Fig. S1

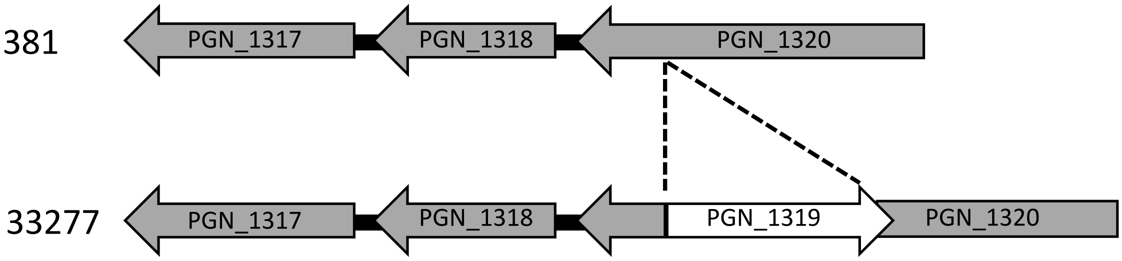

FIG. S1. Illustration of the insertion sequence, PGN_1319, present in the 33277 genome relative to the 381 genome. PGN_1319 disrupts the expression of a putative operon, PGN_1320-PGN_1317 in strain 33277.

Fig. S2

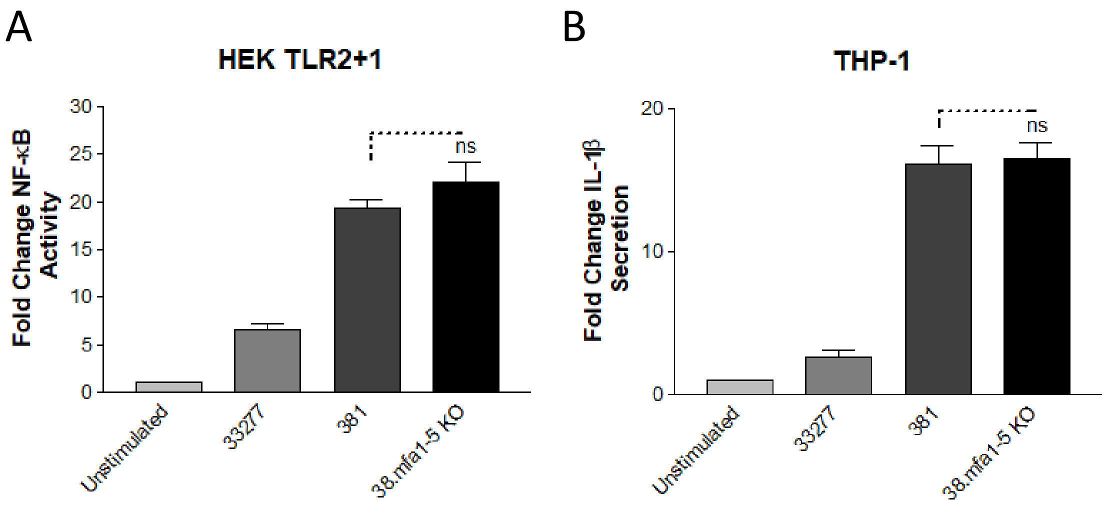

FIG S2. Immune-stimulatory capacity of strain 381 is not appreciably altered in an isogenic mutant strain bearing a deletion of the *mfa1-mfa5* gene cluster. (A) HEK cells expressing TLR2 were stimulated with wild-type strains 33277 and 381 and the indicated isogenic mutant strains (10^5 bacteria). Fold change in NF-κB activation from bacterial stimulations is shown relative to the unstimulated control. (B) Differentiated THP-1 cell were stimulated with wild-type strains 33277 and 381 and the indicated isogenic mutant strains (10^5 bacteria). Fold change in IL-1β production from bacterial stimulations is shown relative to the unstimulated control. Data are presented as means ±SD from triplicate sample determinations and are representative of two independent experiments. Statistical significance was determined by student's unpaired *t* test (ns=not statistically significant).

Fig. S3

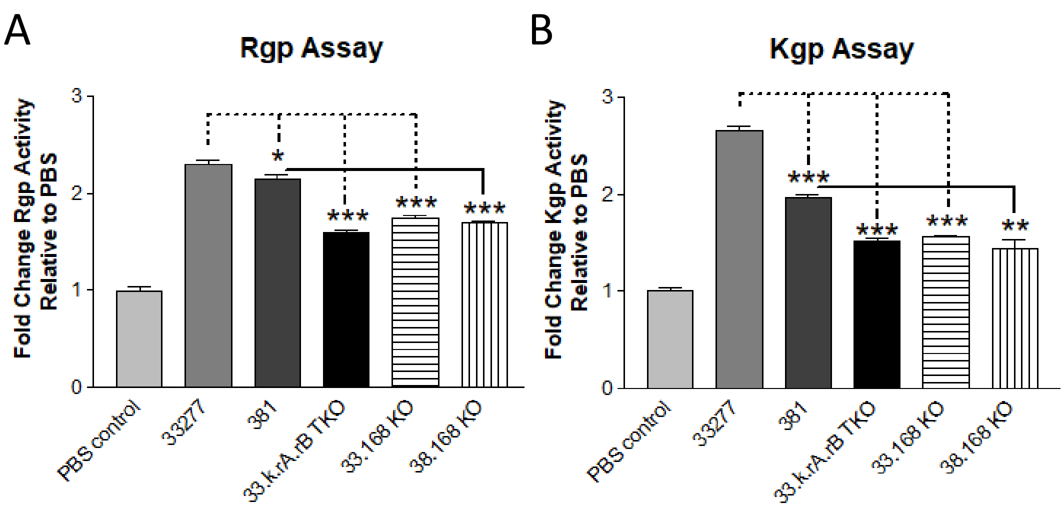

FIG S3. Comparison of gingipain activities for wild-type and gingipain-deficient mutant strains. (A) Arginine (Rgp)-dependent and (B) Lysine (Kgp)-dependent gingipain substrates were exposed to strains 33277 and 381 (10^8 bacteria) and OD450 nm was determined. Fold change in gingipain activity is shown relative to the media control. Data are presented as means ±SD from triplicate sample determinations and are representative of two independent experiments. Asterisks indicate statistical significance as determined by student's unpaired *t* test (*P<0.05,**P<0.001,***P<0.0001).

Fig. S4

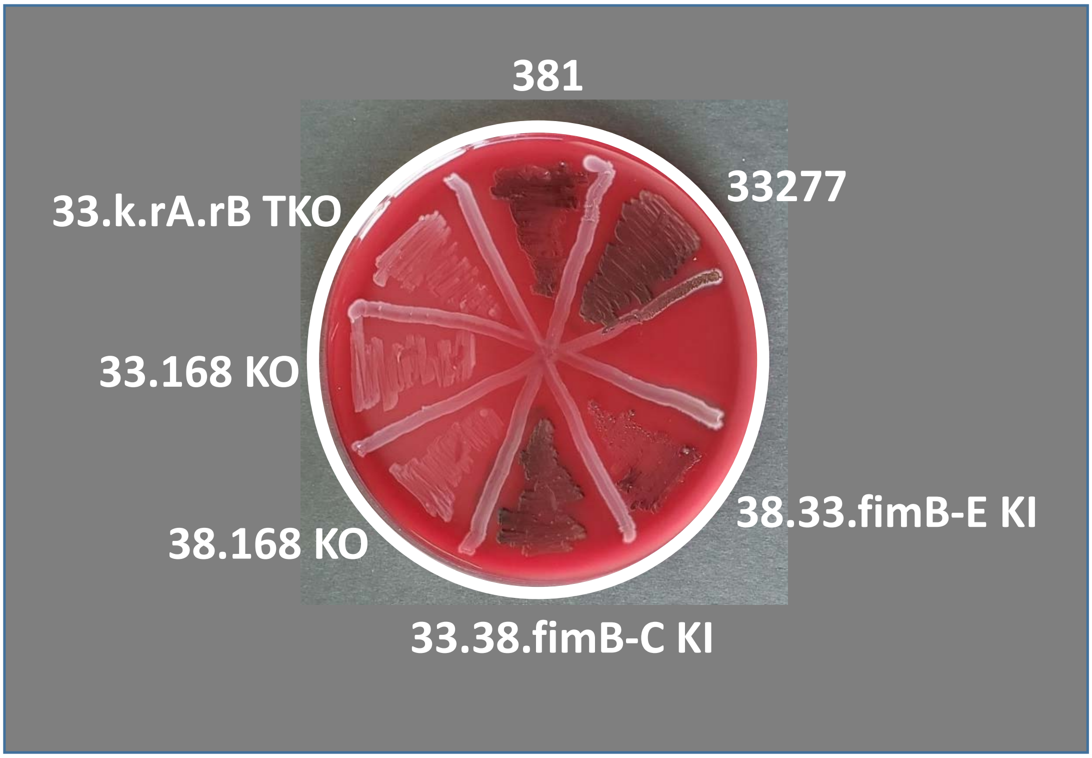

FIG S4. Comparison of pigmentation phenotypes for wild-type, *fimB* mutant, and gingipain-deficient *P. gingivalis* strains. The indicated strains were co-streaked on a blood agar plate and grown anaerobically.

TABLE S1. Complete comparison of 33277 and 381 transcriptomes[a,b].

(Table begins on the next page.)

[a] Gene numbers are listed according to the *P. gingivalis* ATCC 33277 annotations.

[b] Differential expression values are shown as both 33277 fold change relative to 381, and Log2 ratio (33277:381).

Sequence Name	locus_tag	product	gene	Minimum	Maximum	Length	Direction	Fold Change	Differential Expression Log2 Ratio	Differential Expression p-value	Differential Expression Adjusted p-value	Differential Expression Log2 Standard Error	Differential Expression Wald Statistic	Type	db_xref	protein_id
AP009380	PGN_0001	chromosomal replication initiator protein DnaA	dnaA	1	1422	1422	forward	1.177	0.235	0.315	0.465	0.234	1.005	CDS	GI:188593545	BAG32520.1
AP009380	PGN_0002	conserved hypothetical protein		1435	2007	573	forward	1.275	0.351	0.129	0.251	0.231	1.518	CDS	GI:188593546	BAG32521.1
AP009380	PGN_0003	conserved hypothetical protein		2009	3028	1020	reverse	1.426	0.512	0.033	0.098	0.241	2.127	CDS	GI:188593547	BAG32522.1
AP009380	PGN_0004	putative nicotinate mononucleotide:5,6-dimethylbenzimidazole phosphoribosyltransferase		3108	3812	705	forward	0.968	-0.047	0.903	0.942	0.390	-0.121	CDS	GI:188593548	BAG32523.1
AP009380	PGN_0005	conserved hypothetical protein		3887	5041	1155	reverse	0.744	-0.427	0.059	0.144	0.226	-1.890	CDS	GI:188593549	BAG32524.1
AP009380	PGN_0006	putative Na+driven multidrug efflux pump		5094	6473	1380	reverse	0.647	-0.629	0.005	0.028	0.226	-2.784	CDS	GI:188593550	BAG32525.1
AP009380	PGN_0007	hypothetical protein		6487	6642	156	forward	0.347	-1.527	0.010	0.043	0.592	-2.580	CDS	GI:188593551	BAG32526.1
AP009380	PGN_t0001	tRNA-Asn		6601	6677	77	reverse	0.346	-1.530	0.010	0.042	0.592	-2.585	tRNA		
AP009380	PGN_t0002	tRNA-Asn		6700	6773	74	reverse	0.327	-1.613	0.006	0.032	0.591	-2.729	tRNA		
AP009380	PGN_0008	ATP-dependent Clp protease ATP-binding subunit ClpC	clpC	7400	9979	2580	forward	0.459	-1.123	0.001	0.009	0.347	-3.238	CDS	GI:188593552	BAG32527.1
AP009380	PGN_0009	glycosyl hydrolase family 3		10119	13130	3012	forward	1.106	0.146	0.545	0.671	0.241	0.605	CDS	GI:188593553	BAG32528.1
AP009380	PGN_0010	probable L-threonine-O-3-phosphate decarboxylase		13178	14206	1029	forward	1.360	0.443	0.063	0.151	0.239	1.858	CDS	GI:188593554	BAG32529.1
AP009380	PGN_0011	conserved hypothetical protein		14216	14986	771	forward	1.606	0.684	0.004	0.024	0.239	2.855	CDS	GI:188593555	BAG32530.1
AP009380	PGN_0012	two-component system response regulator		15571	16920	1350	forward	1.592	0.671	0.033	0.098	0.315	2.128	CDS	GI:188593556	BAG32531.1
AP009380	PGN_0013	putative two-component system sensor histidine kinase		16930	18267	1338	forward	1.437	0.523	0.147	0.274	0.361	1.449	CDS	GI:188593557	BAG32532.1
AP009380	PGN_0014	conserved hypothetical protein		18271	20517	2247	forward	1.889	0.917	0.049	0.126	0.466	1.968	CDS	GI:188593558	BAG32533.1
AP009380	PGN_0015	probable transcriptional regulator		20602	21306	705	forward	0.969	-0.045	0.824	0.885	0.205	-0.222	CDS	GI:188593559	BAG32534.1
AP009380	PGN_0016	putative TIM-barrel protein		21292	22293	1002	reverse	1.248	0.320	0.212	0.354	0.256	1.247	CDS	GI:188593560	BAG32535.1
AP009380	PGN_0017	sulfate transporter permease		22290	23966	1677	reverse	1.325	0.406	0.101	0.214	0.248	1.639	CDS	GI:188593561	BAG32536.1
AP009380	PGN_0018	hypothetical protein		24234	24404	171	reverse	0.251	-1.994	0.000	0.000	0.303	-6.584	CDS	GI:188593562	BAG32537.1
AP009380	PGN_0019	hypothetical protein		24770	24880	111	forward	0.268	-1.899	0.000	0.003	0.528	-3.600	CDS	GI:188593563	BAG32538.1
AP009380	PGN_0020	probable DNA-binding protein		24952	25608	657	forward	1.021	0.031	0.908	0.945	0.264	0.116	CDS	GI:188593564	BAG32539.1
AP009380	PGN_0021	probable hydrolase		25677	26336	660	forward	0.816	-0.293	0.331	0.481	0.302	-0.971	CDS	GI:188593565	BAG32540.1
AP009380	PGN_0022	Por secretion system protein porU	porU	26349	29825	3477	forward	1.683	0.751	0.001	0.007	0.223	3.360	CDS	GI:188593566	BAG32541.1
AP009380	PGN_0023	Por secretion system protein porV (pg27, lptO)	porV	29901	31076	1176	forward	2.007	1.005	0.000	0.004	0.284	3.536	CDS	GI:188593567	BAG32542.1
AP009380	PGN_0024	putative 2C-methyl-D-erythritol 2,4-cyclodiphosphate synthase		31083	31571	489	forward	1.092	0.127	0.564	0.686	0.221	0.576	CDS	GI:188593568	BAG32543.1
AP009380	PGN_0025	probable SpoU rRNA methylase family protein		31674	32216	543	reverse	0.861	-0.216	0.417	0.555	0.266	-0.812	CDS	GI:188593569	BAG32544.1
AP009380	PGN_t0003	tRNA-Gln		32732	32805	74	forward	0.510	-0.971	0.023	0.075	0.427	-2.276	tRNA		
AP009380	PGN_0026	putative cytidine deaminase		33069	33545	477	forward	1.129	0.176	0.500	0.634	0.261	0.674	CDS	GI:188593570	BAG32545.1
AP009380	PGN_0027	transposase in ISPg1		33765	34850	1086	forward	0.600	-0.736	0.098	0.210	0.445	-1.653	CDS	GI:188593571	BAG32546.1
AP009380	PGN_0028	hypothetical protein		34875	35024	150	forward	0.765	-0.386	0.378	0.520	0.438	-0.882	CDS	GI:188593572	BAG32547.1
AP009380	PGN_0029	conserved hypothetical protein		35420	36004	585	reverse	0.721	-0.471	0.138	0.262	0.318	-1.483	CDS	GI:188593573	BAG32548.1
AP009380	PGN_0030	beta-mannosidase		36142	38688	2547	reverse	1.470	0.556	0.014	0.054	0.226	2.463	CDS	GI:188593574	BAG32549.1
AP009380	PGN_0031	conserved hypothetical protein with RmuC domain		38757	40055	1299	reverse	1.059	0.082	0.723	0.809	0.232	0.355	CDS	GI:188593575	BAG32550.1
AP009380	PGN_0032	conserved hypothetical protein		40103	40276	174	forward	0.971	-0.042	0.926	0.952	0.452	-0.093	CDS	GI:188593576	BAG32551.1
AP009380	PGN_0033	thioredoxin		40685	40999	315	reverse	1.185	0.245	0.471	0.609	0.340	0.721	CDS	GI:188593577	BAG32552.1
AP009380	PGN_0034	DNA polymerase III alpha subunit		41048	44734	3687	reverse	1.064	0.089	0.667	0.766	0.207	0.430	CDS	GI:188593578	BAG32553.1
AP009380	PGN_0035	50S ribosomal protein L19	rplS	45013	45378	366	forward	0.840	-0.252	0.229	0.371	0.209	-1.204	CDS	GI:188593579	BAG32554.1
AP009380	PGN_0036	hypothetical protein		45792	46055	264	forward	0.419	-1.256	0.000	0.003	0.340	-3.692	CDS	GI:188593580	BAG32555.1
AP009380	PGN_0037	conserved hypothetical protein		46140	46259	120	forward	0.467	-1.099	0.002	0.013	0.352	-3.121	CDS	GI:188593581	BAG32556.1
AP009380	PGN_0038	serine hydroxymethyltransferase		46617	47897	1281	forward	1.706	0.770	0.007	0.034	0.287	2.685	CDS	GI:188593582	BAG32557.1
AP009380	PGN_0039	beta-hexosaminidase		48048	50387	2340	forward	2.401	1.264	0.001	0.007	0.377	3.349	CDS	GI:188593583	BAG32558.1
AP009380	PGN_0040	hypothetical protein		50737	50850	114	reverse	3.372	1.754	0.000	0.002	0.453	3.874	CDS	GI:188593584	BAG32559.1
AP009380	PGN_0041	heat shock protein 90	htpG	51051	53105	2055	forward	0.471	-1.085	0.000	0.003	0.294	-3.690	CDS	GI:188593585	BAG32560.1
AP009380	PGN_0042	probable phosphatidate cytidylyltransferase		53288	54142	855	reverse	0.990	-0.015	0.963	0.972	0.316	-0.047	CDS	GI:188593586	BAG32561.1
AP009380	PGN_0043	putative transmembrane AAA-metalloprotease FtsH		54171	56192	2022	reverse	1.355	0.438	0.140	0.263	0.297	1.476	CDS	GI:188593587	BAG32562.1
AP009380	PGN_0044	GTP-binding protein		56393	57496	1104	reverse	1.147	0.198	0.381	0.524	0.226	0.876	CDS	GI:188593588	BAG32563.1
AP009380	PGN_0045	conserved hypothetical protein		57515	57679	165	reverse	0.748	-0.418	0.168	0.301	0.304	-1.378	CDS	GI:188593589	BAG32564.1
AP009380	PGN_0046	hypothetical protein		58549	58815	267	forward	0.757	-0.402	0.180	0.314	0.300	-1.342	CDS	GI:188593590	BAG32565.1
AP009380	PGN_0047	conserved hypothetical protein		58828	59046	219	forward	0.578	-0.790	0.100	0.212	0.480	-1.647	CDS	GI:188593591	BAG32566.1
AP009380	PGN_0048	conserved hypothetical protein		59059	59475	417	forward	0.505	-0.985	0.002	0.013	0.314	-3.134	CDS	GI:188593592	BAG32567.1
AP009380	PGN_0049	probable anti-restriction protein		59497	60027	531	forward	0.594	-0.751	0.056	0.139	0.393	-1.910	CDS	GI:188593593	BAG32568.1
AP009380	PGN_0050	conserved hypothetical protein		60044	61318	1275	forward	0.720	-0.474	0.219	0.362	0.386	-1.228	CDS	GI:188593594	BAG32569.1
AP009380	PGN_0051	conserved hypothetical protein		61345	61599	255	forward	0.751	-0.413	0.305	0.453	0.403	-1.026	CDS	GI:188593595	BAG32570.1
AP009380	PGN_0052	hypothetical protein		61604	61834	231	forward	0.661	-0.598	0.134	0.258	0.399	-1.498	CDS	GI:188593596	BAG32571.1
AP009380	PGN_0053	conserved hypothetical protein		62092	63318	1227	forward	0.277	-1.853	0.000	0.002	0.479	-3.871	CDS	GI:188593597	BAG32572.1
AP009380	PGN_0054	hypothetical protein		63320	63724	405	forward	0.216	-2.213	0.000	0.000	0.472	-4.689	CDS	GI:188593598	BAG32573.1
AP009380	PGN_0055	probable lysozyme		63785	64300	516	reverse	0.197	-2.345	0.000	0.000	0.423	-5.545	CDS	GI:188593599	BAG32574.1
AP009380	PGN_0056	probable conserved protein found in conjugate transposon		64284	64745	462	reverse	0.625	-0.678	0.007	0.034	0.253	-2.678	CDS	GI:188593600	BAG32575.1
AP009380	PGN_0057	probable conserved protein found in conjugate transposon TraP	traP	64770	65624	855	reverse	0.530	-0.916	0.000	0.005	0.263	-3.482	CDS	GI:188593601	BAG32576.1
AP009380	PGN_0058	probable conserved protein found in conjugate transposon		65624	66208	585	reverse	0.466	-1.102	0.000	0.003	0.307	-3.592	CDS	GI:188593602	BAG32577.1
AP009380	PGN_0059	conserved protein found in conjugate transposon TraN	traN	66210	67130	921	reverse	0.642	-0.640	0.018	0.064	0.270	-2.373	CDS	GI:188593603	BAG32578.1
AP009380	PGN_0060	conserved protein found in conjugate transposon TraM	traM	67169	68536	1368	reverse	0.626	-0.675	0.003	0.017	0.224	-3.011	CDS	GI:188593604	BAG32579.1
AP009380	PGN_0061	hypothetical protein		68487	68819	333	reverse	0.746	-0.423	0.137	0.261	0.285	-1.485	CDS	GI:188593605	BAG32580.1
AP009380	PGN_0062	putative conserved protein found in conjugate transposon TraK	traK	68816	69439	624	reverse	0.557	-0.846	0.000	0.005	0.242	-3.491	CDS	GI:188593606	BAG32581.1
AP009380	PGN_0063	conserved transmembrane protein found in conjugate transposon TraJ	traJ	69459	70535	1077	reverse	0.618	-0.693	0.008	0.036	0.260	-2.662	CDS	GI:188593607	BAG32582.1
AP009380	PGN_0064	putative conserved protein found in conjugate transposon TraI	traI	70538	71167	630	reverse	0.642	-0.640	0.023	0.075	0.281	-2.272	CDS	GI:188593608	BAG32583.1
AP009380	PGN_0065	conserved protein found in conjugate transposon TraG	traG	71302	73803	2502	reverse	0.368	-1.441	0.000	0.000	0.300	-4.801	CDS	GI:188593609	BAG32584.1
AP009380	PGN_0066	probable conserved transmembrane protein found in conjugate transposon TraF	traF	73800	74177	378	reverse	0.772	-0.374	0.205	0.346	0.295	-1.267	CDS	GI:188593610	BAG32585.1
AP009380	PGN_0067	probable conserved transmembrane protein found in conjugate transposon TraE	traF	74182	74481	300	reverse	0.753	-0.409	0.096	0.207	0.245	-1.665	CDS	GI:188593611	BAG32586.1
AP009380	PGN_0068	hypothetical protein		74657	75244	588	reverse	0.656	-0.608	0.046	0.122	0.305	-1.995	CDS	GI:188593612	BAG32587.1
AP009380	PGN_0069	probable conserved protein found in conjugate transposon TraA	traA	75232	75972	741	reverse	0.747	-0.421	0.081	0.181	0.241	-1.748	CDS	GI:188593613	BAG32588.1
AP009380	PGN_0070	hypothetical protein		76002	76592	591	reverse	0.851	-0.232	0.369	0.513	0.259	-0.898	CDS	GI:188593614	BAG32589.1
AP009380	PGN_0071	hypothetical protein		76589	76942	354	reverse	0.896	-0.159	0.548	0.674	0.264	-0.600	CDS	GI:188593615	BAG32590.1
AP009380	PGN_0072	hypothetical protein		76968	77399	432	reverse	0.644	-0.636	0.039	0.108	0.308	-2.068	CDS	GI:188593616	BAG32591.1
AP009380	PGN_0073	putative conserved protein found in conjugate transposon TraA	traA	77383	78165	783	reverse	0.607	-0.720	0.026	0.083	0.323	-2.227	CDS	GI:188593617	BAG32592.1
AP009380	PGN_0074	conserved hypothetical protein		78954	79367	414	forward	0.447	-1.163	0.000	0.000	0.256	-4.548	CDS	GI:188593618	BAG32593.1
AP009380	PGN_0075	conserved hypothetical protein		79352	80587	1236	forward	0.561	-0.834	0.000	0.003	0.229	-3.642	CDS	GI:188593619	BAG32594.1
AP009380	PGN_0076	putative mobilization protein TraG family		80770	82779	2010	forward	0.814	-0.297	0.225	0.366	0.245	-1.214	CDS	GI:188593620	BAG32595.1
AP009380	PGN_0077	hypothetical protein		82878	83033	156	forward	0.490	-1.028	0.013	0.051	0.413	-2.486	CDS	GI:188593621	BAG32596.1
AP009380	PGN_0078	hypothetical protein		83075	83287	213	forward	0.558	-0.843	0.034	0.100	0.399	-2.115	CDS	GI:188593622	BAG32597.1

AP009380	PGN_0079	conserved hypothetical protein with DUF1016 domain	83317	84354	1038	forward	0.498	-1.005	0.015	0.056	0.412	-2.440	CDS	GI:188593623	BAG32598.1
AP009380	PGN_0080	probable tetracycline resistance element mobilization regulatory protein RteC	84397	84723	327	reverse	0.682	-0.552	0.093	0.203	0.329	-1.678	CDS	GI:188593624	BAG32599.1
AP009380	PGN_0081	putative Na driven multidrug efflux pump	85010	86368	1359	reverse	0.681	-0.554	0.119	0.238	0.356	-1.558	CDS	GI:188593625	BAG32600.1
AP009380	PGN_0082	probable transcriptional regulator AraC family	86465	87313	849	reverse	0.545	-0.877	0.006	0.029	0.317	-2.766	CDS	GI:188593626	BAG32601.1
AP009380	PGN_0083	conserved hypothetical protein	87598	88992	1395	forward	0.976	-0.034	0.879	0.925	0.227	-0.152	CDS	GI:188593627	BAG32602.1
AP009380	PGN_0084	DNA topoisomerase I	89027	91156	2130	forward	0.673	-0.571	0.020	0.069	0.246	-2.325	CDS	GI:188593628	BAG32603.1
AP009380	PGN_0085	hypothetical protein	91296	91727	432	forward	0.922	-0.117	0.705	0.798	0.310	-0.379	CDS	GI:188593629	BAG32604.1
AP009380	PGN_0086	putative DNA methylase	91714	97200	5487	forward	0.861	-0.215	0.381	0.524	0.246	-0.876	CDS	GI:188593630	BAG32605.1
AP009380	PGN_0087	conserved hypothetical protein	97257	99167	1911	reverse	0.515	-0.957	0.006	0.030	0.347	-2.756	CDS	GI:188593631	BAG32606.1
AP009380	PGN_0088	putative transcriptional regulator	99167	99376	210	reverse	0.555	-0.850	0.036	0.103	0.405	-2.096	CDS	GI:188593632	BAG32607.1
AP009380	PGN_0089	hypothetical protein	99529	99849	321	reverse	0.875	-0.193	0.505	0.638	0.290	-0.666	CDS	GI:188593633	BAG32608.1
AP009380	PGN_0090	hypothetical protein	99833	100186	354	reverse	1.037	0.052	0.878	0.925	0.339	0.154	CDS	GI:188593634	BAG32609.1
AP009380	PGN_0091	hypothetical protein	100407	100685	279	forward	0.725	-0.464	0.103	0.216	0.285	-1.630	CDS	GI:188593635	BAG32610.1
AP009380	PGN_0092	conserved hypothetical protein	100714	101025	312	forward	0.584	-0.776	0.006	0.032	0.285	-2.728	CDS	GI:188593636	BAG32611.1
AP009380	PGN_0093	conserved hypothetical protein	101075	101440	366	reverse	1.207	0.272	0.231	0.373	0.227	1.197	CDS	GI:188593637	BAG32612.1
AP009380	PGN_0094	putative bacteriophage integrase	101455	102690	1236	reverse	1.362	0.446	0.052	0.132	0.230	1.942	CDS	GI:188593638	BAG32613.1
AP009380	PGN_0095	hypothetical protein	102733	102882	150	reverse	0.666	-0.587	0.013	0.051	0.236	-2.487	CDS	GI:188593639	BAG32614.1
AP009380	PGN_0096	aspartate kinase	103084	104424	1341	reverse	0.987	-0.019	0.926	0.952	0.203	-0.093	CDS	GI:188593640	BAG32615.1
AP009380	PGN_0097	putative cell-division ATP-binding protein	104442	105182	741	reverse	1.054	0.076	0.793	0.861	0.288	0.263	CDS	GI:188593641	BAG32616.1
AP009380	PGN_0098	hypothetical protein	105346	105519	174	reverse	0.994	-0.009	0.982	0.984	0.394	-0.023	CDS	GI:188593642	BAG32617.1
AP009380	PGN_0099	probable peptidase	105575	106588	1014	forward	1.300	0.379	0.261	0.407	0.337	1.125	CDS	GI:188593643	BAG32618.1
AP009380	PGN_0100	diaminopimelate decarboxylase	106598	107746	1149	forward	0.870	-0.202	0.618	0.729	0.404	-0.499	CDS	GI:188593644	BAG32619.1
AP009380	PGN_0101	putative 1,4-dihydroxy-2-naphthoate octaprenyltransferase	107736	108623	888	forward	0.848	-0.239	0.282	0.430	0.222	-1.075	CDS	GI:188593645	BAG32620.1
AP009380	PGN_0102	conserved hypothetical protein	108715	109095	381	forward	0.643	-0.638	0.103	0.216	0.391	-1.630	CDS	GI:188593646	BAG32621.1
AP009380	PGN_0103	putative TonB	109130	110446	1317	forward	0.698	-0.519	0.190	0.328	0.396	-1.311	CDS	GI:188593647	BAG32622.1
AP009380	PGN_0104	transposase in ISPg1	111347	112432	1086	reverse	0.658	-0.604	0.198	0.336	0.469	-1.287	CDS	GI:188593648	BAG32623.1
AP009380	PGN_0105	conserved hypothetical protein	112565	112798	234	forward	0.357	-1.487	0.010	0.043	0.579	-2.568	CDS	GI:188593649	BAG32624.1
AP009380	PGN_0106	partial transposase in ISPg3	113293	114081	789	forward	0.565	-0.824	0.042	0.115	0.406	-2.032	CDS	GI:188593650	BAG32625.1
AP009380	PGN_0107	partial transposase in ISPg3	114121	114441	321	forward	0.756	-0.403	0.309	0.457	0.396	-1.017	CDS	GI:188593651	BAG32626.1
AP009380	PGN_0108	partial transposase in ISPg1	114428	114859	432	reverse	0.701	-0.512	0.224	0.366	0.422	-1.215	CDS	GI:188593652	BAG32627.1
AP009380	PGN_0109	conserved hypothetical protein	114823	115275	453	reverse	0.825	-0.277	0.408	0.547	0.335	-0.828	CDS	GI:188593653	BAG32628.1
AP009380	PGN_0110	hypothetical protein	115327	115455	129	reverse	0.731	-0.452	0.167	0.299	0.327	-1.382	CDS	GI:188593654	BAG32629.1
AP009380	PGN_t0004	tRNA-Val	115467	115544	78	reverse	0.458	-1.126	0.001	0.007	0.338	-3.328	tRNA		
AP009380	PGN_t0005	tRNA-Val	115587	115661	75	reverse	0.370	-1.433	0.000	0.003	0.387	-3.706	tRNA		
AP009380	PGN_0111	partial transposase in ISPg6	115776	115976	201	reverse	0.477	-1.069	0.007	0.032	0.395	-2.709	CDS	GI:188593655	BAG32630.1
AP009380	PGN_0112	partial transposase Orf1 in ISPg5	116468	116686	219	reverse	0.596	-0.746	0.009	0.041	0.287	-2.598	CDS	GI:188593656	BAG32631.1
AP009380	PGN_0113	hypothetical protein	116703	116849	147	reverse	1.097	0.133	0.744	0.823	0.408	0.326	CDS	GI:188593657	BAG32632.1
AP009380	PGN_0114	Na translocating NADH-quinone reductase subunit A	117168	118523	1356	forward	1.659	0.730	0.000	0.004	0.208	3.519	CDS	GI:188593658	BAG32633.1
AP009380	PGN_0115	Na translocating NADH-quinone reductase subunit B	118554	119753	1200	forward	1.608	0.685	0.003	0.018	0.230	2.983	CDS	GI:188593659	BAG32634.1
AP009380	PGN_0116	probable Na translocating NADH-quinone reductase subunit C	119777	120511	735	forward	2.031	1.022	0.000	0.003	0.278	3.670	CDS	GI:188593660	BAG32635.1
AP009380	PGN_0117	putative Na translocating NADH-quinone reductase subunit D	120517	121146	630	forward	1.989	0.992	0.000	0.002	0.259	3.838	CDS	GI:188593661	BAG32636.1
AP009380	PGN_0118	putative Na translocating NADH-quinone reductase subunit E	121186	121800	615	forward	1.789	0.839	0.001	0.010	0.263	3.196	CDS	GI:188593662	BAG32637.1
AP009380	PGN_0119	Na translocating NADH-quinone reductase subunit F	121819	123057	1239	forward	1.554	0.636	0.003	0.020	0.217	2.926	CDS	GI:188593663	BAG32638.1
AP009380	PGN_t0006	tRNA-Met	123389	123463	75	reverse	0.279	-1.841	0.000	0.002	0.484	-3.807	tRNA		
AP009380	PGN_0120	conserved hypothetical protein	123989	124471	483	forward	1.235	0.304	0.266	0.413	0.274	1.112	CDS	GI:188593664	BAG32639.1
AP009380	PGN_0121	conserved hypothetical protein	124527	126272	1746	forward	1.311	0.391	0.032	0.096	0.183	2.140	CDS	GI:188593665	BAG32640.1
AP009380	PGN_0122	28 kDa outer membrane protein Omp28	126292	127167	876	forward	1.041	0.058	0.787	0.857	0.214	0.271	CDS	GI:188593666	BAG32641.1
AP009380	PGN_0123	conserved hypothetical protein	127167	127907	741	forward	0.528	-0.922	0.005	0.027	0.329	-2.800	CDS	GI:188593667	BAG32642.1
AP009380	PGN_0124	hypothetical protein	127938	128045	108	forward	0.567	-0.818	0.009	0.041	0.314	-2.602	CDS	GI:188593668	BAG32643.1
AP009380	PGN_0125	D-isomer specific 2-hydroxyacid dehydrogenase family protein	128126	129085	960	forward	0.993	-0.010	0.966	0.975	0.245	-0.042	CDS	GI:188593669	BAG32644.1
AP009380	PGN_0126	putative transmembrane glucose/galactose transporter	129124	130413	1290	forward	1.017	0.024	0.916	0.949	0.228	0.106	CDS	GI:188593670	BAG32645.1
AP009380	PGN_0127	hypothetical protein	130930	131103	174	reverse	0.884	-0.179	0.744	0.823	0.546	-0.327	CDS	GI:188593671	BAG32646.1
AP009380	PGN_0128	immunoreactive 53 kDa antigen	131555	132994	1440	reverse	0.873	-0.197	0.354	0.499	0.212	-0.927	CDS	GI:188593672	BAG32647.1
AP009380	PGN_0129	conserved hypothetical protein	133035	133628	594	reverse	0.843	-0.246	0.302	0.450	0.239	-1.031	CDS	GI:188593673	BAG32648.1
AP009380	PGN_0130	partial transposase in ISPg1	134082	134726	645	reverse	0.642	-0.639	0.173	0.307	0.469	-1.362	CDS	GI:188593674	BAG32649.1
AP009380	PGN_0131	partial transposase in ISPg1	134772	135167	396	reverse	0.793	-0.334	0.421	0.559	0.416	-0.804	CDS	GI:188593675	BAG32650.1
AP009380	PGN_0132	conserved hypothetical protein	135438	135914	477	reverse	1.945	0.960	0.003	0.018	0.322	2.983	CDS	GI:188593676	BAG32651.1
AP009380	PGN_0133	adenosylmethionine--8-amino-7-oxononanoate aminotransferase	135926	137227	1302	reverse	1.238	0.308	0.321	0.472	0.310	0.992	CDS	GI:188593677	BAG32652.1
AP009380	PGN_0134	putative biotin synthetase	137217	138275	1059	reverse	1.103	0.141	0.585	0.703	0.258	0.546	CDS	GI:188593678	BAG32653.1
AP009380	PGN_0135	putative H+/peptide symporter	138390	139931	1542	reverse	1.173	0.230	0.388	0.531	0.267	0.863	CDS	GI:188593679	BAG32654.1
AP009380	PGN_0136	conserved hypothetical protein	139957	141048	1092	reverse	1.050	0.070	0.737	0.818	0.209	0.336	CDS	GI:188593680	BAG32655.1
AP009380	PGN_0137	putative tryptophanyl-tRNA synthetase	142131	143114	984	forward	1.276	0.351	0.051	0.130	0.180	1.951	CDS	GI:188593681	BAG32656.1
AP009380	PGN_0138	conserved hypothetical protein	143169	143588	420	forward	1.183	0.243	0.305	0.452	0.236	1.027	CDS	GI:188593682	BAG32657.1
AP009380	PGN_0139	conserved hypothetical protein	143588	144061	474	forward	1.256	0.329	0.207	0.348	0.261	1.261	CDS	GI:188593683	BAG32658.1
AP009380	PGN_0140	peptide methionine sulfoxide reductase	144123	145181	1059	forward	1.607	0.684	0.019	0.066	0.291	2.355	CDS	GI:188593684	BAG32659.1
AP009380	PGN_0141	conserved hypothetical protein	145238	146422	1185	forward	1.069	0.097	0.709	0.801	0.259	0.373	CDS	GI:188593685	BAG32660.1
AP009380	PGN_0142	putative cation efflux protein	146829	147737	909	forward	0.885	-0.176	0.471	0.609	0.244	-0.721	CDS	GI:188593686	BAG32661.1
AP009380	PGN_0143	probable dihydroneopterin aldolase	147780	148133	354	forward	1.133	0.181	0.499	0.633	0.268	0.676	CDS	GI:188593687	BAG32662.1
AP009380	PGN_0144	hypothetical protein	148204	149463	1260	reverse	0.828	-0.272	0.412	0.551	0.332	-0.821	CDS	GI:188593688	BAG32663.1
AP009380	PGN_0145	conserved hypothetical protein	149877	154424	4548	reverse	1.517	0.602	0.039	0.109	0.292	2.062	CDS	GI:188593689	BAG32664.1
AP009380	PGN_0146	hypothetical protein	154445	154588	144	reverse	0.821	-0.285	0.486	0.623	0.408	-0.697	CDS	GI:188593690	BAG32665.1
AP009380	PGN_0147	conserved hypothetical protein	154846	157173	2328	reverse	1.933	0.950	0.018	0.065	0.403	2.360	CDS	GI:188593691	BAG32666.1
AP009380	PGN_0148	conserved hypothetical protein	157181	161929	4749	reverse	1.703	0.768	0.021	0.072	0.333	2.304	CDS	GI:188593692	BAG32667.1
AP009380	PGN_0149	ribose-phosphate pyrophosphokinase	162077	163018	942	reverse	1.571	0.651	0.010	0.043	0.254	2.567	CDS	GI:188593693	BAG32668.1
AP009380	PGN_0150	putative ATP-dependent RNA helicase	163205	164488	1284	reverse	1.487	0.572	0.003	0.017	0.191	2.996	CDS	GI:188593694	BAG32669.1
AP009380	PGN_0151	conserved hypothetical protein	165089	166063	975	reverse	0.735	-0.444	0.452	0.590	0.590	-0.753	CDS	GI:188593695	BAG32670.1
AP009380	PGN_0152	immunoreactive 61 kDa antigen	166236	167858	1623	reverse	0.679	-0.558	0.345	0.494	0.591	-0.945	CDS	GI:188593696	BAG32671.1
AP009380	PGN_0153	conserved hypothetical protein	168040	168174	135	reverse	0.261	-1.937	0.000	0.001	0.483	-4.011	CDS	GI:188593697	BAG32672.1
AP009380	PGN_t0007	tRNA-Met	168503	168579	77	forward	0.165	-2.599	0.000	0.000	0.545	-4.771	tRNA		
AP009380	PGN_0154	conserved hypothetical protein	168799	169359	561	forward	3.227	1.690	0.000	0.002	0.448	3.769	CDS	GI:188593698	BAG32673.1
AP009380	PGN_0155	hypothetical protein	169400	169534	135	forward	1.237	0.306	0.367	0.511	0.339	0.903	CDS	GI:188593699	BAG32674.1
AP009380	PGN_0156	conserved hypothetical protein	169555	170238	684	forward	0.915	-0.128	0.583	0.702	0.234	-0.549	CDS	GI:188593700	BAG32675.1
AP009380	PGN_0157	putative thiamine biosynthesis protein ThiH	170357	171469	1113	reverse	0.752	-0.411	0.079	0.179	0.234	-1.754	CDS	GI:188593701	BAG32676.1
AP009380	PGN_0158	putative thiazole biosynthesis protein ThiG	171482	172261	780	reverse	0.819	-0.288	0.522	0.652	0.451	-0.640	CDS	GI:188593702	BAG32677.1
AP009380	PGN_0159	probable thiamin-phosphate pyrophosphorylase	172320	174263	1944	reverse	0.786	-0.347	0.404	0.544	0.415	-0.835	CDS	GI:188593703	BAG32678.1
AP009380	PGN_0160	thiamine biosynthesis protein	174260	176023	1764	reverse	0.834	-0.262	0.375	0.518	0.295	-0.887	CDS	GI:188593704	BAG32679.1
AP009380	PGN_0161	putative thiamine biosynthesis protein ThiS	176093	176347	255	reverse	0.467	-1.097	0.000	0.002	0.294	-3.734	CDS	GI:188593705	BAG32680.1

AP009380	PGN_0162	conserved hypothetical protein		176666	177436	771	forward	0.450	-1.151	0.000	0.003	0.314	-3.664	CDS	GI:188593706	BAG32681.1
AP009380	PGN_0163	hypothetical protein		177696	178004	309	forward	0.794	-0.332	0.291	0.440	0.315	-1.056	CDS	GI:188593707	BAG32682.1
AP009380	PGN_0164	conserved hypothetical protein		178270	178503	234	reverse	0.687	-0.541	0.214	0.356	0.435	-1.242	CDS	GI:188593708	BAG32683.1
AP009380	PGN_0165	conserved hypothetical protein		178645	178812	168	forward	0.805	-0.314	0.445	0.584	0.411	-0.764	CDS	GI:188593709	BAG32684.1
AP009380	PGN_0166	conserved hypothetical protein		178991	179143	153	forward	0.720	-0.474	0.256	0.401	0.417	-1.137	CDS	GI:188593710	BAG32685.1
AP009380	PGN_0167	30S ribosomal protein S16	rpsP	179295	179873	579	reverse	0.994	-0.009	0.977	0.983	0.304	-0.029	CDS	GI:188593711	BAG32686.1
AP009380	PGN_0168	lipopolysaccharide biosynthesis protein WbpB	wbpB	180659	181630	972	forward	0.948	-0.077	0.781	0.853	0.279	-0.278	CDS	GI:188593712	BAG32687.1
AP009380	PGN_0169	probable metallo-beta-lactamase superfamily protein		181748	182557	810	reverse	1.395	0.480	0.092	0.201	0.285	1.683	CDS	GI:188593713	BAG32688.1
AP009380	PGN_0170	L-asparaginase		182610	183623	1014	reverse	1.651	0.723	0.006	0.029	0.261	2.769	CDS	GI:188593714	BAG32689.1
AP009380	PGN_0171	partial transposase in ISPg2		183701	184012	312	reverse	1.336	0.418	0.257	0.403	0.369	1.134	CDS	GI:188593715	BAG32690.1
AP009380	PGN_0172	conserved hypothetical protein		184006	184278	273	forward	0.771	-0.376	0.053	0.133	0.194	-1.936	CDS	GI:188593716	BAG32691.1
AP009380	PGN_0173	glyceraldehyde 3-phosphate dehydrogenase type I		184289	185299	1011	forward	0.993	-0.011	0.951	0.966	0.172	-0.062	CDS	GI:188593717	BAG32692.1
AP009380	PGN_0174	probable transcriptional regulator AraC family		185439	186377	939	reverse	1.238	0.308	0.192	0.331	0.236	1.304	CDS	GI:188593718	BAG32693.1
AP009380	PGN_0175	conserved hypothetical protein		186498	187172	675	reverse	1.146	0.196	0.391	0.532	0.229	0.858	CDS	GI:188593719	BAG32694.1
AP009380	PGN_0176	conserved hypothetical protein		187169	187612	444	reverse	1.127	0.173	0.507	0.638	0.260	0.664	CDS	GI:188593720	BAG32695.1
AP009380	PGN_0177	hypothetical protein		187634	187957	324	forward	0.556	-0.848	0.033	0.097	0.397	-2.135	CDS	GI:188593721	BAG32696.1
AP009380	PGN_0178	conserved hypothetical protein		188162	188743	582	forward	0.393	-1.348	0.001	0.007	0.402	-3.350	CDS	GI:188593722	BAG32697.1
AP009380	PGN_0179	60 kDa protein		188769	190241	1473	forward	0.556	-0.847	0.055	0.137	0.441	-1.920	CDS	GI:188593723	BAG32698.1
AP009380	PGN_0180	FimA type I fimbrilin	fimA	190297	191448	1152	forward	0.296	-1.755	0.000	0.000	0.298	-5.887	CDS	GI:188593724	BAG32699.1
AP009380	PGN_0181	conserved hypothetical protein		191587	191943	357	forward	0.506	-0.982	0.002	0.015	0.322	-3.049	CDS	GI:188593725	BAG32700.1
AP009380	PGN_0182	conserved hypothetical protein		192172	192498	327	forward	0.914	-0.130	0.709	0.801	0.348	-0.373	CDS	GI:188593726	BAG32701.1
AP009380	PGN_0183	minor component FimC	fimC	192485	193873	1389	forward	0.782	-0.354	0.335	0.485	0.367	-0.964	CDS	GI:188593727	BAG32702.1
AP009380	PGN_0184	minor component FimD	fimD	193888	195900	2013	forward	0.842	-0.248	0.451	0.590	0.329	-0.754	CDS	GI:188593728	BAG32703.1
AP009380	PGN_0185	minor component FimE	fimE	195897	197549	1653	forward	1.225	0.293	0.327	0.476	0.298	0.981	CDS	GI:188593729	BAG32704.1
AP009380	PGN_0186	hypothetical protein		197572	197799	228	reverse	1.263	0.337	0.230	0.372	0.281	1.199	CDS	GI:188593730	BAG32705.1
AP009380	PGN_0187	conserved hypothetical protein		198082	198633	552	forward	0.961	-0.057	0.753	0.830	0.182	-0.315	CDS	GI:188593731	BAG32706.1
AP009380	PGN_0188	50S ribosomal protein L32	rpmF	198640	198825	186	forward	0.796	-0.329	0.097	0.208	0.198	-1.661	CDS	GI:188593732	BAG32707.1
AP009380	PGN_0189	beta-ketoacyl-acyl-carrier-protein synthase III		199005	200012	1008	forward	1.370	0.454	0.161	0.291	0.324	1.403	CDS	GI:188593733	BAG32708.1
AP009380	PGN_0190	putative GTP-binding protein		200091	200990	900	forward	1.971	0.979	0.017	0.063	0.411	2.384	CDS	GI:188593734	BAG32709.1
AP009380	PGN_0191	GTP-binding protein EngA		201053	202366	1314	forward	1.599	0.677	0.102	0.215	0.414	1.635	CDS	GI:188593735	BAG32710.1
AP009380	PGN_0192	conserved hypothetical protein		202417	205716	3300	forward	1.792	0.841	0.048	0.125	0.426	1.974	CDS	GI:188593736	BAG32711.1
AP009380	PGN_0193	putative polysaccharide deacetylase		205717	206364	648	forward	1.970	0.978	0.035	0.101	0.464	2.109	CDS	GI:188593737	BAG32712.1
AP009380	PGN_0194	conserved hypothetical protein		206390	207076	687	forward	2.059	1.042	0.036	0.103	0.496	2.098	CDS	GI:188593738	BAG32713.1
AP009380	PGN_0195	putative xanthine phosphoribosyltransferase		207275	207856	582	reverse	1.515	0.599	0.025	0.081	0.268	2.239	CDS	GI:188593739	BAG32714.1
AP009380	PGN_0196	xanthine/uracil permease		207893	209230	1338	reverse	1.672	0.742	0.010	0.042	0.287	2.586	CDS	GI:188593740	BAG32715.1
AP009380	PGN_0197	conserved hypothetical protein		209391	210062	672	reverse	1.022	0.031	0.892	0.934	0.229	0.136	CDS	GI:188593741	BAG32716.1
AP009380	PGN_0198	conserved hypothetical protein		210122	211627	1506	reverse	1.420	0.506	0.028	0.087	0.230	2.196	CDS	GI:188593742	BAG32717.1
AP009380	PGN_t0008	tRNA-Pro		212909	212984	76	forward	0.416	-1.264	0.009	0.039	0.480	-2.631	tRNA		
AP009380	PGN_0199	hypothetical protein		213103	213288	186	reverse	1.548	0.630	0.001	0.007	0.189	3.342	CDS	GI:188593743	BAG32718.1
AP009380	PGN_0200	conserved hypothetical protein		213315	214205	891	reverse	1.603	0.681	0.002	0.014	0.221	3.086	CDS	GI:188593744	BAG32719.1
AP009380	PGN_0201	conserved hypothetical protein with DUF558 domain		214251	214997	747	reverse	0.979	-0.030	0.891	0.934	0.219	-0.137	CDS	GI:188593745	BAG32720.1
AP009380	PGN_0202	probable leucine aminopeptidase precursor		215327	216328	1002	forward	1.239	0.309	0.281	0.429	0.286	1.079	CDS	GI:188593746	BAG32721.1
AP009380	PGN_0203	probable SufE Fe/S-cluster-related protein		216352	216777	426	forward	1.600	0.678	0.011	0.045	0.266	2.549	CDS	GI:188593747	BAG32722.1
AP009380	PGN_0204	protoporphyrinogen oxidase		216781	218178	1398	forward	2.121	1.085	0.000	0.003	0.297	3.653	CDS	GI:188593748	BAG32723.1
AP009380	PGN_0205	conserved hypothetical protein		219032	219931	900	reverse	1.822	0.865	0.050	0.129	0.442	1.957	CDS	GI:188593749	BAG32724.1
AP009380	PGN_0206	putative lipid A disaccharide synthase		219928	221079	1152	reverse	2.491	1.316	0.000	0.002	0.352	3.736	CDS	GI:188593750	BAG32725.1
AP009380	PGN_0207	probable stationary-phase survival protein		221116	221886	771	reverse	2.648	1.405	0.000	0.000	0.274	5.127	CDS	GI:188593751	BAG32726.1
AP009380	PGN_0208	conserved hypothetical protein		221883	222440	558	reverse	2.340	1.226	0.000	0.000	0.249	4.922	CDS	GI:188593752	BAG32727.1
AP009380	PGN_0209	glycyl-tRNA synthetase		222437	223984	1548	reverse	2.080	1.056	0.000	0.002	0.273	3.872	CDS	GI:188593753	BAG32728.1
AP009380	PGN_0210	transposase in ISPg1		224297	225382	1086	forward	0.907	-0.140	0.758	0.834	0.455	-0.308	CDS	GI:188593754	BAG32729.1
AP009380	PGN_0211	conserved hypothetical protein		225616	226788	1173	forward	0.687	-0.543	0.086	0.190	0.316	-1.719	CDS	GI:188593755	BAG32730.1
AP009380	PGN_0212	transposase in ISPg1		226942	228027	1086	reverse	0.609	-0.716	0.138	0.261	0.482	-1.485	CDS	GI:188593756	BAG32731.1
AP009380	PGN_0213	conserved hypothetical protein		228170	228556	387	forward	0.514	-0.961	0.058	0.142	0.507	-1.896	CDS	GI:188593757	BAG32732.1
AP009380	PGN_0214	conserved hypothetical protein		228667	228975	309	reverse	0.810	-0.304	0.196	0.335	0.235	-1.292	CDS	GI:188593758	BAG32733.1
AP009380	PGN_0215	conserved hypothetical protein		228974	229342	369	forward	0.751	-0.413	0.041	0.114	0.202	-2.041	CDS	GI:188593759	BAG32734.1
AP009380	PGN_r0001	16S ribosomal RNA		229311	230785	1475	forward	0.601	-0.735	0.000	0.003	0.199	-3.694	rRNA		
AP009380	PGN_0216	conserved hypothetical protein		230898	231056	159	forward	0.903	-0.148	0.499	0.633	0.219	-0.675	CDS	GI:188593760	BAG32735.1
AP009380	PGN_0217	conserved hypothetical protein		231183	231338	156	forward	1.095	0.132	0.518	0.648	0.203	0.647	CDS	GI:188593761	BAG32736.1
AP009380	PGN_t0009	tRNA-Ile		231348	231421	74	forward	0.398	-1.327	0.006	0.032	0.488	-2.722	tRNA		
AP009380	PGN_t0010	tRNA-Ala		231423	231499	77	forward	0.494	-1.018	0.006	0.031	0.372	-2.739	tRNA		
AP009380	PGN_r0002	23S ribosomal RNA		231618	234450	2833	forward	0.487	-1.039	0.000	0.001	0.258	-4.032	rRNA		
AP009380	PGN_r0003	5S ribosomal RNA		234597	234704	108	forward	0.251	-1.992	0.000	0.000	0.459	-4.344	rRNA		
AP009380	PGN_0218	transposase in ISPg1		235110	236195	1086	forward	0.669	-0.581	0.210	0.351	0.463	-1.253	CDS	GI:188593762	BAG32737.1
AP009380	PGN_0219	partial transposase in ISPg1		236434	237003	570	forward	0.577	-0.793	0.107	0.220	0.492	-1.613	CDS	GI:188593763	BAG32738.1
AP009380	PGN_0220	partial transposase in ISPg1		237092	237517	426	forward	0.572	-0.806	0.101	0.214	0.491	-1.640	CDS	GI:188593764	BAG32739.1
AP009380	PGN_0221	DNA topoisomerase III		237886	240018	2133	forward	0.863	-0.213	0.407	0.546	0.257	-0.830	CDS	GI:188593765	BAG32740.1
AP009380	PGN_0222	conserved hypothetical protein		240698	240988	291	reverse	0.775	-0.369	0.325	0.474	0.375	-0.984	CDS	GI:188593766	BAG32741.1
AP009380	PGN_0223	glycosyl transferase family 4	wecA	241404	242510	1107	forward	0.869	-0.202	0.388	0.530	0.234	-0.864	CDS	GI:188593767	BAG32742.1
AP009380	PGN_0224	UDP-N-acetyl-D-mannosaminuronic acid dehydrogenase		242758	243966	1209	forward	1.104	0.143	0.621	0.732	0.289	0.494	CDS	GI:188593768	BAG32743.1
AP009380	PGN_0225	probable glycosyltransferase		244252	245238	987	forward	1.501	0.586	0.112	0.228	0.369	1.589	CDS	GI:188593769	BAG32744.1
AP009380	PGN_0226	conserved hypothetical protein		245244	246413	1170	forward	2.297	1.200	0.003	0.019	0.407	2.944	CDS	GI:188593770	BAG32745.1
AP009380	PGN_0227	probable glycosyl transferase family 1		246423	247481	1059	forward	2.432	1.282	0.002	0.012	0.406	3.161	CDS	GI:188593771	BAG32746.1
AP009380	PGN_0228	probable coenzyme F390 synthetase		247494	248828	1335	forward	2.169	1.117	0.005	0.027	0.399	2.798	CDS	GI:188593772	BAG32747.1
AP009380	PGN_0229	putative DNA-binding protein histone-like family		249123	249608	486	forward	1.472	0.558	0.010	0.043	0.216	2.577	CDS	GI:188593773	BAG32748.1
AP009380	PGN_0230	probable serine acetyltransferase		249728	250162	435	forward	1.260	0.333	0.222	0.365	0.273	1.222	CDS	GI:188593774	BAG32749.1
AP009380	PGN_0231	probable delta-aminolevulinic acid dehydratase		250156	251340	1185	forward	1.591	0.670	0.005	0.027	0.239	2.804	CDS	GI:188593775	BAG32750.1
AP009380	PGN_0232	probable glycosyl transferase family 2		251361	252401	1041	forward	1.593	0.672	0.001	0.010	0.210	3.198	CDS	GI:188593776	BAG32751.1
AP009380	PGN_0233	conserved hypothetical protein with glycosyl transferase WecB/TagA/CpsF family domain		252443	253141	699	forward	1.559	0.641	0.001	0.005	0.184	3.480	CDS	GI:188593777	BAG32752.1
AP009380	PGN_0234	UDP-N-acetylglucosamine 2-epimerase		253147	254307	1161	forward	1.340	0.422	0.047	0.123	0.212	1.989	CDS	GI:188593778	BAG32753.1
AP009380	PGN_0235	DNA-binding protein HU		254613	254879	267	forward	1.509	0.594	0.020	0.069	0.255	2.328	CDS	GI:188593779	BAG32754.1
AP009380	PGN_0236	conserved hypothetical protein		255081	255650	570	forward	1.222	0.290	0.371	0.514	0.324	0.894	CDS	GI:188593780	BAG32755.1
AP009380	PGN_0237	conserved hypothetical protein		255710	256330	621	reverse	1.690	0.757	0.001	0.008	0.229	3.302	CDS	GI:188593781	BAG32756.1
AP009380	PGN_0238	conserved hypothetical protein		256334	256882	549	reverse	1.393	0.478	0.013	0.053	0.193	2.471	CDS	GI:188593782	BAG32757.1
AP009380	PGN_0239	putative type I phosphodiesterase-nucleotide pyrophosphatase		256879	258114	1236	reverse	0.823	-0.280	0.206	0.347	0.222	-1.264	CDS	GI:188593783	BAG32758.1
AP009380	PGN_0240	putative ferrochelatase		258611	259648	1038	forward	1.038	0.054	0.881	0.926	0.363	0.149	CDS	GI:188593784	BAG32759.1
AP009380	PGN_0241	conserved hypothetical protein		259655	260629	975	forward	1.248	0.320	0.316	0.466	0.319	1.002	CDS	GI:188593785	BAG32760.1
AP009380	PGN_0242	probable glycosyl transferase family 1		260646	261794	1149	forward	0.737	-0.440	0.066	0.157	0.240	-1.835	CDS	GI:188593786	BAG32761.1

AP009380	PGN_0243	phosphoglycerate mutase		261930	262676	747	reverse	2.002	1.001	0.020	0.068	0.429	2.331	CDS	GI:188593787	BAG32762.1
AP009380	PGN_0244	hypothetical protein		262690	262899	210	reverse	0.926	-0.111	0.782	0.854	0.401	-0.276	CDS	GI:188593788	BAG32763.1
AP009380	PGN_0245	hypothetical protein		262960	264270	1311	reverse	0.931	-0.104	0.679	0.778	0.250	-0.414	CDS	GI:188593789	BAG32764.1
AP009380	PGN_0246	conserved hypothetical protein		264267	265772	1506	reverse	0.991	-0.014	0.948	0.964	0.207	-0.066	CDS	GI:188593790	BAG32765.1
AP009380	PGN_0247	putative magnesium transporter		265791	267143	1353	reverse	0.686	-0.545	0.066	0.157	0.297	-1.836	CDS	GI:188593791	BAG32766.1
AP009380	PGN_0248	putative dimethyladenosine transferase		267175	267951	777	reverse	0.709	-0.496	0.052	0.132	0.256	-1.943	CDS	GI:188593792	BAG32767.1
AP009380	PGN_0249	conserved hypothetical protein		268082	269131	1050	forward	1.138	0.186	0.497	0.632	0.274	0.679	CDS	GI:188593793	BAG32768.1
AP009380	PGN_0250	aminoacyl-histidine dipeptidase		269162	270616	1455	forward	1.354	0.437	0.199	0.337	0.340	1.284	CDS	GI:188593794	BAG32769.1
AP009380	PGN_0251	malonyl CoA-acyl carrier protein transacylase		270731	271612	882	forward	1.856	0.892	0.021	0.072	0.388	2.301	CDS	GI:188593795	BAG32770.1
AP009380	PGN_0252	putative membrane-bound lytic murein transglycosylase D		271793	273139	1347	reverse	2.063	1.045	0.001	0.008	0.317	3.292	CDS	GI:188593796	BAG32771.1
AP009380	PGN_0253	conserved hypothetical protein		273158	273865	708	reverse	1.115	0.158	0.515	0.646	0.242	0.651	CDS	GI:188593797	BAG32772.1
AP009380	PGN_0254	putative ParB chromosome partitioning protein		273885	274754	870	reverse	1.054	0.076	0.704	0.798	0.201	0.380	CDS	GI:188593798	BAG32773.1
AP009380	PGN_0255	putative ParA chromosome partitioning protein		274762	275538	777	reverse	1.499	0.584	0.015	0.057	0.240	2.432	CDS	GI:188593799	BAG32774.1
AP009380	PGN_0256	hydrolase		275754	276632	879	reverse	0.672	-0.574	0.013	0.051	0.231	-2.489	CDS	GI:188593800	BAG32775.1
AP009380	PGN_0257	putative arginine deiminase		276650	277675	1026	reverse	0.917	-0.124	0.635	0.744	0.262	-0.475	CDS	GI:188593801	BAG32776.1
AP009380	PGN_0258	hypothetical protein		277959	278345	387	reverse	0.984	-0.023	0.936	0.956	0.293	-0.080	CDS	GI:188593802	BAG32777.1
AP009380	PGN_0259	conserved hypothetical protein		278348	279055	708	reverse	1.029	0.041	0.893	0.934	0.303	0.135	CDS	GI:188593803	BAG32778.1
AP009380	PGN_0260	conserved hypothetical protein		279068	279607	540	reverse	0.996	-0.006	0.979	0.983	0.242	-0.026	CDS	GI:188593804	BAG32779.1
AP009380	PGN_0261	sigma-54-dependent transcriptional regulator		279594	280847	1254	reverse	1.200	0.263	0.354	0.499	0.283	0.928	CDS	GI:188593805	BAG32780.1
AP009380	PGN_0262	conserved hypothetical protein		280875	282143	1269	reverse	1.050	0.070	0.788	0.858	0.262	0.269	CDS	GI:188593806	BAG32781.1
AP009380	PGN_0263	putative Fe-S oxidoreductase		282180	283484	1305	reverse	0.928	-0.108	0.720	0.808	0.301	-0.358	CDS	GI:188593807	BAG32782.1
AP009380	PGN_0264	signal recognition particle-docking protein		283481	284434	954	reverse	0.950	-0.073	0.815	0.878	0.314	-0.234	CDS	GI:188593808	BAG32783.1
AP009380	PGN_0265	carboxynorspermidine decarboxylase		284461	285597	1137	reverse	1.073	0.101	0.741	0.821	0.306	0.330	CDS	GI:188593809	BAG32784.1
AP009380	PGN_0266	aspartyl-tRNA synthetase		285607	287370	1764	reverse	1.215	0.281	0.337	0.487	0.293	0.959	CDS	GI:188593810	BAG32785.1
AP009380	PGN_0267	putative riboflavin biosynthesis protein		287800	288792	993	reverse	0.728	-0.459	0.071	0.165	0.254	-1.803	CDS	GI:188593811	BAG32786.1
AP009380	PGN_0268	protoporphyrinogen oxidase		288817	289698	882	forward	0.873	-0.197	0.488	0.625	0.283	-0.694	CDS	GI:188593812	BAG32787.1
AP009380	PGN_0269	putative transcriptional regulatory protein		289695	290180	486	forward	0.819	-0.287	0.303	0.451	0.279	-1.030	CDS	GI:188593813	BAG32788.1
AP009380	PGN_0270	probable amidophosphoribosyl-transferase		290164	290904	741	forward	0.821	-0.285	0.189	0.327	0.217	-1.313	CDS	GI:188593814	BAG32789.1
AP009380	PGN_0271	endopeptidase PepO		291034	293103	2070	reverse	1.468	0.553	0.027	0.085	0.251	2.208	CDS	GI:188593815	BAG32790.1
AP009380	PGN_0272	conserved hypothetical protein		293122	294024	903	reverse	1.272	0.347	0.129	0.252	0.229	1.517	CDS	GI:188593816	BAG32791.1
AP009380	PGN_0273	conserved hypothetical protein		294206	294340	135	reverse	2.665	1.414	0.000	0.000	0.297	4.770	CDS	GI:188593817	BAG32792.1
AP009380	PGN_0274	putative RNA polymerase sigma-70 factor ECF subfamily		294444	295025	582	reverse	1.815	0.860	0.001	0.006	0.252	3.409	CDS	GI:188593818	BAG32793.1
AP009380	PGN_0275	phosphofructokinase		295174	296823	1650	reverse	0.684	-0.547	0.057	0.141	0.288	-1.902	CDS	GI:188593819	BAG32794.1
AP009380	PGN_0276	hypothetical protein		297019	297333	315	reverse	0.846	-0.241	0.388	0.531	0.279	-0.863	CDS	GI:188593820	BAG32795.1
AP009380	PGN_0277	putative heat shock protein 15	hslR	297308	297745	438	reverse	0.930	-0.104	0.653	0.759	0.233	-0.449	CDS	GI:188593821	BAG32796.1
AP009380	PGN_0278	putative peptidyl-tRNA hydrolase		297751	298308	558	reverse	0.813	-0.298	0.139	0.263	0.202	-1.478	CDS	GI:188593822	BAG32797.1
AP009380	PGN_0279	putative 50S ribosomal protein L25	rplY	298449	299027	579	reverse	1.409	0.494	0.118	0.237	0.316	1.562	CDS	GI:188593823	BAG32798.1
AP009380	PGN_0280	hypothetical protein		299185	299475	291	reverse	0.620	-0.690	0.182	0.317	0.517	-1.336	CDS	GI:188593824	BAG32799.1
AP009380	PGN_0281	methionyl-tRNA synthetase		299637	301679	2043	forward	1.159	0.213	0.348	0.497	0.227	0.939	CDS	GI:188593825	BAG32800.1
AP009380	PGN_0282	2',3'-cyclic-nucleotide 2'-phosphodiesterase precursor		301700	303481	1782	forward	1.257	0.331	0.184	0.320	0.249	1.329	CDS	GI:188593826	BAG32801.1
AP009380	PGN_0283	probable exonuclease		303478	304260	783	forward	1.553	0.635	0.031	0.094	0.295	2.152	CDS	GI:188593827	BAG32802.1
AP009380	PGN_0284	probable transcriptional regulator		304323	304676	354	reverse	0.773	-0.372	0.359	0.503	0.406	-0.918	CDS	GI:188593828	BAG32803.1
AP009380	PGN_0285	pyridine nucleotide-disulphide oxidoreductase		304747	307227	2481	reverse	0.849	-0.236	0.266	0.413	0.212	-1.112	CDS	GI:188593829	BAG32804.1
AP009380	PGN_0286	hypothetical protein frame-shifted with PGN0285		307239	307562	324	reverse	0.262	-1.930	0.000	0.003	0.536	-3.598	CDS	GI:188593830	BAG32805.1
AP009380	PGN_0287	Mfa1fimbrilin	mfa1	308593	310284	1692	forward	0.270	-1.887	0.000	0.000	0.196	-9.641	CDS	GI:188593831	BAG32806.1
AP009380	PGN_0288	conserved hypothetical protein		310364	311338	975	forward	0.239	-2.063	0.000	0.000	0.289	-7.150	CDS	GI:188593832	BAG32807.1
AP009380	PGN_0289	conserved hypothetical protein		311639	312979	1341	forward	0.281	-1.834	0.000	0.000	0.269	-6.826	CDS	GI:188593833	BAG32808.1
AP009380	PGN_0290	immunoreactive 32 kDa antigen		312988	313989	1002	forward	0.342	-1.547	0.000	0.000	0.297	-5.202	CDS	GI:188593834	BAG32809.1
AP009380	PGN_0291	conserved hypothetical protein		314139	317825	3687	forward	0.341	-1.550	0.000	0.000	0.245	-6.329	CDS	GI:188593835	BAG32810.1
AP009380	PGN_0292	hypothetical protein		318212	318334	123	forward	0.286	-1.807	0.000	0.000	0.246	-7.340	CDS	GI:188593836	BAG32811.1
AP009380	PGN_0293	receptor antigen A	ragA	318767	321877	3111	forward	1.327	0.408	0.135	0.258	0.273	1.496	CDS	GI:188593837	BAG32812.1
AP009380	PGN_0294	receptor antigen B	ragB	321911	323422	1512	forward	1.497	0.582	0.078	0.177	0.331	1.761	CDS	GI:188593838	BAG32813.1
AP009380	PGN_0295	C-terminal domain of Arg- and Lys-gingipain proteinase		323591	324472	882	forward	1.100	0.138	0.725	0.809	0.391	0.352	CDS	GI:188593839	BAG32814.1
AP009380	PGN_0296	conserved hypothetical protein		324678	325841	1164	forward	0.907	-0.141	0.580	0.700	0.255	-0.553	CDS	GI:188593840	BAG32815.1
AP009380	PGN_0297	conserved hypothetical protein		326030	326737	708	forward	1.025	0.035	0.861	0.911	0.202	0.175	CDS	GI:188593841	BAG32816.1
AP009380	PGN_0298	putative undecaprenyl diphosphate synthase		326815	327579	765	forward	1.004	0.005	0.979	0.983	0.210	0.026	CDS	GI:188593842	BAG32817.1
AP009380	PGN_0299	putative outer membrane protein		327597	330272	2676	forward	1.107	0.147	0.529	0.656	0.233	0.630	CDS	GI:188593843	BAG32818.1
AP009380	PGN_0300	conserved hypothetical protein		330329	330853	525	forward	0.890	-0.168	0.352	0.498	0.180	-0.931	CDS	GI:188593844	BAG32819.1
AP009380	PGN_0301	conserved hypothetical protein		330888	331379	492	forward	1.095	0.131	0.590	0.707	0.242	0.540	CDS	GI:188593845	BAG32820.1
AP009380	PGN_0302	rubrerythrin		331708	332286	579	forward	0.522	-0.939	0.016	0.059	0.388	-2.418	CDS	GI:188593846	BAG32821.1
AP009380	PGN_0303	putative zinc protease		332564	335389	2826	forward	0.944	-0.084	0.725	0.809	0.238	-0.351	CDS	GI:188593847	BAG32822.1
AP009380	PGN_0304	conserved hypothetical protein		335560	335721	162	forward	0.452	-1.145	0.013	0.051	0.460	-2.487	CDS	GI:188593848	BAG32823.1
AP009380	PGN_0305	conserved hypothetical protein		335938	336096	159	forward	0.600	-0.738	0.122	0.242	0.478	-1.545	CDS	GI:188593849	BAG32824.1
AP009380	PGN_0306	conserved hypothetical protein		336239	337081	843	forward	0.486	-1.041	0.000	0.000	0.232	-4.497	CDS	GI:188593850	BAG32825.1
AP009380	PGN_0307	conserved hypothetical protein		337034	337759	726	reverse	0.896	-0.159	0.586	0.704	0.292	-0.545	CDS	GI:188593851	BAG32826.1
AP009380	PGN_0308	conserved hypothetical protein		337731	337961	231	reverse	0.726	-0.462	0.248	0.393	0.400	-1.155	CDS	GI:188593852	BAG32827.1
AP009380	PGN_0309	probable ribonuclease P protein component		337967	338380	414	reverse	0.851	-0.233	0.296	0.443	0.223	-1.046	CDS	GI:188593853	BAG32828.1
AP009380	PGN_0310	putative uroporphyrinogen-III synthase		338377	339123	747	reverse	0.638	-0.647	0.006	0.030	0.235	-2.753	CDS	GI:188593854	BAG32829.1
AP009380	PGN_0311	conserved hypothetical protein		339114	339821	708	reverse	0.980	-0.029	0.894	0.935	0.219	-0.133	CDS	GI:188593855	BAG32830.1
AP009380	PGN_0312	hypothetical protein		339872	340117	246	reverse	1.176	0.234	0.371	0.514	0.262	0.895	CDS	GI:188593856	BAG32831.1
AP009380	PGN_0313	peptide chain release factor 3		340123	341703	1581	reverse	1.432	0.518	0.038	0.107	0.249	2.076	CDS	GI:188593857	BAG32832.1
AP009380	PGN_0314	probable formate/nitrite transporter		342110	342895	786	forward	2.177	1.123	0.017	0.063	0.471	2.383	CDS	GI:188593858	BAG32833.1
AP009380	PGN_0315	precorrin-6x reductase/cobalamin biosynthetic protein CbiD		342990	344798	1809	reverse	3.314	1.729	0.000	0.001	0.425	4.071	CDS	GI:188593859	BAG32834.1
AP009380	PGN_0316	precorrin-4 C11-methyltransferase		344795	346639	1845	reverse	2.567	1.360	0.001	0.009	0.418	3.253	CDS	GI:188593860	BAG32835.1
AP009380	PGN_0317	decarboxylating precorrin-6Y C5,15-methyltransferase		346653	347894	1242	reverse	2.143	1.099	0.003	0.019	0.371	2.964	CDS	GI:188593861	BAG32836.1
AP009380	PGN_0318	precorrin-3B C17-methyltransferase		347887	349293	1407	reverse	1.611	0.688	0.014	0.054	0.280	2.457	CDS	GI:188593862	BAG32837.1
AP009380	PGN_0319	probable RNA polymerase sigma-70 factor ECF subfamily		349809	350342	534	forward	0.544	-0.880	0.012	0.048	0.349	-2.521	CDS	GI:188593863	BAG32838.1
AP009380	PGN_0320	conserved hypothetical protein		350342	350827	486	forward	0.406	-1.299	0.000	0.002	0.335	-3.874	CDS	GI:188593864	BAG32839.1
AP009380	PGN_0321	conserved hypothetical protein		350835	351335	501	forward	0.428	-1.223	0.000	0.001	0.310	-3.940	CDS	GI:188593865	BAG32840.1
AP009380	PGN_0322	conserved hypothetical protein		351369	352262	894	forward	0.451	-1.150	0.000	0.000	0.263	-4.368	CDS	GI:188593866	BAG32841.1
AP009380	PGN_0323	conserved hypothetical protein		352276	353133	858	forward	0.395	-1.339	0.000	0.000	0.271	-4.949	CDS	GI:188593867	BAG32842.1
AP009380	PGN_0324	transposase in ISPg1		353426	354511	1086	reverse	0.884	-0.178	0.682	0.780	0.435	-0.410	CDS	GI:188593868	BAG32843.1
AP009380	PGN_0325	hypothetical protein		354680	355045	366	reverse	0.878	-0.188	0.390	0.532	0.218	-0.860	CDS	GI:188593869	BAG32844.1
AP009380	PGN_0326	DNA-binding protein histone-like family		355912	356379	468	reverse	0.662	-0.594	0.077	0.174	0.336	-1.770	CDS	GI:188593870	BAG32845.1
AP009380	PGN_0327	putative DNA polymerase III epsilon chain		357180	357671	492	reverse	0.844	-0.245	0.352	0.498	0.263	-0.930	CDS	GI:188593871	BAG32846.1
AP009380	PGN_0328	conserved hypothetical protein		357675	358313	639	reverse	0.811	-0.302	0.192	0.331	0.232	-1.303	CDS	GI:188593872	BAG32847.1
AP009380	PGN_0329	conserved hypothetical protein		358494	361187	2694	reverse	1.687	0.755	0.015	0.057	0.310	2.433	CDS	GI:188593873	BAG32848.1

AP009380	PGN_0330	DNA repair protein		361249	362634	1386	reverse	1.599	0.677	0.018	0.065	0.287	2.359	CDS	GI:188593874	BAG32849.1
AP009380	PGN_0331	conserved hypothetical protein		362680	363564	885	reverse	1.314	0.394	0.127	0.249	0.259	1.525	CDS	GI:188593875	BAG32850.1
AP009380	PGN_0332	conserved hypothetical protein		363578	363982	405	forward	1.026	0.038	0.884	0.928	0.258	0.146	CDS	GI:188593876	BAG32851.1
AP009380	PGN_0333	putative transaldolase		364085	364747	663	forward	1.009	0.012	0.941	0.959	0.167	0.075	CDS	GI:188593877	BAG32852.1
AP009380	PGN_0334	conserved hypothetical protein with DUF1343 domain		364744	366042	1299	forward	1.418	0.504	0.039	0.109	0.244	2.065	CDS	GI:188593878	BAG32853.1
AP009380	PGN_0335	conserved hypothetical protein with Zinc carboxypeptidase domain		366121	368586	2466	reverse	1.362	0.445	0.208	0.348	0.353	1.260	CDS	GI:188593879	BAG32854.1
AP009380	PGN_0336	immunoreactive 23 kDa antigen		369407	370030	624	reverse	1.609	0.686	0.071	0.164	0.379	1.808	CDS	GI:188593880	BAG32855.1
AP009380	PGN_0337	conserved hypothetical protein		370232	370390	159	reverse	1.444	0.531	0.362	0.506	0.582	0.912	CDS	GI:188593881	BAG32856.1
AP009380	PGN_0338	hypothetical protein		370525	370725	201	reverse	1.242	0.313	0.596	0.713	0.591	0.530	CDS	GI:188593882	BAG32857.1
AP009380	PGN_0339	hypothetical protein		370817	370948	132	forward	0.669	-0.581	0.326	0.476	0.592	-0.981	CDS	GI:188593883	BAG32858.1
AP009380	PGN_0340	carboxyl-terminal processing protease		370966	372567	1602	forward	1.088	0.122	0.648	0.754	0.267	0.457	CDS	GI:188593884	BAG32859.1
AP009380	PGN_0341	conserved hypothetical protein		372639	374159	1521	forward	1.592	0.671	0.017	0.062	0.281	2.387	CDS	GI:188593885	BAG32860.1
AP009380	PGN_0342	putative uracil-DNA glycosylase		374193	374861	669	forward	2.531	1.340	0.000	0.000	0.205	6.523	CDS	GI:188593886	BAG32861.1
AP009380	PGN_0343	hypothetical protein		375660	375797	138	reverse	1.707	0.772	0.067	0.158	0.422	1.829	CDS	GI:188593887	BAG32862.1
AP009380	PGN_0344	probable haloacid dehalogenase-like hydrolase		375803	376618	816	reverse	2.118	1.083	0.001	0.007	0.323	3.347	CDS	GI:188593888	BAG32863.1
AP009380	PGN_0345	conserved hypothetical protein		376767	377621	855	reverse	1.324	0.404	0.105	0.218	0.249	1.621	CDS	GI:188593889	BAG32864.1
AP009380	PGN_0346	putative methyltransferase		377666	378367	702	reverse	1.133	0.180	0.521	0.651	0.280	0.642	CDS	GI:188593890	BAG32865.1
AP009380	PGN_0347	conserved hypothetical protein		378383	378859	477	reverse	0.703	-0.509	0.045	0.121	0.254	-2.001	CDS	GI:188593891	BAG32866.1
AP009380	PGN_0348	putative universal stress protein UspA	uspA	379179	380291	1113	reverse	0.968	-0.047	0.926	0.952	0.503	-0.092	CDS	GI:188593892	BAG32867.1
AP009380	PGN_0349	upregulated in stationary phase protein A	ustA	380456	380710	255	reverse	0.781	-0.357	0.386	0.529	0.412	-0.867	CDS	GI:188593893	BAG32868.1
AP009380	PGN_0350	probable translation initation factor SUI1		380917	381249	333	reverse	0.986	-0.021	0.954	0.969	0.359	-0.057	CDS	GI:188593894	BAG32869.1
AP009380	PGN_0351	pyruvate carboxylase subunit B		381346	383205	1860	reverse	0.910	-0.136	0.665	0.766	0.315	-0.433	CDS	GI:188593895	BAG32870.1
AP009380	PGN_0352	conserved hypothetical protein		383312	383488	177	reverse	0.558	-0.842	0.005	0.025	0.298	-2.829	CDS	GI:188593896	BAG32871.1
AP009380	PGN_0353	conserved hypothetical protein		384064	384522	459	forward	0.932	-0.102	0.662	0.764	0.234	-0.437	CDS	GI:188593897	BAG32872.1
AP009380	PGN_0354	putative nitrogen utilization substance protein A		384569	385903	1335	forward	1.339	0.421	0.108	0.222	0.262	1.607	CDS	GI:188593898	BAG32873.1
AP009380	PGN_0355	translation initiation factor IF-2		385999	388938	2940	forward	1.349	0.431	0.101	0.214	0.263	1.640	CDS	GI:188593899	BAG32874.1
AP009380	PGN_0356	conserved hypothetical protein		388966	389457	492	forward	1.187	0.247	0.249	0.393	0.214	1.154	CDS	GI:188593900	BAG32875.1
AP009380	PGN_0357	ABC transporter membrane protein		389491	390936	1446	forward	1.641	0.714	0.002	0.012	0.226	3.160	CDS	GI:188593901	BAG32876.1
AP009380	PGN_0358	putative ABC transporter ATP-binding protein		390976	391728	753	forward	1.571	0.652	0.007	0.033	0.242	2.693	CDS	GI:188593902	BAG32877.1
AP009380	PGN_0359	putative ABC transporter permease protein		391735	393078	1344	forward	1.574	0.655	0.026	0.083	0.294	2.224	CDS	GI:188593903	BAG32878.1
AP009380	PGN_0360	tyrosyl-tRNA synthetase		394043	395335	1293	forward	1.253	0.325	0.080	0.180	0.186	1.751	CDS	GI:188593904	BAG32879.1
AP009380	PGN_0361	putative glycosyl transferase family 2		395355	396422	1068	forward	1.114	0.156	0.482	0.619	0.222	0.704	CDS	GI:188593905	BAG32880.1
AP009380	PGN_0362	hypothetical protein		396600	396725	126	reverse	1.334	0.416	0.353	0.498	0.447	0.929	CDS	GI:188593906	BAG32881.1
AP009380	PGN_0363	conserved hypothetical protein		396722	396916	195	reverse	1.036	0.052	0.928	0.953	0.573	0.090	CDS	GI:188593907	BAG32882.1
AP009380	PGN_0364	hypothetical protein		397291	397491	201	reverse	0.460	-1.120	0.028	0.087	0.510	-2.197	CDS	GI:188593908	BAG32883.1
AP009380	PGN_0365	arginyl-tRNA synthetase		397663	399456	1794	forward	0.748	-0.419	0.186	0.322	0.316	-1.324	CDS	GI:188593909	BAG32884.1
AP009380	PGN_0366	putative tRNA 5-methylaminomethyl-2-thiouridylate 5-methyltransferase		399461	400546	1086	forward	0.847	-0.240	0.396	0.537	0.283	-0.848	CDS	GI:188593910	BAG32885.1
AP009380	PGN_0367	exodeoxyribonuclease III		400591	401355	765	forward	0.990	-0.015	0.938	0.958	0.192	-0.078	CDS	GI:188593911	BAG32886.1
AP009380	PGN_0368	redox-sensitive transcriptional activator OxyR	oxyR	401428	402354	927	forward	1.154	0.207	0.357	0.502	0.225	0.921	CDS	GI:188593912	BAG32887.1
AP009380	PGN_0369	probable single-stranded binding protein		402405	402875	471	forward	0.769	-0.379	0.135	0.258	0.253	-1.496	CDS	GI:188593913	BAG32888.1
AP009380	PGN_0370	conserved hypothetical protein		402893	404221	1329	forward	1.110	0.150	0.625	0.735	0.306	0.489	CDS	GI:188593914	BAG32889.1
AP009380	PGN_0371	conserved hypothetical protein		404257	404853	597	forward	1.237	0.306	0.298	0.446	0.294	1.041	CDS	GI:188593915	BAG32890.1
AP009380	PGN_0372	hypothetical protein		404909	405001	93	forward	1.115	0.157	0.605	0.718	0.303	0.518	CDS	GI:188593916	BAG32891.1
AP009380	PGN_0373	putative thioredoxin		405469	405978	510	reverse	1.218	0.284	0.253	0.399	0.248	1.144	CDS	GI:188593917	BAG32892.1
AP009380	PGN_0374	conserved hypothetical protein		406116	407243	1128	reverse	0.751	-0.412	0.045	0.120	0.205	-2.007	CDS	GI:188593918	BAG32893.1
AP009380	PGN_0375	phosphoribulose/uridine kinase		407334	408998	1665	forward	0.791	-0.338	0.353	0.499	0.364	-0.928	CDS	GI:188593919	BAG32894.1
AP009380	PGN_0376	2-dehydro-3-deoxyphosphooctonate aldolase		410086	410904	819	forward	1.196	0.258	0.258	0.405	0.228	1.131	CDS	GI:188593920	BAG32895.1
AP009380	PGN_0377	aspartate ammonia-lyase		411152	412579	1428	forward	1.333	0.414	0.138	0.261	0.279	1.485	CDS	GI:188593921	BAG32896.1
AP009380	PGN_0378	putative exopolyphosphatase		412726	413634	909	forward	0.851	-0.234	0.230	0.372	0.194	-1.201	CDS	GI:188593922	BAG32897.1
AP009380	PGN_0379	conserved hypothetical protein		413733	414665	933	forward	1.143	0.192	0.530	0.657	0.307	0.627	CDS	GI:188593923	BAG32898.1
AP009380	PGN_0380	partial ROK family transcriptional repressor with glucose kinase domain		414732	415511	780	forward	1.538	0.621	0.004	0.021	0.214	2.908	CDS	GI:188593924	BAG32899.1
AP009380	PGN_0381	partial ROK family transcriptional repressor with glucose kinase domain		415480	415938	459	forward	1.878	0.909	0.000	0.003	0.251	3.621	CDS	GI:188593925	BAG32900.1
AP009380	PGN_0382	conserved hypothetical protein		415923	416477	555	forward	1.000	0.000	1.000	1.000	0.234	0.000	CDS	GI:188593926	BAG32901.1
AP009380	PGN_0383	probable transporter		416474	417385	912	forward	1.237	0.307	0.292	0.441	0.291	1.053	CDS	GI:188593927	BAG32902.1
AP009380	PGN_0384	conserved hypothetical protein		417382	417819	438	forward	1.995	0.996	0.007	0.033	0.369	2.702	CDS	GI:188593928	BAG32903.1
AP009380	PGN_0385	putative integrase/recombinase XerD		417859	418785	927	reverse	1.053	0.074	0.773	0.847	0.257	0.288	CDS	GI:188593929	BAG32904.1
AP009380	PGN_0386	probable 3-dehydroquinate dehydratase type II		418903	419328	426	forward	0.736	-0.441	0.045	0.119	0.220	-2.009	CDS	GI:188593930	BAG32905.1
AP009380	PGN_0387	putative O-methyltransferase		419429	420079	651	forward	1.050	0.070	0.789	0.858	0.261	0.268	CDS	GI:188593931	BAG32906.1
AP009380	PGN_0388	putative thiol peroxidase		420125	420664	540	forward	0.827	-0.274	0.279	0.427	0.253	-1.082	CDS	GI:188593932	BAG32907.1
AP009380	PGN_0389	putative cytidine/deoxycytidylate deaminase		420860	421339	480	reverse	1.707	0.772	0.008	0.037	0.292	2.646	CDS	GI:188593933	BAG32908.1
AP009380	PGN_0390	conserved hypothetical protein		421385	422248	864	reverse	1.480	0.565	0.047	0.123	0.285	1.986	CDS	GI:188593934	BAG32909.1
AP009380	PGN_0391	conserved hypothetical protein		422258	423676	1419	reverse	0.945	-0.082	0.697	0.792	0.212	-0.389	CDS	GI:188593935	BAG32910.1
AP009380	PGN_0392	conserved hypothetical protein with competence-damaged protein domain		423709	424191	483	reverse	0.494	-1.017	0.002	0.016	0.336	-3.029	CDS	GI:188593936	BAG32911.1
AP009380	PGN_0393	putative O-sialoglycoprotein endopeptidase		424191	425216	1026	reverse	0.655	-0.609	0.006	0.032	0.224	-2.723	CDS	GI:188593937	BAG32912.1
AP009380	PGN_t0011	tRNA-Glu		425498	425569	72	reverse	0.360	-1.475	0.001	0.005	0.425	-3.473	tRNA		
AP009380	PGN_0394	probable 30S ribosomal protein S20	rpsT	425634	425888	255	reverse	0.627	-0.673	0.004	0.022	0.232	-2.899	CDS	GI:188593938	BAG32913.1
AP009380	PGN_t0012	tRNA-Glu		425918	425989	72	reverse	0.358	-1.481	0.000	0.003	0.406	-3.650	tRNA		
AP009380	PGN_0395	conserved hypothetical protein		426069	426374	306	forward	0.844	-0.245	0.406	0.546	0.295	-0.830	CDS	GI:188593939	BAG32914.1
AP009380	PGN_0396	ribonuclease R		426565	428760	2196	reverse	2.346	1.230	0.001	0.005	0.357	3.446	CDS	GI:188593940	BAG32915.1
AP009380	PGN_0397	putative auxin-regulated protein		428813	430342	1530	reverse	1.885	0.915	0.001	0.006	0.270	3.389	CDS	GI:188593941	BAG32916.1
AP009380	PGN_0398	ABC transporter ATP-binding protein MsbA family		430358	432175	1818	reverse	1.518	0.603	0.006	0.029	0.217	2.772	CDS	GI:188593942	BAG32917.1
AP009380	PGN_0399	conserved hypothetical protein		432200	432475	276	forward	1.108	0.148	0.655	0.759	0.331	0.447	CDS	GI:188593943	BAG32918.1
AP009380	PGN_0400	conserved hypothetical protein		432834	435614	2781	forward	0.446	-1.165	0.000	0.002	0.309	-3.765	CDS	GI:188593944	BAG32919.1
AP009380	PGN_0401	conserved hypothetical protein		436189	436380	192	reverse	0.348	-1.523	0.006	0.030	0.553	-2.755	CDS	GI:188593945	BAG32920.1
AP009380	PGN_0402	hypothetical protein		436435	436653	219	reverse	0.289	-1.791	0.000	0.004	0.509	-3.519	CDS	GI:188593946	BAG32921.1
AP009380	PGN_0403	putative pyridoxamine-phosphate oxidase		436686	437330	645	forward	0.964	-0.053	0.811	0.875	0.224	-0.239	CDS	GI:188593947	BAG32922.1
AP009380	PGN_0404	conserved hypothetical protein		437367	437771	405	forward	0.898	-0.155	0.498	0.633	0.228	-0.677	CDS	GI:188593948	BAG32923.1
AP009380	PGN_0405	alpha-1,2-mannosidase family protein		437860	440205	2346	forward	1.227	0.295	0.209	0.350	0.235	1.256	CDS	GI:188593949	BAG32924.1
AP009380	PGN_0406	conserved hypothetical protein with glycosyl hydrolase family 92 domain		440230	442533	2304	forward	1.357	0.440	0.116	0.234	0.280	1.573	CDS	GI:188593950	BAG32925.1
AP009380	PGN_0407	hypothetical protein		442691	442897	207	reverse	1.793	0.842	0.049	0.126	0.427	1.972	CDS	GI:188593951	BAG32926.1
AP009380	PGN_0408	conserved hypothetical protein		443080	443433	354	forward	1.039	0.055	0.844	0.900	0.279	0.197	CDS	GI:188593952	BAG32927.1
AP009380	PGN_0409	conserved hypothetical protein		443454	443816	363	forward	1.291	0.369	0.232	0.374	0.309	1.196	CDS	GI:188593953	BAG32928.1
AP009380	PGN_0410	probable RNA pseudouridylate synthase		443836	444810	975	forward	1.771	0.825	0.002	0.012	0.263	3.142	CDS	GI:188593954	BAG32929.1
AP009380	PGN_0411	thiol-disulfide interchange protein		444847	446895	2049	forward	1.823	0.866	0.007	0.033	0.321	2.700	CDS	GI:188593955	BAG32930.1
AP009380	PGN_0412	conserved hypothetical protein		446913	447698	786	forward	1.945	0.960	0.014	0.055	0.391	2.454	CDS	GI:188593956	BAG32931.1
AP009380	PGN_0413	DNA gyrase B subunit	gyrB	447756	449720	1965	forward	0.923	-0.115	0.664	0.765	0.265	-0.434	CDS	GI:188593957	BAG32932.1
AP009380	PGN_0414	probable membrane-bound dipeptidase		449713	451521	1809	forward	1.155	0.208	0.351	0.498	0.222	0.933	CDS	GI:188593958	BAG32933.1

AP009380	PGN_0415	restriction endonuclease	452503	456477	3975	reverse	1.201	0.264	0.170	0.303	0.192	1.372	CDS	GI:188593959	BAG32934.1
AP009380	PGN_0416	putative type II DNA modification methyltransferase	456487	457500	1014	reverse	0.635	-0.654	0.015	0.056	0.268	-2.440	CDS	GI:188593960	BAG32935.1
AP009380	PGN_0417	conserved hypothetical protein	457693	457986	294	reverse	0.499	-1.004	0.006	0.029	0.363	-2.763	CDS	GI:188593961	BAG32936.1
AP009380	PGN_0418	conserved hypothetical protein with aminodeoxychorismate lyase domain	458560	459654	1095	forward	0.887	-0.174	0.491	0.628	0.252	-0.688	CDS	GI:188593962	BAG32937.1
AP009380	PGN_0419	putative dinucleotide-utilizing enzyme involved in molybdopterin and thiamine biosynthesis	459651	460400	750	forward	0.903	-0.147	0.572	0.692	0.260	-0.565	CDS	GI:188593963	BAG32938.1
AP009380	PGN_0420	putative lipoprotein releasing system ATP-binding protein	460397	461056	660	forward	1.466	0.552	0.010	0.042	0.213	2.590	CDS	GI:188593964	BAG32939.1
AP009380	PGN_0421	conserved hypothetical protein	461086	461790	705	forward	1.345	0.427	0.044	0.117	0.212	2.019	CDS	GI:188593965	BAG32940.1
AP009380	PGN_0422	conserved hypothetical protein	461797	462399	603	forward	1.257	0.330	0.104	0.218	0.203	1.624	CDS	GI:188593966	BAG32941.1
AP009380	PGN_0423	putative transcription elongation factor	462882	463352	471	forward	0.822	-0.282	0.281	0.429	0.262	-1.077	CDS	GI:188593967	BAG32942.1
AP009380	PGN_0424	putative HIT family protein	463368	463757	390	forward	0.966	-0.050	0.842	0.898	0.252	-0.200	CDS	GI:188593968	BAG32943.1
AP009380	PGN_0425	partial transposase in ISPg3	463896	464033	138	reverse	0.532	-0.912	0.014	0.054	0.371	-2.458	CDS	GI:188593969	BAG32944.1
AP009380	PGN_0426	conserved hypothetical protein	464668	465144	477	reverse	0.370	-1.434	0.000	0.000	0.274	-5.234	CDS	GI:188593970	BAG32945.1
AP009380	PGN_0427	putative glycosyl hydrolase	465141	466427	1287	reverse	0.572	-0.806	0.010	0.042	0.311	-2.593	CDS	GI:188593971	BAG32946.1
AP009380	PGN_0428	putative glycosyl transferase family 1	466424	467686	1263	reverse	0.747	-0.421	0.220	0.363	0.343	-1.228	CDS	GI:188593972	BAG32947.1
AP009380	PGN_0429	putative 4-alpha-glucanotransferase	467683	469659	1977	reverse	0.655	-0.610	0.154	0.283	0.428	-1.426	CDS	GI:188593973	BAG32948.1
AP009380	PGN_0430	putative ATP-binding component of ABC transporter protein	470146	470847	702	reverse	0.918	-0.123	0.724	0.809	0.347	-0.354	CDS	GI:188593974	BAG32949.1
AP009380	PGN_0431	conserved hypothetical protein	470882	472240	1359	reverse	0.640	-0.644	0.013	0.052	0.260	-2.476	CDS	GI:188593975	BAG32950.1
AP009380	PGN_0432	conserved hypothetical protein	472260	472367	108	forward	0.800	-0.322	0.583	0.702	0.587	-0.549	CDS	GI:188593976	BAG32951.1
AP009380	PGN_0433	phosphoglycerate kinase	472474	473730	1257	reverse	1.650	0.723	0.025	0.079	0.322	2.247	CDS	GI:188593977	BAG32952.1
AP009380	PGN_0434	phosphoenolpyruvate carboxykinase	474026	475633	1608	forward	2.020	1.014	0.007	0.032	0.373	2.717	CDS	GI:188593978	BAG32953.1
AP009380	PGN_0435	probable partial hemagglutinin-related protein	475829	476041	213	reverse	0.414	-1.273	0.030	0.093	0.588	-2.164	CDS	GI:188593979	BAG32954.1
AP009380	PGN_0436	probable partial hemagglutinin-related protein	476041	476403	363	reverse	0.475	-1.074	0.048	0.125	0.544	-1.974	CDS	GI:188593980	BAG32955.1
AP009380	PGN_0437	conserved hypothetical protein	476631	476939	309	reverse	0.793	-0.334	0.113	0.230	0.211	-1.584	CDS	GI:188593981	BAG32956.1
AP009380	PGN_0438	conserved hypothetical protein	476938	477306	369	forward	0.760	-0.396	0.041	0.112	0.193	-2.047	CDS	GI:188593982	BAG32957.1
AP009380	PGN_r0004	16S ribosomal RNA	477275	478749	1475	forward	0.612	-0.709	0.001	0.009	0.219	-3.237	rRNA		
AP009380	PGN_0439	conserved hypothetical protein	478862	479020	159	forward	0.854	-0.228	0.344	0.494	0.241	-0.946	CDS	GI:188593983	BAG32958.1
AP009380	PGN_0440	conserved hypothetical protein	479147	479302	156	forward	1.079	0.110	0.587	0.705	0.203	0.543	CDS	GI:188593984	BAG32959.1
AP009380	PGN_t0013	tRNA-Ile	479312	479385	74	forward	0.394	-1.345	0.006	0.029	0.486	-2.770	tRNA		
AP009380	PGN_t0014	tRNA-Ala	479387	479463	77	forward	0.452	-1.146	0.003	0.018	0.384	-2.986	tRNA		
AP009380	PGN_r0005	23S ribosomal RNA	479582	482414	2833	forward	0.484	-1.047	0.000	0.001	0.262	-3.993	rRNA		
AP009380	PGN_r0006	5S ribosomal RNA	482561	482668	108	forward	0.251	-1.992	0.000	0.000	0.457	-4.363	rRNA		
AP009380	PGN_0441	hypothetical protein	482818	482919	102	reverse	0.614	-0.703	0.039	0.109	0.341	-2.065	CDS	GI:188593985	BAG32960.1
AP009380	PGN_0442	transposase in ISPg3	482969	483871	903	reverse	0.709	-0.497	0.156	0.285	0.350	-1.418	CDS	GI:188593986	BAG32961.1
AP009380	PGN_0443	hypothetical protein	484199	484372	174	forward	0.688	-0.539	0.358	0.503	0.586	-0.919	CDS	GI:188593987	BAG32962.1
AP009380	PGN_0444	probable outer membrane efflux protein	484845	486212	1368	reverse	0.652	-0.618	0.057	0.141	0.325	-1.901	CDS	GI:188593988	BAG32963.1
AP009380	PGN_0445	membrane fusion efflux protein	486209	487315	1107	reverse	0.596	-0.746	0.040	0.110	0.362	-2.058	CDS	GI:188593989	BAG32964.1
AP009380	PGN_0446	putative ABC transporter ATP-binding protein	487385	488647	1263	reverse	0.606	-0.724	0.026	0.084	0.326	-2.220	CDS	GI:188593990	BAG32965.1
AP009380	PGN_0447	putative ABC transporter permease protein	488670	489944	1275	reverse	0.582	-0.781	0.022	0.073	0.340	-2.294	CDS	GI:188593991	BAG32966.1
AP009380	PGN_0448	putative ABC transporter ATP-binding protein	489969	490628	660	reverse	0.695	-0.525	0.139	0.263	0.355	-1.478	CDS	GI:188593992	BAG32967.1
AP009380	PGN_0449	conserved hypothetical protein	490647	491054	408	reverse	0.593	-0.754	0.031	0.094	0.351	-2.151	CDS	GI:188593993	BAG32968.1
AP009380	PGN_0450	putative RNA polymerase sigma-70 factor ECF subfamily	491540	492064	525	forward	0.846	-0.241	0.378	0.520	0.273	-0.882	CDS	GI:188593994	BAG32969.1
AP009380	PGN_0451	conserved hypothetical protein	492061	492453	393	forward	0.680	-0.557	0.045	0.121	0.278	-2.001	CDS	GI:188593995	BAG32970.1
AP009380	PGN_0452	conserved hypothetical protein	492540	492602	63	reverse	0.634	-0.657	0.038	0.108	0.317	-2.070	CDS	GI:188593996	BAG32971.1
AP009380	PGN_0453	partial transposase Orf1 in ISPg5	492650	492766	117	reverse	0.473	-1.081	0.000	0.001	0.273	-3.959	CDS	GI:188593997	BAG32972.1
AP009380	PGN_0454	transposase in ISPg3	492790	493692	903	reverse	0.592	-0.756	0.015	0.058	0.312	-2.421	CDS	GI:188593998	BAG32973.1
AP009380	PGN_0455	partial transposase Orf1 in ISPg5	493799	494002	204	reverse	0.367	-1.448	0.000	0.000	0.306	-4.728	CDS	GI:188593999	BAG32974.1
AP009380	PGN_0456	methylmalonyl-CoA mutase large subunit	494428	496575	2148	reverse	1.041	0.057	0.844	0.900	0.292	0.197	CDS	GI:188594000	BAG32975.1
AP009380	PGN_0457	methylmalonyl-CoA mutase small subunit	496604	498460	1857	reverse	0.649	-0.624	0.020	0.068	0.267	-2.333	CDS	GI:188594001	BAG32976.1
AP009380	PGN_0458	hypothetical protein	498707	500233	1527	forward	1.291	0.369	0.090	0.198	0.218	1.695	CDS	GI:188594002	BAG32977.1
AP009380	PGN_0459	transposase in ISPg3	501114	502016	903	forward	0.421	-1.249	0.001	0.007	0.373	-3.346	CDS	GI:188594003	BAG32978.1
AP009380	PGN_0460	DNA-binding protein histone-like family	502076	502513	438	forward	0.211	-2.248	0.000	0.000	0.304	-7.393	CDS	GI:188594004	BAG32979.1
AP009380	PGN_0461	probable D-alanyl-D-alanine dipeptidase	503654	504277	624	reverse	1.005	0.007	0.979	0.983	0.282	0.027	CDS	GI:188594005	BAG32980.1
AP009380	PGN_0462	probable haloacid dehalogenase-like hydrolase	504357	505580	1224	reverse	0.953	-0.069	0.798	0.865	0.270	-0.256	CDS	GI:188594006	BAG32981.1
AP009380	PGN_0463	conserved hypothetical protein	505605	507386	1782	reverse	1.021	0.030	0.914	0.948	0.280	0.108	CDS	GI:188594007	BAG32982.1
AP009380	PGN_0464	conserved hypothetical protein	507422	510409	2988	reverse	0.860	-0.218	0.503	0.636	0.325	-0.669	CDS	GI:188594008	BAG32983.1
AP009380	PGN_0465	GTP pyrophosphokinase	510667	512907	2241	reverse	0.988	-0.018	0.959	0.970	0.352	-0.051	CDS	GI:188594009	BAG32984.1
AP009380	PGN_0466	putative cardiolipin synthetase	512975	514396	1422	reverse	0.924	-0.115	0.716	0.806	0.315	-0.364	CDS	GI:188594010	BAG32985.1
AP009380	PGN_0467	conserved hypothetical protein	514628	514804	177	forward	0.584	-0.776	0.072	0.165	0.430	-1.802	CDS	GI:188594011	BAG32986.1
AP009380	PGN_0468	conserved hypothetical protein with DUF452 domain	514794	515546	753	forward	2.232	1.158	0.001	0.007	0.347	3.338	CDS	GI:188594012	BAG32987.1
AP009380	PGN_0469	probable biotin synthesis protein	515537	516292	756	forward	1.344	0.426	0.196	0.334	0.330	1.293	CDS	GI:188594013	BAG32988.1
AP009380	PGN_0470	conserved hypothetical protein	516322	517398	1077	reverse	1.069	0.096	0.681	0.779	0.233	0.411	CDS	GI:188594014	BAG32989.1
AP009380	PGN_0471	conserved hypothetical protein	517391	518338	948	reverse	0.945	-0.082	0.646	0.752	0.179	-0.460	CDS	GI:188594015	BAG32990.1
AP009380	PGN_0472	DNA topoisomerase IV A subunit	518325	521021	2697	reverse	0.781	-0.357	0.227	0.369	0.295	-1.209	CDS	GI:188594016	BAG32991.1
AP009380	PGN_0473	conserved hypothetical protein	521082	522275	1194	reverse	1.031	0.044	0.866	0.916	0.260	0.169	CDS	GI:188594017	BAG32992.1
AP009380	PGN_0474	hypothetical protein	522300	522398	99	forward	0.585	-0.774	0.098	0.210	0.469	-1.653	CDS	GI:188594018	BAG32993.1
AP009380	PGN_0475	hypothetical protein	522487	522897	411	forward	0.918	-0.123	0.701	0.795	0.322	-0.384	CDS	GI:188594019	BAG32994.1
AP009380	PGN_0476	conserved hypothetical protein	523058	524257	1200	forward	0.855	-0.226	0.565	0.687	0.392	-0.575	CDS	GI:188594020	BAG32995.1
AP009380	PGN_0477	conserved hypothetical protein	524362	526026	1665	forward	0.699	-0.517	0.242	0.386	0.442	-1.171	CDS	GI:188594021	BAG32996.1
AP009380	PGN_0478	partial transposase in ISPg4	526319	526489	171	reverse	0.634	-0.656	0.032	0.096	0.307	-2.141	CDS	GI:188594022	BAG32997.1
AP009380	PGN_0479	hypothetical protein	527100	527192	93	reverse	0.657	-0.605	0.218	0.361	0.491	-1.233	CDS	GI:188594023	BAG32998.1
AP009380	PGN_0480	partial transposase in ISPg4	527564	528007	444	reverse	0.336	-1.573	0.000	0.001	0.376	-4.179	CDS	GI:188594024	BAG32999.1
AP009380	PGN_0481	hypothetical protein	528038	529306	1269	forward	0.259	-1.951	0.000	0.000	0.206	-9.486	CDS	GI:188594025	BAG33000.1
AP009380	PGN_0482	probable immunoreactive 23 kDa antigen	529331	529960	630	forward	0.277	-1.852	0.000	0.000	0.204	-9.080	CDS	GI:188594026	BAG33001.1
AP009380	PGN_0483	putative aldose 1-epimerase	530166	531233	1068	forward	1.050	0.070	0.721	0.809	0.196	0.357	CDS	GI:188594027	BAG33002.1
AP009380	PGN_0484	putative galactokinase	531283	532437	1155	forward	1.362	0.446	0.047	0.123	0.225	1.984	CDS	GI:188594028	BAG33003.1
AP009380	PGN_0485	conserved hypothetical protein	532570	532995	426	reverse	0.636	-0.652	0.005	0.025	0.230	-2.839	CDS	GI:188594029	BAG33004.1
AP009380	PGN_0486	conserved hypothetical protein	533061	533708	648	reverse	0.561	-0.835	0.000	0.001	0.207	-4.039	CDS	GI:188594030	BAG33005.1
AP009380	PGN_0487	FtsK/SpoIIIE family cell division protein	533722	536307	2586	reverse	1.351	0.435	0.122	0.242	0.281	1.546	CDS	GI:188594031	BAG33006.1
AP009380	PGN_0488	conserved hypothetical protein	536511	537626	1116	reverse	2.019	1.014	0.004	0.023	0.354	2.866	CDS	GI:188594032	BAG33007.1
AP009380	PGN_0489	conserved hypothetical protein	537623	537766	144	reverse	2.254	1.172	0.003	0.017	0.391	3.001	CDS	GI:188594033	BAG33008.1
AP009380	PGN_0490	putative DNA-damage-inducible protein F	537782	539092	1311	reverse	2.152	1.106	0.000	0.002	0.293	3.770	CDS	GI:188594034	BAG33009.1
AP009380	PGN_0491	probable phosphotyrosine protein phosphatase	539107	539610	504	reverse	1.649	0.722	0.003	0.019	0.245	2.950	CDS	GI:188594035	BAG33010.1
AP009380	PGN_0492	cation-transporting ATPase	539618	541825	2208	reverse	1.518	0.602	0.049	0.127	0.306	1.967	CDS	GI:188594036	BAG33011.1
AP009380	PGN_0493	hypothetical protein	541861	542124	264	reverse	0.697	-0.520	0.047	0.123	0.262	-1.986	CDS	GI:188594037	BAG33012.1
AP009380	PGN_0494	hypothetical protein	542233	542379	147	reverse	0.785	-0.349	0.541	0.667	0.571	-0.611	CDS	GI:188594038	BAG33013.1
AP009380	PGN_0495	conserved hypothetical protein	542412	542804	393	forward	0.631	-0.663	0.065	0.154	0.360	-1.844	CDS	GI:188594039	BAG33014.1
AP009380	PGN_0496	putative cytochrome B subunit	542851	543543	693	forward	1.290	0.368	0.096	0.206	0.221	1.667	CDS	GI:188594040	BAG33015.1

AP009380	PGN_0497	fumarate reductase flavoprotein subunit		543574	545517	1944	forward	1.100	0.137	0.612	0.725	0.271	0.507	CDS	GI:188594041	BAG33016.1
AP009380	PGN_0498	fumarate reductase iron-sulfur protein		545546	546301	756	forward	0.420	-1.251	0.000	0.002	0.327	-3.828	CDS	GI:188594042	BAG33017.1
AP009380	PGN_0499	conserved hypothetical protein		546534	546938	405	forward	1.220	0.286	0.216	0.359	0.231	1.237	CDS	GI:188594043	BAG33018.1
AP009380	PGN_0500	methylmalonyl-CoA decarboxylase alpha subunit		547037	548590	1554	forward	1.570	0.650	0.019	0.068	0.278	2.339	CDS	GI:188594044	BAG33019.1
AP009380	PGN_0501	conserved hypothetical protein		548615	549556	942	forward	2.024	1.017	0.001	0.009	0.314	3.239	CDS	GI:188594045	BAG33020.1
AP009380	PGN_0502	conserved hypothetical protein		549553	549789	237	forward	2.111	1.078	0.002	0.011	0.340	3.169	CDS	GI:188594046	BAG33021.1
AP009380	PGN_0503	putative biotin carboxyl carrier protein		549828	550274	447	forward	1.986	0.990	0.001	0.007	0.297	3.336	CDS	GI:188594047	BAG33022.1
AP009380	PGN_0504	methylmalonyl-CoA decarboxylase beta subunit		550279	551430	1152	forward	1.531	0.615	0.033	0.098	0.289	2.130	CDS	GI:188594048	BAG33023.1
AP009380	PGN_0505	hypothetical protein		551410	551571	162	reverse	2.713	1.440	0.006	0.031	0.526	2.735	CDS	GI:188594049	BAG33024.1
AP009380	PGN_0506	hypothetical protein		551990	552127	138	forward	0.772	-0.374	0.449	0.588	0.495	-0.757	CDS	GI:188594050	BAG33025.1
AP009380	PGN_0507	putative ion transporter		552508	553230	723	forward	1.296	0.374	0.149	0.277	0.259	1.443	CDS	GI:188594051	BAG33026.1
AP009380	PGN_0508	putative aminopeptidase		553557	554960	1404	reverse	4.033	2.012	0.000	0.000	0.463	4.346	CDS	GI:188594052	BAG33027.1
AP009380	PGN_0509	immunoreactive 84 kDa antigen		555012	557318	2307	reverse	1.542	0.624	0.076	0.173	0.352	1.775	CDS	GI:188594053	BAG33028.1
AP009380	PGN_0510	probable xanthosine triphosphate pyrophosphatase		557330	557914	585	reverse	1.124	0.169	0.638	0.747	0.359	0.471	CDS	GI:188594054	BAG33029.1
AP009380	PGN_0511	conserved hypothetical protein		557985	558365	381	forward	0.699	-0.518	0.105	0.219	0.320	-1.619	CDS	GI:188594055	BAG33030.1
AP009380	PGN_0512	probable biotin--acetyl-CoA-carboxylase ligase		558337	559110	774	forward	1.227	0.296	0.156	0.285	0.208	1.420	CDS	GI:188594056	BAG33031.1
AP009380	PGN_0513	conserved hypothetical protein		559145	560170	1026	forward	1.055	0.077	0.820	0.881	0.340	0.228	CDS	GI:188594057	BAG33032.1
AP009380	PGN_0514	conserved hypothetical protein		560204	560992	789	reverse	1.617	0.693	0.051	0.129	0.354	1.955	CDS	GI:188594058	BAG33033.1
AP009380	PGN_0515	probable lipoprotein signal peptidase		560989	561669	681	reverse	1.054	0.075	0.806	0.871	0.308	0.245	CDS	GI:188594059	BAG33034.1
AP009380	PGN_0516	putative DnaK suppressor protein		561673	562053	381	reverse	1.391	0.476	0.034	0.100	0.225	2.117	CDS	GI:188594060	BAG33035.1
AP009380	PGN_0517	isoleucyl-tRNA synthetase		562123	565536	3414	reverse	1.543	0.626	0.007	0.032	0.230	2.718	CDS	GI:188594061	BAG33036.1
AP009380	PGN_0518	putative ribulose-phosphate 3-epimerase		565878	566534	657	forward	1.111	0.152	0.565	0.687	0.264	0.575	CDS	GI:188594062	BAG33037.1
AP009380	PGN_0519	probable competence protein		566592	568076	1485	forward	1.504	0.589	0.027	0.085	0.266	2.210	CDS	GI:188594063	BAG33038.1
AP009380	PGN_0520	probable shikimate kinase		568015	568575	561	reverse	1.356	0.439	0.030	0.092	0.203	2.165	CDS	GI:188594064	BAG33039.1
AP009380	PGN_0521	conserved hypothetical protein		568623	570695	2073	reverse	1.103	0.141	0.506	0.638	0.213	0.665	CDS	GI:188594065	BAG33040.1
AP009380	PGN_t0015	tRNA-His		570911	570985	75	reverse	0.503	-0.992	0.024	0.078	0.440	-2.256	tRNA		
AP009380	PGN_0522	putative dihydropteroate synthase		571504	572349	846	forward	1.098	0.134	0.625	0.735	0.274	0.489	CDS	GI:188594066	BAG33041.1
AP009380	PGN_0523	conserved hypothetical protein		572409	573176	768	forward	1.431	0.517	0.155	0.284	0.364	1.421	CDS	GI:188594067	BAG33042.1
AP009380	PGN_0524	lipid A 4'-phosphatase		573192	573902	711	reverse	1.626	0.701	0.054	0.136	0.365	1.923	CDS	GI:188594068	BAG33043.1
AP009380	PGN_0525	probable aerotolerance-related exported protein BatE	batE	573929	574837	909	reverse	1.916	0.938	0.007	0.032	0.345	2.720	CDS	GI:188594069	BAG33044.1
AP009380	PGN_0526	aerotolerance-related exported protein BatD	batD	574834	576636	1803	reverse	1.470	0.556	0.053	0.134	0.288	1.932	CDS	GI:188594070	BAG33045.1
AP009380	PGN_0527	probable aerotolerance-related exported protein BatC	batC	576817	577563	747	reverse	1.410	0.496	0.047	0.123	0.250	1.983	CDS	GI:188594071	BAG33046.1
AP009380	PGN_0528	putative aerotolerance-related exported protein BatB	batB	577560	578579	1020	reverse	1.170	0.226	0.336	0.485	0.235	0.963	CDS	GI:188594072	BAG33047.1
AP009380	PGN_0529	aerotolerance-related membrane protein BatA	batA	578590	579573	984	reverse	1.005	0.007	0.973	0.979	0.195	0.034	CDS	GI:188594073	BAG33048.1
AP009380	PGN_0530	conserved hypothetical protein		579570	580526	957	reverse	0.861	-0.215	0.373	0.515	0.241	-0.892	CDS	GI:188594074	BAG33049.1
AP009380	PGN_0531	putative von Willebrand factor type A		580523	581395	873	reverse	0.867	-0.206	0.524	0.652	0.324	-0.637	CDS	GI:188594075	BAG33050.1
AP009380	PGN_0532	magnesium chelatase subunit I		581406	582401	996	reverse	1.005	0.007	0.978	0.983	0.271	0.027	CDS	GI:188594076	BAG33051.1
AP009380	PGN_0533	putative quinolinate synthetase complex subunit A		582503	583429	927	reverse	2.132	1.092	0.009	0.041	0.420	2.602	CDS	GI:188594077	BAG33052.1
AP009380	PGN_0534	putative nicotinate-nucleotide pyrophosphorylase		583449	584291	843	reverse	1.849	0.887	0.019	0.067	0.378	2.344	CDS	GI:188594078	BAG33053.1
AP009380	PGN_0535	L-aspartate oxidase		584323	585879	1557	reverse	1.388	0.473	0.126	0.247	0.310	1.529	CDS	GI:188594079	BAG33054.1
AP009380	PGN_0536	conserved hypothetical protein		586345	586479	135	forward	0.455	-1.135	0.002	0.014	0.368	-3.085	CDS	GI:188594080	BAG33055.1
AP009380	PGN_0537	probable transcriptional regulator Crp family		586999	587622	624	forward	0.371	-1.430	0.000	0.003	0.393	-3.642	CDS	GI:188594081	BAG33056.1
AP009380	PGN_0538	conserved hypothetical protein		587687	588493	807	forward	0.723	-0.468	0.126	0.247	0.305	-1.531	CDS	GI:188594082	BAG33057.1
AP009380	PGN_0539	metallo-beta-lactamase superfamily protein		588586	590001	1416	forward	0.938	-0.093	0.762	0.837	0.307	-0.303	CDS	GI:188594083	BAG33058.1
AP009380	PGN_0540	conserved hypothetical protein		589974	590357	384	forward	0.910	-0.136	0.723	0.809	0.385	-0.354	CDS	GI:188594084	BAG33059.1
AP009380	PGN_0541	hypothetical protein		590351	590527	177	reverse	1.125	0.170	0.754	0.831	0.542	0.313	CDS	GI:188594085	BAG33060.1
AP009380	PGN_0542	partial transposase in ISPg2		590955	591218	264	reverse	0.431	-1.215	0.000	0.003	0.330	-3.681	CDS	GI:188594086	BAG33061.1
AP009380	PGN_0543	glutamyl-tRNA synthetase		591535	593058	1524	forward	1.562	0.643	0.065	0.153	0.348	1.849	CDS	GI:188594087	BAG33062.1
AP009380	PGN_0544	3-deoxy-D-manno-octulosonic-acid transferase		593083	594321	1239	forward	2.278	1.188	0.003	0.019	0.402	2.955	CDS	GI:188594088	BAG33063.1
AP009380	PGN_0545	putative sulfatase		594406	596361	1956	forward	3.235	1.694	0.000	0.003	0.471	3.592	CDS	GI:188594089	BAG33064.1
AP009380	PGN_0546	glucose-1-phosphate thymidylyltransferase		596476	597345	870	forward	1.250	0.322	0.293	0.441	0.306	1.051	CDS	GI:188594090	BAG33065.1
AP009380	PGN_0547	dTDP-4-dehydrorhamnose 3,5-epimerase		597360	597950	591	forward	1.836	0.876	0.018	0.065	0.371	2.362	CDS	GI:188594091	BAG33066.1
AP009380	PGN_0548	putative dTDP-4-dehydrorhamnose reductase		597947	598804	858	forward	1.691	0.758	0.049	0.127	0.385	1.966	CDS	GI:188594092	BAG33067.1
AP009380	PGN_0549	dTDP-glucose 4,6-dehydratase		598811	599875	1065	forward	1.944	0.959	0.020	0.070	0.413	2.320	CDS	GI:188594093	BAG33068.1
AP009380	PGN_0550	aminomethyltransferase		599950	601038	1089	forward	1.520	0.604	0.044	0.118	0.300	2.014	CDS	GI:188594094	BAG33069.1
AP009380	PGN_0551	conserved hypothetical protein		601328	601423	96	reverse	0.963	-0.054	0.925	0.952	0.574	-0.094	CDS	GI:188594095	BAG33070.1
AP009380	PGN_0552	hypothetical protein		601640	601777	138	reverse	0.576	-0.797	0.177	0.311	0.591	-1.349	CDS	GI:188594096	BAG33071.1
AP009380	PGN_0553	conserved hypothetical protein		602002	602328	327	reverse	3.224	1.689	0.002	0.013	0.542	3.117	CDS	GI:188594097	BAG33072.1
AP009380	PGN_0554	conserved hypothetical protein		602334	602903	570	reverse	1.549	0.631	0.270	0.417	0.572	1.103	CDS	GI:188594098	BAG33073.1
AP009380	PGN_0555	conserved hypothetical protein		602982	603659	678	reverse	0.334	-1.582	0.000	0.004	0.443	-3.569	CDS	GI:188594099	BAG33074.1
AP009380	PGN_0556	putative cobalamin biosynthesis-related protein		603656	608065	4410	reverse	0.754	-0.407	0.075	0.171	0.228	-1.782	CDS	GI:188594100	BAG33075.1
AP009380	PGN_0557	TonB-dependent receptor HmuR	hmuR	608102	610042	1941	reverse	1.280	0.356	0.099	0.210	0.215	1.651	CDS	GI:188594101	BAG33076.1
AP009380	PGN_0558	conserved hypothetical protein		610057	610707	651	reverse	1.932	0.950	0.001	0.009	0.293	3.246	CDS	GI:188594102	BAG33077.1
AP009380	PGN_0559	conserved hypothetical protein		611026	611166	141	forward	0.374	-1.417	0.004	0.023	0.492	-2.880	CDS	GI:188594103	BAG33078.1
AP009380	PGN_0560	hypothetical protein		611390	611563	174	reverse	1.116	0.158	0.639	0.748	0.337	0.469	CDS	GI:188594104	BAG33079.1
AP009380	PGN_0561	trypsin like proteinase PrtT	prtT	611560	614082	2523	reverse	1.206	0.270	0.352	0.498	0.290	0.930	CDS	GI:188594105	BAG33080.1
AP009380	PGN_t0016	tRNA-Arg		614228	614304	77	reverse	0.663	-0.594	0.162	0.292	0.424	-1.399	tRNA		
AP009380	PGN_0562	conserved hypothetical protein		614309	614662	354	reverse	0.768	-0.380	0.201	0.340	0.297	-1.279	CDS	GI:188594106	BAG33081.1
AP009380	PGN_0563	conserved hypothetical protein		614741	614836	96	reverse	1.364	0.448	0.105	0.219	0.277	1.619	CDS	GI:188594107	BAG33082.1
AP009380	PGN_0564	superoxide dismutase Fe-Mn	sod	614848	615423	576	reverse	1.152	0.204	0.419	0.557	0.252	0.808	CDS	GI:188594108	BAG33083.1
AP009380	PGN_0565	conserved hypothetical protein		615561	616352	792	reverse	1.831	0.873	0.027	0.084	0.394	2.215	CDS	GI:188594109	BAG33084.1
AP009380	PGN_0566	probable thioesterase protein		616416	616835	420	reverse	1.964	0.974	0.018	0.065	0.411	2.369	CDS	GI:188594110	BAG33085.1
AP009380	PGN_0567	collagenase	prtC	616891	618144	1254	reverse	1.896	0.923	0.009	0.041	0.353	2.612	CDS	GI:188594111	BAG33086.1
AP009380	PGN_0568	2-amino-4-hydroxy-6- hydroxymethyldihydropteridine pyrophosphokinase		618148	618582	435	reverse	1.607	0.685	0.011	0.045	0.268	2.551	CDS	GI:188594112	BAG33087.1
AP009380	PGN_0569	S-adenosylmethionine:tRNA ribosyltransferase-isomerase		618594	619646	1053	reverse	1.543	0.626	0.006	0.032	0.229	2.727	CDS	GI:188594113	BAG33088.1
AP009380	PGN_0570	putative tRNA pseudouridine synthase B		619664	620440	777	reverse	1.164	0.219	0.421	0.558	0.272	0.805	CDS	GI:188594114	BAG33089.1
AP009380	PGN_0571	putative undecaprenol kinase		620450	621292	843	reverse	1.227	0.295	0.284	0.432	0.275	1.072	CDS	GI:188594115	BAG33090.1
AP009380	PGN_0572	conserved hypothetical protein		621400	621627	228	reverse	1.112	0.154	0.553	0.676	0.259	0.594	CDS	GI:188594116	BAG33091.1
AP009380	PGN_0573	putative cell division protein FtsX		621674	622561	888	reverse	0.737	-0.441	0.052	0.132	0.227	-1.939	CDS	GI:188594117	BAG33092.1
AP009380	PGN_0574	conserved hypothetical protein		624175	624516	342	forward	0.593	-0.754	0.073	0.168	0.421	-1.793	CDS	GI:188594118	BAG33093.1
AP009380	PGN_0575	transposase in ISPg1		624688	625749	1062	reverse	0.625	-0.677	0.165	0.296	0.488	-1.388	CDS	GI:188594119	BAG33094.1
AP009380	PGN_0576	hypothetical protein		625842	625943	102	forward	0.255	-1.970	0.000	0.000	0.466	-4.231	CDS	GI:188594120	BAG33095.1
AP009380	PGN_t0017	tRNA-Ser		626045	626129	85	forward	0.335	-1.579	0.000	0.001	0.405	-3.896	tRNA		
AP009380	PGN_0577	transposase in ISPg1		626732	627817	1086	forward	0.724	-0.467	0.288	0.436	0.439	-1.062	CDS	GI:188594121	BAG33096.1
AP009380	PGN_0578	conserved hypothetical protein found in conjugate transposon		627916	628137	222	reverse	0.520	-0.944	0.005	0.028	0.338	-2.792	CDS	GI:188594122	BAG33097.1
AP009380	PGN_0579	conserved hypothetical protein		628159	629265	1107	forward	0.794	-0.333	0.106	0.219	0.206	-1.616	CDS	GI:188594123	BAG33098.1
AP009380	PGN_0580	conserved hypothetical protein		629353	634965	5613	forward	0.646	-0.630	0.015	0.057	0.259	-2.437	CDS	GI:188594124	BAG33099.1

AP009380	PGN_0581	conserved hypothetical protein		635151	636635	1485	forward	0.687	-0.543	0.036	0.102	0.258	-2.100	CDS	GI:188594125	BAG33100.1
AP009380	PGN_0582	DNA topoisomerase I		636731	638812	2082	forward	0.698	-0.519	0.068	0.159	0.284	-1.826	CDS	GI:188594126	BAG33101.1
AP009380	PGN_0583	conserved hypothetical protein		638954	640594	1641	forward	0.594	-0.752	0.021	0.071	0.325	-2.312	CDS	GI:188594127	BAG33102.1
AP009380	PGN_0584	conserved hypothetical protein		640869	642197	1329	reverse	0.696	-0.523	0.075	0.171	0.294	-1.782	CDS	GI:188594128	BAG33103.1
AP009380	PGN_0585	transposase in ISPg3		642231	643133	903	forward	0.773	-0.372	0.262	0.408	0.332	-1.122	CDS	GI:188594129	BAG33104.1
AP009380	PGN_0586	conserved hypothetical protein		643172	643486	315	forward	0.406	-1.301	0.000	0.003	0.358	-3.634	CDS	GI:188594130	BAG33105.1
AP009380	PGN_0587	transposase in ISPg1		643570	644655	1086	forward	0.677	-0.563	0.223	0.366	0.462	-1.219	CDS	GI:188594131	BAG33106.1
AP009380	PGN_0588	conserved hypothetical protein		644756	645304	549	forward	0.726	-0.463	0.320	0.471	0.466	-0.994	CDS	GI:188594132	BAG33107.1
AP009380	PGN_0589	conserved hypothetical protein		645609	645830	222	forward	0.576	-0.796	0.057	0.140	0.418	-1.906	CDS	GI:188594133	BAG33108.1
AP009380	PGN_0590	putative Fic family protein		646047	647105	1059	forward	0.582	-0.780	0.003	0.019	0.265	-2.947	CDS	GI:188594134	BAG33109.1
AP009380	PGN_0591	conserved hypothetical protein		647136	648518	1383	reverse	0.647	-0.629	0.036	0.103	0.300	-2.098	CDS	GI:188594135	BAG33110.1
AP009380	PGN_0592	putative conserved protein found in conjugate transposon TraQ	traQ	648638	649075	438	reverse	0.852	-0.231	0.447	0.585	0.304	-0.761	CDS	GI:188594136	BAG33111.1
AP009380	PGN_0593	putative conserved protein found in conjugate transposon TraO	traO	649095	649679	585	reverse	0.784	-0.352	0.266	0.413	0.316	-1.113	CDS	GI:188594137	BAG33112.1
AP009380	PGN_0594	conserved protein found in conjugate transposon TraN	traN	649684	650619	936	reverse	0.782	-0.354	0.175	0.308	0.261	-1.357	CDS	GI:188594138	BAG33113.1
AP009380	PGN_0595	putative conserved protein found in conjugate transposon TraM	traM	650693	652054	1362	reverse	0.514	-0.961	0.009	0.041	0.370	-2.596	CDS	GI:188594139	BAG33114.1
AP009380	PGN_0596	conserved hypothetical protein found in conjugate transposon		652051	652314	264	reverse	0.641	-0.641	0.157	0.285	0.452	-1.417	CDS	GI:188594140	BAG33115.1
AP009380	PGN_0597	putative conserved protein found in conjugate transposon TraK	traK	652318	652941	624	reverse	0.475	-1.074	0.022	0.073	0.469	-2.290	CDS	GI:188594141	BAG33116.1
AP009380	PGN_0598	conserved transmembrane protein found in conjugate transposon TraJ	traJ	652959	653945	987	reverse	0.498	-1.006	0.007	0.032	0.372	-2.708	CDS	GI:188594142	BAG33117.1
AP009380	PGN_0599	putative conserved protein found in conjugate transposon TraI	traI	653966	654589	624	reverse	0.513	-0.963	0.004	0.024	0.338	-2.850	CDS	GI:188594143	BAG33118.1
AP009380	PGN_0600	conserved hypothetical protein		654641	655108	468	reverse	0.451	-1.149	0.012	0.048	0.455	-2.526	CDS	GI:188594144	BAG33119.1
AP009380	PGN_0601	conserved hypothetical protein		655186	655605	420	reverse	0.815	-0.296	0.318	0.468	0.297	-0.998	CDS	GI:188594145	BAG33120.1
AP009380	PGN_0602	transposase in ISPg1		655769	656854	1086	forward	0.635	-0.655	0.157	0.286	0.462	-1.416	CDS	GI:188594146	BAG33121.1
AP009380	PGN_0603	hypothetical protein		657387	657560	174	reverse	0.973	-0.039	0.931	0.955	0.455	-0.086	CDS	GI:188594147	BAG33122.1
AP009380	PGN_0604	ferritin		657990	658472	483	forward	1.820	0.864	0.016	0.059	0.358	2.415	CDS	GI:188594148	BAG33123.1
AP009380	PGN_0605	transposase in ISPg1		658720	659805	1086	reverse	0.620	-0.689	0.122	0.242	0.445	-1.548	CDS	GI:188594149	BAG33124.1
AP009380	PGN_0606	glucosamine-6-phosphate isomerase		659925	661913	1989	reverse	1.112	0.153	0.600	0.715	0.291	0.525	CDS	GI:188594150	BAG33125.1
AP009380	PGN_0607	dipeptidyl peptidase 11	dpp11	662070	664232	2163	reverse	1.385	0.470	0.042	0.115	0.231	2.033	CDS	GI:188594151	BAG33126.1
AP009380	PGN_0608	conserved hypothetical protein		664295	664750	456	reverse	0.988	-0.018	0.933	0.955	0.214	-0.084	CDS	GI:188594152	BAG33127.1
AP009380	PGN_0609	probable DNA mismatch repair protein		664774	665898	1125	reverse	0.894	-0.162	0.442	0.581	0.211	-0.768	CDS	GI:188594153	BAG33128.1
AP009380	PGN_0610	conserved hypothetical protein with DUF1015 domain		666064	667311	1248	reverse	1.943	0.958	0.003	0.017	0.318	3.011	CDS	GI:188594154	BAG33129.1
AP009380	PGN_0611	D-3-phosphoglycerate dehydrogenase		667330	668250	921	reverse	2.047	1.034	0.004	0.023	0.361	2.862	CDS	GI:188594155	BAG33130.1
AP009380	PGN_0612	phosphoserine aminotransferase		668351	669433	1083	reverse	1.465	0.551	0.061	0.147	0.294	1.875	CDS	GI:188594156	BAG33131.1
AP009380	PGN_0613	UDP-glucose 6-dehydrogenase	ugdA	669767	671074	1308	reverse	0.802	-0.318	0.247	0.392	0.274	-1.159	CDS	GI:188594157	BAG33132.1
AP009380	PGN_0614	DNA-binding protein histone-like family		671337	671843	507	reverse	0.891	-0.166	0.593	0.711	0.312	-0.534	CDS	GI:188594158	BAG33133.1
AP009380	PGN_0615	hypothetical protein		671866	672081	216	reverse	0.743	-0.429	0.104	0.218	0.264	-1.624	CDS	GI:188594159	BAG33134.1
AP009380	PGN_0616	probable elongation factor P		672379	672945	567	reverse	1.414	0.500	0.023	0.076	0.220	2.269	CDS	GI:188594160	BAG33135.1
AP009380	PGN_0617	conserved hypothetical protein		673077	674633	1557	reverse	0.976	-0.035	0.898	0.938	0.273	-0.128	CDS	GI:188594161	BAG33136.1
AP009380	PGN_0618	aspartate-semialdehyde dehydrogenase		674829	675842	1014	forward	0.863	-0.212	0.305	0.453	0.207	-1.025	CDS	GI:188594162	BAG33137.1
AP009380	PGN_0619	conserved hypothetical protein		675814	675951	138	reverse	1.307	0.386	0.355	0.500	0.417	0.926	CDS	GI:188594163	BAG33138.1
AP009380	PGN_0620	putative S-adenosyl-methyltransferase MraW		676513	677448	936	forward	0.974	-0.038	0.910	0.946	0.338	-0.113	CDS	GI:188594164	BAG33139.1
AP009380	PGN_0621	conserved hypothetical protein		677448	677921	474	forward	0.741	-0.433	0.191	0.330	0.331	-1.307	CDS	GI:188594165	BAG33140.1
AP009380	PGN_0622	penicillin-binding protein		677931	680132	2202	forward	1.028	0.040	0.841	0.898	0.199	0.201	CDS	GI:188594166	BAG33141.1
AP009380	PGN_0623	UDP-N-acetylmuramoylalanyl-D-glutamyl-2, 6-diaminopimelate ligase		680143	681606	1464	forward	1.415	0.501	0.096	0.206	0.300	1.666	CDS	GI:188594167	BAG33142.1
AP009380	PGN_0624	phospho-N-acetylmuramoyl-pentapeptide- transferase		681621	682880	1260	forward	0.937	-0.093	0.695	0.790	0.238	-0.391	CDS	GI:188594168	BAG33143.1
AP009380	PGN_0625	UDP-N-acetylmuramoylalanine--D-glutamate ligase		682904	684256	1353	forward	1.732	0.792	0.015	0.057	0.326	2.431	CDS	GI:188594169	BAG33144.1
AP009380	PGN_0626	putative rod shape-determining protein RodA		684268	685524	1257	forward	1.812	0.858	0.017	0.061	0.358	2.397	CDS	GI:188594170	BAG33145.1
AP009380	PGN_0627	N-acetylglucosaminyl transferase		685521	686660	1140	forward	1.733	0.793	0.012	0.050	0.317	2.502	CDS	GI:188594171	BAG33146.1
AP009380	PGN_0628	UDP-N-acetylmuramate-alanine ligase		686660	688030	1371	forward	1.696	0.762	0.022	0.073	0.332	2.295	CDS	GI:188594172	BAG33147.1
AP009380	PGN_0629	putative cell division protein FtsQ		688024	688800	777	forward	0.834	-0.261	0.378	0.520	0.296	-0.882	CDS	GI:188594173	BAG33148.1
AP009380	PGN_0630	probable cell division protein FtsA		688858	690288	1431	forward	1.121	0.164	0.553	0.676	0.277	0.594	CDS	GI:188594174	BAG33149.1
AP009380	PGN_0631	putative cell division protein FtsZ		690291	691664	1374	forward	1.107	0.146	0.621	0.732	0.295	0.495	CDS	GI:188594175	BAG33150.1
AP009380	PGN_0632	conserved hypothetical protein		691696	692145	450	forward	0.849	-0.235	0.541	0.667	0.385	-0.611	CDS	GI:188594176	BAG33151.1
AP009380	PGN_0633	conserved hypothetical protein		693082	693714	633	reverse	1.778	0.831	0.012	0.049	0.331	2.506	CDS	GI:188594177	BAG33152.1
AP009380	PGN_0634	3-methyl-2-oxobutanoate hydroxymethyltransferase		693766	694587	822	reverse	1.364	0.448	0.026	0.083	0.201	2.228	CDS	GI:188594178	BAG33153.1
AP009380	PGN_0635	glutamine-hydrolyzing GMP synthase		694658	696178	1521	reverse	1.436	0.522	0.012	0.048	0.208	2.514	CDS	GI:188594179	BAG33154.1
AP009380	PGN_0636	50S ribosomal protein L31	rpmE	696895	697152	258	forward	0.789	-0.341	0.057	0.141	0.179	-1.903	CDS	GI:188594180	BAG33155.1
AP009380	PGN_0637	putative heat shock-related protease htrA protein		697369	698865	1497	forward	0.645	-0.633	0.065	0.154	0.343	-1.845	CDS	GI:188594181	BAG33156.1
AP009380	PGN_0638	RNA polymerase sigma factor RpoD	rpoD	699055	699918	864	forward	1.006	0.008	0.966	0.975	0.197	0.043	CDS	GI:188594182	BAG33157.1
AP009380	PGN_0639	30S ribosomal protein S6	rpsF	700015	700368	354	forward	1.264	0.339	0.172	0.305	0.248	1.366	CDS	GI:188594183	BAG33158.1
AP009380	PGN_0640	30S ribosomal protein S18	rpsR	700372	700644	273	forward	1.042	0.060	0.761	0.836	0.196	0.304	CDS	GI:188594184	BAG33159.1
AP009380	PGN_0641	50S ribosomal protein L9	rplI	700669	701208	540	forward	0.802	-0.319	0.134	0.258	0.213	-1.500	CDS	GI:188594185	BAG33160.1
AP009380	PGN_0642	conserved hypothetical protein		701484	703439	1956	forward	1.108	0.148	0.476	0.613	0.208	0.712	CDS	GI:188594186	BAG33161.1
AP009380	PGN_0643	3,4-dihydroxy-2-butanone 4-phosphate synthase		703442	704659	1218	forward	1.028	0.040	0.850	0.904	0.213	0.189	CDS	GI:188594187	BAG33162.1
AP009380	PGN_0644	transposase in ISPg1		705140	706225	1086	forward	0.723	-0.468	0.325	0.474	0.475	-0.984	CDS	GI:188594188	BAG33163.1
AP009380	PGN_0645	Por secretion system protein porQ	porQ	706384	707424	1041	forward	1.253	0.325	0.158	0.288	0.231	1.410	CDS	GI:188594189	BAG33164.1
AP009380	PGN_0646	probable cytidylate kinase		707454	708149	696	forward	1.473	0.558	0.023	0.074	0.245	2.280	CDS	GI:188594190	BAG33165.1
AP009380	PGN_0647	hydroxymethylbutenyl pyrophosphate reductase		708146	709015	870	forward	1.562	0.644	0.004	0.023	0.225	2.864	CDS	GI:188594191	BAG33166.1
AP009380	PGN_0648	conserved hypothetical protein		708999	710054	1056	reverse	0.924	-0.114	0.717	0.806	0.314	-0.363	CDS	GI:188594192	BAG33167.1
AP009380	PGN_0649	conserved hypothetical protein		710285	710392	108	reverse	0.584	-0.775	0.028	0.086	0.352	-2.203	CDS	GI:188594193	BAG33168.1
AP009380	PGN_0650	conserved hypothetical protein		710436	710798	363	forward	0.687	-0.542	0.023	0.074	0.238	-2.281	CDS	GI:188594194	BAG33169.1
AP009380	PGN_0651	conserved hypothetical protein		711069	711161	93	forward	0.346	-1.530	0.000	0.002	0.410	-3.730	CDS	GI:188594195	BAG33170.1
AP009380	PGN_0652	conserved hypothetical protein		711268	711414	147	forward	1.260	0.334	0.166	0.297	0.241	1.386	CDS	GI:188594196	BAG33171.1
AP009380	PGN_0653	conserved hypothetical protein		711578	711850	273	reverse	0.808	-0.308	0.293	0.441	0.293	-1.051	CDS	GI:188594197	BAG33172.1
AP009380	PGN_0654	conserved hypothetical protein		711901	712842	942	forward	0.905	-0.144	0.560	0.684	0.247	-0.583	CDS	GI:188594198	BAG33173.1
AP009380	PGN_0655	conserved hypothetical protein		712839	713042	204	forward	0.758	-0.400	0.109	0.224	0.250	-1.603	CDS	GI:188594199	BAG33174.1
AP009380	PGN_0656	conserved hypothetical protein		713066	713761	696	forward	0.817	-0.291	0.296	0.444	0.279	-1.044	CDS	GI:188594200	BAG33175.1
AP009380	PGN_0657	conserved hypothetical protein		713769	714695	927	forward	0.611	-0.710	0.054	0.136	0.369	-1.923	CDS	GI:188594201	BAG33176.1
AP009380	PGN_0658	GTP-binding elongation factor family protein TypA/BipA		714902	716701	1800	forward	1.364	0.448	0.087	0.194	0.262	1.709	CDS	GI:188594202	BAG33177.1
AP009380	PGN_0659	35 kDa hemin binding protein		716804	717838	1035	forward	2.243	1.166	0.001	0.010	0.363	3.209	CDS	GI:188594203	BAG33178.1
AP009380	PGN_0660	putative alkyl hydroperoxide reductase C subunit		718242	718808	567	forward	0.683	-0.550	0.111	0.227	0.345	-1.593	CDS	GI:188594204	BAG33179.1
AP009380	PGN_0661	alkyl hydroperoxide reductase F subunit		718974	720521	1548	forward	1.166	0.222	0.570	0.690	0.390	0.569	CDS	GI:188594205	BAG33180.1
AP009380	PGN_0662	ATP-dependent protease La	serB	720727	723264	2538	forward	1.454	0.540	0.009	0.041	0.207	2.611	CDS	GI:188594206	BAG33181.1
AP009380	PGN_0663	conserved hypothetical protein		723261	723809	549	forward	1.470	0.556	0.031	0.093	0.257	2.162	CDS	GI:188594207	BAG33182.1
AP009380	PGN_0664	conserved hypothetical protein		723806	725098	1293	forward	1.889	0.918	0.004	0.022	0.318	2.886	CDS	GI:188594208	BAG33183.1
AP009380	PGN_0665	putative triosephosphate isomerase		725130	725885	756	forward	2.382	1.252	0.001	0.009	0.385	3.253	CDS	GI:188594209	BAG33184.1
AP009380	PGN_0666	conserved hypothetical protein		725947	726453	507	forward	2.395	1.260	0.001	0.011	0.397	3.177	CDS	GI:188594210	BAG33185.1
AP009380	PGN_0667	putative GTP cyclohydrolase I		726457	727038	582	forward	1.743	0.802	0.021	0.071	0.347	2.311	CDS	GI:188594211	BAG33186.1

AP009380	PGN_0668	RNA-binding protein		728247	728540	294	reverse	2.270	1.183	0.012	0.048	0.468	2.527	CDS	GI:188594212	BAG33187.1
AP009380	PGN_0669	ABC transporter ATP-binding protein		728790	729545	756	reverse	1.503	0.588	0.022	0.072	0.256	2.299	CDS	GI:188594213	BAG33188.1
AP009380	PGN_0670	probable inorganic polyphosphate/ATP-NAD kinase		729604	730470	867	reverse	1.303	0.382	0.160	0.290	0.272	1.404	CDS	GI:188594214	BAG33189.1
AP009380	PGN_0671	putative pyridoxal phosphate biosynthetic protein		730548	731264	717	forward	1.384	0.469	0.091	0.199	0.277	1.692	CDS	GI:188594215	BAG33190.1
AP009380	PGN_0672	probable biopolymer transport protein		731422	732036	615	forward	1.713	0.776	0.027	0.084	0.350	2.217	CDS	GI:188594216	BAG33191.1
AP009380	PGN_0673	probable biopolymer transport protein		732033	732452	420	forward	1.631	0.706	0.026	0.084	0.318	2.220	CDS	GI:188594217	BAG33192.1
AP009380	PGN_0674	conserved hypothetical protein		732457	733284	828	forward	2.116	1.081	0.001	0.009	0.332	3.259	CDS	GI:188594218	BAG33193.1
AP009380	PGN_0675	conserved hypothetical protein		733299	733844	546	forward	2.427	1.279	0.002	0.016	0.423	3.027	CDS	GI:188594219	BAG33194.1
AP009380	PGN_0676	putative ribosomal protein L11 methyltransferase		733944	734879	936	reverse	2.017	1.012	0.012	0.048	0.401	2.524	CDS	GI:188594220	BAG33195.1
AP009380	PGN_0677	putative multi antimicrobial extrusion protein MatE		734813	736177	1365	reverse	1.769	0.823	0.007	0.032	0.304	2.708	CDS	GI:188594221	BAG33196.1
AP009380	PGN_0678	thiamine monophosphate kinase		736170	737210	1041	reverse	1.369	0.453	0.063	0.151	0.243	1.859	CDS	GI:188594222	BAG33197.1
AP009380	PGN_0679	putative tetraacyldisaccharide 4'-kinase		737216	738289	1074	reverse	1.134	0.181	0.427	0.565	0.229	0.794	CDS	GI:188594223	BAG33198.1
AP009380	PGN_0680	signal peptide peptidase SppA 67K type		738319	740106	1788	reverse	0.910	-0.136	0.611	0.724	0.267	-0.508	CDS	GI:188594224	BAG33199.1
AP009380	PGN_0681	hypothetical protein		740195	740290	96	forward	0.436	-1.197	0.002	0.012	0.378	-3.162	CDS	GI:188594225	BAG33200.1
AP009380	PGN_0682	hypothetical protein		741622	741762	141	forward	0.647	-0.629	0.015	0.056	0.258	-2.442	CDS	GI:188594226	BAG33201.1
AP009380	PGN_0683	TonB-linked receptor Tlr		741759	743879	2121	reverse	1.240	0.310	0.368	0.511	0.344	0.901	CDS	GI:188594227	BAG33202.1
AP009380	PGN_0684	conserved hypothetical protein with adenosylcobinamide amidohydrolase domain		743893	745056	1164	reverse	0.843	-0.246	0.246	0.391	0.212	-1.159	CDS	GI:188594228	BAG33203.1
AP009380	PGN_0685	putative iron compound ABC transporter ATP-binding protein		745080	746081	1002	reverse	0.732	-0.451	0.018	0.065	0.191	-2.359	CDS	GI:188594229	BAG33204.1
AP009380	PGN_0686	putative iron compound ABC transporter permease protein		746089	747123	1035	reverse	0.742	-0.430	0.207	0.348	0.341	-1.261	CDS	GI:188594230	BAG33205.1
AP009380	PGN_0687	putative iron compound ABC transporter periplasmic iron compound-binding protein		747120	748295	1176	reverse	0.709	-0.496	0.230	0.372	0.413	-1.200	CDS	GI:188594231	BAG33206.1
AP009380	PGN_0688	conserved hypothetical protein		748877	749461	585	forward	0.927	-0.110	0.590	0.707	0.204	-0.539	CDS	GI:188594232	BAG33207.1
AP009380	PGN_0689	conserved hypothetical protein		749586	749969	384	reverse	0.895	-0.160	0.518	0.648	0.248	-0.646	CDS	GI:188594233	BAG33208.1
AP009380	PGN_0690	conserved hypothetical protein		750076	750624	549	reverse	0.938	-0.092	0.702	0.796	0.240	-0.383	CDS	GI:188594234	BAG33209.1
AP009380	PGN_t0018	tRNA-Leu		750654	750737	84	reverse	0.306	-1.708	0.000	0.003	0.472	-3.622	tRNA		
AP009380	PGN_0691	conserved hypothetical protein		750904	751206	303	reverse	1.904	0.929	0.036	0.103	0.443	2.095	CDS	GI:188594235	BAG33210.1
AP009380	PGN_0692	phosphoserine phosphatase		751218	752459	1242	reverse	1.977	0.983	0.022	0.073	0.428	2.295	CDS	GI:188594236	BAG33211.1
AP009380	PGN_0693	conserved hypothetical protein		752518	753690	1173	reverse	1.618	0.694	0.088	0.196	0.407	1.704	CDS	GI:188594237	BAG33212.1
AP009380	PGN_0694	50S ribosomal protein L34	rpmH	753943	754095	153	reverse	0.732	-0.449	0.065	0.155	0.244	-1.842	CDS	GI:188594238	BAG33213.1
AP009380	PGN_0695	probable septum formation protein Maf		754157	754756	600	reverse	1.078	0.109	0.609	0.723	0.213	0.511	CDS	GI:188594239	BAG33214.1
AP009380	PGN_0696	probable hydrolase		754796	755317	522	reverse	1.140	0.189	0.343	0.494	0.200	0.947	CDS	GI:188594240	BAG33215.1
AP009380	PGN_0697	conserved hypothetical protein		755334	756146	813	reverse	1.018	0.026	0.922	0.951	0.266	0.098	CDS	GI:188594241	BAG33216.1
AP009380	PGN_0698	probable nitroreductase		756139	756693	555	reverse	0.718	-0.479	0.178	0.312	0.355	-1.347	CDS	GI:188594242	BAG33217.1
AP009380	PGN_0699	conserved hypothetical protein		756915	757124	210	forward	0.874	-0.195	0.713	0.804	0.529	-0.368	CDS	GI:188594243	BAG33218.1
AP009380	PGN_0700	putative oxidoreductase Gfo/Idh/MocA family		757343	758830	1488	forward	1.623	0.699	0.005	0.027	0.249	2.810	CDS	GI:188594244	BAG33219.1
AP009380	PGN_0701	beta-galactosidase	lacZI	758844	762215	3372	forward	1.735	0.795	0.021	0.072	0.345	2.305	CDS	GI:188594245	BAG33220.1
AP009380	PGN_0702	conserved hypothetical protein		762298	763386	1089	forward	1.577	0.658	0.111	0.227	0.412	1.594	CDS	GI:188594246	BAG33221.1
AP009380	PGN_0703	hypothetical protein		763542	764468	927	forward	2.823	1.497	0.001	0.009	0.458	3.272	CDS	GI:188594247	BAG33222.1
AP009380	PGN_0704	putative tonB-linked outer membrane receptor		764983	767256	2274	forward	1.229	0.298	0.103	0.216	0.182	1.633	CDS	GI:188594248	BAG33223.1
AP009380	PGN_0705	heme-binding protein FetB		767285	768166	882	forward	1.202	0.265	0.394	0.536	0.311	0.852	CDS	GI:188594249	BAG33224.1
AP009380	PGN_0706	putative exported periplasmic protein		768284	769423	1140	forward	1.490	0.575	0.131	0.254	0.381	1.510	CDS	GI:188594250	BAG33225.1
AP009380	PGN_0707	putative iron compound ABC transporter permease protein		769420	770490	1071	forward	1.647	0.720	0.028	0.086	0.327	2.201	CDS	GI:188594251	BAG33226.1
AP009380	PGN_0708	putative iron compound ABC transporter ATP-binding protein		770534	771292	759	forward	1.835	0.876	0.002	0.016	0.288	3.040	CDS	GI:188594252	BAG33227.1
AP009380	PGN_0709	putative indolepyruvate ferredoxin oxidoreductase beta subunit		771684	772277	594	reverse	1.522	0.606	0.042	0.115	0.299	2.030	CDS	GI:188594253	BAG33228.1
AP009380	PGN_0710	indolepyruvate ferredoxin oxidoreductase alpha subunit		772304	773911	1608	reverse	1.672	0.741	0.005	0.028	0.267	2.782	CDS	GI:188594254	BAG33229.1
AP009380	PGN_0711	putative oxidoreductase short chain dehydrogenase/reductase family		773989	774750	762	reverse	1.358	0.441	0.036	0.102	0.210	2.102	CDS	GI:188594255	BAG33230.1
AP009380	PGN_0712	conserved hypothetical protein		774861	774998	138	reverse	0.532	-0.910	0.106	0.219	0.563	-1.617	CDS	GI:188594256	BAG33231.1
AP009380	PGN_0713	saccharopine dehydrogenase		775178	776371	1194	forward	1.155	0.208	0.377	0.520	0.236	0.883	CDS	GI:188594257	BAG33232.1
AP009380	PGN_0714	probable pyrazinamidase/nicotinamidase		776408	776920	513	forward	1.172	0.229	0.437	0.575	0.294	0.778	CDS	GI:188594258	BAG33233.1
AP009380	PGN_0715	outer membrane efflux protein		777123	778457	1335	forward	0.508	-0.977	0.011	0.046	0.384	-2.547	CDS	GI:188594259	BAG33234.1
AP009380	PGN_0716	ABC transporter permease		778497	779750	1254	forward	0.712	-0.491	0.193	0.332	0.377	-1.302	CDS	GI:188594260	BAG33235.1
AP009380	PGN_0717	conserved hypothetical protein		779851	780198	348	reverse	0.547	-0.871	0.068	0.160	0.478	-1.822	CDS	GI:188594261	BAG33236.1
AP009380	PGN_0718	putative ABC transporter permease protein		780400	782751	2352	forward	0.474	-1.078	0.000	0.002	0.287	-3.749	CDS	GI:188594262	BAG33237.1
AP009380	PGN_0719	probable ABC transporter permease protein		782790	785159	2370	forward	0.551	-0.860	0.001	0.006	0.254	-3.390	CDS	GI:188594263	BAG33238.1
AP009380	PGN_0720	putative ABC transporter permease protein		785186	787561	2376	forward	0.576	-0.795	0.007	0.034	0.297	-2.679	CDS	GI:188594264	BAG33239.1
AP009380	PGN_0721	putative ABC transporter ATP-binding protein		787654	788313	660	forward	0.505	-0.985	0.000	0.000	0.225	-4.379	CDS	GI:188594265	BAG33240.1
AP009380	PGN_0722	conserved hypothetical protein		788619	790172	1554	reverse	0.969	-0.046	0.800	0.866	0.181	-0.253	CDS	GI:188594266	BAG33241.1
AP009380	PGN_0723	succinate-semialdehyde dehydrogenase		790656	792011	1356	reverse	2.507	1.326	0.002	0.012	0.420	3.154	CDS	GI:188594267	BAG33242.1
AP009380	PGN_0724	NAD-dependent 4-hydroxybutyrate dehydrogenase		792207	793322	1116	reverse	1.206	0.270	0.371	0.514	0.302	0.894	CDS	GI:188594268	BAG33243.1
AP009380	PGN_0725	4-hydroxybutyrate CoA-transferase		793373	794668	1296	reverse	1.215	0.281	0.332	0.482	0.289	0.970	CDS	GI:188594269	BAG33244.1
AP009380	PGN_0726	conserved hypothetical protein		794674	794958	285	reverse	0.991	-0.014	0.958	0.970	0.256	-0.053	CDS	GI:188594270	BAG33245.1
AP009380	PGN_0727	4-hydroxybutyryl-CoA dehydratase		795031	796491	1461	reverse	0.695	-0.525	0.046	0.122	0.264	-1.992	CDS	GI:188594271	BAG33246.1
AP009380	PGN_0728	outer membrane protein 40 precursor		797192	798334	1143	reverse	0.576	-0.795	0.029	0.090	0.364	-2.182	CDS	GI:188594272	BAG33247.1
AP009380	PGN_0729	outer membrane protein 41 precursor		798381	799556	1176	reverse	0.520	-0.943	0.003	0.018	0.318	-2.968	CDS	GI:188594273	BAG33248.1
AP009380	PGN_0730	hypothetical protein		799607	799699	93	reverse	0.413	-1.274	0.000	0.003	0.352	-3.618	CDS	GI:188594274	BAG33249.1
AP009380	PGN_0731	hypothetical protein		799718	799843	126	reverse	1.116	0.158	0.499	0.633	0.234	0.676	CDS	GI:188594275	BAG33250.1
AP009380	PGN_0732	conserved hypothetical protein		799865	800848	984	reverse	1.097	0.133	0.471	0.609	0.185	0.720	CDS	GI:188594276	BAG33251.1
AP009380	PGN_0733	alpha-glucan phosphorylase		800880	803450	2571	reverse	1.170	0.227	0.261	0.407	0.202	1.124	CDS	GI:188594277	BAG33252.1
AP009380	PGN_0734	conserved hypothetical protein		803660	804028	369	reverse	0.428	-1.225	0.009	0.041	0.471	-2.600	CDS	GI:188594278	BAG33253.1
AP009380	PGN_0735	putative bifunctional cobalamin biosynthesis protein		804054	804590	537	forward	0.757	-0.402	0.155	0.284	0.283	-1.421	CDS	GI:188594279	BAG33254.1
AP009380	PGN_0736	putative nicotinate-nucleotide-dimethylbenzimidazole phosphoribosyltransferase		804643	805680	1038	forward	0.752	-0.412	0.170	0.303	0.300	-1.373	CDS	GI:188594280	BAG33255.1
AP009380	PGN_0737	probable cobalamin-5'-phosphate synthase		805687	806469	783	forward	0.841	-0.250	0.391	0.532	0.291	-0.858	CDS	GI:188594281	BAG33256.1
AP009380	PGN_0738	putative phosphoglycerate mutase		806471	807010	540	forward	0.752	-0.412	0.122	0.242	0.267	-1.545	CDS	GI:188594282	BAG33257.1
AP009380	PGN_0739	glutamate racemase		807072	807896	825	forward	0.801	-0.319	0.164	0.294	0.229	-1.393	CDS	GI:188594283	BAG33258.1
AP009380	PGN_0740	conserved hypothetical protein		807914	808345	432	forward	0.627	-0.673	0.018	0.064	0.284	-2.371	CDS	GI:188594284	BAG33259.1
AP009380	PGN_0741	TonB-dependent receptor		808579	811125	2547	reverse	0.607	-0.720	0.009	0.041	0.276	-2.607	CDS	GI:188594285	BAG33260.1
AP009380	PGN_0742	probable FKBP-type peptidyl-prolyl cis-trans isomerase		811291	812121	831	reverse	1.577	0.657	0.075	0.171	0.368	1.783	CDS	GI:188594286	BAG33261.1
AP009380	PGN_0743	probable FKBP-type peptidyl-prolyl cis-trans isomerase FkpA		812149	812922	774	reverse	0.792	-0.336	0.193	0.332	0.258	-1.302	CDS	GI:188594287	BAG33262.1
AP009380	PGN_0744	probable FKBP-type peptidyl-prolyl cis-trans isomerase		812943	813527	585	reverse	0.845	-0.243	0.318	0.468	0.244	-0.998	CDS	GI:188594288	BAG33263.1
AP009380	PGN_0745	hypothetical protein		813613	813744	132	forward	0.535	-0.903	0.012	0.048	0.359	-2.512	CDS	GI:188594289	BAG33264.1
AP009380	PGN_0746	conserved hypothetical protein		814254	814601	348	reverse	1.293	0.371	0.333	0.483	0.383	0.968	CDS	GI:188594290	BAG33265.1
AP009380	PGN_0747	probable anthranilate synthase component II		814623	815219	597	reverse	1.147	0.198	0.597	0.714	0.375	0.528	CDS	GI:188594291	BAG33266.1
AP009380	PGN_0748	gingipain-sensitive ligand A	gslA	815845	820437	4593	forward	0.372	-1.425	0.000	0.004	0.399	-3.575	CDS	GI:188594292	BAG33267.1
AP009380	PGN_0749	transposase in ISPg1		821642	822727	1086	forward	0.638	-0.648	0.150	0.278	0.450	-1.438	CDS	GI:188594293	BAG33268.1
AP009380	PGN_0750	putative copper homeostasis protein CutC		823067	823813	747	reverse	1.212	0.278	0.230	0.372	0.231	1.199	CDS	GI:188594294	BAG33269.1
AP009380	PGN_0751	putative cationic transporter		823818	824738	921	reverse	1.438	0.524	0.036	0.103	0.250	2.094	CDS	GI:188594295	BAG33270.1
AP009380	PGN_0752	hypothetical protein		825133	825297	165	reverse	0.470	-1.089	0.002	0.013	0.350	-3.114	CDS	GI:188594296	BAG33271.1
AP009380	PGN_0753	probable two component system response regulator		825294	826031	738	reverse	0.445	-1.170	0.001	0.005	0.336	-3.480	CDS	GI:188594297	BAG33272.1

AP009380	PGN_0754	conserved hypothetical protein		826263	826871	609	forward	1.082	0.114	0.600	0.715	0.217	0.524	CDS	GI:188594298	BAG33273.1
AP009380	PGN_0755	hypothetical protein		826991	827188	198	forward	1.440	0.527	0.167	0.299	0.381	1.382	CDS	GI:188594299	BAG33274.1
AP009380	PGN_0756	prolyl oligopeptidase		827536	829590	2055	forward	1.575	0.655	0.006	0.029	0.237	2.759	CDS	GI:188594300	BAG33275.1
AP009380	PGN_0757	conserved hypothetical protein		829675	830301	627	forward	1.503	0.588	0.017	0.062	0.246	2.387	CDS	GI:188594301	BAG33276.1
AP009380	PGN_0758	conserved hypothetical protein		830368	830757	390	reverse	2.925	1.548	0.003	0.016	0.513	3.020	CDS	GI:188594302	BAG33277.1
AP009380	PGN_0759	conserved hypothetical protein		831006	832166	1161	reverse	1.467	0.553	0.106	0.219	0.342	1.618	CDS	GI:188594303	BAG33278.1
AP009380	PGN_0760	putative D-alanine--D-alanine ligase		832191	833183	993	reverse	1.344	0.427	0.174	0.307	0.314	1.361	CDS	GI:188594304	BAG33279.1
AP009380	PGN_0761	ribosomal large subunit pseudouridine synthase		833250	834347	1098	reverse	1.073	0.102	0.643	0.750	0.221	0.463	CDS	GI:188594305	BAG33280.1
AP009380	PGN_0762	conserved hypothetical protein		834385	835041	657	reverse	0.900	-0.152	0.540	0.666	0.248	-0.613	CDS	GI:188594306	BAG33281.1
AP009380	PGN_0763	conserved hypothetical protein		835036	835353	318	forward	0.648	-0.625	0.097	0.209	0.377	-1.658	CDS	GI:188594307	BAG33282.1
AP009380	PGN_0764	putative riboflavin synthase alpha subunit		835634	836236	603	forward	1.474	0.559	0.020	0.068	0.240	2.333	CDS	GI:188594308	BAG33283.1
AP009380	PGN_0765	probable nitroreductase		836233	836784	552	forward	1.687	0.754	0.002	0.016	0.249	3.032	CDS	GI:188594309	BAG33284.1
AP009380	PGN_0766	aminotransferase class V		836843	838057	1215	forward	2.431	1.282	0.001	0.005	0.368	3.480	CDS	GI:188594310	BAG33285.1
AP009380	PGN_0767	putative ribonuclease HII		838068	838673	606	forward	1.886	0.915	0.016	0.059	0.379	2.413	CDS	GI:188594311	BAG33286.1
AP009380	PGN_0768	conserved hypothetical protein		838648	838926	279	forward	1.098	0.135	0.630	0.739	0.280	0.482	CDS	GI:188594312	BAG33287.1
AP009380	PGN_0769	putative cytosine/adenosine deaminase		838923	839375	453	forward	1.411	0.496	0.106	0.219	0.307	1.616	CDS	GI:188594313	BAG33288.1
AP009380	PGN_0770	conserved hypothetical protein		839407	840321	915	forward	1.421	0.507	0.063	0.151	0.273	1.861	CDS	GI:188594314	BAG33289.1
AP009380	PGN_0771	conserved hypothetical protein		840296	840865	570	forward	1.338	0.420	0.239	0.383	0.356	1.178	CDS	GI:188594315	BAG33290.1
AP009380	PGN_0772	probable tRNA/rRNA methyltransferase		841665	842429	765	reverse	1.665	0.736	0.015	0.056	0.301	2.444	CDS	GI:188594316	BAG33291.1
AP009380	PGN_0773	putative lactoylglutathione lyase		842514	842912	399	reverse	1.552	0.634	0.067	0.157	0.346	1.832	CDS	GI:188594317	BAG33292.1
AP009380	PGN_0774	two-component system sensor histidine kinase		843068	844405	1338	reverse	1.796	0.845	0.004	0.021	0.290	2.913	CDS	GI:188594318	BAG33293.1
AP009380	PGN_0775	two-component system response regulator		844431	845825	1395	reverse	1.277	0.353	0.255	0.401	0.310	1.139	CDS	GI:188594319	BAG33294.1
AP009380	PGN_0776	conserved hypothetical protein		846070	846186	117	reverse	0.697	-0.522	0.227	0.369	0.432	-1.208	CDS	GI:188594320	BAG33295.1
AP009380	PGN_t0019	tRNA-Arg		846341	846417	77	reverse	0.370	-1.435	0.001	0.011	0.450	-3.189	tRNA		
AP009380	PGN_0777	probable glycosyl transferase		846478	847224	747	reverse	1.335	0.417	0.058	0.143	0.220	1.894	CDS	GI:188594321	BAG33296.1
AP009380	PGN_0778	Por secretion system protein porT/sprT	porT	847377	848111	735	reverse	1.888	0.917	0.000	0.000	0.217	4.216	CDS	GI:188594322	BAG33297.1
AP009380	PGN_0779	probable uracil phosphoribosyltransferase		848250	848900	651	forward	1.321	0.401	0.116	0.234	0.255	1.571	CDS	GI:188594323	BAG33298.1
AP009380	PGN_0780	PrtQ, protease	prtQ	848884	850791	1908	forward	0.768	-0.380	0.155	0.284	0.267	-1.423	CDS	GI:188594324	BAG33299.1
AP009380	PGN_0781	DNA topoisomerase I		851527	853893	2367	forward	1.439	0.525	0.111	0.227	0.329	1.594	CDS	GI:188594325	BAG33300.1
AP009380	PGN_0782	putative tRNA pseudouridine synthase A		853897	854655	759	forward	0.979	-0.030	0.921	0.951	0.303	-0.100	CDS	GI:188594326	BAG33301.1
AP009380	PGN_0783	putative DNA-binding protein histone-like family		855387	855869	483	forward	0.666	-0.587	0.084	0.188	0.340	-1.726	CDS	GI:188594327	BAG33302.1
AP009380	PGN_0784	hypothetical protein		856085	857338	1254	forward	0.606	-0.723	0.044	0.118	0.359	-2.015	CDS	GI:188594328	BAG33303.1
AP009380	PGN_0785	hypothetical protein		857556	857897	342	forward	1.485	0.570	0.214	0.357	0.460	1.241	CDS	GI:188594329	BAG33304.1
AP009380	PGN_0786	conserved hypothetical protein		858011	859363	1353	reverse	2.268	1.182	0.008	0.037	0.447	2.646	CDS	GI:188594330	BAG33305.1
AP009380	PGN_0787	conserved hypothetical protein		859413	860060	648	reverse	2.095	1.067	0.013	0.050	0.427	2.497	CDS	GI:188594331	BAG33306.1
AP009380	PGN_0788	peptidyl-dipeptidase		860157	862283	2127	reverse	1.225	0.293	0.386	0.529	0.338	0.867	CDS	GI:188594332	BAG33307.1
AP009380	PGN_0789	conserved hypothetical protein		862322	864460	2139	reverse	1.261	0.335	0.170	0.303	0.244	1.373	CDS	GI:188594333	BAG33308.1
AP009380	PGN_0790	transposase in ISPg3		864734	865636	903	forward	0.667	-0.583	0.096	0.207	0.351	-1.662	CDS	GI:188594334	BAG33309.1
AP009380	PGN_0791	putative cell division trigger factor		866097	867569	1473	forward	1.813	0.859	0.018	0.065	0.363	2.367	CDS	GI:188594335	BAG33310.1
AP009380	PGN_0792	polyribonucleotide nucleotidyltransferase		868221	870545	2325	reverse	1.323	0.403	0.144	0.269	0.276	1.460	CDS	GI:188594336	BAG33311.1
AP009380	PGN_0793	4-alpha-glucanotransferase		870605	873298	2694	reverse	1.226	0.294	0.192	0.331	0.225	1.305	CDS	GI:188594337	BAG33312.1
AP009380	PGN_0794	conserved hypothetical protein		873323	874429	1107	reverse	1.091	0.125	0.623	0.733	0.254	0.492	CDS	GI:188594338	BAG33313.1
AP009380	PGN_0795	conserved hypothetical protein		874603	876744	2142	reverse	1.251	0.323	0.397	0.538	0.381	0.847	CDS	GI:188594339	BAG33314.1
AP009380	PGN_0796	hypothetical protein		877005	877154	150	forward	0.286	-1.805	0.002	0.014	0.587	-3.075	CDS	GI:188594340	BAG33315.1
AP009380	PGN_0797	conserved hypothetical protein		877161	877298	138	forward	0.465	-1.105	0.060	0.146	0.588	-1.880	CDS	GI:188594341	BAG33316.1
AP009380	PGN_0798	conserved hypothetical protein		877785	878915	1131	reverse	1.022	0.032	0.901	0.940	0.257	0.125	CDS	GI:188594342	BAG33317.1
AP009380	PGN_t0020	tRNA-Pro		879184	879261	78	forward	0.383	-1.383	0.000	0.000	0.317	-4.369	tRNA		
AP009380	PGN_0799	putative acyl-CoA dehydrogenase		879406	881127	1722	reverse	1.137	0.185	0.415	0.553	0.226	0.816	CDS	GI:188594343	BAG33318.1
AP009380	PGN_0800	putative electron transfer flavoprotein alpha subunit		881139	882158	1020	reverse	0.992	-0.012	0.958	0.970	0.219	-0.053	CDS	GI:188594344	BAG33319.1
AP009380	PGN_0801	probable electron transfer flavoprotein beta subunit		882167	883033	867	reverse	1.011	0.015	0.930	0.955	0.176	0.087	CDS	GI:188594345	BAG33320.1
AP009380	PGN_0802	probable glycoprotease		883124	883843	720	reverse	0.829	-0.271	0.155	0.284	0.191	-1.421	CDS	GI:188594346	BAG33321.1
AP009380	PGN_0803	conserved hypothetical protein		884073	884546	474	reverse	1.399	0.484	0.048	0.125	0.245	1.975	CDS	GI:188594347	BAG33322.1
AP009380	PGN_0804	conserved hypothetical protein		884562	885176	615	reverse	1.399	0.484	0.067	0.157	0.264	1.832	CDS	GI:188594348	BAG33323.1
AP009380	PGN_0805	conserved hypothetical protein		885212	885682	471	reverse	1.438	0.524	0.063	0.151	0.282	1.860	CDS	GI:188594349	BAG33324.1
AP009380	PGN_0806	putative MotA/TolQ/ExbB proton channel protein		885691	886503	813	reverse	1.341	0.423	0.142	0.267	0.288	1.467	CDS	GI:188594350	BAG33325.1
AP009380	PGN_t0021	tRNA-Ser		886571	886658	88	reverse	0.511	-0.968	0.000	0.003	0.262	-3.699	tRNA		
AP009380	PGN_0807	putative DNAse related protein		886851	887678	828	reverse	1.859	0.894	0.013	0.052	0.361	2.475	CDS	GI:188594351	BAG33326.1
AP009380	PGN_0808	probable isoprenyl synthetase		887725	888702	978	reverse	1.409	0.495	0.176	0.309	0.366	1.353	CDS	GI:188594352	BAG33327.1
AP009380	PGN_0809	putative TonB protein		888873	889565	693	reverse	1.166	0.222	0.253	0.399	0.194	1.142	CDS	GI:188594353	BAG33328.1
AP009380	PGN_0810	conserved hypothetical protein		889699	889941	243	forward	1.521	0.605	0.182	0.317	0.453	1.336	CDS	GI:188594354	BAG33329.1
AP009380	PGN_0811	conserved hypothetical protein		890017	892635	2619	reverse	2.149	1.103	0.007	0.033	0.409	2.696	CDS	GI:188594355	BAG33330.1
AP009380	PGN_0812	conserved hypothetical protein		892676	893392	717	reverse	1.358	0.442	0.193	0.331	0.339	1.303	CDS	GI:188594356	BAG33331.1
AP009380	PGN_0813	GTP-binding protein		893373	894557	1185	reverse	1.305	0.384	0.051	0.130	0.197	1.952	CDS	GI:188594357	BAG33332.1
AP009380	PGN_0814	probable adenylate kinase		894567	895151	585	reverse	1.251	0.323	0.110	0.226	0.202	1.596	CDS	GI:188594358	BAG33333.1
AP009380	PGN_0815	putative hypoxanthine phosphoribosyltransferase		895152	895688	537	reverse	1.432	0.518	0.035	0.101	0.246	2.107	CDS	GI:188594359	BAG33334.1
AP009380	PGN_0816	fructose-1,6-bisphosphatase		896282	898279	1998	forward	1.140	0.190	0.476	0.613	0.266	0.713	CDS	GI:188594360	BAG33335.1
AP009380	PGN_0817	penicillin-binding protein 1A		898435	900789	2355	forward	1.820	0.864	0.012	0.048	0.342	2.523	CDS	GI:188594361	BAG33336.1
AP009380	PGN_0818	conserved hypothetical protein		900837	901547	711	forward	1.969	0.977	0.001	0.009	0.300	3.260	CDS	GI:188594362	BAG33337.1
AP009380	PGN_0819	leucyl-tRNA synthetase		901712	904489	2778	reverse	0.791	-0.338	0.082	0.183	0.194	-1.742	CDS	GI:188594363	BAG33338.1
AP009380	PGN_0820	hypothetical protein		904586	904750	165	forward	0.592	-0.756	0.006	0.029	0.273	-2.767	CDS	GI:188594364	BAG33339.1
AP009380	PGN_0821	hypothetical protein		905494	905643	150	reverse	0.717	-0.480	0.383	0.525	0.549	-0.873	CDS	GI:188594365	BAG33340.1
AP009380	PGN_0822	conserved hypothetical protein		905691	905876	186	forward	0.411	-1.283	0.012	0.048	0.509	-2.519	CDS	GI:188594366	BAG33341.1
AP009380	PGN_t0022	tRNA-Gly		905888	905960	73	reverse	0.359	-1.476	0.001	0.010	0.458	-3.220	tRNA		
AP009380	PGN_0823	NAD-utilizing dehydrogenases		906026	907585	1560	reverse	1.052	0.073	0.746	0.825	0.225	0.324	CDS	GI:188594367	BAG33342.1
AP009380	PGN_0824	tRNA nucleotidyltransferase		907570	909021	1452	reverse	1.085	0.118	0.579	0.699	0.212	0.555	CDS	GI:188594368	BAG33343.1
AP009380	PGN_0825	conserved hypothetical protein		909154	909384	231	reverse	1.509	0.593	0.185	0.321	0.447	1.326	CDS	GI:188594369	BAG33344.1
AP009380	PGN_0826	dihydrolipoamide dehydrogenase		909661	911010	1350	reverse	1.503	0.588	0.132	0.256	0.391	1.505	CDS	GI:188594370	BAG33345.1
AP009380	PGN_0827	glucosamine-6-phosphate isomerase		911015	911806	792	reverse	1.810	0.856	0.036	0.102	0.407	2.102	CDS	GI:188594371	BAG33346.1
AP009380	PGN_0828	flavoprotein		911844	913055	1212	reverse	1.543	0.625	0.088	0.194	0.366	1.708	CDS	GI:188594372	BAG33347.1
AP009380	PGN_0829	putative prolipoprotein diacylglyceryl transferase		913086	913937	852	reverse	1.447	0.533	0.127	0.249	0.350	1.525	CDS	GI:188594373	BAG33348.1
AP009380	PGN_0830	meso-diaminopimelate D-dehydrogenase		913974	914879	906	reverse	1.461	0.547	0.069	0.161	0.300	1.819	CDS	GI:188594374	BAG33349.1
AP009380	PGN_0831	probable nitrogen utilization substance protein		914917	915963	1047	reverse	1.403	0.488	0.063	0.151	0.263	1.858	CDS	GI:188594375	BAG33350.1
AP009380	PGN_0832	Por secretion system protein sov/gliding motility protein SprA	sov	916648	924147	7500	reverse	1.740	0.799	0.009	0.041	0.307	2.606	CDS	GI:188594376	BAG33351.1
AP009380	PGN_0833	probable Holliday junction DNA helicase RuvA	ruvA	924187	924795	609	reverse	1.123	0.167	0.403	0.543	0.200	0.837	CDS	GI:188594377	BAG33352.1
AP009380	PGN_0834	transposase in ISPg1		925239	926324	1086	reverse	0.771	-0.374	0.401	0.541	0.445	-0.840	CDS	GI:188594378	BAG33353.1
AP009380	PGN_0835	conserved hypothetical protein		926428	926592	165	reverse	0.630	-0.667	0.073	0.167	0.372	-1.795	CDS	GI:188594379	BAG33354.1
AP009380	PGN_0836	conserved hypothetical protein		926879	929554	2676	reverse	0.535	-0.902	0.031	0.093	0.417	-2.160	CDS	GI:188594380	BAG33355.1

AP009380	PGN_0837	conserved hypothetical protein		929571	930287	717	reverse	0.565	-0.823	0.082	0.184	0.473	-1.738	CDS	GI:188594381	BAG33356.1
AP009380	PGN_0838	conserved hypothetical protein		930384	930596	213	reverse	0.527	-0.925	0.059	0.144	0.490	-1.887	CDS	GI:188594382	BAG33357.1
AP009380	PGN_0839	transposase in ISPg2		930874	931980	1107	reverse	1.483	0.569	0.122	0.242	0.368	1.546	CDS	GI:188594383	BAG33358.1
AP009380	PGN_0840	conserved hypothetical protein		932089	932283	195	forward	0.662	-0.595	0.098	0.210	0.360	-1.653	CDS	GI:188594384	BAG33359.1
AP009380	PGN_0841	putative 4-diphosphocytidyl-2C-methyl-D-erythritol synthase		932280	932948	669	forward	0.771	-0.375	0.205	0.345	0.296	-1.268	CDS	GI:188594385	BAG33360.1
AP009380	PGN_t0023	tRNA-Asp		933331	933407	77	forward	0.416	-1.266	0.004	0.021	0.435	-2.907	tRNA		
AP009380	PGN_0842	transposase in ISPg1		933734	934819	1086	reverse	0.634	-0.658	0.145	0.270	0.451	-1.457	CDS	GI:188594386	BAG33361.1
AP009380	PGN_0843	conserved hypothetical protein		935043	935576	534	forward	0.570	-0.812	0.002	0.015	0.266	-3.050	CDS	GI:188594387	BAG33362.1
AP009380	PGN_0844	conserved hypothetical protein		935603	936061	459	forward	0.486	-1.041	0.005	0.027	0.371	-2.803	CDS	GI:188594388	BAG33363.1
AP009380	PGN_0845	conserved hypothetical protein		936419	936778	360	forward	0.494	-1.019	0.040	0.111	0.496	-2.054	CDS	GI:188594389	BAG33364.1
AP009380	PGN_0846	conserved hypothetical protein		936785	937306	522	forward	0.605	-0.724	0.055	0.137	0.378	-1.918	CDS	GI:188594390	BAG33365.1
AP009380	PGN_0847	conserved hypothetical protein		937319	937546	228	forward	0.630	-0.667	0.052	0.132	0.344	-1.939	CDS	GI:188594391	BAG33366.1
AP009380	PGN_0848	conserved hypothetical protein		937569	937850	282	forward	0.577	-0.793	0.015	0.057	0.326	-2.432	CDS	GI:188594392	BAG33367.1
AP009380	PGN_0849	conserved hypothetical protein		937863	938165	303	forward	0.516	-0.954	0.005	0.027	0.340	-2.805	CDS	GI:188594393	BAG33368.1
AP009380	PGN_0850	conserved hypothetical protein		938178	938309	132	forward	0.845	-0.243	0.444	0.583	0.318	-0.765	CDS	GI:188594394	BAG33369.1
AP009380	PGN_0851	conserved hypothetical protein		938363	938593	231	forward	0.770	-0.378	0.116	0.235	0.241	-1.570	CDS	GI:188594395	BAG33370.1
AP009380	PGN_0852	immunoreactive 47 kDa antigen		938887	940173	1287	reverse	0.688	-0.540	0.029	0.090	0.248	-2.180	CDS	GI:188594396	BAG33371.1
AP009380	PGN_0853	conserved hypothetical protein		940236	940346	111	forward	0.581	-0.782	0.023	0.076	0.345	-2.269	CDS	GI:188594397	BAG33372.1
AP009380	PGN_0854	hypothetical protein		941025	941138	114	reverse	0.616	-0.700	0.003	0.018	0.236	-2.970	CDS	GI:188594398	BAG33373.1
AP009380	PGN_0855	hypothetical protein		941192	941329	138	reverse	0.689	-0.537	0.227	0.369	0.445	-1.207	CDS	GI:188594399	BAG33374.1
AP009380	PGN_0856	putative A/G-specific adenine glycosylase		941353	942576	1224	reverse	1.214	0.280	0.262	0.409	0.250	1.121	CDS	GI:188594400	BAG33375.1
AP009380	PGN_0857	conserved hypothetical protein		942626	943564	939	forward	0.898	-0.155	0.441	0.579	0.201	-0.771	CDS	GI:188594401	BAG33376.1
AP009380	PGN_0858	probable ABC transporter ATP-binding protein		943616	944314	699	forward	1.343	0.426	0.104	0.218	0.262	1.626	CDS	GI:188594402	BAG33377.1
AP009380	PGN_0859	probable ABC transporter permease protein		944311	945060	750	forward	1.322	0.403	0.162	0.292	0.288	1.400	CDS	GI:188594403	BAG33378.1
AP009380	PGN_0860	conserved hypothetical protein		945110	946159	1050	forward	2.682	1.423	0.001	0.006	0.417	3.409	CDS	GI:188594404	BAG33379.1
AP009380	PGN_0861	conserved hypothetical protein		946343	946996	654	forward	0.910	-0.135	0.492	0.628	0.197	-0.687	CDS	GI:188594405	BAG33380.1
AP009380	PGN_0862	Type III restriction enzyme, res subunit		947073	949814	2742	reverse	1.222	0.289	0.268	0.415	0.261	1.107	CDS	GI:188594406	BAG33381.1
AP009380	PGN_0863	DNA methylase N-4/N-6		949807	951441	1635	reverse	0.969	-0.046	0.819	0.880	0.201	-0.229	CDS	GI:188594407	BAG33382.1
AP009380	PGN_0864	transposase in ISPg3		951638	952540	903	forward	0.680	-0.556	0.092	0.201	0.330	-1.686	CDS	GI:188594408	BAG33383.1
AP009380	PGN_0865	bifunctional phosphoribosylaminoimidazolecarboxamide formyltransferase/IMP cyclohydrolas		952701	954218	1518	forward	0.619	-0.692	0.043	0.116	0.342	-2.025	CDS	GI:188594409	BAG33384.1
AP009380	PGN_0866	cell shape-determining protein MreB		954321	955340	1020	forward	0.933	-0.100	0.706	0.798	0.264	-0.378	CDS	GI:188594410	BAG33385.1
AP009380	PGN_0867	probable cell shape-determining protein MreC		955378	956265	888	forward	1.542	0.625	0.012	0.048	0.248	2.521	CDS	GI:188594411	BAG33386.1
AP009380	PGN_0868	conserved hypothetical protein		956265	956783	519	forward	2.091	1.064	0.000	0.002	0.285	3.738	CDS	GI:188594412	BAG33387.1
AP009380	PGN_0869	penicillin-binding protein 2		956776	958641	1866	forward	1.506	0.591	0.046	0.122	0.297	1.993	CDS	GI:188594413	BAG33388.1
AP009380	PGN_0870	putative rod shape-determining protein RodA		958631	960088	1458	forward	1.446	0.533	0.057	0.140	0.280	1.904	CDS	GI:188594414	BAG33389.1
AP009380	PGN_0871	conserved hypothetical protein		960116	961327	1212	reverse	0.845	-0.243	0.242	0.386	0.207	-1.171	CDS	GI:188594415	BAG33390.1
AP009380	PGN_0872	DNA-binding protein histone-like family		961559	962017	459	forward	0.957	-0.063	0.847	0.902	0.325	-0.193	CDS	GI:188594416	BAG33391.1
AP009380	PGN_0873	conserved hypothetical protein		962082	962792	711	forward	0.988	-0.018	0.957	0.970	0.337	-0.053	CDS	GI:188594417	BAG33392.1
AP009380	PGN_0874	conserved hypothetical protein		962829	963755	927	forward	1.242	0.312	0.279	0.427	0.289	1.082	CDS	GI:188594418	BAG33393.1
AP009380	PGN_0875	DNA gyrase A subunit	gyrA	963939	966518	2580	forward	1.550	0.632	0.004	0.021	0.217	2.913	CDS	GI:188594419	BAG33394.1
AP009380	PGN_0876	TPR domain protein		966552	967754	1203	forward	1.751	0.808	0.010	0.043	0.314	2.575	CDS	GI:188594420	BAG33395.1
AP009380	PGN_0877	SNF2-related helicase		968346	971243	2898	forward	1.079	0.110	0.725	0.809	0.313	0.352	CDS	GI:188594421	BAG33396.1
AP009380	PGN_0878	hypothetical protein		971275	971727	453	forward	1.750	0.808	0.043	0.116	0.399	2.025	CDS	GI:188594422	BAG33397.1
AP009380	PGN_0879	transposase in ISPg3		971813	972715	903	reverse	0.804	-0.314	0.286	0.434	0.295	-1.067	CDS	GI:188594423	BAG33398.1
AP009380	PGN_0880	tyrosine phenol-lyase		973197	974576	1380	reverse	1.163	0.218	0.489	0.626	0.316	0.691	CDS	GI:188594424	BAG33399.1
AP009380	PGN_0881	conserved hypothetical protein		974829	975956	1128	reverse	1.721	0.783	0.054	0.135	0.407	1.926	CDS	GI:188594425	BAG33400.1
AP009380	PGN_0882	conserved hypothetical protein		975971	976837	867	reverse	2.004	1.003	0.008	0.037	0.378	2.652	CDS	GI:188594426	BAG33401.1
AP009380	PGN_0883	conserved hypothetical protein		976869	977585	717	reverse	1.799	0.847	0.042	0.114	0.416	2.037	CDS	GI:188594427	BAG33402.1
AP009380	PGN_0884	organic solvent tolerance protein OstA		977612	980467	2856	reverse	1.497	0.582	0.117	0.236	0.371	1.566	CDS	GI:188594428	BAG33403.1
AP009380	PGN_0885	probable nitroimidazole resistance protein		980940	981476	537	reverse	1.081	0.112	0.782	0.854	0.404	0.277	CDS	GI:188594429	BAG33404.1
AP009380	PGN_0886	putative cation efflux protein		981739	982704	966	forward	0.939	-0.090	0.725	0.809	0.256	-0.352	CDS	GI:188594430	BAG33405.1
AP009380	PGN_0887	conserved hypothetical protein		982701	983093	393	reverse	1.126	0.172	0.650	0.755	0.378	0.454	CDS	GI:188594431	BAG33406.1
AP009380	PGN_0888	conserved hypothetical protein		983139	983234	96	forward	1.186	0.246	0.521	0.651	0.383	0.642	CDS	GI:188594432	BAG33407.1
AP009380	PGN_0889	potassium uptake protein TrkA		983309	984994	1686	reverse	1.298	0.376	0.271	0.419	0.342	1.100	CDS	GI:188594433	BAG33408.1
AP009380	PGN_0890	putative TonB-dependent outer membrane receptor protein		986905	989508	2604	forward	0.965	-0.052	0.815	0.878	0.222	-0.234	CDS	GI:188594434	BAG33409.1
AP009380	PGN_0891	dioxygenase		989941	990882	942	forward	1.158	0.211	0.475	0.613	0.296	0.714	CDS	GI:188594435	BAG33410.1
AP009380	PGN_0892	hypothetical protein		990928	991068	141	forward	0.779	-0.360	0.264	0.411	0.322	-1.117	CDS	GI:188594436	BAG33411.1
AP009380	PGN_0893	fumarate hydratase class I anaerobic		991178	992824	1647	forward	1.474	0.559	0.100	0.212	0.340	1.644	CDS	GI:188594437	BAG33412.1
AP009380	PGN_0894	DNA polymerase III, gamma and tau subunits		992947	994755	1809	forward	1.026	0.037	0.879	0.925	0.244	0.153	CDS	GI:188594438	BAG33413.1
AP009380	PGN_0895	ferredoxin 4Fe-4S		995192	995362	171	reverse	0.367	-1.447	0.000	0.001	0.349	-4.147	CDS	GI:188594439	BAG33414.1
AP009380	PGN_0896	probable D-alanyl-D-alanine carboxypeptidase		995698	997200	1503	reverse	0.839	-0.253	0.348	0.497	0.270	-0.939	CDS	GI:188594440	BAG33415.1
AP009380	PGN_0897	conserved hypothetical protein		997197	997397	201	reverse	0.759	-0.397	0.344	0.494	0.420	-0.946	CDS	GI:188594441	BAG33416.1
AP009380	PGN_0898	probable peptidylarginine deiminase		997443	999113	1671	reverse	1.772	0.826	0.062	0.150	0.443	1.863	CDS	GI:188594442	BAG33417.1
AP009380	PGN_0899	conserved hypothetical protein		999285	999383	99	reverse	1.113	0.154	0.722	0.809	0.434	0.355	CDS	GI:188594443	BAG33418.1
AP009380	PGN_0900	thiol protease		1000329	1002860	2532	reverse	2.137	1.096	0.009	0.040	0.419	2.615	CDS	GI:188594444	BAG33419.1
AP009380	PGN_0901	putative riboflavin synthase beta subunit		1003000	1003485	486	reverse	1.761	0.816	0.034	0.100	0.386	2.117	CDS	GI:188594445	BAG33420.1
AP009380	PGN_0902	conserved hypothetical protein		1003577	1004263	687	reverse	1.025	0.036	0.902	0.941	0.296	0.123	CDS	GI:188594446	BAG33421.1
AP009380	PGN_0903	two-component system response regulator FimR	fimR	1004449	1005132	684	reverse	1.205	0.269	0.255	0.401	0.236	1.138	CDS	GI:188594447	BAG33422.1
AP009380	PGN_0904	two-component system sensor histidine kinase FimS	fimS	1005145	1007040	1896	reverse	0.889	-0.170	0.410	0.550	0.206	-0.823	CDS	GI:188594448	BAG33423.1
AP009380	PGN_0905	putative dihydroorotate dehydrogenase		1007223	1007921	699	reverse	0.789	-0.342	0.237	0.381	0.289	-1.183	CDS	GI:188594449	BAG33424.1
AP009380	PGN_0906	probable dihydroorotate dehydrogenase electron transfer subunit		1007957	1008754	798	reverse	0.871	-0.199	0.465	0.605	0.273	-0.730	CDS	GI:188594450	BAG33425.1
AP009380	PGN_0907	conserved hypothetical protein		1008806	1009246	441	reverse	0.756	-0.403	0.351	0.498	0.431	-0.933	CDS	GI:188594451	BAG33426.1
AP009380	PGN_0908	hypothetical protein		1010126	1010311	186	reverse	0.935	-0.098	0.868	0.917	0.589	-0.166	CDS	GI:188594452	BAG33427.1
AP009380	PGN_0909	transposase in ISPg3		1010418	1011320	903	reverse	0.727	-0.460	0.138	0.262	0.310	-1.482	CDS	GI:188594453	BAG33428.1
AP009380	PGN_0910	conserved hypothetical protein		1011518	1012690	1173	reverse	1.402	0.488	0.117	0.236	0.311	1.567	CDS	GI:188594454	BAG33429.1
AP009380	PGN_0911	putative ribonuclease H		1012705	1013355	651	reverse	0.992	-0.012	0.969	0.977	0.314	-0.038	CDS	GI:188594455	BAG33430.1
AP009380	PGN_0912	conserved hypothetical protein		1013383	1014384	1002	reverse	1.022	0.032	0.911	0.946	0.282	0.112	CDS	GI:188594456	BAG33431.1
AP009380	PGN_0913	putative acetyltransferase		1014409	1014948	540	reverse	0.835	-0.259	0.276	0.424	0.238	-1.090	CDS	GI:188594457	BAG33432.1
AP009380	PGN_0914	peptidase M24 family		1014957	1016744	1788	reverse	0.909	-0.137	0.484	0.621	0.196	-0.700	CDS	GI:188594458	BAG33433.1
AP009380	PGN_0915	conserved hypothetical protein		1016793	1018340	1548	reverse	0.709	-0.496	0.043	0.116	0.245	-2.023	CDS	GI:188594459	BAG33434.1
AP009380	PGN_0916	molecular chaperone DnaK	dnaK	1018923	1020845	1923	forward	0.415	-1.268	0.009	0.039	0.482	-2.629	CDS	GI:188594460	BAG33435.1
AP009380	PGN_0917	tyrosine type site-specific recombinase		1021623	1022885	1263	forward	0.722	-0.469	0.334	0.484	0.486	-0.966	CDS	GI:188594461	BAG33436.1
AP009380	PGN_0918	transposase in ISPg1		1023531	1024616	1086	forward	0.918	-0.123	0.785	0.856	0.452	-0.273	CDS	GI:188594462	BAG33437.1
AP009380	PGN_0919	hypothetical protein		1025094	1025738	645	reverse	0.709	-0.496	0.143	0.267	0.338	-1.465	CDS	GI:188594463	BAG33438.1
AP009380	PGN_0920	putative partial excisionase		1026238	1026375	138	forward	0.295	-1.761	0.000	0.001	0.436	-4.042	CDS	GI:188594464	BAG33439.1
AP009380	PGN_0921	hypothetical protein		1026426	1026593	168	forward	0.835	-0.260	0.657	0.760	0.586	-0.444	CDS	GI:188594465	BAG33440.1
AP009380	PGN_0922	conserved hypothetical protein		1026608	1027813	1206	forward	0.411	-1.282	0.000	0.001	0.328	-3.903	CDS	GI:188594466	BAG33441.1

AP009380	PGN_0923	putative DNA primase		1028044	1028931	888	forward	0.509	-0.973	0.003	0.018	0.327	-2.974	CDS	GI:188594467	BAG33442.1
AP009380	PGN_0924	mobilization protein		1029061	1029423	363	forward	0.483	-1.050	0.004	0.023	0.366	-2.867	CDS	GI:188594468	BAG33443.1
AP009380	PGN_0925	putative mobilization protein		1029413	1030354	942	forward	0.485	-1.043	0.000	0.004	0.292	-3.572	CDS	GI:188594469	BAG33444.1
AP009380	PGN_0926	conserved hypothetical protein		1030380	1031102	723	forward	0.608	-0.718	0.022	0.073	0.314	-2.289	CDS	GI:188594470	BAG33445.1
AP009380	PGN_0927	conserved hypothetical protein		1031232	1031435	204	forward	0.642	-0.640	0.036	0.102	0.305	-2.100	CDS	GI:188594471	BAG33446.1
AP009380	PGN_0928	conserved hypothetical protein		1031507	1032715	1209	forward	0.848	-0.238	0.192	0.330	0.182	-1.306	CDS	GI:188594472	BAG33447.1
AP009380	PGN_0929	conserved hypothetical protein		1032705	1034606	1902	forward	0.773	-0.371	0.090	0.198	0.219	-1.697	CDS	GI:188594473	BAG33448.1
AP009380	PGN_0930	hypothetical protein		1034802	1035848	1047	forward	0.732	-0.450	0.072	0.166	0.250	-1.800	CDS	GI:188594474	BAG33449.1
AP009380	PGN_0931	conserved hypothetical protein		1035904	1036683	780	forward	0.887	-0.173	0.570	0.690	0.304	-0.569	CDS	GI:188594475	BAG33450.1
AP009380	PGN_0932	probable GCN5-related N-acetyltransferase		1037241	1037696	456	forward	1.265	0.339	0.390	0.532	0.394	0.860	CDS	GI:188594476	BAG33451.1
AP009380	PGN_0933	probable transcriptional regulator		1037750	1039207	1458	forward	1.005	0.008	0.981	0.984	0.322	0.024	CDS	GI:188594477	BAG33452.1
AP009380	PGN_0934	transposase in ISPg3		1039361	1040263	903	forward	0.908	-0.139	0.552	0.676	0.234	-0.595	CDS	GI:188594478	BAG33453.1
AP009380	PGN_0935	conserved hypothetical protein		1040509	1042389	1881	forward	0.837	-0.256	0.343	0.493	0.270	-0.949	CDS	GI:188594479	BAG33454.1
AP009380	PGN_0936	putative glycerate dehydrogenase		1042630	1043583	954	forward	1.334	0.415	0.103	0.216	0.255	1.631	CDS	GI:188594480	BAG33455.1
AP009380	PGN_0937	hypothetical protein		1043701	1043811	111	forward	1.228	0.297	0.346	0.496	0.315	0.942	CDS	GI:188594481	BAG33456.1
AP009380	PGN_0938	8-amino-7-oxononanoate synthase		1043970	1045118	1149	forward	0.830	-0.268	0.199	0.337	0.209	-1.285	CDS	GI:188594482	BAG33457.1
AP009380	PGN_0939	conserved hypothetical protein		1045118	1045537	420	forward	0.903	-0.148	0.524	0.652	0.232	-0.638	CDS	GI:188594483	BAG33458.1
AP009380	PGN_0940	partial transposase in ISPg2		1045629	1045856	228	forward	0.855	-0.226	0.362	0.507	0.249	-0.911	CDS	GI:188594484	BAG33459.1
AP009380	PGN_0941	conserved hypothetical protein		1046329	1047720	1392	forward	0.781	-0.356	0.116	0.233	0.226	-1.574	CDS	GI:188594485	BAG33460.1
AP009380	PGN_0942	conserved hypothetical protein		1047725	1048531	807	forward	1.292	0.370	0.071	0.165	0.205	1.806	CDS	GI:188594486	BAG33461.1
AP009380	PGN_0943	alginate O-acetyltransferase		1048552	1050087	1536	forward	0.981	-0.028	0.907	0.945	0.237	-0.117	CDS	GI:188594487	BAG33462.1
AP009380	PGN_0944	transposase in ISPg3		1050241	1051143	903	reverse	0.795	-0.330	0.199	0.337	0.257	-1.286	CDS	GI:188594488	BAG33463.1
AP009380	PGN_0945	putative TetR family transcriptional regulator		1052312	1052959	648	forward	0.772	-0.373	0.195	0.334	0.288	-1.296	CDS	GI:188594489	BAG33464.1
AP009380	PGN_0946	conserved hypothetical protein		1053000	1055405	2406	forward	0.752	-0.411	0.059	0.144	0.218	-1.887	CDS	GI:188594490	BAG33465.1
AP009380	PGN_0947	conserved hypothetical protein		1055483	1056274	792	forward	1.057	0.080	0.767	0.842	0.269	0.296	CDS	GI:188594491	BAG33466.1
AP009380	PGN_0948	conserved hypothetical protein		1056278	1057555	1278	forward	0.961	-0.057	0.816	0.878	0.244	-0.233	CDS	GI:188594492	BAG33467.1
AP009380	PGN_0949	ABC transporter ATP-binding protein		1057580	1059334	1755	forward	1.060	0.083	0.728	0.811	0.240	0.347	CDS	GI:188594493	BAG33468.1
AP009380	PGN_0950	ABC transporter ATP-binding protein		1059381	1061087	1707	forward	0.838	-0.256	0.250	0.395	0.222	-1.150	CDS	GI:188594494	BAG33469.1
AP009380	PGN_0951	conserved hypothetical protein		1061257	1061634	378	reverse	0.660	-0.600	0.023	0.075	0.264	-2.277	CDS	GI:188594495	BAG33470.1
AP009380	PGN_0952	carboxyl-terminal processing protease		1061884	1063593	1710	forward	1.009	0.013	0.963	0.972	0.268	0.047	CDS	GI:188594496	BAG33471.1
AP009380	PGN_0953	transposase in ISPg3		1064180	1065082	903	forward	0.763	-0.391	0.240	0.385	0.333	-1.175	CDS	GI:188594497	BAG33472.1
AP009380	PGN_0954	partial transposase in ISPg6		1065426	1065938	513	reverse	0.427	-1.227	0.000	0.000	0.280	-4.386	CDS	GI:188594498	BAG33473.1
AP009380	PGN_0955	transposase in ISPg3		1066019	1066921	903	reverse	0.866	-0.207	0.548	0.674	0.345	-0.601	CDS	GI:188594499	BAG33474.1
AP009380	PGN_0956	hypothetical protein		1067028	1067300	273	reverse	1.045	0.063	0.795	0.863	0.242	0.260	CDS	GI:188594500	BAG33475.1
AP009380	PGN_0957	conserved hypothetical protein		1067323	1067865	543	reverse	1.124	0.169	0.533	0.659	0.271	0.624	CDS	GI:188594501	BAG33476.1
AP009380	PGN_0958	conserved hypothetical protein		1067870	1067965	96	reverse	0.675	-0.567	0.120	0.240	0.365	-1.554	CDS	GI:188594502	BAG33477.1
AP009380	PGN_0959	probable transcriptional regulator		1067962	1068285	324	reverse	0.616	-0.700	0.020	0.070	0.302	-2.321	CDS	GI:188594503	BAG33478.1
AP009380	PGN_0960	conserved hypothetical protein		1068395	1069285	891	reverse	0.765	-0.386	0.137	0.261	0.260	-1.485	CDS	GI:188594504	BAG33479.1
AP009380	PGN_0961	conserved hypothetical protein		1069360	1069476	117	forward	0.471	-1.087	0.019	0.068	0.465	-2.339	CDS	GI:188594505	BAG33480.1
AP009380	PGN_0962	threonyl-tRNA synthetase		1070862	1072823	1962	forward	1.381	0.465	0.051	0.129	0.238	1.955	CDS	GI:188594506	BAG33481.1
AP009380	PGN_0963	translation initiation factor IF-3		1072925	1073563	639	forward	1.238	0.308	0.158	0.287	0.218	1.412	CDS	GI:188594507	BAG33482.1
AP009380	PGN_0964	probable 50S ribosomal protein L35	rpmI	1073607	1073804	198	forward	1.208	0.273	0.163	0.293	0.195	1.397	CDS	GI:188594508	BAG33483.1
AP009380	PGN_0965	putative 50S ribosomal protein L20	rplT	1073917	1074264	348	forward	1.194	0.255	0.203	0.343	0.201	1.272	CDS	GI:188594509	BAG33484.1
AP009380	PGN_0966	partial transposase in ISPg1		1074727	1075296	570	forward	0.629	-0.668	0.169	0.302	0.486	-1.375	CDS	GI:188594510	BAG33485.1
AP009380	PGN_0967	partial transposase in ISPg1		1075517	1075942	426	forward	0.602	-0.733	0.136	0.260	0.491	-1.491	CDS	GI:188594511	BAG33486.1
AP009380	PGN_0968	conserved hypothetical protein		1076269	1077045	777	reverse	1.001	0.001	0.998	0.998	0.451	0.003	CDS	GI:188594512	BAG33487.1
AP009380	PGN_0969	conserved hypothetical protein		1077061	1077621	561	reverse	0.745	-0.424	0.322	0.472	0.428	-0.991	CDS	GI:188594513	BAG33488.1
AP009380	PGN_0970	putative RNA polymerase sigma-70 factor ECF subfamily		1077611	1078117	507	reverse	0.734	-0.445	0.293	0.441	0.424	-1.051	CDS	GI:188594514	BAG33489.1
AP009380	PGN_0971	transposase in ISPg1		1078414	1079499	1086	forward	0.712	-0.490	0.272	0.419	0.446	-1.099	CDS	GI:188594515	BAG33490.1
AP009380	PGN_0972	TPR domain protein		1079830	1082286	2457	reverse	0.670	-0.578	0.026	0.083	0.260	-2.223	CDS	GI:188594516	BAG33491.1
AP009380	PGN_t0024	tRNA-Phe		1082680	1082755	76	reverse	0.535	-0.901	0.047	0.123	0.454	-1.987	tRNA		
AP009380	PGN_0973	conserved hypothetical protein		1083418	1085742	2325	reverse	1.248	0.320	0.349	0.498	0.342	0.936	CDS	GI:188594517	BAG33492.1
AP009380	PGN_0974	putative shikimate 5-dehydrogenase		1085770	1086519	750	reverse	1.798	0.846	0.027	0.085	0.383	2.210	CDS	GI:188594518	BAG33493.1
AP009380	PGN_0975	putative ubiquinone/menaquinone biosynthesis methyltransferase		1086516	1087253	738	reverse	2.227	1.155	0.001	0.006	0.339	3.404	CDS	GI:188594519	BAG33494.1
AP009380	PGN_0976	phosphoribosylaminoimidazole-succinocarboxamide synthase		1087285	1088226	942	reverse	1.852	0.889	0.004	0.023	0.310	2.869	CDS	GI:188594520	BAG33495.1
AP009380	PGN_0977	phosphate starvation-inducible PhoH-like protein		1088283	1089275	993	reverse	1.793	0.842	0.009	0.041	0.324	2.602	CDS	GI:188594521	BAG33496.1
AP009380	PGN_0978	hypothetical protein		1089588	1089680	93	forward	0.944	-0.083	0.849	0.903	0.438	-0.190	CDS	GI:188594522	BAG33497.1
AP009380	PGN_0979	hypothetical protein		1089723	1089815	93	reverse	0.778	-0.363	0.536	0.662	0.586	-0.619	CDS	GI:188594523	BAG33498.1
AP009380	PGN_0980	putative alpha-1,2-mannosidase family protein		1089895	1092210	2316	reverse	0.863	-0.212	0.394	0.536	0.249	-0.852	CDS	GI:188594524	BAG33499.1
AP009380	PGN_0981	S-adenosylmethionine:tRNA ribosyltransferase-isomerase		1092349	1093566	1218	forward	0.647	-0.629	0.014	0.054	0.255	-2.463	CDS	GI:188594525	BAG33500.1
AP009380	PGN_t0025	tRNA-Leu		1093748	1093832	85	reverse	0.430	-1.218	0.028	0.086	0.553	-2.203	tRNA		
AP009380	PGN_0982	putative Mrr restriction system protein		1093971	1094888	918	reverse	0.371	-1.429	0.000	0.000	0.274	-5.219	CDS	GI:188594526	BAG33501.1
AP009380	PGN_0983	hypothetical protein		1095644	1095754	111	forward	0.440	-1.186	0.009	0.039	0.452	-2.626	CDS	GI:188594527	BAG33502.1
AP009380	PGN_0984	probable phosphatidylserine decarboxylase proenzyme		1095991	1096656	666	forward	0.803	-0.317	0.300	0.448	0.306	-1.036	CDS	GI:188594528	BAG33503.1
AP009380	PGN_0985	probable phosphatidylserine synthase		1096658	1097368	711	forward	1.069	0.096	0.669	0.768	0.226	0.427	CDS	GI:188594529	BAG33504.1
AP009380	PGN_0986	hypothetical protein		1097435	1097680	246	forward	1.255	0.327	0.189	0.328	0.249	1.313	CDS	GI:188594530	BAG33505.1
AP009380	PGN_0987	prolyl-tRNA synthetase		1097961	1099442	1482	forward	1.464	0.550	0.017	0.062	0.230	2.387	CDS	GI:188594531	BAG33506.1
AP009380	PGN_0988	hypothetical protein		1099497	1099826	330	forward	1.586	0.666	0.017	0.062	0.278	2.391	CDS	GI:188594532	BAG33507.1
AP009380	PGN_0989	putative methyltransferase		1099841	1100608	768	forward	1.931	0.949	0.006	0.032	0.348	2.725	CDS	GI:188594533	BAG33508.1
AP009380	PGN_0990	ATP-binding protein Mrp/Nbp35 family		1100628	1101746	1119	forward	1.987	0.991	0.002	0.013	0.317	3.130	CDS	GI:188594534	BAG33509.1
AP009380	PGN_0991	putative ribonuclease BN		1102207	1103634	1428	forward	1.761	0.816	0.002	0.014	0.263	3.100	CDS	GI:188594535	BAG33510.1
AP009380	PGN_0992	putative riboflavin biosynthesis protein		1103668	1104639	972	reverse	1.233	0.302	0.144	0.269	0.207	1.460	CDS	GI:188594536	BAG33511.1
AP009380	PGN_0993	putative peptidase M23/M37 family		1104627	1105922	1296	reverse	1.623	0.699	0.007	0.034	0.260	2.684	CDS	GI:188594537	BAG33512.1
AP009380	PGN_0994	conserved hypothetical protein		1105934	1106797	864	reverse	1.382	0.467	0.030	0.092	0.215	2.167	CDS	GI:188594538	BAG33513.1
AP009380	PGN_0995	TPR domain protein		1106794	1107309	516	reverse	1.283	0.360	0.098	0.210	0.218	1.653	CDS	GI:188594539	BAG33514.1
AP009380	PGN_0996	TPR domain protein		1107351	1108532	1182	reverse	1.613	0.690	0.023	0.074	0.303	2.280	CDS	GI:188594540	BAG33515.1
AP009380	PGN_0997	putative deoxyuridine 5'-triphosphate nucleotidohydrolase		1108560	1108994	435	reverse	1.492	0.577	0.047	0.123	0.291	1.987	CDS	GI:188594541	BAG33516.1
AP009380	PGN_0998	4-hydroxy-3-methylbut-2-en-1-yl diphosphate synthase		1109051	1110796	1746	reverse	1.540	0.623	0.022	0.073	0.272	2.288	CDS	GI:188594542	BAG33517.1
AP009380	PGN_0999	putative phosphoribosylaminoimidazole carboxylase		1110970	1111476	507	reverse	1.249	0.320	0.288	0.436	0.302	1.063	CDS	GI:188594543	BAG33518.1
AP009380	PGN_1000	putative glycine cleavage system H protein		1111477	1111857	381	reverse	0.950	-0.074	0.709	0.801	0.199	-0.373	CDS	GI:188594544	BAG33519.1
AP009380	PGN_1001	conserved hypothetical protein		1112025	1113032	1008	reverse	1.203	0.267	0.227	0.369	0.221	1.207	CDS	GI:188594545	BAG33520.1
AP009380	PGN_1002	AMP nucleosidase		1113051	1113827	777	reverse	1.230	0.299	0.226	0.368	0.247	1.211	CDS	GI:188594546	BAG33521.1
AP009380	PGN_1003	conserved hypothetical protein		1113896	1114369	474	forward	0.843	-0.247	0.295	0.443	0.236	-1.047	CDS	GI:188594547	BAG33522.1
AP009380	PGN_1004	putative ABC transporter ATP-binding protein		1114372	1115331	960	forward	1.538	0.622	0.004	0.021	0.213	2.913	CDS	GI:188594548	BAG33523.1
AP009380	PGN_1005	probable ABC transporter permease protein		1115336	1116664	1329	forward	1.472	0.558	0.020	0.069	0.240	2.323	CDS	GI:188594549	BAG33524.1
AP009380	PGN_1006	transposase in ISPg3		1117001	1117903	903	reverse	0.840	-0.252	0.470	0.609	0.349	-0.722	CDS	GI:188594550	BAG33525.1
AP009380	PGN_1007	conserved hypothetical protein		1118041	1118262	222	reverse	1.003	0.004	0.992	0.993	0.413	0.010	CDS	GI:188594551	BAG33526.1

AP009380	PGN_1008	partial transposase in ISPg1		1118534	1119226	693	forward	0.741	-0.432	0.330	0.480	0.444	-0.973	CDS	GI:188594552	BAG33527.1
AP009380	PGN_1009	calcium-transporting ATPase		1119487	1122312	2826	forward	0.863	-0.212	0.485	0.623	0.304	-0.698	CDS	GI:188594553	BAG33528.1
AP009380	PGN_1010	conserved hypothetical protein		1122312	1123034	723	forward	1.666	0.737	0.045	0.120	0.368	2.003	CDS	GI:188594554	BAG33529.1
AP009380	PGN_1011	xanthine/uracil/vitamin C permease		1123055	1124356	1302	forward	1.667	0.737	0.033	0.098	0.346	2.127	CDS	GI:188594555	BAG33530.1
AP009380	PGN_1012	putative 4-diphosphocytidyl-2C-methyl-D-erythritol kinase		1124385	1125209	825	forward	1.346	0.428	0.188	0.326	0.325	1.316	CDS	GI:188594556	BAG33531.1
AP009380	PGN_1013	putative Fe-S oxidoreductase		1125188	1127092	1905	forward	1.880	0.911	0.018	0.065	0.385	2.364	CDS	GI:188594557	BAG33532.1
AP009380	PGN_1014	elongation factor G		1127300	1129459	2160	reverse	0.985	-0.022	0.918	0.950	0.213	-0.103	CDS	GI:188594558	BAG33533.1
AP009380	PGN_1015	putative DNA polymerase III delta prime subunit		1129703	1130953	1251	reverse	1.110	0.150	0.552	0.676	0.252	0.595	CDS	GI:188594559	BAG33534.1
AP009380	PGN_1016	conserved hypothetical protein		1131341	1131955	615	forward	1.346	0.428	0.038	0.106	0.206	2.080	CDS	GI:188594560	BAG33535.1
AP009380	PGN_1017	conserved hypothetical protein		1131963	1132352	390	forward	0.838	-0.255	0.328	0.478	0.261	-0.977	CDS	GI:188594561	BAG33536.1
AP009380	PGN_1018	conserved hypothetical protein		1132404	1133570	1167	forward	1.245	0.316	0.099	0.210	0.192	1.651	CDS	GI:188594562	BAG33537.1
AP009380	PGN_1019	Por secretion system response regulatr protein porX	porX	1133660	1135216	1557	forward	0.879	-0.187	0.415	0.553	0.229	-0.815	CDS	GI:188594563	BAG33538.1
AP009380	PGN_1020	probable ATP/GTP-binding transmembrane protein		1135228	1135644	417	forward	1.209	0.274	0.191	0.330	0.210	1.308	CDS	GI:188594564	BAG33539.1
AP009380	PGN_1021	hypothetical protein		1135644	1135871	228	forward	1.295	0.373	0.101	0.214	0.227	1.640	CDS	GI:188594565	BAG33540.1
AP009380	PGN_1022	putative thymidine kinase		1135999	1136613	615	forward	0.879	-0.186	0.510	0.640	0.283	-0.660	CDS	GI:188594566	BAG33541.1
AP009380	PGN_1023	acid phosphatase OlpA		1136610	1137425	816	forward	1.251	0.324	0.164	0.295	0.233	1.392	CDS	GI:188594567	BAG33542.1
AP009380	PGN_1024	putative ribosome-binding factor A		1137464	1137799	336	forward	1.316	0.396	0.115	0.232	0.251	1.578	CDS	GI:188594568	BAG33543.1
AP009380	PGN_1025	conserved hypothetical protein		1137827	1139050	1224	forward	1.232	0.301	0.282	0.430	0.280	1.075	CDS	GI:188594569	BAG33544.1
AP009380	PGN_1026	glycosyl transferase family 2		1139196	1139933	738	forward	1.166	0.222	0.286	0.434	0.208	1.066	CDS	GI:188594570	BAG33545.1
AP009380	PGN_1027	dihydroorotase		1139944	1141293	1350	forward	1.485	0.570	0.007	0.034	0.213	2.682	CDS	GI:188594571	BAG33546.1
AP009380	PGN_1028	conserved hypothetical protein		1141553	1142215	663	forward	1.052	0.073	0.693	0.788	0.186	0.394	CDS	GI:188594572	BAG33547.1
AP009380	PGN_1029	conserved hypothetical protein		1142181	1142576	396	forward	1.476	0.561	0.042	0.114	0.276	2.036	CDS	GI:188594573	BAG33548.1
AP009380	PGN_t0026	tRNA-Ala		1142632	1142708	77	forward	0.710	-0.494	0.196	0.334	0.382	-1.293	tRNA		
AP009380	PGN_1030	hypothetical protein		1142678	1142863	186	forward	0.663	-0.594	0.092	0.200	0.352	-1.688	CDS	GI:188594574	BAG33549.1
AP009380	PGN_1031	conserved hypothetical protein		1143165	1143644	480	reverse	0.370	-1.435	0.001	0.005	0.416	-3.452	CDS	GI:188594575	BAG33550.1
AP009380	PGN_1032	conserved hypothetical protein		1143862	1144575	714	forward	0.327	-1.611	0.000	0.001	0.408	-3.953	CDS	GI:188594576	BAG33551.1
AP009380	PGN_1033	O-antigen flippase	wzx	1144923	1146488	1566	forward	0.495	-1.015	0.001	0.007	0.301	-3.374	CDS	GI:188594577	BAG33552.1
AP009380	PGN_1034	conserved hypothetical protein		1146614	1147186	573	forward	1.050	0.070	0.794	0.862	0.269	0.262	CDS	GI:188594578	BAG33553.1
AP009380	PGN_1035	conserved hypothetical protein with DUF1063 domain		1147241	1148542	1302	forward	1.205	0.269	0.335	0.484	0.279	0.965	CDS	GI:188594579	BAG33554.1
AP009380	PGN_1036	putative G/U mismatch-specific DNA glycosylase		1148568	1149050	483	forward	1.148	0.199	0.517	0.647	0.307	0.648	CDS	GI:188594580	BAG33555.1
AP009380	PGN_1037	conserved hypothetical protein		1149162	1149614	453	reverse	0.859	-0.219	0.344	0.494	0.232	-0.946	CDS	GI:188594581	BAG33556.1
AP009380	PGN_1038	conserved hypothetical protein		1150639	1151181	543	forward	0.825	-0.277	0.254	0.401	0.243	-1.140	CDS	GI:188594582	BAG33557.1
AP009380	PGN_1039	putative alpha-1,2-mannosidase precursor		1151266	1153533	2268	forward	1.476	0.562	0.052	0.132	0.289	1.944	CDS	GI:188594583	BAG33558.1
AP009380	PGN_1040	conserved hypothetical protein		1153713	1153961	249	forward	0.639	-0.646	0.021	0.072	0.280	-2.304	CDS	GI:188594584	BAG33559.1
AP009380	PGN_1041	cytochrome d ubiquinol oxidase subunit I		1153981	1155570	1590	forward	0.796	-0.329	0.227	0.369	0.273	-1.207	CDS	GI:188594585	BAG33560.1
AP009380	PGN_1042	cytochrome d ubiquinol oxidase subunit II		1155616	1156779	1164	forward	1.117	0.160	0.459	0.598	0.215	0.741	CDS	GI:188594586	BAG33561.1
AP009380	PGN_1043	conserved hypothetical protein		1156926	1157717	792	forward	1.136	0.184	0.401	0.541	0.219	0.841	CDS	GI:188594587	BAG33562.1
AP009380	PGN_1044	alpha-amylase		1157714	1159408	1695	forward	1.090	0.124	0.602	0.717	0.238	0.521	CDS	GI:188594588	BAG33563.1
AP009380	PGN_1045	beta-galactosidase	lacZII	1159873	1163079	3207	reverse	1.091	0.125	0.553	0.676	0.211	0.594	CDS	GI:188594589	BAG33564.1
AP009380	PGN_t0027	tRNA-Met		1164040	1164116	77	reverse	0.756	-0.403	0.423	0.561	0.503	-0.801	tRNA		
AP009380	PGN_1046	putative DNA repair protein		1164289	1164981	693	forward	1.053	0.075	0.772	0.846	0.257	0.290	CDS	GI:188594590	BAG33565.1
AP009380	PGN_1047	hydroxylamine reductase		1165206	1166858	1653	forward	0.734	-0.447	0.109	0.223	0.278	-1.605	CDS	GI:188594591	BAG33566.1
AP009380	PGN_1048	hypothetical protein		1167592	1167738	147	reverse	0.915	-0.128	0.689	0.786	0.319	-0.400	CDS	GI:188594592	BAG33567.1
AP009380	PGN_1049	putative alkaline phosphatase		1168010	1169701	1692	reverse	1.279	0.355	0.255	0.401	0.312	1.138	CDS	GI:188594593	BAG33568.1
AP009380	PGN_1050	conserved hypothetical protein		1169737	1170933	1197	reverse	1.379	0.463	0.211	0.352	0.370	1.251	CDS	GI:188594594	BAG33569.1
AP009380	PGN_1051	hypothetical protein		1171115	1171243	129	reverse	2.033	1.024	0.033	0.098	0.481	2.130	CDS	GI:188594595	BAG33570.1
AP009380	PGN_1052	conserved hypothetical protein		1171432	1172196	765	reverse	2.182	1.126	0.005	0.025	0.397	2.835	CDS	GI:188594596	BAG33571.1
AP009380	PGN_1053	putative phospho-2-dehydro-3-deoxyheptonate aldolase/chorismate mutase		1172193	1173293	1101	reverse	1.980	0.986	0.031	0.093	0.456	2.160	CDS	GI:188594597	BAG33572.1
AP009380	PGN_1054	virulence modulating gene F	vimF	1173309	1174559	1251	reverse	2.371	1.246	0.003	0.019	0.423	2.944	CDS	GI:188594598	BAG33573.1
AP009380	PGN_1055	virulence modulating gene E	vimE	1174556	1175917	1362	reverse	1.819	0.863	0.022	0.073	0.376	2.297	CDS	GI:188594599	BAG33574.1
AP009380	PGN_1056	virulence modulating gene A	vimA	1175914	1176879	966	reverse	0.867	-0.206	0.378	0.520	0.234	-0.881	CDS	GI:188594600	BAG33575.1
AP009380	PGN_1057	recombinase A	recA	1176953	1177975	1023	reverse	0.801	-0.320	0.267	0.414	0.288	-1.109	CDS	GI:188594601	BAG33576.1
AP009380	PGN_1058	putative bacterioferritin comigratory protein	bcp	1177996	1178451	456	reverse	0.826	-0.276	0.261	0.407	0.246	-1.124	CDS	GI:188594602	BAG33577.1
AP009380	PGN_1059	conserved hypothetical protein		1178752	1179021	270	forward	1.084	0.116	0.728	0.811	0.335	0.348	CDS	GI:188594603	BAG33578.1
AP009380	PGN_1060	transposase in ISPg3		1179008	1179910	903	reverse	0.668	-0.582	0.119	0.239	0.374	-1.557	CDS	GI:188594604	BAG33579.1
AP009380	PGN_1061	conserved hypothetical protein		1180396	1181307	912	forward	0.979	-0.031	0.896	0.936	0.237	-0.131	CDS	GI:188594605	BAG33580.1
AP009380	PGN_1062	tRNA modification GTPase		1181339	1182895	1557	forward	1.372	0.457	0.021	0.072	0.198	2.307	CDS	GI:188594606	BAG33581.1
AP009380	PGN_1063	partial transposase Orf2 in ISPg5		1183205	1183396	192	reverse	1.216	0.282	0.415	0.553	0.346	0.815	CDS	GI:188594607	BAG33582.1
AP009380	PGN_1064	transposase in ISPg3		1183610	1184512	903	reverse	0.656	-0.607	0.072	0.165	0.337	-1.802	CDS	GI:188594608	BAG33583.1
AP009380	PGN_1065	transposase in ISPg3		1184666	1185568	903	reverse	0.758	-0.400	0.267	0.413	0.360	-1.111	CDS	GI:188594609	BAG33584.1
AP009380	PGN_1066	transposase in ISPg3		1185976	1186878	903	forward	0.698	-0.518	0.095	0.205	0.310	-1.670	CDS	GI:188594610	BAG33585.1
AP009380	PGN_1067	hypothetical protein		1186924	1188018	1095	reverse	0.762	-0.393	0.044	0.119	0.195	-2.012	CDS	GI:188594611	BAG33586.1
AP009380	PGN_1068	conserved hypothetical protein		1188515	1189525	1011	reverse	0.600	-0.736	0.004	0.023	0.257	-2.866	CDS	GI:188594612	BAG33587.1
AP009380	PGN_1069	hypothetical protein		1189492	1190520	1029	reverse	1.024	0.034	0.919	0.950	0.336	0.102	CDS	GI:188594613	BAG33588.1
AP009380	PGN_1070	hypothetical protein		1190495	1191574	1080	reverse	1.155	0.208	0.546	0.672	0.344	0.604	CDS	GI:188594614	BAG33589.1
AP009380	PGN_1071	hypothetical protein		1191492	1192352	861	reverse	0.939	-0.091	0.787	0.857	0.338	-0.270	CDS	GI:188594615	BAG33590.1
AP009380	PGN_1072	hypothetical protein		1192349	1193278	930	reverse	0.823	-0.281	0.446	0.585	0.369	-0.761	CDS	GI:188594616	BAG33591.1
AP009380	PGN_1073	hypothetical protein		1193286	1194362	1077	reverse	0.894	-0.162	0.570	0.690	0.285	-0.568	CDS	GI:188594617	BAG33592.1
AP009380	PGN_1074	hypothetical protein		1194416	1195786	1371	reverse	0.656	-0.608	0.031	0.094	0.282	-2.153	CDS	GI:188594618	BAG33593.1
AP009380	PGN_1075	hypothetical protein		1196079	1196237	159	forward	0.587	-0.767	0.011	0.045	0.300	-2.556	CDS	GI:188594619	BAG33594.1
AP009380	PGN_1076	putative DNA methylase		1196323	1199790	3468	reverse	0.605	-0.725	0.090	0.198	0.428	-1.695	CDS	GI:188594620	BAG33595.1
AP009380	PGN_1077	transposase in ISPg1		1199815	1200900	1086	reverse	0.597	-0.744	0.122	0.242	0.481	-1.546	CDS	GI:188594621	BAG33596.1
AP009380	PGN_1078	GDP-mannose 4,6-dehydratase		1201181	1202278	1098	forward	1.395	0.480	0.057	0.141	0.253	1.902	CDS	GI:188594622	BAG33597.1
AP009380	PGN_1079	GDP-fucose synthetase		1202271	1203344	1074	forward	1.791	0.841	0.001	0.011	0.264	3.189	CDS	GI:188594623	BAG33598.1
AP009380	PGN_1080	branched-chain amino acid aminotransferase		1203483	1204502	1020	forward	0.956	-0.064	0.860	0.910	0.365	-0.177	CDS	GI:188594624	BAG33599.1
AP009380	PGN_1081	conserved hypothetical protein		1204631	1206352	1722	reverse	0.777	-0.364	0.290	0.439	0.344	-1.057	CDS	GI:188594625	BAG33600.1
AP009380	PGN_1082	hypothetical protein		1206592	1206759	168	forward	0.686	-0.545	0.324	0.474	0.552	-0.986	CDS	GI:188594626	BAG33601.1
AP009380	PGN_1083	hypothetical protein		1206831	1206923	93	forward	1.016	0.024	0.941	0.959	0.317	0.074	CDS	GI:188594627	BAG33602.1
AP009380	PGN_1084	hypothetical protein		1206957	1207061	105	reverse	0.662	-0.594	0.120	0.239	0.382	-1.555	CDS	GI:188594628	BAG33603.1
AP009380	PGN_1085	ferrous iron transport protein B		1207318	1209852	2535	forward	1.123	0.167	0.473	0.611	0.233	0.717	CDS	GI:188594629	BAG33604.1
AP009380	PGN_1086	hypothetical protein		1209872	1210057	186	forward	1.111	0.152	0.723	0.809	0.429	0.355	CDS	GI:188594630	BAG33605.1
AP009380	PGN_1087	conserved hypothetical protein		1210065	1210520	456	forward	1.255	0.328	0.433	0.571	0.418	0.785	CDS	GI:188594631	BAG33606.1
AP009380	PGN_1088	30S ribosomal protein S1	rpsA	1211098	1212897	1800	forward	1.527	0.610	0.018	0.065	0.258	2.366	CDS	GI:188594632	BAG33607.1
AP009380	PGN_1089	probable methyltransferase		1213749	1214288	540	reverse	0.890	-0.169	0.643	0.750	0.364	-0.463	CDS	GI:188594633	BAG33608.1
AP009380	PGN_1090	conserved hypothetical protein		1214325	1215140	816	reverse	0.913	-0.132	0.598	0.714	0.250	-0.528	CDS	GI:188594634	BAG33609.1
AP009380	PGN_1091	conserved hypothetical protein		1215158	1215790	633	reverse	0.850	-0.234	0.259	0.405	0.208	-1.129	CDS	GI:188594635	BAG33610.1
AP009380	PGN_1092	ATP-dependent exoDNAse alpha subunit		1215922	1217337	1416	forward	0.918	-0.123	0.582	0.701	0.224	-0.550	CDS	GI:188594636	BAG33611.1

AP009380	PGN_1093	conserved hypothetical protein		1217354	1218685	1332	reverse	0.500	-1.001	0.000	0.000	0.187	-5.340	CDS	GI:188594637	BAG33612.1
AP009380	PGN_1094	glycine dehydrogenase		1218891	1221758	2868	reverse	1.461	0.547	0.021	0.072	0.238	2.301	CDS	GI:188594638	BAG33613.1
AP009380	PGN_1095	probable metallo-beta-lactamase		1221762	1222406	645	reverse	1.088	0.122	0.575	0.695	0.217	0.561	CDS	GI:188594639	BAG33614.1
AP009380	PGN_1096	glucose-inhibited division protein B		1222403	1223077	675	reverse	0.873	-0.195	0.454	0.592	0.261	-0.749	CDS	GI:188594640	BAG33615.1
AP009380	PGN_1097	conserved hypothetical protein		1223103	1223915	813	reverse	0.869	-0.202	0.501	0.635	0.301	-0.673	CDS	GI:188594641	BAG33616.1
AP009380	PGN_1098	probable succinoglycan biosynthesis regulator ExsB protein		1224353	1225015	663	forward	1.418	0.504	0.084	0.188	0.292	1.729	CDS	GI:188594642	BAG33617.1
AP009380	PGN_1099	probable phosphoesterase		1225050	1225544	495	forward	1.312	0.391	0.197	0.336	0.304	1.289	CDS	GI:188594643	BAG33618.1
AP009380	PGN_1100	putative capsule biosynthesis protein CapA		1225555	1226685	1131	forward	1.469	0.554	0.096	0.207	0.333	1.665	CDS	GI:188594644	BAG33619.1
AP009380	PGN_1101	conserved hypothetical protein		1226727	1226906	180	reverse	1.876	0.908	0.015	0.057	0.373	2.436	CDS	GI:188594645	BAG33620.1
AP009380	PGN_1102	hypothetical protein		1227469	1227561	93	reverse	0.431	-1.213	0.009	0.040	0.463	-2.621	CDS	GI:188594646	BAG33621.1
AP009380	PGN_1103	dipeptidase		1227855	1229513	1659	forward	1.334	0.415	0.235	0.379	0.350	1.187	CDS	GI:188594647	BAG33622.1
AP009380	PGN_t0028	tRNA-Arg		1229586	1229660	75	forward	0.583	-0.778	0.042	0.114	0.382	-2.036	tRNA		
AP009380	PGN_1104	chorismate synthase		1229886	1230992	1107	reverse	0.595	-0.748	0.052	0.131	0.385	-1.946	CDS	GI:188594648	BAG33623.1
AP009380	PGN_1105	probable FKBP-type peptidyl-prolyl cis-trans isomerase		1231142	1231714	573	reverse	0.541	-0.885	0.035	0.101	0.420	-2.109	CDS	GI:188594649	BAG33624.1
AP009380	PGN_1106	conserved hypothetical protein		1231765	1232271	507	reverse	0.589	-0.763	0.039	0.109	0.370	-2.062	CDS	GI:188594650	BAG33625.1
AP009380	PGN_1107	conserved hypothetical protein		1232268	1232678	411	reverse	0.761	-0.394	0.281	0.429	0.365	-1.079	CDS	GI:188594651	BAG33626.1
AP009380	PGN_1108	putative RNA polymerase ECF-type sigma factor		1232726	1233277	552	reverse	0.544	-0.879	0.002	0.015	0.286	-3.069	CDS	GI:188594652	BAG33627.1
AP009380	PGN_1109	hypothetical protein		1233914	1234141	228	forward	0.918	-0.123	0.643	0.750	0.266	-0.463	CDS	GI:188594653	BAG33628.1
AP009380	PGN_1110	partial transposase in ISPg1		1234332	1234967	636	forward	0.729	-0.456	0.337	0.487	0.475	-0.960	CDS	GI:188594654	BAG33629.1
AP009380	PGN_1111	formate-tetrahydrofolate ligase		1235184	1236851	1668	reverse	1.257	0.330	0.223	0.366	0.271	1.219	CDS	GI:188594655	BAG33630.1
AP009380	PGN_1112	PhoH-like protein		1237008	1238342	1335	forward	1.086	0.119	0.562	0.685	0.206	0.579	CDS	GI:188594656	BAG33631.1
AP009380	PGN_1113	putative crossover junction endodeoxyribonuclease RuvC	ruvC	1238390	1238959	570	reverse	0.816	-0.294	0.170	0.303	0.214	-1.372	CDS	GI:188594657	BAG33632.1
AP009380	PGN_1114	conserved hypothetical protein		1238967	1239275	309	reverse	0.913	-0.132	0.603	0.717	0.254	-0.520	CDS	GI:188594658	BAG33633.1
AP009380	PGN_1115	putative hemagglutinin		1239496	1240605	1110	forward	0.535	-0.902	0.035	0.102	0.429	-2.103	CDS	GI:188594659	BAG33634.1
AP009380	PGN_1116	putative aminotransferase		1240734	1242044	1311	reverse	1.772	0.825	0.008	0.036	0.310	2.662	CDS	GI:188594660	BAG33635.1
AP009380	PGN_1117	acetyl-CoA synthetase		1242087	1244144	2058	reverse	1.766	0.820	0.012	0.048	0.326	2.516	CDS	GI:188594661	BAG33636.1
AP009380	PGN_1118	transposase in ISPg1		1244914	1245999	1086	forward	0.928	-0.108	0.811	0.874	0.451	-0.240	CDS	GI:188594662	BAG33637.1
AP009380	PGN_1119	probable large conductance mechanosensitive channel protein		1246529	1246948	420	forward	1.069	0.097	0.692	0.788	0.245	0.396	CDS	GI:188594663	BAG33638.1
AP009380	PGN_1120	putative NADPH-NAD transhydrogenase		1247326	1248483	1158	forward	1.631	0.706	0.036	0.103	0.337	2.096	CDS	GI:188594664	BAG33639.1
AP009380	PGN_1121	probable NADPH-NAD transhydrogenase alpha subunit		1248593	1248907	315	forward	1.727	0.788	0.019	0.068	0.337	2.340	CDS	GI:188594665	BAG33640.1
AP009380	PGN_1122	NADPH-NAD transhydrogenase beta subunit		1248904	1251441	2538	forward	1.909	0.932	0.003	0.018	0.314	2.968	CDS	GI:188594666	BAG33641.1
AP009380	PGN_1123	conserved hypothetical protein		1251587	1252786	1200	reverse	1.598	0.676	0.006	0.030	0.246	2.749	CDS	GI:188594667	BAG33642.1
AP009380	PGN_1124	Band 7 protein		1252783	1253763	981	reverse	1.120	0.163	0.529	0.656	0.259	0.630	CDS	GI:188594668	BAG33643.1
AP009380	PGN_1125	conserved hypothetical protein		1253790	1254254	465	reverse	0.985	-0.022	0.936	0.956	0.273	-0.080	CDS	GI:188594669	BAG33644.1
AP009380	PGN_1126	putative error-prone repair: SOS-response transcriptional repressor UmuD homolog		1255263	1255688	426	forward	0.882	-0.181	0.396	0.537	0.213	-0.849	CDS	GI:188594670	BAG33645.1
AP009380	PGN_1127	putative SOS mutagenesis and repair protein UmuC homolog		1255696	1257057	1362	forward	1.002	0.002	0.990	0.991	0.179	0.013	CDS	GI:188594671	BAG33646.1
AP009380	PGN_1128	L-lactate permease		1257066	1258616	1551	reverse	1.054	0.076	0.668	0.767	0.178	0.429	CDS	GI:188594672	BAG33647.1
AP009380	PGN_1129	conserved hypothetical protein		1258932	1259402	471	forward	0.554	-0.853	0.009	0.041	0.328	-2.602	CDS	GI:188594673	BAG33648.1
AP009380	PGN_1130	putative UDP-N-acetylenolpyruvoylglucosamine reductase		1259402	1260418	1017	forward	0.603	-0.729	0.010	0.043	0.283	-2.575	CDS	GI:188594674	BAG33649.1
AP009380	PGN_1131	conserved hypothetical protein		1260445	1261923	1479	forward	0.560	-0.836	0.037	0.105	0.401	-2.083	CDS	GI:188594675	BAG33650.1
AP009380	PGN_1132	transposase in ISPg1		1262252	1263337	1086	reverse	0.669	-0.581	0.222	0.366	0.476	-1.220	CDS	GI:188594676	BAG33651.1
AP009380	PGN_1133	hypothetical protein		1263359	1263559	201	reverse	0.331	-1.596	0.004	0.021	0.548	-2.911	CDS	GI:188594677	BAG33652.1
AP009380	PGN_1134	conserved hypothetical protein		1263752	1264873	1122	forward	1.143	0.193	0.435	0.574	0.248	0.780	CDS	GI:188594678	BAG33653.1
AP009380	PGN_1135	putative glycosyltransferase		1264870	1266141	1272	forward	1.175	0.233	0.370	0.514	0.259	0.896	CDS	GI:188594679	BAG33654.1
AP009380	PGN_1136	probable GTP-cyclohydrolase protein		1266278	1266742	465	forward	0.955	-0.066	0.755	0.831	0.212	-0.312	CDS	GI:188594680	BAG33655.1
AP009380	PGN_1137	conserved hypothetical protein		1266770	1267651	882	forward	1.096	0.133	0.573	0.693	0.235	0.563	CDS	GI:188594681	BAG33656.1
AP009380	PGN_1138	conserved hypothetical protein		1268039	1268527	489	reverse	1.158	0.212	0.366	0.510	0.234	0.904	CDS	GI:188594682	BAG33657.1
AP009380	PGN_1139	conserved hypothetical protein		1268538	1268951	414	reverse	1.324	0.405	0.104	0.218	0.250	1.624	CDS	GI:188594683	BAG33658.1
AP009380	PGN_1140	putative orotate phosphoribosyltransferase		1269002	1269634	633	reverse	1.551	0.633	0.018	0.065	0.268	2.359	CDS	GI:188594684	BAG33659.1
AP009380	PGN_1141	putative amidohydrolase		1269745	1270566	822	reverse	1.180	0.239	0.387	0.530	0.276	0.865	CDS	GI:188594685	BAG33660.1
AP009380	PGN_1142	probable acetyltransferase		1270563	1271111	549	reverse	0.984	-0.024	0.935	0.956	0.293	-0.081	CDS	GI:188594686	BAG33661.1
AP009380	PGN_1143	conserved hypothetical protein		1271162	1271587	426	reverse	0.736	-0.442	0.246	0.391	0.381	-1.159	CDS	GI:188594687	BAG33662.1
AP009380	PGN_1144	hypothetical protein		1271814	1271957	144	reverse	0.578	-0.792	0.015	0.056	0.324	-2.443	CDS	GI:188594688	BAG33663.1
AP009380	PGN_1145	conserved hypothetical protein		1272128	1272259	132	reverse	0.768	-0.381	0.117	0.236	0.243	-1.566	CDS	GI:188594689	BAG33664.1
AP009380	PGN_1146	conserved hypothetical protein		1272454	1273134	681	reverse	0.956	-0.065	0.722	0.809	0.184	-0.356	CDS	GI:188594690	BAG33665.1
AP009380	PGN_1147	conserved hypothetical protein		1273445	1274416	972	reverse	0.696	-0.524	0.019	0.066	0.223	-2.352	CDS	GI:188594691	BAG33666.1
AP009380	PGN_1148	phosphoribosylamine-glycine ligase		1274419	1275714	1296	reverse	0.725	-0.464	0.076	0.174	0.262	-1.771	CDS	GI:188594692	BAG33667.1
AP009380	PGN_1149	prolyl tripeptidase A		1275711	1277909	2199	reverse	0.769	-0.378	0.122	0.242	0.245	-1.547	CDS	GI:188594693	BAG33668.1
AP009380	PGN_1150	putative N6-adenine-specific DNA methylase		1277941	1279395	1455	reverse	0.786	-0.348	0.244	0.389	0.299	-1.166	CDS	GI:188594694	BAG33669.1
AP009380	PGN_1151	1-deoxy-D-xylulose-5-phosphate reductoisomerase		1280014	1281171	1158	reverse	1.382	0.467	0.103	0.216	0.286	1.632	CDS	GI:188594695	BAG33670.1
AP009380	PGN_1152	probable 16S rRNA processing protein		1281168	1281695	528	reverse	0.941	-0.088	0.641	0.749	0.188	-0.466	CDS	GI:188594696	BAG33671.1
AP009380	PGN_1153	UDP-N-acetylglucosamine 1-carboxyvinyltransferase		1281702	1283006	1305	reverse	1.039	0.056	0.780	0.853	0.200	0.279	CDS	GI:188594697	BAG33672.1
AP009380	PGN_1154	conserved hypothetical protein		1283037	1283621	585	reverse	0.965	-0.052	0.798	0.865	0.203	-0.257	CDS	GI:188594698	BAG33673.1
AP009380	PGN_1155	glucose-6-phosphate isomerase		1283659	1284996	1338	reverse	0.860	-0.218	0.339	0.489	0.228	-0.956	CDS	GI:188594699	BAG33674.1
AP009380	PGN_1156	glycerol-3-phosphate dehydrogenase		1285029	1286033	1005	reverse	0.650	-0.621	0.047	0.123	0.313	-1.985	CDS	GI:188594700	BAG33675.1
AP009380	PGN_1157	lysyl-tRNA synthetase		1286119	1287855	1737	reverse	0.776	-0.365	0.294	0.442	0.348	-1.049	CDS	GI:188594701	BAG33676.1
AP009380	PGN_1158	putative purine nucleoside phosphorylase		1287978	1288856	879	reverse	0.835	-0.261	0.508	0.639	0.394	-0.663	CDS	GI:188594702	BAG33677.1
AP009380	PGN_1159	conserved hypothetical protein		1288927	1290348	1422	reverse	0.774	-0.370	0.323	0.473	0.374	-0.989	CDS	GI:188594703	BAG33678.1
AP009380	PGN_1160	transposase in ISPg2		1290555	1291637	1083	forward	1.324	0.405	0.115	0.233	0.257	1.576	CDS	GI:188594704	BAG33679.1
AP009380	PGN_1161	transposase in ISPg1		1291755	1292840	1086	reverse	0.506	-0.981	0.043	0.116	0.484	-2.028	CDS	GI:188594705	BAG33680.1
AP009380	PGN_1162	putative CoA transferase subunit A		1293589	1294233	645	forward	0.675	-0.568	0.012	0.048	0.225	-2.521	CDS	GI:188594706	BAG33681.1
AP009380	PGN_1163	conserved hypothetical protein		1294302	1294676	375	forward	0.572	-0.806	0.006	0.029	0.292	-2.760	CDS	GI:188594707	BAG33682.1
AP009380	PGN_1164	conserved hypothetical protein with prokaryotic DUF849 domain		1294712	1295524	813	forward	0.876	-0.191	0.461	0.599	0.259	-0.738	CDS	GI:188594708	BAG33683.1
AP009380	PGN_1165	conserved hypothetical protein		1295566	1296609	1044	forward	0.729	-0.456	0.092	0.201	0.270	-1.687	CDS	GI:188594709	BAG33684.1
AP009380	PGN_1166	L-lysine 2,3-aminomutase		1296696	1297946	1251	forward	0.880	-0.185	0.585	0.703	0.338	-0.546	CDS	GI:188594710	BAG33685.1
AP009380	PGN_1167	conserved hypothetical protein		1297973	1299052	1080	forward	0.835	-0.261	0.413	0.552	0.318	-0.819	CDS	GI:188594711	BAG33686.1
AP009380	PGN_1168	probable DNA mismatch repair protein MutS		1299052	1300443	1392	forward	0.887	-0.174	0.531	0.657	0.277	-0.626	CDS	GI:188594712	BAG33687.1
AP009380	PGN_1169	D-lysine 5,6-aminomutase alpha subunit		1300471	1302042	1572	forward	0.882	-0.181	0.420	0.558	0.225	-0.806	CDS	GI:188594713	BAG33688.1
AP009380	PGN_1170	D-lysine 5,6-aminomutase beta subunit		1302039	1302830	792	forward	1.085	0.118	0.682	0.780	0.288	0.409	CDS	GI:188594714	BAG33689.1
AP009380	PGN_1171	coenzyme A transferase beta subunit		1302853	1303515	663	forward	1.211	0.276	0.353	0.498	0.297	0.929	CDS	GI:188594715	BAG33690.1
AP009380	PGN_1172	acyl-CoA dehydrogenase short-chain specific		1303561	1304700	1140	forward	1.713	0.777	0.047	0.123	0.391	1.984	CDS	GI:188594716	BAG33691.1
AP009380	PGN_1173	putative electron transfer flavoprotein beta subunit		1304715	1305500	786	forward	1.718	0.781	0.049	0.126	0.396	1.971	CDS	GI:188594717	BAG33692.1
AP009380	PGN_1174	electron transfer flavoprotein alpha subunit		1305514	1306521	1008	forward	1.263	0.337	0.340	0.490	0.353	0.954	CDS	GI:188594718	BAG33693.1
AP009380	PGN_1175	putative enoyl-CoA hydratase		1306625	1307395	771	forward	1.258	0.332	0.407	0.546	0.400	0.830	CDS	GI:188594719	BAG33694.1
AP009380	PGN_1176	putative 3-hydroxybutyryl-CoA dehydrogenase		1307442	1308287	846	forward	1.128	0.174	0.644	0.750	0.375	0.463	CDS	GI:188594720	BAG33695.1
AP009380	PGN_1177	transposase in ISPg1		1308536	1309621	1086	forward	0.772	-0.373	0.396	0.537	0.440	-0.849	CDS	GI:188594721	BAG33696.1
AP009380	PGN_1178	acetate kinase		1309802	1310998	1197	reverse	2.680	1.422	0.000	0.000	0.219	6.492	CDS	GI:188594722	BAG33697.1

AP009380	PGN_1179	phosphotransacetylase		1311044	1312054	1011	reverse	2.110	1.077	0.000	0.000	0.208	5.178	CDS	GI:188594723	BAG33698.1
AP009380	PGN_1180	conserved hypothetical protein		1312263	1313111	849	reverse	1.663	0.734	0.000	0.001	0.186	3.946	CDS	GI:188594724	BAG33699.1
AP009380	PGN_1181	probable thiol:disulfide oxidoreductase		1313252	1314355	1104	reverse	2.204	1.140	0.000	0.001	0.282	4.041	CDS	GI:188594725	BAG33700.1
AP009380	PGN_1182	conserved hypothetical protein		1314623	1314871	249	forward	0.665	-0.588	0.057	0.140	0.308	-1.907	CDS	GI:188594726	BAG33701.1
AP009380	PGN_1183	hypothetical protein		1315054	1315197	144	forward	0.875	-0.193	0.503	0.636	0.288	-0.670	CDS	GI:188594727	BAG33702.1
AP009380	PGN_1184	conserved hypothetical protein		1315228	1316160	933	forward	1.803	0.850	0.000	0.004	0.238	3.565	CDS	GI:188594728	BAG33703.1
AP009380	PGN_1185	conserved hypothetical protein		1316212	1316775	564	reverse	2.616	1.387	0.000	0.000	0.201	6.906	CDS	GI:188594729	BAG33704.1
AP009380	PGN_1186	putative DNA-binding response regulator RprY	rprY	1316892	1317629	738	reverse	1.440	0.526	0.016	0.061	0.219	2.399	CDS	GI:188594730	BAG33705.1
AP009380	PGN_1187	conserved hypothetical protein		1318389	1319432	1044	forward	2.905	1.539	0.000	0.000	0.239	6.449	CDS	GI:188594731	BAG33706.1
AP009380	PGN_1188	conserved hypothetical protein		1319510	1320121	612	forward	2.852	1.512	0.000	0.000	0.207	7.309	CDS	GI:188594732	BAG33707.1
AP009380	PGN_1189	phosphoglucomutase/phosphomannomutase		1320175	1321563	1389	forward	3.041	1.604	0.000	0.000	0.292	5.494	CDS	GI:188594733	BAG33708.1
AP009380	PGN_1190	RNA methyltransferase		1321608	1323044	1437	forward	2.626	1.393	0.000	0.000	0.296	4.701	CDS	GI:188594734	BAG33709.1
AP009380	PGN_1191	transposase in ISPg1		1323484	1324569	1086	reverse	0.710	-0.493	0.270	0.417	0.447	-1.102	CDS	GI:188594735	BAG33710.1
AP009380	PGN_1192	DNA-binding protein histone-like family		1324680	1325165	486	forward	0.407	-1.296	0.000	0.001	0.334	-3.884	CDS	GI:188594736	BAG33711.1
AP009380	PGN_1193	conserved hypothetical protein		1325303	1326409	1107	forward	1.215	0.282	0.351	0.498	0.302	0.932	CDS	GI:188594737	BAG33712.1
AP009380	PGN_1194	alanine racemase		1326445	1328916	2472	forward	1.731	0.791	0.019	0.066	0.336	2.353	CDS	GI:188594738	BAG33713.1
AP009380	PGN_1195	conserved hypothetical protein		1329224	1330447	1224	reverse	0.850	-0.234	0.276	0.424	0.215	-1.089	CDS	GI:188594739	BAG33714.1
AP009380	PGN_t0029	tRNA-Arg		1330508	1330581	74	reverse	0.418	-1.258	0.019	0.066	0.535	-2.351	tRNA		
AP009380	PGN_t0030	tRNA-Arg		1330617	1330690	74	reverse	1.134	0.182	0.737	0.818	0.540	0.336	tRNA		
AP009380	PGN_1196	putative sugar phosphate isomerase		1330785	1331609	825	reverse	1.584	0.663	0.026	0.083	0.298	2.222	CDS	GI:188594740	BAG33715.1
AP009380	PGN_1197	conserved hypothetical protein		1331602	1332453	852	reverse	1.288	0.365	0.138	0.261	0.246	1.485	CDS	GI:188594741	BAG33716.1
AP009380	PGN_1198	putative sodium-solute transporter		1332450	1333910	1461	reverse	0.985	-0.022	0.921	0.951	0.218	-0.099	CDS	GI:188594742	BAG33717.1
AP009380	PGN_1199	DNA-binding protein histone-like family		1334281	1334739	459	forward	1.796	0.845	0.003	0.017	0.280	3.018	CDS	GI:188594743	BAG33718.1
AP009380	PGN_1200	ATPase AAA family		1334823	1336127	1305	forward	1.196	0.258	0.224	0.366	0.212	1.216	CDS	GI:188594744	BAG33719.1
AP009380	PGN_1201	conserved hypothetical protein		1336210	1336920	711	forward	1.093	0.128	0.602	0.716	0.245	0.522	CDS	GI:188594745	BAG33720.1
AP009380	PGN_1202	RNA polymerase sigma-54 factor	rpoN	1336884	1338341	1458	reverse	1.375	0.459	0.047	0.123	0.231	1.985	CDS	GI:188594746	BAG33721.1
AP009380	PGN_1203	UDP-N-acetylmuramoylalanyl-D-glutamyl-2, 6-diaminopimelate–D-alanyl-D-alanyl ligase		1338335	1339639	1305	reverse	0.974	-0.038	0.858	0.909	0.209	-0.179	CDS	GI:188594747	BAG33722.1
AP009380	PGN_1204	probable aspartate-1-decarboxylase		1339841	1340197	357	forward	0.936	-0.095	0.741	0.821	0.288	-0.330	CDS	GI:188594748	BAG33723.1
AP009380	PGN_1205	signal recognition particle protein		1340274	1341611	1338	forward	1.468	0.554	0.031	0.093	0.256	2.161	CDS	GI:188594749	BAG33724.1
AP009380	PGN_1206	putative methylenetetrahydrofolate dehydrogenase/methenyltetrahydrofolate cyclohydrola		1341732	1342622	891	forward	0.864	-0.210	0.284	0.432	0.196	-1.071	CDS	GI:188594750	BAG33725.1
AP009380	PGN_1207	putative transport multidrug efflux protein		1342915	1344261	1347	forward	0.940	-0.089	0.748	0.825	0.275	-0.322	CDS	GI:188594751	BAG33726.1
AP009380	PGN_1208	ClpB protein	clpB	1344903	1347494	2592	reverse	0.366	-1.451	0.002	0.014	0.471	-3.080	CDS	GI:188594752	BAG33727.1
AP009380	PGN_1209	probable flavodoxin		1347713	1348273	561	forward	0.987	-0.019	0.946	0.962	0.280	-0.068	CDS	GI:188594753	BAG33728.1
AP009380	PGN_1210	hypothetical protein		1349272	1350174	903	forward	0.681	-0.553	0.018	0.064	0.234	-2.370	CDS	GI:188594754	BAG33729.1
AP009380	PGN_1211	hypothetical protein		1350327	1351196	870	forward	1.091	0.126	0.608	0.722	0.246	0.513	CDS	GI:188594755	BAG33730.1
AP009380	PGN_1212	hypothetical protein		1351214	1351858	645	forward	0.963	-0.055	0.839	0.897	0.272	-0.203	CDS	GI:188594756	BAG33731.1
AP009380	PGN_1213	putative ATP-binding protein		1351855	1355046	3192	forward	1.074	0.103	0.659	0.761	0.233	0.441	CDS	GI:188594757	BAG33732.1
AP009380	PGN_1214	hypothetical protein		1355050	1355760	711	forward	1.176	0.233	0.429	0.567	0.295	0.791	CDS	GI:188594758	BAG33733.1
AP009380	PGN_1215	hypothetical protein		1355767	1356297	531	forward	1.094	0.130	0.661	0.763	0.296	0.438	CDS	GI:188594759	BAG33734.1
AP009380	PGN_1216	transposase in ISPg1		1356488	1357573	1086	forward	0.630	-0.666	0.126	0.247	0.435	-1.530	CDS	GI:188594760	BAG33735.1
AP009380	PGN_1217	hypothetical protein		1357785	1357895	111	forward	0.724	-0.465	0.128	0.250	0.306	-1.522	CDS	GI:188594761	BAG33736.1
AP009380	PGN_1218	asparaginyl-tRNA synthetase		1357947	1359356	1410	reverse	2.288	1.194	0.001	0.006	0.349	3.426	CDS	GI:188594762	BAG33737.1
AP009380	PGN_1219	ribosomal large subunit pseudouridine synthase B		1359388	1360707	1320	reverse	1.970	0.978	0.003	0.018	0.328	2.979	CDS	GI:188594763	BAG33738.1
AP009380	PGN_1220	adenylosuccinate lyase		1360808	1362151	1344	reverse	1.681	0.749	0.028	0.087	0.341	2.198	CDS	GI:188594764	BAG33739.1
AP009380	PGN_1221	probable ATP:corrinoid adenosyltransferase		1362286	1362849	564	reverse	0.769	-0.380	0.093	0.202	0.226	-1.681	CDS	GI:188594765	BAG33740.1
AP009380	PGN_1222	conserved hypothetical protein		1362872	1363528	657	reverse	1.061	0.086	0.849	0.903	0.452	0.190	CDS	GI:188594766	BAG33741.1
AP009380	PGN_1223	uracil permease		1363547	1364734	1188	reverse	0.526	-0.927	0.016	0.060	0.385	-2.407	CDS	GI:188594767	BAG33742.1
AP009380	PGN_1224	probable transcriptional regulator		1365074	1365541	468	forward	1.170	0.227	0.248	0.393	0.196	1.156	CDS	GI:188594768	BAG33743.1
AP009380	PGN_1225	probable exodeoxyribonuclease VII large subunit		1365594	1366976	1383	forward	1.630	0.705	0.034	0.099	0.332	2.125	CDS	GI:188594769	BAG33744.1
AP009380	PGN_1226	ribonucleotide reductase		1367249	1369801	2553	forward	1.321	0.402	0.086	0.191	0.234	1.718	CDS	GI:188594770	BAG33745.1
AP009380	PGN_1227	TPR domain protein		1370001	1372175	2175	forward	1.076	0.105	0.718	0.806	0.291	0.362	CDS	GI:188594771	BAG33746.1
AP009380	PGN_1228	hypothetical protein		1372442	1372552	111	forward	0.917	-0.126	0.691	0.787	0.317	-0.397	CDS	GI:188594772	BAG33747.1
AP009380	PGN_1229	valyl-tRNA synthetase		1372931	1375561	2631	forward	1.740	0.799	0.016	0.061	0.333	2.400	CDS	GI:188594773	BAG33748.1
AP009380	PGN_1230	conserved hypothetical protein		1375590	1376042	453	forward	1.847	0.885	0.011	0.047	0.350	2.529	CDS	GI:188594774	BAG33749.1
AP009380	PGN_1231	hypothetical protein		1376094	1376336	243	reverse	0.421	-1.250	0.002	0.016	0.411	-3.044	CDS	GI:188594775	BAG33750.1
AP009380	PGN_t0031	tRNA-Thr		1376103	1376175	73	forward	0.378	-1.402	0.005	0.027	0.499	-2.812	tRNA		
AP009380	PGN_1232	thioredoxin reductase		1376369	1377310	942	forward	1.090	0.124	0.489	0.626	0.180	0.691	CDS	GI:188594776	BAG33751.1
AP009380	PGN_1233	conserved hypothetical protein		1377879	1378493	615	forward	0.967	-0.049	0.868	0.917	0.295	-0.167	CDS	GI:188594777	BAG33752.1
AP009380	PGN_1234	conserved hypothetical protein		1378668	1380269	1602	reverse	1.506	0.591	0.048	0.123	0.298	1.982	CDS	GI:188594778	BAG33753.1
AP009380	PGN_1235	membrane protein PorS	porS	1380259	1381566	1308	reverse	0.849	-0.237	0.350	0.498	0.253	-0.934	CDS	GI:188594779	BAG33754.1
AP009380	PGN_1236	regulator PorR	porR	1381563	1382717	1155	reverse	1.765	0.819	0.053	0.134	0.424	1.934	CDS	GI:188594780	BAG33755.1
AP009380	PGN_1237	hypothetical protein		1382872	1382964	93	forward	0.884	-0.178	0.749	0.826	0.555	-0.320	CDS	GI:188594781	BAG33756.1
AP009380	PGN_1238	conserved hypothetical protein		1383104	1384240	1137	reverse	1.625	0.700	0.050	0.128	0.357	1.959	CDS	GI:188594782	BAG33757.1
AP009380	PGN_1239	probable lipopolysaccharide biosynthesis glycosyltransferase		1384351	1385211	861	reverse	1.843	0.882	0.025	0.081	0.394	2.237	CDS	GI:188594783	BAG33758.1
AP009380	PGN_1240	conserved hypothetical protein		1385217	1386368	1152	reverse	1.328	0.409	0.236	0.380	0.345	1.185	CDS	GI:188594784	BAG33759.1
AP009380	PGN_1241	hypothetical protein		1386415	1386726	312	reverse	1.024	0.034	0.915	0.949	0.321	0.106	CDS	GI:188594785	BAG33760.1
AP009380	PGN_1242	putative O-antigen polymerase Wzy	wzy	1386747	1387790	1044	reverse	0.576	-0.796	0.015	0.057	0.327	-2.431	CDS	GI:188594786	BAG33761.1
AP009380	PGN_1243	UDP-glucose 6-dehydrogenase		1387806	1389374	1569	reverse	0.828	-0.273	0.158	0.287	0.193	-1.413	CDS	GI:188594787	BAG33762.1
AP009380	PGN_1244	putative peptide chain release factor RF-2		1389418	1390377	960	reverse	1.160	0.214	0.341	0.490	0.225	0.953	CDS	GI:188594788	BAG33763.1
AP009380	PGN_1245	long-chain-fatty-acid-CoA ligase		1390657	1392483	1827	reverse	0.969	-0.046	0.828	0.887	0.210	-0.217	CDS	GI:188594789	BAG33764.1
AP009380	PGN_1246	hypothetical protein		1392638	1396789	4152	reverse	0.397	-1.333	0.000	0.000	0.302	-4.407	CDS	GI:188594790	BAG33765.1
AP009380	PGN_1247	hypothetical protein		1397064	1397213	150	forward	0.550	-0.863	0.031	0.094	0.401	-2.154	CDS	GI:188594791	BAG33766.1
AP009380	PGN_1248	hypothetical protein		1397280	1397396	117	forward	0.523	-0.935	0.110	0.225	0.585	-1.600	CDS	GI:188594792	BAG33767.1
AP009380	PGN_1249	conserved hypothetical protein		1397475	1397627	153	reverse	0.339	-1.561	0.000	0.001	0.389	-4.010	CDS	GI:188594793	BAG33768.1
AP009380	PGN_1250	hypothetical protein		1397708	1397926	219	forward	0.665	-0.590	0.219	0.362	0.479	-1.230	CDS	GI:188594794	BAG33769.1
AP009380	PGN_1251	probable glycosyltransferase	gtfB	1398046	1399173	1128	forward	0.785	-0.350	0.050	0.128	0.178	-1.961	CDS	GI:188594795	BAG33770.1
AP009380	PGN_1252	iron-containing alcohol dehydrogenase		1399553	1400701	1149	forward	0.830	-0.268	0.470	0.609	0.371	-0.723	CDS	GI:188594796	BAG33771.1
AP009380	PGN_1253	hypothetical protein		1400840	1401256	417	forward	1.003	0.005	0.984	0.986	0.233	0.020	CDS	GI:188594797	BAG33772.1
AP009380	PGN_1254	hypothetical protein		1401417	1402022	606	forward	0.860	-0.218	0.301	0.449	0.211	-1.035	CDS	GI:188594798	BAG33773.1
AP009380	PGN_1255	putative heptosyltransferase	rfa	1402106	1403161	1056	forward	1.106	0.145	0.677	0.777	0.348	0.416	CDS	GI:188594799	BAG33774.1
AP009380	PGN_1256	conserved hypothetical protein		1403145	1403597	453	forward	1.088	0.121	0.745	0.824	0.372	0.326	CDS	GI:188594800	BAG33775.1
AP009380	PGN_1257	hypothetical protein		1403714	1403806	93	forward	0.814	-0.297	0.522	0.652	0.464	-0.640	CDS	GI:188594801	BAG33776.1
AP009380	PGN_1258	cobalamin biosynthesis protein		1404353	1405375	1023	reverse	1.445	0.531	0.098	0.209	0.320	1.656	CDS	GI:188594802	BAG33777.1
AP009380	PGN_1259	probable histidinol-phosphate aminotransferase		1405389	1406396	1008	reverse	1.621	0.697	0.022	0.073	0.305	2.287	CDS	GI:188594803	BAG33778.1
AP009380	PGN_1260	cobyric acid synthase		1406389	1407885	1497	reverse	1.447	0.533	0.030	0.092	0.246	2.171	CDS	GI:188594804	BAG33779.1
AP009380	PGN_1261	probable cobalamin adenosyltransferase		1407882	1408448	567	reverse	1.513	0.598	0.032	0.096	0.279	2.139	CDS	GI:188594805	BAG33780.1
AP009380	PGN_1262	cobyrinic acid a,c-diamide synthase		1408471	1409790	1320	reverse	1.421	0.507	0.042	0.115	0.250	2.030	CDS	GI:188594806	BAG33781.1

AP009380	PGN_1263	conserved hypothetical protein		1410847	1414254	3408	reverse	0.981	-0.028	0.908	0.945	0.242	-0.116	CDS	GI:188594807	BAG33782.1
AP009380	PGN_1264	conserved hypothetical protein		1414251	1414967	717	reverse	0.660	-0.599	0.031	0.093	0.277	-2.158	CDS	GI:188594808	BAG33783.1
AP009380	PGN_1265	hypothetical protein		1415080	1415286	207	reverse	0.723	-0.467	0.402	0.543	0.558	-0.837	CDS	GI:188594809	BAG33784.1
AP009380	PGN_1266	conserved hypothetical protein		1415796	1415924	129	reverse	1.123	0.168	0.600	0.715	0.319	0.525	CDS	GI:188594810	BAG33785.1
AP009380	PGN_1267	conserved hypothetical protein		1415956	1416828	873	forward	1.365	0.449	0.104	0.218	0.276	1.625	CDS	GI:188594811	BAG33786.1
AP009380	PGN_1268	putative oxidoreductase		1417068	1417889	822	forward	0.778	-0.363	0.263	0.410	0.324	-1.118	CDS	GI:188594812	BAG33787.1
AP009380	PGN_1269	putative electron transport protein		1417886	1419253	1368	forward	0.981	-0.028	0.933	0.955	0.328	-0.084	CDS	GI:188594813	BAG33788.1
AP009380	PGN_1270	conserved hypothetical protein		1419259	1419843	585	forward	0.978	-0.033	0.912	0.947	0.294	-0.111	CDS	GI:188594814	BAG33789.1
AP009380	PGN_1271	probable thioesterase superfamily protein		1419954	1420427	474	reverse	0.711	-0.492	0.011	0.047	0.194	-2.530	CDS	GI:188594815	BAG33790.1
AP009380	PGN_1272	putative diaminopimelate decarboxylase		1420667	1421815	1149	forward	0.727	-0.460	0.241	0.385	0.393	-1.172	CDS	GI:188594816	BAG33791.1
AP009380	PGN_1273	probable 1,4-dihydroxy-2-naphthoate octaprenyltransferase		1421805	1422692	888	forward	0.737	-0.441	0.080	0.181	0.252	-1.749	CDS	GI:188594817	BAG33792.1
AP009380	PGN_1274	conserved hypothetical protein		1422784	1423164	381	forward	0.652	-0.618	0.109	0.224	0.385	-1.603	CDS	GI:188594818	BAG33793.1
AP009380	PGN_1275	conserved hypothetical protein		1423199	1424515	1317	forward	0.715	-0.485	0.223	0.366	0.398	-1.219	CDS	GI:188594819	BAG33794.1
AP009380	PGN_1276	transposase in ISPg1		1425416	1426501	1086	reverse	0.692	-0.532	0.261	0.407	0.473	-1.125	CDS	GI:188594820	BAG33795.1
AP009380	PGN_1277	conserved hypothetical protein		1426697	1426867	171	forward	0.864	-0.211	0.693	0.788	0.535	-0.395	CDS	GI:188594821	BAG33796.1
AP009380	PGN_1278	partial transposase in ISPg3		1427362	1428150	789	forward	0.559	-0.839	0.031	0.094	0.390	-2.152	CDS	GI:188594822	BAG33797.1
AP009380	PGN_1279	partial transposase in ISPg3		1428190	1428510	321	forward	0.786	-0.347	0.391	0.532	0.404	-0.859	CDS	GI:188594823	BAG33798.1
AP009380	PGN_1280	partial transposase in ISPg1		1428497	1428928	432	reverse	0.679	-0.558	0.196	0.334	0.431	-1.293	CDS	GI:188594824	BAG33799.1
AP009380	PGN_1281	putative conserved protein found in conjugate transposon TraM	traM	1429021	1430160	1140	forward	0.561	-0.834	0.000	0.003	0.232	-3.601	CDS	GI:188594825	BAG33800.1
AP009380	PGN_1282	conserved protein found in conjugate transposon TraN	traN	1430199	1431119	921	forward	0.636	-0.652	0.019	0.068	0.279	-2.336	CDS	GI:188594826	BAG33801.1
AP009380	PGN_1283	conserved protein found in conjugate transposon TraO	traO	1431151	1431705	555	forward	0.441	-1.180	0.000	0.003	0.320	-3.692	CDS	GI:188594827	BAG33802.1
AP009380	PGN_1284	putative DNA primase involved in conjugation TraP	traP	1431705	1432559	855	forward	0.533	-0.908	0.000	0.001	0.233	-3.906	CDS	GI:188594828	BAG33803.1
AP009380	PGN_1285	conserved protein found in conjugate transposon TraQ	traQ	1432584	1433045	462	forward	0.610	-0.714	0.007	0.033	0.265	-2.696	CDS	GI:188594829	BAG33804.1
AP009380	PGN_1286	probable lysozyme		1433029	1433544	516	forward	0.213	-2.229	0.000	0.000	0.426	-5.238	CDS	GI:188594830	BAG33805.1
AP009380	PGN_1287	conserved hypothetical protein		1433605	1434009	405	reverse	0.214	-2.222	0.000	0.000	0.469	-4.736	CDS	GI:188594831	BAG33806.1
AP009380	PGN_1288	conserved hypothetical protein		1434011	1435237	1227	reverse	0.276	-1.857	0.000	0.001	0.478	-3.885	CDS	GI:188594832	BAG33807.1
AP009380	PGN_1289	conserved hypothetical protein		1435495	1435725	231	reverse	0.576	-0.797	0.049	0.126	0.404	-1.971	CDS	GI:188594833	BAG33808.1
AP009380	PGN_1290	conserved hypothetical protein		1435730	1435984	255	reverse	0.667	-0.585	0.150	0.278	0.406	-1.441	CDS	GI:188594834	BAG33809.1
AP009380	PGN_1291	conserved hypothetical protein related to phage		1436011	1437285	1275	reverse	0.668	-0.582	0.138	0.262	0.392	-1.482	CDS	GI:188594835	BAG33810.1
AP009380	PGN_1292	probable anti-restriction protein		1437302	1437832	531	reverse	0.612	-0.710	0.130	0.253	0.469	-1.512	CDS	GI:188594836	BAG33811.1
AP009380	PGN_1293	conserved hypothetical protein		1437854	1438270	417	reverse	0.457	-1.129	0.002	0.014	0.365	-3.096	CDS	GI:188594837	BAG33812.1
AP009380	PGN_1294	conserved hypothetical protein		1438283	1438501	219	reverse	0.499	-1.003	0.020	0.068	0.429	-2.335	CDS	GI:188594838	BAG33813.1
AP009380	PGN_1295	hypothetical protein		1438514	1438780	267	reverse	0.673	-0.571	0.073	0.168	0.319	-1.791	CDS	GI:188594839	BAG33814.1
AP009380	PGN_1296	putative OmpA family protein		1439480	1441498	2019	reverse	0.785	-0.350	0.223	0.366	0.287	-1.219	CDS	GI:188594840	BAG33815.1
AP009380	PGN_1297	conserved hypothetical protein		1441520	1442113	594	reverse	0.804	-0.315	0.251	0.397	0.274	-1.147	CDS	GI:188594841	BAG33816.1
AP009380	PGN_1298	conserved hypothetical protein		1442133	1442552	420	reverse	0.750	-0.416	0.081	0.182	0.238	-1.744	CDS	GI:188594842	BAG33817.1
AP009380	PGN_1299	hypothetical protein		1442549	1442665	117	reverse	0.627	-0.673	0.093	0.203	0.401	-1.678	CDS	GI:188594843	BAG33818.1
AP009380	PGN_1300	probable transcriptional regulator		1442769	1443455	687	reverse	0.982	-0.027	0.908	0.945	0.233	-0.115	CDS	GI:188594844	BAG33819.1
AP009380	PGN_1301	probable transcriptional regulator		1443472	1443828	357	reverse	1.045	0.063	0.825	0.885	0.287	0.221	CDS	GI:188594845	BAG33820.1
AP009380	PGN_1302	O-antigen ligase waaL	waaL	1443893	1445308	1416	reverse	1.842	0.881	0.005	0.025	0.310	2.840	CDS	GI:188594846	BAG33821.1
AP009380	PGN_1303	hypothetical protein		1445350	1446237	888	reverse	1.615	0.692	0.019	0.067	0.295	2.346	CDS	GI:188594847	BAG33822.1
AP009380	PGN_1304	conserved hypothetical protein		1446253	1447131	879	reverse	1.109	0.149	0.497	0.632	0.220	0.679	CDS	GI:188594848	BAG33823.1
AP009380	PGN_1305	putative N-acetylmuramoyl-L-alanine amidase		1447172	1448362	1191	reverse	0.740	-0.435	0.064	0.153	0.235	-1.849	CDS	GI:188594849	BAG33824.1
AP009380	PGN_t0032	tRNA-Thr		1448555	1448631	77	reverse	0.411	-1.283	0.001	0.010	0.400	-3.205	tRNA		
AP009380	PGN_1306	hypothetical protein		1448901	1449152	252	reverse	0.587	-0.767	0.017	0.061	0.320	-2.394	CDS	GI:188594850	BAG33825.1
AP009380	PGN_1307	hypothetical protein		1449432	1449659	228	reverse	0.251	-1.994	0.000	0.000	0.282	-7.068	CDS	GI:188594851	BAG33826.1
AP009380	PGN_1308	probable iron dependent repressor		1449706	1450638	933	forward	0.929	-0.106	0.599	0.715	0.202	-0.525	CDS	GI:188594852	BAG33827.1
AP009380	PGN_1309	ferrous iron transport protein B		1450675	1452849	2175	forward	0.609	-0.717	0.011	0.045	0.281	-2.551	CDS	GI:188594853	BAG33828.1
AP009380	PGN_1310	glycogen synthase		1452886	1454532	1647	forward	0.815	-0.294	0.308	0.456	0.289	-1.019	CDS	GI:188594854	BAG33829.1
AP009380	PGN_1311	putative K+dependent Na+exchanger related-protein		1454601	1455554	954	forward	0.640	-0.645	0.025	0.080	0.287	-2.244	CDS	GI:188594855	BAG33830.1
AP009380	PGN_1312	probable transcriptional regulator		1455575	1456039	465	forward	0.679	-0.559	0.076	0.173	0.315	-1.774	CDS	GI:188594856	BAG33831.1
AP009380	PGN_1313	conserved hypothetical protein		1456472	1458199	1728	forward	0.795	-0.330	0.310	0.457	0.325	-1.016	CDS	GI:188594857	BAG33832.1
AP009380	PGN_1314	ATP-dependent DNA helicase		1458433	1460730	2298	reverse	0.551	-0.859	0.000	0.001	0.210	-4.091	CDS	GI:188594858	BAG33833.1
AP009380	PGN_1315	conserved hypothetical protein		1460730	1462109	1380	reverse	0.513	-0.964	0.014	0.055	0.393	-2.453	CDS	GI:188594859	BAG33834.1
AP009380	PGN_1316	excinuclease ABC A subunit	uvrAI	1462135	1465038	2904	reverse	0.479	-1.063	0.000	0.003	0.289	-3.674	CDS	GI:188594860	BAG33835.1
AP009380	PGN_1317	conserved hypothetical protein		1465109	1466599	1491	reverse	0.089	-3.489	0.000	0.000	0.226	-15.473	CDS	GI:188594861	BAG33836.1
AP009380	PGN_1318	putative ABC transporter ATP-binding protein		1466577	1467311	735	reverse	0.059	-4.085	0.000	0.000	0.214	-19.127	CDS	GI:188594862	BAG33837.1
AP009380	PGN_1319	transposase in ISPg1		1467551	1468636	1086	forward	0.605	-0.726	0.105	0.218	0.448	-1.622	CDS	GI:188594863	BAG33838.1
AP009380	PGN_1320	conserved hypothetical protein		1468766	1469419	654	reverse	0.039	-4.696	0.000	0.000	0.206	-22.755	CDS	GI:188594864	BAG33839.1
AP009380	PGN_1321	conserved hypothetical protein		1469657	1470997	1341	reverse	0.763	-0.389	0.403	0.544	0.466	-0.836	CDS	GI:188594865	BAG33840.1
AP009380	PGN_1322	conserved hypothetical protein		1471140	1471316	177	reverse	0.738	-0.438	0.064	0.153	0.237	-1.852	CDS	GI:188594866	BAG33841.1
AP009380	PGN_1323	TPR domain protein		1471380	1473077	1698	reverse	1.828	0.871	0.008	0.036	0.328	2.658	CDS	GI:188594867	BAG33842.1
AP009380	PGN_1324	probable ABC transporter membrane protein		1473255	1474157	903	reverse	1.750	0.808	0.059	0.144	0.428	1.886	CDS	GI:188594868	BAG33843.1
AP009380	PGN_1325	probable ABC transporter membrane protein		1474157	1475041	885	reverse	1.403	0.489	0.136	0.259	0.328	1.492	CDS	GI:188594869	BAG33844.1
AP009380	PGN_1326	hypothetical protein		1475108	1476331	1224	reverse	1.131	0.178	0.415	0.553	0.219	0.815	CDS	GI:188594870	BAG33845.1
AP009380	PGN_1327	hypothetical protein		1476335	1477345	1011	reverse	1.207	0.272	0.242	0.386	0.232	1.169	CDS	GI:188594871	BAG33846.1
AP009380	PGN_1328	hypothetical protein		1477342	1478463	1122	reverse	0.930	-0.104	0.580	0.700	0.188	-0.553	CDS	GI:188594872	BAG33847.1
AP009380	PGN_1329	hypothetical protein		1478460	1478912	453	reverse	0.822	-0.282	0.299	0.447	0.272	-1.038	CDS	GI:188594873	BAG33848.1
AP009380	PGN_1330	probable branched chain amino acid ABC transporter ATP-binding protein		1479164	1479901	738	reverse	0.737	-0.440	0.033	0.097	0.206	-2.134	CDS	GI:188594874	BAG33849.1
AP009380	PGN_1331	conserved hypothetical protein		1480142	1480453	312	reverse	1.547	0.629	0.057	0.140	0.330	1.905	CDS	GI:188594875	BAG33850.1
AP009380	PGN_1332	putative para-aminobenzoate synthase component I		1480507	1481484	978	forward	1.605	0.683	0.034	0.099	0.322	2.121	CDS	GI:188594876	BAG33851.1
AP009380	PGN_1333	probable para-aminobenzoate synthase component I		1481491	1482090	600	forward	1.743	0.801	0.039	0.109	0.389	2.060	CDS	GI:188594877	BAG33852.1
AP009380	PGN_1334	conserved hypothetical protein		1482135	1483616	1482	reverse	0.654	-0.612	0.069	0.160	0.336	-1.821	CDS	GI:188594878	BAG33853.1
AP009380	PGN_1335	conserved hypothetical protein		1483775	1486585	2811	reverse	0.891	-0.166	0.509	0.639	0.251	-0.661	CDS	GI:188594879	BAG33854.1
AP009380	PGN_1336	conserved hypothetical protein		1486757	1487938	1182	reverse	0.521	-0.942	0.001	0.007	0.279	-3.372	CDS	GI:188594880	BAG33855.1
AP009380	PGN_1337	conserved hypothetical protein		1487951	1488232	282	reverse	0.730	-0.455	0.116	0.234	0.290	-1.571	CDS	GI:188594881	BAG33856.1
AP009380	PGN_1338	pyruvate phosphate dikinase		1488289	1491015	2727	reverse	0.863	-0.212	0.495	0.631	0.310	-0.683	CDS	GI:188594882	BAG33857.1
AP009380	PGN_1339	conserved hypothetical protein		1491183	1491326	144	forward	0.834	-0.262	0.368	0.511	0.291	-0.901	CDS	GI:188594883	BAG33858.1
AP009380	PGN_1340	conserved hypothetical protein		1491379	1494342	2964	reverse	0.736	-0.443	0.124	0.244	0.288	-1.539	CDS	GI:188594884	BAG33859.1
AP009380	PGN_1341	putative CoA transferase		1494874	1496370	1497	reverse	1.129	0.175	0.473	0.610	0.243	0.718	CDS	GI:188594885	BAG33860.1
AP009380	PGN_1342	putative SAM/TRAM family methylase protein		1496674	1498071	1398	forward	1.311	0.391	0.070	0.163	0.216	1.812	CDS	GI:188594886	BAG33861.1
AP009380	PGN_1343	probable ABC transporter ATP-binding protein		1498978	1499805	828	forward	1.294	0.371	0.237	0.381	0.314	1.183	CDS	GI:188594887	BAG33862.1
AP009380	PGN_1344	conserved hypothetical protein		1499819	1500673	855	forward	0.769	-0.379	0.241	0.385	0.323	-1.172	CDS	GI:188594888	BAG33863.1
AP009380	PGN_1345	conserved hypothetical protein		1500670	1501428	759	forward	1.033	0.046	0.872	0.919	0.288	0.161	CDS	GI:188594889	BAG33864.1
AP009380	PGN_1346	putative transcriptional regulator		1501425	1501796	372	forward	1.219	0.285	0.392	0.533	0.333	0.857	CDS	GI:188594890	BAG33865.1
AP009380	PGN_1347	putative TonB-dependent receptor exported protein		1502016	1504520	2505	forward	1.085	0.118	0.632	0.741	0.246	0.479	CDS	GI:188594891	BAG33866.1
AP009380	PGN_1348	conserved hypothetical protein		1504551	1505291	741	forward	1.119	0.163	0.511	0.641	0.247	0.657	CDS	GI:188594892	BAG33867.1

AP009380	PGN_1349	probable dipeptidyl anminopeptidase		1505647	1507926	2280	forward	1.577	0.657	0.034	0.100	0.310	2.117	CDS	GI:188594893	BAG33868.1
AP009380	PGN_1350	conserved hypothetical protein		1508085	1509077	993	reverse	0.901	-0.151	0.530	0.656	0.240	-0.628	CDS	GI:188594894	BAG33869.1
AP009380	PGN_1351	conserved hypothetical protein		1509152	1509436	285	reverse	0.840	-0.252	0.304	0.452	0.245	-1.027	CDS	GI:188594895	BAG33870.1
AP009380	PGN_1352	conserved hypothetical protein with DUF1706 domain		1509570	1510106	537	reverse	0.893	-0.163	0.514	0.645	0.250	-0.653	CDS	GI:188594896	BAG33871.1
AP009380	PGN_1353	conserved hypothetical protein		1510110	1510526	417	reverse	0.833	-0.263	0.357	0.502	0.286	-0.921	CDS	GI:188594897	BAG33872.1
AP009380	PGN_1354	conserved hypothetical protein		1510702	1511634	933	forward	1.203	0.267	0.216	0.359	0.216	1.237	CDS	GI:188594898	BAG33873.1
AP009380	PGN_1355	conserved hypothetical protein		1511631	1511786	156	forward	1.524	0.607	0.012	0.049	0.242	2.506	CDS	GI:188594899	BAG33874.1
AP009380	PGN_1356	conserved hypothetical protein		1511776	1512108	333	forward	1.287	0.364	0.114	0.231	0.230	1.582	CDS	GI:188594900	BAG33875.1
AP009380	PGN_1357	conserved hypothetical protein		1512186	1512596	411	forward	1.096	0.133	0.634	0.743	0.279	0.476	CDS	GI:188594901	BAG33876.1
AP009380	PGN_1358	conserved hypothetical protein		1512872	1513183	312	forward	0.805	-0.313	0.261	0.407	0.279	-1.124	CDS	GI:188594902	BAG33877.1
AP009380	PGN_1359	putative erythronate-4-phosphate dehydrogenase		1513187	1514320	1134	forward	0.947	-0.079	0.740	0.821	0.238	-0.332	CDS	GI:188594903	BAG33878.1
AP009380	PGN_1360	probable oxidoreductase		1514330	1515055	726	forward	1.068	0.095	0.739	0.820	0.286	0.333	CDS	GI:188594904	BAG33879.1
AP009380	PGN_1361	conserved hypothetical protein		1515640	1515843	204	forward	0.573	-0.804	0.010	0.043	0.312	-2.574	CDS	GI:188594905	BAG33880.1
AP009380	PGN_1362	probable exported transglycosylase protein		1515974	1517539	1566	forward	1.052	0.073	0.743	0.823	0.221	0.328	CDS	GI:188594906	BAG33881.1
AP009380	PGN_1363	ABC transporter ATP-binding protein	wzt	1517564	1519435	1872	forward	1.802	0.849	0.000	0.003	0.233	3.647	CDS	GI:188594907	BAG33882.1
AP009380	PGN_1364	probable peptidyl-prolyl cis-trans isomerase cyclophilin-type		1519443	1520147	705	forward	1.359	0.442	0.172	0.305	0.323	1.366	CDS	GI:188594908	BAG33883.1
AP009380	PGN_1365	conserved hypothetical protein		1520290	1520640	351	reverse	0.913	-0.131	0.655	0.759	0.293	-0.447	CDS	GI:188594909	BAG33884.1
AP009380	PGN_1366	conserved hypothetical protein		1520745	1522853	2109	reverse	0.966	-0.049	0.829	0.888	0.229	-0.215	CDS	GI:188594910	BAG33885.1
AP009380	PGN_1367	NAD-specific glutamate dehydrogenase		1523059	1524396	1338	reverse	1.509	0.594	0.046	0.122	0.298	1.992	CDS	GI:188594911	BAG33886.1
AP009380	PGN_1368	conserved hypothetical protein		1524720	1524830	111	forward	0.446	-1.164	0.001	0.006	0.342	-3.406	CDS	GI:188594912	BAG33887.1
AP009380	PGN_1369	conserved hypothetical protein		1524947	1525075	129	forward	1.059	0.083	0.853	0.905	0.448	0.185	CDS	GI:188594913	BAG33888.1
AP009380	PGN_1370	NAD-dependent nucleotide-diphosphate-sugar epimerase		1525085	1526041	957	reverse	0.791	-0.338	0.286	0.434	0.317	-1.067	CDS	GI:188594914	BAG33889.1
AP009380	PGN_1371	hypothetical protein		1526100	1526189	90	forward	0.275	-1.862	0.000	0.000	0.442	-4.213	CDS	GI:188594915	BAG33890.1
AP009380	PGN_1372	conserved hypothetical protein		1526357	1527067	711	forward	0.956	-0.064	0.774	0.848	0.225	-0.287	CDS	GI:188594916	BAG33891.1
AP009380	PGN_1373	probable transcriptional regulator		1527064	1527663	600	forward	1.116	0.159	0.433	0.571	0.202	0.784	CDS	GI:188594917	BAG33892.1
AP009380	PGN_1374	putative ribosomal large subunit pseudouridine synthase D		1527681	1528364	684	reverse	0.912	-0.133	0.467	0.606	0.183	-0.728	CDS	GI:188594918	BAG33893.1
AP009380	PGN_1375	putative beta-ketoacyl-acyl carrier protein reductase		1528408	1529154	747	reverse	0.919	-0.122	0.625	0.735	0.249	-0.489	CDS	GI:188594919	BAG33894.1
AP009380	PGN_1376	putative transcriptional regulator		1529238	1529873	636	reverse	0.768	-0.381	0.184	0.320	0.287	-1.328	CDS	GI:188594920	BAG33895.1
AP009380	PGN_t0033	tRNA-Gln		1530097	1530170	74	reverse	0.362	-1.468	0.000	0.003	0.399	-3.675	tRNA		
AP009380	PGN_1377	GTP-binding protein LepA		1530449	1532236	1788	forward	1.667	0.737	0.012	0.050	0.295	2.502	CDS	GI:188594921	BAG33896.1
AP009380	PGN_1378	replicative DNA helicase		1532328	1533857	1530	forward	1.527	0.610	0.031	0.093	0.282	2.163	CDS	GI:188594922	BAG33897.1
AP009380	PGN_1379	hypothetical protein		1534341	1534478	138	forward	0.435	-1.199	0.000	0.002	0.310	-3.865	CDS	GI:188594923	BAG33898.1
AP009380	PGN_1380	hypothetical protein		1534517	1534639	123	reverse	0.458	-1.127	0.003	0.018	0.379	-2.971	CDS	GI:188594924	BAG33899.1
AP009380	PGN_1381	alanyl-tRNA synthetase		1535303	1537933	2631	forward	1.204	0.268	0.224	0.366	0.221	1.215	CDS	GI:188594925	BAG33900.1
AP009380	PGN_1382	putative 3-dehydroquinate synthase		1538005	1539009	1005	forward	1.438	0.524	0.139	0.262	0.354	1.480	CDS	GI:188594926	BAG33901.1
AP009380	PGN_t0034	tRNA-Pro		1539045	1539119	75	forward	0.604	-0.727	0.032	0.096	0.340	-2.141	tRNA		
AP009380	PGN_1383	conserved hypothetical protein		1539254	1539985	732	reverse	0.936	-0.095	0.777	0.850	0.335	-0.284	CDS	GI:188594927	BAG33902.1
AP009380	PGN_1384	probable 1-acyl-sn-glycerol-3-phosphate acetyltransferase		1540000	1540785	786	reverse	0.551	-0.860	0.002	0.014	0.277	-3.101	CDS	GI:188594928	BAG33903.1
AP009380	PGN_1385	hypothetical protein		1540791	1541057	267	forward	0.624	-0.681	0.015	0.057	0.280	-2.436	CDS	GI:188594929	BAG33904.1
AP009380	PGN_1386	conserved hypothetical protein		1541300	1541569	270	forward	1.045	0.063	0.860	0.910	0.357	0.177	CDS	GI:188594930	BAG33905.1
AP009380	PGN_1387	putative ABC transporter permease protein		1541838	1543073	1236	reverse	0.978	-0.032	0.933	0.955	0.381	-0.084	CDS	GI:188594931	BAG33906.1
AP009380	PGN_1388	DNA ligase		1543086	1545095	2010	reverse	1.277	0.353	0.363	0.507	0.388	0.910	CDS	GI:188594932	BAG33907.1
AP009380	PGN_1389	probable acetyltransferase		1545083	1545610	528	reverse	1.229	0.297	0.428	0.566	0.375	0.792	CDS	GI:188594933	BAG33908.1
AP009380	PGN_1390	putative recombination protein RecR		1545617	1546240	624	reverse	1.070	0.098	0.790	0.859	0.366	0.267	CDS	GI:188594934	BAG33909.1
AP009380	PGN_1391	putative ribonuclease E		1546237	1547796	1560	reverse	1.055	0.077	0.752	0.829	0.244	0.317	CDS	GI:188594935	BAG33910.1
AP009380	PGN_1392	conserved hypothetical protein		1547949	1548041	93	reverse	1.089	0.123	0.655	0.759	0.276	0.446	CDS	GI:188594936	BAG33911.1
AP009380	PGN_1393	putative DNA-binding protein HU		1548072	1548350	279	reverse	1.092	0.127	0.629	0.738	0.262	0.484	CDS	GI:188594937	BAG33912.1
AP009380	PGN_1394	transposase in ISPg2		1548462	1549592	1131	reverse	1.736	0.796	0.038	0.107	0.384	2.075	CDS	GI:188594938	BAG33913.1
AP009380	PGN_1395	putative anaerobic ribonucleoside-triphosphate reductase activating protein		1549744	1550247	504	reverse	1.018	0.025	0.925	0.952	0.268	0.095	CDS	GI:188594939	BAG33914.1
AP009380	PGN_1396	anaerobic ribonucleoside-triphosphate reductase		1550268	1552664	2397	reverse	0.588	-0.766	0.011	0.047	0.302	-2.534	CDS	GI:188594940	BAG33915.1
AP009380	PGN_1397	transposase in ISPg1		1553593	1554678	1086	forward	0.633	-0.659	0.139	0.263	0.446	-1.478	CDS	GI:188594941	BAG33916.1
AP009380	PGN_r0007	5S ribosomal RNA		1554965	1555072	108	reverse	0.259	-1.950	0.000	0.000	0.461	-4.227	rRNA		
AP009380	PGN_r0008	23S ribosomal RNA		1555219	1558051	2833	reverse	0.490	-1.028	0.000	0.001	0.260	-3.953	rRNA		
AP009380	PGN_t0035	tRNA-Ala		1558170	1558246	77	reverse	0.495	-1.015	0.006	0.032	0.373	-2.724	tRNA		
AP009380	PGN_t0036	tRNA-Ile		1558248	1558321	74	reverse	0.413	-1.277	0.007	0.033	0.474	-2.697	tRNA		
AP009380	PGN_1398	conserved hypothetical protein		1558331	1558486	156	reverse	1.076	0.106	0.618	0.729	0.212	0.499	CDS	GI:188594942	BAG33917.1
AP009380	PGN_1399	conserved hypothetical protein		1558613	1558771	159	reverse	0.885	-0.176	0.468	0.607	0.242	-0.725	CDS	GI:188594943	BAG33918.1
AP009380	PGN_r0009	16S ribosomal RNA		1558884	1560358	1475	reverse	0.636	-0.654	0.002	0.015	0.214	-3.056	rRNA		
AP009380	PGN_1400	conserved hypothetical protein		1560609	1560773	165	forward	0.962	-0.056	0.809	0.873	0.231	-0.242	CDS	GI:188594944	BAG33919.1
AP009380	PGN_1401	delta-1-pyrroline-5-carboxylate dehydrogenase		1561167	1562798	1632	reverse	1.876	0.908	0.004	0.021	0.311	2.919	CDS	GI:188594945	BAG33920.1
AP009380	PGN_1402	putative amidinotransferase		1562875	1563804	930	reverse	1.246	0.317	0.150	0.278	0.220	1.440	CDS	GI:188594946	BAG33921.1
AP009380	PGN_1403	ornithine aminotransferase		1563811	1565040	1230	reverse	1.174	0.231	0.278	0.426	0.213	1.084	CDS	GI:188594947	BAG33922.1
AP009380	PGN_1404	conserved hypothetical protein		1565279	1565434	156	reverse	0.990	-0.015	0.953	0.968	0.248	-0.059	CDS	GI:188594948	BAG33923.1
AP009380	PGN_1405	elongation factor P		1565490	1566056	567	forward	1.419	0.505	0.034	0.099	0.238	2.119	CDS	GI:188594949	BAG33924.1
AP009380	PGN_1406	hypothetical protein		1566354	1566569	216	forward	0.804	-0.315	0.230	0.372	0.262	-1.201	CDS	GI:188594950	BAG33925.1
AP009380	PGN_1407	DNA-binding protein histone-like family		1566592	1567098	507	forward	0.886	-0.174	0.561	0.684	0.300	-0.582	CDS	GI:188594951	BAG33926.1
AP009380	PGN_1408	conserved hypothetical protein with predicted permease membrane region		1567240	1568916	1677	reverse	1.118	0.161	0.483	0.620	0.230	0.702	CDS	GI:188594952	BAG33927.1
AP009380	PGN_1409	putative peptidase		1569133	1570488	1356	forward	1.257	0.330	0.131	0.254	0.218	1.511	CDS	GI:188594953	BAG33928.1
AP009380	PGN_1410	conserved hypothetical protein		1570470	1570715	246	reverse	1.017	0.024	0.918	0.950	0.236	0.103	CDS	GI:188594954	BAG33929.1
AP009380	PGN_1411	putative N-ethylammeline chlorohydrolase		1570563	1571837	1275	forward	0.880	-0.184	0.395	0.537	0.217	-0.850	CDS	GI:188594955	BAG33930.1
AP009380	PGN_1412	putative purine nucleoside phosphorylase I		1571857	1572678	822	forward	0.769	-0.379	0.174	0.307	0.279	-1.360	CDS	GI:188594956	BAG33931.1
AP009380	PGN_1413	conserved hypothetical protein		1573210	1573755	546	reverse	0.947	-0.079	0.778	0.851	0.279	-0.282	CDS	GI:188594957	BAG33932.1
AP009380	PGN_1414	hypothetical protein		1574322	1574456	135	reverse	0.655	-0.611	0.278	0.426	0.563	-1.085	CDS	GI:188594958	BAG33933.1
AP009380	PGN_1415	DNA-binding protein histone-like family		1574605	1575123	519	forward	2.258	1.175	0.000	0.000	0.216	5.435	CDS	GI:188594959	BAG33934.1
AP009380	PGN_1416	probable lysyl endopeptidase precursor		1575649	1578471	2823	forward	0.640	-0.643	0.016	0.059	0.266	-2.419	CDS	GI:188594960	BAG33935.1
AP009380	PGN_1417	hypothetical protein		1579304	1579516	213	reverse	0.229	-2.127	0.000	0.000	0.465	-4.574	CDS	GI:188594961	BAG33936.1
AP009380	PGN_1418	pyruvate-flavodoxin oxidoreductase		1579766	1583347	3582	reverse	0.883	-0.179	0.479	0.616	0.253	-0.708	CDS	GI:188594962	BAG33937.1
AP009380	PGN_1419	conserved hypothetical protein		1583536	1584717	1182	reverse	0.775	-0.369	0.309	0.457	0.362	-1.018	CDS	GI:188594963	BAG33938.1
AP009380	PGN_1420	transposase in ISPg1		1585174	1586259	1086	forward	0.744	-0.427	0.335	0.484	0.442	-0.965	CDS	GI:188594964	BAG33939.1
AP009380	PGN_1421	hypothetical protein		1586614	1586718	105	reverse	0.815	-0.294	0.524	0.652	0.462	-0.636	CDS	GI:188594965	BAG33940.1
AP009380	PGN_1422	putative partial DNA-binding protein histone-like family		1586885	1587172	288	forward	0.938	-0.092	0.679	0.778	0.222	-0.414	CDS	GI:188594966	BAG33941.1
AP009380	PGN_1423	putative partial DNA-binding protein histone-like family		1587188	1587358	171	forward	0.895	-0.159	0.496	0.632	0.234	-0.681	CDS	GI:188594967	BAG33942.1
AP009380	PGN_1424	putative partial Type II restriction enzyme		1587436	1587753	318	forward	0.885	-0.177	0.520	0.650	0.275	-0.644	CDS	GI:188594968	BAG33943.1
AP009380	PGN_1425	putative partial Type II restriction enzyme		1587756	1588271	516	forward	0.881	-0.182	0.424	0.562	0.228	-0.799	CDS	GI:188594969	BAG33944.1
AP009380	PGN_1426	adenine-specific methyltransferase		1588291	1589259	969	forward	1.053	0.074	0.729	0.811	0.214	0.347	CDS	GI:188594970	BAG33945.1
AP009380	PGN_1427	hypothetical protein		1589551	1589691	141	forward	1.053	0.075	0.809	0.873	0.311	0.241	CDS	GI:188594971	BAG33946.1
AP009380	PGN_1428	transposase in ISPg3		1589940	1590842	903	reverse	0.698	-0.518	0.099	0.211	0.315	-1.647	CDS	GI:188594972	BAG33947.1

AP009380	PGN_1429	conserved hypothetical protein		1591072	1591371	300	reverse	4.301	2.105	0.000	0.000	0.275	7.661	CDS	GI:188594973	BAG33948.1
AP009380	PGN_1430	putative transmembrane Acr-type transport protein		1591356	1594505	3150	reverse	4.824	2.270	0.000	0.000	0.235	9.672	CDS	GI:188594974	BAG33949.1
AP009380	PGN_1431	putative cation efflux system protein		1594502	1595563	1062	reverse	3.999	2.000	0.000	0.000	0.205	9.743	CDS	GI:188594975	BAG33950.1
AP009380	PGN_1432	probable outer membrane efflux protein		1595599	1596987	1389	reverse	2.848	1.510	0.000	0.000	0.182	8.274	CDS	GI:188594976	BAG33951.1
AP009380	PGN_1433	transposase in ISPg1		1597755	1598840	1086	reverse	0.621	-0.688	0.139	0.262	0.465	-1.481	CDS	GI:188594977	BAG33952.1
AP009380	PGN_1434	aminoacyl-histidine dipeptidase		1599206	1600666	1461	reverse	1.006	0.009	0.968	0.976	0.234	0.039	CDS	GI:188594978	BAG33953.1
AP009380	PGN_1435	hypothetical protein		1600747	1600962	216	forward	0.649	-0.623	0.056	0.140	0.327	-1.908	CDS	GI:188594979	BAG33954.1
AP009380	PGN_1436	conserved hypothetical protein		1600995	1601615	621	forward	0.745	-0.425	0.183	0.319	0.319	-1.331	CDS	GI:188594980	BAG33955.1
AP009380	PGN_1437	conserved hypothetical protein		1601796	1604279	2484	reverse	1.212	0.278	0.183	0.319	0.209	1.331	CDS	GI:188594981	BAG33956.1
AP009380	PGN_1438	hypothetical protein		1604431	1604523	93	reverse	0.663	-0.593	0.029	0.090	0.272	-2.180	CDS	GI:188594982	BAG33957.1
AP009380	PGN_t0037	tRNA-Gly		1604695	1604770	76	reverse	0.379	-1.401	0.002	0.015	0.460	-3.048	tRNA		
AP009380	PGN_1439	hypothetical protein		1604744	1604854	111	forward	0.393	-1.346	0.002	0.015	0.442	-3.046	CDS	GI:188594983	BAG33958.1
AP009380	PGN_t0038	tRNA-Leu		1604819	1604903	85	reverse	0.595	-0.748	0.008	0.039	0.284	-2.632	tRNA		
AP009380	PGN_t0039	tRNA-Gly		1604920	1604992	73	reverse	0.547	-0.870	0.010	0.044	0.339	-2.566	tRNA		
AP009380	PGN_t0040	tRNA-Tyr		1605026	1605108	83	reverse	0.530	-0.915	0.005	0.029	0.329	-2.777	tRNA		
AP009380	PGN_1440	putative vancomycin B-type resistance protein VanW		1605477	1606325	849	forward	1.273	0.348	0.151	0.278	0.242	1.438	CDS	GI:188594984	BAG33959.1
AP009380	PGN_1441	glutamine-dependent NAD synthetase		1606435	1608378	1944	forward	1.738	0.798	0.003	0.017	0.265	3.009	CDS	GI:188594985	BAG33960.1
AP009380	PGN_1442	transposase in ISPg1		1608491	1609576	1086	forward	0.626	-0.676	0.124	0.245	0.440	-1.537	CDS	GI:188594986	BAG33961.1
AP009380	PGN_1443	carbamoyl-phosphate synthase large subunit		1609916	1613143	3228	reverse	0.986	-0.021	0.943	0.961	0.286	-0.072	CDS	GI:188594987	BAG33962.1
AP009380	PGN_1444	carbamoyl-phosphate synthase small subunit		1613162	1614235	1074	reverse	0.779	-0.360	0.152	0.280	0.252	-1.432	CDS	GI:188594988	BAG33963.1
AP009380	PGN_1445	putative amidophosphoribosyltransferase		1614269	1616152	1884	reverse	1.084	0.117	0.657	0.760	0.264	0.443	CDS	GI:188594989	BAG33964.1
AP009380	PGN_1446	conserved hypothetical protein		1616242	1618125	1884	reverse	1.725	0.786	0.003	0.019	0.267	2.945	CDS	GI:188594990	BAG33965.1
AP009380	PGN_1447	CTP synthase		1618253	1619872	1620	reverse	1.241	0.312	0.136	0.260	0.209	1.490	CDS	GI:188594991	BAG33966.1
AP009380	PGN_1448	conserved hypothetical protein		1619988	1620272	285	reverse	0.420	-1.251	0.002	0.016	0.414	-3.026	CDS	GI:188594992	BAG33967.1
AP009380	PGN_1449	inosine-5'-monophosphate dehydrogenase		1620527	1622023	1497	forward	1.833	0.874	0.010	0.042	0.338	2.588	CDS	GI:188594993	BAG33968.1
AP009380	PGN_1450	putative tRNA isopentenyltransferase		1622020	1622928	909	forward	2.237	1.161	0.004	0.022	0.400	2.900	CDS	GI:188594994	BAG33969.1
AP009380	PGN_1451	chaperonin GroES	groES	1623145	1623414	270	forward	0.354	-1.498	0.002	0.013	0.480	-3.121	CDS	GI:188594995	BAG33970.1
AP009380	PGN_1452	chaperonin GroEL	groEL	1623453	1625090	1638	forward	0.392	-1.352	0.001	0.006	0.397	-3.404	CDS	GI:188594996	BAG33971.1
AP009380	PGN_t0041	tRNA-Ser		1625476	1625562	87	forward	0.341	-1.550	0.002	0.014	0.504	-3.079	tRNA		
AP009380	PGN_1453	conserved hypothetical protein		1625660	1625770	111	reverse	0.441	-1.181	0.000	0.002	0.310	-3.816	CDS	GI:188594997	BAG33972.1
AP009380	PGN_1454	probable abortive infection protein		1625770	1626495	726	forward	1.034	0.048	0.853	0.905	0.257	0.185	CDS	GI:188594998	BAG33973.1
AP009380	PGN_1455	conserved hypothetical protein		1626471	1629494	3024	forward	1.108	0.148	0.528	0.656	0.235	0.631	CDS	GI:188594999	BAG33974.1
AP009380	PGN_1456	conserved hypothetical protein		1629525	1630772	1248	forward	0.713	-0.489	0.022	0.073	0.213	-2.290	CDS	GI:188595000	BAG33975.1
AP009380	PGN_1457	probable alkaline phosphatase		1630769	1632346	1578	forward	1.096	0.133	0.502	0.635	0.198	0.672	CDS	GI:188595001	BAG33976.1
AP009380	PGN_1458	preprotein translocase SecA subunit		1632440	1635781	3342	forward	1.366	0.450	0.073	0.168	0.251	1.792	CDS	GI:188595002	BAG33977.1
AP009380	PGN_1459	conserved hypothetical protein		1635885	1636763	879	forward	1.768	0.822	0.027	0.085	0.372	2.209	CDS	GI:188595003	BAG33978.1
AP009380	PGN_1460	putative guanylate kinase		1636796	1637362	567	forward	1.493	0.578	0.108	0.222	0.360	1.608	CDS	GI:188595004	BAG33979.1
AP009380	PGN_1461	putative spore maturation protein A/B		1637382	1638614	1233	forward	1.683	0.751	0.059	0.144	0.398	1.888	CDS	GI:188595005	BAG33980.1
AP009380	PGN_1462	conserved hypothetical protein		1638650	1639105	456	forward	1.090	0.124	0.728	0.811	0.356	0.347	CDS	GI:188595006	BAG33981.1
AP009380	PGN_1463	probable UbiA prenyltransferase		1639122	1639982	861	forward	1.782	0.834	0.040	0.110	0.406	2.055	CDS	GI:188595007	BAG33982.1
AP009380	PGN_1464	probable HAD-superfamily subfamily IB hydrolase		1639972	1640574	603	forward	2.371	1.246	0.003	0.019	0.421	2.960	CDS	GI:188595008	BAG33983.1
AP009380	PGN_1465	hypothetical protein		1640938	1641126	189	reverse	1.951	0.964	0.024	0.078	0.428	2.252	CDS	GI:188595009	BAG33984.1
AP009380	PGN_1466	arginine-specific cysteine proteinase RgpB	rgpB	1641155	1643365	2211	reverse	2.118	1.082	0.006	0.029	0.392	2.760	CDS	GI:188595010	BAG33985.1
AP009380	PGN_1467	conserved hypothetical protein		1643383	1643505	123	reverse	1.214	0.279	0.405	0.545	0.336	0.832	CDS	GI:188595011	BAG33986.1
AP009380	PGN_1468	putative lipoic acid synthase		1643618	1644466	849	reverse	1.796	0.845	0.020	0.070	0.364	2.319	CDS	GI:188595012	BAG33987.1
AP009380	PGN_1469	dipeptidyl peptidase IV	dppIV	1644569	1646740	2172	reverse	2.159	1.110	0.001	0.009	0.342	3.248	CDS	GI:188595013	BAG33988.1
AP009380	PGN_1470	putative SsrA-binding protein		1646780	1647241	462	reverse	2.013	1.009	0.000	0.005	0.289	3.493	CDS	GI:188595014	BAG33989.1
AP009380	PGN_1471	conserved hypothetical protein		1647274	1648365	1092	reverse	1.646	0.719	0.005	0.028	0.258	2.788	CDS	GI:188595015	BAG33990.1
AP009380	PGN_1472	queuine tRNA-ribosyltransferase		1648372	1649502	1131	reverse	1.194	0.256	0.237	0.381	0.216	1.182	CDS	GI:188595016	BAG33991.1
AP009380	PGN_1473	hypothetical protein		1649813	1649947	135	reverse	1.662	0.733	0.042	0.115	0.361	2.030	CDS	GI:188595017	BAG33992.1
AP009380	PGN_1474	putative autoinducer-2 production protein LuxS		1650319	1650798	480	reverse	1.657	0.729	0.040	0.110	0.355	2.056	CDS	GI:188595018	BAG33993.1
AP009380	PGN_1475	probable 5'-methylthioadenosine/S-adenosylhomocysteine nucleosidase		1650823	1651509	687	reverse	1.321	0.401	0.244	0.389	0.345	1.165	CDS	GI:188595019	BAG33994.1
AP009380	PGN_1476	conserved hypothetical protein		1651912	1653306	1395	reverse	0.899	-0.153	0.491	0.628	0.222	-0.689	CDS	GI:188595020	BAG33995.1
AP009380	PGN_1477	conserved hypothetical protein		1653471	1653725	255	forward	0.405	-1.303	0.000	0.000	0.308	-4.235	CDS	GI:188595021	BAG33996.1
AP009380	PGN_1478	conserved hypothetical protein		1653919	1654077	159	forward	0.564	-0.826	0.095	0.205	0.494	-1.670	CDS	GI:188595022	BAG33997.1
AP009380	PGN_1479	dipeptidyl peptidase 7	dpp7	1654445	1656583	2139	reverse	1.331	0.413	0.213	0.355	0.331	1.245	CDS	GI:188595023	BAG33998.1
AP009380	PGN_1480	conserved hypothetical protein with DUF389 domain		1656599	1657939	1341	reverse	1.087	0.120	0.611	0.724	0.236	0.509	CDS	GI:188595024	BAG33999.1
AP009380	PGN_1481	putative polysaccharide biosynthesis protein		1658039	1659523	1485	reverse	0.699	-0.516	0.038	0.107	0.249	-2.072	CDS	GI:188595025	BAG34000.1
AP009380	PGN_1482	holliday junction DNA helicase RuvB	ruvB	1659567	1660661	1095	reverse	0.844	-0.245	0.453	0.592	0.327	-0.750	CDS	GI:188595026	BAG34001.1
AP009380	PGN_1483	conserved hypothetical protein		1661050	1661259	210	reverse	0.573	-0.804	0.172	0.305	0.589	-1.366	CDS	GI:188595027	BAG34002.1
AP009380	PGN_1484	putative methylated-DNA-protein-cysteine methyltransferase		1661501	1662013	513	forward	0.850	-0.234	0.396	0.537	0.276	-0.848	CDS	GI:188595028	BAG34003.1
AP009380	PGN_1485	conserved hypothetical protein		1662096	1662434	339	forward	0.833	-0.263	0.303	0.451	0.255	-1.030	CDS	GI:188595029	BAG34004.1
AP009380	PGN_1486	conserved hypothetical protein		1662562	1663569	1008	forward	1.328	0.410	0.021	0.071	0.177	2.311	CDS	GI:188595030	BAG34005.1
AP009380	PGN_1487	probable dephospho-CoA kinase		1663576	1664184	609	forward	1.379	0.463	0.071	0.165	0.257	1.804	CDS	GI:188595031	BAG34006.1
AP009380	PGN_1488	conserved hypothetical protein		1664291	1664722	432	forward	1.577	0.657	0.020	0.068	0.282	2.332	CDS	GI:188595032	BAG34007.1
AP009380	PGN_1489	2-amino-3-ketobutyrate CoA ligase		1664798	1665988	1191	forward	2.010	1.007	0.001	0.007	0.301	3.346	CDS	GI:188595033	BAG34008.1
AP009380	PGN_1490	probable precorrin-2 C20-methyltransferase		1666101	1666814	714	forward	1.063	0.089	0.691	0.787	0.223	0.398	CDS	GI:188595034	BAG34009.1
AP009380	PGN_1491	conserved hypothetical protein		1666905	1667663	759	reverse	0.892	-0.165	0.503	0.636	0.247	-0.669	CDS	GI:188595035	BAG34010.1
AP009380	PGN_1492	putative pantoate-beta-alanine ligase		1667824	1668669	846	forward	1.350	0.433	0.206	0.347	0.342	1.265	CDS	GI:188595036	BAG34011.1
AP009380	PGN_1493	conserved hypothetical protein		1668659	1670206	1548	forward	1.301	0.380	0.261	0.407	0.338	1.124	CDS	GI:188595037	BAG34012.1
AP009380	PGN_1494	putative oxygen-independent coproporphyrinogen III oxidase		1670203	1671333	1131	forward	2.021	1.015	0.018	0.065	0.429	2.365	CDS	GI:188595038	BAG34013.1
AP009380	PGN_1495	putative low-specificity L-threonine aldolase		1671373	1672407	1035	forward	1.702	0.768	0.045	0.120	0.383	2.003	CDS	GI:188595039	BAG34014.1
AP009380	PGN_1496	hypothetical protein		1672503	1672904	402	reverse	1.341	0.423	0.171	0.304	0.309	1.369	CDS	GI:188595040	BAG34015.1
AP009380	PGN_1497	putative iron-sulfur cluster binding protein		1673034	1674005	972	reverse	1.182	0.242	0.410	0.549	0.293	0.824	CDS	GI:188595041	BAG34016.1
AP009380	PGN_1498	conserved hypothetical protein		1674016	1675074	1059	reverse	0.967	-0.049	0.858	0.909	0.273	-0.179	CDS	GI:188595042	BAG34017.1
AP009380	PGN_1499	conserved hypothetical protein		1675539	1675685	147	forward	0.419	-1.254	0.031	0.094	0.583	-2.151	CDS	GI:188595043	BAG34018.1
AP009380	PGN_1500	conserved hypothetical protein		1675764	1676015	252	forward	0.881	-0.183	0.563	0.686	0.317	-0.578	CDS	GI:188595044	BAG34019.1
AP009380	PGN_1501	putative mannose-6-phosphate isomerase		1676038	1677048	1011	forward	1.238	0.308	0.365	0.509	0.340	0.906	CDS	GI:188595045	BAG34020.1
AP009380	PGN_1502	conserved hypothetical protein		1677061	1677933	873	forward	1.219	0.286	0.322	0.472	0.288	0.991	CDS	GI:188595046	BAG34021.1
AP009380	PGN_1503	probable ferric uptake transcriptional regulator		1678019	1678519	501	forward	1.088	0.122	0.523	0.652	0.191	0.639	CDS	GI:188595047	BAG34022.1
AP009380	PGN_1504	adenylosuccinate synthetase		1678548	1679819	1272	forward	1.794	0.843	0.000	0.004	0.237	3.565	CDS	GI:188595048	BAG34023.1
AP009380	PGN_1505	putative folylpolyglutamate synthase		1679819	1681105	1287	forward	1.716	0.779	0.001	0.005	0.225	3.465	CDS	GI:188595049	BAG34024.1
AP009380	PGN_1506	putative transporter		1681143	1682546	1404	forward	2.424	1.277	0.002	0.014	0.415	3.075	CDS	GI:188595050	BAG34025.1
AP009380	PGN_1507	hypothetical protein		1683500	1684105	606	forward	0.543	-0.880	0.002	0.014	0.284	-3.103	CDS	GI:188595051	BAG34026.1
AP009380	PGN_1508	hypothetical protein		1684707	1684805	99	forward	0.882	-0.181	0.564	0.686	0.314	-0.577	CDS	GI:188595052	BAG34027.1
AP009380	PGN_1509	conserved hypothetical protein		1685165	1686439	1275	reverse	0.655	-0.610	0.079	0.179	0.347	-1.756	CDS	GI:188595053	BAG34028.1
AP009380	PGN_1510	putative peptidyl-prolyl cis-trans isomerase		1686729	1688876	2148	reverse	0.972	-0.041	0.869	0.917	0.252	-0.164	CDS	GI:188595054	BAG34029.1

AP009380	PGN_1511	probable hemolysin		1688983	1690236	1254	reverse	0.758	-0.399	0.146	0.271	0.274	-1.455	CDS	GI:188595055	BAG34030.1
AP009380	PGN_1512	conserved hypothetical protein		1690233	1690937	705	reverse	1.032	0.045	0.842	0.899	0.226	0.199	CDS	GI:188595056	BAG34031.1
AP009380	PGN_1513	conserved hypothetical protein		1690968	1692320	1353	reverse	0.821	-0.284	0.277	0.425	0.262	-1.087	CDS	GI:188595057	BAG34032.1
AP009380	PGN_1514	conserved hypothetical protein		1692362	1693666	1305	reverse	1.102	0.140	0.525	0.652	0.220	0.636	CDS	GI:188595058	BAG34033.1
AP009380	PGN_1515	conserved hypothetical protein		1693659	1694393	735	reverse	1.830	0.872	0.004	0.021	0.299	2.918	CDS	GI:188595059	BAG34034.1
AP009380	PGN_1516	probable molybdopterin biosynthesis MoeB protein		1694449	1695198	750	reverse	1.597	0.675	0.030	0.091	0.310	2.175	CDS	GI:188595060	BAG34035.1
AP009380	PGN_1517	peptidase T	pepT	1695286	1696503	1218	reverse	1.908	0.932	0.000	0.000	0.197	4.732	CDS	GI:188595061	BAG34036.1
AP009380	PGN_1518	putative oligopeptide transporter		1696520	1698499	1980	reverse	1.427	0.513	0.010	0.043	0.200	2.571	CDS	GI:188595062	BAG34037.1
AP009380	PGN_1519	hemagglutinin-related protein		1698688	1699734	1047	reverse	1.076	0.105	0.613	0.725	0.208	0.506	CDS	GI:188595063	BAG34038.1
AP009380	PGN_1520	conserved hypothetical protein		1700387	1703017	2631	reverse	0.716	-0.481	0.159	0.288	0.342	-1.409	CDS	GI:188595064	BAG34039.1
AP009380	PGN_1521	conserved hypothetical protein		1703024	1703923	900	reverse	0.604	-0.728	0.046	0.122	0.365	-1.994	CDS	GI:188595065	BAG34040.1
AP009380	PGN_1522	conserved hypothetical protein		1703920	1704861	942	reverse	0.709	-0.497	0.150	0.278	0.345	-1.441	CDS	GI:188595066	BAG34041.1
AP009380	PGN_1523	putative polysaccharide export outer membrane protein		1705044	1705850	807	forward	1.566	0.647	0.011	0.047	0.255	2.533	CDS	GI:188595067	BAG34042.1
AP009380	PGN_1524	conserved hypothetical protein		1705857	1708322	2466	forward	1.209	0.274	0.238	0.382	0.232	1.180	CDS	GI:188595068	BAG34043.1
AP009380	PGN_1525	probable capsular polysaccharide biosynthesis protein		1708332	1709075	744	forward	1.356	0.439	0.134	0.258	0.293	1.498	CDS	GI:188595069	BAG34044.1
AP009380	PGN_1526	conserved hypothetical protein		1709234	1710349	1116	forward	1.392	0.477	0.099	0.210	0.289	1.651	CDS	GI:188595070	BAG34045.1
AP009380	PGN_1527	conserved hypothetical protein		1710390	1711100	711	forward	1.676	0.745	0.018	0.065	0.315	2.366	CDS	GI:188595071	BAG34046.1
AP009380	PGN_1528	conserved hypothetical protein		1711104	1712510	1407	forward	1.168	0.224	0.452	0.591	0.299	0.751	CDS	GI:188595072	BAG34047.1
AP009380	PGN_1529	putative oxidoreductase		1712740	1713747	1008	reverse	1.512	0.596	0.079	0.179	0.339	1.757	CDS	GI:188595073	BAG34048.1
AP009380	PGN_1530	putative 2-oxoglutarate ferredoxin oxidoreductase subunit		1713774	1715633	1860	reverse	1.126	0.171	0.562	0.685	0.294	0.580	CDS	GI:188595074	BAG34049.1
AP009380	PGN_1531	hypothetical protein		1715781	1715924	144	reverse	0.358	-1.482	0.001	0.006	0.436	-3.396	CDS	GI:188595075	BAG34050.1
AP009380	PGN_1532	conserved hypothetical protein		1716139	1716351	213	forward	0.853	-0.229	0.595	0.712	0.431	-0.531	CDS	GI:188595076	BAG34051.1
AP009380	PGN_1533	putative carbonic anhydrase		1716533	1717261	729	reverse	1.492	0.577	0.014	0.054	0.235	2.462	CDS	GI:188595077	BAG34052.1
AP009380	PGN_1534	hypothetical protein		1717564	1718631	1068	forward	3.323	1.732	0.000	0.000	0.281	6.174	CDS	GI:188595078	BAG34053.1
AP009380	PGN_1535	hypothetical protein		1718720	1719772	1053	forward	2.217	1.149	0.000	0.001	0.286	4.014	CDS	GI:188595079	BAG34054.1
AP009380	PGN_1536	hypothetical protein		1719926	1720966	1041	forward	0.617	-0.697	0.045	0.121	0.349	-2.000	CDS	GI:188595080	BAG34055.1
AP009380	PGN_1537	probable cation efflux system protein		1720984	1722084	1101	forward	0.716	-0.482	0.136	0.259	0.323	-1.492	CDS	GI:188595081	BAG34056.1
AP009380	PGN_1538	putative cation efflux system		1722119	1725190	3072	forward	0.950	-0.075	0.718	0.806	0.206	-0.361	CDS	GI:188595082	BAG34057.1
AP009380	PGN_1539	putative ABC transport system exported protein		1725168	1726658	1491	forward	1.200	0.263	0.435	0.573	0.337	0.781	CDS	GI:188595083	BAG34058.1
AP009380	PGN_1540	putative ABC transport membrane protein		1726698	1729829	3132	forward	1.143	0.193	0.563	0.685	0.334	0.579	CDS	GI:188595084	BAG34059.1
AP009380	PGN_1541	hypothetical protein		1730076	1730201	126	forward	1.648	0.721	0.067	0.157	0.393	1.833	CDS	GI:188595085	BAG34060.1
AP009380	PGN_1542	putative esterase		1730198	1731037	840	forward	1.326	0.407	0.060	0.146	0.217	1.880	CDS	GI:188595086	BAG34061.1
AP009380	PGN_1543	conserved hypothetical protein		1731073	1731732	660	reverse	0.947	-0.078	0.714	0.805	0.214	-0.366	CDS	GI:188595087	BAG34062.1
AP009380	PGN_1544	conserved hypothetical protein		1731713	1732057	345	reverse	0.445	-1.167	0.001	0.007	0.350	-3.334	CDS	GI:188595088	BAG34063.1
AP009380	PGN_1545	hypothetical protein		1732120	1732305	186	reverse	0.946	-0.080	0.889	0.932	0.575	-0.140	CDS	GI:188595089	BAG34064.1
AP009380	PGN_1546	hypothetical protein		1732358	1732561	204	reverse	0.464	-1.107	0.009	0.042	0.427	-2.594	CDS	GI:188595090	BAG34065.1
AP009380	PGN_1547	conserved hypothetical protein		1732564	1733421	858	forward	1.022	0.032	0.916	0.949	0.300	0.105	CDS	GI:188595091	BAG34066.1
AP009380	PGN_1548	conserved hypothetical protein		1733705	1734565	861	forward	0.428	-1.225	0.001	0.007	0.368	-3.327	CDS	GI:188595092	BAG34067.1
AP009380	PGN_1549	putative ATP-dependent Clp protease proteolytic subunit	clpP	1734938	1735606	669	forward	0.795	-0.331	0.322	0.472	0.334	-0.990	CDS	GI:188595093	BAG34068.1
AP009380	PGN_1550	ATP-dependent Clp protease ATP-binding subunit ClpX	clpX	1735643	1736878	1236	forward	0.614	-0.703	0.069	0.161	0.387	-1.819	CDS	GI:188595094	BAG34069.1
AP009380	PGN_1551	ATP-dependent DNA helicase RecQ	recQI	1736957	1739134	2178	forward	0.722	-0.470	0.079	0.179	0.268	-1.755	CDS	GI:188595095	BAG34070.1
AP009380	PGN_1552	putative peptidyl-prolyl cis-trans isomerase		1739171	1740553	1383	forward	0.905	-0.143	0.550	0.675	0.240	-0.598	CDS	GI:188595096	BAG34071.1
AP009380	PGN_1553	conserved hypothetical protein		1740615	1742495	1881	forward	1.303	0.382	0.160	0.289	0.271	1.406	CDS	GI:188595097	BAG34072.1
AP009380	PGN_1554	conserved hypothetical protein		1742486	1742830	345	forward	1.626	0.701	0.017	0.062	0.293	2.391	CDS	GI:188595098	BAG34073.1
AP009380	PGN_1555	DNA mismatch repair protein MutL		1742827	1744683	1857	forward	0.716	-0.482	0.141	0.265	0.328	-1.471	CDS	GI:188595099	BAG34074.1
AP009380	PGN_1556	putative hemagglutinin		1744939	1747716	2778	reverse	0.490	-1.030	0.037	0.104	0.493	-2.091	CDS	GI:188595100	BAG34075.1
AP009380	PGN_1557	conserved hypothetical protein		1748075	1748896	822	reverse	1.105	0.144	0.655	0.759	0.323	0.446	CDS	GI:188595101	BAG34076.1
AP009380	PGN_1558	conserved hypothetical protein		1748910	1749380	471	forward	1.230	0.299	0.330	0.480	0.307	0.974	CDS	GI:188595102	BAG34077.1
AP009380	PGN_1559	hypothetical protein		1749467	1749682	216	reverse	0.365	-1.454	0.000	0.000	0.333	-4.366	CDS	GI:188595103	BAG34078.1
AP009380	PGN_1560	conserved hypothetical protein		1749838	1749981	144	forward	0.775	-0.368	0.270	0.417	0.334	-1.103	CDS	GI:188595104	BAG34079.1
AP009380	PGN_1561	conserved hypothetical protein		1750327	1750623	297	forward	0.837	-0.256	0.337	0.487	0.267	-0.960	CDS	GI:188595105	BAG34080.1
AP009380	PGN_1562	conserved hypothetical protein		1750630	1750938	309	forward	0.955	-0.066	0.803	0.868	0.265	-0.250	CDS	GI:188595106	BAG34081.1
AP009380	PGN_1563	hypothetical protein		1750980	1751078	99	reverse	0.882	-0.181	0.657	0.760	0.407	-0.445	CDS	GI:188595107	BAG34082.1
AP009380	PGN_1564	conserved hypothetical protein		1751085	1752626	1542	forward	0.944	-0.084	0.799	0.866	0.330	-0.254	CDS	GI:188595108	BAG34083.1
AP009380	PGN_1565	conserved hypothetical protein with PSP1 C-terminal conserved region		1752731	1754143	1413	forward	1.335	0.417	0.180	0.314	0.310	1.342	CDS	GI:188595109	BAG34084.1
AP009380	PGN_1566	conserved hypothetical protein		1754151	1754681	531	forward	1.278	0.354	0.208	0.349	0.281	1.258	CDS	GI:188595110	BAG34085.1
AP009380	PGN_1567	putative DNA replication and repair protein RecF		1754678	1755772	1095	forward	1.098	0.135	0.613	0.725	0.267	0.506	CDS	GI:188595111	BAG34086.1
AP009380	PGN_1568	conserved hypothetical protein		1755786	1756076	291	forward	1.207	0.271	0.368	0.511	0.301	0.901	CDS	GI:188595112	BAG34087.1
AP009380	PGN_1569	probable transcriptional regulator Crp/Fnr family		1756125	1756823	699	reverse	0.911	-0.135	0.530	0.656	0.215	-0.628	CDS	GI:188595113	BAG34088.1
AP009380	PGN_1570	DNA-directed RNA polymerase beta' subunit	rpoC	1757112	1761413	4302	reverse	1.210	0.275	0.324	0.474	0.279	0.987	CDS	GI:188595114	BAG34089.1
AP009380	PGN_1571	DNA-directed RNA polymerase beta subunit	rpoB	1761479	1765288	3810	reverse	1.304	0.383	0.151	0.279	0.266	1.436	CDS	GI:188595115	BAG34090.1
AP009380	PGN_1572	putative 50S ribosomal protein L7/L12	rplL	1765400	1765777	378	reverse	0.875	-0.192	0.471	0.609	0.266	-0.721	CDS	GI:188595116	BAG34091.1
AP009380	PGN_1573	putative 50S ribosomal protein L10	rplJ	1765819	1766343	525	reverse	0.820	-0.285	0.222	0.365	0.234	-1.221	CDS	GI:188595117	BAG34092.1
AP009380	PGN_1574	50S ribosomal protein L1	rplA	1766359	1767057	699	reverse	0.896	-0.159	0.552	0.676	0.268	-0.594	CDS	GI:188595118	BAG34093.1
AP009380	PGN_1575	50S ribosomal protein L11	rplK	1767078	1767515	438	reverse	0.766	-0.385	0.103	0.217	0.236	-1.629	CDS	GI:188595119	BAG34094.1
AP009380	PGN_1576	putative transcription antitermination protein		1767584	1768123	540	reverse	0.817	-0.291	0.245	0.390	0.250	-1.163	CDS	GI:188595120	BAG34095.1
AP009380	PGN_1577	putative preprotein translocase SecE subunit		1768145	1768348	204	reverse	0.648	-0.626	0.011	0.047	0.247	-2.534	CDS	GI:188595121	BAG34096.1
AP009380	PGN_t0042	tRNA-Trp		1768361	1768436	76	reverse	0.768	-0.380	0.051	0.130	0.195	-1.950	tRNA		
AP009380	PGN_1578	translation elongation factor Tu		1768507	1769694	1188	reverse	0.766	-0.384	0.151	0.278	0.267	-1.438	CDS	GI:188595122	BAG34097.1
AP009380	PGN_t0043	tRNA-Thr		1769762	1769833	72	reverse	0.592	-0.755	0.034	0.099	0.356	-2.120	tRNA		
AP009380	PGN_t0044	tRNA-Tyr		1769863	1769948	86	reverse	0.489	-1.032	0.006	0.030	0.375	-2.752	tRNA		
AP009380	PGN_1579	putative site-specific recombinase		1770088	1771293	1206	reverse	0.664	-0.590	0.131	0.254	0.391	-1.508	CDS	GI:188595123	BAG34098.1
AP009380	PGN_1580	putative 30S ribosomal protein S21	rpsU	1771370	1771561	192	reverse	0.755	-0.406	0.110	0.226	0.254	-1.597	CDS	GI:188595124	BAG34099.1
AP009380	PGN_1581	DNA mismatch repair protein MutS		1771723	1774245	2523	reverse	1.626	0.701	0.007	0.034	0.261	2.690	CDS	GI:188595125	BAG34100.1
AP009380	PGN_1582	membrane-associated zinc metalloprotease		1774255	1775574	1320	reverse	1.046	0.064	0.800	0.866	0.254	0.253	CDS	GI:188595126	BAG34101.1
AP009380	PGN_1583	hypothetical protein		1775727	1775918	192	reverse	1.038	0.053	0.895	0.935	0.402	0.132	CDS	GI:188595127	BAG34102.1
AP009380	PGN_1584	putative sodium/hydrogen antiporter		1776051	1777571	1521	forward	1.118	0.160	0.507	0.638	0.241	0.664	CDS	GI:188595128	BAG34103.1
AP009380	PGN_1585	excinuclease ABC B subunit	uvrB	1777568	1779604	2037	reverse	1.268	0.342	0.198	0.337	0.266	1.287	CDS	GI:188595129	BAG34104.1
AP009380	PGN_1586	hypothetical protein		1779637	1779792	156	forward	0.477	-1.067	0.006	0.032	0.391	-2.728	CDS	GI:188595130	BAG34105.1
AP009380	PGN_1587	putative translation elongation factor Ts		1779957	1780781	825	reverse	0.891	-0.166	0.505	0.638	0.250	-0.666	CDS	GI:188595131	BAG34106.1
AP009380	PGN_1588	putative 30S ribosomal protein S2	rpsB	1780920	1781765	846	reverse	0.780	-0.359	0.121	0.240	0.231	-1.552	CDS	GI:188595132	BAG34107.1
AP009380	PGN_1589	putative 30S ribosomal protein S9	rpsI	1781900	1782286	387	reverse	0.875	-0.192	0.439	0.577	0.248	-0.774	CDS	GI:188595133	BAG34108.1
AP009380	PGN_1590	putative 50S ribosomal protein L13	rplM	1782296	1782751	456	reverse	0.895	-0.160	0.460	0.599	0.216	-0.739	CDS	GI:188595134	BAG34109.1
AP009380	PGN_1591	conserved hypothetical protein		1783313	1783981	669	reverse	0.588	-0.766	0.000	0.003	0.208	-3.675	CDS	GI:188595135	BAG34110.1
AP009380	PGN_1592	conserved hypothetical protein		1784541	1784642	102	reverse	0.546	-0.873	0.016	0.059	0.362	-2.412	CDS	GI:188595136	BAG34111.1
AP009380	PGN_1593	putative phosphopantetheine adenylyltransferase		1785017	1785478	462	reverse	1.228	0.296	0.352	0.498	0.319	0.930	CDS	GI:188595137	BAG34112.1
AP009380	PGN_1594	DNA topoisomerase IV B subunit		1785509	1787443	1935	reverse	1.092	0.127	0.579	0.699	0.230	0.555	CDS	GI:188595138	BAG34113.1

AP009380	PGN_1595	conserved hypothetical protein		1787923	1788483	561	forward	0.941	-0.088	0.681	0.779	0.215	-0.411	CDS	GI:188595139	BAG34114.1
AP009380	PGN_1596	probable 3'-5' exonuclease		1788524	1789126	603	forward	1.415	0.501	0.030	0.091	0.230	2.176	CDS	GI:188595140	BAG34115.1
AP009380	PGN_1597	conserved hypothetical protein		1789123	1790328	1206	forward	1.335	0.417	0.062	0.149	0.223	1.869	CDS	GI:188595141	BAG34116.1
AP009380	PGN_1598	probable glutamine ABC transporter		1790391	1791218	828	reverse	1.675	0.744	0.004	0.024	0.260	2.858	CDS	GI:188595142	BAG34117.1
AP009380	PGN_1599	conserved hypothetical protein		1791219	1793309	2091	reverse	1.636	0.710	0.002	0.014	0.230	3.083	CDS	GI:188595143	BAG34118.1
AP009380	PGN_1600	conserved hypothetical protein		1793287	1794555	1269	reverse	0.913	-0.132	0.659	0.761	0.299	-0.441	CDS	GI:188595144	BAG34119.1
AP009380	PGN_1601	conserved hypothetical protein with lemA family domain		1794616	1795212	597	reverse	1.058	0.081	0.759	0.835	0.265	0.307	CDS	GI:188595145	BAG34120.1
AP009380	PGN_1602	putative flavoredoxin		1795250	1795837	588	reverse	1.297	0.375	0.142	0.266	0.255	1.469	CDS	GI:188595146	BAG34121.1
AP009380	PGN_1603	aspartate carbamoyltransferase regulatory subunit		1795866	1796321	456	reverse	1.514	0.598	0.048	0.124	0.302	1.979	CDS	GI:188595147	BAG34122.1
AP009380	PGN_1604	aspartate carbamoyltransferase catalytic subunit		1796334	1797248	915	reverse	1.255	0.327	0.152	0.279	0.228	1.434	CDS	GI:188595148	BAG34123.1
AP009380	PGN_1605	conserved hypothetical protein		1797295	1798032	738	reverse	1.237	0.307	0.130	0.252	0.202	1.515	CDS	GI:188595149	BAG34124.1
AP009380	PGN_1606	conserved hypothetical protein		1798061	1799044	984	reverse	1.203	0.267	0.220	0.363	0.217	1.227	CDS	GI:188595150	BAG34125.1
AP009380	PGN_1607	hypothetical protein		1799172	1799357	186	forward	0.616	-0.698	0.134	0.258	0.466	-1.499	CDS	GI:188595151	BAG34126.1
AP009380	PGN_1608	neuraminidase		1799422	1801002	1581	reverse	0.904	-0.146	0.621	0.732	0.295	-0.495	CDS	GI:188595152	BAG34127.1
AP009380	PGN_1609	hypothetical protein		1801024	1801113	90	forward	0.592	-0.755	0.101	0.214	0.461	-1.639	CDS	GI:188595153	BAG34128.1
AP009380	PGN_1610	conserved hypothetical protein		1801155	1801415	261	reverse	0.427	-1.228	0.000	0.000	0.273	-4.497	CDS	GI:188595154	BAG34129.1
AP009380	PGN_1611	conserved hypothetical protein		1801429	1802886	1458	forward	1.204	0.267	0.198	0.337	0.208	1.286	CDS	GI:188595155	BAG34130.1
AP009380	PGN_1612	probable beta-phosphoglucomutase		1802981	1803733	753	reverse	1.233	0.302	0.240	0.384	0.257	1.176	CDS	GI:188595156	BAG34131.1
AP009380	PGN_1613	ATP-dependent DNA helicase RecG		1803751	1805847	2097	reverse	0.817	-0.292	0.378	0.520	0.331	-0.881	CDS	GI:188595157	BAG34132.1
AP009380	PGN_1614	UDP-glucose 4-epimerase	galE	1805890	1806918	1029	reverse	0.823	-0.281	0.487	0.624	0.404	-0.695	CDS	GI:188595158	BAG34133.1
AP009380	PGN_1615	putative GTP-binding protein		1806928	1807533	606	reverse	0.565	-0.823	0.030	0.092	0.379	-2.170	CDS	GI:188595159	BAG34134.1
AP009380	PGN_1616	conserved hypothetical protein		1807634	1808227	594	forward	0.790	-0.339	0.360	0.505	0.371	-0.915	CDS	GI:188595160	BAG34135.1
AP009380	PGN_1617	probable metallophosphoesterase		1808230	1809699	1470	forward	1.041	0.058	0.881	0.926	0.388	0.150	CDS	GI:188595161	BAG34136.1
AP009380	PGN_1618	methionine gamma-lyase		1809862	1811061	1200	forward	1.118	0.161	0.438	0.576	0.208	0.775	CDS	GI:188595162	BAG34137.1
AP009380	PGN_1619	transposase in ISPg1		1811402	1812487	1086	reverse	0.726	-0.462	0.305	0.453	0.451	-1.025	CDS	GI:188595163	BAG34138.1
AP009380	PGN_1620	hypothetical protein		1813060	1813158	99	reverse	0.707	-0.501	0.176	0.309	0.370	-1.354	CDS	GI:188595164	BAG34139.1
AP009380	PGN_1621	conserved hypothetical protein		1813177	1813413	237	reverse	0.434	-1.204	0.000	0.000	0.284	-4.243	CDS	GI:188595165	BAG34140.1
AP009380	PGN_1622	conserved hypothetical protein		1813728	1814273	546	reverse	0.404	-1.308	0.000	0.003	0.363	-3.603	CDS	GI:188595166	BAG34141.1
AP009380	PGN_1623	conserved hypothetical protein		1814278	1817637	3360	reverse	0.749	-0.417	0.152	0.279	0.291	-1.434	CDS	GI:188595167	BAG34142.1
AP009380	PGN_1624	conserved hypothetical protein		1817688	1817840	153	forward	0.460	-1.120	0.004	0.021	0.384	-2.916	CDS	GI:188595168	BAG34143.1
AP009380	PGN_1625	conserved hypothetical protein		1817925	1818494	570	forward	0.704	-0.507	0.028	0.086	0.230	-2.202	CDS	GI:188595169	BAG34144.1
AP009380	PGN_1626	putative tRNA isopentenyltransferase		1818514	1819416	903	forward	1.212	0.277	0.325	0.474	0.282	0.984	CDS	GI:188595170	BAG34145.1
AP009380	PGN_1627	probable 4-amino-4-deoxy-L-arabinose transferase		1819556	1821070	1515	forward	0.697	-0.521	0.064	0.152	0.281	-1.855	CDS	GI:188595171	BAG34146.1
AP009380	PGN_1628	putative glycosyltransferases		1821098	1822057	960	forward	0.833	-0.263	0.382	0.524	0.301	-0.874	CDS	GI:188595172	BAG34147.1
AP009380	PGN_1629	conserved hypothetical protein with integral membrane domain DUF6		1822068	1823141	1074	reverse	0.940	-0.089	0.766	0.841	0.298	-0.298	CDS	GI:188595173	BAG34148.1
AP009380	PGN_1630	transcription termination factor Rho		1823204	1825180	1977	reverse	1.311	0.391	0.056	0.139	0.204	1.912	CDS	GI:188595174	BAG34149.1
AP009380	PGN_1631	piutative DNA-binding protein histone-like family		1825857	1826375	519	forward	0.839	-0.253	0.405	0.545	0.303	-0.834	CDS	GI:188595175	BAG34150.1
AP009380	PGN_1632	hypothetical protein		1826408	1827403	996	forward	0.767	-0.383	0.085	0.190	0.223	-1.720	CDS	GI:188595176	BAG34151.1
AP009380	PGN_1633	formiminotransferase-cyclodeaminase		1827444	1828346	903	forward	0.738	-0.439	0.054	0.135	0.228	-1.929	CDS	GI:188595177	BAG34152.1
AP009380	PGN_1634	imidazolonepropionase		1828447	1829718	1272	forward	1.019	0.027	0.923	0.951	0.274	0.097	CDS	GI:188595178	BAG34153.1
AP009380	PGN_1635	conserved hypothetical protein with nucleoside recognition domain		1829812	1830966	1155	forward	0.790	-0.341	0.300	0.448	0.329	-1.037	CDS	GI:188595179	BAG34154.1
AP009380	PGN_1636	conserved hypothetical protein		1830986	1832134	1149	forward	1.276	0.352	0.225	0.366	0.290	1.215	CDS	GI:188595180	BAG34155.1
AP009380	PGN_1637	putative methenyltetrahydrofolate cyclohydrolase		1832159	1832788	630	forward	1.395	0.480	0.175	0.309	0.354	1.356	CDS	GI:188595181	BAG34156.1
AP009380	PGN_1638	histidine ammonia-lyase		1832791	1834284	1494	forward	1.037	0.052	0.867	0.916	0.310	0.168	CDS	GI:188595182	BAG34157.1
AP009380	PGN_1639	conserved hypothetical protein		1834485	1834814	330	forward	3.833	1.938	0.000	0.000	0.249	7.784	CDS	GI:188595183	BAG34158.1
AP009380	PGN_1640	serine/threonine transporter		1834937	1836115	1179	reverse	1.126	0.171	0.378	0.520	0.194	0.882	CDS	GI:188595184	BAG34159.1
AP009380	PGN_1641	arginine/ornithine transport system ATPase		1836144	1837250	1107	reverse	1.092	0.127	0.530	0.656	0.202	0.628	CDS	GI:188595185	BAG34160.1
AP009380	PGN_1642	conserved hypothetical protein		1837326	1838414	1089	reverse	0.720	-0.474	0.090	0.198	0.280	-1.694	CDS	GI:188595186	BAG34161.1
AP009380	PGN_1643	conserved hypothetical protein		1838446	1838829	384	reverse	0.531	-0.913	0.001	0.005	0.264	-3.453	CDS	GI:188595187	BAG34162.1
AP009380	PGN_1644	transposase in ISPg1		1839297	1840382	1086	reverse	0.831	-0.267	0.562	0.685	0.461	-0.580	CDS	GI:188595188	BAG34163.1
AP009380	PGN_1645	putative dipeptidyl peptidase III		1840723	1843443	2721	forward	1.098	0.135	0.497	0.632	0.199	0.679	CDS	GI:188595189	BAG34164.1
AP009380	PGN_1646	seryl-tRNA synthetase		1843456	1844727	1272	reverse	1.118	0.160	0.370	0.514	0.179	0.896	CDS	GI:188595190	BAG34165.1
AP009380	PGN_1647	putative 50S ribosomal protein L27	rpmA	1844827	1845084	258	reverse	0.987	-0.019	0.936	0.956	0.234	-0.080	CDS	GI:188595191	BAG34166.1
AP009380	PGN_1648	putative 50S ribosomal protein L21	rplU	1845112	1845429	318	reverse	0.968	-0.047	0.849	0.903	0.246	-0.190	CDS	GI:188595192	BAG34167.1
AP009380	PGN_1649	conserved hypothetical protein		1845490	1845798	309	reverse	1.128	0.173	0.667	0.766	0.403	0.431	CDS	GI:188595193	BAG34168.1
AP009380	PGN_1650	conserved hypothetical protein		1846156	1846695	540	forward	0.857	-0.223	0.299	0.446	0.214	-1.040	CDS	GI:188595194	BAG34169.1
AP009380	PGN_1651	putative glycosyltransferase		1846692	1847645	954	forward	1.453	0.539	0.005	0.028	0.193	2.793	CDS	GI:188595195	BAG34170.1
AP009380	PGN_1652	probable nitroreductase		1847645	1848184	540	forward	1.334	0.415	0.023	0.075	0.182	2.277	CDS	GI:188595196	BAG34171.1
AP009380	PGN_1653	putative thiamine biosynthesis lipoprotein ApbE		1848181	1849194	1014	forward	1.251	0.323	0.089	0.196	0.190	1.702	CDS	GI:188595197	BAG34172.1
AP009380	PGN_1654	putative electron transport complex RnfABCDGE type A subunit		1849409	1849981	573	reverse	1.325	0.406	0.166	0.297	0.293	1.386	CDS	GI:188595198	BAG34173.1
AP009380	PGN_1655	putative electron transport complex RnfABCDGE type E subunit		1850006	1850596	591	reverse	1.216	0.283	0.223	0.366	0.232	1.218	CDS	GI:188595199	BAG34174.1
AP009380	PGN_1656	putative electron transport complex RnfABCDGE type G subunit		1850593	1851270	678	reverse	1.129	0.175	0.438	0.576	0.226	0.776	CDS	GI:188595200	BAG34175.1
AP009380	PGN_1657	electron transport complex RnfABCDGE type D subunit		1851267	1852250	984	reverse	1.121	0.164	0.459	0.598	0.222	0.740	CDS	GI:188595201	BAG34176.1
AP009380	PGN_1658	electron transport complex RnfABCDGE type C subunit		1852266	1853597	1332	reverse	1.242	0.312	0.133	0.256	0.208	1.503	CDS	GI:188595202	BAG34177.1
AP009380	PGN_1659	putative electron transport complex RnfABCDGE type B subunit		1853633	1854505	873	reverse	0.992	-0.011	0.958	0.970	0.220	-0.052	CDS	GI:188595203	BAG34178.1
AP009380	PGN_1660	conserved hypothetical protein		1854515	1854898	384	reverse	0.758	-0.399	0.087	0.193	0.233	-1.713	CDS	GI:188595204	BAG34179.1
AP009380	PGN_1661	conserved hypothetical protein		1855294	1856586	1293	reverse	1.044	0.062	0.818	0.880	0.269	0.230	CDS	GI:188595205	BAG34180.1
AP009380	PGN_1662	partial transposase in ISPg3		1856750	1857088	339	forward	0.692	-0.531	0.062	0.149	0.284	-1.869	CDS	GI:188595206	BAG34181.1
AP009380	PGN_1663	hypothetical protein		1857149	1857331	183	forward	0.973	-0.040	0.921	0.951	0.404	-0.099	CDS	GI:188595207	BAG34182.1
AP009380	PGN_1664	conserved hypothetical protein		1857680	1857850	171	forward	0.350	-1.513	0.005	0.028	0.543	-2.788	CDS	GI:188595208	BAG34183.1
AP009380	PGN_1665	hypothetical protein		1858023	1858127	105	reverse	0.554	-0.852	0.043	0.117	0.422	-2.020	CDS	GI:188595209	BAG34184.1
AP009380	PGN_1666	phosphoribosylformylglycinamidine synthase		1858201	1861905	3705	forward	1.409	0.495	0.030	0.092	0.228	2.166	CDS	GI:188595210	BAG34185.1
AP009380	PGN_1667	putative DNA processing Smf-like protein		1861898	1863022	1125	forward	1.350	0.433	0.177	0.311	0.321	1.350	CDS	GI:188595211	BAG34186.1
AP009380	PGN_1668	conserved hypothetical protein		1863037	1863933	897	forward	1.288	0.365	0.202	0.342	0.286	1.275	CDS	GI:188595212	BAG34187.1
AP009380	PGN_1669	transposase in ISPg1		1864131	1865216	1086	reverse	0.967	-0.049	0.910	0.946	0.432	-0.113	CDS	GI:188595213	BAG34188.1
AP009380	PGN_1670	conserved hypothetical protein with predicted lysozyme domain		1865870	1866448	579	forward	0.494	-1.018	0.012	0.049	0.406	-2.508	CDS	GI:188595214	BAG34189.1
AP009380	PGN_1671	probable chromate transport protein		1866586	1867179	594	reverse	0.621	-0.686	0.056	0.139	0.359	-1.913	CDS	GI:188595215	BAG34190.1
AP009380	PGN_1672	probable chromate transport protein		1867198	1867779	582	reverse	0.578	-0.791	0.016	0.060	0.329	-2.404	CDS	GI:188595216	BAG34191.1
AP009380	PGN_1673	Por secretion system protein porN/gldN	porN	1867949	1869028	1080	reverse	1.919	0.940	0.000	0.002	0.250	3.762	CDS	GI:188595217	BAG34192.1
AP009380	PGN_1674	Por secretion system protein porM/gldM	porM	1869037	1870587	1551	reverse	1.962	0.973	0.000	0.003	0.265	3.664	CDS	GI:188595218	BAG34193.1
AP009380	PGN_1675	Por secretion system protein porL/gldL	porL	1870591	1871520	930	reverse	1.844	0.883	0.000	0.000	0.205	4.312	CDS	GI:188595219	BAG34194.1
AP009380	PGN_1676	Por secretion system protein porK/gldK	porK	1871561	1873036	1476	reverse	1.841	0.880	0.000	0.002	0.230	3.836	CDS	GI:188595220	BAG34195.1
AP009380	PGN_1677	Por secretion system protein porP	porP	1873093	1874034	942	reverse	1.563	0.644	0.029	0.090	0.295	2.183	CDS	GI:188595221	BAG34196.1
AP009380	PGN_1678	conserved hypothetical protein		1874117	1874374	258	reverse	0.845	-0.242	0.581	0.700	0.439	-0.553	CDS	GI:188595222	BAG34197.1
AP009380	PGN_1679	conserved hypothetical protein		1874527	1876032	1506	reverse	0.575	-0.799	0.016	0.059	0.330	-2.418	CDS	GI:188595223	BAG34198.1
AP009380	PGN_1680	putative ABC transporter permease protein		1876209	1877546	1338	forward	0.776	-0.365	0.291	0.440	0.346	-1.055	CDS	GI:188595224	BAG34199.1
AP009380	PGN_1681	putative ABC transporter ATP-binding protein		1877626	1878297	672	forward	0.514	-0.960	0.023	0.076	0.423	-2.270	CDS	GI:188595225	BAG34200.1

AP009380	PGN_1682	probable ABC transporter permease protein		1878518	1879894	1377	forward	0.570	-0.812	0.009	0.041	0.311	-2.610	CDS	GI:188595226	BAG34201.1
AP009380	PGN_1683	probable ABC transporter permease protein		1879916	1881244	1329	forward	0.877	-0.189	0.542	0.669	0.311	-0.609	CDS	GI:188595227	BAG34202.1
AP009380	PGN_1684	hypothetical protein		1881385	1881489	105	reverse	0.546	-0.872	0.009	0.041	0.335	-2.606	CDS	GI:188595228	BAG34203.1
AP009380	PGN_1685	NADP-dependent malate dehydrogenase		1881584	1883866	2283	forward	0.992	-0.012	0.961	0.971	0.242	-0.049	CDS	GI:188595229	BAG34204.1
AP009380	PGN_1686	hypothetical protein		1883933	1884091	159	forward	1.004	0.006	0.982	0.984	0.265	0.023	CDS	GI:188595230	BAG34205.1
AP009380	PGN_1687	conserved hypothetical protein		1884094	1884531	438	reverse	0.836	-0.258	0.299	0.446	0.248	-1.040	CDS	GI:188595231	BAG34206.1
AP009380	PGN_1688	putative ribose 5-phosphate isomerase B		1884566	1885003	438	reverse	1.224	0.292	0.327	0.477	0.298	0.979	CDS	GI:188595232	BAG34207.1
AP009380	PGN_1689	transketolase		1885090	1887117	2028	reverse	1.552	0.634	0.003	0.017	0.211	3.011	CDS	GI:188595233	BAG34208.1
AP009380	PGN_1690	putative exported fucosidase		1887561	1889381	1821	forward	0.926	-0.111	0.755	0.831	0.355	-0.312	CDS	GI:188595234	BAG34209.1
AP009380	PGN_1691	putative cysteine desulfurase		1889518	1890648	1131	forward	1.179	0.237	0.293	0.441	0.225	1.052	CDS	GI:188595235	BAG34210.1
AP009380	PGN_1692	conserved hypothetical protein		1890632	1890856	225	forward	1.735	0.795	0.022	0.072	0.346	2.299	CDS	GI:188595236	BAG34211.1
AP009380	PGN_1693	selenide water dikinase		1890853	1891899	1047	forward	1.792	0.842	0.017	0.063	0.354	2.379	CDS	GI:188595237	BAG34212.1
AP009380	PGN_1694	putative alanyl dipeptidyl peptidase		1891917	1894442	2526	forward	2.992	1.581	0.000	0.002	0.413	3.832	CDS	GI:188595238	BAG34213.1
AP009380	PGN_1695	putative fructose-bisphosphate aldolase class I		1894585	1895466	882	reverse	0.908	-0.140	0.596	0.713	0.264	-0.530	CDS	GI:188595239	BAG34214.1
AP009380	PGN_1696	conserved hypothetical protein		1895731	1895940	210	forward	0.950	-0.075	0.872	0.919	0.463	-0.161	CDS	GI:188595240	BAG34215.1
AP009380	PGN_1697	conserved hypothetical protein		1896118	1897149	1032	reverse	1.625	0.700	0.001	0.006	0.205	3.411	CDS	GI:188595241	BAG34216.1
AP009380	PGN_1698	putative 30S ribosomal protein S15	rpsO	1897422	1897691	270	forward	0.966	-0.050	0.872	0.919	0.309	-0.161	CDS	GI:188595242	BAG34217.1
AP009380	PGN_1699	probable zinc ABC transporter zinc-binding protein		1897807	1898754	948	forward	1.177	0.236	0.349	0.497	0.251	0.937	CDS	GI:188595243	BAG34218.1
AP009380	PGN_1700	probable metal uptake system ABC transporter ATP-binding protein		1898759	1899373	615	forward	1.244	0.315	0.367	0.511	0.350	0.902	CDS	GI:188595244	BAG34219.1
AP009380	PGN_1701	conserved hypothetical protein		1899336	1899875	540	forward	1.195	0.257	0.279	0.427	0.238	1.082	CDS	GI:188595245	BAG34220.1
AP009380	PGN_1702	protein-export membrane protein SecD/SecF		1900113	1903058	2946	forward	1.214	0.279	0.208	0.348	0.222	1.260	CDS	GI:188595246	BAG34221.1
AP009380	PGN_1703	putative ribonuclease III		1903185	1903970	786	reverse	1.088	0.122	0.747	0.825	0.379	0.322	CDS	GI:188595247	BAG34222.1
AP009380	PGN_1704	beta-ketoacyl-acyl-carrier-protein synthase II		1903982	1905238	1257	reverse	1.062	0.087	0.786	0.857	0.322	0.272	CDS	GI:188595248	BAG34223.1
AP009380	PGN_1705	putative acyl carrier protein		1905248	1905484	237	reverse	1.010	0.014	0.962	0.972	0.287	0.048	CDS	GI:188595249	BAG34224.1
AP009380	PGN_1706	probable phosphoribosylglycinamide formyltransferase		1905653	1906234	582	forward	0.914	-0.130	0.600	0.715	0.247	-0.525	CDS	GI:188595250	BAG34225.1
AP009380	PGN_1707	conserved hypothetical protein		1906231	1907271	1041	forward	1.309	0.389	0.207	0.348	0.308	1.261	CDS	GI:188595251	BAG34226.1
AP009380	PGN_1708	magnesium chelatase subunit ChlI		1907297	1908838	1542	forward	1.738	0.798	0.009	0.039	0.304	2.624	CDS	GI:188595252	BAG34227.1
AP009380	PGN_1709	conserved hypothetical protein		1908843	1909166	324	forward	1.556	0.638	0.004	0.023	0.223	2.863	CDS	GI:188595253	BAG34228.1
AP009380	PGN_1710	conserved hypothetical protein		1909520	1910197	678	forward	0.881	-0.183	0.463	0.602	0.250	-0.734	CDS	GI:188595254	BAG34229.1
AP009380	PGN_1711	phenylalanyl-tRNA synthetase alpha subunit		1910274	1911296	1023	forward	1.535	0.619	0.015	0.056	0.254	2.439	CDS	GI:188595255	BAG34230.1
AP009380	PGN_1712	putative endonuclease III		1911315	1911989	675	forward	1.340	0.422	0.072	0.166	0.234	1.801	CDS	GI:188595256	BAG34231.1
AP009380	PGN_1713	conserved hypothetical protein		1912051	1913388	1338	forward	1.077	0.107	0.661	0.763	0.243	0.438	CDS	GI:188595257	BAG34232.1
AP009380	PGN_1714	transcription-repair coupling factor		1913365	1916733	3369	reverse	1.045	0.064	0.780	0.853	0.230	0.279	CDS	GI:188595258	BAG34233.1
AP009380	PGN_1715	putative chaperone protein GrpE	grpE	1917128	1917712	585	forward	0.580	-0.785	0.081	0.182	0.450	-1.746	CDS	GI:188595259	BAG34234.1
AP009380	PGN_1716	chaperone protein DnaJ	dnaJ	1917755	1918906	1152	forward	0.585	-0.772	0.095	0.205	0.462	-1.671	CDS	GI:188595260	BAG34235.1
AP009380	PGN_1717	conserved hypothetical protein		1918992	1919309	318	forward	0.603	-0.731	0.090	0.198	0.431	-1.695	CDS	GI:188595261	BAG34236.1
AP009380	PGN_1718	probable UDP-2,3-diacylglucosamine hydrolase		1919338	1920126	789	forward	0.688	-0.539	0.169	0.302	0.392	-1.375	CDS	GI:188595262	BAG34237.1
AP009380	PGN_1719	conserved hypothetical protein with appr-1-p processing enzyme domain		1920208	1920702	495	forward	0.662	-0.595	0.118	0.236	0.380	-1.565	CDS	GI:188595263	BAG34238.1
AP009380	PGN_1720	hypothetical protein		1920714	1920827	114	forward	0.665	-0.589	0.091	0.199	0.348	-1.692	CDS	GI:188595264	BAG34239.1
AP009380	PGN_1721	8-amino-7-oxononanoate synthase		1921069	1922256	1188	forward	1.364	0.447	0.076	0.173	0.252	1.773	CDS	GI:188595265	BAG34240.1
AP009380	PGN_1722	putative uridine kinase		1922311	1922934	624	forward	1.203	0.267	0.348	0.497	0.284	0.939	CDS	GI:188595266	BAG34241.1
AP009380	PGN_1723	conserved hypothetical protein		1922976	1924163	1188	forward	1.728	0.789	0.043	0.116	0.390	2.024	CDS	GI:188595267	BAG34242.1
AP009380	PGN_1724	conserved hypothetical protein		1924165	1924860	696	forward	1.361	0.445	0.156	0.285	0.313	1.419	CDS	GI:188595268	BAG34243.1
AP009380	PGN_1725	probable polysaccharide deacetylase		1924848	1925642	795	forward	0.652	-0.617	0.063	0.151	0.332	-1.858	CDS	GI:188595269	BAG34244.1
AP009380	PGN_1726	transposase in ISPg3		1926046	1926948	903	forward	0.818	-0.289	0.359	0.503	0.315	-0.918	CDS	GI:188595270	BAG34245.1
AP009380	PGN_1727	transposase in ISPg1		1927072	1928133	1062	forward	0.620	-0.689	0.132	0.256	0.458	-1.505	CDS	GI:188595271	BAG34246.1
AP009380	PGN_1728	lysine-specific cysteine proteinase Kgp	kgp	1928550	1933721	5172	reverse	2.023	1.017	0.027	0.085	0.461	2.208	CDS	GI:188595272	BAG34247.1
AP009380	PGN_1729	probable acetyltransferase		1934169	1935161	993	reverse	0.753	-0.410	0.136	0.260	0.275	-1.490	CDS	GI:188595273	BAG34248.1
AP009380	PGN_1730	conserved hypothetical protein		1935169	1936092	924	reverse	1.659	0.730	0.010	0.042	0.282	2.591	CDS	GI:188595274	BAG34249.1
AP009380	PGN_1731	conserved hypothetical protein		1936187	1936300	114	reverse	0.952	-0.070	0.852	0.905	0.377	-0.187	CDS	GI:188595275	BAG34250.1
AP009380	PGN_1732	hypothetical protein		1936519	1936638	120	reverse	1.011	0.016	0.971	0.978	0.455	0.036	CDS	GI:188595276	BAG34251.1
AP009380	PGN_1733	hemagglutinin protein HagA	hagA	1936748	1944634	7887	reverse	0.520	-0.943	0.011	0.046	0.371	-2.542	CDS	GI:188595277	BAG34252.1
AP009380	PGN_1734	nucleoside permease NupG		1945016	1946239	1224	reverse	0.641	-0.641	0.010	0.043	0.249	-2.578	CDS	GI:188595278	BAG34253.1
AP009380	PGN_1735	conserved hypothetical protein		1946354	1947721	1368	reverse	0.763	-0.391	0.196	0.334	0.302	-1.293	CDS	GI:188595279	BAG34254.1
AP009380	PGN_1736	putative glycogen synthase		1947824	1948639	816	reverse	0.716	-0.482	0.061	0.147	0.257	-1.874	CDS	GI:188595280	BAG34255.1
AP009380	PGN_1737	ATP-dependent DNA helicase RecQ	recQII	1949266	1951389	2124	forward	0.837	-0.256	0.421	0.558	0.318	-0.805	CDS	GI:188595281	BAG34256.1
AP009380	PGN_1738	putative long-chain-fatty-acid-CoA ligase		1951864	1953537	1674	forward	1.691	0.758	0.044	0.119	0.377	2.010	CDS	GI:188595282	BAG34257.1
AP009380	PGN_1739	conserved hypothetical protein		1953709	1953921	213	forward	0.876	-0.191	0.473	0.610	0.266	-0.718	CDS	GI:188595283	BAG34258.1
AP009380	PGN_1740	putative RNA polymerase ECF-type sigma factor		1954140	1954643	504	reverse	0.402	-1.313	0.000	0.002	0.347	-3.783	CDS	GI:188595284	BAG34259.1
AP009380	PGN_1741	conserved hypothetical protein		1954780	1955199	420	forward	1.133	0.180	0.549	0.674	0.300	0.599	CDS	GI:188595285	BAG34260.1
AP009380	PGN_1742	conserved hypothetical protein		1955174	1955335	162	forward	0.901	-0.150	0.627	0.737	0.308	-0.486	CDS	GI:188595286	BAG34261.1
AP009380	PGN_1743	phosphopyruvate hydratase		1955415	1956692	1278	forward	1.334	0.416	0.022	0.073	0.181	2.294	CDS	GI:188595287	BAG34262.1
AP009380	PGN_1744	conserved hypothetical protein		1956817	1957500	684	reverse	0.673	-0.572	0.044	0.119	0.285	-2.011	CDS	GI:188595288	BAG34263.1
AP009380	PGN_t0045	tRNA-Lys		1957668	1957743	76	forward	0.412	-1.278	0.000	0.001	0.329	-3.886	tRNA		
AP009380	PGN_1745	putative NapC/NirT cytochrome c-type protein		1958308	1958919	612	forward	0.650	-0.622	0.067	0.158	0.340	-1.830	CDS	GI:188595289	BAG34264.1
AP009380	PGN_1746	cytochrome c nitrite reductase catalytic subunit NrfA		1959362	1960501	1140	forward	0.620	-0.689	0.046	0.121	0.344	-1.999	CDS	GI:188595290	BAG34265.1
AP009380	PGN_1747	conserved hypothetical protein		1960572	1961867	1296	forward	0.682	-0.552	0.078	0.177	0.313	-1.763	CDS	GI:188595291	BAG34266.1
AP009380	PGN_1748	putative cytochrome c biogenesis protein CcsA		1961860	1962675	816	forward	0.563	-0.828	0.004	0.022	0.286	-2.898	CDS	GI:188595292	BAG34267.1
AP009380	PGN_1749	probable NADPH-quinone reductase		1962944	1963465	522	forward	1.103	0.141	0.459	0.598	0.191	0.741	CDS	GI:188595293	BAG34268.1
AP009380	PGN_1750	putative 3-deoxy-D-manno-octulosonate cytidylyltransferase		1963462	1964226	765	forward	1.409	0.495	0.036	0.102	0.235	2.100	CDS	GI:188595294	BAG34269.1
AP009380	PGN_1751	DNA primase		1964270	1966291	2022	forward	1.657	0.728	0.005	0.027	0.259	2.808	CDS	GI:188595295	BAG34270.1
AP009380	PGN_1752	putative ferredoxin 4Fe-4S		1966523	1966750	228	forward	0.931	-0.103	0.667	0.766	0.239	-0.431	CDS	GI:188595296	BAG34271.1
AP009380	PGN_1753	putative 2-oxoglutarate oxidoreductase alpha subunit		1966769	1967851	1083	forward	1.155	0.208	0.241	0.385	0.177	1.172	CDS	GI:188595297	BAG34272.1
AP009380	PGN_1754	hypothetical protein		1967872	1968051	180	forward	1.423	0.509	0.012	0.048	0.202	2.527	CDS	GI:188595298	BAG34273.1
AP009380	PGN_1755	putative 2-oxoglutarate oxidoreductase beta subunit		1968125	1968832	708	forward	1.267	0.342	0.068	0.159	0.187	1.825	CDS	GI:188595299	BAG34274.1
AP009380	PGN_1756	putative 2-oxoglutarate oxidoreductase gamma subunit		1968861	1969406	546	forward	1.289	0.366	0.115	0.232	0.232	1.577	CDS	GI:188595300	BAG34275.1
AP009380	PGN_1757	GTP pyrophosphokinase		1969658	1971946	2289	forward	0.807	-0.309	0.266	0.413	0.278	-1.112	CDS	GI:188595301	BAG34276.1
AP009380	PGN_1758	putative v-type ATPase subunit K		1972305	1972781	477	reverse	1.516	0.600	0.135	0.259	0.402	1.494	CDS	GI:188595302	BAG34277.1
AP009380	PGN_1759	putative v-type ATPase subunit I		1972836	1974650	1815	reverse	1.821	0.865	0.021	0.072	0.375	2.303	CDS	GI:188595303	BAG34278.1
AP009380	PGN_1760	putative v-type ATPase subunit D		1974647	1975261	615	reverse	1.585	0.664	0.060	0.146	0.353	1.881	CDS	GI:188595304	BAG34279.1
AP009380	PGN_1761	v-type ATPase subunit B		1975277	1976596	1320	reverse	1.386	0.471	0.142	0.267	0.321	1.467	CDS	GI:188595305	BAG34280.1
AP009380	PGN_1762	v-type ATPase subunit A		1976608	1978362	1755	reverse	1.494	0.579	0.099	0.210	0.351	1.652	CDS	GI:188595306	BAG34281.1
AP009380	PGN_1763	conserved hypothetical protein		1978372	1979310	939	reverse	1.495	0.580	0.068	0.159	0.318	1.826	CDS	GI:188595307	BAG34282.1
AP009380	PGN_1764	putative v-type ATPase subunit E		1979314	1979904	591	reverse	1.261	0.335	0.309	0.457	0.329	1.017	CDS	GI:188595308	BAG34283.1
AP009380	PGN_1765	hypothetical protein		1979944	1980084	141	reverse	0.656	-0.609	0.181	0.317	0.456	-1.336	CDS	GI:188595309	BAG34284.1
AP009380	PGN_1766	conserved hypothetical protein		1980095	1980352	258	reverse	0.636	-0.653	0.162	0.292	0.466	-1.400	CDS	GI:188595310	BAG34285.1
AP009380	PGN_1767	immunoreactive 46 kDa antigen		1980602	1981873	1272	forward	0.985	-0.022	0.944	0.962	0.314	-0.070	CDS	GI:188595311	BAG34286.1

AP009380	PGN_1768	putative DNA-binding response regulator/sensor histidine kinase		1981953	1984838	2886	reverse	1.299	0.377	0.113	0.230	0.238	1.584	CDS	GI:188595312	BAG34287.1
AP009380	PGN_1769	hypothetical protein		1984961	1985137	177	reverse	0.662	-0.596	0.038	0.106	0.287	-2.077	CDS	GI:188595313	BAG34288.1
AP009380	PGN_1770	conserved hypothetical protein		1985158	1985946	789	forward	0.801	-0.320	0.195	0.334	0.247	-1.296	CDS	GI:188595314	BAG34289.1
AP009380	PGN_1771	DNA polymerase I		1986093	1988873	2781	reverse	0.987	-0.018	0.946	0.962	0.270	-0.068	CDS	GI:188595315	BAG34290.1
AP009380	PGN_1772	1,4-alpha-glucan branching enzyme		1988924	1990930	2007	reverse	0.926	-0.110	0.679	0.778	0.266	-0.414	CDS	GI:188595316	BAG34291.1
AP009380	PGN_1773	sodium/hydrogen antiporter		1990927	1993230	2304	reverse	0.830	-0.269	0.359	0.503	0.293	-0.917	CDS	GI:188595317	BAG34292.1
AP009380	PGN_1774	conserved hypothetical protein		1993781	1993996	216	forward	1.181	0.240	0.399	0.540	0.284	0.843	CDS	GI:188595318	BAG34293.1
AP009380	PGN_1775	conserved hypothetical protein		1993993	1995477	1485	forward	1.093	0.128	0.644	0.750	0.276	0.463	CDS	GI:188595319	BAG34294.1
AP009380	PGN_1776	peptidyl-dipeptidase		1995494	1997530	2037	forward	2.395	1.260	0.002	0.015	0.412	3.055	CDS	GI:188595320	BAG34295.1
AP009380	PGN_1777	bleomycin hydrolase		1997647	1998918	1272	reverse	1.937	0.954	0.027	0.084	0.430	2.216	CDS	GI:188595321	BAG34296.1
AP009380	PGN_1778	hypothetical protein		1999341	1999436	96	reverse	0.531	-0.914	0.034	0.100	0.432	-2.115	CDS	GI:188595322	BAG34297.1
AP009380	PGN_1779	conserved hypothetical protein		2000160	2000297	138	forward	1.260	0.334	0.523	0.652	0.522	0.639	CDS	GI:188595323	BAG34298.1
AP009380	PGN_1780	putative YjgF-like protein		2000300	2000680	381	reverse	2.245	1.167	0.003	0.017	0.390	2.992	CDS	GI:188595324	BAG34299.1
AP009380	PGN_1781	putative tRNA:rRNA methyltransferase		2000706	2001455	750	reverse	1.799	0.847	0.013	0.051	0.341	2.488	CDS	GI:188595325	BAG34300.1
AP009380	PGN_1782	DNA repair protein RecN		2001452	2003107	1656	reverse	1.548	0.631	0.024	0.077	0.279	2.259	CDS	GI:188595326	BAG34301.1
AP009380	PGN_1783	conserved hypothetical protein		2003122	2004030	909	reverse	1.294	0.371	0.042	0.115	0.183	2.033	CDS	GI:188595327	BAG34302.1
AP009380	PGN_1784	DNA/pantothenate metabolism flavoprotein		2004027	2005241	1215	reverse	1.333	0.414	0.089	0.196	0.243	1.701	CDS	GI:188595328	BAG34303.1
AP009380	PGN_1785	putative DNA polymerase III epsilon chain		2005267	2006046	780	reverse	1.105	0.144	0.587	0.705	0.265	0.543	CDS	GI:188595329	BAG34304.1
AP009380	PGN_1786	putative DNA polymerase III beta chain		2006059	2007192	1134	reverse	1.104	0.143	0.612	0.725	0.281	0.507	CDS	GI:188595330	BAG34305.1
AP009380	PGN_1787	probable 5-formyltetrahydrofolate cyclo-ligase		2007398	2007901	504	reverse	1.352	0.435	0.125	0.245	0.284	1.535	CDS	GI:188595331	BAG34306.1
AP009380	PGN_1788	carboxyl-terminal processing protease		2007915	2009549	1635	reverse	1.872	0.905	0.026	0.083	0.407	2.222	CDS	GI:188595332	BAG34307.1
AP009380	PGN_1789	putative deoxycytidylate deaminase		2009557	2010012	456	reverse	1.375	0.460	0.248	0.393	0.398	1.156	CDS	GI:188595333	BAG34308.1
AP009380	PGN_1790	conserved hypothetical protein		2010093	2010446	354	reverse	2.103	1.072	0.000	0.001	0.268	4.006	CDS	GI:188595334	BAG34309.1
AP009380	PGN_1791	putative flavodoxin		2010611	2011108	498	reverse	1.116	0.159	0.425	0.562	0.199	0.799	CDS	GI:188595335	BAG34310.1
AP009380	PGN_1792	glycerate kinase		2011247	2012407	1161	reverse	0.873	-0.196	0.488	0.625	0.283	-0.693	CDS	GI:188595336	BAG34311.1
AP009380	PGN_1793	conserved hypothetical protein		2012647	2013831	1185	reverse	0.689	-0.538	0.022	0.073	0.234	-2.295	CDS	GI:188595337	BAG34312.1
AP009380	PGN_1794	conserved hypothetical protein		2013960	2014130	171	reverse	0.626	-0.676	0.013	0.051	0.271	-2.489	CDS	GI:188595338	BAG34313.1
AP009380	PGN_1795	conserved hypothetical protein		2014143	2014589	447	reverse	0.621	-0.687	0.022	0.073	0.299	-2.294	CDS	GI:188595339	BAG34314.1
AP009380	PGN_1796	conserved hypothetical protein		2014582	2017959	3378	reverse	0.684	-0.547	0.060	0.146	0.291	-1.878	CDS	GI:188595340	BAG34315.1
AP009380	PGN_1797	conserved hypothetical protein		2018735	2019256	522	reverse	0.904	-0.145	0.623	0.734	0.296	-0.491	CDS	GI:188595341	BAG34316.1
AP009380	PGN_1798	conserved hypothetical protein		2019507	2020172	666	reverse	0.736	-0.441	0.118	0.237	0.283	-1.562	CDS	GI:188595342	BAG34317.1
AP009380	PGN_1799	hypothetical protein		2020208	2020381	174	reverse	0.731	-0.452	0.289	0.437	0.427	-1.060	CDS	GI:188595343	BAG34318.1
AP009380	PGN_1800	urocanate hydratase		2020569	2022548	1980	reverse	1.639	0.713	0.004	0.025	0.251	2.842	CDS	GI:188595344	BAG34319.1
AP009380	PGN_1801	conserved hypothetical protein		2022889	2023296	408	reverse	0.987	-0.019	0.944	0.962	0.268	-0.071	CDS	GI:188595345	BAG34320.1
AP009380	PGN_1802	hemolysin		2023283	2024257	975	reverse	1.166	0.222	0.347	0.496	0.236	0.941	CDS	GI:188595346	BAG34321.1
AP009380	PGN_1803	conserved hypothetical protein		2024269	2025096	828	reverse	1.491	0.576	0.076	0.173	0.325	1.774	CDS	GI:188595347	BAG34322.1
AP009380	PGN_1804	Na+/H+ antiporter		2025125	2026483	1359	reverse	0.704	-0.506	0.123	0.243	0.328	-1.541	CDS	GI:188595348	BAG34323.1
AP009380	PGN_1805	cysteinyl-tRNA synthetase		2026626	2028086	1461	forward	0.952	-0.071	0.803	0.868	0.286	-0.250	CDS	GI:188595349	BAG34324.1
AP009380	PGN_1806	conserved hypothetical protein		2028137	2029156	1020	forward	0.838	-0.255	0.360	0.505	0.278	-0.914	CDS	GI:188595350	BAG34325.1
AP009380	PGN_1807	putative glycosyltransferase		2029167	2030177	1011	forward	0.917	-0.125	0.570	0.690	0.220	-0.568	CDS	GI:188595351	BAG34326.1
AP009380	PGN_1808	conserved hypothetical protein		2030210	2031652	1443	forward	1.058	0.081	0.643	0.750	0.175	0.464	CDS	GI:188595352	BAG34327.1
AP009380	PGN_1809	hypothetical protein		2031685	2031780	96	forward	1.084	0.117	0.710	0.801	0.314	0.372	CDS	GI:188595353	BAG34328.1
AP009380	PGN_1810	hypothetical protein		2032072	2032338	267	forward	2.203	1.140	0.000	0.002	0.296	3.857	CDS	GI:188595354	BAG34329.1
AP009380	PGN_1811	putative alpha-L-fucosidase		2032472	2034565	2094	reverse	1.439	0.525	0.006	0.029	0.189	2.770	CDS	GI:188595355	BAG34330.1
AP009380	PGN_1812	polyphosphate kinase		2034569	2036656	2088	reverse	1.057	0.080	0.770	0.845	0.275	0.292	CDS	GI:188595356	BAG34331.1
AP009380	PGN_1813	GTP-binding protein		2036819	2038039	1221	reverse	0.704	-0.505	0.031	0.094	0.235	-2.155	CDS	GI:188595357	BAG34332.1
AP009380	PGN_1814	conserved hypothetical protein		2038118	2039152	1035	forward	1.277	0.353	0.156	0.285	0.249	1.418	CDS	GI:188595358	BAG34333.1
AP009380	PGN_1815	conserved hypothetical protein		2039149	2039763	615	forward	2.038	1.027	0.001	0.005	0.298	3.449	CDS	GI:188595359	BAG34334.1
AP009380	PGN_1816	conserved hypothetical protein		2039904	2040566	663	forward	1.250	0.322	0.257	0.403	0.284	1.135	CDS	GI:188595360	BAG34335.1
AP009380	PGN_1817	conserved hypothetical protein		2041168	2041605	438	forward	1.019	0.027	0.919	0.950	0.267	0.101	CDS	GI:188595361	BAG34336.1
AP009380	PGN_1818	conserved hypothetical protein		2041638	2047895	6258	forward	1.469	0.555	0.152	0.280	0.388	1.431	CDS	GI:188595362	BAG34337.1
AP009380	PGN_1819	hypothetical protein		2047889	2048422	534	forward	1.509	0.594	0.173	0.307	0.436	1.362	CDS	GI:188595363	BAG34338.1
AP009380	PGN_1820	conserved hypothetical protein		2048526	2048987	462	forward	1.389	0.474	0.295	0.443	0.452	1.048	CDS	GI:188595364	BAG34339.1
AP009380	PGN_1821	conserved hypothetical protein		2049047	2050444	1398	forward	1.460	0.546	0.124	0.245	0.355	1.537	CDS	GI:188595365	BAG34340.1
AP009380	PGN_1822	hypothetical protein		2051009	2051110	102	reverse	2.005	1.004	0.037	0.105	0.482	2.085	CDS	GI:188595366	BAG34341.1
AP009380	PGN_1823	conserved hypothetical protein		2051588	2052361	774	forward	2.843	1.507	0.000	0.003	0.416	3.625	CDS	GI:188595367	BAG34342.1
AP009380	PGN_1824	hypothetical protein		2052465	2052776	312	forward	2.087	1.062	0.006	0.032	0.389	2.728	CDS	GI:188595368	BAG34343.1
AP009380	PGN_1825	hypothetical protein		2052907	2054094	1188	forward	0.447	-1.161	0.013	0.052	0.468	-2.480	CDS	GI:188595369	BAG34344.1
AP009380	PGN_1826	conserved hypothetical protein		2054091	2054789	699	forward	0.859	-0.220	0.548	0.674	0.365	-0.601	CDS	GI:188595370	BAG34345.1
AP009380	PGN_1827	S-adenosylmethionine synthase		2055213	2056502	1290	forward	0.574	-0.800	0.088	0.196	0.469	-1.704	CDS	GI:188595371	BAG34346.1
AP009380	PGN_1828	conserved hypothetical protein		2056631	2057350	720	reverse	0.549	-0.866	0.006	0.032	0.318	-2.722	CDS	GI:188595372	BAG34347.1
AP009380	PGN_1829	probable nicotinamide mononucleotide transporter		2057305	2057886	582	reverse	0.691	-0.533	0.122	0.242	0.344	-1.547	CDS	GI:188595373	BAG34348.1
AP009380	PGN_1830	putative TonB-dependent receptor		2057918	2060302	2385	reverse	0.810	-0.304	0.115	0.232	0.193	-1.577	CDS	GI:188595374	BAG34349.1
AP009380	PGN_1831	putative GTPase		2060378	2061325	948	reverse	1.081	0.112	0.709	0.801	0.300	0.373	CDS	GI:188595375	BAG34350.1
AP009380	PGN_1832	putative ribosome recycling factor		2061410	2061970	561	reverse	1.363	0.447	0.072	0.167	0.249	1.796	CDS	GI:188595376	BAG34351.1
AP009380	PGN_1833	putative uridylate kinase		2062007	2062726	720	reverse	0.942	-0.086	0.685	0.782	0.211	-0.406	CDS	GI:188595377	BAG34352.1
AP009380	PGN_1834	conserved hypothetical protein		2062809	2064800	1992	reverse	1.260	0.333	0.074	0.169	0.186	1.788	CDS	GI:188595378	BAG34353.1
AP009380	PGN_1835	conserved hypothetical protein		2065011	2065316	306	reverse	0.607	-0.721	0.105	0.218	0.445	-1.623	CDS	GI:188595379	BAG34354.1
AP009380	PGN_1836	transposase in ISPg3		2065490	2066392	903	reverse	0.745	-0.424	0.165	0.296	0.306	-1.388	CDS	GI:188595380	BAG34355.1
AP009380	PGN_1837	conserved hypothetical protein		2067081	2067926	846	forward	0.714	-0.485	0.136	0.260	0.326	-1.490	CDS	GI:188595381	BAG34356.1
AP009380	PGN_1838	partial transposase in ISPg1		2068225	2068869	645	reverse	0.749	-0.417	0.352	0.498	0.448	-0.931	CDS	GI:188595382	BAG34357.1
AP009380	PGN_1839	partial transposase in ISPg1		2068915	2069310	396	reverse	0.794	-0.333	0.413	0.552	0.406	-0.819	CDS	GI:188595383	BAG34358.1
AP009380	PGN_1840	50S ribosomal protein L17	rplQ	2069522	2070004	483	reverse	3.683	1.881	0.000	0.000	0.187	10.079	CDS	GI:188595384	BAG34359.1
AP009380	PGN_1841	DNA-directed RNA polymerase alpha subunit	rpoA	2070010	2071002	993	reverse	4.100	2.036	0.000	0.000	0.272	7.497	CDS	GI:188595385	BAG34360.1
AP009380	PGN_1842	30S ribosomal protein S4	rpsD	2071015	2071620	606	reverse	3.917	1.970	0.000	0.000	0.241	8.166	CDS	GI:188595386	BAG34361.1
AP009380	PGN_1843	30S ribosomal protein S11	rpsK	2071780	2072166	387	reverse	3.976	1.991	0.000	0.000	0.302	6.598	CDS	GI:188595387	BAG34362.1
AP009380	PGN_1844	30S ribosomal protein S13	rpsM	2072178	2072558	381	reverse	3.765	1.913	0.000	0.000	0.280	6.825	CDS	GI:188595388	BAG34363.1
AP009380	PGN_1845	50S ribosomal protein L36	rpmJ	2072591	2072707	117	reverse	3.628	1.859	0.000	0.000	0.226	8.214	CDS	GI:188595389	BAG34364.1
AP009380	PGN_1846	translation initiation factor IF-1		2072724	2072942	219	reverse	3.458	1.790	0.000	0.000	0.226	7.933	CDS	GI:188595390	BAG34365.1
AP009380	PGN_1847	putative methionine aminopeptidase type I		2072945	2073730	786	reverse	3.212	1.683	0.000	0.000	0.236	7.140	CDS	GI:188595391	BAG34366.1
AP009380	PGN_1848	preprotein translocase SecY subunit		2073730	2075070	1341	reverse	2.815	1.493	0.000	0.000	0.242	6.166	CDS	GI:188595392	BAG34367.1
AP009380	PGN_1849	50S ribosomal protein L15	rplO	2075075	2075521	447	reverse	3.064	1.615	0.000	0.000	0.193	8.386	CDS	GI:188595393	BAG34368.1
AP009380	PGN_1850	50S ribosomal protein L30	rpmD	2075547	2075723	177	reverse	3.118	1.641	0.000	0.000	0.240	6.830	CDS	GI:188595394	BAG34369.1
AP009380	PGN_1851	30S ribosomal protein S5	rpsE	2075743	2076261	519	reverse	3.291	1.719	0.000	0.000	0.242	7.095	CDS	GI:188595395	BAG34370.1
AP009380	PGN_1852	50S ribosomal protein L18	rplR	2076267	2076611	345	reverse	3.234	1.693	0.000	0.000	0.254	6.655	CDS	GI:188595396	BAG34371.1
AP009380	PGN_1853	50S ribosomal protein L6	rplF	2076630	2077181	552	reverse	3.107	1.636	0.000	0.000	0.254	6.443	CDS	GI:188595397	BAG34372.1
AP009380	PGN_1854	30S ribosomal protein S8	rpsH	2077200	2077595	396	reverse	3.125	1.644	0.000	0.000	0.236	6.955	CDS	GI:188595398	BAG34373.1

AP009380	PGN_1855	30S ribosomal protein S14	rpsN	2077646	2077915	270	reverse	2.496	1.319	0.000	0.000	0.225	5.864	CDS	GI:188595399	BAG34374.1
AP009380	PGN_1856	50S ribosomal protein L5	rplE	2077917	2078477	561	reverse	2.820	1.496	0.000	0.000	0.254	5.880	CDS	GI:188595400	BAG34375.1
AP009380	PGN_1857	50S ribosomal protein L24	rplX	2078477	2078797	321	reverse	2.795	1.483	0.000	0.000	0.237	6.246	CDS	GI:188595401	BAG34376.1
AP009380	PGN_1858	50S ribosomal protein L14	rplN	2078820	2079185	366	reverse	3.534	1.821	0.000	0.000	0.317	5.750	CDS	GI:188595402	BAG34377.1
AP009380	PGN_1859	30S ribosomal protein S17	rpsQ	2079187	2079441	255	reverse	3.305	1.725	0.000	0.000	0.288	5.994	CDS	GI:188595403	BAG34378.1
AP009380	PGN_1860	50S ribosomal protein L29	rpmC	2079455	2079649	195	reverse	3.488	1.802	0.000	0.000	0.296	6.089	CDS	GI:188595404	BAG34379.1
AP009380	PGN_1861	50S ribosomal protein L16	rplP	2079655	2080089	435	reverse	3.264	1.707	0.000	0.000	0.311	5.492	CDS	GI:188595405	BAG34380.1
AP009380	PGN_1862	30S ribosomal protein S3	rpsC	2080110	2080850	741	reverse	2.966	1.569	0.000	0.000	0.270	5.800	CDS	GI:188595406	BAG34381.1
AP009380	PGN_1863	50S ribosomal protein L22	rplV	2080857	2081261	405	reverse	3.043	1.605	0.000	0.000	0.320	5.022	CDS	GI:188595407	BAG34382.1
AP009380	PGN_1864	30S ribosomal protein S19	rpsS	2081316	2081585	270	reverse	3.062	1.615	0.000	0.000	0.261	6.181	CDS	GI:188595408	BAG34383.1
AP009380	PGN_1865	50S ribosomal protein L2	rplB	2081608	2082432	825	reverse	2.565	1.359	0.000	0.000	0.241	5.642	CDS	GI:188595409	BAG34384.1
AP009380	PGN_1866	50S ribosomal protein L23	rplW	2082439	2082732	294	reverse	2.682	1.423	0.000	0.000	0.243	5.851	CDS	GI:188595410	BAG34385.1
AP009380	PGN_1867	50S ribosomal protein L4	rplD	2082747	2083376	630	reverse	3.167	1.663	0.000	0.000	0.262	6.356	CDS	GI:188595411	BAG34386.1
AP009380	PGN_1868	50S ribosomal protein L3	rplC	2083376	2083993	618	reverse	3.310	1.727	0.000	0.000	0.258	6.693	CDS	GI:188595412	BAG34387.1
AP009380	PGN_1869	30S ribosomal protein S10	rpsJ	2084016	2084321	306	reverse	3.320	1.731	0.000	0.000	0.251	6.899	CDS	GI:188595413	BAG34388.1
AP009380	PGN_1870	translation elongation factor G		2084337	2086460	2124	reverse	2.208	1.143	0.000	0.000	0.210	5.446	CDS	GI:188595414	BAG34389.1
AP009380	PGN_1871	30S ribosomal protein S7	rpsG	2086473	2086949	477	reverse	2.407	1.267	0.000	0.000	0.221	5.740	CDS	GI:188595415	BAG34390.1
AP009380	PGN_1872	30S ribosomal protein S12	rpsL	2087186	2087590	405	reverse	2.216	1.148	0.000	0.000	0.190	6.036	CDS	GI:188595416	BAG34391.1
AP009380	PGN_1873	conserved hypothetical protein		2088187	2089473	1287	reverse	2.144	1.100	0.000	0.000	0.262	4.206	CDS	GI:188595417	BAG34392.1
AP009380	PGN_1874	putative 3-phosphoshikimate 1-carboxyvinyltransferase		2089679	2090938	1260	forward	2.132	1.092	0.000	0.004	0.307	3.563	CDS	GI:188595418	BAG34393.1
AP009380	PGN_1875	conserved hypothetical protein		2090960	2091403	444	forward	2.130	1.091	0.002	0.015	0.358	3.046	CDS	GI:188595419	BAG34394.1
AP009380	PGN_1876	putative ABC transporter membrane protein		2091396	2092202	807	forward	1.873	0.906	0.007	0.034	0.337	2.687	CDS	GI:188595420	BAG34395.1
AP009380	PGN_1877	Por secretion system protein porW/sprE	porW	2092195	2095677	3483	forward	2.561	1.357	0.000	0.000	0.270	5.022	CDS	GI:188595421	BAG34396.1
AP009380	PGN_1878	conserved hypothetical protein		2095702	2097123	1422	forward	2.780	1.475	0.000	0.000	0.310	4.764	CDS	GI:188595422	BAG34397.1
AP009380	PGN_1879	hypothetical protein		2097131	2097292	162	forward	1.129	0.175	0.553	0.676	0.294	0.593	CDS	GI:188595423	BAG34398.1
AP009380	PGN_1880	malate dehydrogenase		2097400	2098404	1005	reverse	1.440	0.526	0.092	0.201	0.312	1.683	CDS	GI:188595424	BAG34399.1
AP009380	PGN_1881	conserved hypothetical protein		2098575	2098853	279	forward	1.870	0.903	0.007	0.032	0.333	2.714	CDS	GI:188595425	BAG34400.1
AP009380	PGN_1882	probable permease		2098866	2100026	1161	forward	1.545	0.628	0.049	0.127	0.320	1.964	CDS	GI:188595426	BAG34401.1
AP009380	PGN_1883	glutaminyl-tRNA synthetase		2100406	2102106	1701	forward	2.025	1.018	0.000	0.002	0.272	3.748	CDS	GI:188595427	BAG34402.1
AP009380	PGN_1884	probable alkaline phosphatase		2102134	2102781	648	forward	2.606	1.382	0.000	0.000	0.264	5.229	CDS	GI:188595428	BAG34403.1
AP009380	PGN_1885	conserved hypothetical protein		2102844	2103779	936	forward	2.708	1.437	0.000	0.000	0.188	7.653	CDS	GI:188595429	BAG34404.1
AP009380	PGN_1886	putative NAD dependent epimerase		2103783	2104802	1020	forward	3.352	1.745	0.000	0.000	0.258	6.764	CDS	GI:188595430	BAG34405.1
AP009380	PGN_1887	hypothetical protein		2105127	2105300	174	reverse	2.720	1.444	0.000	0.000	0.287	5.038	CDS	GI:188595431	BAG34406.1
AP009380	PGN_1888	4-hydroxybutyrate CoA-transferase		2105523	2106818	1296	reverse	2.139	1.097	0.000	0.000	0.216	5.067	CDS	GI:188595432	BAG34407.1
AP009380	PGN_1889	conserved hypothetical protein		2107357	2107506	150	reverse	2.056	1.040	0.001	0.006	0.308	3.376	CDS	GI:188595433	BAG34408.1
AP009380	PGN_1890	50S ribosomal protein L33	rpmG	2107525	2107713	189	reverse	2.048	1.035	0.003	0.019	0.351	2.947	CDS	GI:188595434	BAG34409.1
AP009380	PGN_1891	50S ribosomal protein L28	rpmB	2107733	2107972	240	reverse	1.922	0.943	0.001	0.007	0.282	3.338	CDS	GI:188595435	BAG34410.1
AP009380	PGN_1892	conserved hypothetical protein		2108195	2110462	2268	reverse	2.902	1.537	0.000	0.000	0.242	6.363	CDS	GI:188595436	BAG34411.1
AP009380	PGN_1893	hypothetical protein		2110659	2111270	612	reverse	3.047	1.607	0.000	0.000	0.298	5.387	CDS	GI:188595437	BAG34412.1
AP009380	PGN_1894	conserved hypothetical protein		2111397	2111549	153	reverse	0.890	-0.168	0.705	0.798	0.444	-0.378	CDS	GI:188595438	BAG34413.1
AP009380	PGN_1895	conserved hypothetical protein		2111697	2112272	576	forward	2.748	1.459	0.000	0.000	0.206	7.085	CDS	GI:188595439	BAG34414.1
AP009380	PGN_1896	galactose-1-phosphate transferase	wbaP	2112269	2113675	1407	forward	3.117	1.640	0.000	0.000	0.299	5.477	CDS	GI:188595440	BAG34415.1
AP009380	PGN_1897	putative transport related membrane protein		2113672	2115468	1797	forward	3.141	1.651	0.000	0.000	0.315	5.243	CDS	GI:188595441	BAG34416.1
AP009380	PGN_1898	probable transport protein		2115429	2116427	999	reverse	2.340	1.227	0.000	0.000	0.273	4.498	CDS	GI:188595442	BAG34417.1
AP009380	PGN_1899	conserved hypothetical protein		2116530	2117414	885	forward	1.856	0.892	0.003	0.019	0.301	2.963	CDS	GI:188595443	BAG34418.1
AP009380	PGN_1900	hypothetical protein		2117698	2117823	126	reverse	1.218	0.284	0.374	0.517	0.320	0.889	CDS	GI:188595444	BAG34419.1
AP009380	PGN_1901	transposase in ISPg1		2118544	2119629	1086	reverse	0.989	-0.016	0.970	0.977	0.426	-0.037	CDS	GI:188595445	BAG34420.1
AP009380	PGN_1902	conserved hypothetical protein		2119733	2120473	741	reverse	1.465	0.551	0.010	0.043	0.214	2.571	CDS	GI:188595446	BAG34421.1
AP009380	PGN_1903	putative adenine-specific DNA methyltransferase		2120466	2121305	840	reverse	1.299	0.377	0.175	0.309	0.278	1.355	CDS	GI:188595447	BAG34422.1
AP009380	PGN_1904	hemagglutinin protein HagB	hagB	2121869	2122921	1053	forward	3.126	1.644	0.000	0.000	0.198	8.287	CDS	GI:188595448	BAG34423.1
AP009380	PGN_1905	conserved hypothetical protein		2123712	2124776	1065	reverse	0.771	-0.375	0.175	0.308	0.276	-1.357	CDS	GI:188595449	BAG34424.1
AP009380	PGN_1906	hemagglutinin protein HagC	hagC	2125016	2126068	1053	forward	3.004	1.587	0.000	0.000	0.267	5.939	CDS	GI:188595450	BAG34425.1
AP009380	PGN_1907	conserved hypothetical protein		2126435	2128441	2007	reverse	1.657	0.728	0.002	0.016	0.240	3.038	CDS	GI:188595451	BAG34426.1
AP009380	PGN_1908	hypothetical protein		2128438	2128557	120	reverse	2.485	1.313	0.000	0.003	0.361	3.639	CDS	GI:188595452	BAG34427.1
AP009380	PGN_1909	conserved hypothetical protein		2128566	2128736	171	forward	1.893	0.921	0.006	0.029	0.334	2.760	CDS	GI:188595453	BAG34428.1
AP009380	PGN_1910	conserved hypothetical protein		2129007	2129177	171	reverse	0.704	-0.506	0.140	0.263	0.343	-1.475	CDS	GI:188595454	BAG34429.1
AP009380	PGN_1911	transposase in ISPg3		2129806	2130708	903	forward	0.915	-0.128	0.689	0.785	0.321	-0.401	CDS	GI:188595455	BAG34430.1
AP009380	PGN_1912	partial transposase in ISPg6		2130789	2131301	513	forward	0.534	-0.906	0.000	0.003	0.245	-3.697	CDS	GI:188595456	BAG34431.1
AP009380	PGN_1913	transposase in ISPg3		2131645	2132547	903	reverse	0.799	-0.323	0.302	0.450	0.313	-1.031	CDS	GI:188595457	BAG34432.1
AP009380	PGN_1914	carboxyl-terminal processing protease		2133134	2134843	1710	reverse	1.048	0.068	0.804	0.869	0.273	0.248	CDS	GI:188595458	BAG34433.1
AP009380	PGN_1915	conserved hypothetical protein		2135093	2135470	378	forward	0.630	-0.667	0.031	0.093	0.309	-2.160	CDS	GI:188595459	BAG34434.1
AP009380	PGN_1916	putative ABC transporter ATP-binding protein		2135640	2137346	1707	reverse	0.736	-0.443	0.029	0.088	0.202	-2.190	CDS	GI:188595460	BAG34435.1
AP009380	PGN_1917	putative ABC transporter ATP-binding protein		2137393	2139147	1755	reverse	1.105	0.144	0.641	0.749	0.309	0.466	CDS	GI:188595461	BAG34436.1
AP009380	PGN_1918	conserved hypothetical protein		2139172	2140449	1278	reverse	0.935	-0.097	0.699	0.794	0.252	-0.386	CDS	GI:188595462	BAG34437.1
AP009380	PGN_1919	conserved hypothetical protein		2140453	2141244	792	reverse	1.196	0.259	0.372	0.515	0.290	0.892	CDS	GI:188595463	BAG34438.1
AP009380	PGN_1920	conserved hypothetical protein		2141322	2143727	2406	reverse	0.749	-0.417	0.135	0.258	0.279	-1.496	CDS	GI:188595464	BAG34439.1
AP009380	PGN_1921	probable transcriptional regulator		2143768	2144415	648	reverse	0.714	-0.486	0.065	0.155	0.264	-1.843	CDS	GI:188595465	BAG34440.1
AP009380	PGN_1922	transposase in ISPg3		2145584	2146486	903	forward	0.557	-0.845	0.010	0.043	0.328	-2.577	CDS	GI:188595466	BAG34441.1
AP009380	PGN_1923	hypothetical protein		2146688	2146798	111	reverse	0.664	-0.591	0.164	0.294	0.424	-1.393	CDS	GI:188595467	BAG34442.1
AP009380	PGN_1924	conserved hypothetical protein		2146958	2147248	291	reverse	0.519	-0.946	0.022	0.073	0.414	-2.286	CDS	GI:188595468	BAG34443.1
AP009380	PGN_1925	conserved hypothetical protein		2147268	2148026	759	reverse	0.796	-0.329	0.405	0.545	0.395	-0.833	CDS	GI:188595469	BAG34444.1
AP009380	PGN_1926	transposase in ISPg1		2148230	2149315	1086	reverse	0.585	-0.773	0.095	0.205	0.463	-1.671	CDS	GI:188595470	BAG34445.1
AP009380	PGN_1927	conserved hypothetical protein		2149419	2151707	2289	reverse	0.533	-0.909	0.002	0.013	0.291	-3.122	CDS	GI:188595471	BAG34446.1
AP009380	PGN_1928	conserved hypothetical protein		2151763	2152509	747	reverse	1.545	0.628	0.218	0.361	0.509	1.233	CDS	GI:188595472	BAG34447.1
AP009380	PGN_1929	conserved hypothetical protein		2152506	2152943	438	reverse	1.390	0.476	0.348	0.497	0.507	0.938	CDS	GI:188595473	BAG34448.1
AP009380	PGN_1930	conserved hypothetical protein		2152940	2153641	702	reverse	1.326	0.407	0.416	0.554	0.501	0.813	CDS	GI:188595474	BAG34449.1
AP009380	PGN_1931	conserved hypothetical protein		2153655	2154836	1182	reverse	1.372	0.457	0.356	0.501	0.495	0.923	CDS	GI:188595475	BAG34450.1
AP009380	PGN_1932	conserved hypothetical protein		2154838	2156418	1581	reverse	1.408	0.494	0.318	0.468	0.494	0.998	CDS	GI:188595476	BAG34451.1
AP009380	PGN_1933	conserved hypothetical protein		2156423	2157667	1245	reverse	1.170	0.226	0.611	0.724	0.444	0.509	CDS	GI:188595477	BAG34452.1
AP009380	PGN_1934	conserved hypothetical protein		2157683	2157919	237	reverse	0.946	-0.079	0.829	0.888	0.368	-0.216	CDS	GI:188595478	BAG34453.1
AP009380	PGN_1935	hypothetical protein		2157921	2159504	1584	reverse	0.840	-0.251	0.398	0.538	0.297	-0.846	CDS	GI:188595479	BAG34454.1
AP009380	PGN_1936	conserved hypothetical protein		2159810	2159983	174	reverse	0.311	-1.685	0.001	0.009	0.517	-3.259	CDS	GI:188595480	BAG34455.1
AP009380	PGN_1937	glucose-inhibited division protein A		2160244	2162121	1878	forward	0.949	-0.075	0.817	0.879	0.324	-0.232	CDS	GI:188595481	BAG34456.1
AP009380	PGN_1938	excinuclease ABC C subunit	uvrC	2162152	2163954	1803	forward	1.173	0.231	0.314	0.464	0.229	1.007	CDS	GI:188595482	BAG34457.1
AP009380	PGN_1939	putative D-tyrosyl-tRNA deacylase		2163961	2164413	453	forward	1.070	0.097	0.666	0.766	0.226	0.431	CDS	GI:188595483	BAG34458.1
AP009380	PGN_1940	conserved hypothetical protein		2164418	2164768	351	forward	1.170	0.227	0.355	0.500	0.246	0.925	CDS	GI:188595484	BAG34459.1
AP009380	PGN_1941	putative deoxyribose-phosphate aldolase		2164695	2165624	930	forward	1.290	0.367	0.121	0.240	0.237	1.551	CDS	GI:188595485	BAG34460.1

AP009380	PGN_1942	hypothetical protein		2165665	2165826	162	forward	0.967	-0.049	0.849	0.903	0.257	-0.191	CDS	GI:188595486	BAG34461.1
AP009380	PGN_1943	putative polyprenyl synthetase		2165935	2166909	975	reverse	1.009	0.012	0.956	0.969	0.219	0.056	CDS	GI:188595487	BAG34462.1
AP009380	PGN_1944	conserved hypothetical protein		2166967	2167605	639	reverse	1.224	0.291	0.362	0.506	0.320	0.911	CDS	GI:188595488	BAG34463.1
AP009380	PGN_1945	probable signal peptidase-related protein		2167626	2168252	627	reverse	2.100	1.070	0.002	0.013	0.344	3.114	CDS	GI:188595489	BAG34464.1
AP009380	PGN_1946	signal peptidase I		2168242	2169639	1398	reverse	1.575	0.655	0.021	0.072	0.285	2.303	CDS	GI:188595490	BAG34465.1
AP009380	PGN_1947	putative dihydrodipicolinate reductase	dapB	2169655	2170371	717	reverse	1.590	0.669	0.004	0.022	0.231	2.896	CDS	GI:188595491	BAG34466.1
AP009380	PGN_1948	deoxyguanosinetriphosphate triphosphohydrolase		2170432	2171775	1344	reverse	0.920	-0.120	0.653	0.759	0.267	-0.450	CDS	GI:188595492	BAG34467.1
AP009380	PGN_1949	conserved hypothetical protein		2171919	2172911	993	reverse	1.731	0.792	0.018	0.065	0.335	2.360	CDS	GI:188595493	BAG34468.1
AP009380	PGN_1950	hypothetical protein		2173007	2173114	108	reverse	0.808	-0.308	0.552	0.676	0.518	-0.595	CDS	GI:188595494	BAG34469.1
AP009380	PGN_1951	conserved hypothetical protein		2173420	2173779	360	forward	1.131	0.178	0.568	0.689	0.311	0.571	CDS	GI:188595495	BAG34470.1
AP009380	PGN_1952	hypothetical protein		2173877	2173996	120	reverse	1.200	0.263	0.567	0.688	0.459	0.573	CDS	GI:188595496	BAG34471.1
AP009380	PGN_1953	TonB-dependent outer membrane receptor		2174086	2176587	2502	forward	1.411	0.496	0.126	0.247	0.324	1.530	CDS	GI:188595497	BAG34472.1
AP009380	PGN_1954	probable DNA repair protein RecO		2177157	2177894	738	forward	0.958	-0.062	0.827	0.886	0.284	-0.219	CDS	GI:188595498	BAG34473.1
AP009380	PGN_1955	phosphomannomutase		2177967	2179715	1749	forward	0.874	-0.194	0.324	0.474	0.197	-0.986	CDS	GI:188595499	BAG34474.1
AP009380	PGN_1956	hypothetical protein		2179819	2179920	102	reverse	1.019	0.028	0.923	0.952	0.287	0.096	CDS	GI:188595500	BAG34475.1
AP009380	PGN_1957	transposase in ISPg1		2180321	2181370	1050	reverse	1.040	0.056	0.894	0.935	0.423	0.133	CDS	GI:188595501	BAG34476.1
AP009380	PGN_1959	CRISPR-associated protein Cas2		2189610	2189873	264	reverse	1.142	0.192	0.477	0.614	0.270	0.711	CDS	GI:188595502	BAG34477.1
AP009380	PGN_1960	CRISPR-associated protein Cas1		2189873	2190889	1017	reverse	1.351	0.434	0.215	0.358	0.350	1.239	CDS	GI:188595503	BAG34478.1
AP009380	PGN_1961	CRISPR-associated protein Cas4		2190886	2191395	510	reverse	1.483	0.568	0.093	0.203	0.338	1.679	CDS	GI:188595504	BAG34479.1
AP009380	PGN_1962	conserved hypothetical protein		2191513	2192571	1059	reverse	1.349	0.432	0.132	0.254	0.286	1.508	CDS	GI:188595505	BAG34480.1
AP009380	PGN_1963	conserved hypothetical protein		2192592	2193887	1296	reverse	0.853	-0.230	0.275	0.423	0.211	-1.092	CDS	GI:188595506	BAG34481.1
AP009380	PGN_1964	probable CRISPR-associated helicase Cas3 core		2193898	2196018	2121	reverse	0.696	-0.524	0.054	0.135	0.272	-1.926	CDS	GI:188595507	BAG34482.1
AP009380	PGN_1965	hypothetical protein		2196035	2196622	588	reverse	0.733	-0.449	0.197	0.336	0.348	-1.289	CDS	GI:188595508	BAG34483.1
AP009380	PGN_1966	conserved hypothetical protein		2196629	2197294	666	reverse	0.645	-0.633	0.053	0.132	0.327	-1.939	CDS	GI:188595509	BAG34484.1
AP009380	PGN_1967	putative sulfatase		2197942	2199864	1923	reverse	1.454	0.540	0.131	0.253	0.357	1.512	CDS	GI:188595510	BAG34485.1
AP009380	PGN_1968	conserved hypothetical protein		2199877	2202420	2544	reverse	1.127	0.173	0.508	0.639	0.262	0.662	CDS	GI:188595511	BAG34486.1
AP009380	PGN_1969	putative methionyl-tRNA formyltransferase		2202585	2203556	972	reverse	0.990	-0.015	0.950	0.966	0.238	-0.063	CDS	GI:188595512	BAG34487.1
AP009380	PGN_t0046	tRNA-Asp		2203780	2203856	77	reverse	0.405	-1.304	0.003	0.017	0.434	-3.006	tRNA		
AP009380	PGN_1970	arginine-specific cysteine proteinase RgpA	rgpA	2204102	2209213	5112	reverse	2.277	1.187	0.001	0.010	0.370	3.210	CDS	GI:188595513	BAG34488.1
AP009380	PGN_1971	hypothetical protein		2209654	2209800	147	forward	0.606	-0.723	0.151	0.279	0.503	-1.436	CDS	GI:188595514	BAG34489.1
AP009380	PGN_1972	conserved hypothetical protein		2209781	2209903	123	forward	0.781	-0.357	0.449	0.588	0.472	-0.756	CDS	GI:188595515	BAG34490.1
AP009380	PGN_1973	probable phosphoglycerate mutase		2210019	2210537	519	forward	1.436	0.522	0.007	0.032	0.192	2.716	CDS	GI:188595516	BAG34491.1
AP009380	PGN_1974	conserved hypothetical protein		2210566	2211090	525	forward	1.066	0.093	0.655	0.759	0.208	0.446	CDS	GI:188595517	BAG34492.1
AP009380	PGN_1975	putative regulatory protein		2211099	2211608	510	forward	1.115	0.157	0.492	0.628	0.228	0.687	CDS	GI:188595518	BAG34493.1
AP009380	PGN_1976	conserved hypothetical protein		2211615	2214194	2580	forward	1.072	0.101	0.720	0.808	0.281	0.359	CDS	GI:188595519	BAG34494.1
AP009380	PGN_1977	conserved hypothetical protein		2214763	2215398	636	forward	0.823	-0.280	0.416	0.554	0.345	-0.813	CDS	GI:188595520	BAG34495.1
AP009380	PGN_1978	conserved hypothetical protein		2215466	2215861	396	forward	0.389	-1.360	0.001	0.010	0.422	-3.222	CDS	GI:188595521	BAG34496.1
AP009380	PGN_1979	primosomal protein N		2215888	2218401	2514	reverse	0.571	-0.809	0.083	0.186	0.467	-1.733	CDS	GI:188595522	BAG34497.1
AP009380	PGN_1980	putative NADPH-dependent glutamate synthase		2218435	2219823	1389	reverse	1.258	0.331	0.181	0.317	0.248	1.336	CDS	GI:188595523	BAG34498.1
AP009380	PGN_1981	conserved hypothetical protein		2219930	2220721	792	reverse	0.841	-0.251	0.347	0.496	0.266	-0.940	CDS	GI:188595524	BAG34499.1
AP009380	PGN_1982	putative tRNA guanine 1-methyltransferase		2220923	2221600	678	forward	0.948	-0.077	0.731	0.813	0.226	-0.343	CDS	GI:188595525	BAG34500.1
AP009380	PGN_1983	putative ion transporter		2221632	2222543	912	forward	1.073	0.102	0.687	0.784	0.254	0.403	CDS	GI:188595526	BAG34501.1
AP009380	PGN_1984	hypothetical protein		2222612	2222833	222	reverse	1.072	0.100	0.715	0.805	0.274	0.365	CDS	GI:188595527	BAG34502.1
AP009380	PGN_1985	probable N-acetylmuramoyl-L-alanine amidase		2222830	2223279	450	reverse	1.066	0.093	0.726	0.810	0.265	0.350	CDS	GI:188595528	BAG34503.1
AP009380	PGN_1986	DNA-binding protein, histone-like family		2223419	2223895	477	reverse	1.313	0.393	0.194	0.333	0.303	1.298	CDS	GI:188595529	BAG34504.1
AP009380	PGN_1987	conserved hypothetical protein		2224256	2224987	732	reverse	1.379	0.464	0.039	0.109	0.225	2.062	CDS	GI:188595530	BAG34505.1
AP009380	PGN_1988	conserved hypothetical protein		2225115	2226632	1518	reverse	0.990	-0.015	0.959	0.970	0.286	-0.051	CDS	GI:188595531	BAG34506.1
AP009380	PGN_1989	conserved hypothetical protein with NIF3 domain		2227223	2228377	1155	forward	0.779	-0.360	0.129	0.251	0.237	-1.520	CDS	GI:188595532	BAG34507.1
AP009380	PGN_1990	conserved hypothetical protein		2228395	2229150	756	forward	0.721	-0.473	0.060	0.145	0.251	-1.882	CDS	GI:188595533	BAG34508.1
AP009380	PGN_1991	putative cell-cycle protein		2229414	2230778	1365	forward	1.321	0.402	0.247	0.392	0.347	1.157	CDS	GI:188595534	BAG34509.1
AP009380	PGN_1992	putative helicase		2230773	2233058	2286	reverse	0.597	-0.745	0.000	0.001	0.187	-3.980	CDS	GI:188595535	BAG34510.1
AP009380	PGN_1993	conserved hypothetical protein		2233149	2233529	381	reverse	0.561	-0.833	0.001	0.010	0.260	-3.200	CDS	GI:188595536	BAG34511.1
AP009380	PGN_1994	conserved hypothetical protein		2233542	2233919	378	reverse	0.403	-1.310	0.000	0.000	0.302	-4.335	CDS	GI:188595537	BAG34512.1
AP009380	PGN_1995	conserved hypothetical protein		2234175	2234450	276	reverse	0.684	-0.548	0.144	0.268	0.375	-1.462	CDS	GI:188595538	BAG34513.1
AP009380	PGN_1996	putative dihydrodipicolinate synthase	dapA	2234676	2235569	894	forward	0.737	-0.440	0.041	0.112	0.215	-2.046	CDS	GI:188595539	BAG34514.1
AP009380	PGN_1997	putative dethiobiotin synthase		2235598	2236251	654	forward	0.981	-0.027	0.908	0.945	0.235	-0.115	CDS	GI:188595540	BAG34515.1
AP009380	PGN_1998	immunoreactive 23 kDa antigen		2236357	2237028	672	reverse	0.804	-0.315	0.220	0.363	0.256	-1.227	CDS	GI:188595541	BAG34516.1
AP009380	PGN_1999	putative dihydroorotate dehydrogenase		2237094	2238074	981	reverse	0.952	-0.071	0.688	0.784	0.176	-0.402	CDS	GI:188595542	BAG34517.1
AP009380	PGN_t0047	tRNA-Lys		2238677	2238752	76	reverse	0.379	-1.400	0.000	0.003	0.390	-3.593	tRNA		
AP009380	PGN_2000	hypothetical protein		2238976	2239449	474	reverse	0.905	-0.144	0.716	0.806	0.395	-0.364	CDS	GI:188595543	BAG34518.1
AP009380	PGN_2001	Por secretion system protein porY/putative sensor histidine kinase	porY	2239546	2240733	1188	forward	1.053	0.074	0.727	0.810	0.212	0.349	CDS	GI:188595544	BAG34519.1
AP009380	PGN_2002	conserved hypothetical protein		2241053	2241163	111	reverse	0.907	-0.141	0.648	0.754	0.309	-0.456	CDS	GI:188595545	BAG34520.1
AP009380	PGN_2003	single-stranded-DNA-specific exonuclease		2241193	2242947	1755	forward	1.062	0.086	0.731	0.813	0.251	0.344	CDS	GI:188595546	BAG34521.1
AP009380	PGN_2004	conserved hypothetical protein		2242944	2243999	1056	forward	1.492	0.577	0.005	0.028	0.207	2.787	CDS	GI:188595547	BAG34522.1
AP009380	PGN_2005	conserved hypothetical protein		2244148	2245830	1683	forward	0.773	-0.371	0.118	0.236	0.237	-1.565	CDS	GI:188595548	BAG34523.1
AP009380	PGN_2006	nicotinate phosphoribosyltransferase		2245863	2247047	1185	forward	0.934	-0.098	0.603	0.717	0.188	-0.521	CDS	GI:188595549	BAG34524.1
AP009380	PGN_2007	probable nicotinamide-nucleotide adenylyltransferase		2247047	2247640	594	forward	1.306	0.385	0.187	0.324	0.291	1.321	CDS	GI:188595550	BAG34525.1
AP009380	PGN_2008	conserved hypothetical protein		2247654	2248037	384	forward	1.245	0.316	0.273	0.421	0.289	1.096	CDS	GI:188595551	BAG34526.1
AP009380	PGN_2009	conserved hypothetical protein		2248044	2248226	183	forward	1.356	0.439	0.193	0.332	0.337	1.300	CDS	GI:188595552	BAG34527.1
AP009380	PGN_2010	putative secreted protein		2248330	2249811	1482	forward	1.509	0.593	0.122	0.242	0.384	1.545	CDS	GI:188595553	BAG34528.1
AP009380	PGN_2011	putative helicase		2249816	2251858	2043	forward	2.406	1.266	0.000	0.002	0.332	3.817	CDS	GI:188595554	BAG34529.1
AP009380	PGN_2012	outer membrane efflux protein		2251956	2253134	1179	reverse	2.603	1.380	0.000	0.000	0.288	4.787	CDS	GI:188595555	BAG34530.1
AP009380	PGN_2013	cation efflux system protein		2253151	2256270	3120	reverse	2.636	1.398	0.000	0.000	0.303	4.608	CDS	GI:188595556	BAG34531.1
AP009380	PGN_2014	cation efflux system protein		2256290	2257468	1179	reverse	2.096	1.068	0.000	0.001	0.262	4.083	CDS	GI:188595557	BAG34532.1
AP009380	PGN_2015	conserved hypothetical protein		2257341	2257628	288	reverse	2.102	1.072	0.000	0.004	0.301	3.557	CDS	GI:188595558	BAG34533.1
AP009380	PGN_2016	hypothetical protein		2258007	2258426	420	reverse	1.201	0.265	0.222	0.365	0.217	1.221	CDS	GI:188595559	BAG34534.1
AP009380	PGN_2017	conserved hypothetical protein		2258498	2260012	1515	reverse	1.089	0.123	0.655	0.759	0.276	0.447	CDS	GI:188595560	BAG34535.1
AP009380	PGN_2018	putative UDP-N-acetylglucosamine acyltransferase		2260017	2260808	792	reverse	1.264	0.338	0.211	0.352	0.270	1.252	CDS	GI:188595561	BAG34536.1
AP009380	PGN_2019	UDP-3-O-[3-hydroxymyristoyl] N-acetylglucosamine deacetylase		2260808	2262196	1389	reverse	1.184	0.244	0.277	0.425	0.224	1.088	CDS	GI:188595562	BAG34537.1
AP009380	PGN_2020	UDP-3-O-[3-hydroxymyristoyl] glucosamine N-acyltransferase		2262175	2263224	1050	reverse	1.025	0.035	0.884	0.928	0.240	0.146	CDS	GI:188595563	BAG34538.1
AP009380	PGN_2021	orotidine 5'-phosphate decarboxylase		2263317	2264147	831	reverse	1.334	0.416	0.143	0.267	0.284	1.464	CDS	GI:188595564	BAG34539.1
AP009380	PGN_2022	peptide chain release factor 1		2264164	2265222	1059	reverse	1.257	0.330	0.141	0.265	0.224	1.471	CDS	GI:188595565	BAG34540.1
AP009380	PGN_2023	putative phosphoribosylformylglycinamidine cyclo-ligase		2265274	2266440	1167	reverse	1.021	0.030	0.882	0.926	0.201	0.148	CDS	GI:188595566	BAG34541.1
AP009380	PGN_2024	putative hemagglutinin		2266469	2267410	942	reverse	1.013	0.018	0.929	0.954	0.202	0.089	CDS	GI:188595567	BAG34542.1
AP009380	PGN_2025	conserved hypothetical protein		2267643	2268341	699	reverse	1.098	0.135	0.502	0.636	0.202	0.671	CDS	GI:188595568	BAG34543.1
AP009380	PGN_2026	putative abortive infection protein		2268314	2269615	1302	reverse	1.008	0.012	0.959	0.970	0.227	0.051	CDS	GI:188595569	BAG34544.1
AP009380	PGN_2027	conserved hypothetical protein		2269630	2269908	279	reverse	0.952	-0.071	0.839	0.897	0.351	-0.203	CDS	GI:188595570	BAG34545.1

AP009380	PGN_2028	conserved hypothetical protein		2270124	2272109	1986	forward	1.307	0.386	0.064	0.152	0.208	1.853	CDS	GI:188595571	BAG34546.1
AP009380	PGN_2029	conserved hypothetical protein		2272171	2273073	903	forward	1.208	0.272	0.164	0.294	0.196	1.393	CDS	GI:188595572	BAG34547.1
AP009380	PGN_2030	conserved hypothetical protein		2273079	2273864	786	forward	1.188	0.249	0.345	0.494	0.263	0.944	CDS	GI:188595573	BAG34548.1
AP009380	PGN_2031	L-serine dehydratase		2273960	2275159	1200	forward	0.817	-0.292	0.211	0.352	0.233	-1.252	CDS	GI:188595574	BAG34549.1
AP009380	PGN_2032	putative alpha-galactosidase		2275159	2276604	1446	forward	1.765	0.820	0.004	0.023	0.286	2.866	CDS	GI:188595575	BAG34550.1
AP009380	PGN_2033	ATP-dependent RNA helicase		2276623	2278437	1815	reverse	1.422	0.508	0.095	0.205	0.304	1.672	CDS	GI:188595576	BAG34551.1
AP009380	PGN_2034	probable sugar isomerase		2278583	2279224	642	reverse	1.038	0.054	0.856	0.907	0.295	0.182	CDS	GI:188595577	BAG34552.1
AP009380	PGN_2035	putative peptidase		2279403	2280620	1218	forward	0.584	-0.776	0.001	0.010	0.242	-3.214	CDS	GI:188595578	BAG34553.1
AP009380	PGN_2036	hypothetical protein		2280768	2280926	159	forward	0.837	-0.257	0.506	0.638	0.386	-0.665	CDS	GI:188595579	BAG34554.1
AP009380	PGN_2037	DNA-binding protein from starved cells Dps	dps	2281649	2282128	480	forward	0.397	-1.332	0.000	0.000	0.313	-4.259	CDS	GI:188595580	BAG34555.1
AP009380	PGN_2038	conserved hypothetical protein		2282257	2283531	1275	reverse	2.048	1.035	0.001	0.007	0.307	3.373	CDS	GI:188595581	BAG34556.1
AP009380	PGN_2039	conserved hypothetical protein		2283533	2284714	1182	reverse	1.593	0.672	0.001	0.009	0.207	3.241	CDS	GI:188595582	BAG34557.1
AP009380	PGN_2040	conserved hypothetical protein		2284717	2285712	996	reverse	1.187	0.248	0.285	0.433	0.232	1.069	CDS	GI:188595583	BAG34558.1
AP009380	PGN_2041	putative alkaline protease AprF		2285761	2287266	1506	reverse	1.348	0.431	0.029	0.088	0.197	2.189	CDS	GI:188595584	BAG34559.1
AP009380	PGN_2042	DNA mismatch repair protein MutS		2288182	2290830	2649	reverse	2.091	1.064	0.000	0.004	0.302	3.528	CDS	GI:188595585	BAG34560.1
AP009380	PGN_2043	conserved hypothetical protein		2291150	2291842	693	reverse	1.268	0.343	0.195	0.334	0.264	1.295	CDS	GI:188595586	BAG34561.1
AP009380	PGN_2044	conserved hypothetical protein		2291839	2291937	99	reverse	1.917	0.939	0.000	0.001	0.242	3.885	CDS	GI:188595587	BAG34562.1
AP009380	PGN_2045	phenylalanyl-tRNA synthetase beta subunit		2291921	2294380	2460	reverse	1.507	0.591	0.004	0.023	0.206	2.869	CDS	GI:188595588	BAG34563.1
AP009380	PGN_2046	conserved hypothetical protein		2294909	2295217	309	reverse	0.830	-0.270	0.227	0.369	0.223	-1.207	CDS	GI:188595589	BAG34564.1
AP009380	PGN_2047	conserved hypothetical protein		2295216	2295584	369	forward	0.772	-0.372	0.065	0.154	0.202	-1.845	CDS	GI:188595590	BAG34565.1
AP009380	PGN_r0010	16S ribosomal RNA		2295553	2297027	1475	forward	0.610	-0.712	0.001	0.009	0.218	-3.267	rRNA		
AP009380	PGN_2048	conserved hypothetical protein		2297140	2297298	159	forward	0.983	-0.025	0.912	0.947	0.223	-0.110	CDS	GI:188595591	BAG34566.1
AP009380	PGN_2049	conserved hypothetical protein		2297425	2297580	156	forward	1.104	0.143	0.496	0.632	0.210	0.681	CDS	GI:188595592	BAG34567.1
AP009380	PGN_t0048	tRNA-Ile		2297590	2297663	74	forward	0.408	-1.295	0.007	0.034	0.482	-2.687	tRNA		
AP009380	PGN_t0049	tRNA-Ala		2297665	2297741	77	forward	0.469	-1.092	0.005	0.028	0.391	-2.790	tRNA		
AP009380	PGN_r0011	23S ribosomal RNA		2297860	2300692	2833	forward	0.478	-1.065	0.000	0.001	0.255	-4.180	rRNA		
AP009380	PGN_r0012	5S ribosomal RNA		2300839	2300946	108	forward	0.261	-1.939	0.000	0.000	0.461	-4.208	rRNA		
AP009380	PGN_2050	ATP-dependent helicase		2301152	2304376	3225	reverse	2.194	1.134	0.005	0.025	0.400	2.832	CDS	GI:188595593	BAG34568.1
AP009380	PGN_2051	conserved hypothetical protein		2304373	2305308	936	reverse	2.861	1.517	0.000	0.000	0.343	4.416	CDS	GI:188595594	BAG34569.1
AP009380	PGN_2052	conserved hypothetical protein		2305278	2306204	927	reverse	1.849	0.887	0.001	0.005	0.256	3.464	CDS	GI:188595595	BAG34570.1
AP009380	PGN_2053	conserved hypothetical protein		2306216	2306947	732	reverse	1.814	0.860	0.000	0.000	0.196	4.390	CDS	GI:188595596	BAG34571.1
AP009380	PGN_2054	putative glycerol-3-phosphate cytidylyltransferase		2306953	2307411	459	reverse	1.307	0.386	0.085	0.189	0.224	1.723	CDS	GI:188595597	BAG34572.1
AP009380	PGN_2055	putative 4-hydroxythreonine-4-phosphate dehydrogenase		2307433	2308530	1098	reverse	1.564	0.645	0.015	0.057	0.265	2.435	CDS	GI:188595598	BAG34573.1
AP009380	PGN_2056	conserved hypothetical protein		2308574	2309629	1056	reverse	1.303	0.381	0.046	0.122	0.191	1.994	CDS	GI:188595599	BAG34574.1
AP009380	PGN_2057	conserved hypothetical protein		2309720	2310778	1059	reverse	1.025	0.036	0.926	0.952	0.386	0.093	CDS	GI:188595600	BAG34575.1
AP009380	PGN_2058	conserved hypothetical protein		2310791	2311195	405	reverse	0.571	-0.808	0.003	0.017	0.268	-3.010	CDS	GI:188595601	BAG34576.1
AP009380	PGN_2059	conserved hypothetical protein		2311199	2311405	207	forward	1.542	0.625	0.037	0.106	0.300	2.081	CDS	GI:188595602	BAG34577.1
AP009380	PGN_2060	histidyl-tRNA synthetase		2311410	2312774	1365	reverse	1.739	0.798	0.001	0.008	0.243	3.283	CDS	GI:188595603	BAG34578.1
AP009380	PGN_2061	probable dihydrofolate reductase		2312835	2313323	489	reverse	1.677	0.746	0.000	0.003	0.202	3.698	CDS	GI:188595604	BAG34579.1
AP009380	PGN_2062	thymidylate synthase		2313369	2314172	804	reverse	1.038	0.054	0.838	0.896	0.264	0.205	CDS	GI:188595605	BAG34580.1
AP009380	PGN_2063	hypothetical protein		2314204	2314305	102	forward	0.728	-0.458	0.350	0.498	0.491	-0.934	CDS	GI:188595606	BAG34581.1
AP009380	PGN_2064	putative peptidase M48 family		2314396	2315193	798	forward	1.033	0.047	0.823	0.884	0.210	0.223	CDS	GI:188595607	BAG34582.1
AP009380	PGN_2065	putative Lys- and Rgp- gingipain domain protein		2315403	2316284	882	forward	0.448	-1.160	0.005	0.027	0.414	-2.800	CDS	GI:188595608	BAG34583.1
AP009380	PGN_2066	putative ABC transporter ATP-binding protein		2316526	2318463	1938	reverse	0.963	-0.054	0.826	0.886	0.248	-0.219	CDS	GI:188595609	BAG34584.1
AP009380	PGN_2067	TPR domain protein		2318460	2320547	2088	reverse	1.023	0.033	0.886	0.929	0.231	0.144	CDS	GI:188595610	BAG34585.1
AP009380	PGN_2068	putative peptide deformylase		2320583	2321152	570	reverse	0.811	-0.302	0.253	0.399	0.264	-1.143	CDS	GI:188595611	BAG34586.1
AP009380	PGN_2069	probable endonuclease		2321257	2321709	453	reverse	0.661	-0.598	0.012	0.048	0.238	-2.519	CDS	GI:188595612	BAG34587.1
AP009380	PGN_2070	conserved hypothetical protein		2322232	2327898	5667	forward	0.679	-0.560	0.059	0.144	0.297	-1.886	CDS	GI:188595613	BAG34588.1
AP009380	PGN_2071	probable ketopantoate reductase ApbA/PanE		2327912	2328856	945	forward	0.788	-0.343	0.112	0.228	0.216	-1.589	CDS	GI:188595614	BAG34589.1
AP009380	PGN_2072	ABC transporter ATP-binding protein		2328991	2330607	1617	reverse	1.114	0.156	0.525	0.652	0.245	0.636	CDS	GI:188595615	BAG34590.1
AP009380	PGN_2073	conserved hypothetical protein		2330881	2331900	1020	reverse	0.674	-0.568	0.100	0.212	0.345	-1.645	CDS	GI:188595616	BAG34591.1
AP009380	PGN_2074	conserved hypothetical protein		2332150	2332404	255	reverse	0.528	-0.922	0.000	0.005	0.264	-3.490	CDS	GI:188595617	BAG34592.1
AP009380	PGN_2075	excinuclease ABC A subunit	uvrAII	2332428	2335289	2862	reverse	0.973	-0.039	0.882	0.926	0.266	-0.148	CDS	GI:188595618	BAG34593.1
AP009380	PGN_t0050	tRNA-Leu		2335414	2335497	84	reverse	0.430	-1.217	0.003	0.017	0.404	-3.009	tRNA		
AP009380	PGN_t0051	tRNA-Leu		2335529	2335614	86	reverse	0.367	-1.446	0.001	0.009	0.446	-3.244	tRNA		
AP009380	PGN_t0052	tRNA-Gly		2335702	2335777	76	reverse	0.374	-1.417	0.000	0.004	0.398	-3.560	tRNA		
AP009380	PGN_2076	conserved hypothetical protein		2335963	2336247	285	reverse	0.548	-0.867	0.006	0.032	0.318	-2.724	CDS	GI:188595619	BAG34594.1
AP009380	PGN_2077	conserved hypothetical protein		2336328	2336510	183	reverse	0.441	-1.181	0.002	0.015	0.388	-3.046	CDS	GI:188595620	BAG34595.1
AP009380	PGN_2078	conserved hypothetical protein		2336702	2338054	1353	reverse	1.192	0.253	0.218	0.362	0.206	1.231	CDS	GI:188595621	BAG34596.1
AP009380	PGN_2079	mannose-1-phosphate guanylyltransferase		2338089	2339174	1086	reverse	0.986	-0.021	0.933	0.955	0.246	-0.084	CDS	GI:188595622	BAG34597.1
AP009380	PGN_2080	conserved hypothetical protein		2339249	2340979	1731	forward	1.789	0.839	0.036	0.102	0.400	2.100	CDS	GI:188595623	BAG34598.1
AP009380	PGN_2081	1-deoxy-D-xylulose 5-phosphate synthase		2341152	2343056	1905	forward	1.177	0.235	0.274	0.422	0.215	1.094	CDS	GI:188595624	BAG34599.1
AP009380	PGN_2082	putative potassium uptake protein TrkA		2343110	2344450	1341	forward	1.012	0.017	0.935	0.956	0.210	0.081	CDS	GI:188595625	BAG34600.1
AP009380	PGN_2083	potassium uptake protein TrkH		2344477	2345940	1464	forward	1.128	0.173	0.412	0.551	0.211	0.820	CDS	GI:188595626	BAG34601.1
AP009380	PGN_t0053	tRNA-Cys		2346132	2346202	71	reverse	0.652	-0.617	0.111	0.226	0.387	-1.596	tRNA		
AP009380	PGN_2084	conserved hypothetical protein		2346590	2346742	153	forward	1.105	0.144	0.663	0.764	0.330	0.436	CDS	GI:188595627	BAG34602.1
AP009380	PGN_2085	putative Fe-S oxidoreductases		2346976	2348310	1335	forward	1.396	0.481	0.023	0.076	0.212	2.265	CDS	GI:188595628	BAG34603.1
AP009380	PGN_2086	probable acetyltransferase		2348358	2349224	867	forward	1.320	0.401	0.158	0.287	0.284	1.413	CDS	GI:188595629	BAG34604.1
AP009380	PGN_2087	glycosyltransferase		2349263	2350231	969	forward	1.913	0.936	0.001	0.006	0.276	3.394	CDS	GI:188595630	BAG34605.1
AP009380	PGN_2088	conserved hypothetical protein		2350373	2350969	597	forward	0.761	-0.395	0.209	0.350	0.314	-1.256	CDS	GI:188595631	BAG34606.1
AP009380	PGN_2089	conserved hypothetical protein		2350962	2351258	297	forward	0.954	-0.068	0.800	0.866	0.270	-0.253	CDS	GI:188595632	BAG34607.1
AP009380	PGN_2090	conserved hypothetical protein		2351338	2353560	2223	forward	0.817	-0.292	0.409	0.549	0.353	-0.825	CDS	GI:188595633	BAG34608.1
AP009380	PGN_2091	conserved hypothetical protein		2353557	2354213	657	forward	0.807	-0.309	0.281	0.429	0.287	-1.078	CDS	GI:188595634	BAG34609.1