393	0.208592	0.25899
AB57_1594		hypothetical protein	-0.077274286	0.480073	0.540393
AB57_1595		indolepyruvate ferredoxin oxidoreductase	-0.915230748	9.37E-09	4.30E-08
AB57_1596		transcriptional regulator, LysR family	-0.366797748	0.004498	0.007933
AB57_1597		hydroxymethylglutaryl-CoA lyase	-0.773774297	8.22E-09	3.81E-08
AB57_1598		methylcrotonoyl-CoA carboxylase subunit alpha	-0.293679681	0.100234	0.132832
AB57_1599		3-methylglutaconyl-CoA hydratase	0.338948833	0.058308	0.081535
AB57_1600		methylcrotonoyl-CoA carboxylase beta chain	0.793952739	3.37E-05	8.72E-05
AB57_1601		isovaleryl-CoA dehydrogenase	1.246310293	9.11E-14	1.00E-12
AB57_1602		transcriptional regulator AcrR family	-0.272095657	0.15798	0.20073
AB57_1603		long-chain fatty-acid-CoA ligase	0.136566001	0.375612	0.435937
AB57_1604		putative SAM-dependent methyltransferase	0.118590652	0.351452	0.411249
AB57_1605		hypothetical protein	0.27744271	0.02873	0.042846
AB57_1606		lipolytic enzyme	-0.416116145	0.00072	0.001468
AB57_1608		transcriptional regulator, LysR family	-0.433588587	0.006646	0.011326
AB57_1610		hypothetical protein	-1.144410585	2.65E-10	1.59E-09
AB57_1611		hypothetical protein	-0.917768582	4.89E-09	2.35E-08
AB57_1612		hypothetical protein	-0.851299072	1.07E-14	1.38E-13
AB57_1613		surface antigen	-0.957855507	4.63E-10	2.67E-09
AB57_1614		hypothetical protein	-1.226571647	1.84E-16	3.41E-15
AB57_1615	cinA	competence/damage-inducible protein CinA	-1.008917589	1.05E-16	2.03E-15
AB57_1616		hypothetical protein	-1.426914986	4.98E-13	4.85E-12
AB57_1617		catalase	-0.288877678	0.088907	0.119447
AB57_1620		hypothetical protein	-0.674282358	0.000621	0.001278
AB57_1621		hypothetical protein	-0.750785197	8.86E-06	2.54E-05
AB57_1622		hypothetical protein	0.157312764	0.610655	0.661037
AB57_1623		DNA polymerase V component	-0.363244278	0.037951	0.055088
AB57_1624		transporter, LysE family	-0.460847416	0.000418	0.000887
AB57_1625		proline dehydrogenase transcriptional activator	0.007687032	0.972856	0.978409
AB57_1626		sensor histidine kinase/response regulator	-0.719156355	8.24E-09	3.81E-08
AB57_1629		two component transcriptional regulator, LuxR family	-0.253907534	0.135418	0.17452
AB57_1630		acetyltransferase, gnat family	-0.166996543	0.131579	0.170047
AB57_1631		ABC-type amino acid transport system	-1.146018613	0.00157	0.003008
AB57_1632		ArtM protein	-1.440268857	0.0052	0.009054
AB57_1633		glutamate/aspartate ABC transporter, ATP-binding protein	-1.273490064	0.004782	0.008382
AB57_1634		ABC transporter, periplasmic binding protein	-1.058920609	2.63E-11	1.90E-10
AB57_1635		ABC transporter, periplasmic binding protein	-0.756228145	6.02E-11	4.05E-10
AB57_1636		transcriptional regulator, LysR family	-0.257914837	0.024295	0.036781
AB57_1637		lysine exporter protein	-0.571757892	4.14E-05	0.000106
AB57_1638		cysteine desulfurase	0.078968309	0.529988	0.58764
AB57_1639		hypothetical protein	-0.742001788	1.14E-09	6.18E-09
AB57_1640		serine acetyltransferase	-1.609953079	0.000535	0.001113
AB57_1641		rhodanese domain protein	-1.603371528	4.94E-05	0.000124
AB57_1642		3-oxoacyl-[acyl-carrier-protein] reductase	-0.541913165	0.00325	0.005877
AB57_1643		transcriptional regulator, LysR family	-0.49028826	0.001193	0.002335
AB57_1644		glutathione S-transferase family protein	-0.34921025	0.001214	0.002374

AB57_1645		glutathione S-transferase family protein	-1.125393342	2.44E-16	4.43E-15
AB57_1646		transcriptional regulator, LysR family	-0.565947273	0.000253	0.000558
AB57_1647		LrgA family protein	-0.311728901	0.239713	0.294077
AB57_1648		LrgB family protein	-0.682479278	0.00049	0.001029
AB57_1649		transcriptional regulator, GntR family	-0.756712523	3.68E-05	9.48E-05
AB57_1650		negative transcriptional regulator	0.051573081	0.751773	0.788424
AB57_1651		acetyltransferase	0.478135376	0.005191	0.009043
AB57_1652		MFS permease	-0.352634996	0.007465	0.012589
AB57_1654	mdcA	malonate decarboxylase, alpha subunit	-0.584244673	0.000603	0.001246
AB57_1655	mdcB	triphosphoribosyl-dephospho-CoA synthase	-0.660986676	0.000557	0.001154
AB57_1656	mdcC	malonate decarboxylase subunit delta	-0.459256747	0.031572	0.046671
AB57_1657	mdcD	malonate decarboxylase subunit beta	-0.233220696	0.076867	0.104793
AB57_1658	mdcE	malonate decarboxylase, gamma subunit	-0.515795006	0.000334	0.00072
AB57_1659	mdcG	phosphoribosyl-dephospho-CoA transferase	-0.583711747	0.004167	0.007384
AB57_1660	mdcH	malonate decarboxylase, epsilon subunit	-0.474455528	0.012792	0.020516
AB57_1661	madL	malonate transporter, MadL subunit	0.00818907	0.956973	0.966112
AB57_1662	madM	malonate transporter, MadM subunit	-0.052727459	0.630352	0.6776
AB57_1663	mdcR	malonate utilization transcriptional regulator, LysR family	-0.294534906	0.012298	0.019784
AB57_1664		aminotransferase	0.151396825	0.179508	0.226296
AB57_1666	cydB	cytochrome D ubiquinol oxidase, subunit II	0.204250087	0.158507	0.201261
AB57_1667		cytochrome bd ubiquinol oxidase, subunit I	0.07427579	0.563509	0.619057
AB57_1669		hypothetical protein	-0.389944015	0.094639	0.126095
AB57_1670		acyl-CoA dehydrogenase family protein	-0.878715016	6.07E-05	0.000149
AB57_1671		monooxygenase, NtaA/SnaA/SoxA family	-1.649279408	2.09E-22	1.02E-20
AB57_1672		sugar transport protein	-1.135328034	1.90E-11	1.42E-10
AB57_1673		hypothetical protein	-0.321051104	0.009294	0.015331
AB57_1674	tauA	taurine ABC transporter, periplasmic binding protein	-1.446303705	0.002891	0.005272
AB57_1675	tauB	taurine import ATP-binding protein	-1.469627237	0.003774	0.006746
AB57_1676	tauC	taurine transport system permease protein	-1.507820303	0.000123	0.000289
AB57_1677	tauD	taurine dioxygenase	-1.673356802	1.75E-25	1.54E-23
AB57_1678		Asp/Glu racemase	-0.989929095	8.99E-12	7.17E-11
AB57_1679		permease for cytosine/purines, uracil, thiamine, allantoin	-0.694584684	7.39E-05	0.000179
AB57_1680		transcriptional regulator, GntR family	-0.035035662	0.771405	0.806271
AB57_1681		transcriptional regulator, LysR family	-0.408180135	0.002359	0.004373
AB57_1682		isochorismatase hydrolase	-0.883198153	3.70E-08	1.55E-07
AB57_1683		amidohydrolase	-0.428385182	0.000191	0.000433
AB57_1687	arsB	arsenical-resistance protein	-0.616446795	0.000827	0.001668
AB57_1688		transcriptional regulator, LysR family	-0.420014509	0.001452	0.002794
AB57_1689		chromate transporter	-0.613992791	0.003461	0.006225
AB57_1690		chromate transporter	-0.836183636	3.82E-05	9.80E-05
AB57_1691		FAD-dependent pyridine nucleotide-disulphide oxidoreductase	0.566032061	5.63E-05	0.00014
AB57_1692		hypothetical protein	-0.260801053	0.014931	0.023509
AB57_1693		hypothetical protein	1.094505627	1.47E-11	1.11E-10
AB57_1694		serine acetyltransferase	0.413577859	0.000607	0.001253
AB57_1695		RNA methyltransferase, TrmH family, group 1	0.668663854	1.87E-08	8.20E-08
AB57_1696		DNA polymerase III subunit alpha	0.166421332	0.216585	0.267836
AB57_1697		L-asparaginase 2	-0.297965924	0.052914	0.074526
AB57_1698		proton/sodium-glutamate symport protein	-0.267755615	0.085592	0.115286
AB57_1699		aminotransferase AlaT	-0.071725651	0.611675	0.661754
AB57_1700	msrB	methionine-R-sulfoxide reductase	-1.08258309	1.55E-17	3.47E-16
AB57_1701		glutathione peroxidase	-0.431723201	0.000105	0.000248
AB57_1702		transcriptional regulator, AraC family	-0.41397799	0.002156	0.004031
AB57_1703		lysine exporter protein	-0.371911197	0.013515	0.021545
AB57_1704		succinyldiaminopimelate transaminase	1.183816778	1.71E-09	9.00E-09
AB57_1705	glnD	[protein-PII] uridylyltransferase	0.249223129	0.066945	0.092459
AB57_1706	purT	phosphoribosylglycinamide formyltransferase 2	0.295366543	0.01117	0.018096
AB57_1707		hypothetical protein	-0.308582255	0.014909	0.023484
AB57_1708		hypothetical protein	-0.612888187	7.66E-06	2.23E-05

AB57_1709		putative amino acid transporter	-0.438195569	0.000105	0.000249
AB57_1710		hypothetical protein	1.2505913	7.00E-25	5.28E-23
AB57_1711		hypothetical protein	-0.901361087	8.64E-11	5.65E-10
AB57_1712		transcriptional regulator, Crp/Fnr family	-0.321409363	0.017178	0.026717
AB57_1713		hypothetical protein	-0.646835477	4.14E-05	0.000106
AB57_1714	ychF	GTP-dependent nucleic acid-binding protein EngD	2.407378071	1.58E-21	7.13E-20
AB57_1715		D-methionine transport system permease protein MetI	0.339020826	0.030305	0.045032
AB57_1716		D-and L-methionine transport protein	1.118929461	3.35E-15	4.86E-14
AB57_1717		D-methionine transport protein	1.536689293	8.07E-27	9.33E-25
AB57_1718		D-methionine transport protein	0.934824056	1.13E-12	1.06E-11
AB57_1719		hypothetical protein	-0.929750229	4.16E-13	4.11E-12
AB57_1722		putative Acyl-CoA dehydrogenase	-0.871733053	0.021176	0.032444
AB57_1723		acyl-CoA dehydrogenase family protein	-1.186867422	0.001545	0.002963
AB57_1724		glutathione S-transferase	-0.734093282	3.52E-09	1.75E-08
AB57_1725	gltI	glutamate/aspartate ABC transporter, periplasmic glutamate/as	-1.302788119	4.32E-14	4.96E-13
AB57_1726	gltJ	glutamate/aspartate transport system permease protein GltJ	-0.144835296	0.213093	0.264224
AB57_1727	gltK	glutamate/aspartate transport system permease protein GltK	0.244279185	0.085154	0.114822
AB57_1728	gltL	glutamate/aspartate transport ATP-binding protein GltL	0.082438557	0.584435	0.637314
AB57_1729		hypothetical protein	-0.448411076	0.017825	0.027641
AB57_1730		transcriptional regulator, AsnC family	-0.29282045	0.004202	0.007443
AB57_1731		hypothetical protein	0.768890265	8.47E-10	4.71E-09
AB57_1732		1-acyl-sn-glycerol-3-phosphate acyltransferase	0.57814749	9.78E-06	2.77E-05
AB57_1733		transcriptional regulator, TetR family	-0.432386752	0.000455	0.000959
AB57_1734		hypothetical protein	-1.261490992	2.44E-16	4.43E-15
AB57_1735		phage integrase	-0.55891964	6.85E-07	2.38E-06
AB57_1736		hypothetical protein	-0.635037834	0.006326	0.010831
AB57_1737		transcriptional Regulator, LysR family	-0.501374357	1.76E-05	4.75E-05
AB57_1738		hypothetical protein	-0.314319191	0.014617	0.023072
AB57_1739		cytosine/purines/uracil/thiamine/allantoin permease family pro	0.134726028	0.266878	0.323436
AB57_1740		hypothetical protein	-1.383103362	4.82E-16	8.21E-15
AB57_1741		hypothetical protein	-1.206686603	2.75E-12	2.42E-11
AB57_1742		transcriptional regulator, LysR family	-0.450630147	0.000808	0.001636
AB57_1743		hypothetical protein	-0.27824275	0.164803	0.208897
AB57_1744		fimbrial protein	-0.295898777	0.076298	0.104132
AB57_1745		fimbrial biogenesis outer membrane usher protein	-0.274449337	0.087989	0.118299
AB57_1746		pili assembly chaperone	-0.458145045	0.008715	0.014505
AB57_1747		fimbrial protein	0.192013375	0.139794	0.179409
AB57_1748		hypothetical protein	-0.277740188	0.299653	0.358113
AB57_1749		hypothetical protein	0.416446126	0.009245	0.01527
AB57_1750	bioB	biotin synthase	0.808371519	4.78E-09	2.31E-08
AB57_1751		iron-sulfur cluster binding protein	0.162801581	0.166075	0.210438
AB57_1752		carbohydrate kinase family	-0.728143919	1.53E-09	8.16E-09
AB57_1753	ruvC	Holliday junction resolvase	-0.215749008	0.083831	0.113203
AB57_1755		transcriptional regulator, XRE family	0.011214505	0.943006	0.954355
AB57_1756	yncA	phosphinothricin acetyltransferase	-0.07960927	0.548718	0.606047
AB57_1757		carbapenem-hydrolyzing oxacillinase OXA-69	-0.598598121	0.002921	0.005319
AB57_1758	fxsA	suppressor of F exclusion of phage T7	-0.539695501	5.84E-05	0.000144
AB57_1759		hypothetical protein	-0.556890849	7.43E-06	2.17E-05
AB57_1760		hypothetical protein	-0.802274329	5.44E-05	0.000135
AB57_1761	metK	S-adenosylmethionine synthetase	1.220967364	1.57E-14	1.96E-13
AB57_1762	tkt	transketolase	1.577505077	1.89E-11	1.41E-10
AB57_1763		OsmC family protein	-0.420680512	9.38E-05	0.000224
AB57_1764		hypothetical protein	0.093282716	0.473365	0.533979
AB57_1765		hypothetical protein	-0.736510246	5.64E-11	3.84E-10
AB57_1766		hypothetical protein	-0.819060724	2.28E-11	1.66E-10
AB57_1767		hypothetical protein	-0.808242408	3.82E-10	2.24E-09
AB57_1768	trmA	tRNA (uracil-5-)-methyltransferase	1.329476994	1.47E-13	1.54E-12
AB57_1769		hypothetical protein	-0.257171102	0.105393	0.13922

AB57_1770		bifunctional proline dehydrogenase/pyrroline-5-carboxylate deh	3.510271945	2.99E-25	2.41E-23
AB57_1771		leucine-responsive regulatory protein	-0.351277172	0.006723	0.011432
AB57_1772	putP	sodium/proline symporter	1.695307841	3.50E-15	5.06E-14
AB57_1773		NAD-dependent deacetylase regulatory protein	-0.153154879	0.271784	0.328628
AB57_1774	gcvH	glycine cleavage system protein H	1.236318337	1.81E-18	4.79E-17
AB57_1775		transcriptional regulator, AraC family	0.006251726	0.957389	0.966268
AB57_1776		MaoC domain protein dehydratase	-0.021153699	0.886341	0.907365
AB57_1779		nucleoprotein/polynucleotide-associated enzyme	0.967576577	6.65E-14	7.37E-13
AB57_1780		permease	1.038038579	3.82E-11	2.69E-10
AB57_1781		serine/threonine transporter SstT	1.509621801	6.43E-15	8.95E-14
AB57_1782		transcriptional regulator, ArsR family	-0.62495168	6.46E-09	3.05E-08
AB57_1783		transcriptional regulator, TetR family	0.388388744	0.001086	0.002144
AB57_1784		cupin family protein	1.459267989	6.50E-21	2.51E-19
AB57_1785	maf	septum formation protein Maf	0.217149053	0.039347	0.056913
AB57_1786		hypothetical protein	-0.594051434	9.08E-08	3.60E-07
AB57_1787	pgk	phosphoglycerate kinase	1.913388781	9.03E-12	7.19E-11
AB57_1788		hypothetical protein	1.113488849	7.04E-08	2.84E-07
AB57_1789	fba	fructose-1,6-bisphosphate aldolase	1.50702831	3.93E-15	5.64E-14
AB57_1790		PpiC-type peptidyl-prolyl cis-trans isomerase	0.563023697	0.000141	0.000327
AB57_1791		organic solvent tolerance protein	0.43083674	0.002533	0.004669
AB57_1792		aminoglycoside phosphotransferase	0.96051272	6.81E-16	1.14E-14
AB57_1793		nucleotidyl transferase family protein	0.733760045	5.48E-08	2.24E-07
AB57_1794	gidB	16S rRNA methyltransferase GidB	0.643281463	4.44E-09	2.17E-08
AB57_1795		sporulation initiation inhibitor protein soj	0.789051104	1.32E-15	2.08E-14
AB57_1796		chromosome partitioning protein ParB	0.543034942	5.42E-06	1.61E-05
AB57_1797		MotA/TolQ/ExbB proton channel	-0.685052779	2.14E-08	9.37E-08
AB57_1798		biopolymer transport protein ExbD/TolR	-0.158493249	0.200019	0.249518
AB57_1799	msbA	lipid A export permease/ATP-binding protein MsbA	0.485603662	0.003906	0.006954
AB57_1800	lpxK	tetraacyldisaccharide 4'-kinase	0.278144602	0.014268	0.022581
AB57_1801		3-deoxy-manno-octulosonate cytidylyltransferase	0.733825481	7.52E-08	3.03E-07
AB57_1802		3-deoxy-manno-octulosonate cytidylyltransferase	0.649928418	1.19E-07	4.62E-07
AB57_1803		DNA polymerase III delta prime subunit	0.43341939	9.06E-05	0.000217
AB57_1804		type 4 fimbrial biogenesis protein	0.214975184	0.065972	0.091217
AB57_1805		TatD-related deoxyribonuclease	0.419491768	0.000174	0.000395
AB57_1806		transcriptional regulator, TetR family	0.38589945	0.000321	0.000694
AB57_1807	gspG	general secretion pathway protein G	0.091926581	0.403964	0.464905
AB57_1808	gspI	general secretion pathway protein I	-0.402157589	0.034236	0.050148
AB57_1809	gspJ	general secretion pathway protein J	-0.338773868	0.022391	0.034149
AB57_1810	gspK	general secretion pathway protein K	-0.13024088	0.325923	0.385646
AB57_1811		putative 6-pyruvoyl tetrahydrobiopterin synthase	-0.220258595	0.105019	0.13884
AB57_1812	ung	uracil-DNA glycosylase	0.568575386	5.35E-08	2.19E-07
AB57_1813		putative enoyl-CoA hydratase/isomerase	1.017122372	5.43E-10	3.11E-09
AB57_1814		tRNA-specific adenosine deaminase	0.37197721	0.000557	0.001154
AB57_1815		hypothetical protein	0.836798979	1.41E-12	1.29E-11
AB57_1816	cmk	cytidylate kinase	0.666655497	0.000238	0.000529
AB57_1817	rpsA	30S ribosomal protein S1	1.02894102	4.52E-09	2.20E-08
AB57_1818	ihfB	integration host factor, beta subunit	-0.011154454	0.928835	0.941817
AB57_1819		hypothetical protein	-0.317920997	0.016035	0.025075
AB57_1820		hypothetical protein	0.059106217	0.589177	0.641918
AB57_1821	pyrF	orotidine 5'-phosphate decarboxylase	1.825960422	5.47E-29	8.43E-27
AB57_1822		monooxygenase, flavin-binding family	-0.347203582	0.015293	0.023987
AB57_1823		transcriptional regulator, AraC family	-0.40568926	0.008745	0.014549
AB57_1824		AFG1-family ATPase	0.756022699	2.42E-06	7.67E-06
AB57_1825	glcB	malate synthase G	0.828581021	9.65E-07	3.28E-06
AB57_1826		acetyltransferase, gnat family	0.388112556	0.17295	0.218476
AB57_1827		biopolymer transport protein ExbD/TolR	-0.788080285	1.92E-09	1.00E-08
AB57_1828		biopolymer transport protein ExbD/TolR	-0.393769861	0.047348	0.067199
AB57_1829		biopolymer transport protein	0.031979521	0.786761	0.820929

AB57_1830		TonB family protein	-0.701205612	1.71E-06	5.58E-06
AB57_1831		TonB-dependent receptor	-1.206139072	4.81E-17	9.87E-16
AB57_1832		heme-binding protein A	0.109915814	0.346945	0.407135
AB57_1833		heme-binding protein A	0.260523761	0.06803	0.093782
AB57_1834		Zn-dependent oligopeptidase	0.330577742	0.019698	0.030342
AB57_1835		ABC-type dipeptide/oligopeptide/nickel transport system perme	0.112241577	0.415401	0.476436
AB57_1836		ABC-type dipeptide/oligopeptide/nickel transport system perme	-0.18431661	0.129046	0.16724
AB57_1837		glutathione import ATP-binding protein GsiA	0.188553038	0.070781	0.09714
AB57_1838		hypothetical protein	-0.355382788	0.001312	0.002549
AB57_1839		hypothetical protein	-0.764908796	2.86E-08	1.22E-07
AB57_1840		3'(2'),5'-bisphosphate nucleotidase	0.110855963	0.313912	0.372626
AB57_1841		phosphoglycerate mutase	-0.266123129	0.025362	0.038192
AB57_1842	rpsT	30S ribosomal protein S20	0.514790569	0.036597	0.053331
AB57_1843		nucleoside-diphosphate-sugar epimerase	-0.558129254	0.000812	0.001642
AB57_1844		ribonuclease activity regulator protein RraA	-0.322490349	0.007205	0.012201
AB57_1845		glutaredoxin	-0.457770485	0.000254	0.00056
AB57_1846		Dyp-type peroxidase	0.056631977	0.569566	0.624413
AB57_1847		hypothetical protein	-0.615400057	1.61E-08	7.13E-08
AB57_1848	mfd	transcription-repair coupling factor	-0.09921584	0.407336	0.468202
AB57_1849		histidine triad protein	-0.120107752	0.367523	0.427487
AB57_1850		adenylate/guanylate cyclase	-0.27228813	0.043272	0.06196
AB57_1851	fdx	ferredoxin, 2Fe-2S type	1.039120262	1.09E-15	1.75E-14
AB57_1852	hscA	chaperone protein HscA	0.893789006	1.43E-06	4.74E-06
AB57_1853	hscB	Fe-S protein assembly co-chaperone HscB	0.164786599	0.191704	0.240198
AB57_1854	iscA	iron-sulfur cluster assembly protein IscA	0.006334964	0.965656	0.972673
AB57_1855	iscU	scaffold protein	-0.203758952	0.187338	0.235205
AB57_1856	iscS	cysteine desulfurase IscS	0.799697477	2.75E-05	7.24E-05
AB57_1857		iscRSUA operon repressor	0.695568516	7.15E-10	4.03E-09
AB57_1858		hypothetical protein	-0.17933817	0.319334	0.378297
AB57_1859		hypothetical protein	-0.364280598	0.000391	0.000834
AB57_1860	hup	DNA-binding protein HU	-0.498988076	0.000462	0.000972
AB57_1861		peptidyl-prolyl cis-trans isomerase	1.088381298	4.97E-09	2.38E-08
AB57_1862		transcriptional regulator, AraC family	-0.593303519	2.13E-06	6.81E-06
AB57_1863		alkane 1-monooxygenase	-0.376659475	0.000446	0.000944
AB57_1864		acyl-CoA dehydrogenase, middle domain protein	-0.402969077	0.000166	0.000377
AB57_1865		acyl-CoA dehydrogenase	-0.679975956	8.00E-11	5.26E-10
AB57_1866		ABC-1 domain protein	-0.078525049	0.570563	0.625136
AB57_1867		hypothetical protein	-1.022638782	1.33E-14	1.69E-13
AB57_1868		hypothetical protein	0.208815213	0.135276	0.174397
AB57_1869		hypothetical protein	-0.46587402	0.000204	0.000459
AB57_1870		hypothetical protein	-0.611057853	1.53E-06	5.05E-06
AB57_1871		transporter, major facilitator family	-0.670307829	9.88E-08	3.89E-07
AB57_1872		siderophore biosynthesis protein	-0.479407881	1.44E-06	4.77E-06
AB57_1873		siderophore biosynthesis protein	0.091491562	0.446838	0.507303
AB57_1874		hypothetical protein	-0.157293316	0.329417	0.389283
AB57_1875		dimethylmenaquinone methyltransferase	-0.237819421	0.086561	0.116464
AB57_1876		TonB-dependent receptor	1.607211543	9.76E-11	6.33E-10
AB57_1877		hypothetical protein	0.038979932	0.825798	0.85539
AB57_1878		hypothetical protein	-0.24650748	0.02641	0.039657
AB57_1879		hypothetical protein	-0.021927412	0.910264	0.927306
AB57_1880		rhizobactin siderophore biosynthesis protein RhbD	0.15056112	0.288341	0.346159
AB57_1882		HAD-superfamily hydrolase	-0.039421249	0.756912	0.793139
AB57_1883		hypothetical protein	0.013818428	0.92252	0.936183
AB57_1884		bifunctional adenosylcobalamin biosynthesis protein CobP	0.165934188	0.188222	0.236236
AB57_1885	cobT	nicotinate-nucleotide--dimethylbenzimidazole phosphoribosyltr	0.666193533	1.36E-09	7.26E-09
AB57_1886		fructose-2,6-bisphosphatase	0.186986159	0.14672	0.187453
AB57_1887		histidine acid phosphatase family protein	-0.18895244	0.213265	0.264273
AB57_1888	cobS	cobalamin 5'-phosphate synthase	-0.591225445	2.17E-07	8.07E-07

AB57_1889		phospho-2-dehydro-3-deoxyheptonate aldolase	0.874058489	1.95E-09	1.02E-08
AB57_1890		hypothetical protein	-0.373672022	0.170853	0.216122
AB57_1891		hypothetical protein	-0.33595539	0.00662	0.011288
AB57_1893		outer-membrane receptor for Fe(III)-coprogen,Fe(III)-ferrioxami	-0.137067632	0.253641	0.309421
AB57_1894	lpxB	lipid-A-disaccharide synthase	0.04801504	0.649379	0.695025
AB57_1895		hypothetical protein	0.836635203	6.77E-09	3.18E-08
AB57_1896		hypothetical protein	-0.239054898	0.033604	0.049339
AB57_1897		hypothetical protein	-0.989353311	3.61E-08	1.51E-07
AB57_1898		putative porin	0.510374259	1.06E-06	3.57E-06
AB57_1899		histidine triad protein	0.284073523	0.042821	0.061409
AB57_1900		hypothetical protein	-0.179174174	0.112548	0.147669
AB57_1901		hypothetical protein	-0.653250341	2.88E-05	7.55E-05
AB57_1902		hypothetical protein	-0.835361306	9.13E-12	7.23E-11
AB57_1903		hypothetical protein	0.751616048	5.01E-09	2.40E-08
AB57_1904		hypothetical protein	-0.226103662	0.03216	0.047413
AB57_1905		UbiE/COQ5 methyltransferase	-0.615338636	2.51E-07	9.25E-07
AB57_1906		poly(R)-hydroxyalkanoic acid synthase	-0.55061217	3.29E-07	1.19E-06
AB57_1907	metZ	O-succinylhomoserine sulfhydrylase	1.193312138	2.05E-18	5.37E-17
AB57_1908		hypothetical protein	-0.917515121	4.08E-11	2.86E-10
AB57_1909		hypothetical protein	0.411722982	0.001229	0.0024
AB57_1910	recR	recombination protein RecR	0.456166585	1.74E-05	4.69E-05
AB57_1911		ribonuclease D	0.505096964	1.03E-06	3.49E-06
AB57_1912		hypothetical protein	-0.608109867	6.27E-05	0.000154
AB57_1914		hypothetical protein	-0.468524244	0.000155	0.000356
AB57_1915		hypothetical protein	-1.148786072	1.06E-14	1.38E-13
AB57_1916		hypothetical protein	-0.324229774	0.007101	0.012046
AB57_1919		AAA ATPase family protein	0.311453318	0.036891	0.053717
AB57_1920		hypothetical protein	0.550164245	0.002658	0.004877
AB57_1921	trpB	tryptophan synthase subunit beta	0.577414282	1.58E-05	4.31E-05
AB57_1922	prmB	N5-glutamine S-adenosyl-L-methionine-dependent methyltrans	2.373108687	2.15E-26	2.21E-24
AB57_1923	aroC	chorismate synthase	1.747739757	2.25E-17	4.97E-16
AB57_1924		GGDEF domain protein	-0.475214495	5.41E-06	1.61E-05
AB57_1925		hypothetical protein	-0.301722283	0.010744	0.017474
AB57_1926		hypothetical protein	-1.698541725	1.26E-13	1.34E-12
AB57_1927	lipA	lipoyl synthase	-0.365287078	0.001544	0.002963
AB57_1928		acetoin:2,6-dichlorophenolindophenol oxidoreductase alpha sul	-0.941128336	8.92E-19	2.42E-17
AB57_1929		acetoin:2,6-dichlorophenolindophenol oxidoreductase subunit	-0.79627024	5.04E-15	7.18E-14
AB57_1930		dihydrolipoamide acetyltransferase	-0.32250713	0.003241	0.005866
AB57_1931	lpdA	dihydrolipoamide dehydrogenase	-0.104584122	0.350711	0.410642
AB57_1932		acetoin dehydrogenase	-0.232414347	0.031335	0.046394
AB57_1933		zinc-binding alcohol dehydrogenase	-0.18710262	0.077278	0.105275
AB57_1934		hypothetical protein	0.402975696	0.001786	0.003407
AB57_1935		sigma-54 specific, transcriptional regulator, Fis family	-0.565554924	0.001789	0.00341
AB57_1936		metallo-beta-lactamase family protein	1.588559026	3.96E-08	1.65E-07
AB57_1937		oxidoreductase	2.146534046	4.13E-09	2.04E-08
AB57_1938		hypothetical protein	0.926174176	4.18E-06	1.28E-05
AB57_1939		homoserine dehydrogenase	-0.421501678	0.000256	0.000565
AB57_1940		hypothetical protein	-0.342307695	0.008575	0.014304
AB57_1941		transcriptional regulatory protein	-0.625028528	0.000286	0.000624
AB57_1942		transcriptional regulator, AraC type	-0.870599417	4.19E-16	7.37E-15
AB57_1943		fmn-dependent NADH-azoreductase	-0.057651023	0.677839	0.721467
AB57_1944		chromate transporter	-1.058886976	9.78E-20	3.07E-18
AB57_1945		transcriptional regulator, GntR family	0.526270035	0.000244	0.000542
AB57_1946		putative oxidoreductase	0.652422917	1.02E-09	5.57E-09
AB57_1947		4Fe-4S ferredoxin iron-sulfur binding	1.303211198	7.58E-13	7.23E-12
AB57_1948		ABC-type transporter, periplasmic component: TauT family	1.657489716	1.45E-26	1.63E-24
AB57_1949		ABC-type nitrate/sulfonate/bicarbonate transport system perm	1.700354332	2.06E-35	6.36E-33
AB57_1950		aliphatic sulfonates import ATP-binding protein SsuB	2.114631942	1.69E-47	1.25E-44

AB57_1951		HEAT domain containing protein	0.983301666	1.13E-14	1.45E-13
AB57_1952		hypothetical protein	-0.770108626	2.78E-07	1.01E-06
AB57_1953		dicarboxylic acid transport protein; alpha-ketoglutarate permea	-1.08656334	1.06E-12	1.00E-11
AB57_1954		TonB-dependent siderophore receptor	1.138877486	1.21E-08	5.48E-08
AB57_1955		aspartate ammonia-lyase	0.588756409	0.000234	0.00052
AB57_1956		hypothetical protein	1.010615107	2.77E-06	8.67E-06
AB57_1958		transcriptional regulator, LysR family	-0.244544399	0.022884	0.034801
AB57_1959		transcriptional regulator, LysR family	-0.01407521	0.890862	0.911053
AB57_1960		acetyl-CoA acetyltransferase	0.114029055	0.490092	0.549377
AB57_1961		short-chain fatty acid transporter	-0.697428778	5.77E-08	2.36E-07
AB57_1962		3-oxoacid CoA-transferase, subunit B	-0.268847283	0.042888	0.061483
AB57_1963		3-oxoacid CoA-transferase, subunit A	-0.006941907	0.955305	0.964692
AB57_1964		transcriptional regulator, LysR family	-0.607587787	1.17E-05	3.28E-05
AB57_1966		GntP family transporter	-0.473936145	7.10E-05	0.000173
AB57_1967		3-hydroxybutyrate dehydrogenase	-0.283689916	0.011314	0.018305
AB57_1968		transcriptional regulator, AraC family	-2.046919506	1.31E-22	6.63E-21
AB57_1969		4-hydroxybenzoate transporter	-0.700964528	4.88E-07	1.73E-06
AB57_1970		dienelactone hydrolase	1.687183801	2.13E-34	5.37E-32
AB57_1971		short chain dehydrogenase	1.385931837	4.51E-11	3.12E-10
AB57_1972		oxygenase subunit	1.441124057	6.72E-12	5.45E-11
AB57_1973		nitrilotriacetate monooxygenase component B	1.171087476	5.84E-07	2.04E-06
AB57_1974		hypothetical protein	0.673754013	0.001066	0.002107
AB57_1975		transcriptional regulator, AraC family	-1.392482498	3.83E-13	3.80E-12
AB57_1976		anthranilate dioxygenase reductase	0.665508856	4.51E-07	1.60E-06
AB57_1977	antB	anthranilate 1,2-dioxygenase, small subunit	1.207369045	1.19E-08	5.37E-08
AB57_1978	antA	anthranilate 1,2-dioxygenase, large subunit	1.14536873	1.58E-12	1.43E-11
AB57_1979		transcriptional regulator, ModE family	-0.710563823	0.000925	0.001853
AB57_1980	modA	molybdate ABC transporter, periplasmic molybdate-binding pro	-0.254153726	0.022556	0.034373
AB57_1981	modB	molybdate ABC transporter, permease protein	-0.122762033	0.365279	0.425412
AB57_1982	modC	molybdenum import ATP-binding protein ModC	-0.308882557	0.077643	0.105734
AB57_1983		2,3-dihydro-2,3-dihydroxybenzoate dehydrogenase	-0.885202996	1.59E-06	5.24E-06
AB57_1984		isochorismatase	-0.197484043	0.184504	0.231962
AB57_1985		transcriptional regulator, fur family	-0.587024891	0.005372	0.009341
AB57_1986		5'-nucleotidase	0.227902384	0.068248	0.094047
AB57_1987	ppk	polyphosphate kinase	-0.824256906	1.72E-12	1.54E-11
AB57_1988		hypothetical protein	-0.285670892	0.075991	0.103752
AB57_1989	pqqB	pyrroloquinoline quinone biosynthesis protein PqqB	0.652462841	2.71E-09	1.38E-08
AB57_1990	pqqC	pyrroloquinoline quinone biosynthesis protein PqqC	0.547700687	6.23E-06	1.84E-05
AB57_1991	pqqD	pyrroloquinoline quinone biosynthesis protein PqqD	0.441112888	0.00205	0.003857
AB57_1992	pqqE	pyrroloquinoline quinone biosynthesis protein PqqE	0.478459181	1.29E-05	3.57E-05
AB57_1993		dipeptidase	-0.661436496	8.38E-08	3.34E-07
AB57_1994		hypothetical protein	-1.181698377	5.14E-13	4.98E-12
AB57_1995		hypothetical protein	-1.069278121	2.02E-11	1.49E-10
AB57_1996		hypothetical protein	-0.742796993	2.54E-08	1.09E-07
AB57_1997		phospholipase D/Transphosphatidylase	-0.601996051	4.34E-05	0.00011
AB57_1998		hypothetical protein	-1.160885033	1.29E-12	1.19E-11
AB57_1999		hypothetical protein	-0.571460039	9.38E-06	2.66E-05
AB57_2000		hypothetical protein	-0.27638594	0.015232	0.023901
AB57_2001		hypothetical protein	-0.524435345	4.38E-07	1.56E-06
AB57_2002		alcohol dehydrogenase	0.109199705	0.309519	0.368356
AB57_2003		hypothetical protein	0.033609814	0.759167	0.794826
AB57_2004		fimbrial protein	0.668874923	4.31E-07	1.54E-06
AB57_2005		outer membrane fimbrial usher protein	1.534427145	7.24E-13	6.94E-12
AB57_2006		pili assembly chaperone	2.241373529	2.16E-14	2.61E-13
AB57_2007		fimbrial subunit	1.263290287	5.28E-07	1.86E-06
AB57_2008		phage replication protein	0.777234057	0.015055	0.023683
AB57_2009		hypothetical protein	0.422125218	0.000416	0.000886
AB57_2010		hypothetical protein	-0.146491127	0.33236	0.392009

AB57_2011	hypothetical protein	0.032057656	0.805925	0.838561
AB57_2012	hypothetical protein	-0.73684071	3.68E-09	1.83E-08
AB57_2014	putative phage-related protein	-0.5713923	3.21E-06	9.96E-06
AB57_2015	hypothetical protein	-0.662318489	3.31E-08	1.40E-07
AB57_2017	replication protein	0.566938593	0.020014	0.030804
AB57_2018	hypothetical protein	-0.07615274	0.473689	0.534019
AB57_2019	mobilization protein BmgB	-0.32865625	0.011369	0.018385
AB57_2020	hypothetical protein	1.205719587	0.01861	0.028786
AB57_2021	phage replication protein	0.764453464	0.014736	0.023252
AB57_2022	hypothetical protein	0.413652576	0.000497	0.00104
AB57_2023	hypothetical protein	-0.012181787	0.934343	0.946468
AB57_2024	hypothetical protein	0.014809245	0.91843	0.934034
AB57_2025	hypothetical protein	-0.782088487	1.06E-09	5.78E-09
AB57_2027	putative phage-related protein	-0.58658978	6.21E-07	2.16E-06
AB57_2028	hypothetical protein	-0.675234586	1.60E-08	7.10E-08
AB57_2030	replication protein	0.433446684	0.061766	0.085916
AB57_2031	hypothetical protein	-0.121631276	0.261068	0.31733
AB57_2032	hypothetical protein	-0.408423893	8.73E-05	0.00021
AB57_2033	hypothetical protein	-0.227544046	0.218776	0.270274
AB57_2035	putative phage-related protein	-0.349899267	0.027948	0.041815
AB57_2037	replication protein	0.486874607	0.039231	0.056767
AB57_2038	hypothetical protein	-0.020036101	0.856998	0.88252
AB57_2039	mobilization protein BmgB	-0.466908663	0.000344	0.000739
AB57_2040	phage replication protein	0.760376904	0.014784	0.023317
AB57_2041	hypothetical protein	0.355716294	0.003619	0.006492
AB57_2042	hypothetical protein	-0.141555492	0.318225	0.377261
AB57_2043	hypothetical protein	-0.225918165	0.093791	0.125145
AB57_2044	hypothetical protein	-0.805528553	4.24E-10	2.46E-09
AB57_2046	putative phage-related protein	-0.706429437	1.82E-07	6.85E-07
AB57_2047	hypothetical protein	-0.668897028	4.37E-08	1.81E-07
AB57_2048	mobilization protein BmgB	-0.442791212	0.000872	0.001754
AB57_2049	phage replication protein	0.702594085	0.03145	0.046528
AB57_2050	hypothetical protein	0.436184972	0.000517	0.001079
AB57_2052	replication protein	0.485230961	0.043378	0.062088
AB57_2053	hypothetical protein	-0.095625459	0.385725	0.445994
AB57_2054	mobilization protein BmgB	-0.437893268	0.000975	0.001942
AB57_2055	hypothetical protein	1.281017398	0.002143	0.004011
AB57_2056	phage replication protein	0.788941932	0.015449	0.024211
AB57_2057	hypothetical protein	0.400429628	0.002111	0.003961
AB57_2058	hypothetical protein	-0.128989827	0.347675	0.407732
AB57_2059	hypothetical protein	-0.125697876	0.341601	0.402011
AB57_2060	hypothetical protein	-0.730662417	1.56E-08	6.93E-08
AB57_2062	putative phage-related protein	-0.609884148	3.20E-07	1.16E-06
AB57_2063	hypothetical protein	-0.636442928	1.14E-07	4.44E-07
AB57_2064	hypothetical protein	-0.081665652	0.574488	0.628878
AB57_2065	hypothetical protein	0.049762601	0.719543	0.760008
AB57_2066	hypothetical protein	-0.768350669	4.15E-11	2.90E-10
AB57_2067	hypothetical protein	-0.614801473	0.021294	0.032611
AB57_2068	putative phage-related protein	-0.581539629	4.65E-06	1.41E-05
AB57_2069	hypothetical protein	-0.630531122	7.97E-09	3.71E-08
AB57_2070	hypothetical protein	-0.543977859	1.94E-06	6.26E-06
AB57_2071	hypothetical protein	-0.595725813	6.40E-05	0.000157
AB57_2072	phage replication protein	0.848121636	0.008893	0.014769
AB57_2073	hypothetical protein	0.460421468	0.000112	0.000264
AB57_2074	outer membrane protein E	-0.535898613	4.36E-06	1.33E-05
AB57_2075	hypothetical protein	0.083120929	0.553447	0.610359
AB57_2076	putative oxidoreductase	0.182231393	0.110602	0.14527
AB57_2077	transcriptional regulator, TetR family	-0.023932719	0.821273	0.851418

AB57_2078		flavin binding monooxygenase	-0.440988846	0.001428	0.002754
AB57_2079		hypothetical protein	0.100925191	0.367389	0.427466
AB57_2080	adeC	multidrug efflux protein AdeC	0.442546663	0.004554	0.008009
AB57_2081	adeB	multidrug efflux protein AdeB	0.33538607	0.067813	0.093552
AB57_2082	adeA	multidrug efflux protein AdeA	1.704819852	1.09E-14	1.41E-13
AB57_2083	adeR	AdeR	-0.512218797	1.91E-06	6.19E-06
AB57_2084	adeS	AdeS	-0.38450281	0.00113	0.002223
AB57_2085		hypothetical protein	-0.736972893	9.67E-05	0.00023
AB57_2086		hypothetical protein	-0.353000606	0.091641	0.122852
AB57_2087		transcriptional regulator, AraC family	-0.206277844	0.129994	0.168292
AB57_2088		alpha/beta hydrolase	-0.599810687	0.00016	0.000365
AB57_2089		short-chain dehydrogenase/reductase	-0.054965872	0.722061	0.76245
AB57_2090		short-chain dehydrogenase/reductase	0.051538493	0.706195	0.74826
AB57_2091		transcriptional regulator, LysR family	-0.400075923	0.0283	0.04229
AB57_2092		dienelactone hydrolase	-0.728986376	4.15E-08	1.73E-07
AB57_2093		acetyltransferase	-0.069498055	0.526464	0.584609
AB57_2094		hypothetical protein	-0.155178104	0.274817	0.331645
AB57_2095		endonuclease/exonuclease/phosphatase	-0.729509863	2.92E-07	1.06E-06
AB57_2096		hypothetical protein	-0.443435975	0.000197	0.000444
AB57_2097		transcriptional regulator, TetR family	-0.63802903	0.007167	0.012147
AB57_2099		type III restriction enzyme, res subunit	-0.839493454	6.94E-11	4.61E-10
AB57_2100		guanosine-3',5'-bis(diphosphate) 3'-pyrophosphohydrolase ((pp	-0.382225027	0.0133	0.02123
AB57_2101		hypothetical protein	-0.398064946	0.001182	0.002317
AB57_2102		putative acid phosphatase	-0.14163115	0.347376	0.407512
AB57_2103		hypothetical protein	-0.568666517	1.25E-05	3.47E-05
AB57_2104		outer membrane efflux protein	0.202408711	0.189191	0.23729
AB57_2105		auxin-responsive GH3-related protein	0.572736548	1.98E-05	5.32E-05
AB57_2106		hypothetical protein	0.562010707	3.60E-06	1.10E-05
AB57_2107		multidrug resistance protein VceB	0.273434539	0.043808	0.062655
AB57_2108		RND family drug transporter	-0.355403251	0.01815	0.028111
AB57_2109		indoleacetamide hydrolase	-0.941862568	2.17E-10	1.32E-09
AB57_2110		transcriptional regulator, LuxR family	-1.611988945	1.46E-16	2.73E-15
AB57_2112		methylenetetrahydrofolate reductase domain protein	0.85665658	9.57E-07	3.25E-06
AB57_2113		ADP-ribose pyrophosphatase	-0.108435041	0.344804	0.405007
AB57_2114		putative nicotinate phosphoribosyltransferase	-0.106114784	0.352745	0.412372
AB57_2115		ribose-phosphate pyrophosphokinase	-0.123516155	0.598536	0.650392
AB57_2118		2-hydroxy-3-oxopropionate reductase	-0.549973745	0.000332	0.000716
AB57_2119		transporter, anion:cation symporter family	-0.967885872	1.40E-13	1.48E-12
AB57_2120		nucleoside-diphosphate-sugar epimerase	-0.87575614	6.39E-05	0.000156
AB57_2121		transcriptional regulator, LysR family	-0.025290667	0.826876	0.856267
AB57_2122		fumarylacetoacetate hydrolase	-0.078848074	0.639801	0.68676
AB57_2123		dihydroxy-acid dehydratase	0.182917741	0.161065	0.20437
AB57_2124		NADP-dependent fatty aldehyde dehydrogenase	0.483401616	0.000104	0.000246
AB57_2125		transcriptional regulator, TetR family	-0.039875371	0.733946	0.772795
AB57_2126		transporter, major facilitator family	-0.363011437	0.044926	0.064032
AB57_2127		multidrug resistance efflux pump	-0.646707363	1.28E-07	4.96E-07
AB57_2128		hypothetical protein	-0.494739113	0.004506	0.007943
AB57_2129		hypothetical protein	-0.238933576	0.287527	0.345406
AB57_2130		transcriptional regulator, LysR family	-0.373851602	0.007824	0.013147
AB57_2131		transporter, major facilitator family	-1.007056499	6.99E-15	9.51E-14
AB57_2132		senescence marker protein-30	-0.672192094	0.000233	0.000518
AB57_2133		transcriptional regulator, GntR family	-0.368336833	0.005691	0.009831
AB57_2134		hypothetical protein	-0.206907836	0.083625	0.113006
AB57_2135		amidohydrolase family protein	-0.136908881	0.376873	0.436851
AB57_2136		transporter, anion:cation symporter (ACS) family	-0.482482202	4.93E-06	1.48E-05
AB57_2137		hypothetical protein	-0.146549292	0.156602	0.199115
AB57_2138		hypothetical protein	-0.46969674	8.28E-05	0.000199
AB57_2139		hypothetical protein	-0.865377637	4.75E-07	1.69E-06

AB57_2140		hypothetical protein	-0.442000531	2.84E-05	7.45E-05
AB57_2141		hypothetical protein	-0.267522965	0.044304	0.063267
AB57_2142		hypothetical protein	-0.819815872	8.00E-06	2.31E-05
AB57_2143		hypothetical protein	-0.563444605	4.63E-05	0.000117
AB57_2144		hypothetical protein	-0.375946211	0.007956	0.013356
AB57_2145		transcriptional regulator, TetR family	0.023331101	0.92504	0.938226
AB57_2147		thermostable carboxypeptidase 1	-0.295283659	0.05267	0.074212
AB57_2148		hypothetical protein	-0.466338263	0.00731	0.012356
AB57_2149		glutathione-regulated potassium-efflux system protein	-0.067027412	0.510098	0.569168
AB57_2150		quinoprotein glucose dehydrogenase-B	0.621000109	1.16E-05	3.25E-05
AB57_2151		transcriptional regulator, LysR family	-0.321734038	0.003044	0.005529
AB57_2152		isochorismatase hydrolase	0.712329953	1.28E-09	6.87E-09
AB57_2153		antibiotic biosynthesis monooxygenase	0.404155047	0.00045	0.000951
AB57_2154		hypothetical protein	-0.831324889	2.42E-07	8.96E-07
AB57_2155		L-sorbosone dehydrogenase	-1.195167531	5.22E-21	2.06E-19
AB57_2156		oxidoreductase, FAD/FMN-binding	-0.249648781	0.054501	0.076617
AB57_2157		hypothetical protein	-0.079902985	0.627607	0.675632
AB57_2158		putative acetoacetate decarboxylase	-0.316025169	0.14435	0.184617
AB57_2159		short-chain dehydrogenase	-0.26816924	0.290806	0.348666
AB57_2160		transcriptional regulator, AraC family	-0.613788919	0.003969	0.007064
AB57_2161		transcriptional regulator, TetR family	0.0860609	0.660667	0.705474
AB57_2162		zinc-dependent hydrolase	-0.683148287	1.04E-08	4.72E-08
AB57_2163		transcriptional regulator, BadM/Rrf2 family	0.219039382	0.065957	0.091217
AB57_2164		NADH dehydrogenase fad-containing subunit	0.071689486	0.531695	0.589356
AB57_2165		ThiJ/PfpI domain protein	-1.641238475	2.55E-36	8.58E-34
AB57_2166		transcriptional regulator, MerR family	-0.57079324	0.00824	0.01377
AB57_2167		ThiJ/PfpI domain protein	-0.458321106	0.010239	0.016718
AB57_2168		saccharopine dehydrogenase	-0.900862211	2.89E-09	1.46E-08
AB57_2169		oxidoreductase FMN-binding	-0.561292022	0.00029	0.000633
AB57_2170		alpha/beta hydrolase	-0.352074115	0.002742	0.005022
AB57_2171		hypothetical protein	-0.711187722	4.58E-08	1.89E-07
AB57_2172		NADP-dependent fatty aldehyde dehydrogenase	0.580768773	0.001271	0.002477
AB57_2173		hypothetical protein	0.456218384	0.027444	0.041111
AB57_2174		MFS family permease	-0.653437856	9.74E-05	0.000232
AB57_2175		dihydroxy-acid dehydratase	-0.485367915	0.002186	0.004079
AB57_2176		transcriptional regulator, GntR family	-0.206928789	0.051177	0.072246
AB57_2177		hypothetical protein	-0.213759569	0.061345	0.08549
AB57_2178	catR	ben operon transcriptional regulator BenM	-0.169730408	0.189049	0.237193
AB57_2179		muconate cycloisomerase	-0.987934095	2.45E-11	1.77E-10
AB57_2180	catC	muconolactone delta-isomerase	-0.377921363	0.001238	0.002415
AB57_2181	catA	catechol 1,2-dioxygenase	0.145329828	0.360394	0.420517
AB57_2182		3-oxoadipate CoA-transferase subunit A	0.094210473	0.372249	0.43244
AB57_2183		3-oxoadipate CoA-transferase subunit B	-0.29669327	0.004885	0.008546
AB57_2184	pcaF	beta-ketoadipyl CoA thiolase	0.5293954	0.00025	0.000553
AB57_2185	pcaD	3-oxoadipate enol-lactonase	0.156278783	0.204246	0.254191
AB57_2186		peptidase S45, penicillin amidase	-0.516603152	1.83E-06	5.96E-06
AB57_2187		phenylacetaldehyde dehydrogenase	-0.104192052	0.441241	0.50249
AB57_2188		hypothetical protein	-0.188952796	0.365453	0.42548
AB57_2189		tyramine oxidase	-0.68715743	2.66E-07	9.77E-07
AB57_2190		transcriptional regulator, AraC family	-0.718444507	0.002314	0.0043
AB57_2191		P-hydroxyphenylacetate hydroxylase C1:reductase component	0.569040744	0.000181	0.00041
AB57_2192		2Fe-2S iron-sulfur cluster binding domain protein	1.0073271	5.14E-13	4.98E-12
AB57_2193		short-chain dehydrogenase/reductase	0.808186892	4.41E-09	2.16E-08
AB57_2194		aromatic-ring-hydroxylating dioxygenase beta subunit	0.671337553	6.10E-07	2.13E-06
AB57_2195		ring hydroxylating dioxygenase, Rieske	0.476223838	0.004001	0.007118
AB57_2196		hypothetical protein	-0.055058928	0.662272	0.706984
AB57_2197		hypothetical protein	-0.091348295	0.481114	0.541286
AB57_2198		acyl-CoA dehydrogenase	-0.456151274	0.000422	0.000897

AB57_2199		Glu-tRNA amidotransferase	-0.721925508	1.12E-10	7.12E-10
AB57_2200		transcriptional regulator, MarR-family	-0.102183295	0.399408	0.459947
AB57_2202		general substrate transporter:Major facilitator superfamily	-1.439472182	2.18E-34	5.37E-32
AB57_2203		benzoate transport porin	-1.456220265	1.33E-22	6.63E-21
AB57_2204		short chain dehydrogenase	0.070779307	0.539844	0.597316
AB57_2205		phosphoglycerate mutase	0.401926666	0.000845	0.001702
AB57_2206		aminoglycoside phosphotransferase	-0.054788392	0.607731	0.658449
AB57_2207		acyl-CoA dehydrogenase domain protein	-0.041499013	0.697012	0.739377
AB57_2208		transcriptional regulator, LysR family	0.02924771	0.832865	0.861128
AB57_2209		pca operon regulatory protein	0.362206034	0.005821	0.010036
AB57_2210		metallo-beta-lactamase family protein	-0.576225704	2.63E-06	8.24E-06
AB57_2211		hypothetical protein	-0.973215391	1.64E-15	2.54E-14
AB57_2212		hypothetical protein	-0.45327867	0.001313	0.00255
AB57_2213		hypothetical protein	-0.199728304	0.085444	0.115171
AB57_2214		quinate/shikimate dehydrogenase	-0.336375445	0.033371	0.049036
AB57_2215		porin B	0.547691263	0.000175	0.000396
AB57_2216		3-dehydroshikimate dehydratase	0.535569799	0.001522	0.002923
AB57_2217	aroD	3-dehydroquinate dehydratase	0.896571198	4.20E-10	2.45E-09
AB57_2218	pcaG	protocatechuate 3,4-dioxygenase, alpha subunit	1.220450836	2.25E-16	4.13E-15
AB57_2219	pcaH	protocatechuate 3,4-dioxygenase, beta subunit	1.24123999	2.39E-17	5.24E-16
AB57_2220	pcaC	4-carboxymuconolactone decarboxylase	1.451032065	4.85E-21	1.93E-19
AB57_2221		4-hydroxybenzoate transporter	0.996146758	4.21E-10	2.45E-09
AB57_2222	pcaD	3-oxoadipate enol-lactonase	0.606610397	3.49E-06	1.07E-05
AB57_2223	pcaB	3-carboxy-cis,cis-muconate cycloisomerase	0.333771208	0.015212	0.02388
AB57_2224	pcaF	beta-ketoadipyl CoA thiolase	0.375064625	0.00403	0.007159
AB57_2225		3-oxoadipate CoA-transferase subunit B	0.361121764	0.001006	0.001998
AB57_2226		3-oxoadipate CoA-transferase subunit A	0.154190971	0.130605	0.168965
AB57_2227	ispD	2-C-methyl-D-erythritol 4-phosphate cytidylyltransferase	0.08629036	0.522845	0.581288
AB57_2228		septum formation initiator	-0.887228708	8.47E-11	5.56E-10
AB57_2229		hypothetical protein	-0.829516633	1.41E-12	1.29E-11
AB57_2230	eno	phosphopyruvate hydratase	1.691288509	2.05E-16	3.79E-15
AB57_2231		2-dehydro-3-deoxyphosphooctonate aldolase	1.33835918	2.23E-15	3.35E-14
AB57_2232	pyrG	CTP synthetase	0.754962928	4.57E-05	0.000115
AB57_2233		hypothetical protein	1.046419737	2.99E-13	3.01E-12
AB57_2236		alpha/beta hydrolase	-0.161510347	0.131666	0.170099
AB57_2237		hypothetical protein	-0.373099734	0.002132	0.003994
AB57_2238		NADH:flavin oxidoreductase/nadh oxidase	-0.109852728	0.505982	0.565185
AB57_2239		FAD/FMN-binding/pyridine nucleotide-disulphide oxidoreducta	-0.282373618	0.039917	0.057693
AB57_2240		transcriptional regulator, PadR family	-0.196477002	0.110873	0.145574
AB57_2241		putative peroxidase	-0.633686971	4.50E-10	2.60E-09
AB57_2242		phospho-2-dehydro-3-deoxyheptonate aldolase	-0.215673603	0.110153	0.144784
AB57_2243		hypothetical protein	-0.551026998	1.31E-06	4.37E-06
AB57_2244	clpA	ATP-dependent Clp protease ATP-binding subunit	-1.123284154	1.20E-12	1.11E-11
AB57_2245	clpS	ATP-dependent Clp protease adaptor protein ClpS	0.099796212	0.329296	0.389264
AB57_2246		hypothetical protein	0.375126905	0.000612	0.001262
AB57_2247	argC	N-acetyl-gamma-glutamyl-phosphate reductase	0.806972971	2.21E-09	1.14E-08
AB57_2249		hypothetical protein	0.125688758	0.239495	0.294005
AB57_2250		hypothetical protein	-0.736614396	2.05E-07	7.61E-07
AB57_2251	rpiA	ribose-5-phosphate isomerase A	0.53062348	9.15E-05	0.000219
AB57_2252	ilvA	threonine dehydratase	1.019547145	1.35E-08	6.07E-08
AB57_2253		K+ uptake system component	-0.052839481	0.647526	0.693243
AB57_2254		K+ uptake system component	-0.576546644	7.87E-09	3.67E-08
AB57_2255		phospholipase	0.324252223	0.047842	0.067875
AB57_2256		peptidase M16 domain protein	0.707172841	0.000347	0.000745
AB57_2257		ferrichrome-iron receptor	0.386848219	0.00484	0.008475
AB57_2258		ferrichrome-iron receptor	1.005878197	1.36E-09	7.26E-09
AB57_2259		sugar kinase, ribokinase family	1.543206088	1.16E-16	2.23E-15
AB57_2260		iron-sulfur cluster-binding protein, Rieske family	0.841733269	9.79E-07	3.32E-06

AB57_2261		hypothetical protein	-0.516355147	1.13E-06	3.80E-06
AB57_2262		cytochrome D ubiquinol oxidase subunit I	-0.107680267	0.505244	0.564604
AB57_2263	cydB	cytochrome D ubiquinol oxidase, subunit II	0.104258434	0.555024	0.611916
AB57_2264		hypothetical protein	-0.266815235	0.147001	0.187747
AB57_2265		hypothetical protein	0.961636232	2.17E-06	6.91E-06
AB57_2266		nitroreductase family protein	0.288364433	0.018895	0.029178
AB57_2267	ftsY	signal recognition particle-docking protein FtsY	0.898032316	1.51E-09	8.07E-09
AB57_2268		hypothetical protein	-0.091183435	0.418438	0.479771
AB57_2269		hypothetical protein	-0.332144165	0.266636	0.323354
AB57_2270		hypothetical protein	-1.004131755	3.79E-06	1.16E-05
AB57_2272		hypothetical protein	0.269061212	0.014614	0.023072
AB57_2273		CBS domain containing protein	-0.131714272	0.308698	0.367498
AB57_2274		acetylornithine aminotransferase	0.847690186	1.00E-11	7.86E-11
AB57_2275		glutaredoxin-related protein	0.932095209	7.48E-12	6.03E-11
AB57_2276		hypothetical protein	-0.589418282	1.22E-07	4.73E-07
AB57_2277		transcriptional regulator, LysR family	-0.174275098	0.119355	0.15562
AB57_2278	map	methionine aminopeptidase, type I	-0.332397197	0.000904	0.001814
AB57_2279	brnQ	branched-chain amino acid transport system II carrier protein	1.170654669	3.08E-09	1.56E-08
AB57_2280		glycolate/propanediol utilization protein	0.045420531	0.712637	0.754006
AB57_2281		hypothetical protein	-0.180611889	0.276127	0.333117
AB57_2282		hypothetical protein	-0.464122115	0.000151	0.000347
AB57_2283		alpha/beta hydrolase	-0.576285805	0.00349	0.006275
AB57_2284		alpha/beta hydrolase	-0.296114468	0.09537	0.126932
AB57_2285		multiphosphoryl transfer protein	0.902616405	2.23E-11	1.63E-10
AB57_2286	pfkB	1-phosphofructokinase	0.940095269	1.05E-15	1.70E-14
AB57_2287		PTS system fructose-specific EIIBC component	0.680948162	4.56E-06	1.38E-05
AB57_2288		hypothetical protein	-0.597832626	1.14E-07	4.44E-07
AB57_2289		transcriptional regulator, MarR-family	-0.905244109	3.86E-14	4.51E-13
AB57_2290		hypothetical protein	-0.079835654	0.653978	0.699745
AB57_2291		GGDEF family protein	-0.557114094	1.15E-07	4.47E-07
AB57_2292		UspA domain protein	-0.552444684	4.22E-05	0.000108
AB57_2293		quinoprotein glucose dehydrogenase-B	-1.89222851	2.34E-23	1.31E-21
AB57_2294		hypothetical protein	-1.282781021	4.26E-22	2.00E-20
AB57_2295		sulfate permease	-0.105024153	0.427142	0.488238
AB57_2296		extracellular serine protease	-1.250961061	4.79E-10	2.76E-09
AB57_2297		hypothetical protein	-0.523679041	0.000116	0.000273
AB57_2298		proline-specific permease ProY	-0.154993634	0.182477	0.229725
AB57_2299	kynU	kynureninase	-0.002309789	0.985964	0.9881
AB57_2300		transcriptional regulator, AsnC family	-0.707655107	0.000354	0.000758
AB57_2301		acetyltransferase gnat family	-0.783471695	4.00E-09	1.98E-08
AB57_2302		hypothetical protein	-0.848791182	2.53E-09	1.29E-08
AB57_2303		hypothetical protein	-0.680045701	4.82E-09	2.32E-08
AB57_2304		putative prophage protein	-0.465577084	0.00023	0.000512
AB57_2305		HAD-superfamily hydrolase	0.622334236	2.70E-07	9.90E-07
AB57_2306		heat shock protein 15	0.284650769	0.038271	0.055509
AB57_2307	recA	recombinase A	0.46239164	0.005453	0.009458
AB57_2308	recX	regulatory protein RecX	-0.317298036	0.025089	0.037828
AB57_2309		hypothetical protein	0.113930751	0.386539	0.446796
AB57_2310	lpxA	UDP-N-acetylglucosamine acyltransferase	1.141677694	1.63E-12	1.46E-11
AB57_2311	fabZ	(3R)-hydroxymyristoyl-ACP dehydratase	0.975871393	7.07E-11	4.69E-10
AB57_2312	lpxD	UDP-3-O-[3-hydroxymyristoyl] glucosamine N-acyltransferase	0.635120007	1.85E-05	4.99E-05
AB57_2313		putative outer membrane protein	-0.053730214	0.67838	0.721473
AB57_2314		outer membrane protein assembly complex	0.330044554	0.045806	0.065135
AB57_2315	rseP	peptidase M50, putative membrane-associated zinc metallopep	0.40870147	0.010375	0.016931
AB57_2316	dxr	1-deoxy-D-xylulose 5-phosphate reductoisomerase	1.272992085	6.74E-15	9.24E-14
AB57_2317	cdsA	phosphatidate cytidylyltransferase	0.943404021	8.76E-09	4.04E-08
AB57_2318	uppS	undecaprenyl diphosphate synthase	1.239468555	2.35E-12	2.08E-11
AB57_2319	frr	ribosome recycling factor	1.518659581	2.42E-17	5.26E-16

AB57_2320	pyrH	uridylate kinase	2.252804223	5.55E-24	3.60E-22
AB57_2321		ribosomal protein S12 methylthiotransferase	1.709954135	6.91E-15	9.43E-14
AB57_2323	ntrB	signal transduction histidine kinase, nitrogen specific, NtrB	0.085203813	0.447582	0.50768
AB57_2324	ntrC	nitrogen metabolism transcriptional regulator, NtrC, Fis Family	0.306415987	0.044481	0.063496
AB57_2325		transcriptional regulator, TetR family	0.085948705	0.442262	0.503343
AB57_2326	argF	ornithine carbamoyltransferase	0.930545942	2.87E-11	2.05E-10
AB57_2327	ispF	2-C-methyl-D-erythritol 2,4-cyclodiphosphate synthase	-0.084454838	0.422107	0.483379
AB57_2328		hypothetical protein	-0.298649137	0.029241	0.043555
AB57_2329		hypothetical protein	-0.75816077	5.79E-12	4.76E-11
AB57_2330		D-amino acid dehydrogenase small subunit	-0.805613374	1.97E-09	1.03E-08
AB57_2331		hypothetical protein	0.351616197	0.024962	0.037666
AB57_2333		hypothetical protein	-1.023015865	1.40E-16	2.64E-15
AB57_2334	fumC	fumarate hydratase	-0.256585416	0.050245	0.071066
AB57_2335		UDP-glucose 4-epimerase	-0.55205603	0.000277	0.000608
AB57_2336	tusD	sulfur relay protein TusD/DsrE	-0.7936547	2.34E-10	1.42E-09
AB57_2337		hypothetical protein	-0.276928694	0.014403	0.022765
AB57_2338		hypothetical protein	-0.024397929	0.879927	0.901614
AB57_2339		DsrC family protein	-0.230085408	0.115762	0.15135
AB57_2340		hypothetical protein	-0.300843038	0.094796	0.126258
AB57_2341		transcriptional regulator, HxlR family	-0.217570574	0.04127	0.059508
AB57_2342		transcriptional regulator, GntR family	-0.024447661	0.864046	0.889035
AB57_2343		molybdopterin biosynthesis protein	-0.103370935	0.380215	0.440174
AB57_2344		molybdopterin biosynthesis protein	0.347702987	0.021941	0.033559
AB57_2345		bifunctional molybdenum cofactor biosynthesis protein MoaC/N	-0.012163468	0.92219	0.936105
AB57_2346	moaE	molybdopterin converting factor, subunit 2	-1.088906423	1.48E-25	1.33E-23
AB57_2347		hypothetical protein	-1.235287421	2.02E-23	1.17E-21
AB57_2348	moaA	molybdenum cofactor biosynthesis protein A	-1.361013905	2.61E-08	1.12E-07
AB57_2349		molybdopterin oxidoreductase	-0.928162609	7.59E-10	4.26E-09
AB57_2350		molybdopterin-guanine dinucleotide synthase	-0.210076254	0.213276	0.264273
AB57_2351		molybdopterin oxidoreductase	-0.478882341	8.60E-05	0.000207
AB57_2352		FAD-dependent pyridine nucleotide-disulphide oxidoreductase	-0.427221109	0.002126	0.003984
AB57_2353	nirB	nitrite reductase [NAD(P)H], large subunit	-0.526671055	4.18E-05	0.000107
AB57_2354		response regulator protein	0.02423734	0.920568	0.934972
AB57_2355		putative nitrate transport protein	-0.354850765	0.0206	0.031653
AB57_2356		DNA repair protein UmuC	-0.224159676	0.273326	0.330169
AB57_2357		DNA repair protein	-0.373680527	0.033791	0.049575
AB57_2358	aroQ	3-dehydroquinate dehydratase	0.239125545	0.066244	0.091558
AB57_2359	accB	acetyl-CoA carboxylase, biotin carboxyl carrier protein	1.350914269	2.62E-20	8.88E-19
AB57_2360	accC	acetyl-CoA carboxylase, biotin carboxylase	1.208532983	2.34E-10	1.42E-09
AB57_2361		hypothetical protein	-0.444366929	0.000122	0.000287
AB57_2362		metabolite transporter, MFS superfamily	0.089949784	0.465445	0.525846
AB57_2363		hypothetical protein	-1.030407178	1.57E-06	5.18E-06
AB57_2364		transcriptional regulator, TetR family	-0.87849616	3.76E-11	2.66E-10
AB57_2366		PepSY-associated TM helix domain protein	-0.069260035	0.632666	0.679694
AB57_2367		PepSY-associated TM helix domain protein	0.073619516	0.557346	0.61411
AB57_2368		Glutamate synthase (NADPH)	-0.021580423	0.833873	0.861824
AB57_2369		hypothetical protein	-0.849915754	1.35E-15	2.10E-14
AB57_2370		hypothetical protein	-0.292110699	0.003601	0.006463
AB57_2371	murB	UDP-N-acetylenolpyruvoylglucosamine reductase	0.728434852	1.10E-08	5.00E-08
AB57_2372		protein tyrosine phosphatase	0.221158915	0.063974	0.088753
AB57_2373		hypothetical protein	-0.034227769	0.735503	0.773994
AB57_2374		iron-containing alcohol dehydrogenase	-0.329932371	0.002038	0.003838
AB57_2375		thioesterase family protein	0.087275006	0.443982	0.504835
AB57_2376		phospholipase C, phosphocholine-specific	0.026464094	0.809285	0.841584
AB57_2377		DNA polymerase III subunit tau	0.22966408	0.072405	0.099201
AB57_2378		methyl viologen resistance protein	0.62267065	0.002488	0.004594
AB57_2379		transcriptional regulator, TetR family	0.34354498	0.002008	0.003793
AB57_2380		beta-lactamase	-0.082652504	0.407112	0.468091

AB57_2381		MaoC domain protein dehydratase	0.827780118	7.87E-08	3.16E-07
AB57_2382		3-ketoacyl-(acyl-carrier-protein) reductase	0.054870572	0.768747	0.80372
AB57_2383		acetyl-CoA acetyltransferase	0.205395406	0.372424	0.432498
AB57_2384		hypothetical protein	0.315561051	0.05686	0.079629
AB57_2385		transcriptional regulator, LysR family	0.007206635	0.964843	0.9722
AB57_2386	tal	transaldolase B	-0.167464625	0.261903	0.318136
AB57_2387		leucine export protein LeuE	0.036816847	0.741724	0.779653
AB57_2388		leucine-responsive transcriptional regulator, AsnC family	-0.310101169	0.006653	0.011333
AB57_2389		benzoate transporter	-0.11806345	0.326471	0.386171
AB57_2390		magesium transporter transmembrane protein	-0.129975451	0.248966	0.304319
AB57_2391	mgtA	magnesium-transporting ATPase MgtA	0.801508651	0.000119	0.000279
AB57_2392		hypothetical protein	-0.617824835	7.20E-05	0.000175
AB57_2393		hypothetical protein	-0.587552384	9.97E-08	3.92E-07
AB57_2394		hypothetical protein	-0.497981162	0.013406	0.02138
AB57_2395		universal stress protein family	-0.219247354	0.142388	0.182422
AB57_2396		ABC transporter, ATP-binding protein	-0.03729219	0.750198	0.787218
AB57_2397		hypothetical protein	-0.718915818	1.93E-11	1.43E-10
AB57_2398		hypothetical protein	-0.45813476	0.010013	0.01639
AB57_2399		hypothetical protein	-1.453743378	3.15E-15	4.64E-14
AB57_2400		OmpW family protein	-0.987796777	2.57E-14	3.07E-13
AB57_2401		TonB-dependent siderophore receptor	-0.436746606	7.25E-05	0.000176
AB57_2402		acetyltransferase, gnat family	-0.782351464	6.66E-11	4.43E-10
AB57_2403		hypothetical protein	-0.536763486	0.013595	0.021642
AB57_2404		hypothetical protein	-1.454989897	2.90E-18	7.40E-17
AB57_2405		hypothetical protein	-1.384292987	7.98E-24	4.84E-22
AB57_2406		hypothetical protein	-1.295525078	1.11E-18	2.94E-17
AB57_2407		mechanosensitive ion channel family protein	0.053935283	0.616508	0.666203
AB57_2408		TonB-dependent siderophore receptor	1.84204063	1.69E-13	1.76E-12
AB57_2409		transcriptional regulator, TetR family	-0.293652839	0.09252	0.123761
AB57_2410		hypothetical protein	-0.359772349	0.008478	0.01415
AB57_2411		hypothetical protein	-0.273188993	0.226898	0.279655
AB57_2412		hypothetical protein	-1.287544356	2.37E-06	7.52E-06
AB57_2413		hypothetical protein	-0.664478086	0.000614	0.001265
AB57_2414		transcriptional regulator, AsnC family	-0.030767188	0.824085	0.853854
AB57_2416		chorismate mutase	0.122035866	0.451499	0.511653
AB57_2417		oxidoreductase short-chain dehydrogenase/reductase family	-0.306666365	0.048572	0.068804
AB57_2418		short chain dehydrogenase	-0.377966517	0.017757	0.027559
AB57_2419		glutathione S-transferase	-0.361451544	0.081276	0.110276
AB57_2420		hypothetical protein	-0.674780801	3.73E-05	9.58E-05
AB57_2421		hypothetical protein	-0.605267829	4.82E-05	0.000121
AB57_2422		hypothetical protein	-0.383454617	0.021054	0.032311
AB57_2423		hypothetical protein	-0.264905402	0.106538	0.140481
AB57_2424	pepN	aminopeptidase N	0.444466214	0.01389	0.022076
AB57_2425		hypothetical protein	-1.479361593	3.60E-23	1.93E-21
AB57_2426		hypothetical protein	-0.036726046	0.74253	0.780279
AB57_2427		hydroxyethylthiazole kinase	-0.116940728	0.296833	0.354971
AB57_2428	hpcD	5-carboxymethyl-2-hydroxymuconate isomerase	-0.011055938	0.912304	0.928873
AB57_2429		putative helicase	0.733808273	5.23E-08	2.15E-07
AB57_2430		alcohol dehydrogenase, iron-containing	-0.127742862	0.395306	0.45579
AB57_2432		putative transcriptional regulator	-0.970672405	1.30E-08	5.87E-08
AB57_2433		hydrolase, alpha/beta fold family	-0.275251714	0.025204	0.037985
AB57_2434		aldehyde dehydrogenase	-0.039872026	0.805717	0.838561
AB57_2435	eat	ethanolamine permease	-0.01045382	0.946997	0.957406
AB57_2436	eutB	ethanolamine ammonia-lyase, large subunit	-0.180078051	0.138267	0.177944
AB57_2437	eutC	ethanolamine ammonia-lyase, light chain	-0.921224438	3.13E-08	1.33E-07
AB57_2438		glutamine amidotransferase	0.222606756	0.070727	0.097102
AB57_2439		hypothetical protein	-0.061300944	0.671837	0.715955
AB57_2440	glnS	glutaminyl-tRNA synthetase	0.608359953	0.001173	0.002303

AB57_2441		peptidyl-prolyl cis-trans isomerase, cyclophilin type	1.246428954	1.49E-14	1.87E-13
AB57_2442	lpxH	UDP-2,3-diacylglucosamine hydrolase	0.855098228	1.30E-13	1.39E-12
AB57_2444		dihydropteridine reductase	-0.222179804	0.032643	0.048043
AB57_2445		integral membrane protein	-0.523181825	1.02E-06	3.44E-06
AB57_2446		host factor Hfq	-0.323266009	0.038296	0.055524
AB57_2447	miaA	tRNA delta(2)-isopentenylpyrophosphate transferase	-1.001916123	2.07E-10	1.27E-09
AB57_2448	mutL	DNA mismatch repair protein MutL	0.481352649	5.73E-05	0.000142
AB57_2449		hypothetical protein	0.179594335	0.106519	0.140481
AB57_2450		RNA pseudouridine synthase family protein	-0.546601104	4.22E-05	0.000108
AB57_2451		hypothetical protein	-0.471318486	7.51E-06	2.19E-05
AB57_2452		16S rRNA pseudouridylate 516 synthase	-0.865551711	2.03E-10	1.25E-09
AB57_2453		putative acetyltransferase	-0.892179604	9.94E-11	6.41E-10
AB57_2454		hypothetical protein	-1.224456763	5.26E-24	3.48E-22
AB57_2455		hypothetical protein	-0.901952117	1.85E-17	4.10E-16
AB57_2456		transcriptional regulator, LysR family	-0.533620777	1.93E-07	7.24E-07
AB57_2457		hypothetical protein	-0.424305888	0.000301	0.000653
AB57_2458		hypothetical protein	-0.601977717	8.29E-07	2.84E-06
AB57_2459		MFS superfamily permease	0.619977591	7.17E-05	0.000174
AB57_2460		ion transport protein	-0.344692188	0.0058	0.01001
AB57_2461		hypothetical protein	-0.470608536	0.000547	0.001136
AB57_2462	acnB	bifunctional aconitate hydratase 2/2-methylisocitrate dehydrata	0.809692757	1.24E-05	3.45E-05
AB57_2463		hypothetical protein	-0.768707282	3.48E-12	2.98E-11
AB57_2464		hypothetical protein	-0.25476093	0.08291	0.112287
AB57_2465		hypothetical protein	-0.405496996	0.002104	0.00395
AB57_2466		major facilitator superfamily MFS_1	-0.158915076	0.140504	0.180133
AB57_2467		ubiquinone biosynthesis protein COQ7	0.071211259	0.485046	0.544996
AB57_2468		hypothetical protein	-0.247072731	0.042008	0.060431
AB57_2469		glutamine synthetase	-0.722592472	4.45E-09	2.17E-08
AB57_2470	kdpE	two-component system regulatory protein KdpE	0.007461157	0.951401	0.961536
AB57_2471	kdpD	two-component system sensor protein KdpD	-0.510515533	1.15E-06	3.86E-06
AB57_2472	kdpC	K+-transporting ATPase, C subunit	-0.136131043	0.386852	0.447018
AB57_2473	kdpB	potassium-transporting ATPase subunit B	0.0598417	0.596058	0.64827
AB57_2474	kdpA	potassium-transporting ATPase subunit A	0.044140852	0.72897	0.768212
AB57_2475		2-amino-4-hydroxy-6-hydroxymethyldihydropteridine pyrophos	-0.035829656	0.785374	0.819713
AB57_2476	folB	dihydroneopterin aldolase	0.32183	0.013934	0.022136
AB57_2477		ABC-1 domain protein	0.586231954	3.07E-05	8.04E-05
AB57_2478		molybdopterin biosynthesis protein	0.426090044	2.21E-05	5.90E-05
AB57_2479		FMN-binding protein	0.472573056	1.33E-05	3.67E-05
AB57_2480		acyl-CoA ligase	2.006034816	8.25E-43	4.36E-40
AB57_2481		acyl-CoA dehydrogenase	2.61695086	1.47E-28	2.01E-26
AB57_2482		short-chain dehydrogenase/reductase	3.050454033	2.17E-75	8.03E-72
AB57_2483		transcriptional regulator, AraC family	-0.570392133	0.000179	0.000406
AB57_2484		aliphatic sulfonates family ABC transporter, periplsmic ligand-bi	-0.996963974	1.69E-05	4.58E-05
AB57_2486		aliphatic sulfonates transport permease protein	-0.665949057	0.002011	0.003795
AB57_2487		protein methylase, HemK family	0.810293921	1.10E-09	6.01E-09
AB57_2488	prfA	peptide chain release factor 1	1.425932619	1.33E-15	2.09E-14
AB57_2489		ThiJ/PfpI domain protein	-0.464633636	0.000632	0.001297
AB57_2490		transcriptional regulator, LysR family	-0.530536797	0.000117	0.000275
AB57_2491		hypothetical protein	-0.553857451	0.000324	0.000698
AB57_2492		hypothetical protein	-0.876860381	4.33E-14	4.96E-13
AB57_2493		luciferase family monooxygenase	0.222390885	0.064334	0.089119
AB57_2494		hypothetical protein	-1.801616435	6.33E-33	1.46E-30
AB57_2495		hypothetical protein	-0.605303126	5.58E-05	0.000138
AB57_2496		glycosyl transferase, family 2 protein	0.165856707	0.228699	0.281686
AB57_2497		polysaccharide deacetylase	0.065080331	0.627952	0.675758
AB57_2498		hypothetical protein	0.298514237	0.024802	0.037471
AB57_2499		hypothetical protein	0.13405409	0.290456	0.348359
AB57_2500		hypothetical protein	-0.170081054	0.124053	0.161334

AB57_2501	ppsA	phosphoenolpyruvate synthase	0.465449561	0.00614	0.010537
AB57_2502		RDD family protein	1.27120249	2.29E-23	1.30E-21
AB57_2503		cytochrome O ubiquinol oxidase subunit II	0.531142467	0.0056	0.009691
AB57_2505	cyoB	cytochrome O ubiquinol oxidase, subunit I	0.296803483	0.093673	0.125143
AB57_2506	cyoC	cytochrome O ubiquinol oxidase, subunit III	0.115452438	0.504627	0.564084
AB57_2507	cyoD	cytochrome O ubiquinol oxidase subunit IV	-0.119153185	0.496122	0.555417
AB57_2508	cyoE	protoheme IX farnesyltransferase	0.298226376	0.107661	0.14181
AB57_2509	rpsF	30S ribosomal protein S6	0.794166336	0.000123	0.000288
AB57_2510	rpsR	30S ribosomal protein S18	0.564296659	0.005816	0.010032
AB57_2511	rplI	50S ribosomal protein L9	0.50059197	0.009951	0.016314
AB57_2512	dnaB	replicative DNA helicase	0.455151231	0.000543	0.001128
AB57_2513	alr	alanine racemase	0.057653363	0.559461	0.615852
AB57_2514		hypothetical protein	-0.514225307	0.001284	0.002501
AB57_2515		transglutaminase	-0.872574265	1.14E-11	8.82E-11
AB57_2516		hypothetical protein	-0.554156706	9.30E-06	2.64E-05
AB57_2517		hypothetical protein	-0.494852361	5.34E-06	1.59E-05
AB57_2518		transcriptional factor	-0.295652977	0.044056	0.062961
AB57_2520	gidA	tRNA uridine 5-carboxymethylaminomethyl modification enzym	2.415531767	8.26E-15	1.11E-13
AB57_2521		hypothetical protein	-0.780402421	5.55E-08	2.27E-07
AB57_2522	prmA	ribosomal protein L11 methyltransferase	1.43325973	8.96E-16	1.47E-14
AB57_2523		hypothetical protein	0.226932296	0.040397	0.058341
AB57_2524		transcriptional regulator, Fis-type	0.734246165	1.86E-07	7.00E-07
AB57_2525	purH	bifunctional phosphoribosylaminoimidazolecarboxamide formyl	1.070765014	4.75E-11	3.26E-10
AB57_2526	purD	phosphoribosylamine--glycine ligase	1.148683383	2.14E-10	1.31E-09
AB57_2527		ABC transporter, methionine-binding protein	-0.082593931	0.601225	0.652547
AB57_2528	metN	ABC transporter, ATP-binding protein	1.05489797	3.31E-10	1.95E-09
AB57_2529	metI	ABC transport system permease protein	0.950928835	2.98E-07	1.09E-06
AB57_2530	gloB	hydroxyacylglutathione hydrolase	-0.317646704	0.004617	0.008107
AB57_2531		hypothetical protein	-1.031770312	5.40E-11	3.68E-10
AB57_2532		C4-dicarboxylate transport protein	0.623803994	0.001129	0.002223
AB57_2533		transcriptional regulator, TetR family	0.086179579	0.572202	0.62656
AB57_2534		transporter, major facilitator family	-0.511216562	1.57E-05	4.28E-05
AB57_2535		acetyltransferase, gnat family	-0.344586655	0.001687	0.003227
AB57_2536		L-sorbosone dehydrogenase	-1.103564611	6.40E-19	1.78E-17
AB57_2537		hypothetical protein	-0.42495994	9.89E-05	0.000235
AB57_2538		aspartate racemase	-0.850003776	3.12E-12	2.70E-11
AB57_2539		acetyltransferase, gnat family	-0.295281015	0.093766	0.125145
AB57_2540		hypothetical protein	-0.916702841	3.34E-05	8.66E-05
AB57_2541		hypothetical protein	-0.835332468	0.000111	0.000261
AB57_2542		two-component system sensor protein	-0.460672922	6.20E-05	0.000152
AB57_2543		two-component system response regulator protein	-0.773468614	5.15E-06	1.54E-05
AB57_2544		cyclopropane-fatty-acyl-phospholipid synthase	-0.3852818	0.000672	0.001375
AB57_2545		cyclopropane-fatty-acyl-phospholipid synthase	-1.141911044	2.44E-11	1.77E-10
AB57_2546		hypothetical protein	-0.993616899	7.00E-05	0.00017
AB57_2547		dehydrogenase	-0.783855868	4.84E-05	0.000122
AB57_2548		delta-9 acyl-lipid desaturase 1	-1.437037053	7.88E-12	6.34E-11
AB57_2549		lipocalin family protein	-1.30419923	9.45E-07	3.22E-06
AB57_2550		two-component heavy metal sensor histidine kinase	-0.199360314	0.078785	0.107052
AB57_2551		two-component heavy metal response regulator protein	-0.438606303	0.01109	0.017998
AB57_2552		hypothetical protein	-0.286352345	0.210338	0.260983
AB57_2553		transthyretin	-0.207498292	0.279022	0.336281
AB57_2554		hypothetical protein	-0.089828492	0.429034	0.490249
AB57_2555		paraquat-inducible protein B	-0.042753192	0.677984	0.721467
AB57_2556		paraquat-inducible protein A	-0.341238485	0.004144	0.007351
AB57_2557		paraquat-inducible protein A	-0.410746209	0.009417	0.015521
AB57_2559		hypothetical protein	-0.816989107	1.60E-12	1.44E-11
AB57_2560		transcriptional regulator, TetR family	-0.553092726	0.030283	0.045017
AB57_2561		proline/glycine betaine transporter	0.14848126	0.319172	0.378263

AB57_2562		hypothetical protein	-0.683277146	6.90E-07	2.39E-06
AB57_2563		hypothetical protein	-0.426759898	0.000248	0.000551
AB57_2564		hypothetical protein	-0.605584214	8.33E-08	3.33E-07
AB57_2565		CsuE	0.189107338	0.142766	0.182779
AB57_2566		CsuD	0.800735982	6.22E-05	0.000153
AB57_2567		CsuC	0.946354299	2.46E-08	1.06E-07
AB57_2568		CsuB	0.687843764	0.000528	0.0011
AB57_2569		CsuA	0.375842071	0.083579	0.112986
AB57_2570		CsuA/B	1.379264361	3.52E-09	1.75E-08
AB57_2572		hypothetical protein	-0.056355929	0.801502	0.834898
AB57_2573		transcriptional regulator, GntR family	0.279618133	0.080321	0.10906
AB57_2574		hypothetical protein	0.132587424	0.238843	0.293302
AB57_2575		hypothetical protein	0.710152569	4.36E-07	1.56E-06
AB57_2576		oxidoreductase, short chain dehydrogenase/reductase family	0.087752047	0.540055	0.59737
AB57_2577		aldo/keto reductase	0.158672867	0.218873	0.270304
AB57_2578		transcriptional regulator, LysR family	0.64082893	4.29E-09	2.11E-08
AB57_2579		cyclase family protein	-0.838451737	2.96E-14	3.51E-13
AB57_2580	gltS	sodium/glutamate symporter	0.349556592	0.003779	0.006752
AB57_2581		alpha/beta hydrolase fold protein	-0.255611657	0.039856	0.057626
AB57_2582		transcriptional regulator, AraC family	-0.56791852	0.00264	0.004847
AB57_2583		threonine efflux protein	-0.184697774	0.112731	0.147858
AB57_2584		hypothetical protein	-0.639124663	8.10E-05	0.000195
AB57_2585		hypothetical protein	-0.328421003	0.013577	0.021625
AB57_2586		hypothetical protein	-1.080608382	3.35E-14	3.94E-13
AB57_2587		glycosyl transferase, family 2	-0.416703491	0.000472	0.000992
AB57_2588		methyltransferase type 12	-0.559070875	0.000249	0.000551
AB57_2589		LmbE-like protein	-0.785056305	7.93E-10	4.44E-09
AB57_2590		acyl-CoA dehydrogenase	-0.738455366	3.49E-05	9.01E-05
AB57_2591		hypothetical protein	-1.015241718	9.89E-10	5.44E-09
AB57_2592		gamma-aminobutyrate permease	-0.781122657	2.11E-11	1.55E-10
AB57_2593	mmsA	methylmalonate-semialdehyde dehydrogenase	-0.352956091	0.021313	0.032627
AB57_2594		beta alanine--pyruvate transaminase	-0.661822905	2.22E-10	1.35E-09
AB57_2595		transcriptional regulator, LysR family	-0.230149453	0.028679	0.042787
AB57_2596		serine/threonine protein kinase	-0.312178462	0.055918	0.078429
AB57_2597		patatin family phospholipase	-0.361117825	0.004875	0.008532
AB57_2598		hypothetical protein	-0.725738007	6.11E-06	1.81E-05
AB57_2599		hypothetical protein	-0.448467843	0.000196	0.000442
AB57_2600		putative DNA-binding/iron metalloprotein/AP endonuclease	1.070866397	7.05E-13	6.77E-12
AB57_2601	rpsU	30S ribosomal protein S21	0.959993589	1.40E-07	5.36E-07
AB57_2602		GatB/Yqey domain protein	1.258424166	1.27E-11	9.71E-11
AB57_2603		hypothetical protein	0.017953516	0.875031	0.897592
AB57_2604		2-ketogluconate reductase	0.348674423	0.001979	0.003741
AB57_2605		hypothetical protein	-0.329321352	0.002907	0.005295
AB57_2606		hypothetical protein	-0.709795936	1.75E-08	7.67E-08
AB57_2607	purF	amidophosphoribosyltransferase	0.618777376	0.000639	0.001312
AB57_2608		colicin V producing membrane protein	0.208585987	0.126499	0.164284
AB57_2609	pyrD	dihydroorotate dehydrogenase 2	0.452759822	0.000276	0.000605
AB57_2610		hypothetical protein	0.633709811	1.60E-07	6.09E-07
AB57_2611		hypothetical protein	0.751424642	1.24E-10	7.87E-10
AB57_2612		general secretion pathway protein L	0.71651511	2.39E-10	1.44E-09
AB57_2613		phosphohistidine phosphatase	0.693898647	6.45E-11	4.31E-10
AB57_2614		NAD(P)H-dependent glycerol-3-phosphate dehydrogenase	0.65317558	2.72E-09	1.38E-08
AB57_2615		nitroreductase	0.581711479	9.67E-09	4.43E-08
AB57_2616		hypothetical protein	-1.053720352	9.83E-25	7.13E-23
AB57_2617		ATP-dependent RNA helicase RhlB	0.514811736	0.00022	0.000494
AB57_2618		cold-shock domain protein	-0.068602076	0.731139	0.770058
AB57_2619		hypothetical protein	-0.203333297	0.079198	0.107574
AB57_2620	rpoH	RNA polymerase factor sigma-32	-0.329553062	0.020871	0.032042

AB57_2621		hypothetical protein	0.308846657	0.002446	0.004526
AB57_2622	thiS	thiamine biosynthesis protein ThiS	1.071495895	2.68E-20	9.00E-19
AB57_2623	thiG	thiazole synthase	0.925005427	2.54E-14	3.04E-13
AB57_2624		hypothetical protein	0.097467346	0.390193	0.450457
AB57_2625		protein YaaA	0.112035074	0.265146	0.321758
AB57_2626		hydrolase	0.628069656	2.46E-05	6.53E-05
AB57_2627		ribonuclease Z	-0.535820981	2.23E-07	8.27E-07
AB57_2628		aminoacyl-histidine dipeptidase	-0.427615585	0.000448	0.000948
AB57_2629		hypothetical protein	-1.391736262	1.19E-28	1.69E-26
AB57_2630		bifunctional cyclohexadienyl dehydrogenase/ 3-phosphoshikima	1.125910672	9.72E-11	6.32E-10
AB57_2631		chorismate mutase	0.661157028	1.92E-07	7.19E-07
AB57_2632		alpha/beta hydrolase fold protein	-0.284733056	0.012648	0.020311
AB57_2633		acyl-CoA dehydrogenase	2.073064416	3.73E-57	6.90E-54
AB57_2634		C4-dicarboxylate transporter DctA	0.820096218	7.96E-08	3.19E-07
AB57_2635		hypothetical protein	-0.45245415	5.14E-05	0.000128
AB57_2636		hypothetical protein	0.667663856	4.65E-11	3.21E-10
AB57_2637		inorganic polyphosphate/ATP-NAD kinase	-0.138118444	0.268712	0.325126
AB57_2640		hypothetical protein	0.159002957	0.133131	0.171811
AB57_2641		MutT/NUDIX family protein	0.386177973	0.00092	0.001846
AB57_2642		hypothetical protein	0.52565369	2.47E-06	7.79E-06
AB57_2643		two-component system sensor protein	0.253031781	0.01863	0.028793
AB57_2644		two-component system response regulator protein	0.539009993	1.51E-05	4.14E-05
AB57_2645		hypothetical protein	0.709724359	1.80E-09	9.42E-09
AB57_2646		type II secretion system protein E	-0.361518642	0.019054	0.0294
AB57_2647		hyp	-0.653388771	1.52E-08	6.76E-08
AB57_2648		hypothetical protein	0.101754535	0.458203	0.518615
AB57_2649		ferredoxin--NADP(+) reductase	1.061980561	1.29E-14	1.66E-13
AB57_2650		phenazine biosynthesis protein PhzF family	0.19267704	0.114855	0.150218
AB57_2651		transcriptional regulator, GntR family	-0.385444984	0.008866	0.014731
AB57_2652		peptidase U32	0.52007941	2.21E-05	5.90E-05
AB57_2653		iron-sulfur cluster-binding protein	0.339090758	0.011993	0.019335
AB57_2654		small multidrug resistance protein	-1.097772728	1.06E-17	2.46E-16
AB57_2657		histidine transport system permease protein HisM	0.005367898	0.97691	0.981153
AB57_2658		histidine transport system permease protein HisQ	0.334759186	0.107165	0.141207
AB57_2659		histidine-binding periplasmic protein	0.514615436	0.008311	0.013876
AB57_2660		transcriptional regulator, LysR family	0.233979189	0.145163	0.185528
AB57_2662		efflux transporter, RND family	-0.029268895	0.816253	0.847401
AB57_2663		efflux transporter, RND family	0.282261734	0.02778	0.04158
AB57_2664		multidrug efflux system outer membrane protein	-0.139703058	0.200287	0.249684
AB57_2665	glyA	serine hydroxymethyltransferase	1.818751458	1.72E-14	2.12E-13
AB57_2667		alkaline lipase	-1.608218861	1.25E-17	2.84E-16
AB57_2668		exodeoxyribonuclease X, putative	0.440786802	0.002143	0.004011
AB57_2669		hypothetical protein	-0.45256049	0.012833	0.020563
AB57_2670		hypothetical protein	-0.394171697	0.000294	0.000641
AB57_2671		lysozyme	-0.604924608	4.88E-05	0.000122
AB57_2674		hypothetical protein	-0.470134659	0.001001	0.001989
AB57_2676		hypothetical protein	0.582379523	0.01264	0.020308
AB57_2679		hypothetical protein	-0.79933897	1.73E-08	7.59E-08
AB57_2680		hypothetical protein	-0.549175347	4.24E-05	0.000108
AB57_2681		hypothetical protein	-0.182201495	0.221971	0.273947
AB57_2682		tail tape meausure protein	-0.588231225	1.09E-07	4.27E-07
AB57_2683		hypothetical protein	0.192095691	0.06257	0.086903
AB57_2684		phage protein	-0.149494144	0.216743	0.267942
AB57_2685		hypothetical protein	-0.095636416	0.421602	0.482949
AB57_2686		hypothetical protein	-0.239637241	0.259836	0.316143
AB57_2687		hypothetical protein	-0.030692667	0.877988	0.900376
AB57_2688		putative tail fiber	-0.662496257	4.70E-09	2.27E-08
AB57_2689		hypothetical protein	-0.924939659	2.04E-06	6.55E-06

AB57_2690		hypothetical protein	-0.650402882	2.42E-08	1.05E-07
AB57_2691		hypothetical protein	-0.896413848	5.93E-07	2.07E-06
AB57_2694		hypothetical protein	-0.444531781	0.072446	0.099205
AB57_2696		hypothetical protein	0.20769959	0.293614	0.351795
AB57_2697		major capsid protein	-0.085324366	0.483178	0.543392
AB57_2698		hypothetical protein	0.098305694	0.657348	0.702742
AB57_2700		hypothetical protein	-0.351763155	0.04092	0.059027
AB57_2701		hypothetical protein	-0.539953043	2.46E-06	7.78E-06
AB57_2702		phage putative head morphogenesis protein	-0.396623482	0.022716	0.034574
AB57_2703		hypothetical protein	-0.276298385	0.061485	0.085622
AB57_2704		hypothetical protein	-0.283831206	0.043186	0.061862
AB57_2705		phage protein	-0.366558005	0.05358	0.075379
AB57_2706		hypothetical protein	-0.164353762	0.268035	0.324519
AB57_2707		hypothetical protein	0.01554388	0.921685	0.93585
AB57_2708		hypothetical protein	-0.834183013	4.85E-08	2.00E-07
AB57_2709		hypothetical protein	-0.733962388	2.17E-13	2.23E-12
AB57_2710		hypothetical protein	-0.878488154	6.95E-18	1.68E-16
AB57_2711		hypothetical protein	-0.238785007	0.038773	0.056149
AB57_2712		hypothetical protein	-0.816053125	1.11E-10	7.12E-10
AB57_2713		hypothetical protein	-0.874373658	0.000181	0.00041
AB57_2715		hypothetical protein	0.201035218	0.360377	0.420517
AB57_2722		replicative DNA helicase	-0.249203378	0.093772	0.125145
AB57_2723		hypothetical protein	-0.349412869	0.048182	0.068305
AB57_2726		hypothetical protein	0.299077482	0.064624	0.089454
AB57_2727		regulator protein, putative	0.305224266	0.147484	0.188299
AB57_2728		peptidase S24 S26A and S26B	-0.062966929	0.570402	0.625136
AB57_2729		hypothetical protein	0.541190811	4.86E-05	0.000122
AB57_2730		hypothetical protein	0.025066848	0.815735	0.847101
AB57_2731		hypothetical protein	0.003296773	0.976823	0.981153
AB57_2732		hypothetical protein	-0.579541522	0.095591	0.127131
AB57_2735		hypothetical protein	-0.169206315	0.430148	0.49137
AB57_2736		hypothetical protein	-0.355214066	0.124313	0.161559
AB57_2742		integrase	0.19998551	0.114523	0.149941
AB57_2743		hypothetical protein	-0.173613941	0.362758	0.422741
AB57_2744		ABC transporter ATP-binding protein	0.636928538	1.12E-07	4.39E-07
AB57_2745		ABC transporter permease protein	1.13910031	3.57E-09	1.78E-08
AB57_2746		7-cyano-7-deazaguanine reductase	1.188299869	5.83E-21	2.27E-19
AB57_2747		EsvE2	1.38017779	3.75E-26	3.65E-24
AB57_2748	mrdB	rod shape-determining protein RodA (EsvE3)	1.213595193	1.45E-12	1.32E-11
AB57_2749	mltB	lytic murein transglycosylase B	1.107049191	4.85E-17	9.87E-16
AB57_2750		rare lipoprotein A	0.512486634	0.001219	0.002382
AB57_2751		hypothetical protein	-0.765625567	4.03E-12	3.42E-11
AB57_2752		branched-chain amino acid permease	-0.644548943	6.90E-10	3.90E-09
AB57_2753		transcriptional regulator, AraC family	-1.136760316	1.77E-16	3.30E-15
AB57_2754		hypothetical protein	0.445365065	0.003837	0.006848
AB57_2755	tsf	elongation factor Ts	1.871218838	2.40E-19	7.23E-18
AB57_2756	rpsB	30S ribosomal protein S2	0.395083868	0.032164	0.047413
AB57_2757	map	methionine aminopeptidase, type I	1.072930118	1.01E-12	9.57E-12
AB57_2758		OmpW family protein	0.271776373	0.035661	0.052071
AB57_2759		MFS transporter, NNP family	-0.444479326	0.002372	0.004393
AB57_2760		major facilitator family transporter	-0.859781717	5.66E-15	8.00E-14
AB57_2762		soluble pyridine nucleotide transhydrogenase	0.542481819	0.000744	0.001513
AB57_2763	lipA	lipoyl synthase	0.583026066	0.000491	0.001029
AB57_2764		acyl-CoA dehydrogenase	-0.495612628	1.42E-05	3.92E-05
AB57_2765		4-carboxymuconolactone decarboxylase	0.84880035	2.84E-10	1.69E-09
AB57_2766		hypothetical protein	0.300261376	0.051806	0.073077
AB57_2767	ahcY	S-adenosyl-L-homocysteine hydrolase	0.848726061	3.34E-06	1.03E-05
AB57_2768	metF	5,10-methylenetetrahydrofolate reductase	0.606848261	0.000141	0.000327

AB57_2769		hypothetical protein	0.432851005	4.28E-05	0.000109
AB57_2770		transposase subunit	-0.833936216	7.20E-08	2.90E-07
AB57_2771		transposase 1	-0.487818983	0.007818	0.013143
AB57_2772		sensory box protein	-0.493063017	0.000302	0.000656
AB57_2773		malic enzyme	0.942256293	2.49E-07	9.16E-07
AB57_2774		multifunctional tRNA nucleotidyl transferase/2'3'-cyclic phosph	-0.033233187	0.796439	0.830794
AB57_2775		peptidase S1 and S6	0.393823292	0.000171	0.000388
AB57_2776		hypothetical protein	0.725410569	1.13E-12	1.05E-11
AB57_2777		superoxide dismutase (Fe)	0.806947553	3.64E-07	1.31E-06
AB57_2778		hypothetical protein	-0.035575336	0.832913	0.861128
AB57_2779		hypothetical protein	0.354754429	0.105321	0.139174
AB57_2780		hypothetical protein	-0.494258748	0.000141	0.000326
AB57_2781	ubiA	4-hydroxybenzoate octaprenyltransferase	0.116842607	0.281174	0.338653
AB57_2782		chorismate lyase	-0.229497916	0.031039	0.04603
AB57_2783	glnA	glutamine synthetase, type I	1.613102409	7.28E-13	6.96E-12
AB57_2784		dipeptide/tripeptide permease	-0.251647224	0.012925	0.020694
AB57_2785		peptidase M24	0.228221395	0.071037	0.097455
AB57_2786		para-aminobenzoate/anthranilate synthase glutamine amidotra	0.613482997	1.69E-09	8.90E-09
AB57_2787		aminopeptidase N	-0.464204262	1.85E-05	5.00E-05
AB57_2788		TonB-dependent receptor	-0.478235821	0.00296	0.005385
AB57_2789	trpD	anthranilate phosphoribosyltransferase	0.719270363	1.23E-07	4.76E-07
AB57_2790	trpC	indole-3-glycerol-phosphate synthase	0.884182218	2.01E-08	8.77E-08
AB57_2791		Smr protein/MutS2	0.512521507	0.000301	0.000653
AB57_2792	xdhC	xanthine dehydrogenase accessory protein XdhC	-0.320381656	0.046855	0.066525
AB57_2793	xdhB	xanthine dehydrogenase, molybdopterin binding subunit	-0.407869383	0.000219	0.000492
AB57_2794	xdhA	xanthine dehydrogenase, small subunit	-0.791353297	1.30E-07	5.00E-07
AB57_2795	folE	GTP cyclohydrolase I	0.941710385	9.60E-14	1.05E-12
AB57_2796	ampC	beta-lactamase	1.332697858	1.44E-11	1.09E-10
AB57_2797		hypothetical protein	0.421739017	0.000482	0.001013
AB57_2798		hypothetical protein	-0.513358208	0.000562	0.001162
AB57_2799		hypothetical protein	1.290363373	2.97E-12	2.58E-11
AB57_2800	hemE	uroporphyrinogen decarboxylase	1.851552992	4.61E-27	5.50E-25
AB57_2801		ErfK/YbiS/YcfS/YnhG family	0.383245782	0.011192	0.018123
AB57_2802		probable acinetobactin biosynthesis protein	-0.754419123	1.62E-11	1.22E-10
AB57_2803		probable acinetobactin biosynthesis protein	-0.385071831	0.091855	0.123088
AB57_2804		probable acinetobactin biosynthesis protein	0.036493646	0.812646	0.844367
AB57_2805		probable ABC transporter	0.166864398	0.29835	0.35667
AB57_2806		probable ABC transporter	-0.017590723	0.905551	0.923013
AB57_2808		histidine decarboxylase	-0.239869583	0.208487	0.258947
AB57_2809		2,3 dihydro-2,3 dihydroxybenzoate synthase	0.070805198	0.725154	0.765062
AB57_2810		enterobactin synthase subunit E	-0.067394551	0.664111	0.708742
AB57_2811	basD	nonribosomal peptide synthetase BasD	-0.357077117	0.002334	0.004333
AB57_2812	basC	nonribosomal peptide synthetase BasC	-0.460716221	0.001995	0.00377
AB57_2813	bauA	ferric acinetobactin receptor	-0.747908748	5.25E-12	4.34E-11
AB57_2814	bauB	ferric acinetobactin transport system periplasmic binding protei	-0.148409072	0.280679	0.338167
AB57_2815	bauE	ferric acinetobactin transport system ATP-binding protein	0.308599911	0.082714	0.112062
AB57_2816	bauC	ferric acinetobactin transport system permease	-0.46815724	0.058632	0.081925
AB57_2817	bauD	ferric acinetobactin transport system permease	-0.226279462	0.313816	0.372626
AB57_2819		non-ribosomal peptide synthetase	-0.608596695	9.78E-06	2.77E-05
AB57_2820		non-ribosomal peptide synthetase	-0.288347387	0.106283	0.140317
AB57_2821		hypothetical protein	0.473183466	0.008233	0.013765
AB57_2822		siderophore-interacting protein	-0.094758388	0.571731	0.62623
AB57_2823		threonine ammonia-lyase	-0.227842163	0.349052	0.409218
AB57_2825		pirin domain protein	-0.696130353	1.46E-10	9.14E-10
AB57_2826		hypothetical protein	-1.708939718	3.69E-22	1.78E-20
AB57_2827		transcriptional regulator, TetR family	-0.52673636	0.010384	0.016934
AB57_2828		hypothetical protein	-0.257771801	0.062103	0.086318
AB57_2829		hypothetical protein	-0.351788133	0.034497	0.050471

AB57_2831		transcriptional regulator, TetR family	-1.09785311	2.06E-14	2.50E-13
AB57_2832		hypothetical protein	-0.197655178	0.230555	0.283783
AB57_2833		hypothetical protein	-0.528348551	0.002595	0.004777
AB57_2834		hypothetical protein	-0.32619476	0.061723	0.085894
AB57_2835		hypothetical protein	-0.000904441	0.996094	0.996633
AB57_2836		hypothetical protein	0.233368927	0.072417	0.099201
AB57_2837		hypothetical protein	0.29325248	0.033388	0.049042
AB57_2838		FAD dependent oxidoreductase	0.082110707	0.514155	0.572832
AB57_2839		rubredoxin-NAD(+) reductase	0.22737976	0.040832	0.058923
AB57_2840		aldehyde dehydrogenase	-0.182661027	0.114856	0.150218
AB57_2841		rieske 2Fe-2S family protein	-0.423233454	0.000656	0.001343
AB57_2842		glycine betaine transporter OpuD	-0.726427744	4.24E-11	2.96E-10
AB57_2843		glycine betaine transporter OpuD	-0.457057248	5.70E-05	0.000141
AB57_2844		proline dipeptidase	-0.536255302	5.35E-07	1.88E-06
AB57_2845		glycine cleavage system transcriptional activator	-0.367506004	0.00052	0.001084
AB57_2846		hypothetical protein	-0.506900706	1.16E-05	3.24E-05
AB57_2847		carbon starvation protein A	-0.843357109	3.17E-09	1.59E-08
AB57_2848	efp	elongation factor P	1.343804621	1.12E-13	1.21E-12
AB57_2849		hypothetical protein	0.18829667	0.067997	0.093771
AB57_2850		hypothetical protein	-0.216329428	0.045658	0.064975
AB57_2853	rpmE	50S ribosomal protein L31	0.919950341	9.46E-08	3.74E-07
AB57_2854		sodium/bile acid symporter family protein	0.333616257	0.00075	0.001523
AB57_2855	gloA	glyoxalase I	0.658598827	2.25E-08	9.79E-08
AB57_2856		major facilitator superfamily MFS_1	0.356489723	0.004928	0.008617
AB57_2857		peptidase S16, lon domain protein	-0.218936363	0.113927	0.149215
AB57_2858		transcriptional regulator, LysR family	0.292682132	0.012824	0.020559
AB57_2859		peptidase M23B	0.284903712	0.010511	0.017118
AB57_2860	surE	5'/3'-nucleotidase SurE	0.537438279	9.75E-05	0.000232
AB57_2861		hypothetical protein	-0.806781862	9.43E-08	3.74E-07
AB57_2862		hypothetical protein	-0.797043511	9.07E-10	5.02E-09
AB57_2863		penicillin-binding protein 6 (D-alanyl-D-alanine carboxypeptidas	1.406141449	4.40E-16	7.61E-15
AB57_2864		putative transferase	0.237931972	0.049771	0.070448
AB57_2865		hydrolase, NUDIX family	0.805278637	4.09E-12	3.46E-11
AB57_2866	trmU	tRNA-specific 2-thiouridylase MnmA	1.294611153	8.68E-16	1.43E-14
AB57_2867		hypothetical protein	0.366300885	0.003549	0.006378
AB57_2868	purB	adenylosuccinate lyase	1.688879577	1.78E-15	2.73E-14
AB57_2869		hypothetical protein	-0.604498388	5.14E-07	1.82E-06
AB57_2870		hypothetical protein	0.3135724	0.009294	0.015331
AB57_2871		putative periplasmic protease	-0.376239325	0.01022	0.016695
AB57_2872	pstB	phosphate transporter ATP-binding protein	0.371886353	0.006598	0.011255
AB57_2873	pstA	phosphate ABC transporter, permease protein	1.611295194	1.42E-24	9.70E-23
AB57_2874	pstC	phosphate ABC transporter, permease protein (EsvD)	1.490587985	2.44E-21	1.03E-19
AB57_2875		phosphate ABC transporter, substrate-binding protein	2.287685487	6.48E-20	2.09E-18
AB57_2876	aroP	aromatic amino acid transport protein	-0.918720471	1.55E-09	8.20E-09
AB57_2877		indole-3-pyruvate decarboxylase	-0.667365745	3.12E-05	8.15E-05
AB57_2878		transcriptional regulator, AsnC family	-0.114341386	0.302037	0.360758
AB57_2879		aldehyde dehydrogenase	-0.693059244	1.30E-05	3.59E-05
AB57_2880		diaminobutyrate decarboxylase	0.769062801	7.90E-05	0.000191
AB57_2881		diaminobutyrate--2-oxoglutarate aminotransferase	0.585924437	0.001323	0.002566
AB57_2882		hypothetical protein	-0.857192645	1.97E-14	2.40E-13
AB57_2883		transcriptional regulator, TetR family	-0.464916802	2.43E-05	6.46E-05
AB57_2884		hypothetical protein	-0.235613048	0.060763	0.084776
AB57_2885		fatty acid desaturase	1.160614663	2.72E-10	1.63E-09
AB57_2886		oxidoreductase	1.649265964	1.08E-17	2.47E-16
AB57_2890		transcriptional regulator, TetR family	0.401876354	0.000249	0.000551
AB57_2891		hypothetical protein	-0.681476014	1.97E-07	7.35E-07
AB57_2892		ATP-dependent helicase HepA	1.214922543	1.14E-08	5.15E-08
AB57_2893		pseudouridine synthase A	1.201467495	8.82E-15	1.17E-13

AB57_2894		hypothetical protein	0.057128539	0.611657	0.661754
AB57_2895	hemL	glutamate-1-semialdehyde aminotransferase	0.891817565	5.88E-11	3.97E-10
AB57_2896	thiE	thiamine-phosphate pyrophosphorylase	0.914219062	5.73E-15	8.06E-14
AB57_2900		hypothetical protein	-0.43338474	0.022085	0.033753
AB57_2901		crispr-associated protein, Csy4 family	0.024497575	0.817884	0.848855
AB57_2902		crispr-associated protein, Csy3 family	0.467817435	0.00029	0.000633
AB57_2903		crispr-associated protein, Csy2 family protein	0.423639462	0.000362	0.000775
AB57_2904		crispr-associated protein, Csy1 family	0.174142129	0.095481	0.127033
AB57_2905		crispr-associated helicase Cas3	-0.193139843	0.070492	0.096851
AB57_2906	cas	crispr-associated protein Cas1	0.16950607	0.11631	0.151959
AB57_2907		hypothetical protein	-1.004783403	1.16E-13	1.25E-12
AB57_2908		adenylate cyclase	-0.712829903	3.60E-06	1.10E-05
AB57_2909		hypothetical protein	-0.156759287	0.210102	0.260777
AB57_2910		hypothetical protein	0.535668856	8.23E-06	2.37E-05
AB57_2911		protease	0.706964543	2.39E-05	6.37E-05
AB57_2912		phenazine biosynthesis protein	0.095644638	0.464867	0.525353
AB57_2913		transport protein	0.442091042	0.00109	0.002149
AB57_2914		transcriptional regulator, LysR family	-0.473013253	0.000117	0.000275
AB57_2915		major facilitator family transporter	-0.764858086	0.008155	0.01364
AB57_2917		hypothetical protein	-0.083382727	0.740876	0.778983
AB57_2919	icd	isocitrate dehydrogenase, NADP-dependent	0.029492454	0.800038	0.833607
AB57_2920		pseudouridine synthase, Rsu	0.925174815	6.04E-12	4.94E-11
AB57_2921		isocitrate dehydrogenase, NADP-dependent	1.262659616	9.98E-10	5.49E-09
AB57_2922		peptidase M61	0.679526585	1.80E-05	4.87E-05
AB57_2923		D-ala-D-ala-carboxypeptidase penicillin-binding protein	1.636352716	7.49E-18	1.80E-16
AB57_2924		NADH dehydrogenase	-0.358915957	0.00101	0.002004
AB57_2925		peptidyl-prolyl cis-trans isomerase, FKBP-type	1.208667042	1.96E-11	1.45E-10
AB57_2926		deoxyribodipyrimidine photo-lyase	-0.999918411	8.26E-10	4.61E-09
AB57_2927		deoxyribodipyrimidine photo-lyase	-0.254676462	0.144626	0.184906
AB57_2928		hypothetical protein	-0.585537433	2.76E-05	7.26E-05
AB57_2929		hypothetical protein	-0.761841332	1.46E-10	9.12E-10
AB57_2930		glycosyltransferase	-0.444785389	7.75E-05	0.000187
AB57_2931		hypothetical protein	-0.286959611	0.006777	0.011514
AB57_2932		hypothetical protein	-0.862908183	3.76E-10	2.21E-09
AB57_2933		UDP-N-acetylglucosamine 2-epimerase	-0.590374806	4.32E-09	2.12E-08
AB57_2934		hypothetical protein	-0.83801669	9.73E-15	1.29E-13
AB57_2935		hypothetical protein	-0.162145469	0.243184	0.29794
AB57_2936		2-nitropropane dioxygenase	-0.527309581	4.51E-05	0.000114
AB57_2937		tRNA-dihydrouridine synthase B	0.120968735	0.288136	0.346026
AB57_2938		hypothetical protein	0.711136515	7.35E-11	4.87E-10
AB57_2939		phophoserine phosphatase	-0.068736142	0.520381	0.579245
AB57_2940	proB	gamma-glutamyl kinase	0.737546027	0.0001	0.000238
AB57_2941		GTPase ObgE	0.862340841	9.81E-06	2.78E-05
AB57_2942		hypothetical protein	-0.250444486	0.03392	0.049727
AB57_2943		hypothetical protein	-0.23814413	0.108221	0.142446
AB57_2944		glyceraldehyde-3-phosphate dehydrogenase	2.203003809	3.91E-16	6.92E-15
AB57_2945	rarD	RarD protein	-0.127383944	0.225342	0.277829
AB57_2946		outer membrane lipoprotein Blc	-0.492697224	5.48E-06	1.63E-05
AB57_2947	uvrB	excinuclease ABC subunit B	-0.216215232	0.176592	0.222772
AB57_2948		hypothetical protein	-0.761728457	6.42E-10	3.65E-09
AB57_2949		GGDEF family protein	-0.002564024	0.980417	0.983874
AB57_2950		hypothetical protein	0.43095353	0.000123	0.000289
AB57_2951		aspartate aminotransferase A	1.892752859	5.08E-18	1.25E-16
AB57_2952		hypothetical protein	-0.718439371	4.94E-09	2.37E-08
AB57_2953		thioesterase superfamily protein	-0.001363615	0.991854	0.992927
AB57_2954		hypothetical protein	-0.726904243	5.05E-08	2.07E-07
AB57_2955		short-chain dehydrogenase/reductase	-0.727356412	1.62E-08	7.16E-08
AB57_2956		tRNA--hydroxylase	1.631673094	3.36E-19	1.00E-17

AB57_2957	pdxJ	pyridoxine 5'-phosphate synthase	1.806390963	3.90E-32	8.02E-30
AB57_2958	recO	DNA repair protein RecO	1.008524084	1.10E-10	7.04E-10
AB57_2959		hypothetical protein	0.759793617	7.80E-07	2.68E-06
AB57_2960	era	GTP-binding protein Era	1.217494263	5.47E-12	4.51E-11
AB57_2961	rnc	ribonuclease III	0.827829368	4.47E-12	3.75E-11
AB57_2962		hypothetical protein	0.820816859	4.15E-11	2.90E-10
AB57_2963	lepB	signal peptidase I	0.92912916	1.85E-10	1.14E-09
AB57_2964	lepA	GTP-binding protein LepA	1.510997608	3.48E-10	2.05E-09
AB57_2965		thioesterase superfamily	0.086367976	0.516866	0.575678
AB57_2966		peptidase S1C, Do	-0.285834298	0.022049	0.033711
AB57_2967	nadB	L-aspartate oxidase	0.14510264	0.212407	0.263462
AB57_2968		thioesterase family protein	-0.136525207	0.234918	0.28877
AB57_2969	tmk	thymidylate kinase	0.457591853	6.39E-05	0.000156
AB57_2970		aminodeoxychorismate lyase	0.402791271	0.000455	0.000959
AB57_2971	pabC	aminodeoxychorismate lyase	-0.397960314	0.000446	0.000944
AB57_2972		thiosulfate-binding protein	-2.320274994	7.16E-07	2.47E-06
AB57_2974		alpha/beta hydrolase fold protein	-1.809312963	0.001344	0.002604
AB57_2975	cysT	sulfate ABC transporter, permease protein CysT	-1.045088798	0.021162	0.032435
AB57_2976	cysW	sulfate ABC transporter, permease protein CysW	-1.391631652	2.76E-13	2.81E-12
AB57_2977	cysA	sulfate ABC transporter, ATP-binding protein CysA	0.614528756	6.85E-05	0.000167
AB57_2978		transcriptional regulator CysB-like protein	1.01331559	1.38E-10	8.70E-10
AB57_2979		outer membrane protein CarO	-0.30234762	0.056065	0.078605
AB57_2980	dapD	2,3,4,5-tetrahydropyridine-2,6-carboxylate N-succinyltransferas	2.271470155	1.13E-23	6.75E-22
AB57_2981		radical SAM domain protein	2.310510033	1.40E-20	5.08E-19
AB57_2982		ExsB protein	1.305181938	4.46E-11	3.09E-10
AB57_2983		hypothetical protein	0.588943541	0.000415	0.000884
AB57_2984		hypothetical protein	0.516905766	0.000307	0.000664
AB57_2985		bacterioferritin comigratory protein	0.274170325	0.0228	0.034687
AB57_2986		hypothetical protein	-0.435004323	0.000203	0.000459
AB57_2987		nicotinamide-nucleotide adenylyltransferase	0.27178662	0.016812	0.02618
AB57_2988		hypothetical protein	-0.84801649	5.25E-09	2.50E-08
AB57_2989		enoyl-CoA hydratase/isomerase	-0.605403696	1.16E-05	3.25E-05
AB57_2991		MFS family drug transporter	-0.884317308	1.64E-09	8.67E-09
AB57_2992	purL	phosphoribosylformylglycinamidine synthase	1.840511905	1.21E-15	1.94E-14
AB57_2993		deoxyguanosinetriphosphate triphosphohydrolase-like protein	0.227756612	0.027225	0.040833
AB57_2994	ruvA	Holliday junction DNA helicase RuvA	1.139998243	1.75E-20	6.30E-19
AB57_2995	ruvB	Holliday junction DNA helicase RuvB	1.112562721	1.32E-15	2.08E-14
AB57_2996		Peptidase M20D, amidohydrolase	-1.246999178	4.23E-21	1.74E-19
AB57_2997	ybgC	tol-pal system-associated acyl-CoA thioesterase	-0.596001101	8.96E-08	3.56E-07
AB57_2998	tolQ	protein TolQ	0.091704103	0.460966	0.521423
AB57_2999	tolR	protein TolR	0.433418032	5.73E-05	0.000142
AB57_3002	tolB	translocation protein TolB	0.066475686	0.591698	0.644285
AB57_3003		peptidoglycan-associated lipoprotein	0.034648487	0.799534	0.833317
AB57_3004		hypothetical protein	-0.638251593	0.000966	0.001927
AB57_3005	fbp	fructose-1,6-bisphosphatase	2.454842175	7.73E-29	1.14E-26
AB57_3006		tRNA/rRNA methyltransferase	1.156290886	1.56E-10	9.75E-10
AB57_3007		RNA polymerase factor sigma-70	-0.664039978	1.22E-06	4.07E-06
AB57_3008		hypothetical protein	-0.384841856	0.000559	0.001157
AB57_3009		hypothetical protein	-0.039648516	0.693983	0.736585
AB57_3010		hypothetical protein	-0.485842656	0.002067	0.003886
AB57_3011		hypothetical protein	-0.11692699	0.462085	0.522528
AB57_3012		DnaA family protein	-0.428882999	0.000676	0.001384
AB57_3013		permease	-0.100456476	0.448261	0.508295
AB57_3014	purM	phosphoribosylaminoimidazole synthetase	1.535769846	1.08E-14	1.39E-13
AB57_3015	purN	phosphoribosylglycinamide formyltransferase	1.731874376	5.69E-24	3.63E-22
AB57_3016		hydrolase	0.655985938	7.38E-09	3.46E-08
AB57_3017		signal peptide peptidase SppA, 36K type	0.478759667	0.000978	0.001945
AB57_3019		lipid A biosynthesis acyltransferase	0.171188676	0.091883	0.123088

AB57_3021	lolD	lipoprotein releasing system, ATP-binding protein	0.754523439	3.80E-07	1.36E-06
AB57_3022		lipoprotein-releasing system transmembrane protein LolE	1.038764267	6.59E-11	4.40E-10
AB57_3023		hypothetical protein	0.200318989	0.106338	0.140317
AB57_3024		hypothetical protein	0.162377471	0.14388	0.184079
AB57_3025		hypothetical protein	-0.361597859	0.001118	0.002203
AB57_3027	serC	phosphoserine aminotransferase	1.329869	4.06E-19	1.19E-17
AB57_3029		putative RND family drug transporter	-0.331112431	0.046652	0.066288
AB57_3030		putative RND family drug transporter	-0.263597027	0.014568	0.023015
AB57_3031		hypothetical protein	-0.157327163	0.157186	0.19979
AB57_3032		ABC-2 type transporter family	-0.355795779	0.003159	0.005729
AB57_3033		hypothetical protein	-0.775522756	4.90E-05	0.000123
AB57_3034		glycosyltransferase	-0.428227487	0.012138	0.019543
AB57_3036		hypothetical protein	-0.557778598	9.62E-07	3.27E-06
AB57_3037	gyrA	DNA gyrase, A subunit	1.453762095	1.28E-09	6.88E-09
AB57_3038		electron transfer flavoprotein subunit alpha	0.644326617	0.000491	0.001029
AB57_3039		electron transfer flavoprotein subunit beta	0.462408553	0.00281	0.005133
AB57_3040	xerC	tyrosine recombinase XerC	-0.473578051	0.000133	0.00031
AB57_3041		lysine exporter protein	0.155911964	0.169008	0.21386
AB57_3042		alpha/beta hydrolase fold protein	-0.243731812	0.038836	0.056217
AB57_3043	dapF	diaminopimelate epimerase	0.920475155	3.05E-07	1.11E-06
AB57_3044	lysA	diaminopimelate decarboxylase	1.50975704	1.39E-13	1.47E-12
AB57_3045		hypothetical protein	1.17915259	4.37E-14	4.99E-13
AB57_3046		D-serine/D-alanine/glycine transporter	-1.408511882	1.23E-12	1.14E-11
AB57_3048	radA	DNA repair protein RadA	0.398187238	0.000299	0.000649
AB57_3049		hypothetical protein	-0.06195119	0.690283	0.733079
AB57_3050		lysyl-tRNA synthetase	0.502626213	3.42E-05	8.85E-05
AB57_3051		D-isomer specific 2-hydroxyacid dehydrogenase, NAD-binding	0.666944977	9.35E-10	5.17E-09
AB57_3052		hypothetical protein	-0.475544633	0.001491	0.002866
AB57_3053	fdhD	formate dehydrogenase accessory protein FdhD	-0.025432671	0.843792	0.87086
AB57_3054		oxidoreductase alpha (molybdopterin) subunit	-0.869495648	2.62E-11	1.89E-10
AB57_3057		transcriptional regulator, TetR family	0.241924791	0.089611	0.120261
AB57_3059		oxidoreductase short chain dehydrogenase/reductase family	0.51411678	0.000468	0.000985
AB57_3060		nitroreductase family protein	-0.060550439	0.583793	0.637314
AB57_3061		transcriptional regulator, TetR family	-0.686777363	0.000497	0.00104
AB57_3062		hypothetical protein	-0.824654591	6.93E-06	2.04E-05
AB57_3064		hypothetical protein	-0.473051136	0.028165	0.042117
AB57_3065		hypothetical protein	-0.782731454	3.33E-08	1.40E-07
AB57_3066		non-ribosomal peptide synthetase	-0.213592263	0.135248	0.174397
AB57_3067		hypothetical protein	-0.537312264	8.35E-06	2.40E-05
AB57_3068	greB	transcription elongation factor GreB	-0.490822483	8.77E-06	2.51E-05
AB57_3069		lytic transglycosylase, catalytic	1.369866191	2.96E-08	1.26E-07
AB57_3070		hypothetical protein	0.780694757	7.89E-06	2.28E-05
AB57_3071		PP-loop domain protein	1.405523811	4.18E-18	1.03E-16
AB57_3072		lytic transglycosylase, catalytic	0.062511112	0.606857	0.658081
AB57_3073	htpX	heat shock protein HtpX	0.42723634	0.006399	0.010931
AB57_3074		hypothetical protein	-0.122603659	0.352908	0.412432
AB57_3075		multidrug efflux protein	-0.269300544	0.010519	0.017123
AB57_3076		glycerophosphoryl diester phosphodiesterase	-0.473869358	0.000324	0.000698
AB57_3077		metal-dependent hydrolase of the beta-lactamase superfamily	-0.231943459	0.043589	0.062366
AB57_3078		diacylglycerol kinase	-0.252554118	0.096388	0.128057
AB57_3079	groL	chaperonin GroEL	0.921045308	4.67E-06	1.41E-05
AB57_3080	groS	co-chaperonin GroES	0.004271597	0.978116	0.982098
AB57_3081		biofilm-associated protein	0.286397206	0.100582	0.133245
AB57_3082		putative outer membrane adhesin like proteiin	0.352073517	0.001407	0.002719
AB57_3083		probable phosphodiesterase	-0.3372347	0.03311	0.048691
AB57_3084		hypothetical protein	-0.873081532	1.89E-06	6.13E-06
AB57_3085		phosphoenolpyruvate carboxykinase	2.391333156	5.21E-17	1.05E-15
AB57_3086		glycerol-3-phosphate dehydrogenase	-0.511475117	8.48E-07	2.90E-06

AB57_3087	glpK	glycerol kinase	0.225104393	0.029857	0.044437
AB57_3088		MFS permease	-0.570021419	5.09E-06	1.53E-05
AB57_3089		hypothetical protein	-0.414425734	3.00E-05	7.85E-05
AB57_3090	prmA	ribosomal protein L11 methyltransferase	0.304215118	0.003003	0.005458
AB57_3091		bifunctional 5,10-methylene-tetrahydrofolate dehydrogenase/	1.075812681	2.10E-15	3.20E-14
AB57_3092		alkaline phosphatase	-0.063523587	0.564193	0.619624
AB57_3093		hypothetical protein	-0.355159188	0.013217	0.021115
AB57_3094		hypothetical protein	0.827106318	8.02E-09	3.73E-08
AB57_3095	folP	dihydropteroate synthase	0.090394112	0.409998	0.470969
AB57_3096	ftsH	cell division protein FtsH	0.314149289	0.072834	0.099681
AB57_3097	rrmJ	ribosomal RNA large subunit methyltransferase J	-0.031527555	0.853513	0.879665
AB57_3098		hypothetical protein	0.681938003	1.91E-06	6.19E-06
AB57_3099		hypothetical protein	1.204167143	1.34E-17	3.03E-16
AB57_3100		hypothetical protein	-0.08197427	0.423743	0.485101
AB57_3101	carA	carbamoyl phosphate synthase small subunit	1.808266679	2.19E-14	2.64E-13
AB57_3102	carB	carbamoyl-phosphate synthase, large subunit	0.730223842	6.21E-05	0.000153
AB57_3103	greA	transcription elongation factor GreA	1.233970025	1.24E-11	9.49E-11
AB57_3104		chloramphenicol acetyltransferase	0.182644787	0.142364	0.182422
AB57_3105		universal stress protein	-0.656456989	3.40E-08	1.43E-07
AB57_3106		methylated-DNA--protein-cysteine methyltransferase	-0.448436199	0.000409	0.000872
AB57_3107		hypothetical protein	-0.460366238	0.001969	0.003727
AB57_3108		hypothetical protein	-0.687198384	2.16E-08	9.44E-08
AB57_3109		hypothetical protein	-0.439999463	0.000227	0.000506
AB57_3110		hypothetical protein	-0.519925234	0.044154	0.063078
AB57_3111		hypothetical protein	-0.43115264	0.000723	0.001473
AB57_3112		hypothetical protein	-0.441021265	0.002352	0.004364
AB57_3113		biofilm-associated protein	-0.525082031	0.001958	0.00371
AB57_3114		transposase (ISN1)	-0.616475642	0.000158	0.000362
AB57_3115		putave Na+/H+ antiporter	-0.342091548	0.013662	0.021732
AB57_3116		metallopeptidase, zinc binding	-0.102140588	0.376509	0.436567
AB57_3117		hypothetical protein	0.136337881	0.285748	0.343492
AB57_3118	trpS	tryptophanyl-tRNA synthetase II	1.391040978	4.44E-16	7.63E-15
AB57_3119		hypothetical protein	-0.74399102	1.38E-08	6.20E-08
AB57_3120		hypothetical protein	-0.707689242	7.76E-11	5.13E-10
AB57_3122	sucD	succinyl-CoA synthetase subunit alpha	0.491896934	0.006678	0.011366
AB57_3123	sucC	succinyl-CoA synthetase subunit beta	0.9317812	5.18E-08	2.13E-07
AB57_3124	lpdA	dihydrolipoamide dehydrogenase	1.267903308	1.16E-11	8.94E-11
AB57_3125	sucB	2-oxoglutarate dehydrogenase, E2 component, dihydrolipoamid	1.185962227	8.25E-10	4.61E-09
AB57_3126	sucA	2-oxoglutarate dehydrogenase E1 component	0.980129475	6.69E-08	2.71E-07
AB57_3128		succinate dehydrogenase iron-sulfur subunit	0.537977481	0.002371	0.004393
AB57_3129	sdhA	succinate dehydrogenase flavoprotein subunit	0.846974436	7.89E-06	2.28E-05
AB57_3130	sdhD	succinate dehydrogenase, hydrophobic membrane anchor prote	0.906311645	7.43E-09	3.48E-08
AB57_3131	sdhC	succinate dehydrogenase, cytochrome b556 subunit	0.359915595	0.018925	0.029213
AB57_3132	gltA	citrate synthase I	1.198301133	7.83E-11	5.16E-10
AB57_3133		hypothetical protein	-0.52944257	2.82E-06	8.80E-06
AB57_3134		rhodanese domain protein	1.43624641	3.67E-20	1.21E-18
AB57_3135		hypothetical protein	0.552432482	1.67E-05	4.55E-05
AB57_3136		hypothetical protein	0.227046096	0.02655	0.039853
AB57_3137	rpoD	RNA polymerase sigma factor sigma-70	0.709187689	0.000417	0.000887
AB57_3138		hypothetical protein	-0.568807211	0.000245	0.000543
AB57_3139	lipB	lipoate-protein ligase B	-0.305922382	0.006188	0.01061
AB57_3140		hypothetical protein	-0.236637113	0.046366	0.065906
AB57_3141		alcohol dehydrogenase, class IV	0.452018498	0.001075	0.002123
AB57_3142		putrescine importer	1.075910667	1.57E-07	5.99E-07
AB57_3143		hypothetical protein	-0.323353351	0.001047	0.002073
AB57_3144		transcriptional regulator, PadR family	-0.638094242	5.53E-06	1.64E-05
AB57_3145		RNA methyltransferase, TrmH family	0.926434283	1.17E-13	1.26E-12
AB57_3146		uroporphyrin-III C-methyltransferase	0.490684583	0.000337	0.000725

AB57_3147	serS	seryl-tRNA synthetase	0.613821509	0.000125	0.000293
AB57_3148		hypothetical protein	-0.833355381	1.07E-11	8.37E-11
AB57_3149	lolA	outer membrane lipoprotein carrier protein LolA	0.016048665	0.895042	0.914569
AB57_3150	rpmA	50S ribosomal protein L27	0.871475598	1.88E-06	6.09E-06
AB57_3151	rplU	50S ribosomal protein L21	0.921919291	5.70E-07	2.00E-06
AB57_3153		trans-hexaprenyltranstransferase	0.728232662	3.79E-11	2.67E-10
AB57_3154		site-specific recombinase	0.382806928	0.000185	0.000419
AB57_3155		hypothetical protein	-0.009827313	0.933415	0.945943
AB57_3156	adeI	multidrug efflux protein AdeI	0.275402683	0.127867	0.165944
AB57_3157	adeJ	multidrug efflux protein AdeJ	0.219433054	0.251103	0.306729
AB57_3158	adeK	multidrug efflux protein AdeK	0.092153808	0.582133	0.636305
AB57_3159		hypothetical protein	-0.443612995	0.008824	0.014668
AB57_3160		hypothetical protein	-0.841226306	8.77E-15	1.17E-13
AB57_3161		hypothetical protein	-0.418849294	0.01014	0.016579
AB57_3162		short-chain dehydrogenase/reductase	0.381606343	0.000125	0.000291
AB57_3163		hypothetical protein	-0.733195093	2.65E-06	8.31E-06
AB57_3164	valS	valyl-tRNA synthetase	1.376631647	2.31E-10	1.40E-09
AB57_3165		hypothetical protein	-0.483177729	5.03E-06	1.51E-05
AB57_3166		DnaJ domain protein	-0.672192191	0.000351	0.000752
AB57_3167		hypothetical protein	-0.395465737	0.015874	0.024834
AB57_3168		hypothetical protein	-0.31922819	0.076364	0.104184
AB57_3169		transcriptional regulator, LysR family	-0.426813638	0.000552	0.001146
AB57_3170		ammonium transporter	-0.587867681	4.51E-07	1.60E-06
AB57_3171		hypothetical protein	-0.676553374	0.000874	0.001756
AB57_3172		two-component system sensor kinase	-0.190889012	0.074146	0.101344
AB57_3173		two-component system DNA-binding response regulator	-0.030213804	0.809711	0.84179
AB57_3174	pmrC	lipid A phosphoethanolamine transferase	-0.294770446	0.011963	0.019296
AB57_3175		hypothetical protein	-0.183897957	0.242657	0.297492
AB57_3176		major facilitator superfamily MFS_1	-0.494707858	0.002104	0.00395
AB57_3177		phospholipid/glycerol acyltransferase	-0.008844449	0.953993	0.963893
AB57_3178		hypothetical protein	0.881856672	1.09E-13	1.18E-12
AB57_3179		hypothetical protein	-0.256692266	0.014846	0.023405
AB57_3180		band 7 protein	0.392785585	0.00027	0.000593
AB57_3181		hypothetical protein	-0.831422645	7.78E-13	7.40E-12
AB57_3182		polyprenyl synthetase	0.136215566	0.206078	0.256126
AB57_3183	prpF	AcnD-accessory protein PrpF	0.292276167	0.007777	0.013086
AB57_3185		aromatic amino acid transport protein	0.240347143	0.113313	0.148515
AB57_3186		hypothetical protein	-0.365570099	0.06221	0.086436
AB57_3187		site-specific recombinase, phage integrase family	-0.377347114	0.005187	0.009043
AB57_3188		hypothetical protein	-0.342518291	0.022522	0.034336
AB57_3189		hypothetical protein	0.116824533	0.332068	0.39179
AB57_3190		hypothetical protein	0.539601112	7.58E-06	2.20E-05
AB57_3191		hypothetical protein	0.184719006	0.327302	0.38703
AB57_3192		hypothetical protein	-0.018996848	0.937415	0.949216
AB57_3193		hypothetical protein	-0.482373596	0.000163	0.000372
AB57_3195		hypothetical protein	0.182319677	0.415382	0.476436
AB57_3197		tail tape meausure protein	-0.699441223	3.74E-09	1.85E-08
AB57_3200		hypothetical protein	-0.833914412	4.35E-05	0.00011
AB57_3202		hypothetical protein	-0.864539119	8.05E-13	7.63E-12
AB57_3203		hypothetical protein	-0.263726177	0.172294	0.217722
AB57_3204		Arc domain protein DNA binding domain protein	-0.198463074	0.262977	0.319336
AB57_3205		hypothetical protein	-0.448914311	1.12E-05	3.15E-05
AB57_3206		lipoprotein, putative	-0.140543367	0.240986	0.295541
AB57_3207		hypothetical protein	0.007261804	0.959554	0.967661
AB57_3208		helix-turn-helix domain protein	-0.171676131	0.13857	0.178148
AB57_3209		hypothetical protein	-0.389122215	0.015138	0.023784
AB57_3210		hypothetical protein	-0.184881648	0.387618	0.447763
AB57_3211		hypothetical protein	0.058736517	0.764909	0.800385

AB57_3212		putative tail fiber	-0.69906198	4.19E-07	1.50E-06
AB57_3213		hypothetical protein	-0.838938153	2.80E-05	7.37E-05
AB57_3214		hypothetical protein	-0.703013695	2.18E-09	1.13E-08
AB57_3215		hypothetical protein	-1.012771815	2.91E-15	4.30E-14
AB57_3216		hypothetical protein	-0.325507095	0.002764	0.005058
AB57_3217		hypothetical protein	-0.505314675	0.054681	0.076782
AB57_3219		hypothetical protein	0.387655853	0.053164	0.074825
AB57_3220		prophage LambdaCh01, coat protein	0.122425983	0.459175	0.519555
AB57_3221		hypothetical protein	0.722097979	1.57E-05	4.29E-05
AB57_3225		phage putative head morphogenesis protein	-0.366815587	0.012863	0.020603
AB57_3226		hypothetical protein	-0.735741438	2.60E-06	8.19E-06
AB57_3227		terminase	-0.605103107	0.002355	0.004368
AB57_3229		hypothetical protein	-0.808969738	3.46E-05	8.93E-05
AB57_3231		hypothetical protein	0.186802908	0.335653	0.395767
AB57_3232		hypothetical protein	0.135140998	0.511478	0.570536
AB57_3233		hypothetical protein	0.262903344	0.009399	0.015497
AB57_3234		hypothetical protein	0.203334277	0.132647	0.171246
AB57_3236		hypothetical protein	-0.697765006	2.05E-06	6.58E-06
AB57_3237		hypothetical protein	-0.765253072	5.31E-05	0.000132
AB57_3239		hypothetical protein	-0.124877776	0.583813	0.637314
AB57_3243		gp12	-0.415475974	0.0367	0.053461
AB57_3246		replicative DNA helicase	-0.256859377	0.149395	0.190541
AB57_3247		prophage LambdaBa04, DnaD replication protein, putative	-0.510154781	0.000664	0.00136
AB57_3248		hypothetical protein	-0.317781613	0.149612	0.190752
AB57_3249		hypothetical protein	0.54807326	0.004808	0.008423
AB57_3251		putative transcriptional regulator, Cro/CI family	0.454538263	1.21E-05	3.38E-05
AB57_3252		hypothetical protein	0.337320285	0.020107	0.030907
AB57_3255		hypothetical protein	-0.614560464	0.001292	0.002514
AB57_3257		hypothetical protein	-0.048667022	0.776095	0.810943
AB57_3258		hypothetical protein	0.037223653	0.856458	0.882454
AB57_3259		hypothetical protein	-0.068040346	0.556197	0.613026
AB57_3260		hypothetical protein	-0.121935456	0.367262	0.427452
AB57_3261		hypothetical protein	0.239899323	0.194561	0.243365
AB57_3265		chaperone protein HchA	-0.294530304	0.010494	0.017098
AB57_3266		NADPH:quinone oxidoreductase	-0.096982381	0.330723	0.390577
AB57_3267		transcriptional regulator, AraC family	-0.379121995	0.008578	0.014304
AB57_3268	uppP	undecaprenyl pyrophosphate phosphatase	1.021151768	7.58E-09	3.54E-08
AB57_3269		hypothetical protein	-0.679049361	1.97E-10	1.21E-09
AB57_3270		fatty acid desaturase	0.157298134	0.134932	0.174075
AB57_3273		NAD(P)H dehydrogenase, quinone family	-0.658194314	1.25E-06	4.18E-06
AB57_3274		aromatic hydrocarbon degradation membrane protein	-0.262741952	0.174284	0.220086
AB57_3275	thrH	phosphoserine phosphatase	1.7239657	3.52E-30	6.20E-28
AB57_3276		phosphoadenosine phosphosulfate reductase	0.336480491	0.001765	0.00337
AB57_3277		hypothetical protein	-0.537220429	0.000127	0.000297
AB57_3278		hypothetical protein	-0.616249979	1.32E-05	3.66E-05
AB57_3279		ribonuclease G	0.681922973	6.24E-06	1.84E-05
AB57_3280	maf	Maf-like protein	0.506798305	3.15E-05	8.23E-05
AB57_3281	mreD	rod shape-determining protein MreD	0.518501421	9.12E-06	2.60E-05
AB57_3282	mreC	rod shape-determining protein MreC	0.956257735	2.91E-10	1.74E-09
AB57_3283	mreB	rod shape-determining protein MreB	0.973225319	2.60E-08	1.12E-07
AB57_3284		glutamyl-tRNA(Gln) amidotransferase, C subunit	1.045374356	4.47E-14	5.08E-13
AB57_3285		aspartyl/glutamyl-tRNA amidotransferase subunit A	1.483197063	2.87E-13	2.90E-12
AB57_3286		aspartyl/glutamyl-tRNA amidotransferase subunit B	1.115895385	2.44E-08	1.06E-07
AB57_3287		intracellular protease, PfpI family	-0.16906973	0.118316	0.154416
AB57_3288		hypothetical protein	-0.691053637	8.32E-05	0.0002
AB57_3289		hypothetical protein	-0.308277384	0.018415	0.028509
AB57_3290		hypothetical protein	-0.715769473	9.60E-08	3.79E-07
AB57_3291		transport protein	-0.488722739	3.34E-05	8.67E-05

AB57_3292	ilvA	threonine dehydratase	0.215716721	0.034235	0.050148
AB57_3293		phospholipase, patatin family	-0.385235871	0.00201	0.003795
AB57_3294		amino-acid transport protein	0.71718207	0.000257	0.000565
AB57_3296		hypothetical protein	0.710973932	5.46E-06	1.62E-05
AB57_3297		nitroreductase	0.560507291	7.62E-08	3.06E-07
AB57_3298		drug resistance transporter, Bcr/CflA subfamily	-0.106025334	0.353795	0.413338
AB57_3299		hypothetical protein	-0.262363071	0.023945	0.036295
AB57_3300		hypothetical protein	0.741061011	6.11E-08	2.49E-07
AB57_3301		flavodoxin/nitric oxide synthase	0.139852485	0.303945	0.362773
AB57_3302		hypothetical protein	0.615001193	2.43E-06	7.68E-06
AB57_3303		ErfK/YbiS/YcfS/YnhG family protein	-0.29668735	0.037795	0.054905
AB57_3304		hypothetical protein	-0.201882661	0.269668	0.326176
AB57_3305		hypothetical protein	-0.629628462	0.000612	0.001263
AB57_3306		entericidin EcnAB	-1.150333546	3.44E-12	2.96E-11
AB57_3307	dapE	succinyl-diaminopimelate desuccinylase	1.857730233	1.37E-24	9.57E-23
AB57_3308		alpha/beta hydrolase fold protein	-0.361381531	0.002714	0.004973
AB57_3309		coproporphyrinogen III oxidase	-0.248964781	0.0314	0.046472
AB57_3310		hypothetical protein	-0.406039533	0.0074	0.01249
AB57_3311	pilL	type IV pilus hybrid sensor kinase/response regulator PilL	-0.410098687	0.001415	0.00273
AB57_3312		type IV pilus methyl-accepting chemotaxis sensory transducer P	-0.022753057	0.857452	0.882741
AB57_3313	pilI	type IV pilus signal transduction protein PilI	0.028164992	0.867892	0.892496
AB57_3314	pilH	type IV pilus response regulator protein PilH	-0.004882724	0.975585	0.980621
AB57_3315	pilG	type IV pilus response regulator receiver protein PilG	0.106778229	0.323788	0.383243
AB57_3316		hypothetical protein	-0.54004234	0.002385	0.004415
AB57_3317		multidrug efflux protein	-0.114593708	0.283879	0.341578
AB57_3318		multidrug efflux protein	0.178281444	0.116502	0.152156
AB57_3319	proS	prolyl-tRNA synthetase	0.907035041	5.03E-06	1.51E-05
AB57_3320		hypothetical protein	-0.771163172	1.08E-08	4.90E-08
AB57_3321	phnA	alkylphosphonate utilization operon protein PhnA	-0.257516074	0.032533	0.0479
AB57_3322		hypothetical protein	-0.946117773	2.16E-06	6.87E-06
AB57_3323		hypothetical protein	-1.048345773	3.47E-18	8.61E-17
AB57_3324		hypothetical protein	0.49987512	9.30E-07	3.17E-06
AB57_3325		thiol:disulfide interchange protein DsbC	0.039460181	0.718164	0.758769
AB57_3326		hypothetical protein	-1.212559476	3.73E-19	1.10E-17
AB57_3327		auxin efflux Carrier	-0.921798787	5.82E-16	9.83E-15
AB57_3328		NADPH dehydrogenase	0.41305308	0.000344	0.000739
AB57_3329		TonB-dependent receptor	0.453196982	0.000129	0.000301
AB57_3330		DNA-3-methyladenine glycosylase	-0.427224455	0.001173	0.002303
AB57_3333		peptidyl-prolyl cis-trans isomerase	-0.026910081	0.805279	0.83836
AB57_3334		hypothetical protein	-0.508858047	3.07E-05	8.02E-05
AB57_3335	mscL	large-conductance mechanosensitive channel	-0.15382072	0.13881	0.178394
AB57_3336	typA	GTP-binding protein TypA/BipA	2.209636441	1.31E-14	1.67E-13
AB57_3338		uracil-xanthine permease	2.012473535	1.77E-19	5.46E-18
AB57_3339		ribosomal RNA small subunit methyltransferase C	2.422153646	1.71E-14	2.12E-13
AB57_3340		ribosomal RNA small subunit methyltransferase C	1.76696831	3.12E-18	7.86E-17
AB57_3341		amino-acid transport protein	1.554236317	2.27E-11	1.66E-10
AB57_3342		hypothetical protein	-0.010905611	0.919174	0.934325
AB57_3343		hypothetical protein	-0.337763758	0.003855	0.006875
AB57_3344		outer membrane protein A	-0.01929904	0.898865	0.917462
AB57_3345		type 4 fimbrial biogenesis protein FimT	-0.257654905	0.090308	0.121153
AB57_3346		acetyl-CoA acetyltransferase	1.091514752	2.29E-14	2.75E-13
AB57_3347		hypothetical protein	-1.284861062	1.29E-20	4.76E-19
AB57_3348		quaternary ammonium compound-resistance protein	-1.446184853	4.54E-21	1.82E-19
AB57_3349		hypothetical protein	0.4161307	0.000224	0.000501
AB57_3350		sulfite reductase	0.862429011	1.27E-11	9.70E-11
AB57_3351		glucose dehydrogenase	0.142897397	0.434386	0.495447
AB57_3353		porin B	-0.001014052	0.994522	0.995329
AB57_3354		alpha-methylacyl-CoA racemase	-0.798896076	1.49E-06	4.94E-06

AB57_3355		transcriptional regulator, AraC family	0.361497247	0.002775	0.005073
AB57_3356		acetyl-CoA acetyltransferase	0.265090171	0.010003	0.01639
AB57_3357		3-hydroxyacyl-CoA dehydrogenase	0.24284174	0.069002	0.094981
AB57_3358		hypothetical protein	0.478655331	0.000304	0.000659
AB57_3359		phospholipase, patatin family	0.88308541	1.21E-15	1.93E-14
AB57_3360		acetyltransferase, gnat family	-0.286783882	0.017479	0.027162
AB57_3363		hemolysin-3	-0.37351481	0.00077	0.001563
AB57_3364		metabolite transport protein	-0.324849381	0.013599	0.021642
AB57_3365		hypothetical protein	-0.251513538	0.031166	0.0462
AB57_3366	secA	preprotein translocase subunit SecA	0.435792472	0.011169	0.018096
AB57_3367		peroxidase	-1.390125758	4.57E-06	1.38E-05
AB57_3368		metallo-beta-lactamase superfamily protein	-0.129631435	0.41063	0.471549
AB57_3369		protein tyrosine/serine phosphatase	-0.044686696	0.814608	0.846167
AB57_3370		hypothetical protein	0.335032732	0.004327	0.007656
AB57_3371	folC	folylpolyglutamate synthetase/dihydrofolate synthase	0.360705177	0.002213	0.004121
AB57_3372	accD	acetyl-CoA carboxylase, carboxyl transferase, beta subunit	0.586031764	5.80E-05	0.000143
AB57_3373	trpA	tryptophan synthase subunit alpha	0.141120624	0.330046	0.389901
AB57_3374		transcriptional regulator, AraC family	-0.042807585	0.727278	0.766864
AB57_3377		hypothetical protein	-0.250952675	0.042561	0.061084
AB57_3378		hypothetical protein	0.718418582	5.76E-11	3.91E-10
AB57_3379	trpB	tryptophan synthase subunit beta	1.057930919	1.22E-09	6.59E-09
AB57_3380	trpF	phosphoribosylanthranilate isomerase	0.613649252	9.95E-09	4.55E-08
AB57_3381		vitamin B12 receptor	0.941301953	4.72E-06	1.42E-05
AB57_3382		cobalamin adenosyltransferase	1.092332274	7.96E-21	3.04E-19
AB57_3383		glycerophosphoryl diester phosphodiesterase	0.314063842	0.002924	0.005321
AB57_3384		hypothetical protein	-0.047247876	0.693586	0.736375
AB57_3385		stearoyl-CoA 9-desaturase	0.807527261	2.43E-05	6.46E-05
AB57_3386		hypothetical protein	-0.531495629	9.92E-06	2.80E-05
AB57_3387		two component signal transduction system response regulator	0.322490256	0.004562	0.008019
AB57_3388		two component signal transduction system kinase sensor comp	-0.358216382	0.000293	0.000638
AB57_3389		hypothetical protein	-0.950753218	1.21E-12	1.12E-11
AB57_3390		acyl-CoA dehydrogenase	0.346006061	0.045443	0.064694
AB57_3391		acyl-CoA dehydrogenase	1.097231538	6.14E-12	5.00E-11
AB57_3392		phosphate-starvation-inducible E	-0.65127624	9.54E-10	5.26E-09
AB57_3393		hypothetical protein	-1.346451306	9.57E-25	7.09E-23
AB57_3394		hypothetical protein	0.366754988	0.000809	0.001638
AB57_3395		hyphotetical protein	0.046887406	0.669569	0.714155
AB57_3396		TonB-dependent receptor	0.439031888	0.001302	0.002531
AB57_3397		hypothetical protein	-0.583673229	5.55E-05	0.000138
AB57_3398	aspS	aspartyl-tRNA synthetase	1.580607304	1.68E-15	2.59E-14
AB57_3399		hypothetical protein	-0.398868589	0.000815	0.001648
AB57_3400		glycosyltransferase	-0.294791813	0.041408	0.059673
AB57_3401		hypothetical protein	0.543403842	5.11E-05	0.000128
AB57_3402		LPS glycosyltransferase subfamily	-0.271731005	0.013562	0.021611
AB57_3403		glycosyltransferase	0.39702675	0.000142	0.000329
AB57_3404		hypothetical protein	-0.061988456	0.599038	0.650745
AB57_3405		glycosyltransferase	0.282061061	0.009071	0.015011
AB57_3406		putative polysaccharide deacetylase	0.628543265	2.70E-08	1.15E-07
AB57_3407		hypothetical protein	0.359631566	0.000265	0.000584
AB57_3408		hypothetical protein	-0.021268952	0.832028	0.860879
AB57_3409	ilvE	branched-chain amino acid aminotransferase	0.744049868	3.48E-06	1.07E-05
AB57_3410	glnE	bifunctional glutamine-synthetase adenylyltransferase/deadeny	-0.151918677	0.23434	0.288155
AB57_3411		two-component system histidine kinase sensor component	-1.366212229	2.07E-16	3.81E-15
AB57_3412	queA	S-adenosylmethionine:tRNA ribosyltransferase-isomerase	0.842460174	2.39E-10	1.44E-09
AB57_3413		hypothetical protein	-0.558195017	3.10E-06	9.63E-06
AB57_3414		LemA family	-0.026092298	0.856962	0.88252
AB57_3415	tgt	queuine tRNA-ribosyltransferase	1.258545797	3.08E-13	3.09E-12
AB57_3416	yajC	preprotein translocase, YajC subunit	0.958002409	4.66E-09	2.26E-08

AB57_3417	secD	preprotein translocase subunit SecD	0.73689686	3.98E-05	0.000102
AB57_3418	secF	preprotein translocase subunit SecF	0.432461666	0.009931	0.016296
AB57_3419	coaBC	phosphopantothenoylcysteine decarboxylase/phosphopantothe	0.331467131	0.004037	0.007167
AB57_3420		DNA repair protein RadC	-0.538161884	3.41E-05	8.84E-05
AB57_3422		hypothetical protein	-0.560747716	0.00015	0.000345
AB57_3423		PHP domain protein	-0.551847232	4.33E-06	1.32E-05
AB57_3424	ispZ	intracellular septation protein A	0.132355677	0.295277	0.353453
AB57_3425		YCII-related protein	0.24442238	0.023152	0.035151
AB57_3426		hypothetical protein	0.893384668	1.38E-14	1.74E-13
AB57_3427		rhodanese domain protein	-0.512062336	2.42E-05	6.46E-05
AB57_3428		hypothetical protein	0.883870377	5.89E-11	3.97E-10
AB57_3429		putative nucleotide-binding protein	0.105068105	0.311267	0.369842
AB57_3430		hypothetical protein	-0.060641315	0.64488	0.69081
AB57_3431		hypothetical protein	0.696485922	4.25E-09	2.10E-08
AB57_3432		thioredoxin	0.367225274	0.003659	0.006555
AB57_3433		hypothetical protein	-0.661992519	1.48E-05	4.08E-05
AB57_3434		hypothetical protein	0.16829418	0.100158	0.132826
AB57_3435		hypothetical protein	-0.583952136	3.97E-08	1.66E-07
AB57_3436		dihydrolipoamide dehydrogenase	-0.395510684	0.002041	0.00384
AB57_3438		hypothetical protein	0.064886236	0.562299	0.617911
AB57_3439		GGDEF domain protein	-0.086820137	0.445497	0.506103
AB57_3440		OmpA/MotB	0.012922665	0.920043	0.934695
AB57_3441		Ser/Thr protein phosphatase family protein	-0.273305377	0.011803	0.019053
AB57_3442		phospholipase D/transphosphatidylase	-0.184314574	0.072848	0.099681
AB57_3443		phospholipid/glycerol acyltransferase	-0.211349741	0.071334	0.097826
AB57_3444		GTP-binding proten	0.329903325	0.000812	0.001642
AB57_3445		hypothetical protein	-0.025049205	0.836329	0.864121
AB57_3446		LrgB family protein	-0.082374555	0.531999	0.589517
AB57_3447		hypothetical protein	-0.787983263	3.13E-13	3.13E-12
AB57_3448		diadenosine tetraphosphatase	0.752840742	8.36E-06	2.40E-05
AB57_3449	ksgA	dimethyladenosine transferase	0.711064875	3.05E-06	9.50E-06
AB57_3450	pdxA	4-hydroxythreonine-4-phosphate dehydrogenase	-0.018101878	0.873128	0.895889
AB57_3451	rplM	50S ribosomal protein L13	2.191144543	2.29E-20	7.83E-19
AB57_3452	rpsI	ribosomal protein S9	1.947927642	4.54E-19	1.32E-17
AB57_3453	sspA	stringent starvation protein A	-0.408837947	0.000977	0.001945
AB57_3454	sspB	ClpXP protease specificity-enhancing factor	-0.069422003	0.50607	0.565185
AB57_3455		hypothetical protein	0.31935355	0.006997	0.011881
AB57_3456		acetyl-/propionyl-coenzyme A carboxylase alpha chain	-0.09654849	0.404907	0.4657
AB57_3457		enoyl-CoA hydratase	0.065359478	0.675096	0.719014
AB57_3458		acyl-CoA dehydrogenase	0.135024003	0.195918	0.244649
AB57_3459		methylcrotonoyl-CoA carboxylase beta chain	0.173504286	0.16735	0.211981
AB57_3460		oxidoreductase short-chain dehydrogenase/reductase family	0.407552593	0.014145	0.022414
AB57_3461		hypothetical protein	0.716258976	1.13E-11	8.76E-11
AB57_3463		transcriptional regulator, TetR family	0.969272214	6.65E-14	7.37E-13
AB57_3464		acyl-CoA dehydrogenase	-0.183679296	0.075744	0.103452
AB57_3465		hypothetical protein	-0.462150445	2.52E-05	6.68E-05
AB57_3466		hypothetical protein	-0.398902279	0.000949	0.001897
AB57_3468		hypothetical protein	-0.692887564	1.07E-10	6.89E-10
AB57_3469		CDP-diacylglycerol--serine O-phosphatidyltransferase	0.65819783	4.51E-06	1.37E-05
AB57_3470		hypothetical protein	0.710533609	1.83E-06	5.96E-06
AB57_3471		oxygenase	0.573381474	7.68E-07	2.64E-06
AB57_3472		hypothetical protein	-0.270078961	0.037024	0.053891
AB57_3473		hypothetical protein	-0.973721354	3.31E-15	4.82E-14
AB57_3474		malate dehydrogenase	1.818847128	2.21E-20	7.63E-19
AB57_3475		hypothetical protein	0.414580689	8.76E-05	0.00021
AB57_3476		lytic transglycosylase, catalytic	-0.068465643	0.566444	0.621727
AB57_3477	miaB	(dimethylallyl)adenosine tRNA methylthiotransferase	1.393044169	1.18E-08	5.34E-08
AB57_3478		phosphate starvation-inducible protein	-0.288173459	0.057422	0.080326

AB57_3479		hypothetical protein	0.54330292	3.58E-06	1.10E-05
AB57_3480		TonB family protein	0.31225746	0.041416	0.059673
AB57_3481		hypothetical protein	0.215486513	0.130302	0.168631
AB57_3482		hypothetical protein	-0.415950641	0.000135	0.000315
AB57_3483	xpt	xanthine phosphoribosyltransferase	1.589919845	1.87E-22	9.23E-21
AB57_3484		flavodoxin/nitric oxide synthase	0.007487857	0.943488	0.954582
AB57_3485		putative ribonuclease	-0.674633481	2.06E-09	1.07E-08
AB57_3486		hypothetical protein	0.048771454	0.684059	0.726886
AB57_3487		transcriptional regulator, AraC family	-0.544029596	5.83E-05	0.000144
AB57_3488		fumarylacetoacetate hydrolase	0.520312877	9.83E-07	3.33E-06
AB57_3489		hypothetical protein	-0.089514204	0.441508	0.50264
AB57_3490		nitroreductase family protein	0.240033807	0.073559	0.100617
AB57_3491		hypothetical protein	-0.757523679	1.52E-07	5.80E-07
AB57_3492		HAD-superfamily subfamily IB hydrolase	0.086073384	0.549277	0.606483
AB57_3493	rnr	ribonuclease R	-0.046377179	0.729856	0.768926
AB57_3494		oligopeptidase A	0.083941016	0.566167	0.621608
AB57_3495		hypothetical protein	0.098962824	0.381157	0.441127
AB57_3496		hypothetical protein	0.561581759	1.78E-06	5.83E-06
AB57_3497		TRAP C4-dicarboxylate transport system permease	-0.075025844	0.678317	0.721473
AB57_3498		rhomboid family peptidase	-1.13472463	1.16E-25	1.07E-23
AB57_3499		hypothetical protein	-1.150355265	9.86E-12	7.74E-11
AB57_3500		hypothetical protein	-0.015943245	0.909127	0.926403
AB57_3501		hypothetical protein	-0.490602431	2.59E-06	8.16E-06
AB57_3502		acyl-CoA dehydrogenase	-0.063526423	0.567243	0.622094
AB57_3503		flavin-containing monooxygenase FMO	-1.178814438	8.28E-20	2.64E-18
AB57_3504	rplQ	50S ribosomal protein L17	1.35212687	2.56E-12	2.26E-11
AB57_3505	rpoA	DNA-directed RNA polymerase subunit alpha	1.265119483	3.31E-11	2.36E-10
AB57_3506	rpsD	30S ribosomal protein S4	1.317232437	1.16E-10	7.36E-10
AB57_3507	rpsK	30S ribosomal protein S11	1.496778344	2.11E-12	1.87E-11
AB57_3508	rpsM	30S ribosomal protein S13	1.319660008	1.54E-10	9.62E-10
AB57_3509	rpmJ	50S ribosomal protein L36	0.772433712	4.55E-05	0.000115
AB57_3510	secY	preprotein translocase subunit SecY	0.674281556	0.000174	0.000395
AB57_3511	rplO	50S ribosomal protein L15	0.673041997	0.000223	0.000499
AB57_3512	rpmD	50S ribosomal protein L30	1.001175821	9.62E-08	3.80E-07
AB57_3513	rpsE	30S ribosomal protein S5	0.979959456	1.09E-07	4.26E-07
AB57_3514	rplR	50S ribosomal protein L18	0.953829974	7.35E-07	2.53E-06
AB57_3515		50S ribosomal protein L6	1.079547939	2.34E-08	1.02E-07
AB57_3516	rpsH	30S ribosomal protein S8	1.396120917	8.55E-12	6.83E-11
AB57_3517		30S ribosomal protein S14	1.451067331	2.24E-12	1.98E-11
AB57_3518		50S ribosomal protein L5	1.25760089	5.65E-10	3.23E-09
AB57_3519	rplX	50S ribosomal protein L24	1.253871162	1.19E-09	6.46E-09
AB57_3520	rplN	50S ribosomal protein L14	1.265147477	2.24E-10	1.36E-09
AB57_3521	rpsQ	30S ribosomal protein S17	0.551782806	0.001926	0.003652
AB57_3522	rpmC	50S ribosomal protein L29	0.557335103	0.00215	0.004022
AB57_3523	rplP	50S ribosomal protein L16	0.750530282	2.82E-05	7.41E-05
AB57_3524	rpsC	30S ribosomal protein S3	0.84079562	1.46E-06	4.82E-06
AB57_3525	rplV	50S ribosomal protein L22	0.964333578	1.58E-07	6.01E-07
AB57_3526	rpsS	30S ribosomal protein S19	0.994790685	1.28E-07	4.94E-07
AB57_3527	rplB	50S ribosomal protein L2	1.106199739	3.45E-09	1.72E-08
AB57_3528	rplW	50S ribosomal protein L23	1.673040743	4.53E-14	5.12E-13
AB57_3529	rplD	50S ribosomal protein L4	1.855682216	4.25E-16	7.41E-15
AB57_3530	rplC	50S ribosomal protein L3	1.955743756	5.61E-17	1.12E-15
AB57_3531	rpsJ	30S ribosomal protein S10	1.977139619	1.30E-16	2.46E-15
AB57_3532		glutamine amidotransferase, class I	-0.403501275	0.011138	0.018067
AB57_3533		cystathionine beta-lyase PLP-dependent	0.195651996	0.054677	0.076782
AB57_3534		hypothetical protein	-0.392616592	0.000374	0.0008
AB57_3535		flavohemoprotein	0.935714446	8.22E-14	9.05E-13
AB57_3536		transcriptional regulator, BadM/Rrf2 family	0.14622863	0.246666	0.301907

AB57_3537		ribosome biogenesis GTP-binding protein YsxC	0.708566448	9.18E-09	4.23E-08
AB57_3538		hypothetical protein	-0.07127285	0.496094	0.555417
AB57_3539		sodium:dicarboxylate symporter	-0.806604383	1.38E-09	7.39E-09
AB57_3540		acyl-CoA thioesterase	0.041353613	0.728367	0.767795
AB57_3541		glycerol-3-phosphate acyltransferase	0.832213135	1.64E-06	5.39E-06
AB57_3542		putative RND type efflux pump involved in aminoglycoside resis	-0.870585922	2.98E-16	5.35E-15
AB57_3543		NAD dependent epimerase/dehydratase family	-0.410149784	0.005407	0.009388
AB57_3544	recG	ATP-dependent DNA helicase RecG	-0.318270521	0.002534	0.004669
AB57_3545		competence protein F	-0.134103444	0.214302	0.265279
AB57_3546		hydrolase, NUDIX family protein	0.289429819	0.012772	0.020492
AB57_3547		hypothetical protein	0.28351984	0.004983	0.008704
AB57_3548		magnesium and cobalt transport protein	0.588987953	8.33E-09	3.85E-08
AB57_3549		putative toluene-tolerance protein	0.414071263	0.009048	0.014979
AB57_3551		putative toluene tolerance protein	0.421175391	0.007155	0.012133
AB57_3552		toluene tolerance efflux transporter	1.072151043	7.14E-10	4.03E-09
AB57_3553		toluene tolerance protein Ttg2B	1.466433253	1.91E-12	1.70E-11
AB57_3554		toluene tolerance efflux transporter	1.338273164	1.05E-18	2.81E-17
AB57_3556		DEAD/DEAH box helicase	1.811802127	4.79E-19	1.36E-17
AB57_3557		inositol-1-monophosphatase	0.760134516	4.81E-05	0.000121
AB57_3558	dxs	1-deoxy-D-xylulose-5-phosphate synthase	0.22062155	0.140013	0.179628
AB57_3559	ribA	GTP cyclohydrolase II	0.103482281	0.34371	0.404236
AB57_3560	hemF	coproporphyrinogen III oxidase	-0.004401522	0.974795	0.980093
AB57_3561	aroE	shikimate 5-dehydrogenase	0.655574784	1.05E-08	4.75E-08
AB57_3562		hypothetical protein	0.653078428	1.84E-08	8.05E-08
AB57_3563		acyl-CoA dehydrogenase	0.126183599	0.500016	0.559438
AB57_3564		hypothetical protein	0.100630508	0.317877	0.376969
AB57_3565		phage shock protein C	-0.729111393	2.51E-06	7.92E-06
AB57_3566		HPP domain protein	-1.059395898	1.69E-09	8.89E-09
AB57_3567		hypothetical protein	-0.337422357	0.01056	0.017181
AB57_3570		tetracycline resistance protein TetA	-0.015675482	0.88652	0.907365
AB57_3571	glyQ	glycyl-tRNA synthetase subunit alpha	1.503246735	3.31E-15	4.82E-14
AB57_3572	glyS	glycyl-tRNA synthetase subunit beta	1.215555185	3.26E-08	1.38E-07
AB57_3573		hypothetical protein	0.070750894	0.519189	0.578092
AB57_3574		hypothetical protein	0.287864831	0.006777	0.011514
AB57_3575		YCII-related protein	-1.129475831	1.09E-22	5.61E-21
AB57_3576		hypothetical protein	-0.642851105	7.19E-09	3.38E-08
AB57_3577		transcriptional regulator, LysR family	-0.40763224	0.014889	0.023463
AB57_3578		hypothetical protein	-1.316617322	3.45E-18	8.61E-17
AB57_3579		hypothetical protein	-1.336147518	2.95E-23	1.63E-21
AB57_3580		peptidase S8/S53 subtilisin	-0.182860524	0.083544	0.112986
AB57_3581		hypothetical protein	-0.245782983	0.129897	0.168225
AB57_3582		hypothetical protein	-0.310312152	0.008058	0.013503
AB57_3583	astE	succinylglutamate desuccinylase	0.004366158	0.976233	0.981005
AB57_3584	astB	succinylarginine dihydrolase	0.315409867	0.059872	0.083595
AB57_3585	astD	succinylglutamic semialdehyde dehydrogenase	1.05393425	5.75E-09	2.73E-08
AB57_3586	astA	arginine N-succinyltransferase	1.65528558	5.25E-19	1.48E-17
AB57_3587		bifunctional succinylornithine transaminase/acetylornithine tra	1.539962465	1.45E-14	1.82E-13
AB57_3588		glutamate dehydrogenase	0.716325313	0.00011	0.00026
AB57_3590		amino-acid permease	-0.455675428	0.002895	0.005277
AB57_3591		hypothetical protein	0.540907679	6.94E-08	2.80E-07
AB57_3592		methyltransferase type 11	-0.657209463	8.98E-06	2.57E-05
AB57_3593		hypothetical protein	-0.654553681	3.04E-10	1.81E-09
AB57_3594		hypothetical protein	-0.841449492	1.09E-13	1.18E-12
AB57_3595		hypothetical protein	0.195153114	0.309839	0.368618
AB57_3596		cobyrinic acid a,c-diamide synthase	-0.506828178	2.02E-06	6.49E-06
AB57_3597		hypothetical protein	0.047414664	0.64443	0.690528
AB57_3598	sodC	copper/zinc superoxide dismutase	-0.747570886	2.48E-09	1.27E-08
AB57_3599		hypothetical protein	-0.589572136	2.54E-08	1.09E-07

AB57_3600		chloramphenicol resistance pump cmr	0.693524312	3.72E-05	9.56E-05
AB57_3601		hypothetical protein	-0.789719147	3.12E-07	1.13E-06
AB57_3603		modulator of drug activity B	-0.005854527	0.959276	0.967644
AB57_3604		hypothetical protein	0.030338102	0.78342	0.817904
AB57_3605		hypothetical protein	-0.478625857	2.62E-05	6.92E-05
AB57_3606		FAD linked oxidase domain protein	0.762016005	5.04E-07	1.78E-06
AB57_3607		D-3-phosphoglycerate dehydrogenase	1.622030078	5.60E-15	7.93E-14
AB57_3608		hypothetical protein	0.352834908	0.001033	0.002048
AB57_3609		hypothetical protein	-0.076593105	0.523373	0.581525
AB57_3610		hemerythrin	-0.748117442	1.80E-07	6.79E-07
AB57_3611		hypothetical protein	0.528872845	0.000144	0.000333
AB57_3612	truB	tRNA pseudouridine synthase B	1.029636886	1.00E-10	6.43E-10
AB57_3613		lipase chaperone	-0.837521717	8.36E-05	0.000201
AB57_3614		lipase	-0.716093417	1.30E-11	9.90E-11
AB57_3615	rplS	50S ribosomal protein L19	1.431211247	5.15E-14	5.79E-13
AB57_3616	trmD	tRNA (guanine-N(1)-)-methyltransferase	1.961584801	9.94E-18	2.33E-16
AB57_3617	rimM	16S rRNA-processing protein RimM	1.931498576	6.15E-15	8.61E-14
AB57_3618	rpsP	30S ribosomal protein S16	1.872471403	4.46E-17	9.22E-16
AB57_3619		pilin like competence factor	0.081947416	0.580426	0.634679
AB57_3620		pilin like competence factor	-0.364159401	0.016803	0.026177
AB57_3621	pilY	pilus assembly protein tip-associated adhesin PilY1	-0.453336128	3.73E-05	9.58E-05
AB57_3622	pilX	pilus assembly protein PilX	-0.278204827	0.127705	0.165793
AB57_3623	pilW	pilus assembly protein PilW	0.121434366	0.524901	0.583048
AB57_3624	pilV	type IV pilus modification protein PilV	0.01466947	0.945831	0.95669
AB57_3625	fimT	pilin protein FimT	-0.51381638	0.025338	0.038171
AB57_3626	ispH	4-hydroxy-3-methylbut-2-enyl diphosphate reductase	-0.332415124	0.009948	0.016314
AB57_3627	gmk	guanylate kinase	0.917019499	9.40E-16	1.54E-14
AB57_3628	rpoZ	DNA-directed RNA polymerase subunit omega	0.457243009	0.00376	0.006724
AB57_3629		guanosine-3,5-bis(diphosphate) 3-pyrophosphohydrolase	-0.113570053	0.364259	0.424357
AB57_3630		hypothetical protein	0.965499143	9.46E-16	1.54E-14
AB57_3631		hypothetical protein	-1.320740178	8.56E-19	2.36E-17
AB57_3632	bfr	bacterioferritin	-0.299687889	0.050618	0.071566
AB57_3633		O-antigen polymerase family	-0.32138125	0.018889	0.029178
AB57_3634		type IV pilin structural subunit	-0.417745243	0.000635	0.001305
AB57_3635		hypothetical protein	-0.773234492	3.40E-09	1.70E-08
AB57_3636		hypothetical protein	-0.787240079	5.79E-07	2.03E-06
AB57_3637		LemA	-1.066076761	1.83E-12	1.63E-11
AB57_3638		hypothetical protein	-0.319980479	0.029826	0.04441
AB57_3639		glutamate synthase subunit beta	0.660547208	3.67E-05	9.47E-05
AB57_3640	gltB	glutamate synthase subunit alpha	0.664917283	0.001075	0.002123
AB57_3641		hypothetical protein	0.264260819	0.011686	0.018874
AB57_3642	aroB	3-dehydroquinate synthase	0.362387026	0.002174	0.004058
AB57_3643	aroK	shikimate kinase	0.333927515	0.003183	0.00577
AB57_3644	comQ	fimbrial assembly protein PilQ	-0.395330315	0.004157	0.00737
AB57_3645	comL	pilus assembly protein, PilQ	-0.030939503	0.87876	0.900918
AB57_3646	comO	pilus assembly protein, PilO	0.146477518	0.408533	0.469432
AB57_3647	comN	type 4 fimbrial biogenesis protein PilN	0.051296012	0.735499	0.773994
AB57_3648	comM	type IV pilus assembly protein PilM	-0.586568684	7.30E-07	2.51E-06
AB57_3649		penicillin-binding protein 1A	0.35600205	0.022288	0.034034
AB57_3650		ribosomal RNA large subunit methyltransferase A	0.388792978	0.000322	0.000695
AB57_3651		hypothetical protein	0.257324303	0.063855	0.08862
AB57_3652	mraY	phospho-N-acetylmuramoyl-pentapeptide-transferase	0.620510361	0.000223	0.000499
AB57_3653		UDP-N-acetylmuramoylalanyl-D-glutamyl-2,6-diaminopimelate-	0.665143379	7.24E-06	2.12E-05
AB57_3654		UDP-N-acetylmuramyl-tripeptide synthetase	0.940495009	4.67E-12	3.90E-11
AB57_3655	ftsI	peptidoglycan glycosyltransferase	0.767134659	7.64E-07	2.63E-06
AB57_3656	ftsL	cell division protein FtsL	0.887537408	1.98E-14	2.41E-13
AB57_3657	mraW	S-adenosyl-methyltransferase MraW	0.764835159	2.63E-11	1.90E-10
AB57_3658		thiosulfate-binding protein	-1.22005554	1.22E-05	3.41E-05

AB57_3659		hypothetical protein	-0.445439006	0.005438	0.009437
AB57_3660	gltX	glutamyl-tRNA synthetase	1.321761116	6.76E-10	3.84E-09
AB57_3661		amino-acid permease	1.418645806	4.27E-13	4.20E-12
AB57_3662		hypothetical protein	-0.636442821	6.88E-08	2.78E-07
AB57_3663		hypothetical protein	-1.057703728	1.49E-08	6.69E-08
AB57_3664		hypothetical protein	0.162290745	0.242773	0.297535
AB57_3665		cation efflux system protein	-0.387631773	0.00011	0.000259
AB57_3666		cation efflux system protein	-0.018974259	0.871815	0.895286
AB57_3667		cation efflux system protein (EsvF1)	-0.338220919	0.00245	0.004529
AB57_3668		cation efflux system protein	-0.369846187	0.001339	0.002595
AB57_3669		cation efflux system protein	-0.823818052	4.16E-11	2.90E-10
AB57_3670		hypothetical protein	-0.518552187	8.03E-06	2.32E-05
AB57_3672		putative ABC transporter ATP-binding protein	1.992991589	8.40E-18	1.99E-16
AB57_3673		O-acetylhomoserine/O-acetylserine sulfhydrylase	-1.277786452	4.54E-08	1.88E-07
AB57_3674		acyl coenzyme A reductase	2.676361601	2.04E-28	2.69E-26
AB57_3675		sulfate transporter	-0.660222708	1.01E-07	3.95E-07
AB57_3676		RNA binding S1 domain protein	1.323549846	4.25E-13	4.19E-12
AB57_3677		osmolarity response regulator	-0.719591487	1.93E-06	6.23E-06
AB57_3678		two-component system sensory histidine kinase	-0.357871864	0.002069	0.003888
AB57_3679		succinyl-CoA:coenzyme A transferase	0.815858193	2.04E-07	7.61E-07
AB57_3680		putative acetyltransferase	-0.110092082	0.474634	0.534921
AB57_3681		hypothetical protein	-1.005449476	2.83E-17	6.02E-16
AB57_3682	hisB	imidazoleglycerol-phosphate dehydratase	0.47376303	3.90E-05	0.0001
AB57_3683	hisH	imidazole glycerol phosphate synthase subunit HisH	0.880197076	1.06E-14	1.38E-13
AB57_3684		hypothetical protein	0.291961773	0.025585	0.038481
AB57_3687	hisA	1-(5-phosphoribosyl)-5-[(5-phosphoribosylamino)methylidenea	1.532625361	2.34E-19	7.11E-18
AB57_3688		transcriptional regulator, XRE family	0.21303781	0.260144	0.316415
AB57_3689		hypothetical protein	-0.579942428	7.52E-06	2.19E-05
AB57_3690		hypothetical protein	-0.913423454	1.16E-09	6.26E-09
AB57_3691		cold-shock DNA-binding domain protein	-0.737766246	4.98E-13	4.85E-12
AB57_3692		homoserine kinase	0.45255722	3.74E-05	9.60E-05
AB57_3693	hisF	imidazole glycerol phosphate synthase subunit HisF	0.286790988	0.008618	0.014356
AB57_3694		hypothetical protein	-0.181481917	0.256948	0.313145
AB57_3695		transcriptional regulator, AraC family	-0.797432289	1.21E-05	3.39E-05
AB57_3696		aquaporin Z	-0.304425642	0.005972	0.010278
AB57_3698		hypothetical protein	-0.666422312	1.64E-09	8.67E-09
AB57_3699		transporter LysE family	-0.334097366	0.006434	0.010986
AB57_3700		DNA/RNA non-specific endonuclease G protein	-0.333991194	0.004541	0.007994
AB57_3701		hypothetical protein	-0.322488548	0.002877	0.005248
AB57_3704		acetyltransferase, gnat family	-0.486215376	0.001211	0.00237
AB57_3705		transcriptional regulator, AraC family	-0.584811262	2.48E-07	9.13E-07
AB57_3706		NAD(P)H oxidoreductase	-0.402099163	0.068328	0.094123
AB57_3707		transcriptional regulator, MarR family	-1.009676974	6.76E-12	5.47E-11
AB57_3708		hypothetical protein	-0.498580685	5.52E-05	0.000137
AB57_3709		hypothetical protein	-0.204610249	0.171748	0.21718
AB57_3710		transcriptional regulator, HxlR family	-0.262970667	0.015171	0.023825
AB57_3711		hypothetical protein	-0.771914349	1.86E-06	6.05E-06
AB57_3712		transcriptional regulator, TetR family	-0.432168369	0.051062	0.072138
AB57_3713		transcriptional regulator, AraC family	-0.080088392	0.513288	0.57221
AB57_3714		aldo-keto reductase	0.038574144	0.737474	0.775847
AB57_3715		hypothetical protein	-0.43974879	0.002456	0.004539
AB57_3716		hypothetical protein	-0.469674618	0.000131	0.000304
AB57_3717		transcriptional regulator, LysR family	-0.019779784	0.898696	0.917462
AB57_3718		permease	-0.053362098	0.710799	0.752276
AB57_3719		major facilitator family transporter	1.075297338	2.14E-06	6.83E-06
AB57_3721		hypothetical protein	-0.729497463	1.30E-06	4.34E-06
AB57_3722		methyltransferase	-0.005324005	0.963178	0.970787
AB57_3723		hypothetical protein	0.549057957	9.78E-07	3.32E-06

AB57_3724		pirin family protein	0.181494772	0.087511	0.1177
AB57_3725		isochorismate hydrolase	0.292650751	0.031539	0.04664
AB57_3726		transcriptional regulator, LysR family	-0.495231117	8.69E-06	2.49E-05
AB57_3727		succinate-semialdehyde dehydrogenase (NADP+)	-0.245816506	0.070163	0.096472
AB57_3728	gabT	4-aminobutyrate transaminase	0.083845465	0.440705	0.502034
AB57_3729		transcriptional regulator, GntR family	-0.084209968	0.438621	0.499815
AB57_3730		GABA permease	-0.188394886	0.094119	0.125537
AB57_3731		transcriptional regulator, XRE family	0.345674444	0.004463	0.007882
AB57_3732		hypothetical protein	0.185872306	0.192048	0.240548
AB57_3733		branched-chain amino acid transport	0.085989459	0.657339	0.702742
AB57_3734	ssb	single-strand binding protein	0.440895151	0.002521	0.00465
AB57_3735		major facilitator family transporter	-0.040357243	0.758913	0.794786
AB57_3736		hypothetical protein	0.530121484	0.002687	0.004927
AB57_3737		transcriptional regulator, TenA family	0.965106242	1.78E-17	3.97E-16
AB57_3738		GlpM family protein	-0.171221353	0.186003	0.233767
AB57_3739		hypothetical protein	-0.411924438	0.00028	0.000614
AB57_3740		alcohol dehydrogenase, zinc-binding	0.488781582	1.64E-06	5.39E-06
AB57_3741		transcriptional regulator, TetR family	0.520021005	0.000155	0.000356
AB57_3742	uvrA	excinuclease ABC, A subunit	0.21788802	0.151442	0.192886
AB57_3743		GGDEF family protein	0.066707076	0.629795	0.677199
AB57_3744		hypothetical protein	1.45291543	9.44E-12	7.45E-11
AB57_3745		high-affinity choline transport protein	0.13112329	0.44897	0.508943
AB57_3746		hypothetical protein	-0.249475687	0.155168	0.197429
AB57_3747		acetate permease	-0.585831434	0.000285	0.000623
AB57_3748		hypothetical protein	-0.665110614	8.05E-09	3.74E-08
AB57_3749		two-component system hybrid histidine kinase/response regula	-0.194823012	0.070257	0.096564
AB57_3750		hypothetical protein	-0.69349209	1.45E-05	3.98E-05
AB57_3751		two-component system response regulator protein	0.094893412	0.343989	0.404307
AB57_3752		NADH-dependent fmn reductase	-1.199337304	3.49E-06	1.07E-05
AB57_3753		alkanesulfonate monooxygenase	-1.467211032	5.34E-05	0.000133
AB57_3754		transcriptional regulator, AsnC/Lrp family	-0.675018195	5.18E-07	1.83E-06
AB57_3755		amidase	-0.152717916	0.393614	0.453981
AB57_3756	acsA	acetate--CoA ligase	-0.869264631	2.81E-08	1.20E-07
AB57_3758		hypothetical protein	-0.38830414	0.001296	0.00252
AB57_3759		16S ribosomal RNA methyltransferase RsmE	0.192189869	0.081981	0.11111
AB57_3760		MscS Mechanosensitive ion channel	0.552914754	6.91E-05	0.000168
AB57_3761	kdtA	3-deoxy-D-manno-2-octulosonate transferase	0.404538673	0.000136	0.000316
AB57_3762		N-ethylmaleimide reductase	0.732798891	3.09E-09	1.56E-08
AB57_3763		transcriptional regulator, ArsR family	0.374666715	0.003806	0.006797
AB57_3765	prfB	peptide chain release factor 2	1.601771342	8.52E-17	1.68E-15
AB57_3766		hypothetical protein	-0.590626025	0.000131	0.000304
AB57_3767	recJ	single-stranded-DNA-specific exonuclease RecJ	0.541756314	1.99E-05	5.35E-05
AB57_3768	pdxH	pyridoxamine 5'-phosphate oxidase	0.76863406	5.04E-09	2.41E-08
AB57_3769	glmM	phosphoglucosamine mutase	0.271444069	0.056764	0.079556
AB57_3770	guaB	inosine-5'-monophosphate dehydrogenase	1.302790922	2.83E-13	2.87E-12
AB57_3771		putative ferredoxin	0.086229146	0.607459	0.658347
AB57_3772		metallo-beta-lactamase family protein	-0.141955903	0.304551	0.363263
AB57_3773		TonB-dependent receptor protein	-0.099279103	0.346547	0.406797
AB57_3774		hypothetical protein	-0.082891128	0.473663	0.534019
AB57_3775		hypothetical protein	-0.817603748	2.79E-12	2.45E-11
AB57_3776	aceF	pyruvate dehydrogenase complex dihydrolipoamide acetyltrans	-0.288812197	0.081978	0.11111
AB57_3777	aceE	pyruvate dehydrogenase subunit E1	0.027227929	0.870157	0.894329
AB57_3778		peptidase, M23/M37 family (EsvJ)	0.396618146	0.002821	0.005149
AB57_3779		hypothetical protein	0.313565222	0.001898	0.003603
AB57_3780		UDP-3-O-[3-hydroxymyristoyl] N-acetylglucosamine deacetylase	0.597959858	8.85E-07	3.02E-06
AB57_3781		UDP-3-O-[3-hydroxymyristoyl] N-acetylglucosamine deacetylase	0.693227366	1.55E-10	9.67E-10
AB57_3782	ftsZ	cell division protein FtsZ	0.983360654	3.08E-08	1.31E-07
AB57_3783	ftsA	cell division protein FtsA	0.81733173	7.19E-07	2.48E-06

AB57_3784	ftsQ	cell division protein FtsQ	0.336626717	0.009272	0.015309
AB57_3785		D-alanine--D-alanine ligase	0.437186089	0.001357	0.002627
AB57_3786	murC	UDP-N-acetylmuramate--L-alanine ligase	1.076234564	3.24E-10	1.92E-09
AB57_3787	murG	undecaprenyldiphospho-muramoylpentapeptide beta-N- acetyl	0.224262996	0.048284	0.068422
AB57_3788	gshB	glutathione synthetase	0.080213906	0.444302	0.505044
AB57_3789		hypothetical protein	-0.13161313	0.468867	0.529389
AB57_3790		TonB-dependent receptor protein	0.241591704	0.103293	0.136738
AB57_3791	pyrE	orotate phosphoribosyltransferase	1.687072664	1.95E-29	3.28E-27
AB57_3792	xth	exodeoxyribonuclease III	0.443420265	2.63E-05	6.96E-05
AB57_3793		putative arsenate reductase	-0.060971969	0.582731	0.636583
AB57_3794		hypothetical protein	-0.252713802	0.110332	0.144968
AB57_3795		esterase	-0.465527743	1.15E-05	3.24E-05
AB57_3796		thiol:disulfide interchange protein	0.452926248	0.000297	0.000646
AB57_3797		GGDEF family protein	-0.537247252	1.67E-05	4.54E-05
AB57_3798		hypothetical protein	0.732495221	3.81E-09	1.89E-08
AB57_3799		hypothetical protein	0.555705089	3.04E-08	1.30E-07
AB57_3800		hypothetical protein	-0.646737418	4.14E-05	0.000106
AB57_3801		polysaccharide deacetylase	0.070762179	0.600788	0.652264
AB57_3802		putative OHCU decarboxylase	-0.305058378	0.085914	0.115635
AB57_3803		transthyretin	-0.25096533	0.223436	0.275571
AB57_3804		uracil-xanthine permease	-0.380104958	0.000956	0.001907
AB57_3805		hypothetical protein	2.005771591	8.24E-18	1.97E-16
AB57_3806		monooxygenase, FAD-binding	-0.301263208	0.203606	0.25348
AB57_3807	allC	allantoicase	0.074911175	0.640673	0.687497
AB57_3808	allA	ureidoglycolate hydrolase	-0.562533442	0.000159	0.000362
AB57_3809	parE	DNA topoisomerase IV subunit B	0.615898665	3.07E-08	1.30E-07
AB57_3810		putative esterase	-0.090959207	0.470057	0.530409
AB57_3811		PGAP1 family protein	-0.37249378	0.003266	0.005904
AB57_3812		hypothetical protein	-0.391250986	0.004384	0.00775
AB57_3813		hypothetical protein	0.396940724	0.000738	0.001501
AB57_3814		hypothetical protein	-0.654204379	6.94E-05	0.000169
AB57_3815		hypothetical protein	-0.53046915	1.15E-06	3.86E-06
AB57_3816		LysM domain protein	-0.302448431	0.005624	0.009729
AB57_3817		hypothetical protein	0.968231118	1.38E-10	8.70E-10
AB57_3818		disulfide bond formation protein	-0.96223889	2.68E-14	3.19E-13
AB57_3819	gshA	glutamate--cysteine ligase	0.124658832	0.257507	0.31362
AB57_3820		hypothetical protein	-0.514390692	0.000153	0.000351
AB57_3821		hypothetical protein	-0.546372583	1.15E-07	4.47E-07
AB57_3822		hypothetical protein	-0.15108019	0.158378	0.201166
AB57_3823		putative aminotransferase	-0.101961652	0.349473	0.409452
AB57_3824		MATE efflux family protein	-0.931890055	6.80E-16	1.14E-14
AB57_3825		short-chain dehydrogenase/reductase	0.31194217	0.094205	0.125606
AB57_3826		transcriptional regulator, TetR family	-0.204405826	0.114759	0.150198
AB57_3827	phoB	phosphate regulon transcriptional regulatory protein PhoB	0.685338372	1.15E-11	8.87E-11
AB57_3828	phoR	phosphate regulon sensor kinase PhoR	0.507906193	2.58E-07	9.46E-07
AB57_3829		hypothetical protein	-0.572753777	1.50E-08	6.71E-08
AB57_3830	psd	phosphatidylserine decarboxylase	1.098847171	4.41E-14	5.02E-13
AB57_3831		hypothetical protein	0.291485112	0.004498	0.007933
AB57_3832	pncB	nicotinate phosphoribosyltransferase	-0.162509354	0.159704	0.202712
AB57_3833	dtd	D-tyrosyl-tRNA(Tyr) deacylase	0.154982637	0.22698	0.279662
AB57_3834		hypothetical protein	0.362262923	0.005968	0.010276
AB57_3835		hypothetical protein	-0.681671877	1.34E-05	3.71E-05
AB57_3836		phosphoserine phosphatase	0.313618467	0.005391	0.009364
AB57_3837		hypothetical protein	0.594846234	4.86E-05	0.000122
AB57_3838		3,4-dihydroxy-2-butanone 4-phosphate synthase	0.922428675	2.82E-09	1.43E-08
AB57_3839	ribH	6,7-dimethyl-8-ribityllumazine synthase	1.18703597	6.60E-15	9.11E-14
AB57_3840	nusB	transcription antitermination protein NusB	1.022660155	1.80E-13	1.86E-12
AB57_3841	thiL	thiamine-monophosphate kinase	0.712275515	5.17E-11	3.54E-10

AB57_3843	pgpA	phosphatidylglycerophosphatase A	0.381425867	0.000155	0.000355
AB57_3844	glmU	UDP-N-acetylglucosamine diphosphorylase/glucosamine-1-phos	1.236130708	4.63E-14	5.22E-13
AB57_3845	glmS	glucosamine--fructose-6-phosphate aminotransferase	1.275322005	5.94E-10	3.39E-09
AB57_3846		hypothetical protein	-0.069358311	0.606314	0.657684
AB57_3847		hypothetical protein	0.216894593	0.136451	0.175668
AB57_3848		hypothetical protein	0.169120947	0.11988	0.156237
AB57_3849		hypothetical protein	0.065869366	0.528601	0.586278
AB57_3850		histidine kinase	0.223180338	0.042324	0.060815
AB57_3851		DNA cytosine methyltransferase	0.415554729	6.86E-05	0.000167
AB57_3852		hypothetical protein	0.126316818	0.430592	0.491528
AB57_3853	murI	glutamate racemase	0.084332164	0.535951	0.593541
AB57_3854		haloacid dehydrogenase	-0.586904117	0.000742	0.00151
AB57_3855		hypothetical protein	-0.484388365	0.000736	0.001499
AB57_3856	hutG	formimidoylglutamase	-0.309304759	0.005518	0.009563
AB57_3857	hutI	imidazolonepropionase	-0.309346631	0.016746	0.0261
AB57_3858		proline-specific permease ProY	-0.043975442	0.797306	0.831464
AB57_3859	hutH	histidine ammonia-lyase	0.104630561	0.507076	0.566138
AB57_3860	hutU	urocanate hydratase	-0.19839956	0.199139	0.248588
AB57_3861		hypothetical protein	0.564615974	1.49E-05	4.08E-05
AB57_3862	hutC	histidine utilization repressor	0.343465424	0.001378	0.002665
AB57_3863		acyltransferase 3	-0.327682663	0.002198	0.004096
AB57_3864		CobW/P47K family protein	-0.406831634	0.045748	0.065078
AB57_3865		peptidase M15 family	-0.474239416	0.017544	0.027252
AB57_3866		aromatic amino acid transport protein	-0.989377684	6.34E-14	7.07E-13
AB57_3867	fahA	fumarylacetoacetase	-1.373447515	1.82E-15	2.79E-14
AB57_3868	maiA	maleylacetoacetate isomerase	-1.151056106	6.25E-24	3.92E-22
AB57_3869		glyoxalase/bleomycin resistance protein/dioxygenase	-0.618386064	3.34E-06	1.03E-05
AB57_3870		transcriptional regulator, IclR family	0.133690758	0.179845	0.226644
AB57_3871	hppD	4-hydroxyphenylpyruvate dioxygenase	-0.287358766	0.083267	0.112729
AB57_3872		hypothetical protein	-0.352805554	0.107037	0.141089
AB57_3873		MATE family drug transporter	-0.698499759	4.26E-07	1.52E-06
AB57_3874		bile acid:sodium symporter	-0.624502471	2.69E-08	1.15E-07
AB57_3875		nicotinamidase	-0.325822707	0.012989	0.020787
AB57_3876	dapA	dihydrodipicolinate synthase	0.669157328	3.32E-05	8.64E-05
AB57_3877		hypothetical protein	0.761912378	1.23E-07	4.76E-07
AB57_3878	purC	phosphoribosylaminoimidazole-succinocarboxamide synthase	1.203899431	1.49E-11	1.13E-10
AB57_3879		hypothetical protein	-1.15199323	2.51E-18	6.48E-17
AB57_3880		formate/nitrite transporter family	-0.577090174	2.75E-05	7.26E-05
AB57_3881		recombination factor protein RarA	-0.11695605	0.250564	0.306171
AB57_3882		glucose sorbosone dehydrogenase	-0.712067168	4.29E-09	2.11E-08
AB57_3883		hypothetical protein	-0.315390943	0.030613	0.045453
AB57_3884		hypothetical protein	-1.364517245	3.82E-13	3.80E-12
AB57_3885		dienelactone hydrolase	0.623278085	3.25E-09	1.63E-08
AB57_3886		histidine triad protein	0.554954076	5.06E-06	1.52E-05
AB57_3887	mutY	A/G-specific adenine glycosylase	1.107464248	3.22E-21	1.34E-19
AB57_3888		peptidase	0.201346788	0.142546	0.182562
AB57_3889		hypothetical protein	0.762243242	4.59E-08	1.89E-07
AB57_3890		DNA-3-methyladenine glycosylase 1	0.354920915	0.002121	0.003978
AB57_3891		hypothetical protein	0.373334767	0.000423	0.000899
AB57_3892		transcriptional regulator, GntR family	-0.209055702	0.081535	0.110586
AB57_3894		transcriptional regulator, LysR family	0.062072515	0.660506	0.705474
AB57_3895		hypothetical protein	0.009063168	0.966783	0.973094
AB57_3896		2,5-diketo-D-gluconate reductase B	-0.5496227	1.39E-07	5.33E-07
AB57_3897		major facilitator family transporter	-0.324574395	0.002598	0.004778
AB57_3898		hypothetical protein	0.35890754	0.000467	0.000983
AB57_3899	dapB	dihydrodipicolinate reductase	0.489604405	0.000224	0.000501
AB57_3900		hypothetical protein	0.745500294	3.59E-06	1.10E-05
AB57_3901	dnaJ	chaperone protein DnaJ	0.42544401	0.006113	0.010505

AB57_3902		hypothetical protein	0.096748714	0.377654	0.43762
AB57_3903		RND efflux transporter	-0.004475103	0.979176	0.982895
AB57_3904		secretion protein HlyD	-0.028845813	0.827689	0.856868
AB57_3905		transcriptional regulator, TetR family	0.215265909	0.104679	0.138474
AB57_3906	ppc	phosphoenolpyruvate carboxylase	-0.133416151	0.306427	0.365382
AB57_3907		uracil-xanthine permease	1.128411122	9.95E-11	6.41E-10
AB57_3908		transcriptional regulator, LysR family	-0.328690052	0.003323	0.00599
AB57_3909		hypothetical protein	-0.099746901	0.361794	0.421884
AB57_3910		hypothetical protein	-0.186811221	0.064101	0.088895
AB57_3911	ilvD	dihydroxy-acid dehydratase	0.459834082	0.000614	0.001265
AB57_3912	fmt	methionyl-tRNA formyltransferase	0.987257768	5.64E-13	5.45E-12
AB57_3913	sun	ribosomal RNA small subunit methyltransferase B	0.992649832	9.12E-12	7.23E-11
AB57_3914		hypothetical protein	-0.692931827	1.59E-11	1.20E-10
AB57_3915		sodium-and chloride-dependent transporter	-0.366210436	0.008918	0.014804
AB57_3916		hypothetical protein	-0.018665619	0.892741	0.91247
AB57_3917		hypothetical protein	0.604666128	1.91E-06	6.17E-06
AB57_3918		glutathione S-transferase	-0.392240597	0.003721	0.00666
AB57_4802	AB57_4802	NA	1.495818655	4.83E-09	2.32E-08
AB57_4846	AB57_4846	NA	-0.58544589	0.003896	0.00694
AB57_4852	AB57_4852	NA	1.061091501	6.40E-07	2.23E-06
AB57_4864	AB57_4864	NA	1.808119109	0.001263	0.002463
AB57_4870	AB57_4870	NA	2.003991143	7.81E-05	0.000189
AB57_4871	AB57_4871	NA	1.808977683	0.003277	0.00592
EBG000012374	6S	NA	-0.724158338	0.001919	0.003642
EBG000012374	Aar	NA	-0.602836987	0.000108	0.000256
EBG000012374	C4	NA	0.127556605	0.705825	0.748081
EBG000012374	C4	NA	-0.064953951	0.749969	0.787202
EBG000012374	C4	NA	-0.278049797	0.213535	0.26447
EBG000012375	C4	NA	0.319985389	0.230494	0.283783
EBG000012375	C4	NA	0.370615578	0.048635	0.068868
EBG000012375	C4	NA	-0.103658126	0.607158	0.658214
EBG000012375	C4	NA	0.16203709	0.479005	0.539492
EBG000012375	C4	NA	-0.238740296	0.175296	0.221288
EBG000012375	C4	NA	-0.695130054	0.002316	0.004302
EBG000012375	C4	NA	-0.034048801	0.900844	0.918975
EBG000012375	C4	NA	-0.160600996	0.50078	0.560123
EBG000012375	C4	NA	-0.353513331	0.180911	0.227832
EBG000012375	RNaseP_bact_	NA	-0.160368616	0.611968	0.661877
EBG000012375	C4	NA	0.296612823	0.293797	0.351795
EBG000012375	tmRNA	NA	-0.337579551	0.136104	0.175282
EBG000012375	C4	NA	-0.085889909	0.70327	0.745801
EBG000012375	C4	NA	-0.21937242	0.350598	0.41064
EBG000012375	C4	NA	-0.037938079	0.879574	0.901502
EBG000012375	C4	NA	0.302678087	0.272161	0.328976
EBG000012375	t44	NA	0.840452945	2.54E-05	6.73E-05
EBG000012375	C4	NA	0.085365399	0.764267	0.79994
EBG000012375	C4	NA	-0.013069399	0.961002	0.968858

Supplemental Table 3: Differential expression by qRT-PCR of select genes from *A. baumannii*

Gene ID	Product	log2FC	
		RNA-seq	qRT-PCR
AB57_2007	P-pili fimbrial subunit	1.2632903	2.1743
AB57_0091	Tyrosine kinase ptk	0.90987727	2.462005
AB57_2570	CsuA/B	1.37926436	2.861655
AB57_1479	T6SS protein, TssB	1.43090804	6.579703
AB57_1527	PaaJ	0.55521847	5.902565