Supplemental Materials for:

Essential Genes in the Core Genome of the Human Pathogen *Streptococcus pyogenes*

Yoann Le Breton¹, Ashton T. Belew¹, Kayla M. Valdes¹, Emrul Islam¹, Patrick Curry¹, Hervé Tettelin^{3, 4}, Mark. E. Shirtliff ^{4, 5}, Najib M. El-Sayed^{1, 2}, and Kevin S. McIver¹

^aDepartment of Cell Biology & Molecular Genetics and Maryland Pathogen Research Institute,
 ^bCenter for Bioinformatics and Computation Biology, University of Maryland, College Park, MD
 20742; ³Institute for Genome Sciences, ⁴Department of Microbiology & Immunology,
 ⁵Department of Microbial Pathogenesis, School of Dentistry, University of Maryland School of Medicine, Baltimore, MD USA

Supplemental Materials Contents:

<u>Supplemental Methods</u>. Methodology of all computation analyses performed in the manuscript, including scripts used, genome alignments, library matrices and statistical analyses.

Supplemental Figures. Following four (4) figures are included:

- **Figure S1.** pKRMIT, a Tn-seq compatible *in vivo mariner* transposition system for GAS.
- **Figure S2.** Additional statistical analyses for pairwise comparisons of the initial libraries produced in GAS 5448.
- **Figure S3.** The GAS core genome.
- **Figure S4.** Conserved essential genes within the GAS core genome.

Supplemental Tables. Following ten (10) tables are included:

- **Table S1.** Complete analysis of Tn-seq read counts and alignments.
- **Table S2.** Selection of reads for the Bayesian analysis.
- **Table S3.** Bayesian analysis of Tn-seq datasets for GAS M1T1 5448 grown *in vitro*.
- **Table S4.** Integrated gene essentiality determination for GAS M1T1 5448 for all time points.
- **Table S5.** Bayesian analysis of Tn-seq datasets for GAS M49 NZ131 grown *in vitro*.
- **Table S6.** Integrated gene essentiality determination for GAS M49 NZ131 for all time points.
- **Table S7.** Conserved GAS essential genes identified in both M1T1 5448 and M49 NZ131 compared to the predicted GAS core genome.
- **Table S8.** Bacterial strains and plasmids.
- **Table S9.** Primers used in this study.
- **Table S10.** Summary of 10 publically available GAS genomes.

Supplemental Methods

Scripts used

Italicized directory names (ending in /) refer to directories within the git repository for this project, italicized scripts are provided in the *scripts*/ directory, and italicized data files reside in the *data*/ directory. The git repository may be downloaded by visiting *https://gitlab.umiacs.umd.edu/abelew/tnseq_gas* or with the command: git clone https://gitlab.umiacs.umd.edu/abelew/tnseq_gas.git.

Annotation Collection.

GenBank genomes including annotation information were downloaded for each of the GAS strains used in this study: CP000017 is the reference MGAS 5005 genome ¹ used for MGAS 5448 alignments as it is the most similar annotated genome available; NC_011375 is the reference genome for NZ131 ². A genbank file for the plasmid was also parsed (*reference/genbank/pOSKAR.gb*) and used to define how many reads did not integrate into the genome properly. For each of the genbank annotations collected, the perl script *gb2gff.pl* was used to split the genbank file into the following: a nucleotide fasta file containing a single genomic sequence, a nucleotide multi-fasta of all annotated coding sequences, a peptide multi-fasta of annotated coding sequences, a gff file of all annotations, a gff file of only the coding sequence annotations, and a gff file describing the inter-cds regions. These may be found in *reference/genbank/*. The resulting fasta and gff files were used as the reference for most of the operations that follow; conversely, gene ontology information was downloaded from microbesonline.org for strains 5448

and NZ131 and cross referenced against these annotations when necessary. Copies are located in *reference/microbesonline/*.

Genome Alignments.

The reads generated from Tn-seq data produced in GAS 5448 and NZ131 were queried for quality with FastQC ³ before demultiplexing against the local indexing adapters with Bio::SeqIO ⁴ and again queried for quality. The *mariner* ITR leading sequences were removed with a combination of Biopieces (biopieces.org), Cutadapt ⁵, and Trimmomatic ⁶, reads lacking the ITR sequence were discarded. This process left libraries of approximately 15,000,000 reads (**Table S1**) of lengths primarily 12<=x<=15 nucleotides. In the cases where are large number of reads did not align to the genome, the primary culprit was invariably the plasmid (**Table S1**).

These libraries were aligned against the appropriate GAS genomes with Bowtie ^{7,8} using options to limit the seed sequence to 10 nucleotides (-1 10), with no mismatch (-v 0), and randomly assign multi-matched reads to one of the possible matching positions (-M 1); these are summarized in **Table S1.** This was later repeated with 1 mismatch. The resulting alignments were converted to sorted/compressed binary alignments using SAMtools ⁹ and counted ¹⁰ against the reference genome CDS and intergenic regions. These operations were performed with the *process_reads.sh* script. The resulting count tables are in *data/count_tables/*; organized by strain, library, and time point; they are referenced in *all_samples.csv* for all operations in R. When R functions are noted, they are italicized and have following parentheses. These functions will be found in *R/myr.R* or rarely in *tnseq.rmd*. All operations performed in R are recorded in *tnseq.rmd*

(tnseqv0.rmd for no-mismatches, and tnseqv1.rmd for 1 mismatch analyses) and knitr (http://yihui.name/knitr/) was used to generate *tnseq.pdf* which provides a (longer than anyone will ever read) report of the operations performed.

Library Metrics

Before using the libraries to quantify the essentiality/fitness of coding sequences in the genome, it was necessary to compare and contrast the libraries and quantify their relative coverage, similarity, and saturation with respect to available TA insertion points. These comparisons in turn require some attention to the normalization strategies employed.

Library Saturation by TA insertion points. The GAS genome is AT rich, providing a relatively large number of possible mariner insertion points: there are 1,838,562 and 1,815,783 TA sites found on the genome of MGAS5005 and NZ131, respectively. Therefore, the bam alignments were read into tnseq_count_hitsv2.pl along with the fasta genome; this script created a simple array of the genome and filled in the number of observed reads, which started (forward strand) or ended (reverse strand) at every TA in the genome. The bowtie parameters used allowed no mismatch, therefore this script excluded any read which did not match exactly the TA insertion point. The resulting text files contain one line for each TA of the genome, include a column for the position of each TA, the number of observed reads on the forward strand, reverse strand, and missed reads. These may be found in data/count_tas/; there is one file for the concatenated 5448 libraries as well as each separate library for all strains, in each case the file ends in 'tas only.txt'. Some reads were observed (again due to bowtie mismatches)

to hit near but not on the TA insertion points. These were also collected in the *tnseqcount.out* files, but were discarded. These same outputs were used to feed the essentiality package ¹¹.

These files were read into the R function *plot_saturation()* and used to visualize the lifespan of each library over time. This was done by taking the log₂(hits + 1) for each position and plotting them as a set of histograms.

Normalization and visualization strategies. The most expedient method of comparing the libraries was to treat them as if they were components of an RNA sequencing experiment and assuming similar normalization strategies 12 apply. This strategy is very similar to that taken by the essentials software package 13, but uses voom/limma instead of EdgeR. Therefore the alignments were counted by reference genome coding sequence and quantile normalized without removing the low-count genes. These normalized counts were adjusted by the size of the library and length of each coding sequence (rpkm implemented in edgeR ¹⁴ with assistance from DESeq ¹⁵ and log₂ transformed. Conversely, the quantile normalized counts were adjusted by library size (cpm), then adjusted by the ratio of TAs observed in the coding sequence divided by the median number of TAs in all coding sequences (all normalizations were performed by my norm and divide seq). The resulting data sets were used to quantify the median coverage of the genome. Pairwise Euclidean distances (Fig. S2B), Spearman correlation coefficients (Fig. 1G, H, I) and principle component analyses (Fig. S2A) were then used to visualize the similarities/differences between normalized libraries.

Pairwise sample comparisons. In order to further explore the similarities and difference between the libraries, they were plotted against one another as a series of

scatter plots (generated by *my_linear_scatter*) and histograms. These provided a visual metric of the similarities and differences among the libraries and time points between libraries. In the case of the 5448 strain, voom ¹⁶ and limma ¹⁷ were used to combine the samples, correct for the batch effect among libraries, and calculate the merged changes between time points (performed by *simple_comparison*), and include significance with respect to the variance in the data.

Essentiality. The essentiality software package ¹¹ provides an opportunity to query statistically significant stretches of TAs which have no observed insertions to further inform its metric of essentiality. The insertion data was therefore converted into its expected format (*tnseq_count_hitsv2.pl*) and passed to the version 1.21 of the implementation python script. The resulting table provided a count of the number of insertions observed in each ORF, the number of observed TAs, the maximum length of non-observed sequence, the nucleotide span of this region, a call on whether each ORF is essential, and the posterior probability for each call. A few different parameters were tested with each strain and settled on a minimum hit parameter of 2 for both strains.

Circos. R was used to massage various data structures into the format expected by circos ¹⁸.

SUPPLEMENTAL REFERENCES

- Sumby, P. *et al.* Evolutionary origin and emergence of a highly successful clone of serotype M1 group A streptococcus involved multiple horizontal gene transfer events. *J. Infect. Dis.* **192**, 771-782 (2005).
- McShan, W. M. *et al.* Genome sequence of a nephritogenic and highly transformable M49 strain of *Streptococcus pyogenes*. *J. Bacteriol.* **190**, 7773-7785, doi:10.1128/JB.00672-08 (2008).

- Patel, R. K. & Jain, M. NGS QC Toolkit: A Toolkit for Quality Control of Next Generation Sequencing Data. *PloS One* 7, e30619 (2012).
- 4 Stajich, J. E. *et al.* The Bioperl toolkit: Perl modules for the life sciences. *Genome Res.* **12**, 1611-1618 (2002).
- Martin, M. Cutadapt removes adapter sequences from high-throughput sequencing reads. *EMBnet J* (2011).
- Bolger, A. M., Lohse, M. & Usadel, B. Trimmomatic: a flexible trimmer for Illumina sequence data. *Bioinformatics* **30**, 2114-2120 (2014).
- 7 Langmead, B. Aligning short sequencing reads with Bowtie. *Current Protocols in Bioinformatics* **11** (2010).
- 8 Langmead, B., Trapnell, C., Pop, M. & Salzberg, S. L. Ultrafast and memory-efficient alignment of short DNA sequences to the human genome. *Genome Biology* **10**, R25 (2009).
- 9 Li, H. *et al.* The Sequence Alignment/Map format and SAMtools. *Bioinformatics* **25**, 2078-2079 (2009).
- Anders, S. & Huber, W. Differential expression analysis for sequence count data. *Genome Biology* **11**, R106 (2010).
- DeJesus, M. A. *et al.* Bayesian analysis of gene essentiality based on sequencing of transposon insertion libraries. *Bioinformatics* **29**, 695-703 (2013).
- Dillies, M. A. *et al.* A comprehensive evaluation of normalization methods for Illumina high-throughput RNA sequencing data analysis. *Briefings in Bioinformatics* **14**, 671-683, doi:10.1093/bib/bbs046 (2013).
- Zomer, A., Burghout, P., Bootsma, H. J., Hermans, P. W. & van Hijum, S. A. ESSENTIALS: software for rapid analysis of high throughput transposon insertion sequencing data. *PloS One* 7, e43012, doi:10.1371/journal.pone.0043012 (2012).
- McCarthy, D. J., Chen, Y. & Smyth, G. K. Differential expression analysis of multifactor RNA-Seq experiments with respect to biological variation. *Nucleic Acids Res.* **40**, 4288-4297, doi:10.1093/nar/gks042 (2012).
- Love, M. I., Huber, W. & Anders, S. Moderated estimation of fold change and dispersion for RNA-Seq data with DESeq2. *bioRxiv*, doi:doi:10.1101/002832 (2014).
- Law, C. W., Chen, Y., Shi, W. & Smyth, G. K. voom: Precision weights unlock linear model analysis tools for RNA-seq read counts. *Genome Biology* **15**, R29, doi:10.1186/gb-2014-15-2-r29 (2014).

- Qin, H., Feng, T., Harding, S. A., Tsai, C. J. & Zhang, S. An efficient method to identify differentially expressed genes in microarray experiments. *Bioinformatics* **24**, 1583-1589, doi:10.1093/bioinformatics/btn215 (2008).
- Krzywinski, M. *et al.* Circos: an information aesthetic for comparative genomics. *Genome Res.* **19**, 1639-1645, doi:10.1101/gr.092759.109 (2009).

Supplemental Figures

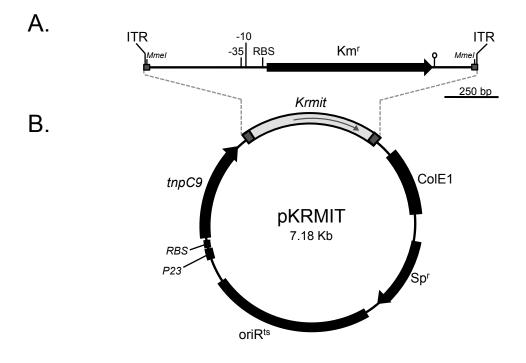
Supplemental Figure S1. pKRMIT, a Tn-seq compatible in vivo mariner **transposition system for GAS.** The Krmit mariner transposable element (A) contains a Kanamycin-resistance (Km^r) cassette surrounded by inverse terminal repeats (ITR) targeted by the *Himar1 mariner* transposase. *Mme*I restriction sites were introduced in the ITR for Tn-seq insertion tag production as indicated. Promoter elements and RBS are also shown. (B) The pKRMIT E. coli/GAS shuttle vector possesses a hyperactive allele of the Himarl mariner transposase (tnpC9) driven from the L. lactis P23 promoter, a ColE1 origin of replication functional in E. coli, a pWV01-derived thermosensitive origin of replication (oriRts) functional in GAS, and a spectinomycin resistance element (Sp^R). (C) Web logo consensus analysis of Krmit transposon insertion sites (TIS) in 120 independent transposants produced in GAS 5448. Nucleotide sequences at the site of Krmit insertion are displayed along the horizontal axis. Positions 31 and 32 correspond to the "TA" dinucleotide targeted by Krmit. The height and order of each letter in the stack of letters at each position correspond to the relative frequency of the nucleotides at that position.

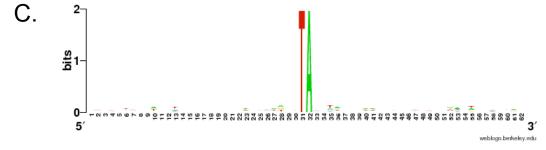
Supplemental Figure S2. Additional statistical analyses for pairwise comparisons of the initial libraries produced in GAS 5448. Libraries 1 to 4 are presented by their original names in the study (Library 9, 11, 12 and 34, respectively) and compared using two additional methods. (A) Principal Component Analysis (PCA) was performed and

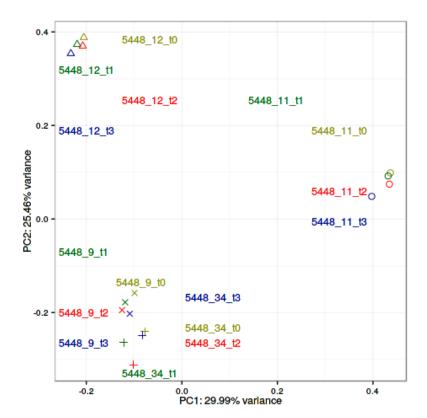
the results are presented graphically with PC1 (x axis) and PC2 (y axis). Libraries are color coded based on time points as follows; T_0 (yellow), T_1 (green), T_2 (red), and T_3 (blue). (B) Euclidean Distance statistical analysis is presented as a heat map.

Supplemental Figure S3. The GAS core genome. Artemis ACT ⁸³ graphical representation of the whole genome multiple sequence alignment of 20 publicly available GAS strains using core clusters of syntenic orthologs (pink lines) as the linking information. Genome order from top to bottom: MGAS5005, NZ131, SF370, MGAS8232, MGAS315, MGAS10394, MGAS6180, MGAS9429, MGAS10270, MGAS2096, MGAS10750. MGAS15252, MGAS1882, Alab49, A20, M1-476, HSC5, HKU, Manfredo and SSI-1.

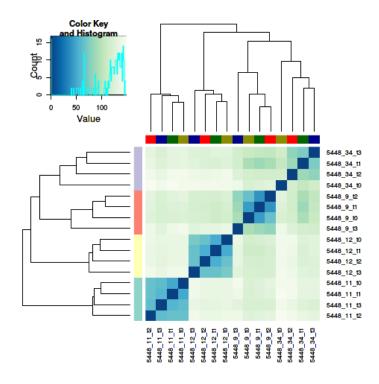
Supplemental Figure S4. Conserved essential genes within the GAS core genome. Artemis ACT ⁸³ graphical representation of the whole genome multiple sequence alignment of 20 publicly available GAS strains using clusters of essential syntenic orthologs (red lines) as the linking information. Genome order from top to bottom: MGAS5005, NZ131, SF370, MGAS8232, MGAS315, MGAS10394, MGAS6180, MGAS9429, MGAS10270, MGAS2096, MGAS10750. MGAS15252, MGAS1882, Alab49, A20, M1-476, HSC5, HKU, Manfredo and SSI-1.

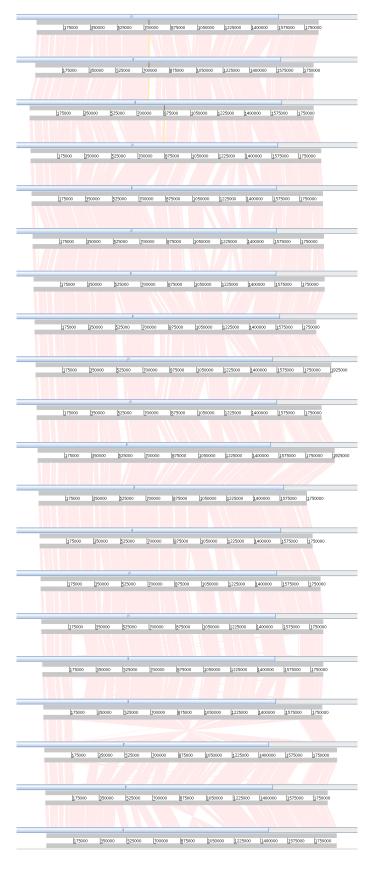














Supplemental Tables

Following nine (9) tables are presented:

- **Table S1.** Complete analysis of Tn-seq read counts and alignments.
- **Table S2.** Selection of reads for the Bayesian analysis.
- **Table S3.** Bayesian analysis of Tn-seq datasets for GAS M1T1 5448 grown *in vitro*.
- **Table S4.** Integrated gene essentiality determination for GAS M1T1 5448 for all time points.
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- **Table S7.** Conserved GAS essential genes identified in both M1T1 5448 and M49 NZ131 compared to the predicted GAS core genome.
- **Table S8.** Bacterial strains and plasmids.
- **Table S9.** Primers used in this study.
- **Table S10.** Summary of the 20 publically available GAS genome sequences.

Table S1. Complete analysis of Tn-seq read counts and alignments.

Sample(a)	Total reads	Strict aligned	Randomly placed(b)	Total aligned (%)(c)	Failed	Plasmid hits (%)(d)	Unique insert sites (TIS)	Saturation index(e)	Av. Distance (f)
5448 Lb1 T0	12,326,943	3,366,045	127,359	3,493,404 (28%)	8,833,539	8,597,058 (97%)	54,757	41	34
5448 Lb1 T1	15,691,922	13,870,884	499,569	14,370,453 (92%)	1,321,469	631,064 (48%)	90,292	68	20
5448 Lb1 T2	14,173,628	11,449,398	1,338,258	12,787,656 (90%)	1,385,972	871,696 (63%)	72,114	54	25
5448 Lb1 T3	12,692,504	11,471,765	632,320	12,104,085 (95%)	588,419	239,739 (41%)	20,132	15	91
5448 Lb2 T0	14,893,811	10,081,697	238,856	10,320,553 (69%)	4,573,258	4,101,079 (90%)	28,705	22	64
5448 Lb2 T1	12,603,471	11,272,221	267,163	11,539,384 (92%)	1,064,087	687,446 (65%)	24,123	18	76
5448 Lb2 T2	10,583,515	9,904,226	198,478	10,102,704 (95%)	480,811	152,719 (32%)	22,297	17	82
5448 Lb2 T3	15,500,886	13,903,253	598,603	14,501,856 (94%)	999,030	437,253 (44%)	33,710	25	55
5448 Lb3 T0	13,394,016	9,867,412	1,192,267	11,059,679 (83%)	2,334,337	2,037,516 (87%)	23,428	18	78
5448 Lb3 T1	15,131,244	13,023,394	1,053,742	14,077,136 (93%)	1,054,108	551,455 (52%)	32,406	24	57
5448 Lb3 T2	13,337,250	11,576,167	1,101,352	12,677,519 (95%)	659,731	402,269 (61%)	24,694	19	74
5448 Lb3 T3	17,623,505	13,938,708	3,080,613	17,019,321 (97%)	604,184	64,548 (11%)	15,840	12	116
5448 Lb4 T0	11,679,250	679,170	32,819	711,989 (6%)	10,967,261	10,879,152 (99%)	8,645	6	213
5448 Lb4 T1	15,856,339	14,747,260	255,938	15,003,198 (95%)	853,141	446,419 (52%)	42,032	32	44
5448 Lb4 T2	10,873,096	10,490,140	58,750	10,548,890 (97%)	324,206	119,664 (37%)	15,401	12	119
5448 Lb4 T3	13,664,074	12,976,990	53,330	13,030,320 (5%)	633,754	401,089 (63%)	26,038	20	71
Master 5448 TO	52,294,020	23,994,324	1,591,301	25,585,625 (49%)	26,708,395	25,614,805 (96%)	79,622	60	23
Master 5448 T1	59,282,976	52,913,759	2,076,412	54,990,171 (93%)	4,292,805	2,316,384 (54%)	107,059	80	17
Master 5448 T2	48,967,489	43,419,931	2,696,838	46,116,769 (94%)	2,850,720	1,546,348 (54%)	90,768	68	20
Master 5448 T3	59,480,969	52,290,716	4,364,866	56,655,582 (95%)	2,825,387	1,142,629 (40%)	65,183	49	28
NZ131 T0	3,460,214	1,652,565	88,035	1,740,600 (50%)	1,719,614	1,579,596 (92%)	52,464	40	35
NZ131 T1	31,730,825	20,195,930	1,717,501	21,913,431 (69%)	9,817,394	7,636,932 (78%)	111,001	84	16
NZ131 T2	17,433,089	10,882,091	220,199	11,102,290 (64%)	6,330,799	5,390,105 (85%)	67,449	51	27
NZ131 T3	44,784,994	36,885,896	307,314	37,193,210 (83%)	7,591,784	4,164,076 (55%)	57,377	44	32

⁽a) Sample name describes the GAS strain (i.e GAS 5448 or NZ131) used to produce the Krmit library. For 5448, 4 independent libraries (Lb1 to Lb4) were analyzed separately. The different libraries produced (T0) were subjected to 3 additional passages in THY (T1 to T3). Master 5448 is the combinaison of the reads from the 4 initial libraries in 5448.

⁽b) Reads aligning to more than one position on the chromosome were randomly placed onto the GAS chromosome.

⁽c) Percentage in parenthesis represents the proportion of the initial reads (sum of strictly aligned and randomly placed) that align to the GAS genome.

⁽d) Percentage in parenthesis coresponds to the proportion of reads among the reads that failed to align to the GAS genome that were aligned to the pKRMIT plasmid sequence.

⁽e) The saturation index depicts the proportion of unique TA sites found on the GAS chromosome hit at least once by Krmit.

⁽f) Calculated distance separating two adjacent TA sites where Krmit inserted.

Table S2. Selection of reads for the Bayesian analysis.

_	All	TIS(a)	TIS with at least 2 Krmit copies(b)					
Library	Unique TIS	Saturation index(c)	Unique TIS	Saturation index(c)				
5448 (T0)	79,622	60	48,250	36				
5448 (T1)	107,059	80	74,428	56				
5448 (T2)	90,768	68	56,967	43				
5448 (T3)	65,183	49	24,716	19				
NZ131 (T0)	52,464	40	39,254	30				
NZ131 (T1)	111,001	84	79,307	60				
NZ131 (T2)	67,449	51	35,787	27				
NZ131 (T3)	57,377	44	11,487	9				

⁽a) Recapitulation of the total number of unique transposon insertion sites (TIS) and saturation indexes for the *Krmit* libraries produced in GAS 5448 and NZ131.

⁽b) The Bayesian analysis for gene essentiality prediction called for eliminating TIS with one *Krmit* insertion. The remaining reads have at least two *Krmit* counts.

⁽c) The saturation index depicts the proportion of unique TA sites found on the GAS chromosome hit at least once by *Krmit*.

Table S3. Bayesian analysis of Tn-seq datasets for GAS M1T1 5448 grown in vitro.

(a) Spy numbers from MGAS5005 genome. (b) When available, gene name is provided.

(b) When available,	anable, gene name is provided.				Bayesian for T ₀		Bayesian for T ₁		Bayesian for T ₂		
Locus Tag(a)	Gene Name(b)	Start	Stop	Length	Z score	Call	Z	score	Call	Z score	Call
M5005_Spy_0001	dnaA	202	1557	451	1	E		1	E	1	E
M5005_Spy_0002	dnaN	1712	2848	378	1	E		1	Ε	1	Ε
M5005_Spy_0003	-	2923	3120	65	0	NE		0	NE	0	NE
M5005_Spy_0004	ychF	3450	4565	371	0	NE		0	NE	0	NE
M5005_Spy_0005	pth	4635	5204	189	0.99875	E	0	.99975	E	0.98	U
M5005_Spy_0006	trcF	5207	8710	1167	0.00025	NE		0	NE	0	NE
M5005_Spy_0007	-	8872	9144	90	0	NE		0	NE	0	NE
M5005_Spy_0008	divIC	9131	9502	123	0.00025	NE	(0.0015	NE	0.001	NE
M5005_Spy_0009	-	9499	9624	41	-1	S		-1	S	-1	S
M5005_Spy_0010	-	9637	10923	428	0	NE		0	NE	0	NE
M5005_Spy_0011	tilS/mesJ	10920	12206	428	1	E		1	E	1	E
M5005_Spy_0012	hpt	12211	12753	180	0.999	E	0	.00025	NE	1	E
M5005_Spy_0013	ftsH	12775	14754	659	0.999	E		1	E	1	E
M5005_Spy_0014	-	15079	16470	463	0	NE		0	NE	0	NE
M5005_Spy_0015c	-	16811	16945	44	-1	S		-1	S	-1	S
M5005_Spy_0017	sibA	31134	32330	398	1	E		1	E	1	E
M5005_Spy_0018	prsA.2	32583	33545	320	0.98775	U		1	E	1	Е
M5005_Spy_0019	recO	33731	34486	251	0	NE		0	NE	0	NE
M5005_Spy_0020	plsX	34589	35596	335	0.99875	E		1	E	1	E
M5005_Spy_0021	acpP.2	35589	35831	80	0.00025	NE	(0.9235	U	0.222	U
M5005_Spy_0022	-	35952	36686	244	0.107	U		0	NE	0	NE
M5005_Spy_0023	-	36762	40535	1257	0.00025	NE		0	NE	0	NE
M5005_Spy_0024	purF	40696	42150	484	0	NE		0	NE	0	NE
M5005_Spy_0025	purM	42178	43200	340	0.00025	NE		0	NE	0	NE
M5005_Spy_0026	purN	43368	43922	184	0	NE		0	NE	0	NE
M5005_Spy_0027	purH -	44106	45653	515	0	NE		0	NE	0	NE
M5005_Spy_0028c		45711	46835	374	0	NE		0	NE	0	NE
M5005_Spy_0029	purD purE	46998	48353	451	0	NE		0	NE	0	NE
M5005_Spy_0030	purK	48511	49122 50182	203 358	0 0.00175	NE NE		0 0	NE NE	0	NE
M5005_Spy_0031 M5005_Spy_0032	pui K -	49106				NE NE				0	NE
M5005_Spy_0032	purB	50209 51870	51852 53162	547 430	0 0.00025	NE NE		0 0	NE NE	0	NE NE
M5005_Spy_0034	- Pui D	53294	54205	303	0.00025	NE		0	NE	0	NE
M5005_Spy_0035	ruvB	54431	55429	332	0.00023	NE		0	NE	0.002	NE
M5005_Spy_0036	-	55567	56004	145	0	NE		0	NE	0.002	NE
M5005_Spy_0037	_	56027	56428	133	0.00025	NE		1	E	0.002	NE
M5005_Spy_0038	_	56425	58200	591	0.40175	U		1	E	1	E
M5005_Spy_0039	adh2/adhE	58509	61151	880	0.40175	NE		0	NE	0	NE
M5005_Spy_0040	adhA/adhP	61403	62419	338	0	NE		0	NE	0	NE
M5005_Spy_0041	norM	62807	63778	323	0	NE		0	NE	0	NE
M5005_Spy_0043	rpsJ	64301	64609	102	0.99	U		1	E	0.999	E
M5005_Spy_0044	rplC	64825	65451	208	0.9915	Ü		1	E	1	E
M5005_Spy_0045	rplD	65475	66098	207	1	E		1	E	1	E
M5005_Spy_0046	rplW	66098	66394	98	0.002	NE		0	NE	0	NE
M5005_Spy_0047	rplB	66412	67245	277	0.99875	Ε		1	Ε	1	Ε
M5005_Spy_0048	rpsS	67384	67662	92	0.992	U	0	.00575	NE	0.999	Ε
M5005_Spy_0049	rplV	67678	68022	114	0.99825	E		1	Ε	1	Ε
M5005_Spy_0050	rpsC	68035	68688	217	0.993	U		1	Ε	1	Ε
M5005_Spy_0051	rpIP	68692	69105	137	0.99925	Ε		1	Ε	1	Ε
M5005_Spy_0052	rpmC	69115	69321	68	0.90175	U		0	NE	0	NE
M5005_Spy_0053	rpsQ	69347	69607	86	0.99925	E		1	Ε	0.009	NE
M5005_Spy_0054	rplN	69632	70000	122	0.00025	NE	0	.01675	NE	1	Ε
M5005_Spy_0055	rplX	70079	70384	101	0.001	NE		.78675	U	0.024	NE
M5005_Spy_0056	rplE	70408	70950	180	1	Е		.70775	U	0.987	U
M5005_Spy_0057	rpsN	70966	71151	61	0.00975	NE		0.999	Ε	0.99	U
M5005_Spy_0058	rpsH	71302	71700	132	0.99875	Е		.02525	NE	0.001	NE
M5005_Spy_0059	rplF	71903	72439	178	1	E		1	Ε	1	Е
M5005_Spy_0060	rplR	72544	72900	118	0.88275	U		1	E	0.991	U

M5005_Spy_0061	rpsE	72919	73413	164	0.9995	Е	1	E	1	Ε
M5005_Spy_0062	rpmD	73428	73610	60	0.00025	NE	1	Ε	1	Ε
M5005_Spy_0063	rplO	73824	74264	146	0.00025	NE	0.00025	NE	0.001	NE
M5005_Spy_0064	secY	74281	75585	434	0.99975	Ε	1	Ε	1	Ε
M5005_Spy_0065	adk	75735	76373	212	0.00025	NE	1	E	0.08	Ū
M5005_Spy_0066	infA	76491	76709	72	0.99125	U	1	E	0.999	E
M5005_Spy_0067										
	rpmJ	76735	76851	38	-1	S	-1	S	-1	S
M5005_Spy_0068	rpsM	76869	77234	121	0.999	E	0.9995	E	0.999	E
M5005_Spy_0069	rpsK	77252	77635	127	0.001	NE	1	E	1	E
M5005_Spy_0070	rpoA	77681	78619	312	1	E	1	E	1	Ε
M5005_Spy_0071	rplQ	78634	79020	128	0.00025	NE	1	E	1	Ε
M5005_Spy_0072c	-	79618	79752	44	-1	S	-1	S	-1	S
M5005_Spy_0073	-	86264	86449	61	0	NE	0	NE	0.004	NE
M5005_Spy_0074	_	87087	87224	45	-1	S	-1	S	-1	S
M5005_Spy_0075	_	87235	87393	52	-1	S	-1	S	-1	S
M5005_Spy_0076	_	87499	87660	53	-1	S	-1	S	-1	S
M5005_Spy_0077	adcR	87770	88213	147	0	NE	0	NE	0	NE
	adcC									
M5005_Spy_0078		88217	88936	239	0	NE	0	NE	0	NE
M5005_Spy_0079	adcB	88929	89744	271	0	NE	0	NE	0	NE
M5005_Spy_0080c	-	89784	90167	127	0	NE	0	NE	0	NE
M5005_Spy_0081c	tyrS	90218	91474	418	1	E	0.99975	E	1	E
M5005_Spy_0082	pbp1b	91566	93878	770	0	NE	0	NE	0	NE
M5005_Spy_0083	rpoB	94142	97708	1188	1	E	1	E	1	Ε
M5005_Spy_0084	rpoC	97799	101440	1213	1	Е	1	Ε	1	Ε
M5005_Spy_0085	-	101592	101957	121	0	NE	0	NE	0	NE
M5005_Spy_0086	comYA	102050	102988	312	0	NE	0	NE	0	NE
M5005_Spy_0087	comYB	102867	103958	363	0.00025	NE	0	NE	0	NE
M5005_Spy_0088	comYC	103960	104286	108	0.00025	NE	0	NE	0	NE
M5005_Spy_0089	-	104360	104280	108	0		0	NE	0	NE
	-					NE				
M5005_Spy_0090	-	104646	104930	94	0	NE	0	NE	0	NE
M5005_Spy_0091	comYD	104923	105357	144	0	NE	0	NE	0	NE
M5005_Spy_0092	-	105341	105667	108	0	NE	0	NE	0	NE
M5005_Spy_0093	-	105765	106718	317	0	NE	0	NE	0	NE
M5005_Spy_0094	ackA	106777	107973	398	0.00025	NE	0	NE	0.001	NE
M5005_Spy_0095	-	108160	108468	102	0	NE	0	NE	0	NE
M5005_Spy_0096c	proC	108551	109321	256	0	NE	0	NE	0	NE
M5005_Spy_0097c	pepA	109369	110436	355	0	NE	0	NE	0	NE
M5005_Spy_0098	-	110546	110710	54	-1	S	-1	S	-1	S
M5005_Spy_0099	_	110892	111185	97	0	NE	0	NE	0	NE
M5005_Spy_0100	trx.1	111182	111499	105	0	NE	0	NE	0	NE
M5005_Spy_0100	-								0	
		111517	112143	208	0	NE	0	NE		NE
M5005_Spy_0102	ssb	112295	112690	131	0	NE	0	NE	0	NE
M5005_Spy_0103c	-	112950	113591	213	0	NE	0	NE	0	NE
M5005_Spy_0104c	-	113611	114588	325	0	NE	0	NE	0	NE
M5005_Spy_0105c	hslO	114575	115447	290	0	NE	0	NE	0	NE
M5005_Spy_0106c	rofA/nra	115594	117087	497	0	NE	0	NE	0	NE
M5005_Spy_0107	cbp	117335	119623	762	0	NE	0	NE	0	NE
M5005_Spy_0108	lepA-1	119616	120173	185	0	NE	0	NE	0	NE
M5005_Spy_0109	prtF	120206	121228	340	0	NE	0	NE	0	NE
M5005_Spy_0110	eftLSL.B	121238	121951	237	0	NE	0	NE	0	NE
M5005_Spy_0111	_	121973	122620	215	0	NE	0	NE	0	NE
M5005_Spy_0112c	_	122807	124129	440	0	NE	0	NE	0	NE
M5005_Spy_0113c	_	124370	124720	116	0	NE	0	NE	0	NE
M5005_Spy_0114	_	125024	125779	251	0	NE	0	NE	0	NE
M5005_Spy_0115c	- ataE	125973	126638	221	0	NE	0	NE	0	NE
M5005_Spy_0116	atoE	126987	128393	468	0	NE	0	NE	0	NE
M5005_Spy_0117c	-	128461	128856	131	0	NE	0	NE	0	NE
M5005_Spy_0118c	-	128952	129371	139	0	NE	0	NE	0	NE
M5005_Spy_0119	-	129492	130676	394	0	NE	0	NE	0	NE
M5005_Spy_0120	atoD.2	130688	131347	219	0	NE	0	NE	0	NE
M5005_Spy_0121	-	131350	131997	215	0	NE	0	NE	0	NE
M5005_Spy_0122c	-	132119	132799	226	0	NE	0	NE	0	NE
M5005_Spy_0123	-	132973	133338	121	0	NE	0	NE	0	NE
–		-								

M5005_Spy_0124	sloR	133375	134394	339	0	NE	0	NE	0	NE
M5005_Spy_0125	-	134849	135169	106	0	NE	0	NE	0	NE
M5005_Spy_0126	ntpI	135159	137180	673	0	NE	0	NE	0	NE
M5005_Spy_0127	ntpK	137182	137661	159	0.00025	NE	0	NE	0	NE
M5005_Spy_0128	ntpE	137729	138313	194	0	NE	0	NE	0	NE
M5005_Spy_0129	ntpC	138329	139327	332	0	NE	0	NE	0	NE
* *	· ·									
M5005_Spy_0130	ntpF	139324	139644	106	0	NE	0	NE	0	NE
M5005_Spy_0131	ntpA	139845	141620	591	0.00025	NE	0	NE	0	NE
M5005_Spy_0132	ntpB	141621	143036	471	0	NE	0	NE	0	NE
M5005_Spy_0133	ntpD	143081	143707	208	0	NE	0	NE	0	NE
M5005_Spy_0134c	-	143827	145089	420	0	NE	0	NE	0	NE
M5005_Spy_0135c	-	145102	145980	292	0	NE	0	NE	0	NE
M5005_Spy_0136	purA	146418	147710	430	0	NE	0	NE	0	NE
M5005_Spy_0137	· _	148037	149080	347	0	NE	0	NE	0	NE
M5005_Spy_0138	nusG	149253	149792	179	0.79375	U	0.47925	U	0.999	E
M5005_Spy_0130		150154	151518	454						
	nga -				0	NE	0	NE	0	NE
M5005_Spy_0140		151523	152008	161	0	NE	0	NE	0	NE
M5005_Spy_0141	slo	152032	153747	571	0	NE	0	NE	0	NE
M5005_Spy_0142	-	154002	154433	143	0	NE	0	NE	0	NE
M5005_Spy_0143c	-	154619	154855	78	0	NE	0	NE	0	NE
M5005_Spy_0144c	-	155265	155432	55	-1	S	-1	S	-1	S
M5005_Spy_0145c	-	155607	155894	95	0	NE	0	NE	0	NE
M5005_Spy_0146	metB	156335	157525	396	0	NE	0	NE	0	NE
M5005_Spy_0147	leuS	157736	160237	833	1	E	1	E	1	E
M5005_Spy_0148	ulaA	160544	161977	477	0	NE	0	NE	0.28	Ū
	-	162048								
M5005_Spy_0149			162326	92	0	NE	0	NE	0	NE
M5005_Spy_0150	-	162449	162934	161	0	NE	0	NE	0	NE
M5005_Spy_0151	ulaD	163025	163687	220	0.00025	NE	0	NE	0	NE
M5005_Spy_0152	-	163692	164555	287	0	NE	0	NE	0	NE
M5005_Spy_0153	araD	164557	165261	234	0	NE	0	NE	0	NE
M5005_Spy_0154	-	165319	165465	48	-1	S	-1	S	-1	S
M5005_Spy_0155	-	165586	167232	548	0	NE	0	NE	0	NE
M5005_Spy_0156	-	167485	168576	363	0	NE	0	NE	0	NE
M5005_Spy_0157	opuAA	169064	170260	398	0	NE	0	NE	0	NE
M5005_Spy_0158	opuABC	170276	172003	575	0	NE	0	NE	0.001	NE
M5005_Spy_0150	polA		174776	880	0.0005	NE	0.999	E		
	poiA	172134							1	E
M5005_Spy_0160	-	174963	175418	151	0	NE	0	NE	0	NE
M5005_Spy_0161	perR	175470	175937	155	0	NE	0	NE	0	NE
M5005_Spy_0162	vlg	176094	176393	99	0	NE	0	NE	0	NE
M5005_Spy_0163	-	176615	177949	444	0.00025	NE	0	NE	0	NE
M5005_Spy_0164	-	177942	178472	176	0	NE	0	NE	0	NE
M5005_Spy_0165c	-	178519	178761	80	0	NE	0	NE	0	NE
M5005_Spy_0166c	-	178801	179016	71	0	NE	0	NE	0	NE
M5005_Spy_0167c	-	179056	179625	189	0	NE	0	NE	0	NE
M5005_Spy_0168c	_	179658	179873	71	0	NE	0	NE	0	NE
M5005_Spy_0169c	_	180029	181339	436	0	NE	0	NE	0	NE
	nadC									
M5005_Spy_0170		181563	182435	290	0	NE	0	NE	0	NE
M5005_Spy_0171c	-	182735	183541	268	0	NE	0	NE	0	NE
M5005_Spy_0172c	-	183562	184077	171	0	NE	0	NE	0	NE
M5005_Spy_0173c	-	184163	185026	287	0	NE	0	NE	0	NE
M5005_Spy_0174	-	185063	185221	52	-1	S	-1	S	-1	S
M5005_Spy_0175	tgt	185245	186387	380	0	NE	0	NE	0	NE
M5005_Spy_0176	-	186604	186915	103	0.00025	NE	0	NE	0	NE
M5005_Spy_0177	bioY	186919	187458	179	0	NE	0	NE	0	NE
M5005_Spy_0178	-	187598	188377	259	0	NE	0	NE	0	NE
M5005_Spy_0179	_	188377	188892	171	0	NE	0	NE	0.001	NE
M5005_Spy_0179	_									
	=	189506	190726	406	0	NE	0	NE	0	NE
M5005_Spy_0181	-	190780	190887	35	-1	S	-1	S	-1	S
M5005_Spy_0182	speG	191138	191842	234	0	NE	0	NE	0	NE
M5005_Spy_0183	-	191927	192046	39	-1	S	-1	S	-1	S
M5005_Spy_0184	-	192082	192201	39	-1	S	-1	S	-1	S
M5005_Spy_0185	pgi	192298	193647	449	1	Ε	1	Ε	1	Е
M5005_Spy_0186c	ralp4	193996	195504	502	0	NE	0	NE	0	NE
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M5005_Spy_0187	-	196059	196763	234	0	NE	0	NE	0	NE
M5005_Spy_0188	-	196666	197181	171	0	NE	0	NE	0	NE
M5005_Spy_0189	-	197165	197290	41	-1	S	-1	S	-1	S
M5005_Spy_0190	-	197371	197478	35	-1	S	-1	S	-1	S
M5005_Spy_0191	-	197506	198177	223	0	NE	0	NE	0	NE
M5005_Spy_0192c	hasC.2	198276	199175	299	0.00025	NE	1	Ε	0.002	NE
M5005_Spy_0194c	gpsA	199408	200223	271	1	E	1	E	1	Ε
M5005_Spy_0195	-	200521	200970	149	0	NE	0	NE	0	NE
M5005_Spy_0196	-	200963	202669	568	0	NE	0	NE	0.001	NE
M5005_Spy_0197	-	202672	204456	594	0.00025	NE	0	NE	0	NE
M5005_Spy_0198	_	204574	205341	255	0	NE	0	NE	0	NE
M5005_Spy_0199	dut	205451	205897	148	0.00025	NE	0	NE	0.001	NE
M5005_Spy_0200	radA	205978	207339	453	0.00025	NE	0	NE	0.001	NE
M5005_Spy_0200	-	203378	208025	165	0.00023	NE	0	NE	1	E
M5005_Spy_0201 M5005_Spy_0202	-									
		208156	208866	236	0	NE	0	NE	0	NE
M5005_Spy_0203	gltX	209048	210493	481	0.98775	U	1	E	1	E
M5005_Spy_0204	fasB	210888	212234	448	0	NE	0	NE	0	NE
M5005_Spy_0205	fasC	212231	213514	427	0.00025	NE	0	NE	0	NE
M5005_Spy_0206	fasA	213518	214258	246	0	NE	0	NE	0	NE
M5005_Spy_0207	rnpA	214798	215157	119	0.15675	U	0.99	U	1	E
M5005_Spy_0208	-	215141	215950	269	0	NE	0	NE	0	NE
M5005_Spy_0209	-	215962	216876	304	0	NE	0	NE	0	NE
M5005_Spy_0210	-	216961	217083	40	-1	S	-1	S	-1	S
M5005_Spy_0211	rpmH	217191	217325	44	-1	S	-1	S	-1	S
M5005_Spy_0212	-	217599	218303	234	0	NE	0	NE	0	NE
M5005_Spy_0213	-	218352	219671	439	0	NE	0	NE	0	NE
M5005_Spy_0214	-	219774	220661	295	0	NE	0	NE	0	NE
M5005_Spy_0215	-	220674	221504	276	0	NE	0	NE	0	NE
M5005_Spy_0216	_	221661	222323	220	0	NE	0	NE	0	NE
M5005_Spy_0217	nanH	222335	223249	304	0	NE	0	NE	0	NE
M5005_Spy_0217	-	22333	223249	312	0	NE	0	NE	0	NE
M5005_Spy_0210	_		225150			NE	0	NE	0	
* *		224320		276	0					NE
M5005_Spy_0220	tatD	225402	226226	274	0	NE	0	NE	0	NE
M5005_Spy_0221	-	226198	226788	196	0	NE	0	NE	0	NE
M5005_Spy_0222	ksgA	226902	227774	290	0.0025	NE	0	NE	0	NE
M5005_Spy_0223	engC	228198	229070	290	0.639	U	0.99975	Е	1	Е
M5005_Spy_0224	rpe	229080	229742	220	0.00025	NE	0	NE	1	E
M5005_Spy_0225	-	229735	230367	210	0	NE	0	NE	0.001	NE
M5005_Spy_0226	-	230369	231640	423	0	NE	0	NE	0	NE
M5005_Spy_0227	cbf	231630	232568	312	0	NE	0	NE	0	NE
M5005_Spy_0228	purR	232835	233674	279	0	NE	0	NE	0	NE
M5005_Spy_0229	prgA	233665	236286	873	0.00025	NE	0	NE	0	NE
M5005_Spy_0230	rpsL	236494	236907	137	0.99225	U	0.99975	Ε	0.992	Ε
M5005_Spy_0231	rpsG	236928	237398	156	0.964	U	1	E	0.998	Ε
M5005_Spy_0232	fus	237765	239843	692	1	Ε	1	Е	1	Ε
M5005_Spy_0233	plr	240191	241201	336	1	Ε	1	Ε	1	Ε
M5005_Spy_0234c	· -	241427	241543	38	-1	S	-1	S	-1	S
M5005_Spy_0235c	_	241685	242425	246	1	E	1	E	1	E
M5005_Spy_0236c	_	242418	243986	522	0.67175	Ū	1	E	1	E
M5005_Spy_02300 M5005_Spy_0237	_	244184	246082	632		NE	0	NE	0	NE
M5005_Spy_0237 M5005_Spy_0238	uppP/bacA				0					
	* *	246148	246987	279	0	NE	0	NE	0	NE
M5005_Spy_0239	mecA	247133	247894	253	0	NE	0	NE	0	NE
M5005_Spy_0240	rgpG	248045	249070	341	1	E	1	E	1	E
M5005_Spy_0241	rgpG	249040	249165	41	-1	S	-1	S	-1	S
M5005_Spy_0242	-	249192	249962	256	0	NE	0	NE	0.998	Е
M5005_Spy_0243	-	250057	251319	420	0	NE	0	NE	1	Ε
M5005_Spy_0244	nifS3	251350	252576	408	0	NE	0.00025	NE	1	Е
M5005_Spy_0245	nifU	252563	253042	159	0.00025	NE	0	NE	1	Ε
M5005_Spy_0246	-	253035	254453	472	0.0005	NE	0	NE	1	Е
M5005_Spy_0247c	pbp7	254605	255786	393	0	NE	0	NE	0	NE
M5005_Spy_0248c	dacA2	255954	257186	410	0	NE	0	NE	0	NE
M5005_Spy_0249	оррА	257517	259487	656	0	NE	0	NE	0	NE
M5005_Spy_0250	оррВ	259540	261054	504	0	NE	0	NE	0	NE
	- r r =	200010		301	J		J		J	

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M5005_Spy_0251	oppC	261054	261980	308	0	NE	0	NE	0	NE
M5005_Spy_0252	oppD	261989	263059	356	0	NE	0	NE	0	NE
M5005_Spy_0253	oppF	263052	263975	307	0	NE	0	NE	0	NE
M5005_Spy_0254c	-	264216	264362	48	-1	S	-1	S	-1	S
M5005_Spy_0255c	-	264737	264871	44	-1	S	-1	S	-1	S
M5005_Spy_0256	comX1.1	270293	270844	183	0	NE	0	NE	0	NE
M5005_Spy_0257	_	271455	272159	234	0	NE	0	NE	0	NE
M5005_Spy_0258	_	272062	272577	171	0	NE	0	NE	0	NE
				34			-1		-1	
M5005_Spy_0259	-	272561	272665		-1	S		S		S
M5005_Spy_0260	-	272683	273267	194	0.99975	E	0.99975	E	1	E
M5005_Spy_0261	-	273267	274385	372	0.86825	U	0.91825	U	1	E
M5005_Spy_0262	-	274410	274718	102	0	NE	0	NE	0	NE
M5005_Spy_0263	nadD	274787	275419	210	0.4555	U	0.99875	Ε	1	Е
M5005_Spy_0264	-	275416	276009	197	0	NE	0	NE	0.001	NE
M5005_Spy_0265	-	276009	276386	125	0.00025	NE	0	NE	0	NE
M5005_Spy_0266	-	276428	277177	249	0	NE	0	NE	0	NE
M5005_Spy_0267	-	277431	278537	368	0	NE	0	NE	0	NE
M5005_Spy_0268	_	278874	279029	51	-1	S	-1	S	-1	S
M5005_Spy_0269	_	279019	279735	238	0	NE	0	NE	0	NE
	atm A									
M5005_Spy_0270	atmA	279938	280780	280	0.00025	NE	0	NE	0	NE
M5005_Spy_0271	atmB	281109	281954	281	0	NE	0	NE	0	NE
M5005_Spy_0272	atmD	282204	283268	354	0	NE	0	NE	0	NE
M5005_Spy_0273	atmE	283269	283961	230	0	NE	0	NE	0	NE
M5005_Spy_0274c	braB	284015	285385	456	0	NE	0	NE	0	NE
M5005_Spy_0275	-	285619	286833	404	0.00025	NE	0	NE	0.001	NE
M5005_Spy_0276c	-	286888	287562	224	0	NE	0	NE	0.997	Ε
M5005_Spy_0277c	-	287572	288963	463	0	NE	0	NE	0.001	NE
M5005_Spy_0278c	gidB	289033	289746	237	0.00025	NE	0	NE	0	NE
M5005_Spy_0279	lemA	289896	290453	185	0	NE	0	NE	0	NE
M5005_Spy_0279	htpX			298		NE		NE		
	- -	290500	291396		0		0		0	NE
M5005_Spy_0281		291630	292163	177	0	NE	0	NE	0	NE
M5005_Spy_0282	covR	292430	293116	228	0	NE	0	NE	0	NE
M5005_Spy_0283	covS	293259	294623	454	0	NE	0	NE	0	NE
M5005_Spy_0284	nrdR	294838	295332	164	0	NE	0	NE	0.001	NE
M5005_Spy_0285	dnaB	295316	296491	391	0.00075	NE	1	E	1	Ε
M5005_Spy_0286	dnaI	296492	297394	300	1	Е	1	E	1	Ε
M5005_Spy_0287	engA	297457	298767	436	1	Е	1	Ε	1	Ε
M5005_Spy_0288	snf	298974	302072	1032	0.00025	NE	0	NE	0.002	NE
M5005_Spy_0289	-	302315	302917	200	0	NE	0	NE	0	NE
M5005 Spy 0290	murC	302957	304285	442	0.0165	NE	1	E	1	E
M5005_Spy_0291	-	304331	304283	160	0.0103	NE	0	NE	0	NE
M5005_Spy_0292	- A	304931	306499	522	0.0005	NE	0	NE	1	E
M5005_Spy_0293	greA	306524	307054	176	0	NE	0	NE	0	NE
M5005_Spy_0294c	-	307269	307412	47	-1	S	-1	S	-1	S
M5005_Spy_0295c	oxaA	307677	308600	307	0.262	U	1	E	1	E
M5005_Spy_0296c	-	308682	308960	92	0	NE	0	NE	0	NE
M5005_Spy_0297c	-	309115	309630	171	0	NE	0	NE	0	NE
M5005_Spy_0298c	-	309533	310237	234	0	NE	0	NE	0	NE
M5005_Spy_0299	-	310535	311272	245	0	NE	0	NE	0	NE
M5005_Spy_0300	-	311311	311811	166	0	NE	0	NE	0	NE
M5005_Spy_0301	-	311826	312515	229	0	NE	0	NE	0	NE
M5005_Spy_0302	_	312693	312935	80	0.001	NE	0.97375	U	0.999	E
M5005_Spy_0303	glr	313113	313907	264	0.62175	U	1	E	1	E
M5005_Spy_0304	gıı			328						
	-	313904	314890		0	NE	0	NE	0	NE
M5005_Spy_0305	-	314869	315390	173	0.00025	NE	0	NE	0	NE
M5005_Spy_0306	-	315387	315848	153	0	NE	0	NE	0	NE
M5005_Spy_0307	xerD	315845	316591	248	0.00025	NE	0	NE	0	NE
M5005_Spy_0308	scpA	316591	317292	233	0	NE	0	NE	0	NE
M5005_Spy_0309	scpB	317289	317840	183	0.00025	NE	0	NE	0.001	NE
M5005_Spy_0310	rluB	317939	318685	248	0.00025	NE	0	NE	0	NE
M5005_Spy_0311	-	318682	318945	87	0	NE	0	NE	0	NE
M5005_Spy_0312	-	319123	319671	182	0.00025	NE	0	NE	0	NE
M5005_Spy_0313	-	319982	320545	187	0.00025	NE	0.00025	NE	1	E
		313302	5=05 +5	107	0.00025		3.00023		-	_

M5005_Spy_0314	-	320547	321200	217	0	NE	0	NE	0	NE
M5005_Spy_0315	-	321493	322413	306	0	NE	0	NE	0	NE
M5005_Spy_0316	-	322452	323006	184	0	NE	0	NE	0	NE
M5005_Spy_0317	hlyX	323139	324473	444	0	NE	0	NE	0	NE
M5005_Spy_0318	pflC	324479	325342	287	0	NE	0	NE	0	NE
M5005_Spy_0319	ppaC	325473	326408	311	0.99825	Ε	0.0255	NE	0.986	U
M5005_Spy_0320	-	326484	327137	217	0	NE	0	NE	0	NE
M5005_Spy_0321c	fhuG	327182	328108	308	0	NE	0	NE	0	NE
M5005_Spy_0322c	fhuB	328180	329232	350	0	NE	0	NE	0	NE
M5005 Spy 0323c	fhuD	329222	330154	310	0	NE	0	NE	0	NE
M5005_Spy_0324c	fhuA	330180	330962	260	0	NE	0	NE	0	NE
M5005_Spy_0325c	murE	331208	332653	481	1	E	1	E	1	E
M5005_Spy_0326	-	332741	334375	544	0.98475	Ū	1	E	1	E
M5005_Spy_0327	upp	334543	335172	209	0.98473	NE	0	NE	0.001	NE
M5005_Spy_0328	clpP		335986	196	0.00025		0.00175	NE	1	E
	СГРР	335396				NE				
M5005_Spy_0329	- 1.	336478	336753	91	0	NE	0	NE	0	NE
M5005_Spy_0330	tmk	337002	337637	211	0.998	E	1	E	1	E
M5005_Spy_0331	dnaX	337655	338530	291	0.99725	E	1	E	1	E
M5005_Spy_0332	-	338549	338788	79	0.00025	NE	0	NE	0	NE
M5005_Spy_0333	-	338877	339038	53	-1	S	-1	S	-1	S
M5005_Spy_0334	-	339193	339516	107	0.00625	NE	0	NE	0.05	U
M5005_Spy_0335	-	339521	340384	287	0	NE	0	NE	0.001	NE
M5005_Spy_0336	-	340411	340803	130	0.00025	NE	0	NE	0.001	NE
M5005_Spy_0337c	cutC	340850	341479	209	0	NE	0	NE	0	NE
M5005_Spy_0338	-	341778	342134	118	0.00025	NE	0	NE	0	NE
M5005_Spy_0339c	exoA	342208	343119	303	0.05625	U	0	NE	0	NE
M5005_Spy_0340	lctO	343269	344450	393	0	NE	0	NE	0	NE
M5005_Spy_0341	prtS	344713	349656	1647	0	NE	0	NE	0	NE
M5005_Spy_0343	-	350145	350324	59	0.01475	NE	0.00025	NE	0.017	NE
M5005_Spy_0344	_	350427	351134	235	0.01173	NE	0	NE	0	NE
M5005_Spy_0345	metG	351377	353374	665	1	E	1	E	1	E
M5005_Spy_0346	-		353872	55	-1	S	-1	S	-1	S
	- nrdF	353705								
M5005_Spy_0347		353869	354882	337	0	NE	0	NE	0	NE
M5005_Spy_0348	nrdI	354886	355374	162	0	NE	0	NE	0	NE
M5005_Spy_0349	nrdE.1	355341	357521	726	0	NE	0	NE	0	NE
M5005_Spy_0350	-	357500	357718	72	-1	S	-1	S	-1	S
M5005_Spy_0351c	spyA	357724	358476	250	0	NE	0	NE	0	NE
M5005_Spy_0352	-	358935	359471	178	0	NE	0	NE	0	NE
M5005_Spy_0353	-	359613	359996	127	0.00025	NE	0	NE	0	NE
M5005_Spy_0354c	-	360090	360722	210	0	NE	0	NE	0	NE
M5005_Spy_0355	-	361401	361721	106	0	NE	0	NE	0	NE
M5005_Spy_0356c	speJ	362034	362732	232	0	NE	0	NE	0	NE
M5005_Spy_0357c	-	362980	363594	204	0.00025	NE	0	NE	0	NE
M5005_Spy_0358	-	363955	364191	78	0	NE	0	NE	0	NE
M5005_Spy_0359	fabG	364175	364882	235	0	NE	0	NE	0	NE
M5005_Spy_0360	-	364928	365917	329	0	NE	0	NE	0	NE
M5005_Spy_0361	glpT	366250	367587	445	0	NE	0	NE	0	NE
M5005_Spy_0362	glmU	367760	369142	460	1	E	1	E	1	E
M5005_Spy_0363	_	369173	369727	184	0.00025	NE	0	NE	0	NE
M5005_Spy_0364	_	369727	369978	83	0.00025	U	0	NE	0	NE
M5005_Spy_0365	pfs	369998	370693	231	0.07723	NE		E	1	E
M5005_Spy_0366	p13 _	370844					1			
	- mtaD		371185	113	0	NE	0	NE	0	NE
M5005_Spy_0367c	mtsR	371286	371933	215	0	NE	0	NE	0.235	U
M5005_Spy_0368	mtsA	372091	373011	306	0	NE	0	NE	0	NE
M5005_Spy_0369	mtsB	373075	373800	241	0	NE	0	NE	0	NE
M5005_Spy_0370	mtsC	373801	374655	284	0	NE	0	NE	0	NE
M5005_Spy_0371c	сурВ	374803	375609	268	0	NE	0	NE	0	NE
M5005_Spy_0372	ftsK	375826	378231	801	1	E	1	Е	1	E
M5005_Spy_0373c	-	378301	378654	117	0	NE	0	NE	0	NE
M5005_Spy_0374	rplK	378898	379323	141	0.9995	Ε	1	Е	0.926	U
M5005_Spy_0375	rplA	379429	380118	229	0.9995	E	1	Е	1	Ε
M5005_Spy_0376	-	380469	381602	377	0	NE	0	NE	0	NE
M5005_Spy_0377	pyrH	381767	381937	56	1	E	1	E	1	E
,	. ,	,		50	_	_	_	_	-	_

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M5005_Spy_0380	frr	382524	383081	185	0.9895	U	1	E	0.997	E
M5005_Spy_0381	-	383190	384047	285	0.00025	NE	0	NE	0	NE
M5005_Spy_0382	msrA.2	384120	384629	169	0	NE	0	NE	0	NE
M5005_Spy_0383	-	384626	384841	71	0	NE	0	NE	0	NE
M5005_Spy_0384	-	384997	386166	389	0	NE	0	NE	0	NE
M5005_Spy_0385	-	386441	388252	603	0	NE	0	NE	0	NE
M5005_Spy_0386	phoH	388411	389463	350	0	NE	0	NE	0	NE
M5005_Spy_0387	-	389509	390084	191	0	NE	0	NE	0	NE
M5005_Spy_0388	-	390192	390740	182	0.00025	NE	0.999	E	1	Е
M5005_Spy_0389	dgk	390721	391128	135	0.0265	NE	1	E	1	E
M5005_Spy_0390	era	391248	392144	298	0.6295	U	0.469	U	1	E
M5005_Spy_0391	-	392128	392640	170	0	NE	0	NE	0	NE
M5005_Spy_0392c	-	392945	393199	84	0	NE	0	NE	0	NE
M5005_Spy_0393	-	393597	393842	81	0	NE	0	NE	0	NE
M5005_Spy_0394	-	393857	394039	60	0	NE	0	NE	0	NE
M5005_Spy_0395c	-	394230	394409	59	0	NE	0	NE	0	NE
M5005_Spy_0396c	-	394348	394497	49	-1	S	-1	S	-1	S
M5005_Spy_0397c	-	394494	394916	140	0	NE	0	NE	0	NE
M5005_Spy_0398	-	395189	395398	69	0	NE	0	NE	0	NE
M5005_Spy_0399	-	395463	395663	66	0	NE	0	NE	0	NE
M5005_Spy_0400	silD	395957	396151	64	0	NE	0	NE	0	NE
M5005_Spy_0401c	-	396344	396460	38	-1	S	-1	S	-1	S
M5005_Spy_0402	-	396644	397639	331	0	NE	0	NE	0	NE
M5005_Spy_0403	-	397684	398130	148	0	NE	0	NE	0	NE
M5005_Spy_0404c	-	398478	398747	89	0	NE	0	NE	0	NE
M5005_Spy_0405	-	398948	399055	35	-1	S	-1	S	-1	S
M5005_Spy_0406c	-	399269	399511	80	0	NE	0	NE	0	NE
M5005_Spy_0407	mutR	399818	400684	288	0	NE	0	NE	0	NE
M5005_Spy_0408	fpg	400856	401683	275	0	NE	0	NE	0	NE
M5005_Spy_0409	coaE	401593	402273	226	1	Е	1	Ε	1	Ε
M5005_Spy_0410	-	402463	403965	500	0	NE	0	NE	0	NE
M5005_Spy_0411	-	404087	405280	397	0	NE	0	NE	0	NE
M5005_Spy_0412	rpmG	405277	405423	48	-1	S	-1	S	-1	S
M5005_Spy_0413	secG	405469	405705	78	0.9975	Е	1	Ε	1	Ε
M5005_Spy_0414	-	405802	408132	776	0	NE	0	NE	0	NE
M5005_Spy_0415	smpB	408135	408602	155	0.00025	NE	0	NE	0.262	U
M5005_Spy_0416	-	408617	409327	236	0	NE	0	NE	0	NE
M5005_Spy_0417c	рср	409443	410090	215	0	NE	0	NE	0	NE
M5005_Spy_0418c	-	410140	411066	308	0	NE	0	NE	0	NE
M5005_Spy_0419c	-	411066	411749	227	0.00025	NE	0	NE	0.001	NE
M5005_Spy_0420c	-	411960	412886	308	0	NE	0	NE	0	NE
M5005_Spy_0421c	gloA	413031	413408	125	0.00025	NE	0	NE	0	NE
M5005_Spy_0422c	-	413419	414084	221	0	NE	0	NE	0	NE
M5005_Spy_0423c	pepQ	414133	415218	361	0.00225	NE	0	NE	0	NE
M5005_Spy_0424	ссрА	415392	416393	333	0.99075	U	0.00025	NE	0.075	U
M5005_Spy_0425	-	416524	417522	332	0.00025	NE	0.5615	U	1	Ε
M5005_Spy_0426	-	417524	418858	444	0.98575	U	1	E	1	E
M5005_Spy_0427	thrS	419280	421223	647	1	E	1	E	1	E
M5005_Spy_0428	drrA/tagH	421364	422356	330	0	NE	0	NE	0	NE
M5005_Spy_0429	-	422358	423176	272	0	NE	0	NE	0	NE
M5005_Spy_0430	-	423178	423963	261	0	NE	0	NE	0	NE
M5005_Spy_0431	-	424164	424313	49	-1	S	-1	S	-1	S
M5005_Spy_0432	-	424708	425856	382	0	NE	0	NE	0	NE
M5005_Spy_0433	-	425813	427060	415	0	NE	0	NE	0	NE
M5005_Spy_0434	-	427116	428150	344	0	NE	0	NE	0	NE
M5005_Spy_0435	vicR	428312	429022	236	1	E	0.99975	E	1	Ε
M5005_Spy_0436	vicK	429015	430367	450	0.00025	NE	0	NE	0.001	NE
M5005_Spy_0437	vicX	430371	431180	269	0	NE	0	NE	0	NE
M5005_Spy_0438	rnc	431624	432316	230	0.00025	NE	0	NE	1	Ε
M5005_Spy_0439	smc	432317	435856	1179	0	NE	0	NE	0	NE
M5005_Spy_0440c	-	436109	436960	283	0	NE	0	NE	0	NE
M5005_Spy_0441	aroE	437234	438106	290	0	NE	0	NE	0	NE
M5005_Spy_0442	-	438205	438939	244	0	NE	0	NE	0.001	NE

ME00E C 0442		420044	420675	244	•		•		0	
M5005_Spy_0443	-	438941	439675	244	0	NE	0	NE	0	NE
M5005_Spy_0444	-	439668	440654	328	0	NE	0	NE	0	NE
M5005_Spy_0445	metK1	440664	441863	399	0	NE	0	NE	0	NE
M5005_Spy_0446	-	441847	442815	322	0.00025	NE	0	NE	0	NE
M5005_Spy_0447	-	442870	443859	329	0	NE	0	NE	0	NE
M5005_Spy_0448	-	444385	444528	47	-1	S	-1	S	-1	S
M5005_Spy_0449	hasB.2	444552	445709	385	0.00025	NE	0	NE	0	NE
M5005_Spy_0450	mefE	445794	447002	402	0	NE	0	NE	0	NE
M5005_Spy_0451c	-	447105	447314	69	0	NE	0	NE	0	NE
M5005_Spy_0452c	-	447304	448149	281	0	NE	0	NE	0	NE
M5005_Spy_0453c	-	448234	448962	242	0	NE	0	NE	0	NE
M5005_Spy_0454c	-	448953	449177	74	0.00025	NE	0	NE	0	NE
M5005_Spy_0455c	-	449177	450271	364	0	NE	0	NE	0	NE
M5005_Spy_0456	-	450317	450619	100	0.07525	U	0.00025	NE	0.606	U
M5005_Spy_0457	-	450619	450924	101	0	NE	0	NE	0	NE
M5005_Spy_0458	-	450943	451215	90	0	NE	0	NE	0	NE
M5005_Spy_0459	-	451320	451772	150	0.00025	NE	0	NE	0	NE
M5005_Spy_0460	-	451838	452152	104	0	NE	0	NE	0	NE
M5005_Spy_0461	_	452569	452907	112	0.00025	NE	0	NE	0	NE
M5005_Spy_0462	_	452931	453755	274	0.00023	NE	0	NE	0	NE
M5005_Spy_0463	-	453769	455016	415	0	NE	0	NE	0	NE
M5005_Spy_0464	mccF	455244	455960	238	0	NE	0	NE	0	NE
M5005_Spy_0465	-	455973	456173	66	0.017	NE	0	NE	0	NE
M5005_Spy_0466	-	456293	457192	299	0	NE	0	NE	0	NE
M5005_Spy_0467c	-	457645	458358	237	0	NE	0	NE	0	NE
M5005_Spy_0468c	-	458406	458681	91	0.00825	NE	0	NE	0	NE
M5005_Spy_0469	-	458701	458919	72	0.00025	NE	0	NE	0	NE
M5005_Spy_0470	-	458986	459783	265	0	NE	0	NE	0	NE
M5005_Spy_0471	_	459787	460611	274	0	NE	0	NE	0	NE
M5005_Spy_0472	ftsY	460611	462161	516	0.99775	E	1	E	1	E
M5005_Spy_0472	-			455		NE	0	NE	0	
		462215	463582		0					NE
M5005_Spy_0474	licT/bglG	463910	464752	280	0	NE	0	NE	0	NE
M5005_Spy_0475	-	464916	466616	566	0	NE	0	NE	0	NE
M5005_Spy_0476	bglA	466635	468059	474	0	NE	0	NE	0	NE
M5005_Spy_0477c	-	468158	468973	271	0	NE	0	NE	0	NE
M5005_Spy_0478c	-	468973	469875	300	0	NE	0	NE	0	NE
M5005_Spy_0479	-	470009	470206	65	0	NE	0	NE	0	NE
M5005_Spy_0480	-	470304	470432	42	0	NE	0	NE	0.001	NE
M5005_Spy_0481c	-	470412	472544	710	-1	S	-1	S	-1	S
M5005_Spy_0482	_	472486	472968	160	0	NE	0	NE	0	NE
M5005_Spy_0483	_	473032	473304	90	0	NE	0	NE	0	NE
M5005_Spy_0484	ptsK	473609	474601	330	0.012	NE	1	E	1	E
	•									
M5005_Spy_0485	lgt	474598	475377	259	0.00025	NE	0	NE	0	NE
M5005_Spy_0486	-	475399	475806	135	0	NE	0	NE	0	NE
M5005_Spy_0487	-	475799	476227	142	0	NE	0	NE	0	NE
M5005_Spy_0488c	-	476386	476670	94	0.00025	NE	0	NE	0.001	NE
M5005_Spy_0489	-	476869	477237	122	0	NE	0	NE	0	NE
M5005_Spy_0491	-	477887	479173	428	0	NE	0	NE	0	NE
M5005_Spy_0492c	-	479186	479314	42	-1	S	-1	S	-1	S
M5005_Spy_0493	-	479383	479595	70	0	NE	0	NE	0	NE
M5005_Spy_0494c	-	479692	479832	46	-1	S	-1	S	-1	S
M5005_Spy_0495c	lysS	479968	481461	497	1	E	1	E	1	E
M5005_Spy_0496	-	481635	482537	300	0.00025	NE	0	NE	0	NE
M5005_Spy_0497c	_	482645	483268	207	0.00023	NE	0	NE	0	NE
M5005_Spy_0498c	-	483609	484088	159	0	NE	0	NE	0	NE
M5005_Spy_0499c	-	484179	484742	187	0	NE	0	NE	0	NE
M5005_Spy_0500c	-	485011	485859	282	0.00025	NE	0	NE	1	E
M5005_Spy_0501	-	486184	486687	167	0	NE	0	NE	0	NE
M5005_Spy_0502	-	486671	487057	128	0.00025	NE	0	NE	0	NE
M5005_Spy_0503c	-	487103	487582	159	0	NE	0	NE	0	NE
M5005_Spy_0504c	pepF	487575	489374	599	0	NE	0	NE	0	NE
M5005_Spy_0505	ррс	489518	492331	937	0	NE	0	NE	0	NE
M5005_Spy_0506	ftsW	492501	493775	424	1	E	1	E	1	E
,					_	_	_	_	_	

M5005_Spy_0507c	-	493792	493932	46	-1	S	-1	S	-1	S
M5005_Spy_0508	tuf	494129	495325	398	1	E	1	Е	1	Ε
M5005_Spy_0509	tpiA	495566	496324	252	0.97425	U	0.98925	U	1	Е
M5005_Spy_0510c	murN	496423	497658	411	1	E	1	E	1	E
M5005_Spy_0511c	murM	497645	498871	408	1	E	1	E	1	E
M5005_Spy_0512c	-	498871	499680	269	0	NE	0	NE	0	NE
M5005_Spy_0513c	-	499831	500064	77	0	NE	0.84975	U	0.584	U
M5005_Spy_0514c	-	500136	501437	433	0	NE	0	NE	0	NE
M5005_Spy_0515	_	501519	501905	128	0	NE	0	NE	0	NE
M5005_Spy_0516	pacL	502136	504817	893	1	E	1	E	1	E
	•									
M5005_Spy_0517c	regR	504901	505896	331	0	NE	0	NE	0	NE
M5005_Spy_0518c		505960	507867	635	0	NE	0	NE	0	NE
M5005_Spy_0519c	agaD	507954	508775	273	0	NE	0	NE	0	NE
M5005_Spy_0520c	agaW	508762	509544	260	0	NE	0	NE	0	NE
M5005_Spy_0521c	agaV	509563	510051	162	0.00025	NE	0	NE	0	NE
M5005_Spy_0522c	ugl	510087	511286	399	0.00025	NE	0	NE	0.001	NE
M5005_Spy_0523	- -	511353	511288	176	0.00023	NE	0	NE	0.001	NE
M5005_Spy_0524	idnO	512059	512853	264	0	NE	0	NE	0	NE
M5005_Spy_0525	-	512878	513519	213	0	NE	0	NE	0	NE
M5005_Spy_0526	kdgK	513548	514549	333	0	NE	0	NE	0	NE
M5005_Spy_0527	kgdA	514554	515189	211	0	NE	0	NE	0	NE
M5005_Spy_0528	-	515485	516135	216	0	NE	0	NE	0.001	NE
M5005_Spy_0529	_	516776	517951	391	0.00025	NE	0	NE	0	NE
M5005_Spy_0530	prfB	518105	519118	337	0.02825	NE	1	E	1	E
M5005_Spy_0531	ftsE	519137	519829	230	0.00025	NE	0.974	U	0.091	U
M5005_Spy_0532	ftsX	519822	520751	309	0.0005	NE	0.985	U	1	E
M5005_Spy_0533c	-	521061	521696	211	0.00025	NE	0	NE	0	NE
M5005_Spy_0534	-	521927	522541	204	0	NE	0	NE	0	NE
M5005_Spy_0535	_	522545	522691	48	-1	S	-1	S	-1	S
	dinG									
M5005_Spy_0536		522841	525300	819	0	NE	0	NE	0	NE
M5005_Spy_0537	aspC	525635	526828	397	0.00025	NE	0	NE	0	NE
M5005_Spy_0538	asnC	526849	528195	448	1	E	1	E	1	E
M5005_Spy_0539	-	528609	529499	296	0.00025	NE	0	NE	0.001	NE
M5005_Spy_0540	-	529496	530473	325	0	NE	0	NE	0	NE
M5005_Spy_0541	-	530470	531381	303	0.00025	NE	0	NE	0.01	NE
M5005_Spy_0542	pepD	531514	532911	465	0.00023	NE	0	NE	0	NE
	adcA									
M5005_Spy_0543		533063	534610	515	0	NE	0	NE	0	NE
M5005_Spy_0544	-	534758	535480	240	0	NE	0	NE	0	NE
M5005_Spy_0545	agaS	535499	536698	399	0	NE	0	NE	0	NE
M5005_Spy_0546c	rpmE2	536795	537055	86	0.9685	U	0	NE	0.998	E
M5005_Spy_0547c	-	537170	538111	313	0.00025	NE	0.00225	NE	0.757	U
M5005_Spy_0548	flaV	538505	538954	149	0.0005	NE	0	NE	1	Ε
M5005_Spy_0549	-	539130	539414	94	0	NE	0	NE	0	NE
M5005_Spy_0550	-	539407	540669	420	0	NE	0	NE	0.001	NE
M5005_Spy_0551	rplS	540784	541131	115	0.822	U	1	E	0.985	U
M5005_Spy_0552	-	542134	542703	189	0.002	NE	0	NE	0.001	NE
M5005_Spy_0553	gyrB	542704	544656	650	1	E	1	Ε	1	E
M5005_Spy_0554	ezrA	545024	546748	574	0.9785	U	1	Ε	1	Е
M5005_Spy_0555c	-	546880	547338	152	0	NE	0	NE	0	NE
M5005_Spy_0556	eno	547565	548872	435	1	E	1	E	1	E
	-									
M5005_Spy_0557c	-	549398	549988	196	0	NE	0	NE	0	NE
M5005_Spy_0558c	-	550037	550288	83	0	NE	0	NE	0	NE
M5005_Spy_0559c	-	550650	551306	218	0	NE	0	NE	0	NE
M5005_Spy_0560c	-	551303	552190	295	0.00025	NE	0	NE	0	NE
M5005_Spy_0561	epf	552662	558841	2059	0	NE	0	NE	0	NE
M5005_Spy_0562	sagA	559706	559867	53	0	NE	0	NE	0	NE
M5005_Spy_0563	sagB									
		560089	561039	316	0	NE	0	NE	0	NE
M5005_Spy_0564	sagC	561036	562094	352	0	NE	0	NE	0	NE
M5005_Spy_0565	sagD	562114	563472	452	0	NE	0	NE	0	NE
M5005_Spy_0566	sagE	563447	564118	223	0	NE	0	NE	0	NE
M5005_Spy_0567	sagF	564115	564798	227	0	NE	0	NE	0	NE
M5005_Spy_0568	sagG	564821	565744	307	0.00025	NE	0	NE	0.003	NE
M5005_Spy_0569	sagH	565753	566880	375	0.00025	NE	0	NE	0.001	NE
	3	555755	223000	3,3	J.550 L 5		J		0.001	

M5005_Spy_0570	sagI	566877	567995	372	0	NE	0	NE	0.001	NE
M5005_Spy_0571	-	568566	571298	910	0.00025	NE	0	NE	0	NE
M5005_Spy_0572	-	571576	572076	166	0	NE	0	NE	0	NE
M5005_Spy_0573	ligA	572270	574228	652	1	Ε	1	E	1	Е
M5005_Spy_0574	-	574242	575264	340	1	Ε	1	E	1	Ε
M5005_Spy_0575	atpE	575657	575854	65	0.88075	U	0.02675	NE	0.989	U
M5005_Spy_0576	atpB	575889	576605	238	1	Ε	1	Ε	0.007	NE
M5005_Spy_0577	atpF	576623	577117	164	0.108	U	1	Ε	1	Ε
M5005_Spy_0578	atpH	577117	577653	178	1	Ε	1	Ε	1	Е
M5005_Spy_0579	atpA	577669	579177	502	1	Е	1	Е	1	Е
M5005_Spy_0580	atpG	579193	580068	291	0.9815	Ū	1	E	1	E
M5005_Spy_0581	atpD	580230	581636	468	1	E	1	E	1	E
M5005_Spy_0582	atpC	581649	582065	138	0.4415	U	0.80875	Ū	0.991	Ū
M5005_Spy_0583	- -	582331	582588	85	0.4413	NE	0.80873	NE	0.991	NE
M5005_Spy_0584	murA	582815	583924	369	0	NE	0	NE	0	NE
M5005_Spy_0585	epuA	583928	584116	62	0	NE	0	NE	0	NE
M5005_Spy_0586	endA	584152	584691	179	0	NE	0	NE	0	NE
M5005_Spy_0587	pheS	584974	586017	347	1	Е	1	E	1	E
M5005_Spy_0588	pheT	586212	588632	806	1	E	1	E	1	E
M5005_Spy_0589	-	588742	589119	125	0	NE	0	NE	0	NE
M5005_Spy_0590	-	589112	589498	128	0	NE	0	NE	0	NE
M5005_Spy_0591	-	589571	590647	358	0	NE	0	NE	0	NE
M5005_Spy_0592	-	590657	591325	222	0	NE	0	NE	0	NE
M5005_Spy_0593c	-	591427	592344	305	0	NE	0	NE	0	NE
M5005_Spy_0594	rexB	592495	595710	1071	0.82275	U	0	NE	0.818	U
M5005_Spy_0595	rexA	595671	599339	1222	0.00025	NE	0	NE	1	Е
M5005_Spy_0596	_	599479	600291	270	0	NE	0	NE	0	NE
M5005_Spy_0597	rpsU	600432	600608	58	0.99425	U	1	E	1	E
M5005_Spy_0598c	mscL	600736	601098	120	0	NE	0	NE	0	NE
M5005_Spy_0599	dnaG	601229	603043	604	1	E	1	E	1	E
M5005_Spy_0600	rpoD		604161	369	1	E	1	E	1	E
	- -	603052								
M5005_Spy_0601		604397	604735	112	0	NE	0	NE	0	NE
M5005_Spy_0602	rmlD	604873	605727	284	1	E	1	E	0.999	E
M5005_Spy_0603	rgpAc	605846	607000	384	0.0005	NE	1	E	1	E
M5005_Spy_0604	rgpBc	606990	607922	310	0.942	U	1	E	1	E
M5005_Spy_0605	rgpCc	607925	608728	267	0.99925	E	1	E	1	E
M5005_Spy_0606	rgpDc	608728	609933	401	0.9975	E	0.999	E	1	E
M5005_Spy_0607	rgpEc	609958	610965	335	1	E	1	E	1	Ε
M5005_Spy_0608	rgpFc	610962	612707	581	1	E	1	E	1	E
M5005_Spy_0609	-	612704	615178	824	0.00025	NE	0	NE	0	NE
M5005_Spy_0610	-	615357	616052	231	0	NE	0	NE	0	NE
M5005_Spy_0611	-	616054	616395	113	0	NE	0	NE	0	NE
M5005_Spy_0612	amrA	616388	617674	428	0.00025	NE	0.00025	NE	1	Ε
M5005_Spy_0613	-	617655	619151	498	0.00025	NE	1	Ε	1	Ε
M5005_Spy_0614	рерТ	619245	620468	407	0	NE	0	NE	0	NE
M5005_Spy_0615	ebsA	620509	620997	162	0	NE	0	NE	0	NE
M5005_Spy_0616c	-	620984	621181	65	0	NE	0	NE	0	NE
M5005_Spy_0617	_	621230	621706	158	0.00025	NE	0	NE	0.302	U
M5005_Spy_0618	cmk	621721	622401	226	0.0005	NE	0.98775	U	0.997	E
M5005_Spy_0619	infC	622563	623093	176	0.995	U	0.99175	U	1	E
M5005_Spy_0620	rpmI	623135	623332	65	0.0065	NE	0.00925	NE	0.995	E
M5005_Spy_0621	rplT			119	0.0003					
		623391	623750			NE	0.99975	E	0.008	NE
M5005_Spy_0622c		624041	626212	723	1	E	1	E	1	E
M5005_Spy_0623	-	626359	627522	387	0	NE	0	NE	0	NE
M5005_Spy_0624	aroD	627519	628205	228	0	NE	0	NE	0	NE
M5005_Spy_0625	aroF	628299	629465	388	0	NE	0	NE	0	NE
M5005_Spy_0626	-	629526	629867	113	0.00025	NE	0	NE	0	NE
M5005_Spy_0627	gor	630088	631440	450	0	NE	0	NE	0	NE
M5005_Spy_0628c	folC.2	631528	632796	422	0	NE	0	NE	0	NE
M5005_Spy_0629c	-	632826	633266	146	0	NE	0	NE	0	NE
M5005_Spy_0630	nifS1	633501	634643	380	0	NE	0	NE	0	NE
M5005_Spy_0631	thiI	634655	635869	404	0	NE	0	NE	0	NE
M5005_Spy_0632	capA	635907	637199	430	0	NE	0	NE	0	NE

M5005_Spy_0633	rplU	637413	637727	104	0.00025	NE	0.62425	U	0.081	U
M5005_Spy_0634	-	637739	638065	108	0.58675	U	0.0325	NE	0.002	NE
M5005_Spy_0635	rpmA	638093	638386	97	0.99825	E	0.029	NE	0.003	NE
M5005_Spy_0636	-	638734	639648	304	0.00025	NE	0	NE	0	NE
M5005_Spy_0637	lsp	639645	640103	152	0	NE	0	NE	0	NE
M5005_Spy_0638	-	640093	640983	296	0	NE	0	NE	0	NE
M5005_Spy_0639	pyrR	641379	641900	173	0.00025	NE	0	NE	0	NE
M5005_Spy_0640	pyrP	641916	643175	419	0.00025	NE	0	NE	0	NE
M5005_Spy_0641	pyrB	643236	644171	311	0.00275	NE	0	NE	0	NE
M5005_Spy_0642	carA	644215	645297	360	0	NE	0	NE	0	NE
M5005_Spy_0643	carB	645523	648699	1058	0.00025	NE	0	NE	0	NE
M5005_Spy_0644	-	648999	650177	392	0	NE	0	NE	0	NE
M5005_Spy_0645	_	650177	650887	236	0	NE	0	NE	0	NE
M5005_Spy_0646	_	650899	652119	406	0	NE	0	NE	0	NE
M5005_Spy_0647	_	652373	654106	577	0	NE	0	NE	0	NE
M5005_Spy_0648	rpsP	654233	654505	90	0.00025	NE	0.00025	NE	0.001	NE
M5005_Spy_0649	1 p31	654515	654754	79	0.00023	NE	0.00023	NE	0.001	NE
M5005_Spy_0650	_	654763	654870	35	-1	S	-1	S	-1	S
M5005_Spy_0651		655665	658691	1008	0	NE	-1	NE	0	NE
	-									
M5005_Spy_0652	- D	658711	659112	133	0	NE	0	NE	0	NE
M5005_Spy_0653c	czcD	659292	660167	291	0.00025	NE	0	NE	0	NE
M5005_Spy_0654	-	660303	660824	173	0	NE	0	NE	0	NE
M5005_Spy_0655	rimM	661039	661557	172	0	NE	0.00225	NE	0.027	NE
M5005_Spy_0656	trmD	661547	662278	243	0.9995	Е	1	E	1	E
M5005_Spy_0657	trxB	662278	663270	330	0.00025	NE	0	NE	0	NE
M5005_Spy_0658	-	663448	664506	352	0	NE	0	NE	0	NE
M5005_Spy_0659	apbA	664519	665442	307	0	NE	0	NE	0	NE
M5005_Spy_0660	fruR	665698	666411	237	0	NE	0	NE	0	NE
M5005_Spy_0661	fruB	666408	667319	303	0	NE	0	NE	0.001	NE
M5005_Spy_0662	fruA	667316	669262	648	0.00025	NE	0	NE	0	NE
M5005_Spy_0663	mur1.1	669361	669954	197	0	NE	0	NE	0.001	NE
M5005_Spy_0664	mur1.2	670106	670813	235	0	NE	0	NE	0	NE
M5005_Spy_0665c	-	670870	671088	72	0	NE	0	NE	0	NE
M5005_Spy_0666c	-	671291	671410	39	-1	S	-1	S	-1	S
M5005_Spy_0667c	-	671385	671594	69	-1	S	-1	S	-1	S
M5005_Spy_0668c	mac	671769	672788	339	0	NE	0	NE	0	NE
M5005_Spy_0669	-	672944	673063	39	-1	S	-1	S	-1	S
M5005_Spy_0670	-	673287	673463	58	0	NE	0	NE	0	NE
M5005_Spy_0671	-	673691	674071	126	0	NE	0	NE	0.001	NE
M5005_Spy_0672	-	674071	674919	282	0	NE	0	NE	0	NE
M5005_Spy_0673	papS	675044	676252	402	1	Е	1	Ε	1	Е
M5005_Spy_0674		676249	678126	625	0.00975	NE	0	NE	0	NE
M5005_Spy_0675	-	678383	678535	50	-1	S	-1	S	-1	S
M5005_Spy_0676	_	678544	678762	72	0	NE	0	NE	0	NE
M5005_Spy_0677	fms	679018	679428	136	0	NE	0	NE	0	NE
M5005_Spy_0678c	-	679510	681522	670	0	NE	0	NE	0	NE
M5005_Spy_0679	_	681742	682392	216	0.00025	NE	0	NE	0.001	NE
M5005_Spy_0680	_	682395	683063	222	0	NE	0	NE	0.001	NE
M5005_Spy_0681	_	683072	684304	410	0	NE	0	NE	0	NE
M5005_Spy_0682	mvaK1	684583	685476	297	0.9995	E	1	E	0.999	E
M5005_Spy_0683	mvaD	685458	686402	314	0.77975	U	1	E	1	E
M5005_Spy_0684	mvaK2	686395	687402	335			0.97825	U	1	E
M5005_Spy_0685	iiivaitz				0.99975	E				
	-	687395	688384	329	0.99975	E	1	E	1	E
M5005_Spy_0686c		688614	689891	425	0.07925	U	0.001	NE	1	E
M5005_Spy_0687c	mvaS.1	689878	691053	391	0.998	E	1	E	1	E
M5005_Spy_0688	thyA	691262	692101	279	0	NE	0.99925	E	0.8	U
M5005_Spy_0689	dyr	692181	692678	165	0.99975	E	1	E	1	E
M5005_Spy_0690	-	692698	692868	56	0	NE	0	NE	0	NE
M5005_Spy_0691	clpX	692998	694227	409	0.00025	NE	0	NE	0.001	NE
M5005_Spy_0692	engB	694237	694836	199	0.97325	U	1	E	1	E
M5005_Spy_0693	-	694984	695727	247	0	NE	0	NE	0	NE
M5005_Spy_0694c	clpL	695785	697884	699	0	NE	0	NE	0.001	NE
M5005_Spy_0695	rpiA	698263	698946	227	0.00025	NE	0.00025	NE	1	E

M5005_Spy_0696	deoB	699023	700234	403	0	NE	0	NE	0	NE
M5005_Spy_0697	arsC	700253	700693	146	0	NE	0	NE	0	NE
M5005_Spy_0698	punA	700677	701486	269	0	NE	0	NE	0.069	U
M5005_Spy_0699	deoD	702149	702862	237	0	NE	0.004	NE	0.012	NE
M5005_Spy_0700	cpsX	702855	703643	262	0	NE	0	NE	0	NE
M5005_Spy_0701c	cpsY	703722	704576	284	0	NE	0	NE	0	NE
M5005_Spy_0702	-	704849	705385	178	0	NE	0	NE	0.001	NE
M5005_Spy_0703	pyrF	705662	706354	230	0	NE	0	NE	0	NE
M5005_Spy_0704	pyrE	706412	707041	209	0	NE	0	NE	0	NE
M5005_Spy_0705	amiC	707238	708692	484	0	NE	0	NE	0	NE
M5005_Spy_0706	-	708810	709673	287	0	NE	0	NE	0	NE
M5005_Spy_0707	_	709702	710352	216	0	NE	0	NE	0	NE
M5005_Spy_0708	ung	710485	710332	217	0	NE	0	NE	0	NE
M5005_Spy_0709	pyrC	710483	711138	422	0.0005	NE	0	NE	0	NE
M5005_Spy_0705	ругс		712336	213	0.0003	U	1	E	1	E
	norE	712596								
M5005_Spy_0711	parE	713372	715321	649	0.981	U	1	E	1	E
M5005_Spy_0712	parC	715412	717871	819	1	E	1	E	1	E
M5005_Spy_0713	bcaT	717994	719016	340	0	NE	0	NE	0	NE
M5005_Spy_0714	-	719080	719310	76	0	NE	0	NE	0.077	U
M5005_Spy_0715	rpsA	719701	720906	401	0.838	U	1	E	1	E
M5005_Spy_0716c	-	721453	721755	100	0	NE	0	NE	0	NE
M5005_Spy_0717	-	721954	722940	328	0	NE	0	NE	0	NE
M5005_Spy_0718	-	723011	723202	63	0.0015	NE	0	NE	0	NE
M5005_Spy_0719	-	723251	723670	139	0	NE	0	NE	0	NE
M5005_Spy_0720	-	723907	724815	302	0	NE	0	NE	0	NE
M5005_Spy_0721c	-	724933	725109	58	0.91575	U	0.97825	U	0.971	U
M5005_Spy_0722	miaA	725243	726142	299	0	NE	0	NE	0	NE
M5005_Spy_0723	hflX	726215	727453	412	0.00025	NE	0	NE	0	NE
M5005_Spy_0724	_	727446	728081	211	0	NE	0	NE	0	NE
M5005_Spy_0725	elaC	728096	729025	309	0.98775	U	1	E	0.999	E
M5005_Spy_0726	-	729025	729789	254	0.38773	NE	0	NE	0.999	NE
M5005_Spy_0720 M5005_Spy_0727	recJ		731996		0		0		0	
		729786		736		NE		NE		NE
M5005_Spy_0728	apt	732147	732665	172	0	NE	0	NE	0	NE
M5005_Spy_0729	dnaD	732746	733429	227	0.98725	U	0.41925	U	0.001	NE
M5005_Spy_0730	nth	733426	734082	218	0	NE	0	NE	0	NE
M5005_Spy_0731	-	734154	734738	194	0.9245	U	1	Е	1	E
M5005_Spy_0732	-	734829	735617	262	0	NE	0	NE	0	NE
M5005_Spy_0733	-	735657	736763	368	0	NE	0	NE	0	NE
M5005_Spy_0734	cpsFO/rmIA	736821	737690	289	0.22075	U	1	E	1	E
M5005_Spy_0735	cpsFP/rmIC	737690	738283	197	0.95275	U	1	E	0.001	NE
M5005_Spy_0736	cpsFQ/rmIB	738527	739567	346	0.9995	E	1	E	1	Ε
M5005_Spy_0737	mutX	739788	740264	158	0	NE	0	NE	0	NE
M5005_Spy_0738	-	740322	741503	393	0	NE	0	NE	0	NE
M5005_Spy_0739	-	741493	742740	415	0	NE	0	NE	0	NE
M5005_Spy_0740c	fbp	742799	744085	428	0	NE	0	NE	0.001	NE
M5005_Spy_0742	-	744497	744622	41	-1	S	-1	S	-1	S
M5005_Spy_0743	-	744804	745802	332	0.00025	NE	0	NE	0	NE
M5005_Spy_0744	_	745792	745971	59	-1	S	-1	S	-1	S
M5005_Spy_0745	_	746148	747017	289	0	NE	0	NE	0	NE
M5005_Spy_0746	_	747014	747772	252	0	NE	0	NE	0	NE
M5005_Spy_0740										
	-	747976	749637	553	0.011	NE	1	E	1	E
M5005_Spy_0748	estA	749770	750555	261	0	NE	0	NE	0	NE
M5005_Spy_0749	-	750585	750911	108	0	NE	0	NE	0	NE
M5005_Spy_0750	-	750957	752864	635	0	NE	0	NE	0	NE
M5005_Spy_0751	acoA	753149	754117	322	0	NE	0	NE	0	NE
M5005_Spy_0752	acoB	754173	755174	333	0	NE	0	NE	0	NE
M5005_Spy_0753	acoC	755359	756768	469	0	NE	0	NE	0	NE
M5005_Spy_0754c	-	756823	757062	79	0.0005	NE	0	NE	0	NE
M5005_Spy_0755	acoL	757095	758858	587	0.0005	NE	0	NE	0	NE
M5005_Spy_0756c	-	758874	759086	70	0	NE	0	NE	0	NE
M5005_Spy_0757c	hylA	759532	761949	805	0.00025	NE	0	NE	0	NE
M5005_Spy_0758	lplB	762182	763171	329	0	NE	0	NE	0	NE
M5005_Spy_0759c	cobQ	763280	764071	263	0.95425	U	1	E	1	E
		. 33200		203	0.55 125	•	-	_	-	-

M5005_Spy_0760c	murC2	764071	765414	447	0.999	E	1	E	1	E
M5005_Spy_0761	-	765521	766372	283	1	E	1	E	1	Ε
M5005_Spy_0762	-	766369	767325	318	0	NE	0	NE	0	NE
M5005_Spy_0763	glmM	767379	768734	451	0.99775	Е	1	Ε	1	Е
M5005_Spy_0764	-	768868	769509	213	0	NE	0	NE	0	NE
M5005_Spy_0765	hemN	769506	770702	398	0	NE	0	NE	0	NE
	-									
M5005_Spy_0766		770712	771464	250	0	NE	0	NE	1	E
M5005_Spy_0767	-	771464	772228	254	0	NE	0	NE	0	NE
M5005_Spy_0768	-	772228	772860	210	0	NE	0	NE	0	NE
M5005_Spy_0769	cas9	773340	777446	1368	0.00025	NE	0	NE	0	NE
M5005_Spy_0770	cas1	777446	778315	289	0	NE	0	NE	0	NE
M5005_Spy_0771	cas2	778312	778653	113	0	NE	0	NE	0	NE
M5005_Spy_0772	csn2	778643	779305	220	0	NE	0	NE	0	NE
M5005_Spy_0773c	_	779352	779639	95	0	NE	0	NE	0	NE
M5005_Spy_0774	_	779772	779951	59	0	NE	0	NE	0	NE
M5005_Spy_0775	_					S		S		S
	- ! ^	780015	780161	48	-1		-1		-1	
M5005_Spy_0776	lepA	780285	782117	610	0	NE	0	NE	0	NE
M5005_Spy_0777	sclB	782375	783256	293	0	NE	0	NE	0	NE
M5005_Spy_0778	msrB/crsA	783442	783879	145	0	NE	0	NE	0.001	NE
M5005_Spy_0779	-	783994	785013	339	0	NE	0	NE	0	NE
M5005_Spy_0780	-	785220	785645	141	0.00025	NE	0	NE	0	NE
M5005_Spy_0781	ptsB	785664	786155	163	0	NE	0	NE	0	NE
M5005_Spy_0782	ptsC	786172	786981	269	0	NE	0	NE	0	NE
M5005_Spy_0783	ptsD	786978	787805	275	0	NE	0	NE	0	NE
M5005_Spy_0784	-	787941	789590	549	0	NE	0	NE	0	NE
	_									
M5005_Spy_0785	-	789594	790382	262	0	NE	0	NE	0	NE
M5005_Spy_0786	-	790376	791422	348	0	NE	0	NE	0	NE
M5005_Spy_0787	-	791519	791866	115	0	NE	0	NE	0	NE
M5005_Spy_0788	-	792201	792767	188	0	NE	0	NE	0	NE
M5005_Spy_0789	-	792783	793472	229	0	NE	0	NE	0	NE
M5005_Spy_0790	gabD	793567	794964	465	0	NE	0	NE	0	NE
M5005_Spy_0791	uvrC	795066	796862	598	0.00025	NE	0	NE	0	NE
M5005_Spy_0792	-	797047	797649	200	0	NE	0	NE	0	NE
M5005_Spy_0793	_	797774	799183	469	0	NE	0	NE	0	NE
M5005_Spy_0794c	trmE	799251	800627	458	0.3345	U	0	NE	1	E
M5005_Spy_0795	rplJ						0.00025			
	•	800960	801460	166	0.0025	NE		NE	0.001	NE
M5005_Spy_0796	rplL	801525	801890	121	0.00175	NE	0.00025	NE	0.001	NE
M5005_Spy_0797	-	802286	802426	46	-1	S	-1	S	-1	S
M5005_Spy_0798	-	802420	802788	122	0	NE	0	NE	0	NE
M5005_Spy_0799	-	802767	802904	45	-1	S	-1	S	-1	S
M5005_Spy_0800	-	802963	803286	107	0	NE	0	NE	0	NE
M5005_Spy_0801	-	803344	803466	40	-1	S	-1	S	-1	S
M5005_Spy_0802	-	803599	803811	70	0	NE	0	NE	0	NE
M5005_Spy_0803	srtI	804076	804771	231	0	NE	0	NE	0	NE
M5005_Spy_0804	srtR	804922	805608	228	0	NE	0	NE	0	NE
M5005_Spy_0805	srtK	805601	806947	448	0.00025	NE	0	NE	0	NE
M5005_Spy_0806	srtA	807095	807235	46	-1	S	-1	S	-1	S
M5005_Spy_0807	srtT	807350	807967	205	0	NE	0	NE	0	NE
M5005_Spy_0808	srtF	808049	808738	229	0	NE	0	NE	0	NE
M5005_Spy_0809	srtE	808744	809493	249	0.00025	NE	0	NE	0	NE
M5005_Spy_0810	srtG	809496	810218	240	0	NE	0	NE	0	NE
M5005_Spy_0811	-	810410	810628	72	0	NE	0	NE	0	NE
M5005_Spy_0812c	-	810737	810952	71	0	NE	0	NE	0	NE
M5005_Spy_0817	dacA1	812371	813699	442	0.00025	NE	0	NE	0.001	NE
M5005_Spy_0818c	-	813816	814778	320	0.00025	NE	0	NE	0	NE
M5005_Spy_0819	_	814866	815021	51	-1	S	-1	S	-1	S
* *	folC.1									
M5005_Spy_0820		815110	816387	425	0.99325	U	1	E	1	E
M5005_Spy_0821	folE	816434	817000	188	0	NE	0	NE	0	NE -
M5005_Spy_0822	folP	817009	817809	266	0.00025	NE	0.0005	NE	1	E
M5005_Spy_0823	folQ	817816	818175	119	0.00025	NE	0	NE	0.001	NE
M5005_Spy_0824	folK	818172	818672	166	0	NE	0	NE	0.696	U
M5005_Spy_0825	murB	818822	819709	295	1	E	1	Ε	1	Ε
M5005_Spy_0826	potA	819755	820909	384	0	NE	0	NE	0.001	NE

M5005_Spy_0827	potB	820893	821687	264	0	NE	0	NE	0	NE
M5005_Spy_0828	potC	821684	822460	258	0	NE	0	NE	0	NE
M5005_Spy_0829	potD	822453	823526	357	0	NE	0	NE	0	NE
M5005_Spy_0830c	dpiA	823581	824246	221	0	NE	0	NE	0	NE
M5005_Spy_0831c	dpiB	824227	825768	513	0	NE	0	NE	0	NE
M5005_Spy_0832	malP	825929	827260	443	0.00025	NE	0	NE	0	NE
M5005_Spy_0833	_	827291	828457	388	0.00025	NE	0	NE	0	NE
M5005_Spy_0834c	_	828540	829631	363	0	NE	0	NE	0	NE
M5005_Spy_0835	aphA	829825	830187	120	0	NE	0	NE	0	NE
	арпа									
M5005_Spy_0837	-	830733	832265	510	0	NE	0	NE	0	NE
M5005_Spy_0838	-	832428	833042	204	0	NE	0	NE	0	NE
M5005_Spy_0839	-	833222	834349	375	0	NE	0	NE	0	NE
M5005_Spy_0840	radC	834398	835078	226	0.00025	NE	0	NE	0	NE
M5005_Spy_0841c	-	835080	835775	231	0	NE	0	NE	0	NE
M5005_Spy_0842c	-	835785	836429	214	0.00025	NE	0	NE	0.99	U
M5005_Spy_0843c	-	836681	837028	115	0	NE	0	NE	0	NE
M5005_Spy_0844c	nifS2	837018	838145	375	0.8785	U	1	Ε	1	Ε
M5005_Spy_0845c	prs	838142	839122	326	0	NE	0	NE	0.001	NE
M5005_Spy_0846c	-	839262	839840	192	0	NE	0	NE	0	NE
M5005_Spy_0847	_	839928	840599	223	0.00025	NE		NE	0.001	NE
	- nnnl/						0			
M5005_Spy_0848	ppnK	840574	841410	278	1	E	1	E	1	E
M5005_Spy_0849	rluD	841407	842312	301	0	NE	0	NE	0	NE
M5005_Spy_0851	pta/eutD	842489	843310	273	0	NE	0	NE	0	NE
M5005_Spy_0852	-	843437	844054	205	0	NE	0	NE	0	NE
M5005_Spy_0853	-	844051	844209	52	-1	S	-1	S	-1	S
M5005_Spy_0854c	-	844403	845092	229	0	NE	0	NE	0	NE
M5005_Spy_0855	proV	845512	846240	242	0	NE	0	NE	0	NE
M5005_Spy_0856	proX	846233	847759	508	0	NE	0	NE	0	NE
M5005_Spy_0857	guaC	848037	849020	327	0	NE	0	NE	0	NE
M5005_Spy_0858	xpt	849325	849906	193	0	NE	0	NE	0	NE
	-						0			
M5005_Spy_0859		849906	851189	427	0.00025	NE		NE	0	NE
M5005_Spy_0860c	apbE	851253	852191	312	0	NE	0	NE	0	NE
M5005_Spy_0861c	-	852244	852429	61	0	NE	0	NE	0	NE
M5005_Spy_0862	tdk2	852567	853136	189	0	NE	0	NE	0	NE
M5005_Spy_0863	prfA	853171	854250	359	1	E	1	E	1	E
M5005_Spy_0864	hemK	854250	855089	279	0	NE	0	NE	0	NE
M5005_Spy_0865	-	855073	855663	196	0.00475	NE	0.00475	NE	0.665	U
M5005_Spy_0866	-	855681	856133	150	0	NE	0	NE	0	NE
M5005_Spy_0867	glyA	856123	857379	418	0	NE	0	NE	0	NE
M5005_Spy_0868	-	857386	858363	325	0.00025	NE	0	NE	0.001	NE
M5005_Spy_0869	_	858364	858963	199	0	NE	0	NE	0	NE
M5005_Spy_0870	_	858973	860697	574	0	NE	0	NE	0	NE
M5005_Spy_0871	_		862421	575			0		0	
	201	860694			0.00025	NE		NE		NE
M5005_Spy_0872	nox	862962	864032	356	0	NE	0	NE	0	NE
M5005_Spy_0873c	ldh	864191	865174	327	0.00025	NE	0	NE	0.002	NE
M5005_Spy_0874	gyrA	865365	867851	828	1	E	1	E	1	E
M5005_Spy_0875	-	867871	868620	249	0.9985	E	1	E	1	E
M5005_Spy_0876	-	868700	869116	138	0	NE	0	NE	0	NE
M5005_Spy_0877	-	869603	869722	39	-1	S	-1	S	-1	S
M5005_Spy_0878	-	869730	870098	122	0.0005	NE	0	NE	0.001	NE
M5005_Spy_0879c	-	870148	871059	303	0	NE	0	NE	0	NE
M5005_Spy_0880c	hlyIII	871176	871826	216	0.00025	NE	0.00025	NE	1	Ε
M5005_Spy_0881c	-	871823	872263	146	0.00025	NE	0	NE	0.001	NE
M5005_Spy_0882	rbgA	872482	873330	282	1	E	1	E	1	E
M5005_Spy_0883	rnhB	873320	874111	263	0.00025	NE	0	NE	0	NE
M5005_Spy_0884	smf				0.00025					
		874176	875012	278		NE	0 060	NE	0	NE
M5005_Spy_0885	topA	875119	877248	709	0	NE	0.069	U	0.995	E
M5005_Spy_0886c	-	877323	877805	160	0	NE	0	NE	0	NE
M5005_Spy_0887c	-	877812	877934	40	-1	S	-1	S	-1	S
M5005_Spy_0888c	-	878080	878205	41	-1	S	-1	S	-1	S
M5005_Spy_0889	-	878218	878763	181	0	NE	0	NE	0	NE
M5005_Spy_0890	ddh	878778	879770	330	0	NE	0	NE	0	NE
M5005_Spy_0891	satD	879875	880540	221	1	E	0.99975	Е	1	Е

M5005_Spy_0892	satE	880533	881249	238	0	NE	0	NE	0	NE
M5005_Spy_0893	gid	881400	882746	448	0.00025	NE	0	NE	0.389	U
M5005_Spy_0894	oadA2	882899	884305	468	0	NE	0	NE	0	NE
M5005_Spy_0895	-	884348	884662	104	0.00025	NE	0	NE	0.001	NE
M5005_Spy_0896	-	884662	885012	116	0	NE	0	NE	0	NE
M5005_Spy_0897	-	885022	886152	376	0	NE	0	NE	0	NE
M5005_Spy_0898c	-	886352	887236	294	0	NE	0	NE	0	NE
M5005_Spy_0899c	citG	887229	887924	231	0	NE	0	NE	0	NE
M5005_Spy_0900c	-	888082	889488	468	0	NE	0	NE	0	NE
M5005_Spy_0901	-	889865	890188	107	0	NE	0	NE	0	NE
M5005_Spy_0902	_	890242	890640	132	0	NE	0	NE	0	NE
M5005_Spy_0903	oadB	890685	891806	373	0	NE	0	NE	0	NE
M5005_Spy_0904	-	891824	891958	44	-1	S	-1	S	-1	S
M5005_Spy_0905	citD	891994	892302	102	0	NE NE	0	NE	0	NE NE
M5005_Spy_0906	citE									
		892320	893177	285	0	NE	0	NE	0	NE
M5005_Spy_0907	citF	893180	894712	510	0.00025	NE	0	NE	0.836	U
M5005_Spy_0908	citX	894642	895283	213	0	NE	0	NE	0	NE
M5005_Spy_0909	oadA1	895298	896692	464	0.00025	NE	0.0005	NE	0.001	NE
M5005_Spy_0910c	citC	896802	897854	350	0	NE	0	NE	0	NE
M5005_Spy_0911c	-	897943	898425	160	0	NE	0	NE	0	NE
M5005_Spy_0912	-	898910	899014	34	-1	S	-1	S	-1	S
M5005_Spy_0913c	xerS	899125	900039	304	0.8115	U	0.61075	U	1	Е
M5005_Spy_0914	-	900733	901362	209	0.00025	NE	0	NE	0.001	NE
M5005_Spy_0915c	ffh	901479	903041	520	0.98975	U	1	Е	0.999	Ε
M5005_Spy_0916c	ylxM	903056	903397	113	0.00025	NE	0.00075	NE	1	Ε
M5005_Spy_0917c	-	903486	904184	232	0.00025	NE	0.00025	NE	1	Ε
M5005_Spy_0918c	-	904267	905700	477	0	NE	0	NE	0	NE
M5005_Spy_0919	guaA	905867	907429	520	0.49925	U	0.001	NE	1	E
M5005_Spy_0920c	murM2	907471	908694	407	0	NE	0	NE	0	NE
M5005_Spy_0921c	-	909059	910603	514	0.00025	NE	0	NE	0	NE
M5005_Spy_0921c	pdxK	910737	911294	185	0.00023	NE	0	NE	0	NE
M5005_Spy_0923c	-			288				NE	0	
* *	-	911272	912138		0	NE	0			NE
M5005_Spy_0924	- - I- D	912228	913496	422	0	NE	0	NE	0	NE
M5005_Spy_0925c	rnhB	913894	914250	118	0	NE	0	NE	0	NE
M5005_Spy_0926c	-	914572	916149	525	0.00025	NE	0	NE	0.148	U
M5005_Spy_0927c	fhs.1	916234	917904	556	1	Е	1	E	1	E
M5005_Spy_0928c	lpIA	918032	919051	339	0	NE	0	NE	0	NE
M5005_Spy_0929c	-	919098	919979	293	0	NE	0	NE	0	NE
M5005_Spy_0930c	-	919972	920784	270	0	NE	0	NE	0	NE
M5005_Spy_0931c	-	920777	921109	110	0	NE	0	NE	0	NE
M5005_Spy_0932c	-	921151	922149	332	0	NE	0	NE	0	NE
M5005_Spy_0933c	-	922146	923345	399	0.00025	NE	0	NE	0	NE
M5005_Spy_0934c	-	923342	924178	278	0	NE	0	NE	0	NE
M5005_Spy_0935	dpfB	924374	925066	230	0	NE	0.00025	NE	1	Ε
M5005_Spy_0936	dfp	925059	925604	181	0.00025	NE	0.996	Ε	1	Ε
M5005_Spy_0937	<u>-</u>	925662	926231	189	0.00025	NE	0	NE	0.001	NE
M5005_Spy_0938	pgmA	926407	928125	572	1	E	1	E	1	E
M5005_Spy_0939c	-	928338	929294	318	0	NE	0	NE	0	NE
M5005_Spy_0940c	_	929296	930360	354	0.00025	NE	0	NE	0	NE
M5005_Spy_0940c	_	930353	931903	516		NE	0	NE	0	NE
M5005_Spy_0941c	-				0					
		932024	933076	350	0	NE	0	NE	0	NE
M5005_Spy_0943c	cdd -	933170	933559	129	0	NE	0	NE	0	NE
M5005_Spy_0944c		934218	934805	195	0	NE	0	NE	0	NE
M5005_Spy_0945	coaA	935073	935993	306	1	E	1	E	1	E
M5005_Spy_0946	rpsT	936062	936295	77	0.0005	NE	0	NE	0	NE
M5005_Spy_0947c	ciaH	936420	937730	436	0.0005	NE	0	NE	0.001	NE
M5005_Spy_0948c	ciaR	937723	938397	224	0	NE	0	NE	0.004	NE
M5005_Spy_0949c	pepN	938743	941280	845	0	NE	0	NE	0	NE
M5005_Spy_0950c	phoU	941485	942138	217	0.00025	NE	0	NE	0.086	U
M5005_Spy_0951c	pstB	942206	942964	252	0.00025	NE	0	NE	0	NE
M5005_Spy_0952c	pstB2	942977	943780	267	0.00025	NE	0	NE	0	NE
M5005_Spy_0953c	pstA	943796	944683	295	0.00025	NE	0	NE	0	NE
M5005_Spy_0954c	pstC	944673	945491	272	0	NE	0.0625	U	0.001	NE
	F	5.1075	5.5.51	-,-	J		0.3023	J	0.001	

M5005_Spy_0955c	pstS	945618	946484	288	0.00025	NE	0	NE	0	NE
M5005_Spy_0956c	-	946623	947933	436	0.00025	NE	1	E	1	Ε
M5005_Spy_0957c	-	947936	948724	262	0.04525	NE	0	NE	0.001	NE
M5005_Spy_0958c	-	948714	948992	92	0	NE	0	NE	0	NE
M5005_Spy_0959c	spxA	948994	949398	134	0	NE	0	NE	0	NE
M5005_Spy_0960c	mreA	949441	950373	310	1	E	1	Е	1	Ε
M5005_Spy_0961c	truB	950402	951286	294	0.00025	NE	0	NE	0	NE
M5005_Spy_0962c	-	951402	952742	446	0	NE	0	NE	0	NE
M5005_Spy_0963c	_	952839	953795	318	0	NE	0	NE	0	NE
M5005_Spy_0964c	-	953806	954402	198	0	NE	0	NE	0	NE
M5005_Spy_0965c	-	954494	955669	391	0	NE	0	NE	0	NE
M5005_Spy_0967c	_	957146	957847	233	0	NE	0	NE	0	NE
M5005_Spy_0968	_	957965	958507	180	0	NE	0	NE	0	NE
M5005_Spy_0969c	_	958504	958647	47	-1	S	-1	S	-1	S
M5005_Spy_0970c	_	958650	959291	213	0	NE	0	NE	0	NE
M5005_Spy_0970c	_				0.00025		0			
	_	959454	959942	162		NE		NE	0.001	NE
M5005_Spy_0972c	-	959953	960153	66	0	NE	0	NE	0	NE
M5005_Spy_0973c	-	960194	960733	179	0	NE	0	NE	0	NE
M5005_Spy_0974c	-	960746	960934	62	0.148	U	0	NE	0.003	NE
M5005_Spy_0975c	-	960945	961532	195	0	NE	0	NE	0	NE
M5005_Spy_0976c		961593	961799	68	0	NE	0	NE	0.001	NE
M5005_Spy_0977c	pcrA	962205	964523	772	0.0245	NE	0.006	NE	1	E
M5005_Spy_0978	-	964891	965061	56	0.00025	NE	0.0415	NE	1	E
M5005_Spy_0979c	-	965052	966374	440	-1	S	-1	S	-1	S
M5005_Spy_0980	-	966494	967729	411	0.00025	NE	0	NE	0	NE
M5005_Spy_0981c	cfa	968098	968871	257	0	NE	0	NE	0	NE
M5005_Spy_0982c	-	969241	970077	278	0	NE	0	NE	0	NE
M5005_Spy_0983c	-	970093	970722	209	0.06425	U	0	NE	0	NE
M5005_Spy_0984c	-	970732	971373	213	0	NE	0	NE	0	NE
M5005_Spy_0985c	-	971479	971814	111	0	NE	0	NE	0	NE
M5005_Spy_0986c	glmS	972010	973824	604	1	E	1	Е	1	Ε
M5005_Spy_0987c	sipC	974000	974557	185	0	NE	0	NE	0	NE
M5005_Spy_0988c	pyk	974775	976277	500	0.999	Ε	1	Ε	1	Ε
M5005_Spy_0989c	pfkA	976340	977353	337	0.99325	U	1	Ε	1	Ε
M5005_Spy_0990c	dnaE	977433	980543	1036	1	Е	1	Е	1	Е
M5005_Spy_0991	-	980728	981099	123	0.00025	NE	0.00075	NE	0.747	Ū
M5005_Spy_0992	-	981099	981797	232	0	NE	0	NE	0	NE
M5005_Spy_0993	_	981807	982592	261	0	NE	0	NE	0	NE
M5005 Spy 0994c	_	982719	983333	204	0.00025	NE	0.00025	NE	1	E
M5005_Spy_0995c	_	983924	984112	62	0	NE	0	NE	0	NE
M5005_Spy_0996	speA2	984332	985087	251	0	NE	0	NE	0	NE
M5005_Spy_0997c	- Sperie	985209	985868	219	0	NE	0	NE	0	NE
M5005_Spy_0998c	_	985868	986089	73	0	NE	0	NE	0	NE
M5005_Spy_0999c	_			257	0.00025		-		-	NE
M5005_Spy_0999C	_	986099	986872			NE	0	NE	0	
M5005_Spy_1000C	_	986883	987485	200	0	NE	0	NE	0	NE
M5005_Spy_1001c	-	987497	988261	254	0	NE	0	NE	0	NE
	-	988263	988595	110	0	NE	0	NE	0	NE
M5005_Spy_1003c	-	988595	988963	122	0	NE	0	NE	0	NE
M5005_Spy_1004c	-	988932	989096	54	-1	S	-1	S	-1	S
M5005_Spy_1005c	-	989068	989415	115	0	NE	0	NE	0	NE
M5005_Spy_1006c	-	989426	991177	583	0	NE	0	NE	0	NE
M5005_Spy_1007c	-	991293	994733	1146	0.00025	NE	0	NE	0	NE
M5005_Spy_1008c	-	994734	996218	494	0	NE	0	NE	0	NE
M5005_Spy_1009c	-	996219	998024	601	0	NE	0	NE	0	NE
M5005_Spy_1010c	-	998017	998475	152	0	NE	0	NE	0.833	U
M5005_Spy_1011c	-	998448	998765	105	0.00025	NE	0	NE	0	NE
M5005_Spy_1012c	-	998778	999284	168	0	NE	0	NE	0	NE
M5005_Spy_1013c	-	999296	999706	136	0.00025	NE	0	NE	0	NE
M5005_Spy_1014c	-	999708	1000103	131	0	NE	0	NE	0	NE
M5005_Spy_1015c	-	1000100	1000411	103	0.00025	NE	0	NE	0.001	NE
M5005_Spy_1016c	-	1000408	1000752	114	0.00025	NE	0	NE	0	NE
M5005_Spy_1017c	-	1000766	1001059	97	0	NE	0	NE	0	NE
M5005_Spy_1018c	-	1001072	1001962	296	0	NE	0	NE	0	NE
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M5005_Spy_1019c	-	1001981	1002550	189	0.00025	NE	0	NE	0	NE
M5005_Spy_1020c	-	1002795	1003064	89	0	NE	0	NE	0	NE
M5005_Spy_1021c	-	1003071	1003979	302	0	NE	0	NE	0	NE
M5005_Spy_1022c	-	1003948	1005273	441	0	NE	0	NE	0	NE
M5005_Spy_1023c	-	1005273	1006547	424	0	NE	0	NE	0	NE
M5005_Spy_1024c	_	1006537	1006917	126	0.00025	NE	0	NE	0	NE
M5005_Spy_1025c	_	1007527	1007961	144	0.00023	NE	0	NE	0	NE
M5005_Spy_1025c							0	NE	0	
	_	1008247	1008513	88	0	NE				NE
M5005_Spy_1027c	-	1008510	1009034	174	0	NE	0	NE	0	NE
M5005_Spy_1028c	-	1009037	1009669	210	0	NE	0	NE	0	NE
M5005_Spy_1029c	-	1009671	1009955	94	0	NE	0	NE	0	NE
M5005_Spy_1030c	-	1009952	1010146	64	0	NE	0	NE	0	NE
M5005_Spy_1031c	-	1010119	1010358	79	0	NE	0	NE	0	NE
M5005_Spy_1032c	-	1010355	1010600	81	0.00025	NE	0	NE	0	NE
M5005_Spy_1033c	-	1010597	1010953	118	0	NE	0	NE	0	NE
M5005_Spy_1034c	-	1010950	1011390	146	0	NE	0	NE	0	NE
M5005_Spy_1035c	_	1011390	1011593	67	0	NE	0	NE	0	NE
M5005_Spy_1036c	ssb2	1011599	1012024	141	0	NE	0	NE	0	NE
	ssb1			224		NE	0	NE	0.001	NE
M5005_Spy_1037c	5501	1012017	1012691		0.00025					
M5005_Spy_1038c	-	1012692	1013174	160	0	NE	0	NE	0	NE
M5005_Spy_1039c	-	1013196	1013450	84	0	NE	0	NE	0	NE
M5005_Spy_1040c	-	1013431	1013784	117	0	NE	0	NE	0	NE
M5005_Spy_1041c	-	1013797	1013934	45	-1	S	-1	S	-1	S
M5005_Spy_1042c	-	1013925	1014707	260	0.91875	U	0	NE	0.333	U
M5005_Spy_1043c	-	1014694	1015524	276	0	NE	0	NE	0	NE
M5005_Spy_1044	-	1015738	1016199	153	0.00025	NE	0	NE	0.001	NE
M5005_Spy_1045c	-	1016649	1016849	66	-1	S	-1	S	-1	S
M5005_Spy_1046	_	1016923	1017309	128	0.00025	NE	0	NE	0	NE
M5005_Spy_1047c	_	1017298	1017507	69	0.00023	NE	0	NE	0	NE
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M5005_Spy_1048	-	1017561	1018160	199	0.00025	NE	0	NE	0	NE
M5005_Spy_1049c	-	1018190	1018348	52	-1	S	-1	S	-1	S
M5005_Spy_1050	-	1018705	1019529	274	0.0005	NE	0.0005	NE	1	E
M5005_Spy_1051	-	1019565	1020458	297	0	NE	0	NE	0	NE
M5005_Spy_1052	int.1	1020579	1021667	362	0	NE	0	NE	0	NE
M5005_Spy_1053	-	1021799	1021912	37	-1	S	-1	S	-1	S
M5005_Spy_1054	-	1022030	1022650	206	0	NE	0	NE	0	NE
M5005_Spy_1055c	glgP	1022907	1025171	754	0	NE	0	NE	0	NE
M5005_Spy_1056c	malM	1025206	1026699	497	0	NE	0	NE	0	NE
M5005_Spy_1057c	malR	1026814	1027833	339	0	NE	0	NE	0	NE
M5005_Spy_1058	malE	1027874	1029325	483	0	NE	0	NE	0	NE
M5005_Spy_1059	malF	1029830	1030960	376	0.00025	NE	0	NE	0.001	NE
M5005_Spy_1060	malG									
	illaiG -	1030960	1031796	278	0	NE	0	NE	0	NE
M5005_Spy_1061		1031951	1032751	266	0.00025	NE	0	NE	0	NE
M5005_Spy_1062c	malA	1032867	1033682	271	0	NE	0	NE	0	NE
M5005_Spy_1063c	malD	1033704	1034564	286	0.00025	NE	0	NE	0	NE
M5005_Spy_1064c	malC	1034561	1035868	435	0	NE	0	NE	0	NE
M5005_Spy_1065c	amyA	1035943	1038078	711	0	NE	0	NE	0	NE
M5005_Spy_1066c	amyB	1038104	1039807	567	0.00025	NE	0	NE	0	NE
M5005_Spy_1067c	malX	1039973	1041232	419	0	NE	0	NE	0	NE
M5005_Spy_1068	-	1041558	1041782	74	0	NE	0	NE	0	NE
M5005_Spy_1069c	-	1041847	1042830	327	0	NE	0	NE	0	NE
M5005_Spy_1070c	dltD	1042861	1044111	416	0	NE	0	NE	0.001	NE
M5005_Spy_1071c	dltC	1044104	1044343	79	0	NE	0	NE	0	NE
M5005_Spy_1072c	dltB	1044361		418	0	NE	0	NE	0	
			1045617							NE
M5005_Spy_1073c	dltA	1045614	1047152	512	0	NE	0	NE	0	NE
M5005_Spy_1074c	-	1047164	1047307	47	-1	S	-1	S	-1	S
M5005_Spy_1075c	uvrB	1047571	1049562	663	0	NE	0	NE	0	NE
M5005_Spy_1076	glnH	1049755	1051929	724	1	E	1	E	1	E
M5005_Spy_1077	glnQ.2	1051929	1052669	246	0.98675	U	0.97275	U	0.285	U
M5005_Spy_1078c	-	1052817	1052969	50	-1	S	-1	S	-1	S
M5005_Spy_1079c	-	1052966	1054345	459	0	NE	0	NE	0	NE
M5005_Spy_1080c	-	1054523	1054972	149	0	NE	0	NE	0	NE
M5005_Spy_1081c	-	1054969	1055304	111	0	NE	0	NE	0	NE
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M5005_Spy_1082c	-	1055307	1055618	103	0	NE	0	NE	0	NE
M5005_Spy_1083c	-	1055641	1057635	664	0.014	NE	0	NE	0.197	U
M5005_Spy_1084c	-	1057741	1058835	364	0	NE	0	NE	0	NE
M5005_Spy_1085c	bglA.2	1058844	1060244	466	0	NE	0	NE	0	NE
M5005_Spy_1086	-	1060469	1061164	231	0	NE	0	NE	0	NE
M5005_Spy_1087c	-	1061169	1061327	52	-1	S	-1	S	-1	S
M5005_Spy_1088c	obgE	1061396	1062703	435	1	E	1	Ε	1	Ε
M5005_Spy_1089c	-	1062766	1062894	42	-1	S	-1	S	-1	S
M5005_Spy_1090	-	1063136	1063651	171	0	NE	0	NE	0	NE
M5005_Spy_1091	-	1063824	1064480	218	0	NE	0	NE	0	NE
M5005_Spy_1092c	rsuA	1064529	1065263	244	0	NE	0	NE	0	NE
M5005_Spy_1093	-	1065375	1065740	121	0	NE	0	NE	0	NE
M5005_Spy_1094c	_	1065860	1067080	406	0	NE	0	NE	0	NE
M5005_Spy_1095	_	1067382	1068938	518	0	NE	0	NE	0	NE
	_									
M5005_Spy_1096c	_	1069045	1069446	133	0	NE	0	NE	0	NE
M5005_Spy_1097c	-	1069531	1070043	170	0	NE	0	NE	0	NE
M5005_Spy_1098c	-	1070348	1071703	451	0	NE	0	NE	0	NE
M5005_Spy_1099c	psr	1071785	1073236	483	0	NE	0	NE	0	NE
M5005_Spy_1100c	aroK	1073444	1073935	163	0	NE	0	NE	0	NE
M5005_Spy_1101c	aroA1	1073928	1075220	430	0	NE	0	NE	0	NE
M5005_Spy_1102c	-	1075322	1076287	321	0.00025	NE	0	NE	0.001	NE
M5005_Spy_1103c	map	1076289	1077149	286	0.00025	NE	1	E	1	Ε
M5005_Spy_1104c	-	1077165	1078448	427	0	NE	0	NE	0.001	NE
M5005_Spy_1105c	-	1078457	1078999	180	0	NE	0	NE	0	NE
M5005_Spy_1106c	grab	1079237	1079890	217	0	NE	0	NE	0	NE
M5005_Spy_1107c	murZ	1080248	1081507	419	0	NE	0	NE	0.001	NE
M5005_Spy_1108c	metK2	1081681	1082877	398	0.98925	U	1	Ε	1	Ε
M5005_Spy_1109c	inlA	1083414	1085792	792	0.00025	NE	0	NE	0	NE
M5005_Spy_1110	birA	1085996	1086937	313	0	NE	1	E	1	E
M5005_Spy_1111c	-	1086912	1087220	102	0	NE	0	NE	0	NE
M5005_Spy_1112c	dnaX	1087210	1087220	556	1	E	1	E	1	E
M5005_Spy_1112c	-	1087210	1088880	165	0	NE	0	NE	0	NE
M5005_Spy_1115C	_			269	0		0	NE	0	
	-	1089522	1090331			NE				NE
M5005_Spy_1115c		1090384	1090647	87	0	NE	0	NE	0	NE
M5005_Spy_1116c	udk	1090727	1091353	208	0	NE	0	NE	0	NE
M5005_Spy_1117	deaD2	1091451	1092536	361	0	NE	0	NE	0	NE
M5005_Spy_1118c	-	1092700	1093920	406	0.00025	NE	0	NE	0	NE
M5005_Spy_1119c	gapN	1094015	1095442	475	1	E	1	E	1	E
M5005_Spy_1120c	pstI	1095627	1097360	577	0	NE	0.9685	U	1	E
M5005_Spy_1121c	ptsH	1097365	1097628	87	0.97675	U	0	NE	0.998	Ε
M5005_Spy_1122	nrdH	1098021	1098239	72	0	NE	0	NE	0.001	NE
M5005_Spy_1123	nrdE.2	1098259	1100418	719	0	NE	0	NE	0	NE
M5005_Spy_1124	nrdF	1100751	1101710	319	0	NE	0	NE	0	NE
M5005_Spy_1125	-	1101685	1102998	437	0	NE	0	NE	0	NE
M5005_Spy_1129c	-	1104384	1105079	231	0	NE	0	NE	0	NE
M5005_Spy_1130c	-	1105098	1105859	253	0	NE	0	NE	0	NE
M5005_Spy_1131c	-	1105856	1106077	73	0.064	U	0	NE	0	NE
M5005_Spy_1132c	alaS	1106432	1109050	872	1	Ε	1	Ε	1	Ε
M5005_Spy_1133c	prsA	1109437	1110492	351	0	NE	0	NE	0	NE
M5005_Spy_1134c	-	1110555	1111262	235	0	NE	0	NE	0	NE
M5005_Spy_1135c	-	1111328	1112524	398	0	NE	0	NE	0	NE
M5005_Spy_1136c	рерВ	1111328	1112324	601	0	NE	0	NE	0	NE
M5005_Spy_1130c M5005_Spy_1137c	рерь								0	
	_	1114718	1115680	320	0	NE	0	NE		NE
M5005_Spy_1138c	- nnaD	1115975	1116691	238	0.00025	NE	0	NE	0	NE
M5005_Spy_1139c	nagB	1116810	1117514	234	0	NE	0	NE	0	NE
M5005_Spy_1140	queA	1117716	1118744	342	0	NE	0	NE	0.001	NE
M5005_Spy_1141	-	1118751	1119971	406	0.00025	NE	0	NE	0	NE
M5005_Spy_1142c	-	1120085	1120675	196	0	NE	0	NE	0	NE
M5005_Spy_1143c	-	1120672	1120920	82	0	NE	0	NE	0	NE
M5005_Spy_1144c	-	1120905	1121132	75	0	NE	0	NE	0	NE
M5005_Spy_1145c	sodA	1121299	1121904	201	0	NE	0	NE	0	NE
M5005_Spy_1146c	holA	1122001	1123041	346	1	Ε	1	Ε	1	Ε
M5005_Spy_1147c	comEC	1123112	1125355	747	0.00025	NE	0	NE	0	NE

MS0015 SP), 1149c - 1125136 1125938		_									
MS005_Soy_1151	M5005_Spy_1148c	comE	1125336	1125998	220	0.00025	NE	0	NE	0	NE
M5905 Spy, 11512c	M5005_Spy_1149c	-	1126198	1126938	246	0.99725	E	1	E	1	E
M5905 Spy, 11512c	M5005_Spy_1150	-	1127056	1127832	258	0	NE	0	NE	0	NE
M5005_Soy_1152c		_									
M5005_Spv_1155c murb 1130251 1131870 539 0 NE		kun									
MS005, Sey, 1155c											
M5005 Spy .1157c											
MSD05, Sey, 1159c murf 1134744 1136135 463 1 E 1 E 1 E MSD05, Sey, 1159c merc 1137473 1138069 1398 0.00025 NE 0 NE 0.001 NE MSD05, Sey, 1159c merc 1138161 11383069 1398 0.00025 NE 0 NE 0 NE MSD05, Sey, 1160c 1138368 1138947 259 0 NE 0 NE 0 NE MSD05, Sey, 1160c 1138368 1138947 259 0 NE 0 NE 0 NE MSD05, Sey, 1160c 1138368 1138947 259 0 NE 0 NE 0 NE MSD05, Sey, 1164c gmm4 114109 1141797 231 0.09975 E 1 E 0.4811 U MSD05, Sey, 1166c 1140474 11440995 173 0 NE 0 NE 0 NE MSD05, Sey, 1166c 1140474 11440995 173 0 NE 0 NE 0 NE MSD05, Sey, 1166c 114306 1142971 311 0.00025 NE 0 NE 0 NE MSD05, Sey, 1166c 114306 11442971 311 0.00025 NE 0 NE 0 NE MSD05, Sey, 1166c 114306 11442971 311 0.00025 NE 0 NE 0 NE MSD05, Sey, 1166c 114306 11442971 311 0.00025 NE 0 NE 0 NE MSD05, Sey, 1166c 114306 11442971 311 0.00025 NE 0 NE 0 NE MSD05, Sey, 1166c 114306 11445133 G20 0 NE 0 NE 0 NE MSD05, Sey, 1169 spd3 1146085 1146085 1146885 266 0 NE 0 NE 0 NE 0 NE MSD05, Sey, 1170 1147060 1147660 1147660 1147660 10.00 NE 0 NE 0 NE 0 NE MSD05, Sey, 1172 1148981 1149205 1149480 91 0 NE 0 NE 0 NE 0 NE MSD05, Sey, 1173c 1149205 1149480 91 0 NE 0 NE 0 NE 0 NE MSD05, Sey, 1176c 1150144 1150107 205 0 NE 0 NE 0 NE 0 NE MSD05, Sey, 1176c 115014 115041 115467 115041 115467 115041 1155467 115041 115467 115041 115467 115041 115047 115041 115047 115041 115047	M5005_Spy_1155c	prfC	1132177	1133721	514	0.00025	NE	0	NE	0	NE
MS005_Spv_1159c	M5005_Spy_1156c	-	1133969	1134664	231	0	NE	0	NE	0	NE
MS005_Spv_1159c	M5005 Spy 1157c	murF	1134744	1136135	463	1	Е	1	Е	1	Е
MS005 Spv 1159c recR		ddl			348			1	F	1	
MS005_Spv_1161c											
M5005_Spy_1162c		recit									
MS005_Spv_1162c		-									
MS005_Spy_1164c											
MS005_Spy_1166	M5005_Spy_1162c	-	1139771	1140313	180	0	NE	0	NE	0	NE
MS005_Spy_1166	M5005_Spy_1163c	-	1140474	1140995	173	0	NE	0	NE	0	NE
MS005_Spy_1166	M5005_Spy_1164c	gpmA	1141102	1141797	231	0.99975	Е	1	Е	0.481	U
M5005_Spy_1166c	M5005 Spv 1165	pvrD						0	NF		
M5005_Spy_1168c		-									
M5005_Spy_1168c											
MS005_Spy_1170		-									
M5005_Spy_1172c		-									
M5005_Spy_1171c -	M5005_Spy_1169	spd3	1146085	1146885	266	0	NE	0	NE	0	NE
M5005_Spy_1173c	M5005_Spy_1170	-	1147096	1147590	164	0	NE	0	NE	0	NE
M5005_Spy_1173c	M5005_Spy_1171c	-	1147660	1148865	401	0	NE	0	NE	0	NE
M5005_Spy_1173c	M5005 Spv 1172c	-	1148981	1149208	75	0	NE	0	NE	0	NE
M5005_Spy_1174c		_									
M5005_Spy_1175c		_									
M5005_Spy_1176c											
M5005_Spy_1177c		-									
M5005_Spy_1178c	- • • -	-									NE
M5005_Spy_1180c -	M5005_Spy_1177c	-	1152418	1153113	231	0	NE	0	NE	0	NE
M5005_Spy_1180c - 1155853 1156116 87 0 NE 0 NE 0 NE NE M5005_Spy_1181c - 1156127 1156720 197 0 NE 0 NE 0 NE NE M5005_Spy_1182c - 1156732 1157067 111 0 NE 0 NE 0 NE M5005_Spy_1183c - 1157068 1157304 78 0 NE 0 NE 0 NE M5005_Spy_1183c - 1157997 1157635 112 0.00025 NE 0 NE 0 NE M5005_Spy_1184c - 1157297 1157635 112 0.00025 NE 0 NE 0 NE M5005_Spy_1186c - 1157595 1158017 140 0 NE 0 NE 0 NE M5005_Spy_1186c - 1158027 1158227 66 0 NE 0 NE 0 NE M5005_Spy_1186c - 1158227 1159138 303 0.00025 NE 0 NE 0 NE M5005_Spy_1186c - 1158227 1159138 303 0.00025 NE 0 NE 0 NE M5005_Spy_1188c - 1159163 1159624 153 0 NE 0 NE 0 NE M5005_Spy_1189c - 1159705 1161120 471 0.00025 NE 0 NE 0 NE M5005_Spy_1190c - 1161230 1161496 88 0 NE 0 NE 0 NE M5005_Spy_1191c - 1161535 1161750 71 0 NE 0 NE 0 NE M5005_Spy_1192c - 116179 1161952 77 0 NE 0 NE 0 NE M5005_Spy_1193c - 1161494 1163442 497 0 NE 0 NE 0 NE M5005_Spy_1195c - 1164700 1165056 118 0.00025 NE 0 NE 0 NE M5005_Spy_1195c - 1164700 1165056 118 0.00025 NE 0 NE 0 NE M5005_Spy_1199c - 1166345 1166980 211 0 NE 0 NE 0 NE M5005_Spy_1199c - 1166345 1166980 211 0 NE 0 NE 0 NE M5005_Spy_1199c - 1166345 1166980 211 0 NE 0 NE 0 NE M5005_Spy_1199c - 1166345 1166980 211 0 NE 0 NE 0 NE M5005_Spy_11200c - 1167844 1168257 137 0 NE 0 NE 0 NE M5005_Spy_11200c - 1167844 1168257 137 0 NE 0 NE 0 NE M5005_Spy_11200c - 1167846 1170056 1170057 68 0 NE 0 NE 0 NE M5005_Spy_11200c - 1166345 1166337 1166337 265 0 NE 0 NE 0 NE M5005_Spy_11200c - 116	M5005_Spy_1178c	-	1153110	1155467	785	0	NE	0	NE	0	NE
M5005_Spy_1181c	M5005_Spy_1179c	-	1155467	1155838	123	0	NE	0	NE	0	NE
M5005_Spy_1181c	M5005_Spy_1180c	-	1155853	1156116	87	0	NE	0	NE	0	NE
M5005_Spy_1182c		_									
M5005_Spy_1183c		_									
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M5005_Spy_1185c - 1157595 1158017 140 0 NE 0 NE 0 NE M5005_Spy_1186c - 1158027 1158227 66 0 NE 0 NE 0 NE M5005_Spy_1188c - 1159163 1159624 153 0 NE 0 NE 0 NE M5005_Spy_1189c - 1159163 1159664 153 0 NE 0 NE 0 NE M5005_Spy_1189c - 1161230 1161496 88 0 NE 0 NE 0 NE M5005_Spy_1191c - 1161351 1161750 71 0 NE 0 NE 0 NE M5005_Spy_1193c - 1161719 1161952 77 0 NE 0 NE 0 NE M5005_Spy_1193c - 1164700 1165042 497 0 NE 0 NE 0		-									
M5005_Spy_1186c - 1158027 1158227 66 0 NE 0 NE 0 NE M5005_Spy_1187c - 1158227 1159138 303 0.00025 NE 0 NE 0 NE M5005_Spy_1188c - 1159705 1161120 471 0.00025 NE 0 NE 0 NE M5005_Spy_1190c - 1161230 1161496 88 0 NE 0 NE 0 NE M5005_Spy_1191c - 1161353 1161750 71 0 NE 0 NE 0 NE M5005_Spy_1192c - 1161719 1161952 77 0 NE 0 NE 0 NE M5005_Spy_1192c - 1163435 1164703 422 0.00025 NE 0 NE 0 NE M5005_Spy_1195c - 1164700 1165056 118 0.00025 NE 0 NE		-									
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M5005_Spy_1188c - 1159163 1159624 153 0 NE 0 NE 0 NE M5005_Spy_11189c - 1159705 1161120 471 0.00025 NE 0 NE 0 NE M5005_Spy_1190c - 1161230 1161496 88 0 NE 0 NE 0 NE M5005_Spy_1191c - 1161535 1161750 71 0 NE 0 NE 0 NE M5005_Spy_1192c - 1161719 1161952 77 0 NE 0 NE 0 NE M5005_Spy_1193c - 1161949 1163442 497 0 NE 0 NE 0 NE M5005_Spy_1194c - 1163435 116703 422 0.00025 NE 0 NE 0 NE M5005_Spy_1196c - 1165058 1166077 139 0 NE 0 NE	M5005_Spy_1186c	-	1158027	1158227	66	0	NE	0	NE	0	NE
M5005_Spy_1189c - 1159705 1161120 471 0.00025 NE 0 NE 0 NE M5005_Spy_1190c - 1161230 1161496 88 0 NE 0 NE 0 NE M5005_Spy_1191c - 1161575 71 0 NE 0 NE 0 NE M5005_Spy_1192c - 1161719 1161952 77 0 NE 0 NE 0 NE M5005_Spy_1193c - 1161949 1163442 497 0 NE 0 NE 0 NE M5005_Spy_1194c - 1163435 1164703 422 0.00025 NE 0 NE 0 NE M5005_Spy_1195c - 1164700 1165056 118 0.00025 NE 0 NE 0 NE M5005_Spy_1199c - 1166345 1166077 139 0 NE 0 NE 0	M5005_Spy_1187c	-	1158227	1159138	303	0.00025	NE	0	NE	0	NE
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M5005_spy_1197c - 1165658 1166077 139 0 NE 0 NE 0 NE M5005_spy_1198c - 1166345 1166980 211 0 NE 0 NE 0 NE M5005_spy_1199c - 1166982 1167251 89 0 NE 0 NE 0 NE M5005_spy_1200c - 1167335 1167847 170 0.00025 NE 0 NE 0 NE M5005_spy_1201c - 1167844 1168257 137 0 NE 0 NE 0 NE M5005_spy_1202c - 1168363 1168530 55 -1 S -1 S -1 S M5005_spy_1203c - 1168540 1169337 265 0 NE 0 NE 0 NE M5005_spy_1204c - 1169334 1170263 309 0.00025 NE 0 NE <td< td=""><td>M5005_Spy_1195c</td><td>-</td><td>1164700</td><td>1165056</td><td>118</td><td>0.00025</td><td>NE</td><td>0</td><td>NE</td><td>0</td><td>NE</td></td<>	M5005_Spy_1195c	-	1164700	1165056	118	0.00025	NE	0	NE	0	NE
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M5005_spy_1198c - 1166345 1166980 211 0 NE 0 NE 0 NE M5005_spy_1199c - 1166982 1167251 89 0 NE 0 NE 0 NE M5005_spy_1200c - 1167335 1167847 170 0.00025 NE 0 NE 0 NE M5005_spy_1201c - 1167844 1168257 137 0 NE 0 NE 0 NE M5005_spy_1202c - 1168363 1168530 55 -1 S -1 S -1 S M5005_spy_1203c - 1168540 1169337 265 0 NE 0 NE 0 NE M5005_spy_1204c - 1169334 1170263 309 0.00025 NE 0 NE 0.001 NE M5005_spy_1206c - 117066 1170857 68 0 NE 0 NE <	M5005 Spy 1197c	-	1165658	1166077	139	0	NE	0	NE	0	NE
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M5005_Spy_1203c - 1168540 1169337 265 0 NE 0 NE 0 NE M5005_Spy_1204c - 1169334 1170263 309 0.00025 NE 0 NE 0.001 NE M5005_Spy_1205c - 1170266 1170595 109 0 NE 0 NE 0 NE M5005_Spy_1206c - 1170861 1170857 68 0 NE 0 NE 0 NE M5005_Spy_1207c - 1170866 1171006 46 -1 S -1 S -1 S M5005_Spy_1208c - 1171003 1171236 77 0 NE 0 NE 0 NE M5005_Spy_1209c - 1171217 1171606 129 0.00025 NE 0 NE 0 NE M5005_Spy_1210c - 1171751 1171990 79 0 NE 0 NE <		-									
M5005_Spy_1204c - 1169334 1170263 309 0.00025 NE 0 NE 0.001 NE M5005_Spy_1205c - 1170266 1170595 109 0 NE 0 NE 0 NE M5005_Spy_1206c - 1170851 1170857 68 0 NE 0 NE 0 NE M5005_Spy_1207c - 1170866 1171006 46 -1 S -1 S -1 S M5005_Spy_1208c - 1171003 1171236 77 0 NE 0 NE 0 NE M5005_Spy_1209c - 1171217 1171606 129 0.00025 NE 0 NE 0 NE M5005_Spy_1210c - 1171751 1171990 79 0 NE 0 NE 0.0001 NE	M5005_Spy_1202c	-	1168363	1168530	55	-1	S	-1	S	-1	S
M5005_Spy_1205c - 1170266 1170595 109 0 NE 0 NE 0 NE M5005_Spy_1206c - 1170651 1170857 68 0 NE 0 NE 0 NE M5005_Spy_1207c - 1170866 1171006 46 -1 S -1 S -1 S M5005_Spy_1208c - 1171003 1171236 77 0 NE 0 NE 0 NE M5005_Spy_1209c - 1171217 1171606 129 0.00025 NE 0 NE 0 NE M5005_Spy_1210c - 1171751 1171990 79 0 NE 0 NE 0.0001 NE	- ' '-	-	1168540	1169337	265	0	NE	0	NE	0	NE
M5005_Spy_1205c - 1170266 1170595 109 0 NE 0 NE 0 NE M5005_Spy_1206c - 1170651 1170857 68 0 NE 0 NE 0 NE M5005_Spy_1207c - 1170866 1171006 46 -1 S -1 S -1 S M5005_Spy_1208c - 1171003 1171236 77 0 NE 0 NE 0 NE M5005_Spy_1209c - 1171217 1171606 129 0.00025 NE 0 NE 0 NE M5005_Spy_1210c - 1171751 1171990 79 0 NE 0 NE 0.0001 NE	M5005_Spy_1204c	-	1169334	1170263	309	0.00025	NE	0	NE	0.001	NE
M5005_Spy_1206c - 1170651 1170857 68 0 NE 0 NE 0 NE M5005_Spy_1207c - 1170866 1171006 46 -1 S -1 S -1 S M5005_Spy_1208c - 1171003 1171236 77 0 NE 0 NE 0 NE M5005_Spy_1209c - 1171217 1171606 129 0.00025 NE 0 NE 0 NE M5005_Spy_1210c - 1171751 1171990 79 0 NE 0 NE 0.0001 NE	M5005_Spy_1205c	-									
M5005_Spy_1207c - 1170866 1171006 46 -1 S -1 S -1 S M5005_Spy_1208c - 1171003 1171236 77 0 NE 0 NE 0 NE M5005_Spy_1209c - 1171217 1171606 129 0.00025 NE 0 NE 0 NE M5005_Spy_1210c - 1171751 1171990 79 0 NE 0 NE 0.0001 NE	: :	-									
M5005_Spy_1208c - 1171003 1171236 77 0 NE 0 NE 0 NE M5005_Spy_1209c - 1171217 1171606 129 0.00025 NE 0 NE 0 NE M5005_Spy_1210c - 1171751 1171990 79 0 NE 0 NE 0.0001 NE		_									
M5005_Spy_1209c - 1171217 1171606 129 0.00025 NE 0 NE 0 NE M5005_Spy_1210c - 1171751 1171990 79 0 NE 0 NE 0.001 NE		_									
M5005_Spy_1210c - 1171751 1171990 79 0 NE 0 NE 0.001 NE		-									
		-									
M5UU5_Spy_1211c - 1172090 1172275 61 -1 S -1 S		-									
	м5005_Spy_1211c	-	1172090	1172275	61	-1	S	-1	S	-1	S

M5005_Spy_1212c	xis	1172277	1172588	103	0.00025	NE	0	NE	0	NE
M5005_Spy_1213c	-	1172666	1172851	61	0.1975	U	0	NE	0	NE
M5005_Spy_1214	-	1173018	1173257	79	0	NE	0	NE	0	NE
M5005_Spy_1215	-	1173399	1174205	268	0.00025	NE	0	NE	0	NE
M5005 Spy 1216c	_	1174140	1174406	88	0	NE	0	NE	0	NE
M5005_Spy_1217c	_	1174438	1175154	238	0.00475	NE	0	NE	0.001	NE
M5005_Spy_1217c										
	-	1175166	1175357	63	0	NE	0	NE	0	NE
M5005_Spy_1219	-	1176511	1176858	115	0.99975	Е	1	E	1	E
M5005_Spy_1220	-	1176862	1177242	126	0	NE	0	NE	0	NE
M5005_Spy_1221	-	1177254	1177520	88	0	NE	0	NE	0	NE
M5005_Spy_1222	int.2	1177644	1178786	380	0	NE	0	NE	0	NE
M5005_Spy_1223c	-	1178876	1179151	91	0.984	U	1	E	0.98	U
M5005_Spy_1224c	-	1179250	1179837	195	0	NE	0	NE	0	NE
M5005_Spy_1225c	_	1179815	1180657	280	0	NE	0	NE	0	NE
M5005_Spy_1226c	_	1180650	1181501	283	0	NE	0	NE	0	NE
M5005_Spy_1227c	_	1181717				NE	0	NE	0	
	- MacM		1182658	313	0					NE
M5005_Spy_1228c	recN	1182830	1184491	553	0	NE	0	NE	0	NE
M5005_Spy_1229c	argR1	1184513	1184983	156	0	NE	0	NE	0	NE
M5005_Spy_1230c	-	1184970	1185797	275	0	NE	0	NE	0	NE
M5005_Spy_1231c	fps	1185790	1186662	290	0	NE	0	NE	0	NE
M5005_Spy_1232c	xseB	1186662	1186877	71	0.782	U	0	NE	0	NE
M5005_Spy_1233c	xseA	1186855	1188195	446	0.00025	NE	0	NE	0	NE
M5005_Spy_1234c	foID	1188348	1189202	284	0	NE	0.00025	NE	1	Ε
M5005_Spy_1235c	-	1189410	1191113	567	0	NE	0	NE	0	NE
M5005_Spy_1236c	phr	1191282	1192691	469	0	NE	0	NE	0	NE
M5005_Spy_1230c	artP/gtr									
	_	1192840	1193574	244	0.04	NE	0	NE	0	NE
M5005_Spy_1238c	artQ	1193574	1194260	228	0	NE	0	NE	0	NE
M5005_Spy_1239c	-	1194387	1194617	76	0.45	U	0.00425	NE	0.954	U
M5005_Spy_1240	clpE	1194915	1197197	760	0	NE	0	NE	0	NE
M5005_Spy_1241	mutT	1197325	1197780	151	0	NE	0	NE	0	NE
M5005_Spy_1242	-	1197831	1198133	100	0	NE	0	NE	0	NE
M5005_Spy_1243c	ileS	1198398	1201199	933	0.99775	Ε	1	Ε	1	Ε
M5005_Spy_1244c	divIVAS	1201472	1202230	252	0.00025	NE	1	Ε	1	Ε
M5005_Spy_1245c	_	1202240	1203031	263	0	NE	0	NE	0	NE
M5005_Spy_1246c	_	1203031	1203285	84	0.00025	NE	0	NE	0.161	U
M5005_Spy_1240c	_									
	-	1203290	1203958	222	0.00025	NE	0	NE	0.001	NE
M5005_Spy_1248c	-	1203958	1204629	223	0	NE	0.00025	NE	0.001	NE
M5005_Spy_1249c	ftsZ	1204632	1205951	439	0.9745	U	1	Е	1	Е
M5005_Spy_1250c	ftsA	1205975	1207339	454	1	E	1	E	1	E
M5005_Spy_1251c	divIB/ftsQ	1207551	1208699	382	0.00075	NE	0.7875	U	0.002	NE
M5005_Spy_1252c	murG	1208700	1209803	367	1	Ε	1	Ε	1	Ε
M5005_Spy_1253c	murD	1209782	1211140	452	1	Ε	1	Ε	1	Ε
M5005_Spy_1254c	-	1211510	1211761	83	0	NE	0	NE	0	NE
M5005_Spy_1255c	typA	1211883	1213724	613	0.00025	NE	0	NE	0.303	U
M5005_Spy_1256c	-	1213907	1214296	129	0	NE	0	NE	0	NE
M5005_Spy_1257c	glcK	1214306	1215277	323	0.00025	NE	0	NE	0	NE
	gick -									
M5005_Spy_1258c		1215282	1215485	67	0	NE	0	NE	0	NE
M5005_Spy_1259c	dpr	1215627	1216154	175	0	NE	0	NE	0	NE
M5005_Spy_1260	-	1216382	1217008	208	0	NE	0	NE	0	NE
M5005_Spy_1261c	-	1217090	1218169	359	0	NE	0	NE	0	NE
M5005_Spy_1262c	-	1218173	1218793	206	0	NE	0	NE	0	NE
M5005_Spy_1263c	-	1219088	1219207	39	-1	S	-1	S	-1	S
M5005_Spy_1264c	-	1219241	1219942	233	0	NE	0	NE	0	NE
M5005_Spy_1265c	_	1220035	1220265	76	0.00025	NE	0	NE	0	NE
M5005_Spy_1266c	_	1220631	1221668	345	0	NE	0	NE	0	NE
M5005_Spy_1267c	coaD									
	-	1221655	1222146	163	0.338	U	1	E	1	E
M5005_Spy_1268c		1222136	1222675	179	0	NE	0	NE	0	NE
M5005_Spy_1269c	asnA	1222798	1223790	330	0	NE	0	NE	0	NE
M5005_Spy_1270c	arcC	1224103	1225053	316	0.0005	NE	0	NE	0.001	NE
M5005_Spy_1271c	-	1225073	1226404	443	0	NE	0	NE	0.001	NE
M5005_Spy_1272c	-	1226421	1227914	497	0	NE	0	NE	0	NE
M5005_Spy_1273c	arcB	1228084	1229097	337	0	NE	0	NE	0	NE
M5005_Spy_1274c	-	1229137	1229565	142	0	NE	0	NE	0	NE
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ME005 0 4075							_			
M5005_Spy_1275c	arcA	1229665	1230900	411	0	NE	0	NE	0	NE
M5005_Spy_1276c	-	1231174	1231854	226	0	NE	0	NE	0.001	NE
M5005_Spy_1277	ahrC.2/argR	1231996	1232469	157	0	NE	0	NE	0	NE
M5005_Spy_1278c	-	1232635	1233351	238	0	NE	0	NE	0	NE
M5005_Spy_1279c	-	1233365	1234444	359	0	NE	0	NE	0	NE
M5005_Spy_1280c	yesM	1234517	1236250	577	0.535	U	0	NE	0	NE
M5005_Spy_1281c	yesN	1236247	1236987	246	0	NE	0	NE	0.001	NE
M5005_Spy_1282c	msrA	1237075	1238181	368	0.00025	NE	0	NE	0.001	NE
M5005_Spy_1283c	tlpA	1238224	1238847	207	0	NE	0	NE	0	NE
M5005_Spy_1284c	ccdA	1238860	1239570	236	0	NE	0	NE	0	NE
M5005_Spy_1285c	-	1240173	1240466	97	0	NE	0	NE	0	NE
M5005_Spy_1286c	-	1240477	1241502	341	0	NE	0	NE	0	NE
M5005_Spy_1287c	-	1241499	1242173	224	0	NE	0	NE	0	NE
M5005_Spy_1288c	-	1242175	1243023	282	0	NE	0	NE	0	NE
M5005_Spy_1289c	-	1243028	1244923	631	0.00025	NE	0	NE	0	NE
M5005_Spy_1290c	-	1244923	1245651	242	0	NE	0	NE	0	NE
M5005_Spy_1291c	-	1245784	1248186	800	0	NE	0	NE	0	NE
M5005_Spy_1292c	valS	1248346	1250751	801	1	Ε	1	Ε	1	Ε
M5005_Spy_1293c	_	1250995	1251558	187	0	NE	0	NE	0	NE
M5005_Spy_1294c	-	1251555	1251734	59	-1	S	-1	S	-1	S
M5005_Spy_1295c	-	1252159	1252554	131	0	NE	0	NE	0	NE
M5005_Spy_1296c	-	1252572	1252826	84	0	NE	0	NE	0	NE
M5005_Spy_1297	aroA2	1253305	1254057	250	0.00025	NE	0	NE	0	NE
M5005_Spy_1298	aroB	1254113	1255186	357	0	NE	0	NE	0	NE
M5005_Spy_1299c	-	1255455	1255613	52	0	NE	0	NE	0	NE
M5005_Spy_1299c	_	1255621	1255926	101	0	NE	0	NE	0	NE
M5005_Spy_1300c	_	1255928	1256266	112	0	NE	0	NE	0	NE
M5005_Spy_1301c	_	1256319	1257074	251	0	NE	0	NE	0	NE
M5005_Spy_1302c	aroE	1257309	1257074	292	0	NE	0	NE	0	NE
M5005_Spy_1304c	lacZ	1257309	1261741	1138	0	NE	0	NE	0	NE
M5005_Spy_1304c	trxR					NE NE			0.001	
	trxS	1261761	1263245	494	0		0	NE		NE
M5005_Spy_1306c		1263245	1264969	574	0	NE	0	NE	0	NE
M5005_Spy_1307c	trxT -	1264959	1265564	201	0	NE	0	NE	0	NE
M5005_Spy_1308c	-	1265870	1267315	481	0	NE	0	NE	0	NE
M5005_Spy_1309c	-	1267396	1268322	308	0	NE	0	NE	0	NE
M5005_Spy_1310c	-	1268332	1269282	316	0	NE	0	NE	0	NE
M5005_Spy_1311	-	1269478	1270356	292	0	NE	0	NE	0	NE
M5005_Spy_1312	-	1270500	1270622	40	-1	S	-1	S	-1	S
M5005_Spy_1313c	-	1270968	1272410	480	0	NE	0	NE	0	NE
M5005_Spy_1314c	hyl	1272434	1274128	564	0	NE	0	NE	0.001	NE
M5005_Spy_1315c	-	1274179	1275219	346	0.00025	NE	0	NE	0	NE
M5005_Spy_1316	-	1275352	1276638	428	0.002	NE	0	NE	0	NE
M5005_Spy_1317	-	1276653	1279358	901	0.001	NE	0	NE	0	NE
M5005_Spy_1318c	rocA	1279459	1280814	451	0	NE	0	NE	0	NE
M5005_Spy_1319c	-	1281479	1282834	451	0	NE	0	NE	0.001	NE
M5005_Spy_1320	recX	1282949	1283725	258	0	NE	0	NE	0	NE
M5005_Spy_1321	-	1283805	1284338	177	0.00025	NE	0	NE	1	E
M5005_Spy_1322c	-	1284437	1284586	49	-1	S	-1	S	-1	S
M5005_Spy_1323	-	1284708	1284986	92	0	NE	0	NE	0	NE
M5005_Spy_1324	-	1291239	1291373	44	-1	S	-1	S	-1	S
M5005_Spy_1325c	-	1292030	1292578	182	0	NE	0	NE	0	NE
M5005_Spy_1326c	comFC	1292658	1293323	221	0.00025	NE	0	NE	0	NE
M5005_Spy_1327c	comFA	1293295	1294509	404	0	NE	0	NE	0	NE
M5005_Spy_1328	-	1294676	1295308	210	0.00025	NE	0	NE	0	NE
M5005_Spy_1329	cysM	1295436	1296377	313	0.00025	NE	0	NE	0	NE
M5005_Spy_1330c	-	1296395	1296772	125	0.00025	NE	0	NE	1	Ε
M5005_Spy_1331c	-	1296772	1298172	466	0	NE	0	NE	0	NE
M5005_Spy_1332c	yvqC	1298209	1298850	213	0	NE	0	NE	0.901	U
M5005_Spy_1333c	yvqE	1298843	1299847	334	0	NE	0	NE	0	NE
M5005_Spy_1334c	yvqF	1299844	1300536	230	0.00025	NE	0	NE	0	NE
M5005_Spy_1335c	-	1300659	1302557	632	1	Е	1	Е	1	E
M5005_Spy_1336c	pppL	1302554	1303294	246	0.003	NE	0.9995	Ε	1	Ε
M5005_Spy_1337c	sunL	1303332	1304654	440	0	NE	0	NE	0	NE
–				-			-			

M5005_Spv_1339s											
MS005_Syn_1340c	M5005_Spy_1338c	fmt	1304644	1305579	311	0.87975	U	1	E	1	E
M5905 Spy, 1341c	M5005_Spy_1339c	priA	1305641	1308025	794	0.00025	NE	0	NE	0.997	Ε
M5005_Syv_1343c	M5005_Spy_1340c	-	1308090	1308407	105	0	NE	0	NE	0	NE
M5005_SPV_1344 abo	M5005_Spy_1341c	gmk	1308423	1309058	211	0.08825	U	1	Ε	0.998	Ε
M5005, Sey, 1344 atoB	M5005_Spy_1342c	-	1309168	1310775	535	0.10175	U	0	NE	0	NE
M5005, Sey, 1344 atoB	M5005_Spy_1343c	-	1310905	1311801	298	0	NE	0	NE	0	NE
MS005, Spv. 1345 atol. 1 313214 313864 216 0 NE 0 NE 0 NE MS005, Spv. 1346 atol. 1 314586 3134525 219 0.00025 NE 0 NE 0 NE MS005, Spv. 1348 - 314588 3136723 3137295 190 0.00025 NE 0 NE 0 NE MS005, Spv. 1349 luxS 3116723 3137295 190 0.00025 NE 0 NE 0 NE MS005, Spv. 1350c -	: :	atoB									
MSD05, Spv, 1346	: :										
MS005 Spv 1348											
MS005 Spv 1348		-									
MS005_Spv_1350c		_									
MS005_Spv_1351c -		luvS									
MS005_Spy_1352	- • • -	_									
MS005_Spy_1354 recU 132166 132145 171 0.00025 NE	: :	_									
MS000_Spy_1355 Pip1A 3121566 3122165 199 0.00025 NE	: :	_									
M5005_Spy_1356c	: :	rocll									
MS000S_Spy_1356c	: :										
M5005_Spy_1358c nadE 1326306 1327130 274 0.948 U	: :										
M5005_Spy_1358c											
M5005_Spy_1350c	: :										
M5005_Spy_1360c	: :										
M5005_Spy_1361c aapA	: :	-									
MS005_Spy_1362c		-									
M5005_Spy_1363c	: :	-									
M5005_Spy_1366c	: :	-									
M5005_Spy_1365c		-	1332357	1333160	267	0		0	NE	0	NE
M5005_Spy_1366c ftsl	M5005_Spy_1364c	-	1333355	1334698	447	1	E	1	E	0.999	E
M5005_Spy_1366c	M5005_Spy_1365c	mraY	1334856	1335866	336		E	1	E	1	Ε
M5005_Spy_1368c mraW 1338455 1339468 337 0 NE 0 NE 1 E M5005_Spy_1370c - 1339492 1341192 416 0 NE 0	M5005_Spy_1366c	ftsI	1335868	1338123	751	0.98025	U	1	E	1	Ε
MS005_Spy_1370c	M5005_Spy_1367c	ftsL	1338127	1338450	107	0.00025	NE	1	Е	1	Е
M5005_Spy_1370c	M5005_Spy_1368c	mraW	1338455	1339468	337	0	NE	0	NE	1	E
M5005_Spy_1371c	M5005_Spy_1369c	-	1339492	1339599	35	-1	S	-1	S	-1	S
M5005_Spy_1372c	M5005_Spy_1370c	proA	1339942	1341192	416	0	NE	0	NE	0	NE
M5005_Spy_1373c - 1343704 1344438 244 0 NE 0 NE 0 NE M5005_Spy_1374c - 134472 1344738 88 0 NE 0 NE 0 NE M5005_Spy_1376c tal 1347134 1347778 214 0 NE 0 NE 0 NE M5005_Spy_1377c - 1347904 1349403 499 0 NE 0 NE 0 NE M5005_Spy_1377c - 1347904 1349403 499 0 NE 0 NE 0 NE M5005_Spy_1379c glpF 1350848 1351549 23 0 NE 0 NE 0 NE M5005_Spy_1381c glpK 1353405 1353389 612 0.00025 NE 0 NE 0 NE M5005_Spy_1388c glyS 135521 1355684 130 0 NE 0 NE	M5005_Spy_1371c	proB	1341185	1342006	273	0	NE	0	NE	0	NE
M5005_Spy_1374c - 1344472 1344738 88 0 NE 0 NE 0 NE M5005_Spy_1375c tkt 1344931 1346916 661 0 NE 0 NE 0.004 NE M5005_Spy_1376c tal 1347904 134903 499 0 NE 0 NE 0 NE M5005_Spy_1377c - 1347904 134903 499 0 NE	M5005_Spy_1372c	proB	1342071	1343699	542	0	NE	0	NE	0	NE
M5005_Spy_1375c tkt 1344931 1346916 661 0 NE 0 NE 0.004 NE M5005_Spy_1377c tal 1347134 1347778 214 0 NE 0 NE 0 NE M5005_Spy_1377c - 1347904 1349403 499 0 NE 0 NE 0 NE M5005_Spy_1378c npx 1349393 1350739 448 0 NE 0 NE 0 NE M5005_Spy_1380c glpF 1350848 1351549 233 0 NE 0 NE 0 NE M5005_Spy_1380c glpO 1351551 1353389 612 0.00025 NE 0 NE <t< td=""><td>M5005_Spy_1373c</td><td>-</td><td>1343704</td><td>1344438</td><td>244</td><td>0</td><td>NE</td><td>0</td><td>NE</td><td>0</td><td>NE</td></t<>	M5005_Spy_1373c	-	1343704	1344438	244	0	NE	0	NE	0	NE
M5005_Spy_1376c tal 1347134 1347778 214 0 NE 0 NE M5005_Spy_1377c - 1347904 134903 499 0 NE 0 NE 0 NE M5005_Spy_1378c npx 1349393 1350739 448 0 NE 0 NE 0 NE M5005_Spy_1387c glpC 1350848 1351549 233 0 NE 0 NE 0 NE M5005_Spy_1380c glpO 1351551 1353349 508 0 NE 0 NE 0 NE M5005_Spy_1381c glpK 1355405 1354931 508 0 NE 0 NE 0 NE M5005_Spy_1382c - 1355891 1356068 85 0 NE 0 NE </td <td>M5005_Spy_1374c</td> <td>-</td> <td>1344472</td> <td>1344738</td> <td>88</td> <td>0</td> <td>NE</td> <td>0</td> <td>NE</td> <td>0</td> <td>NE</td>	M5005_Spy_1374c	-	1344472	1344738	88	0	NE	0	NE	0	NE
M5005_Spy_1377c - 1347904 1349403 499 0 NE 0 NE 0 NE M5005_Spy_1378c npx 1349393 1350739 448 0 NE 0 NE 0 NE M5005_Spy_1389c glpC 1351551 1353389 612 0.00025 NE 0 NE 0 NE M5005_Spy_1381c glpK 1353491 13554931 508 0 NE 0 NE 0 NE M5005_Spy_1382c - 1355811 1355684 130 0 NE 0 NE 0 NE M5005_Spy_1382c - 1355811 1356068 85 0 NE 0 NE 0 NE M5005_Spy_1388c glyS 1356222 1358261 679 0.998 E 1 E 1 E 1 E 1 E 1 E 1 E 1 E 1 E<	M5005_Spy_1375c	tkt	1344931	1346916	661	0	NE	0	NE	0.004	NE
M5005_Spy_1378c npx 1349393 1350739 448 0 NE 0 NE 0 NE M5005_Spy_1379c glpF 1350848 1351549 233 0 NE 0 NE 0 NE M5005_Spy_1380c glpO 1351551 1353389 612 0.00025 NE 0 NE 0 NE M5005_Spy_1381c glpK 1355495 1354931 508 0 NE 0 NE 0 NE M5005_Spy_1382c - 1355291 1355684 130 0 NE 0 NE 0 NE M5005_Spy_1383c - 1355291 1356068 85 0 NE 0 <td>M5005_Spy_1376c</td> <td>tal</td> <td>1347134</td> <td>1347778</td> <td>214</td> <td>0</td> <td>NE</td> <td>0</td> <td>NE</td> <td>0</td> <td>NE</td>	M5005_Spy_1376c	tal	1347134	1347778	214	0	NE	0	NE	0	NE
M5005_Spy_1379c glpF 1350848 1351549 233 0 NE 0 NE 0 NE M5005_Spy_1380c glpO 1351551 1353389 612 0.00025 NE 0 NE 0 NE M5005_Spy_1381c glpK 1353405 13554931 508 0 NE 0 NE 0 NE M5005_Spy_1382c - 1355292 1355684 130 0 NE 0 NE 0 NE M5005_Spy_1383c - 1355811 1356068 85 0 NE 0 NE 0.306 U M5005_Spy_1384c glyQ 1358639 1359556 305 0.9735 U 1 E 1 E 1 E 1 E 1 E 1 E 1 E 1 E 1 E 1 E 1 E 1 E 1 E 1 E 1	M5005_Spy_1377c	-	1347904	1349403	499	0	NE	0	NE	0	NE
M5005_Spy_1380c glpO 1351551 1353389 612 0.00025 NE 0 NE 0 NE M5005_Spy_1381c glpK 1353405 1354931 508 0 NE 0 NE 0 NE M5005_Spy_1382c - 1355292 1355684 130 0 NE 0 NE 0 NE M5005_Spy_1383c - 1355811 1356068 85 0 NE 0 NE 0.306 U M5005_Spy_1384c glyS 1356222 1358261 679 0.998 E 1 E 0 NE 0	M5005_Spy_1378c	npx	1349393	1350739	448	0	NE	0	NE	0	NE
M5005_Spy_1380c glpO 1351551 1353389 612 0.00025 NE 0 NE 0 NE M5005_Spy_1381c glpK 1353405 1354931 508 0 NE 0 NE 0 NE M5005_Spy_1381c - 1355292 1355684 130 0 NE 0 NE 0 NE M5005_Spy_1383c - 1355811 1356068 85 0 NE 0 NE 0.306 U M5005_Spy_1384c glyS 1356222 1358261 679 0.998 E 1 E 0 NE 0	M5005_Spy_1379c	glpF	1350848	1351549	233	0	NE	0	NE	0	NE
M5005_Spy_1381c glpK 1353405 1354931 508 0 NE 0 NE 0 NE M5005_Spy_1382c - 1355292 1355684 130 0 NE 0 NE 0 NE M5005_Spy_1383c - 1355811 1356068 85 0 NE 0 NE 0.306 U M5005_Spy_1384c glyS 1356222 1358261 679 0.998 E 1 E 1 E M5005_Spy_1385c glyQ 1358639 1359556 305 0.9735 U 1 E 1 E 1 E M M NE 0	M5005_Spy_1380c							0		0	
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M5005_Spy_1389c - 1362820 1364469 549 0 NE 0 NE 0 NE M5005_Spy_1390 - 1364653 1365375 240 0 NE 0 NE 0 NE M5005_Spy_1391c - 1365504 1366346 280 0 NE 0 NE 0 NE M5005_Spy_1392 - 1366639 1367196 185 0.00025 NE 0 NE 0 NE M5005_Spy_1393c - 1367232 1368056 274 0 NE 0 NE 0 NE M5005_Spy_1394c - 1368058 1368675 205 0 NE 0 NE 0 NE M5005_Spy_1395c lacD.1 1368872 1369849 325 0 NE 0 NE 0 NE M5005_Spy_1397c lacB.1 1370359 1370874 171 0 NE 0 NE											
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M5005_Spy_1396c lacC1 1369999 1370349 116 0 NE 0 NE 0 NE M5005_Spy_1397c lacB.1 1370359 1370874 171 0 NE 0 NE 0 NE M5005_Spy_1398c lacA.1 1370889 1371314 141 0 NE 0 NE 0 NE M5005_Spy_1399c - 1371554 1373002 482 0 NE 0 NE 0 NE		lacD 1									
M5005_Spy_1397c lacB.1 1370359 1370874 171 0 NE 0 NE 0 NE M5005_Spy_1398c lacA.1 1370889 1371314 141 0 NE 0 NE 0 NE M5005_Spy_1399c - 1371554 1373002 482 0 NE 0 NE 0 NE											
M5005_Spy_1398c lacA.1 1370889 1371314 141 0 NE 0 NE 0 NE M5005_Spy_1399c - 1371554 1373002 482 0 NE 0 NE 0 NE	: :										
M5005_Spy_1399c - 1371554 1373002 482 0 NE 0 NE 0 NE											
13/3031 13/3330 101 U NE U NE U NE		-									
	1.12002_2hA_1400C	-	13/3031	13/3330	101	U	INE	U	INE	U	INE

M5005_Spy_1401c	-	1373329	1373802	157	0	NE	0	NE	0	NE
M5005_Spy_1402	lacR.1	1374039	1374809	256	0	NE	0	NE	0	NE
M5005_Spy_1403c	-	1374836	1375006	56	0.00025	NE	0.0005	NE	0	NE
M5005_Spy_1404c	copZ	1375013	1375216	67	0	NE	0	NE	0	NE
M5005_Spy_1405c	copA	1375230	1377461	743	0	NE	0	NE	0	NE
M5005_Spy_1406c	copY	1377461	1377895	144	0	NE	0	NE	0	NE
M5005_Spy_1407	-	1378067	1379053	328	0	NE	0	NE	0	NE
M5005_Spy_1408c	rbfA	1379187	1379543	118	0.00025	NE	0	NE	0.992	E
M5005_Spy_1409c	infB	1379742	1382603	953	1	E	1	Е	1	E
M5005_Spy_1410c	-	1382623	1382925	100	0.00025	NE	0.0005	NE	0.999	E
M5005_Spy_1411c	-	1382918	1383214	98	0.00225	NE	0.00125	NE	1	Е
M5005_Spy_1412c	nusA	1383230	1384387	385	1	Ε	1	Ε	1	Ε
M5005_Spy_1413c	-	1384562	1385098	178	0	NE	0	NE	0.001	NE
M5005_Spy_1414c	-	1385343	1385522	59	-1	S	-1	S	-1	S
M5005_Spy_1415c	sdaD2	1385761	1386933	390	0	NE	0	NE	0	NE
M5005_Spy_1416c	-						0		0	
		1387049	1388245	398	0	NE		NE		NE
M5005_Spy_1417c	-	1388356	1388541	61	0	NE	0	NE	0	NE
M5005_Spy_1418c	-	1388538	1388837	99	0	NE	0	NE	0	NE
M5005_Spy_1419c	-	1388848	1389468	206	0	NE	0	NE	0	NE
M5005_Spy_1420c	-	1389471	1389632	53	-1	S	-1	S	-1	S
M5005_Spy_1421c	-	1389641	1391548	635	0	NE	0	NE	0.001	NE
M5005_Spy_1422c	-	1391559	1392194	211	0	NE	0	NE	0	NE
M5005_Spy_1423c	_	1392194	1393249	351	0	NE	0	NE	0	NE
M5005_Spy_1424c	_	1393246	1395228	660	0	NE	0	NE	0	NE
M5005_Spy_1425c	-	1395238	1396080	280	0	NE	0	NE	0	NE
M5005_Spy_1426c	-	1396092	1400474	1460	0	NE	0	NE	0	NE
M5005_Spy_1427c	-	1400489	1400722	77	0	NE	0	NE	0	NE
M5005_Spy_1428c	-	1400797	1401252	151	0	NE	0	NE	0	NE
M5005_Spy_1429c	-	1401306	1401905	199	0	NE	0	NE	0	NE
M5005_Spy_1430c	-	1401917	1402276	119	0.00025	NE	0	NE	0	NE
M5005_Spy_1431c	-	1402280	1402606	108	0	NE	0	NE	0	NE
M5005_Spy_1432c	_	1402621	1402899	92	0	NE	0	NE	0	NE
M5005_Spy_1433c	_	1402910	1403266	118	0.00025	NE	0	NE	0	NE
M5005_Spy_1434c	-	1403278	1404165	295	0	NE	0	NE	0	NE
M5005_Spy_1435c	-	1404178	1404747	189	0	NE	0	NE	0	NE
M5005_Spy_1436c	-	1404903	1405169	88	0	NE	0	NE	0	NE
M5005_Spy_1437c	-	1405172	1405360	62	0	NE	0	NE	0	NE
M5005_Spy_1438c	-	1405391	1406830	479	0	NE	0	NE	0	NE
M5005_Spy_1439c	-	1406796	1408328	510	0	NE	0	NE	0	NE
M5005_Spy_1440c	-	1408344	1409621	425	0	NE	0	NE	0	NE
M5005_Spy_1441c	-	1409611	1410105	164	0	NE	0	NE	0	NE
M5005_Spy_1442c	_	1410153	1410569	138	0	NE	0	NE	0	NE
M5005_Spy_1443c	_	1410566	1410757	63	0	NE	0	NE	0	NE
M5005_Spy_1444c	-	1410747	1411598	283	0.00025	NE	0	NE	0	NE
M5005_Spy_1445c	-	1411607	1411873	88	0	NE	0	NE	0	NE
M5005_Spy_1446c	-	1411870	1412037	55	-1	S	-1	S	-1	S
M5005_Spy_1447c	-	1412038	1413360	440	0	NE	0	NE	0	NE
M5005_Spy_1448c	-	1413357	1413632	91	0	NE	0	NE	0	NE
M5005_Spy_1449c	-	1414019	1416403	794	0	NE	0	NE	0	NE
M5005_Spy_1450c	-	1416408	1418330	640	0	NE	0	NE	0	NE
M5005_Spy_1451c	_	1418373	1418930	185	0	NE	0	NE	0	NE
M5005_Spy_1452c	_	1418941	1419339	132	0.00025	NE	0	NE	0	NE
M5005_Spy_1453c	_									
	_	1419343	1420497	384	0	NE	0	NE	0	NE
M5005_Spy_1454c	-	1420497	1420796	99	0.0285	NE	0	NE	0	NE
M5005_Spy_1455c	-	1420884	1421087	67	0.05025	U	0	NE	0	NE
M5005_Spy_1456c	-	1421084	1421236	50	-1	S	-1	S	-1	S
M5005_Spy_1457c	-	1421233	1421619	128	0.00025	NE	0	NE	0.001	NE
M5005_Spy_1458c	-	1421616	1421819	67	0	NE	0	NE	0.127	U
M5005_Spy_1459c	-	1421812	1421982	56	-1	S	-1	S	-1	S
M5005_Spy_1460c	-	1421979	1422254	91	0.424	U	0	NE	0.001	NE
M5005_Spy_1461c	_	1421373	1422531	71	0.001	NE	0.0005	NE	0.001	NE
M5005_Spy_1461C	-									
M5005_Spy_1462 M5005_Spy_1463c	=	1422579	1422992	137	0.00025	NE	0	NE	0	NE
1.12002 2hA 1402C	-	1422973	1423128	51	-1	S	-1	S	-1	S

M5005_Spy_1464	-	1423403	1423804	133	0.99925	E	0.99975	Ε	1	E
M5005_Spy_1465	-	1423818	1424201	127	0	NE	0	NE	0	NE
M5005_Spy_1466	-	1424212	1424763	183	0.00025	NE	0	NE	0	NE
M5005_Spy_1467	int.3	1424880	1425959	359	0	NE	0	NE	0	NE
M5005_Spy_1468c	trmB	1426157	1426792	211	0	NE	0	NE	0	NE
M5005_Spy_1469c	-	1426792	1427583	263	0.9995	Е	1	Е	1	Е
M5005_Spy_1470c	-	1427647	1428681	344	0	NE	0	NE	0	NE
M5005_Spy_1471c	_	1428684	1429409	241	0	NE	0	NE	0	NE
M5005_Spy_1472	hit	1429481	1429900	139	0	NE	0	NE	0	NE
M5005_Spy_1472	-	1429897		118	0	NE	0	NE	0	NE
	lytR		1430253							
M5005_Spy_1474c	- -	1430364	1431638	424	0	NE	0	NE	0	NE
M5005_Spy_1475c	-	1431647	1432171	174	0	NE	0	NE	0	NE
M5005_Spy_1476c	-	1432146	1432607	153	0.00025	NE	0	NE	0.924	U
M5005_Spy_1477c	-	1432761	1434221	486	0	NE	0	NE	0	NE
M5005_Spy_1478	-	1434485	1435297	270	0	NE	0	NE	0	NE
M5005_Spy_1479	manL	1435649	1436641	330	0.00025	NE	0	NE	0	NE
M5005_Spy_1480	manM	1436730	1437539	269	0.00025	NE	0	NE	0	NE
M5005_Spy_1481	manN	1437556	1438467	303	0	NE	0	NE	0	NE
M5005_Spy_1482	manO	1438581	1438940	119	0	NE	0	NE	0	NE
M5005_Spy_1483	serS	1439332	1440609	425	0.9995	E	1	Ε	1	Ε
M5005_Spy_1484c	accD	1440831	1441601	256	0.032	NE	1	Ε	1	Е
M5005_Spy_1485c	accA	1441598	1442464	288	0.99925	E	1	Ε	1	Е
M5005_Spy_1486c	accC	1442473	1443837	454	0.9925	U	1	Ε	1	Ε
M5005_Spy_1487c	fabZ	1443869	1444291	140	0	NE	0.00075	NE	1	Е
M5005_Spy_1488c	accB	1444288	1444788	166	0.9815	U	1	E	1	E
M5005_Spy_1489c	fabF	1444790	1446022	410	1	E	1	E	1	E
M5005_Spy_1490c	fabG	1446037	1446771	244	0.00025	NE	1	E	0.994	E
M5005_Spy_1491c	fabD	1446761	1447699	312	0.00025	NE	1	E	1	E
							0.15275			
M5005_Spy_1492c	fabK	1447724	1448695	323	0.00325	NE		U	0.999	E
M5005_Spy_1493c	acpP	1448897	1449121	74	0.00025	NE -	1	E	0.997	E
M5005_Spy_1494c	fabH	1449182	1450156	324	1	E	1	E	1	E
M5005_Spy_1495c		1450157	1450591	144	0	NE	0	NE	0.857	U
M5005_Spy_1496c	phaB	1450668	1451459	263	1	Е	1	E	1	E
M5005_Spy_1497c	dnaJ	1451679	1452836	385	1	E	1	E	1	E
M5005_Spy_1498c	dnaK	1453117	1454943	608	1	Е	1	E	1	E
M5005_Spy_1499c	grpE	1455124	1455657	177	0.99525	Е	1	E	1	E
M5005_Spy_1500c	hrcA	1455699	1456733	344	0.00025	NE	0.00025	NE	1	Е
M5005_Spy_1501c	-	1456868	1457437	189	0.00025	NE	0	NE	0.001	NE
M5005_Spy_1502c	-	1457434	1458177	247	0	NE	0	NE	0	NE
M5005_Spy_1503c	-	1458167	1458874	235	0	NE	0	NE	0	NE
M5005_Spy_1504c	-	1459265	1459513	82	0	NE	0	NE	0	NE
M5005_Spy_1505c	-	1459723	1459938	71	0	NE	0	NE	0	NE
M5005_Spy_1506c	gatB	1459935	1461374	479	1	Е	1	Е	1	Е
M5005_Spy_1507c	gatA	1461374	1462840	488	1	E	1	E	1	E
M5005_Spy_1508c	gatC	1462840	1463142	100	0.97625	Ū	1	E	0.997	E
M5005_Spy_1509c	-	1463374	1463583	69	0.57025	NE	0	NE	0	NE
M5005_Spy_1509c	_	1463555	1463671	38	-1	S	-1	S	-1	S
M5005_Spy_1510c	-	1463333	1463671	38 148	0	NE	0	NE	0	NE
					0.00575		0.0005			
M5005_Spy_1512c	codY	1464838	1465620	260		NE		NE	1	E
M5005_Spy_1513c	-	1465838	1467052	404	0	NE	0	NE	0	NE
M5005_Spy_1514	-	1467283	1467735	150	0.00025	NE	0	NE	0.001	NE
M5005_Spy_1515c	-	1467858	1469135	425	0.00025	NE	0	NE	0	NE
M5005_Spy_1516	asnB	1469318	1470283	321	0	NE	0	NE	0	NE
M5005_Spy_1517c	-	1470632	1471336	234	0	NE	0	NE	0	NE
M5005_Spy_1518c	-	1471349	1472251	300	0.00025	NE	0	NE	0	NE
M5005_Spy_1519c	recG	1472544	1474559	671	0	NE	0	NE	0	NE
M5005_Spy_1520	-	1474652	1474852	66	0.00275	NE	0	NE	0	NE
M5005_Spy_1521c	-	1474934	1476388	484	0	NE	0	NE	0	NE
M5005_Spy_1522c	-	1476325	1477005	226	0	NE	0	NE	0	NE
M5005_Spy_1523c	-	1477002	1477595	197	0	NE	0	NE	0	NE
M5005_Spy_1524c	cycC	1477592	1479262	556	0	NE	0	NE	0	NE
M5005_Spy_1525c	cycD	1479255	1481018	587	0	NE	0	NE	0	NE
M5005_Spy_1526c	fhuC	1481015	1481851	278	0	NE	0	NE	0	NE
		1.51015	2.02001	2,0	•		J		J	

ME00E 0 4E0E	g						_			
M5005_Spy_1527c	fhuB2	1481848	1482870	340	0	NE	0	NE	0	NE
M5005_Spy_1528c	fhuD2	1482872	1483756	294	0	NE	0	NE	0	NE
M5005_Spy_1529c	shp	1483740	1484615	291	0	NE	0	NE	0	NE
M5005_Spy_1530c	-	1484812	1488639	1275	0	NE	0	NE	0	NE
M5005_Spy_1531c	isp2	1489128	1490639	503	0	NE	0	NE	0	NE
M5005_Spy_1532c	alr	1490726	1491826	366	0.99575	E	0.9555	U	1	E
M5005_Spy_1533c	acpS	1491823	1492179	118	0.999	E	0.05675	NE	1	E
	secA									
M5005_Spy_1534c	SECA	1492295	1494814	839	1	E	1	E	1	E
M5005_Spy_1535c	-	1494892	1494996	34	-1	S	-1	S	-1	S
M5005_Spy_1536c	-	1494980	1495495	171	0	NE	0	NE	0	NE
M5005_Spy_1537c	-	1495398	1496102	234	0	NE	0	NE	0	NE
M5005_Spy_1538c	pmi	1496264	1497217	317	0	NE	0	NE	0	NE
M5005_Spy_1539c	scrK	1497312	1498268	318	0	NE	0	NE	0	NE
M5005_Spy_1540c	endoS	1498460	1501447	995	0	NE	0	NE	0	NE
M5005_Spy_1541c	-	1501471	1501635	54	-1	S	-1	S	-1	S
M5005_Spy_1542c	scrA	1501471	1503561	627	0.00025	NE	0	NE	0	NE
* *										
M5005_Spy_1543	scrB	1503803	1505242	479	0.00025	NE	0.00025	NE	0.001	NE
M5005_Spy_1544	scrR	1505247	1506212	321	0	NE	0	NE	0	NE
M5005_Spy_1545c	nusB	1506353	1506805	150	0.00025	NE	0	NE	1	E
M5005_Spy_1546c	-	1506798	1507187	129	0	NE	0	NE	0.896	U
M5005_Spy_1547c	efp	1507233	1507790	185	0	NE	0	NE	0	NE
M5005_Spy_1548c	comEB	1507886	1508347	153	0	NE	0	NE	0	NE
M5005_Spy_1549c	pepP	1508382	1509455	357	0	NE	0	NE	0	NE
M5005_Spy_1550c	uvrA	1509570	1512428	952	0.00025	NE	0	NE	0	NE
M5005_Spy_15500	corA									
- 17-	COTA	1512601	1513545	314	0.00075	NE	1	E	1	E
M5005_Spy_1552		1513678	1514334	218	0	NE	0	NE	0	NE
M5005_Spy_1553c	rpsR	1514467	1514706	79	0.91925	U	0.997	E	0.99	U
M5005_Spy_1554c	ssb3	1514871	1515362	163	0.00025	NE	0	NE	0.295	U
M5005_Spy_1555c	rpsF	1515384	1515674	96	0.987	U	0	NE	0.172	U
M5005_Spy_1556c	-	1515847	1516140	97	0	NE	0	NE	0	NE
M5005_Spy_1557	mutY	1516461	1517462	333	0	NE	0	NE	0	NE
M5005_Spy_1558	-	1517538	1518125	195	0	NE	0	NE	0	NE
M5005_Spy_1559c	trx	1518177	1518491	104	0.00025	NE	0	NE	0.018	NE
M5005_Spy_1560c	-	1518572	1519075	167	0.00023	NE	0	NE	0.018	NE
* *										
M5005_Spy_1561c	mutS2	1519076	1521415	779	0.0015	NE	0	NE	0	NE
M5005_Spy_1562c	-	1521564	1522109	181	0.00025	NE	0	NE	0	NE
M5005_Spy_1563c	-	1522112	1522420	102	0	NE	0	NE	0	NE
M5005_Spy_1564	-	1522577	1523479	300	0.1885	U	0.00025	NE	1	E
M5005_Spy_1565	spi	1523490	1524083	197	0.75	U	1	Ε	1	Ε
M5005_Spy_1566	recD	1524141	1526594	817	0	NE	0	NE	0	NE
M5005_Spy_1567	-	1526685	1527167	160	0.00025	NE	0	NE	0.001	NE
M5005_Spy_1568c	dinP	1527260	1528354	364	0	NE	0	NE	0	NE
M5005_Spy_1569	pfl	1528563	1530890	775	0	NE	0	NE	0	NE
M5005_Spy_1570c	Pii									
	- ^	1531068	1532018	316	0	NE	0	NE	0	NE
M5005_Spy_1571c	сррА	1532003	1532755	250	0	NE	0	NE	0	NE
M5005_Spy_1572	-	1533053	1533949	298	0	NE	0	NE	0.001	NE
M5005_Spy_1573c	glpF.2	1534285	1535133	282	0.00025	NE	0.00025	NE	1	E
M5005_Spy_1574c	-	1535303	1535449	48	-1	S	-1	S	-1	S
M5005_Spy_1575c	norA	1535635	1536831	398	0.00025	NE	0	NE	0	NE
M5005_Spy_1576	srv	1536937	1537656	239	0	NE	0	NE	0	NE
M5005_Spy_1577	pepXP	1537678	1539960	760	0	NE	0	NE	0	NE
M5005_Spy_1578c		1540040	1540261	73	0	NE	0	NE	0	NE
M5005_Spy_1579	_	1540431	1540805	124	0.00025	NE	0	NE	0	NE
M5005_Spy_1580	-	1540998	1541297	99	0	NE	0	NE	0	NE
M5005_Spy_1581c	-	1541354	1542091	245	0	NE	0	NE	0	NE
M5005_Spy_1582c	dnaQ	1542240	1542827	195	0	NE	0	NE	0	NE
M5005_Spy_1583c	-	1542876	1543406	176	0	NE	0	NE	0.001	NE
M5005_Spy_1584	-	1543612	1544781	389	0	NE	0	NE	0	NE
M5005_Spy_1585c	deoC	1544876	1545547	223	0.00025	NE	0	NE	0	NE
M5005_Spy_1586c	nupC	1545577	1546779	400	0	NE	0	NE	0	NE
M5005_Spy_1587c	udp	1546800	1547579	259	0.00025	NE	0	NE	0	NE
M5005_Spy_1588c		1547644	1547745	33	-1	S	-1	S	-1	S
M5005_Spy_15880	crgR					NE				
112002 2hy_1203	cign	1547819	1548562	247	0	INE	0	NE	0	NE

M5005_Spy_1590	rpsN	1548798	1549067	89	0	NE	0	NE	0	NE
M5005_Spy_1591c	gcp	1549238	1550266	342	0.00025	NE	1	Ε	0.998	Ε
M5005_Spy_1592c	-	1550256	1550711	151	0	NE	0	NE	0	NE
M5005_Spy_1593c	-	1550683	1551381	232	0.00025	NE	0.6645	U	1	Ε
M5005_Spy_1594	-	1551666	1551896	76	0.00025	NE	1	Ε	1	Ε
M5005_Spy_1595	-	1551898	1553580	560	0.99875	Ε	1	Ε	1	Ε
M5005_Spy_1596c	glnA	1553807	1555153	448	0	NE	0	NE	0.001	NE
M5005_Spy_1597c	glnR	1555191	1555562	123	0	NE	0	NE	0	NE
M5005_Spy_1598c	-	1555629	1556180	183	0.00025	NE	0	NE	0.001	NE
M5005_Spy_1599c	pgk	1556443	1557639	398	0.999	E	1	E	1	E
M5005_Spy_1600c	lppC	1557832	1558686	284	0.555	NE	0	NE	0	NE
M5005_Spy_1601c	-	1558916	1559806	296	0	NE	0	NE	0	NE
M5005_Spy_1602c	_	1560043	1561707	554	1	E	1	E	1	E
M5005_Spy_1603c		1561707	1562072	121	0	NE	0	NE	0.001	NE
M5005_Spy_1604c	asp	1562097	1562234	45	-1	S	-1	S	-1	S
M5005_Spy_1605c	_						0		0	
	- D	1562239	1563372	377	0	NE		NE		NE
M5005_Spy_1606c	rpmB	1563550	1563738	62	0.00175	NE	0	NE	0	NE
M5005_Spy_1607c	fba	1564120	1565001	293	1	E	1	E	1	E
M5005_Spy_1608c	-	1565347	1566273	308	0	NE	0	NE	0	NE
M5005_Spy_1610c	pyrG	1567892	1568044	50	0	NE	0	NE	0	NE
M5005_Spy_1611c	rpoE	1568301	1568876	191	0	NE	0	NE	0	NE
M5005_Spy_1612c	tig/ropA	1569093	1570376	427	0.00025	NE	0	NE	0	NE
M5005_Spy_1613	-	1570697	1571542	281	0	NE	0	NE	0.001	NE
M5005_Spy_1614c	-	1571607	1572167	186	0	NE	0	NE	0	NE
M5005_Spy_1615c	-	1572181	1572651	156	0	NE	0	NE	0	NE
M5005_Spy_1616c	thiD	1572641	1573405	254	0	NE	0	NE	0	NE
M5005_Spy_1617c	truA	1573395	1574144	249	0	NE	0	NE	0	NE
M5005_Spy_1618c	comX.2	1574329	1574880	183	0	NE	0	NE	0	NE
M5005_Spy_1619	-	1580302	1580436	44	-1	S	-1	S	-1	S
M5005_Spy_1620c	-	1580598	1581740	380	0.00025	NE	0	NE	0	NE
M5005_Spy_1621	hsdR	1582022	1585000	992	0	NE	0	NE	0	NE
M5005_Spy_1622	hsdS	1585013	1586212	399	0	NE	0	NE	0	NE
M5005_Spy_1623	hsdM	1586225	1587805	526	0.00025	NE	0	NE	0	NE
M5005_Spy_1624c	-	1588015	1588206	63	0	NE	0	NE	0	NE
M5005_Spy_1625c	salR	1588358	1588963	201	0	NE	0	NE	0	NE
M5005_Spy_1626c	salK	1588944	1590506	520	0	NE	0	NE	0	NE
M5005_Spy_1627c	salY	1590546	1592453	635	0	NE	0	NE	0	NE
M5005_Spy_1628c	salX	1592455	1593192	245	0	NE	0	NE	0	NE
M5005_Spy_1629c	salX/salT	1593189	1593650	153	0	NE	0	NE	0	NE
M5005_Spy_1630c	salB	1593724	1595349	541	0	NE	0	NE	0	NE
M5005_Spy_1631c	salA	1595432	1595578	48	-1	S	-1	S	-1	S
M5005_Spy_1632c	lacG	1596090	1597496	468	0	NE	0	NE	0	NE
M5005_Spy_1633c	lacE	1597584	1599281	565	0.00075	NE	0.017	NE	0	NE
M5005_Spy_1634c	lacF	1599281	1599598	105	0	NE	0	NE	0	NE
M5005_Spy_1635c	lacD.2	1599622	1600605	327	0	NE	0	NE	0	NE
M5005_Spy_1636c	lacC.2	1600609	1601538	309	0	NE	0	NE	0	NE
M5005_Spy_1637c	lacB.2	1601586	1602101	171	0	NE	0	NE	0	NE
M5005_Spy_1638c	lacA.2	1602136	1602564	142	0	NE	0	NE	0	NE
M5005_Spy_1639	lacR.2	1603011	1603784	257	0	NE	0	NE	0	NE
M5005_Spy_1640	laciv.2	1604445		95			0		0	
M5005_Spy_1641	_		1604732		0	NE		NE		NE
M5005_Spy_1641 M5005_Spy_1642	-	1604722	1605057	111	0	NE	0	NE	0	NE
	-	1605209	1605391	60	0	NE	0	NE	0.003	NE
M5005_Spy_1643	-	1605380	1605565	61	-1	S	-1	S	-1	S
M5005_Spy_1644c	-	1605479	1605679	66	-1	S	-1	S	-1	S
M5005_Spy_1645	- 	1606013	1606162	49	-1	S	-1	S	-1	S
M5005_Spy_1646c	rpsI	1606282	1606674	130	0.0005	NE	0.0005	NE -	0.445	U
M5005_Spy_1647c	rplM	1606695	1607141	148	0.00025	NE	0.9995	E	0.001	NE
M5005_Spy_1648c	-	1607359	1607565	68	0.0215	NE	0	NE	0.074	U
M5005_Spy_1649c	-	1607562	1608068	168	0	NE	0	NE	0	NE
M5005_Spy_1650c	-	1608204	1609064	286	0	NE	0	NE	0.001	NE
M5005_Spy_1651c	-	1609161	1609679	172	0	NE	0	NE	0	NE
M5005_Spy_1652c	-	1609683	1610429	248	0	NE	0	NE	0	NE
M5005_Spy_1653c	-	1610476	1611273	265	0	NE	0	NE	0	NE

M5005_Spy_1654c	-	1611469	1611882	137	0	NE	0	NE	0	NE
M5005_Spy_1655c	cysS	1611875	1613218	447	1	E	1	E	0.992	E
M5005_Spy_1656c	-	1613246	1613476	76	0	NE	0	NE	0	NE
M5005_Spy_1657c	-	1613489	1613761	90	0	NE	0	NE	0	NE
M5005_Spy_1658c	cysE	1613955	1614536	193	0.958	U	0.9995	E	0.791	U
M5005_Spy_1659c	-	1614545	1615297	250	0.00025	NE	0	NE	0.001	NE
M5005_Spy_1660c	pnp	1615290	1617422	710	0	NE	0	NE	0	NE
M5005_Spy_1661c	-	1617703	1618431	242	0	NE	0	NE	0	NE
M5005_Spy_1662c	ulaA	1618587	1619822	411	0	NE	0	NE	0	NE
M5005_Spy_1663c	-	1619849	1620133	94	0.00025	NE	0	NE	0	NE
M5005_Spy_1664c	_	1620126	1622186	686	0	NE	0	NE	0	NE
M5005_Spy_1665c	_	1622411	1622554	47	-1	S	-1	S	-1	S
M5005_Spy_1666c	rpsO	1622538	1622807	89	0.65075	U	0	NE	0.755	U
M5005_Spy_1667c	-	1622965	1623120	51	-1	S	-1	S	-1	S
M5005_Spy_1668	_	1623246		89	0	NE	0	NE NE	0	NE NE
			1623515							
M5005_Spy_1669	def -	1623616	1624230	204	0.93575	U	1	E	1	E
M5005_Spy_1670c		1624264	1624806	180	0	NE	0	NE	0	NE
M5005_Spy_1671c	-	1624937	1625365	142	0	NE	0	NE	0	NE
M5005_Spy_1672c	polC	1625475	1629872	1465	1	E	1	E	1	E
M5005_Spy_1673c	proS	1630127	1631983	618	1	E	1	E	1	E
M5005_Spy_1674c	eep	1632181	1633440	419	0	NE	0	NE	0	NE
M5005_Spy_1675c	cdsA	1633513	1634307	264	1	E	1	E	1	Ε
M5005_Spy_1676c	uppS	1634320	1635069	249	0.9755	U	1	Е	0.999	Ε
M5005_Spy_1677c	yajC	1635288	1635653	121	0	NE	0	NE	0	NE
M5005_Spy_1678c	-	1635769	1636116	115	0	NE	0	NE	0	NE
M5005_Spy_1680c	pulA	1638902	1639783	293	0	NE	0	NE	0	NE
M5005_Spy_1681c	dexB	1639954	1641567	537	0	NE	0	NE	0	NE
M5005_Spy_1682c	msmK	1641696	1642829	377	0	NE	0	NE	0	NE
M5005_Spy_1683c	lrp	1643127	1643975	282	0	NE	0	NE	0	NE
M5005_Spy_1684	ska	1644335	1645657	440	0	NE	0	NE	0	NE
M5005_Spy_1685c	dtd	1645755	1646198	147	0	NE	0	NE	0	NE
M5005_Spy_1686c	relA	1646213	1648432	739	0.00125	NE	1	E	1	E
M5005_Spy_1687c	scIA	1648684	1648827	47	0.00123	NE	0	NE	0	NE
M5005_Spy_1690	nrdI2	1650113	1650595	160	0	NE	0	NE	0.001	NE
M5005_Spy_1691c	-	1650989	1651807	272	0	NE	0	NE	0.001	NE
M5005_Spy_1693c	_						0		0	
	_	1653782	1654075	97	0	NE		NE		NE
M5005_Spy_1694c	- num 1	1654433	1655182	249	0	NE	0	NE	0	NE
M5005_Spy_1695c	prmA	1655182	1656135	317	0	NE	0	NE	0	NE
M5005_Spy_1696c	- 	1656206	1656676	156	0	NE	0	NE	0	NE
M5005_Spy_1697	papB	1656876	1658633	585	0	NE	0	NE	0	NE
M5005_Spy_1698	trpG	1658666	1659232	188	0	NE	0	NE	0.621	U
M5005_Spy_1699	-	1659265	1660533	422	0	NE	0	NE	0	NE
M5005_Spy_1700	pai1	1661030	1661470	146	0	NE	0	NE	0	NE
M5005_Spy_1701	flaR	1661525	1662031	168	0	NE	0	NE	0	NE
M5005_Spy_1702	smeZ	1662280	1662981	233	0	NE	0	NE	0	NE
M5005_Spy_1703c	-	1663265	1663531	88	0	NE	0	NE	0	NE
M5005_Spy_1704	dppA	1663710	1665338	542	0	NE	0	NE	0	NE
M5005_Spy_1705	dppB	1665451	1666428	325	0	NE	0	NE	0	NE
M5005_Spy_1706	dppC	1666425	1667246	273	0.00025	NE	0	NE	0	NE
M5005_Spy_1707	dppD	1667258	1668061	267	0	NE	0	NE	0	NE
M5005_Spy_1708	dppE	1668045	1668671	208	0	NE	0	NE	0	NE
M5005_Spy_1709c	-	1668752	1668952	66	0	NE	0	NE	0	NE
M5005_Spy_1710c	-	1669121	1671598	825	0.0025	NE	0	NE	0	NE
M5005_Spy_1711c	lmb	1671611	1672531	306	0	NE	0	NE	0	NE
M5005_Spy_1712c	-	1672709	1673842	377	0	NE	0	NE	0	NE
M5005_Spy_1713c	-	1673896	1674048	50	-1	S	-1	S	-1	S
M5005_Spy_1714c	-	1674093	1675160	355	0	NE	0	NE NE	0	NE NE
M5005_Spy_1714c	scpA	1675257	1678751	333 1164	0	NE NE	0	NE NE	0	NE
M5005_Spy_1715C	SCPA						0			
	-	1679185	1680390	401	0	NE		NE	0	NE
M5005_Spy_1717	- cic1_01	1680369	1680551	60	-1	S	-1	S	-1	S
M5005_Spy_1718c	sic1.01	1680969	1681910	313	0	NE	0	NE	0	NE
M5005_Spy_1719c M5005_Spy_1720c	emm1.0	1682099	1683553	484	0	NE	0	NE	0	NE
1/10000_3py_1/20C	mga	1683738	1685327	529	0	NE	0	NE	0	NE

145005 0 4704							_			
M5005_Spy_1721	-	1685712	1685897	61	0.9495	U	0	NE	0.003	NE
M5005_Spy_1722c	-	1686003	1686254	83	0	NE	0	NE	0	NE
M5005_Spy_1723c	isp	1686333	1687934	533	0.00025	NE	0	NE	0	NE
M5005_Spy_1724c	ihk	1688036	1689424	462	0	NE	0	NE	0	NE
M5005_Spy_1725c	irr	1689421	1690074	217	0	NE	0	NE	0	NE
M5005_Spy_1726c	-	1690168	1691385	405	0	NE	0	NE	0	NE
M5005_Spy_1727c	-	1691398	1692072	224	0	NE	0	NE	0	NE
M5005_Spy_1728c	-	1692059	1693327	422	0	NE	0	NE	0	NE
M5005_Spy_1729c	_	1693750	1694154	134	0.00175	NE	0	NE	0	NE
M5005_Spy_1730c	_	1694181	1694477	98	0.00173	NE	0	NE	0	NE
M5005_Spy_17300 M5005_Spy_1731	grm	1694721	1694957	78	0	NE	0	NE	0	NE
	=									
M5005_Spy_1732c	prsA	1695233	1696162	309	0.00025	NE	0	NE	1	E
M5005_Spy_1733c	-	1696218	1696535	105	0	NE	0	NE	0	NE
M5005_Spy_1734c		1696642	1696947	101	0	NE	0.00025	NE	0.003	NE
M5005_Spy_1735c	speB	1696949	1698145	398	0	NE	0	NE	0	NE
M5005_Spy_1736	-	1698670	1698801	43	-1	S	-1	S	-1	S
M5005_Spy_1737	rgg	1699085	1699927	280	0	NE	0	NE	0	NE
M5005_Spy_1738c	spd	1700168	1700983	271	0	NE	0	NE	0	NE
M5005_Spy_1739	-	1701067	1701195	42	-1	S	-1	S	-1	S
M5005_Spy_1740	-	1701347	1701856	169	0	NE	0	NE	0	NE
M5005_Spy_1741c	gldA	1701938	1703026	362	0	NE	0	NE	0	NE
M5005_Spy_1742c	mipB	1703083	1703751	222	0	NE	0	NE	0	NE
M5005_Spy_1743c	pflD	1703764	1706136	790	0	NE	0	NE	0	NE
M5005_Spy_1744c	· _	1706391	1707695	434	0	NE	0	NE	0	NE
M5005 Spy 1745c	_	1707705	1708013	102	0	NE	0	NE	0	NE
M5005_Spy_1746c	_	1708041	1708361	106	0	NE	0	NE	0	NE
M5005_Spy_1747c	_	1708649	1709629	326	0	NE	0	NE	0	NE
M5005_Spy_1748c	_	1709645	1710394	249	0	NE	0	NE	0	NE
M5005_Spy_1749	_	1710517	1711290	257	0	NE	0	NE	0	NE
M5005_Spy_1749	_					NE	0	NE	0	NE
* *	- cocE	1711325	1711525	66 50	0					
M5005_Spy_1751c	secE	1711527	1711703	58	0.755	U	0.998	E	0.944	U
M5005_Spy_1752c	rpmG	1711717	1711869	50	-1	S	-1	S	-1	S
M5005_Spy_1753c	pbp2A	1711918	1714254	778	0	NE	0	NE	0	NE
M5005_Spy_1754c	-	1714293	1714673	126	0	NE	0	NE	0	NE
M5005_Spy_1755	-	1715164	1715355	63	0	NE	0	NE	0	NE
M5005_Spy_1756	-	1715249	1716250	333	0	NE	0	NE	0	NE
M5005_Spy_1757c	-	1716339	1717979	546	0	NE	0	NE	0	NE
M5005_Spy_1758	-	1718226	1719722	498	0	NE	0	NE	0	NE
M5005_Spy_1759c	-	1720207	1720371	54	0	NE	0	NE	0	NE
M5005_Spy_1760c	-	1720350	1720532	60	0	NE	0	NE	0	NE
M5005_Spy_1761c	groEL	1720925	1722556	543	0.773	U	1	E	1	Ε
M5005_Spy_1762c	groES	1722592	1722882	96	0.00025	NE	0.9995	E	0.998	Ε
M5005_Spy_1763c	clpC	1723060	1725504	814	0.00025	NE	0	NE	0.019	NE
M5005_Spy_1764c	ctsR	1725504	1725965	153	0	NE	0	NE	0	NE
M5005_Spy_1765c	csp	1726161	1726370	69	0	NE	0	NE	0.036	NE
M5005_Spy_1766c	-	1726507	1726611	34	-1	S	-1	S	-1	S
M5005_Spy_1767c	-	1726595	1727728	377	0	NE	0	NE	0	NE
M5005_Spy_1768	ahpC	1728685	1729245	186	0	NE	0	NE	0	NE
M5005_Spy_1769	ahpF	1729266	1730798	510	0.00025	NE	0	NE	0	NE
M5005_Spy_1770c	hutI	1730856	1732121	421	0	NE	0	NE	0	NE
M5005_Spy_1771	hutU	1732413	1734443	676	0.00025	NE	0	NE	0	NE
M5005_Spy_1772	-	1734532	1735431	299	0	NE	0	NE	0	NE
M5005_Spy_1773	-	1735442	1736068	208	0	NE	0	NE	0	NE
M5005_Spy_1774	fhs.2	1736086	1737759	557	0	NE	0	NE	0	NE
M5005_Spy_1774 M5005_Spy_1775	-	1737781	1737739	198		NE	0	NE	0	NE
M5005_Spy_1775	-		1738377		0 00025					
M5005_Spy_1770 M5005_Spy_1777		1738597		447 512	0.00025	NE NE	0	NE	0	NE
* *	hutH	1739951	1741492	513	0	NE	0	NE	0	NE
M5005_Spy_1778	hutG	1741678	1742664	328	0	NE	0	NE	0	NE
M5005_Spy_1779c	- 	1742695	1745769	1024	0	NE	0	NE	0	NE
M5005_Spy_1780	rpsB	1746073	1746840	255	0.64925	U	1	E	1	E
M5005_Spy_1781	tsf	1746974	1748014	346	0.99575	E	1	E	1	E
M5005_Spy_1782c	pepO	1748180	1750075	631	0	NE	0	NE	0	NE
M5005_Spy_1783c	dexS	1750283	1751911	542	0.00525	NE	0	NE	0.991	U

M5005_Spy_1784c	-	1751978	1754002	674	0	NE	0	NE	0.001	NE
M5005_Spy_1785	-	1754213	1754926	237	0	NE	0	NE	0.001	NE
M5005_Spy_1786c	-	1755205	1755372	55	0.00025	NE	0	NE	0	NE
M5005_Spy_1787	-	1755730	1756587	285	0.00025	NE	0	NE	0	NE
M5005_Spy_1788	yaaA	1756629	1757360	243	0	NE	0	NE	0	NE
M5005_Spy_1789c	nrdG	1757534	1758148	204	0	NE	0	NE	0.001	NE
M5005_Spy_1790c	-	1758148	1758657	169	0.00025	NE	0	NE	0	NE
M5005_Spy_1791c	-	1758666	1759601	311	0.0005	NE	0.5475	U	0.001	NE
M5005_Spy_1792c	-	1759630	1759776	48	-1	S	-1	S	-1	S
M5005_Spy_1793c	nrdD	1759958	1762156	732	0.00025	NE	0.00025	NE	1	E
M5005_Spy_1794c	_	1762253	1763812	519	0	NE	0	NE	0	NE
M5005_Spy_1795c	_	1764225	1764530	101	0	NE	0	NE	0	NE
M5005_Spy_1796c	_	1764542	1764961	139	0.00025	NE	1	E	1	E
M5005_Spy_1790c	_	1764958	1765227	89	0.00023	NE	0	NE	0	NE
M5005_Spy_1797c	cnvA			132			0		1	E
	spxA	1765340	1765738		0.00025	NE		NE		
M5005_Spy_1799c	recA	1766029	1767165	378	0.00025	NE	0	NE	0.001	NE
M5005_Spy_1800c	cinA	1767254	1768525	423	0	NE	0	NE	0	NE
M5005_Spy_1801c	tag	1768594	1769154	186	0.842	U	0	NE	0	NE
M5005_Spy_1802c	ruvA	1769164	1769760	198	0.00025	NE	0	NE	0.737	U
M5005_Spy_1803c	lmrP	1769762	1770982	406	0	NE	0	NE	0	NE
M5005_Spy_1804c	mutL	1770993	1772975	660	0.27475	U	0	NE	0.006	NE
M5005_Spy_1805c	mutS	1773104	1775659	851	0.26775	U	0	NE	0	NE
M5005_Spy_1806c	-	1775646	1775852	68	0	NE	0	NE	0	NE
M5005_Spy_1807c	argR2	1775995	1776432	145	0	NE	0	NE	0	NE
M5005_Spy_1808	argS	1776723	1778414	563	0.8705	U	1	Ε	1	Ε
M5005_Spy_1809	uviB	1778502	1778810	102	0	NE	0	NE	0	NE
M5005_Spy_1810c	-	1778837	1779709	290	0	NE	0	NE	0	NE
M5005_Spy_1811c	-	1779752	1780687	311	0	NE	0	NE	0	NE
M5005_Spy_1812c	_	1780650	1781591	313	0	NE	0	NE	0.043	NE
M5005_Spy_1813c	aspS	1781584	1783332	582	1	E	1	E	1	E
M5005_Spy_1814c	hisS	17813670	1783332	426	0.99725	E	1	E	1	E
M5005_Spy_1815	rpmF						0		0	
* *	•	1785170	1785352	60	0.00025	NE		NE		NE
M5005_Spy_1816	rpmG	1785368	1785517	49	-1	S	-1	S	-1	S
M5005_Spy_1817	cadD	1785810	1786424	204	0	NE	0	NE	0	NE
M5005_Spy_1818	cadC	1786406	1786774	122	0	NE	0	NE	0	NE
M5005_Spy_1819	-	1786825	1787748	307	0	NE	0	NE	0	NE
M5005_Spy_1820	-	1787814	1788566	250	0	NE	0	NE	0	NE
M5005_Spy_1821	-	1788563	1789165	200	0	NE	0	NE	0	NE
M5005_Spy_1822c	-	1789641	1789925	94	0.00025	NE	0	NE	0	NE
M5005_Spy_1823	-	1790376	1791218	280	0.00025	NE	0	NE	0	NE
M5005_Spy_1824c	-	1791265	1791906	213	0	NE	0	NE	0	NE
M5005_Spy_1825	-	1792113	1792439	108	0	NE	0	NE	0	NE
M5005_Spy_1826	-	1792426	1793013	195	0	NE	0	NE	0.001	NE
M5005_Spy_1827	-	1793010	1794089	359	0.00025	NE	0	NE	0.001	NE
M5005_Spy_1828c	-	1794207	1796075	622	0	NE	0	NE	0	NE
M5005_Spy_1830	-	1796614	1797147	177	0	NE	0	NE	0	NE
M5005_Spy_1831c	rpsD	1797301	1797912	203	1	Ε	1	Ε	1	Ε
M5005_Spy_1832c	` <u>-</u>	1798115	1798219	34	-1	S	-1	S	-1	S
M5005_Spy_1833c	_	1798203	1799336	377	0	NE	0	NE	0	NE
M5005_Spy_1834c	_	1799968	1800240	90	0.00025	NE	0	NE	0.002	NE
M5005_Spy_1835c	holB/dnaC	1800257	1801624	455	1	E	1	E	1	E
M5005_Spy_1836c	rplI	1800257	1802106	150	0	NE	0	NE	0	NE
M5005_Spy_1837c	-									
M5005_Spy_1838c		1802103	1804079	658	0.00025	NE	0	NE	0.001	NE
	gidA	1804170	1806068	632	0.00075	NE	0	NE	1	Ε
M5005_Spy_1839c	-	1806192	1806509	105	0	NE	0	NE	0	NE
M5005_Spy_1840c	mnmA	1807286	1808407	373	1	E	1	E	1	E
M5005_Spy_1841	sdhB	1808705	1809376	223	0	NE	0	NE	0	NE
M5005_Spy_1842	sdhA	1809388	1810260	290	0.00025	NE	0	NE	0	NE
M5005_Spy_1843c	-	1810673	1811287	204	0	NE	0	NE	0	NE
M5005_Spy_1844c	cbiQ	1811659	1812459	266	0	NE	0.9905	U	1	E
M5005_Spy_1845c	cbiO	1812452	1813294	280	1	E	1	Ε	1	Ε
M5005_Spy_1846c	cbiO	1813270	1814160	296	0	NE	1	Ε	1	Ε
M5005_Spy_1847c	pgsA	1814111	1814653	180	0.008	NE	1	Ε	0.731	U

M5005_Spy_1848c	-	1814667	1815692	341	0	NE	0	NE	0.001	NE
M5005_Spy_1849c	-	1815742	1817031	429	0	NE	0	NE	0	NE
M5005_Spy_1850c	-	1817033	1818277	414	0	NE	0	NE	0	NE
M5005_Spy_1851	hasA	1818708	1819967	419	0.00025	NE	0	NE	0	NE
M5005_Spy_1852	hasB	1820003	1821211	402	0	NE	0	NE	0	NE
M5005_Spy_1853	hasC	1821393	1822307	304	0	NE	0	NE	0	NE
M5005_Spy_1854	-	1822615	1823028	137	0	NE	0	NE	0	NE
M5005_Spy_1855	recF	1823030	1824136	368	0	NE	0	NE	0	NE
M5005_Spy_1856c	-	1824191	1825024	277	0.00025	NE	0	NE	0	NE
M5005_Spy_1857c	guaB	1825256	1826737	493	0	NE	0	NE	0	NE
M5005_Spy_1858c	trsA	1827045	1828067	340	1	E	1	E	1	Е
M5005_Spy_1859c	-	1828159	1828284	41	-1	S	-1	S	-1	S
M5005_Spy_1860	-	1828486	1829358	290	0	NE	0	NE	0	NE
M5005_Spy_1861	-	1829437	1831056	539	0.00025	NE	0	NE	0	NE
M5005_Spy_1862	-	1831139	1833715	858	0	NE	0	NE	0	NE
M5005_Spy_1863c	-	1834881	1835162	93	0	NE	0	NE	0	NE
M5005_Spy_1864c	-	1835744	1836223	159	0	NE	0	NE	0	NE
M5005_Spy_1865	htrA	1836435	1837658	407	0.00025	NE	0	NE	1	Е
M5005_Spy_1866	parB	1837717	1838523	268	0.00025	NE	0	NE	0	NE

Table S4. Integrated gene essentiality determination for GAS M1T1 5448 for all time points.

- (a) Spy numbers from MGAS5005 genome.
- (b) When available, gene name is provided.
- (c) Call integrating data from Bayesian analyses on 3 time points.
- (d) Hyperlink to the NCBI Gene website (http://www.ncbi.nlm.nih.gov/gene).
- (e) Information on transcription units based on the work of McClure et al. (2013).
- (f) Asteriks refer to genes found in the GAS core genome.

									Transcri	ptional Unit	(e)
Locus Tag(a)	Gene Name(b)	Call(c)	Start	Stop	Length	Stran	d Gene ID(d) COG Designation		Strand:	+ -	Part of GAS Core Genome (f)
M5005_Spy_0001	dnaA	E	202	1557	451	+	3571011 COG0593L	chromosome replication initiator DnaA			*
M5005_Spy_0002	dnaN	E	1712	2848	378	+	3571012 COG0592L	DNA polymerase III subunit beta			*
M5005_Spy_0003	-	NE	2923	3120	65	+	3571013 COG4481S	hypothetical protein M5005_Spy_0003			
M5005_Spy_0004	ychF	NE	3450	4565	371	+	3571014 COG0012J	GTP-dependent nucleic acid-binding protein EngD			*
M5005_Spy_0005	pth	NC	4635	5204	189	+	3571015 COG0193J	peptidyl-tRNA hydrolase			*
M5005_Spy_0006	trcF	NE	5207	8710	1167	+	3571016 COG1197LK	transcription-repair coupling factor			*
M5005_Spy_0007	-	NE	8872	9144	90	+	3572946 COG1188J	heat shock protein 15			*
M5005_Spy_0008	divIC	NE	9131	9502	123	+	3572947 COG2919D	cell division protein			*
M5005_Spy_0009	-	NC	9499	9624	41	+	<u>3572948</u> -	hypothetical protein M5005_Spy_0009			
M5005_Spy_0010	-	NE	9637	10923	428	+	3572949 COG2367V	beta-lactamase			*
M5005_Spy_0011	tilS/mesJ	E	10920	12206	428	+	3572950 COG0037D	tRNA(Ile)-lysidine synthetase			*
M5005_Spy_0012	hpt	NC	12211	12753	180	+	3572951 COG0634F	hypoxanthine-guanine phosphoribosyltransferase			
M5005_Spy_0013	ftsH	E	12775	14754	659	+	3572952 COG04650	cell division protein			*
M5005_Spy_0014	-	NE	15079	16470	463	+	3572953 COG0531E	amino acid permease			*
M5005_Spy_0015c	-	NC	16811	16945	44	-	<u>3572954</u> -	hypothetical protein M5005_Spy_0015			
M5005_Spy_0017	sibA	E	31134	32330	398	+	3572901 COG3883S	secreted protein			*
M5005_Spy_0018	prsA.2	E	32583	33545	320	+	3572902 COG0462FE	ribose-phosphate pyrophosphokinase			*
M5005_Spy_0019	recO	NE	33731	34486	251	+	3572903 COG1381L	DNA repair protein RecO			*
M5005_Spy_0020	plsX	E	34589	35596	335	+	3572904 COG0416I	glycerol-3-phosphate acyltransferase			*
M5005_Spy_0021	acpP.2	NC	35589	35831	80	+	3572905 COG0236IQ	acyl carrier protein			
M5005_Spy_0022	-	NC	35952	36686	244	+	3572906 COG0152F	synthase			
M5005_Spy_0023	-	NE	36762	40535	1257	+	3572907 COG0046F	phosphoribosylformylglycinamidine synthase			*
M5005_Spy_0024	purF	NE	40696	42150	484	+	3572908 COG0034F	amidophosphoribosyltransferase			*
M5005_Spy_0025	purM	NE	42178	43200	340	+	3572909 COG0150F	phosphoribosylaminoimidazole synthetase			*
M5005_Spy_0026	purN	NE	43368	43922	184	+	3572910 COG0299F	phosphoribosylglycinamide formyltransferase			*
M5005_Spy_0027	purH	NE	44106	45653	515	+	3572911 COG0138F	phosphoribosylaminoimidazolecarboxamide			
M5005_Spy_0028c	-	NE	45711	46835	374	-	3572912 COG3942R	autolysin			*
M5005_Spy_0029	purD	NE	46998	48353	451	+	3572913 COG0151F	phosphoribosylamineglycine ligase			*
M5005_Spy_0030	purE	NE	48511	49122	203	+	3572914 COG0041F	subunit			*
M5005_Spy_0031	purK	NE	49106	50182	358	+	3572915 COG0026F	subunit			*
M5005_Spy_0032	-	NE	50209	51852	547	+	<u>3572916</u> -	hypothetical protein M5005_Spy_0032			
M5005_Spy_0033	purB	NE	51870	53162	430	+	3572917 COG0015F	adenylosuccinate lyase			*
M5005_Spy_0034	-	NE	53294	54205	303	+	<u>3572880</u> -	transcriptional regulator			
M5005_Spy_0035	ruvB	NE	54431	55429	332	+	3572881 COG2255L	Holliday junction DNA helicase RuvB			*
M5005_Spy_0036	-	NE	55567	56004	145	+	3572882 COG0394T	protein tyrosine phosphatase			*
M5005_Spy_0037	-	NC	56027	56428	133	+	3572883 COG4642S	hypothetical protein M5005_Spy_0037			*
M5005_Spy_0038	-	E	56425	58200	591	+	3572884 COG1835I	acyltransferase			*
M5005_Spy_0039	adh2/adhE	NE	58509	61151	880	+	3572885 COG1454C	dehydrogenase			
M5005_Spy_0040	adhA/adhP	NE	61403	62419	338	+	3572886 COG1064R	alcohol dehydrogenase			*
M5005_Spy_0041	norM	NE	62807	63778	323	+	3572887 COG0534V	Na+ driven multidrug efflux pump			*
M5005_Spy_0043	rpsJ	E	64301	64609	102	+	3572889 COG0051J	30S ribosomal protein S10			*
M5005_Spy_0044	rpIC	E	64825	65451	208	+	3572890 COG0087J	50S ribosomal protein L3			*
M5005_Spy_0045	rpID	E	65475	66098	207	+	3572891 COG0088J	50S ribosomal protein L4			*
M5005_Spy_0046	rplW	NE	66098	66394	98	+	3572892 COG0089J	50S ribosomal protein L23			*
M5005_Spy_0047	rplB	E	66412	67245	277	+	3572893 COG0090J	50S ribosomal protein L2			*
M5005_Spy_0048	rpsS	С	67384	67662	92	+	3572894 COG0185J	30S ribosomal protein S19			*
M5005_Spy_0049	rplV	E	67678	68022	114	+	3572895 COG0091J	50S ribosomal protein L22			*
M5005_Spy_0050	rpsC	E	68035	68688	217	+	3572896 COG0092J	30S ribosomal protein S3			*
		_	00033	00000	21,	•					

M5005_Spy_0051	rpIP	E	68692	69105	137	+	3572897 COG0197J	50S ribosomal protein L16	
M5005_Spy_0052	rpmC	NE	69115	69321	68	+	3572898 COG0255J	50S ribosomal protein L29	
M5005_Spy_0053	rpsQ	NC	69347	69607	86	+	3572899 COG0186J	30S ribosomal protein S17	
M5005_Spy_0054	rplN	С	69632	70000	122	+	3572861 COG0093J	50S ribosomal protein L14	
M5005_Spy_0055	rpIX	NC	70079	70384	101	+	3572862 COG0198J	50S ribosomal protein L24	
M5005_Spy_0056	rplE	NC	70408	70950	180	+	3572863 COG0094J	50S ribosomal protein L5	
M5005_Spy_0057	rpsN	NC	70966	71151	61	+	3572864 COG0199J	30S ribosomal protein S14	
M5005_Spy_0058	rpsH	NC	71302	71700	132	+	3572865 COG0096J	30S ribosomal protein S8	
M5005_Spy_0059	rplF	E	71903	72439	178	+	3572866 COG0097J	50S ribosomal protein L6	
M5005_Spy_0060	rplR	NC	72544	72900	118	+	3572867 COG0256J	50S ribosomal protein L18	
M5005_Spy_0061	rpsE	E	72919	73413	164	+	3572868 COG0098J	30S ribosomal protein S5	
M5005_Spy_0062	rpmD	E	73428	73610	60	+	3572869 COG1841J	50S ribosomal protein L30	
M5005_Spy_0063	rplO	NE	73824	74264	146	+	3572870 COG0200J	50S ribosomal protein L15	
M5005_Spy_0064	secY	E	74281	75585	434	+	3572871 COG0201U	preprotein translocase subunit SecY	
M5005_Spy_0065	adk	NC	75735	76373	212	+	3572872 COG0563F	adenylate kinase	
M5005_Spy_0066	infA	E	76491	76709	72	+	3572873 COG0361J	translation initiation factor IF-1	
M5005_Spy_0067	rpmJ	NC	76735	76851	38	+	3572874 COG0257J	50S ribosomal protein L36	
M5005_Spy_0068	rpsM	E	76869	77234	121	+	3572875 COG0099J	30S ribosomal protein S13	
M5005_Spy_0069	rpsK	E	77252	77635	127	+	3572876 COG0100J	30S ribosomal protein S11	
M5005_Spy_0070	rpoA	E	77681	78619	312	+	3572877 COG0202K	DNA-directed RNA polymerase subunit alpha	
M5005_Spy_0071	rplQ	E	78634	79020	128	+	3572878 COG0203J	50S ribosomal protein L17	
M5005_Spy_0072c	-	NC	79618	79752	44	-	<u>3572879</u> -	hypothetical protein M5005_Spy_0072	
M5005_Spy_0073	-	NC	86264	86449	61	+	<u>3572845</u> -	hypothetical protein M5005_Spy_0073	
M5005_Spy_0074	-	NC	87087	87224	45	+	3572846 COG1947I	4-diphosphocytidyl-2-C-methyl-D-erythritol kinase	
M5005_Spy_0075	-	NC	87235	87393	52	+	3572847 COG1947I	partial	_
M5005_Spy_0076	- 4-0	NC	87499	87660	53	+	3572848 COG1947I	4-diphosphocytidyl-2-C-methyl-D-erythritol kinase	
M5005_Spy_0077	adcR	NE	87770	88213	147	+	3572849 COG1846K	MarR family transcriptional regulator	
M5005_Spy_0078 M5005_Spy_0079	adcC adcB	NE NE	88217	88936	239 271	+	3572850 COG1121P 3572819 COG1108P	high-affinity zinc uptake system ATP-binding protein high-affinity zinc uptake system membrane protein	
M5005_Spy_0079	aucb -	NE NE	88929 89784	89744 90167	127	+	3572820 COG0537FGR	bis(5\'-nucleosyl)-tetraphosphatase (asymmetrical)	_
M5005_Spy_0080c	tyrS	E	90218	91474	418	-	3572821 COG0162J	tyrosyl-tRNA synthetase	
M5005_Spy_0001c	pbp1b	NE	91566	93878	770	+	3572822 COG0744M	1B	-
M5005_Spy_0083	rpoB	E	94142	97708	1188	+	3572823 COG0085K	DNA-directed RNA polymerase subunit beta	-
M5005_Spy_0084	rpoC	E	97799	101440	1213	+	3572824 COG0086K	DNA-directed RNA polymerase subunit beta\'	
M5005_Spy_0085	-	NE	101592	101957	121	+	3572825 COG4699S	DNA binding protein	-
M5005_Spy_0086	comYA	NE	102050	102988	312	+	3572826 COG2804NU	competence protein ComG	_
M5005_Spy_0087	comYB	NE	102867	103958	363	+	3572827 COG1459NU	competence protein ComG	
M5005_Spy_0088	comYC	NE	103960	104286	108	+	3572828 COG4537U	competence protein ComG	
M5005_Spy_0089	-	NE	104360	104689	109	+	3572829 -	competence protein ComG	_
M5005_Spy_0090	-	NE	104646	104930	94	+	<u>3572830</u> -	hypothetical protein M5005_Spy_0090	
M5005_Spy_0091	comYD	NE	104923	105357	144	+	3572831 COG4940U	competence protein ComG	
M5005_Spy_0092	-	NE	105341	105667	108	+	<u>3572832</u> -	competence protein ComG	
M5005_Spy_0093	-	NE	105765	106718	317	+	3572833 COG0827L	adenine-specific methyltransferase	
M5005_Spy_0094	ackA	NE	106777	107973	398	+	3572834 COG0282C	acetate kinase	
M5005_Spy_0095	-	NE	108160	108468	102	+	<u>3572835</u> -	hypothetical protein M5005_Spy_0095	
M5005_Spy_0096c	proC	NE	108551	109321	256	-	3572836 COG0345E	pyrroline-5-carboxylate reductase	
M5005_Spy_0097c	pepA	NE	109369	110436	355	-	3572837 COG1363G	glutamyl aminopeptidase	
M5005_Spy_0098	-	NC	110546	110710	54	-	<u>3572838</u> -	hypothetical protein M5005_Spy_0098	
M5005_Spy_0099	-	NE	110892	111185	97	+	<u>3572800</u> -	hypothetical protein M5005_Spy_0099	
M5005_Spy_0100	trx.1	NE	111182	111499	105	+	3572801 COG0526OC	thioredoxin	
M5005_Spy_0101	-	NE	111517	112143	208	+	3572802 COG0073R	tRNA-binding domain-containing protein	
M5005_Spy_0102	ssb	NE	112295	112690	131	+	3572803 COG0629L	single-stranded DNA-binding protein	
M5005_Spy_0103c	-	NE	112950	113591	213	-	3572804 COG1428F	deoxyadenosine kinase/deoxyguanosine kinase	
M5005_Spy_0104c		NE	113611	114588	325	-	3572805 COG0042J	tRNA-dihydrouridine synthase	
M5005_Spy_0105c	hslO rofA/nra	NE	114575	115447	290	-	3572806 COG12810 3572807 -	heat shock protein 33	_
M5005_Spy_0106c M5005 Spy 0107	rora/nra cbp	NE	115594	117087	497	-	3572807 - 3572808 -	transcriptional regulator fibronectin-binding protein	_
M5005_Spy_0107 M5005_Spy_0108	lepA-1	NE NE	117335 119616	119623 120173	762 185	+	3572808 - 3572809 -	signal peptidase I	
M5005_Spy_0108 M5005_Spy_0109	prtF	NE NE	120206	120173	340	+	3572809 - 3572810 -	fibronectin-binding protein	
113303_3py_0103	pro	IVL	120200	121220	340	т	33,2010	noronectar binding protein	

M5005_Spy_0110	eftLSL.B	NE	121238	121951	237	+	3572811 COG4509S	hypothetical protein M5005_Spy_0110
M5005_Spy_0111	-	NE	121973	122620	215	+	<u>3572812</u> -	hypothetical protein M5005_Spy_0111
M5005_Spy_0112c	-	NE	122807	124129	440	-	3572813 COG3436L	transposase
M5005_Spy_0113c	-	NE	124370	124720	116	-	3572814 COG3436L	transposase
M5005_Spy_0114	-	NE	125024	125779	251	+	3572815 COG3764M	sortase
M5005_Spy_0115c	-	NE	125973	126638	221	-	<u>3572816</u> -	hypothetical protein M5005_Spy_0115
M5005_Spy_0116	atoE	NE	126987	128393	468	+	3572817 COG2031I	short-chain fatty acids transporter
M5005_Spy_0117c	-	NE	128461	128856	131	-	<u>3572818</u> -	LysR family transcriptional regulator
M5005_Spy_0118c	-	NE	128952	129371	139	-	3572780 COG0583K	LysR family transcriptional regulator
M5005_Spy_0119	-	NE	129492	130676	394	+	3572781 COG0183I	acetyl-CoA acetyltransferase
M5005_Spy_0120	atoD.2	NE	130688	131347	219	+	3572782 COG1788I	acetate CoA-transferase subunit alpha
M5005_Spy_0121	-	NE	131350	131997	215	+	3572783 COG2057I	acetyl-CoA:acetoacetyl-CoA transferase subunit beta
M5005_Spy_0122c	-	NE	132119	132799	226	-	3572784 COG2964S	DNA-binding protein
M5005_Spy_0123	-	NE	132973	133338	121	+	3572785 COG0251J	translation initiation inhibitor
M5005_Spy_0124	sloR	NE	133375	134394	339	+	3572786 COG1299G	transcriptional regulator
M5005_Spy_0125	-	NE	134849	135169	106	+	<u>3572787</u> -	hypothetical protein M5005_Spy_0125
M5005_Spy_0126	ntpI	NE	135159	137180	673	+	3572788 COG1269C	V-type ATP synthase subunit I
M5005_Spy_0127	ntpK	NE	137182	137661	159	+	3572789 COG0636C	V-type ATP synthase subunit K
M5005_Spy_0128	ntpE	NE	137729	138313	194	+	3572790 -	V-type sodium ATP synthase subunit E
M5005_Spy_0129	ntpC	NE	138329	139327	332	+	3572791 COG1527C	V-type ATP synthase subunit C
M5005_Spy_0130	ntpF	NE	139324	139644	106	+	3572792 COG1436C	V-type ATP synthase subunit F
M5005_Spy_0131	ntpA	NE	139845	141620	591	+	3572793 COG1155C	V-type ATP synthase subunit A
M5005_Spy_0132	ntpB	NE	141621	143036	471	+	3572794 COG1156C	V-type ATP synthase subunit B
M5005_Spy_0133	ntpD	NE	143081	143707	208	+	3572795 COG1394C	V-type ATP synthase subunit D
M5005_Spy_0134c	-	NE	143827	145089	420	-	3572796 COG3853P	tellurite resistance protein
M5005_Spy_0135c	-	NE	145102	145980	292	_	3572797 -	hypothetical protein M5005_Spy_0135
M5005_Spy_0136	purA	NE	146418	147710	430	+	3572798 COG0104F	adenylosuccinate synthetase
M5005_Spy_0137	· -	NE	148037	149080	347	+	3572799 COG1744R	nucleoside-binding protein
M5005_Spy_0138	nusG	С	149253	149792	179	+	3572761 COG0250K	transcription antitermination protein NusG
M5005_Spy_0139	nga	NE	150154	151518	454	+	3572762 -	NAD glycohydrolase
M5005_Spy_0140	-	NE	151523	152008	161	+	3572763 -	hypothetical protein M5005_Spy_0140
M5005_Spy_0141	slo	NE	152032	153747	571	+	3572764 -	streptolysin O
M5005_Spy_0142	-	NE	154002	154433	143	+	3572765 -	hypothetical protein M5005_Spy_0142
M5005_Spy_0143c	-	NE	154619	154855	78	-	3572766 -	hypothetical protein M5005_Spy_0143
M5005_Spy_0144c	-	NC	155265	155432	55	-	3572767 -	hypothetical protein M5005_Spy_0144
M5005_Spy_0145c	-	NE	155607	155894	95	-	3572768 -	hypothetical protein M5005_Spy_0145
M5005_Spy_0146	metB	NE	156335	157525	396	+	3572769 COG0626E	cystathionine beta-lyase
M5005_Spy_0147	leuS	E	157736	160237	833	+	3572770 COG0495J	leucyl-tRNA synthetase
M5005_Spy_0148	ulaA	NC	160544	161977	477	+	3572771 COG3037S	IIC
M5005_Spy_0149	-	NE	162048	162326	92	+	3572772 COG3414G	subunit IIB
M5005_Spy_0150	-	NE	162449	162934	161	+	3572773 COG1762GT	subunit IIA
M5005_Spy_0151	ulaD	NE	163025	163687	220	+	3572774 COG0269G	3-keto-L-gulonate-6-phosphate decarboxylase
M5005_Spy_0152	-	NE	163692	164555	287	+	3572775 COG3623G	L-xylulose 5-phosphate 3-epimerase
M5005_Spy_0153	araD	NE	164557	165261	234	+	3572776 COG0235G	L-ribulose-5-phosphate 4-epimerase
M5005_Spy_0154	-	NC	165319	165465	48	+	3572777 -	hypothetical protein M5005_Spy_0154
M5005_Spy_0155	-	NE	165586	167232	548	+	3572778 COG3711K	BigG family transcription antiterminator
M5005_Spy_0156	-	NE	167485	168576	363	+	3572779 COG2220R	L-ascorbate 6-phosphate lactonase
M5005_Spy_0157	opuAA	NE	169064	170260	398	+	3572741 COG4175E	glycine betaine transport ATP-binding protein
M5005_Spy_0158	opuABC	NE	170276	172003	575	+	3572742 COG4176E	transporter permease
M5005_Spy_0159	polA	E	172134	174776	880	+	3572743 COG0749L	DNA polymerase I
M5005_Spy_0160	-	NE	174963	175418	151	+	3572744 COG1832R	CoA binding protein
M5005_Spy_0161	perR	NE	175470	175937	155	+	3572745 COG0735P	ferric uptake regulation protein
M5005_Spy_0162	vlg	NE	176094	176393	99	+	3572746 -	trans-acting positive regulator Mry
M5005_Spy_0163	-	NE	176615	177949	444	+	3572747 COG3969R	sulfotransferase
M5005_Spy_0164	-	NE	177942	178472	176	+	3572748 COG1475K	parB-like nuclease
M5005_Spy_0165c	-	NE	178519	178761	80	-	3572749 COG3464L	transposase
M5005_Spy_0166c	-	NE	178801	179016	71	-	3572750 COG2801L	transposase
M5005_Spy_0167c	-	NE	179056	179625	189	-	3572751 COG2801L	transposase
M5005_Spy_0168c	-	NE	179658	179873	71	-	3572752 COG2963L	transposase

ME00E C 0160-			100000	404333			2572752 60604740		_	
M5005_Spy_0169c	- 40	NE	180029	181339	436	-	3572753 COG0471P	malonate permease	_	*
M5005_Spy_0170	nadC	NE	181563	182435	290	+	3572754 COG0157H	nicotinate-nucleotide pyrophosphorylase		
M5005_Spy_0171c	-	NE	182735	183541	268	-	3572755 COG2801L	transposase		
M5005_Spy_0172c	-	NE	183562	184077	171	-	3572756 COG2963L	transposase		
M5005_Spy_0173c	-	NE	184163	185026	287	-	3572757 COG5523S	hypothetical protein M5005_Spy_0173	_	*
M5005_Spy_0174	-	NC	185063	185221	52	+	<u>3572758</u> -	hypothetical protein M5005_Spy_0174		
M5005_Spy_0175	tgt	NE	185245	186387	380	+	3572759 COG0343J	queuine tRNA-ribosyltransferase		*
M5005_Spy_0176	-	NE	186604	186915	103	+	3572760 COG4357S	hypothetical protein M5005_Spy_0176		*
M5005_Spy_0177	bioY	NE	186919	187458	179	+	3572722 COG1268R	bioY protein		*
M5005_Spy_0178	-	NE	187598	188377	259	+	3572723 COG1234R	metal-dependent hydrolase		*
M5005_Spy_0179	-	NE	188377	188892	171	+	3572724 COG0590FJ	tRNA-specific adenosine deaminase		
M5005_Spy_0180c	-	NE	189506	190726	406	-	3572725 COG5279D	S-layer protein		*
M5005_Spy_0181	-	NC	190780	190887	35	+	<u>3572726</u> -	hypothetical protein M5005_Spy_0181		
M5005_Spy_0182	speG	NE	191138	191842	234	+	<u>3572727</u> -	exotoxin type G		
M5005_Spy_0183	-	NC	191927	192046	39	+	<u>3572728</u> -	hypothetical protein M5005_Spy_0183		
M5005_Spy_0184	-	NC	192082	192201	39	+	<u>3572729</u> -	hypothetical protein M5005_Spy_0184		
M5005_Spy_0185	pgi	E	192298	193647	449	+	3572730 COG0166G	glucose-6-phosphate isomerase		*
M5005_Spy_0186c	ralp4	NE	193996	195504	502	-	<u>3572731</u> -	transcriptional regulator		*
M5005_Spy_0187	-	NE	196059	196763	234	+	3572732 COG5433L	transposase		
M5005_Spy_0188	-	NE	196666	197181	171	+	<u>3572733</u> -	transposase		
M5005_Spy_0189	-	NC	197165	197290	41	+	<u>3572734</u> -	hypothetical protein M5005_Spy_0189		
M5005_Spy_0190	-	NC	197371	197478	35	+	<u>3572735</u> -	hypothetical protein M5005_Spy_0190		
M5005_Spy_0191	-	NE	197506	198177	223	+	3572736 COG0705R	rhomboid family integral membrane protein		*
M5005_Spy_0192c	hasC.2	NC	198276	199175	299	_	3572737 COG1210M	UTP-glucose-1-phosphate uridylyltransferase	_	*
M5005 Spy 0194c	gpsA	E	199408	200223	271	_	3572739 COG0240C	glycerol-3-phosphate dehydrogenase, partial		*
M5005 Spy 0195	-	NE	200521	200970	149	+	3572740 COG1846K	MarR family transcriptional regulator	_	*
M5005_Spy_0196	-	NE	200963	202669	568	+	3572702 COG1132V	protein/permease		*
M5005_Spy_0197	-	NE	202672	204456	594	+	3572703 COG1132V	protein/permease		*
M5005_Spy_0198	-	NE	204574	205341	255	+	3572704 COG1636S	hypothetical protein M5005_Spy_0198	_	*
M5005_Spy_0199	dut	NE	205451	205897	148	+	3572705 COG0756F	deoxyuridine 5\'-triphosphate nucleotidohydrolase	_	*
M5005_Spy_0200	radA	NE	205978	207339	453	+	3572706 COG10660	DNA repair protein RadA		*
M5005_Spy_0201	-	C	207528	208025	165	+	3572707 COG0288P	carbonic anhydrase	_	*
M5005_Spy_0202	_	NE	208156	208866	236	+	3572708 COG2013S	hypothetical protein M5005_Spy_0202	_	*
M5005_Spy_0203	gltX	E	209048	210493	481	+	3572709 COG0008J	glutamyl-tRNA synthetase	_	*
M5005_Spy_0204	fasB	NE	210888	212234	448	+	3572710 COG2972T	sensory transduction protein kinase	_	*
M5005_Spy_0205	fasC	NE	212231	213514	427	+	3572711 COG2972T	sensory transduction protein kinase		
M5005_Spy_0206	fasA	NE	213518	214258	246	+	3572712 COG3279KT	response regulator		*
M5005_Spy_0207	rnpA	C	214798	215157	119	+	3572713 COG0594J	ribonuclease P	-	*
M5005_Spy_0208	-	NE	215141	215950	269	+	3572714 COG0706U	hypothetical protein M5005_Spy_0208		*
M5005_Spy_0209	_	NE	215962	216876	304	+	3572715 COG1847R	jag protein		*
M5005_Spy_0210	_	NC	216961	217083	40	+	3572716 -	hypothetical protein M5005_Spy_0210		
M5005_Spy_0211	rpmH	NC	217191	217325	44	+	3572717 -	50S ribosomal protein L34	_	
M5005_Spy_0212	-	NE	217599	218303	234	+	3572718 COG3010G	N-acetylmannosamine-6-phosphate 2-epimerase	_	*
M5005_Spy_0212	_	NE	218352	219671	439	+	3572719 COG1653G	N-acetylneuraminate-binding protein		*
M5005_Spy_0214	_	NE	219774	220661	295	+	3572720 COG1175G	N-acetylneuraminate transporter permease	_	*
M5005_Spy_0215	_	NE	220674	221504	276	+	3572721 COG0395G	N-acetylneuraminate transporter permease		*
M5005_Spy_0216	_	NE	221661	222323	220	+	3572683 COG5578S	hypothetical protein M5005_Spy_0216	-	*
M5005_Spy_0217	nanH	NE	222335	22323	304	+	3572684 COG0329EM	N-acetylneuraminate lyase		*
M5005_Spy_0218	-	NE	223271	224209	312	+	3572685 COG1940KG	N-acetylmannosamine kinase		*
M5005_Spy_0219c	_	NE	224320	225150	276	-	3572686 COG1737K	RpiR family transcriptional regulator	_	*
M5005_Spy_0219C	tatD	NE	225402	226226	276	+	3572687 COG0084L	sec-independent protein translocase	_	*
M5005_Spy_0220	-	NE	226198	226226	196	+	3572688 COG1658L	ribonuclease M5		*
M5005_Spy_0221	ksgA	NE	226198	220700	290	+	3572689 COG0030J	dimethyladenosine transferase	-	*
M5005_Spy_0222	engC	E	228198	227774	290	+	3572690 COG1162R	ribosome-associated GTPase	_	*
M5005_Spy_0224	rpe	C	228198	229070	290	+	3572691 COG0036G	ribulose-phosphate 3-epimerase		*
M5005_Spy_0225		NE	229080	230367	210	+	3572692 COG0536G 3572692 COG1564H	thiamin pyrophosphokinase		*
M5005_Spy_0226	-	NE NE	230369	230367	423		3572692 COG1364H 3572693 COG1322S	rmuC family protein		*
M5005_Spy_0226 M5005_Spy_0227	cbf	NE NE	230369 231630	231640 232568	423 312	+	3572693 COG1322S 3572694 COG3481R	CMP-binding factor		*
M5005_Spy_0227 M5005_Spy_0228	purR	NE NE	231630	232568	312 279	+	3572694 COG3481R 3572695 COG0503F	pur operon repressor	_	*
1/12002_3py_0220	purk	INE	232833	2330/4	2/9	+	<u>3372033</u> COG0303f	par operon repressor		**

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M5005_Spy_0229	prgA	NE	233665	236286	873	+	3572696 COG1196D	surface exclusion protein
M5005_Spy_0230	rpsL	E	236494	236907	137	+	3572697 COG0048J	30S ribosomal protein S12
M5005_Spy_0231	rpsG	E	236928	237398	156	+	3572698 COG0049J	30S ribosomal protein S7
M5005_Spy_0232	fus	E	237765	239843	692	+	3572699 COG0480J	elongation factor G
M5005_Spy_0233	plr	E	240191	241201	336	+	3572700 COG0057G	glyceraldehyde-3-phosphate dehydrogenase
M5005_Spy_0234c	-	NC	241427	241543	38	-	<u>3572701</u> -	hypothetical protein M5005_Spy_0234
M5005_Spy_0235c	-	E	241685	242425	246	-	3572663 COG1126E	amino acid transport ATP-binding protein
M5005_Spy_0236c	-	E	242418	243986	522	-	3572664 COG0765E	amino acid ABC transporter permease
M5005_Spy_0237	-	NE	244184	246082	632	+	3572665 COG4907S	hypothetical protein M5005_Spy_0237
M5005_Spy_0238	uppP/bacA	NE	246148	246987	279	+	3572666 COG1968V	undecaprenyl pyrophosphate phosphatase
M5005_Spy_0239	mecA	NE	247133	247894	253	+	3572667 COG48620TN	adaptor protein
M5005_Spy_0240	rgpG	E	248045	249070	341	+	3572668 COG0472M	acetylglucosaminephosphotransferase
M5005_Spy_0241	rgpG	NC	249040	249165	41	+	<u>3572669</u> -	hypothetical protein M5005_Spy_0241
M5005_Spy_0242	-	С	249192	249962	256	+	3572670 COG03960	ABC transporter ATP-binding protein
M5005_Spy_0243	-	С	250057	251319	420	+	3572671 COG07190	ABC transporter
M5005_Spy_0244	nifS3	С	251350	252576	408	+	3572672 COG0520E	cysteine desulfhydrase
M5005_Spy_0245	nifU	С	252563	253042	159	+	3572673 COG0822C	iscU protein
M5005_Spy_0246	-	С	253035	254453	472	+	3572674 COG07190	ABC transporter
M5005_Spy_0247c	pbp7	NE	254605	255786	393	-	3572675 COG1686M	D-alanyl-D-alanine carboxypeptidase
M5005_Spy_0248c	dacA2	NE	255954	257186	410	-	3572676 COG1686M	D-alanyl-D-alanine carboxypeptidase
M5005_Spy_0249	oppA	NE	257517	259487	656	+	3572677 COG4166E	oligopeptide-binding protein
M5005_Spy_0250	oppB	NE	259540	261054	504	+	3572678 COG0601EP	oligopeptide transporter permease
M5005_Spy_0251	oppC	NE	261054	261980	308	+	3572679 COG1173EP	oligopeptide transporter permease
M5005_Spy_0252	oppD	NE	261989	263059	356	+	3572680 COG0444EP	oligopeptide transport ATP-binding protein
M5005_Spy_0253	oppF	NE	263052	263975	307	+	3572681 COG1123R	oligopeptide transport ATP-binding protein
M5005_Spy_0254c	-	NC	264216	264362	48	-	<u>3572682</u> -	transposase
M5005_Spy_0255c	-	NC	264737	264871	44	-	<u>3572650</u> -	hypothetical protein M5005_Spy_0255
M5005_Spy_0256	comX1.1	NE	270293	270844	183	+	3572657 -	competence-specific sigma factor
M5005_Spy_0257	-	NE	271455	272159	234	+	3572658 COG5433L	transposase, partial
M5005_Spy_0258	-	NE	272062	272577	171	+	<u>3572659</u> -	transposase
M5005_Spy_0259	-	NC	272561	272665	34	+	3572660 -	hypothetical protein M5005_Spy_0259
M5005_Spy_0260	-	E	272683	273267	194	+	3572661 COG2179R	lipase
M5005_Spy_0261	-	С	273267	274385	372	+	3572662 COG1161R	GTP-binding protein YgeH
M5005_Spy_0262	-	NE	274410	274718	102	+	3572630 COG1534J	RNA-binding protein
M5005_Spy_0263	nadD	E	274787	275419	210	+	3572631 COG1057H	nicotinic acid mononucleotide adenylyltransferase
M5005_Spy_0264	-	NE	275416	276009	197	+	3572632 COG1713H	HAD superfamily hydrolase
M5005_Spy_0265	-	NE	276009	276386	125	+	3572633 COG0799S	iojap superfamily protein
M5005_Spy_0266	-	NE	276428	277177	249	+	3572634 COG2226H	methyltransferase
M5005_Spy_0267	-	NE	277431	278537	368	+	3572635 COG1323R	hypothetical protein M5005_Spy_0267
M5005_Spy_0268	-	NC	278874	279029	51	+	3572636 -	hypothetical protein M5005_Spy_0268
M5005_Spy_0269	-	NE	279019	279735	238	+	3572637 COG0217S	hypothetical protein M5005_Spy_0269
M5005_Spy_0270	atmA	NE	279938	280780	280	+	3572638 COG0834ET	ABC transporter substrate-binding protein
M5005_Spy_0271	atmB	NE	281109	281954	281	+	3572639 COG1464P	ABC transporter substrate-binding protein
M5005_Spy_0272	atmD	NE	282204	283268	354	+	3572640 COG1135P	ABC transporter ATP-binding protein
M5005_Spy_0273	atmE	NE	283269	283961	230	+	3572641 COG2011P	ABC transporter permease
M5005_Spy_0274c	braB	NE	284015	285385	456	-	3572642 COG1114E	protein
M5005_Spy_0275	-	NE	285619	286833	404	+	3572643 COG3633E	serine/threonine transporter SstT
M5005_Spy_0276c	-	С	286888	287562	224	_	3572644 COG0569P	potassium uptake protein
M5005_Spy_0277c	-	NE	287572	288963	463	-	3572645 COG0168P	potassium uptake protein
M5005 Spy 0278c	gidB	NE	289033	289746	237	-	3572646 COG0357M	16S rRNA methyltransferase GidB
M5005 Spy 0279	lemA	NE	289896	290453	185	+	3572647 COG1704S	hypothetical protein M5005_Spy_0279
M5005_Spy_0280	htpX	NE	290500	291396	298	+	3572648 COG05010	heat shock protein HtpX
M5005_Spy_0281	-	NE	291630	292163	177	+	3572649 COG1399R	hypothetical protein M5005_Spy_0281
M5005_Spy_0282	covR	NE	292430	293116	228	+	3572611 COG0745TK	response regulator
M5005_Spy_0283	covS	NE	293259	294623	454	+	3572612 COG0642T	transmembrane histidine kinase
M5005_Spy_0284	nrdR	NE	294838	295332	164	+	3572613 COG1327K	NrdR family transcriptional regulator
M5005_Spy_0285	dnaB	E	295316	296491	391	+	3572614 COG3611L	replicative DNA helicase
M5005_Spy_0286	dnaI	Ē	296492	297394	300	+	3572615 COG1484L	primosomal protein DnaI
M5005_Spy_0287	engA	E	297457	298767	436	+	3572616 COG1160R	GTP-binding protein EngA
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M5005_Spy_0288 snf NE 298974 302072 1032 + 3572618 - Organization SWF/SNF family helicase MS005_Spy_0289 - NE 302315 302917 200 + 3572619 - Organization hypothetical protein M5005_Spy_0289 MS005_Spy_0291 - NE 304331 304813 160 + 3572619 COG0737M UDP-N-acetylmuramateL-alanine ligase M5005_Spy_0291 - NE 304331 304813 160 + 3572621 COG0782K acetyltransferase M5005_Spy_0292 - C 304931 306499 522 + 3572621 COG0782K aminodeoxychorismate lyase M5005_Spy_0294c - NC 307269 307412 47 - 3572622 COG0782K transposase M5005_Spy_0295c - NE 308682 308960 92 - 3572625 COG1254C acylphosphatase M5005_Spy_0297c - NE 309630 171 - 3572627 COG5433L transposase M5005_Spy_0298c - NE	
M5005_Spy_0290 murC E 302957 304285 442 + 3572619 OG0773M UDP-N-acetylmuramateL-alanine ligase M5005_Spy_0291 - NE 304331 304813 160 + 3572620 C0G0456R acetyltransferase M5005_Spy_0293 greA NE 306524 307054 176 + 3572622 C0G0782K transcription elongation factor GreA M5005_Spy_0295c oxaA E 307677 308600 307 - 3572623 transposase M5005_Spy_0296c - NE 308682 308960 92 - 3572625 C0G1254C acylphosphatase M5005_Spy_0297c - NE 309533 310237 234 - 3572625 C0G1254C acylphosphatase M5005_Spy_0297c - NE 309533 310237 234 - 3572625 C0G1254C acylphosphatase M5005_Spy_0298c - NE 309533 311272 245 + 3572626 C0G566J 235 rRNA methyltransferase M5005_Spy_	
M5005_Spy_0291 - NE 304331 304813 160 + 3572620 COG0456R acetyltransferase M5005_Spy_0293 greA NE 306524 307054 176 + 3572621 COG1559R aminodeoxychorismate lyase M5005_Spy_0294c - NC 307269 307412 47 - 3572623 transposase M5005_Spy_0295c oxaA E 307677 308600 307 - 3572623 cog17600 OxaA-like protein precursor M5005_Spy_0297c - NE 308682 308960 92 - 3572625 COG1254C acylphosphatase M5005_Spy_0297c - NE 309533 310237 234 - 3572625 COG1254C acylphosphatase M5005_Spy_0299 - NE 310537 234 - 3572626 COG1243L transposase M5005_Spy_0300 - NE 311311 311811 166 + 3572629 COG3431L HAD superfamily hydrolase	
M5005_Spy_0292 - C 304931 306499 522 + 3572621 COG1559R aminodeoxychorismate lyase M5005_Spy_0293 greA NE 306524 307054 176 + 3572622 COG0782K transcription elongation factor GreA M5005_Spy_0295c oxaA E 307677 308600 307 - 3572622 COG0706U OxaA-like protein precursor M5005_Spy_0296c - NE 3088682 308960 92 - 3572625 COG1254C acylphosphatase M5005_Spy_0297c - NE 309115 309630 171 - 3572625 COG5433L transposase M5005_Spy_0298c - NE 310535 311272 245 + 3572628 COG05433L transposase M5005_Spy_0300 - NE 311311 311811 166 + 3572629 COG1418R HAD superfamily hydrolase M5005_Spy_0302 - C 312693 312935 80	
M5005_Spy_0293 greA NE 306524 307054 176 + 3572622 COG0782K transcription elongation factor GreA M5005_Spy_0294c - NC 307269 307412 47 - 3572623 transposase M5005_Spy_0295c oxaA E 307677 308600 307 - 3572625 COG0706U OxaA-like protein precursor M5005_Spy_0297c - NE 308860 92 - 3572625 COG1254C acylphosphatase M5005_Spy_0298c - NE 309533 310237 234 - 3572626 transposase M5005_Spy_0299 - NE 310537 234 - 3572628 COG05661 23S rRNA methyltransferase M5005_Spy_0300 - NE 310535 311272 245 + 3572629 COG1418R HAD superfamily hydrolase M5005_Spy_0301 - NE 311826 312515 229 + 3572629 COG0670R hypothetical protein M5005_Spy_0301 M5005_Spy_0302 - C 312693	
M5005_Spy_0294c - NC 307269 307412 47 - 3572623 - transposase M5005_Spy_0295c oxaA E 307677 308600 307 - 3572622 COG1254C OxaA-like protein precursor M5005_Spy_0296c - NE 308960 92 - 3572625 COG1254C acylphosphatase M5005_Spy_0297c - NE 309533 310237 234 - 3572626 - transposase M5005_Spy_0299 - NE 310535 311272 245 + 3572629 COG1418R HAD superfamily hydrolase M5005_Spy_0300 - NE 311311 311811 166 + 3572629 COG1418R HAD superfamily hydrolase M5005_Spy_0301 - NE 311826 312515 229 + 3572592 COG3763S hypothetical protein M5005_Spy_0301 M5005_Spy_0303 glr E 313113 313907 264 + 3572592 COG3763S hypothetical protein M5005_Spy_0302 M5005_Spy_0304	
M5005_Spy_0295c oxaA E 307677 308600 307 - 3572624 COG0706U OxaA-like protein precursor M5005_Spy_0296c - NE 308682 308960 92 - 3572625 COG1254C acylphosphatase M5005_Spy_0297c - NE 309115 309630 171 - 3572626 - transposase M5005_Spy_0298c - NE 310537 234 - 3572627 COG5433L transposase M5005_Spy_0300 - NE 310535 311272 245 + 3572629 COG1418R HAD superfamily hydrolase M5005_Spy_0301 - NE 311826 312515 229 + 3572592 COG0670R hypothetical protein M5005_Spy_0301 M5005_Spy_0303 glr E 313113 313907 264 + 3572592 COG0760R hypothetical protein M5005_Spy_0302 M5005_Spy_0304 - NE 314869 315390 173 + 3572592 COG0622R phosphoesterase M5005_Spy_0306 <td></td>	
M5005_Spy_0296c - NE 308682 308960 92 - 3572625 COG1254C acylphosphatase M5005_Spy_0297c - NE 309115 309630 171 - 3572626 - transposase M5005_Spy_0299 - NE 309533 310237 234 - 3572627 COG5433L transposase M5005_Spy_0300 - NE 311311 311811 166 + 3572629 COG1418R HAD superfamily hydrolase M5005_Spy_0301 - NE 311826 312515 229 + 3572591 COG0670R hypothetical protein M5005_Spy_0301 M5005_Spy_0302 - C 312693 312935 80 + 3572591 COG0670R hypothetical protein M5005_Spy_0302 M5005_Spy_0303 glr E 313113 313907 264 + 3572593 COG0127F pyrophosphatase/unknown domain fusion protein M5005_Spy_0305 - NE 314890 315848 153 +	
M5005_Spy_0297c - NE 309115 309630 171 - 3572626 - transposase M5005_Spy_0298c - NE 309533 310237 234 - 3572622 COG5433L transposase M5005_Spy_0299 - NE 310535 311272 245 + 3572628 COG05661 23S rRNA methyltransferase M5005_Spy_0300 - NE 311311 311811 166 + 3572629 COG1418R HAD superfamily hydrolase M5005_Spy_0301 - NE 311826 312515 229 + 3572591 COG0670R hypothetical protein M5005_Spy_0301 M5005_Spy_0302 - C 312693 312935 80 + 3572592 COG3763S hypothetical protein M5005_Spy_0302 M5005_Spy_0303 glr E 313113 313907 264 + 3572592 COG0768M glutamate racemase M5005_Spy_0305 - NE 314869 315390 173 + 3572594 COG0127F pyrophosphatase/unknown domain fusion protein	
M5005_Spy_0298c - NE 309533 310237 234 - 3572627 COG5433L transposase M5005_Spy_0299 - NE 310535 311272 245 + 3572628 COG05661 23S rRNA methyltransferase M5005_Spy_0300 - NE 311311 311811 166 + 3572629 COG0670R HAD superfamily hydrolase M5005_Spy_0301 - NE 311826 312515 229 + 3572591 COG0670R hypothetical protein M5005_Spy_0301 M5005_Spy_0302 - C 312693 312935 80 + 3572592 COG3763S hypothetical protein M5005_Spy_0302 M5005_Spy_0303 glr E 313113 313907 264 + 3572592 COG0796M glutamate racemase M5005_Spy_0304 - NE 313904 314890 328 + 3572594 COG0127F pyrophosphatase/unknown domain fusion protein M5005_Spy_0306 - NE 315848 153<	
M5005_Spy_0299 - NE 310535 311272 245 + 3572628 COG0566J 23S rRNA methyltransferase M5005_Spy_0300 - NE 311311 311811 166 + 3572629 COG1418R HAD superfamily hydrolase M5005_Spy_0301 - NE 311826 312515 229 + 3572591 COG0670R hypothetical protein M5005_Spy_0301 M5005_Spy_0302 - C 312693 312935 80 + 3572592 COG3763S hypothetical protein M5005_Spy_0302 M5005_Spy_0303 glr E 313113 313907 264 + 3572592 COG0127F pyrophosphatase/unknown domain fusion protein M5005_Spy_0305 - NE 314869 315390 173 + 3572595 COG0127F pyrophosphatase/unknown domain fusion protein M5005_Spy_0306 - NE 315848 153 + 3572595 COG0622R phosphoesterase M5005_Spy_0308 xerD NE 315845	
M5005_Spy_0300 - NE 311311 311811 166 + 3572629 COG1418R HAD superfamily hydrolase M5005_Spy_0301 - NE 311826 312515 229 + 3572591 COG0670R hypothetical protein M5005_Spy_0301 M5005_Spy_0302 - C 312693 312935 80 + 3572592 COG3763S hypothetical protein M5005_Spy_0302 M5005_Spy_0303 glr E 313113 313907 264 + 3572593 COG0796M glutamate racemase M5005_Spy_0304 - NE 314890 328 + 3572594 COG0127F pyrophosphatase/unknown domain fusion protein M5005_Spy_0305 - NE 314869 315390 173 + 3572595 COG0622R phosphoesterase M5005_Spy_0306 - NE 315848 153 + 3572596 COG4109K hypothetical protein M5005_Spy_0306 M5005_Spy_0308 scpA NE 315845 316591 248 + 3572596 COG4197K hypothetical protein M5005_Spy_0306 <tr< td=""><td></td></tr<>	
M5005_Spy_0301 - NE 311826 312515 229 + 3572591 COG0670R hypothetical protein M5005_Spy_0301 M5005_Spy_0302 - C 312693 312935 80 + 3572592 COG3763S hypothetical protein M5005_Spy_0302 M5005_Spy_0303 glr E 313113 313907 264 + 3572593 COG0796M glutamate racemase M5005_Spy_0304 - NE 314890 328 + 3572594 COG0127F pyrophosphatase/unknown domain fusion protein M5005_Spy_0305 - NE 314869 315390 173 + 3572595 COG0622R phosphoesterase M5005_Spy_0306 - NE 315848 153 + 3572596 COG4109K hypothetical protein M5005_Spy_0306 M5005_Spy_0307 xerD NE 315845 316591 248 + 3572596 COG41974L site-specific tyrosine recombinase XerD M5005_Spy_0309 scpA NE 315289 317289	
M5005_Spy_0302 - C 312693 312935 80 + 3572592 COG3763S hypothetical protein M5005_Spy_0302 M5005_Spy_0303 glr E 313113 313907 264 + 3572593 COG0796M glutamate racemase M5005_Spy_0304 - NE 313904 314890 328 + 3572594 COG0127F pyrophosphatase/unknown domain fusion protein M5005_Spy_0305 - NE 314869 315390 173 + 3572595 COG0622R phosphoesterase M5005_Spy_0306 - NE 315848 153 + 3572596 COG4109K hypothetical protein M5005_Spy_0306 M5005_Spy_0307 xerD NE 315845 316591 248 + 3572596 COG4974L site-specific tyrosine recombinase XerD M5005_Spy_0309 scpA NE 316591 317292 233 + 3572598 COG1354S segregation and condensation protein A M5005_Spy_0310 rluB NE 317289	
M5005_Spy_0303 glr E 313113 313907 264 + 3572593 COG0796M glutamate racemase M5005_Spy_0304 - NE 313904 314890 328 + 3572594 COG0127F pyrophosphatase/unknown domain fusion protein M5005_Spy_0305 - NE 314869 315390 173 + 3572595 COG0622R phosphoesterase M5005_Spy_0306 - NE 315387 315848 153 + 3572596 COG4109K hypothetical protein M5005_Spy_0306 M5005_Spy_0307 xerD NE 315845 316591 248 + 3572597 COG4974L site-specific tyrosine recombinase XerD M5005_Spy_0308 scpA NE 316591 317292 233 + 3572598 COG1354S segregation and condensation protein A M5005_Spy_0309 scpB NE 317289 317840 183 + 3572599 COG1386K segregation and condensation protein B M5005_Spy_0310 rluB NE	
M5005_Spy_0304 - NE 313904 314890 328 + 3572594 COG0127F pyrophosphatase/unknown domain fusion protein protein phosphoesterase M5005_Spy_0305 - NE 314869 315390 173 + 3572595 COG0622R phosphoesterase M5005_Spy_0306 - NE 315387 315848 153 + 3572596 COG4109K hypothetical protein M5005_Spy_0306 M5005_Spy_0307 xerD NE 315845 316591 248 + 3572597 COG4974L site-specific tyrosine recombinase XerD M5005_Spy_0308 scpA NE 316591 317292 233 + 3572598 COG1354S segregation and condensation protein B M5005_Spy_0310 rluB NE 317840 183 + 3572599 COG1386K segregation and condensation protein B NE 317939 318685 248 + 3572600 COG1187J ribosomal large subunit pseudouridine synthase B	
M5005_Spy_0305 - NE M5005_Spy_0306 314869 315390 173 + 3572595 COG0622R phosphoesterase phosphoesterase M5005_Spy_0306 - NE M5005_Spy_0306 - NE M5005_Spy_0306 + 3572596 COG4109K phyothetical protein M5005_Spy_0306 hyothetical protein M5005_Spy_0306 M5005_Spy_0308 scpA NE M50591 248 phosphoesterase hyothetical protein M5005_Spy_0306 M5005_Spy_0308 scpA NE M50591 317292 233 phosphoesterase M5005_Spy_0309 scpB NE M507591 317289 317840 183 phosphoesterase Head S72598 phosphoesterase M5005_Spy_0310 rluB NE M507599 317840 183 phosphoesterase Head S72598 phosphoesterase phosphoesterase M5005_Spy_0308 scpA NE M507599 317289 317292 233 phosphoesterase Head S72598 phosphoesterase Head S72598 phosphoesterase Head S72598 phosphoesterase M5005_Spy_0308 scpB NE M507599 317840 183 phosphoesterase Head S72598 phosphoesterase Site-specific tyrosine recombinase XerD M5005_Spy_0308 scpB NE M507599	
M5005_Spy_0306 - NE 315387 315848 153 + 3572596 COG4109K hypothetical protein M5005_Spy_0306 M5005_Spy_0307 xerD NE 315845 316591 248 + 3572592 COG4974L site-specific tyrosine recombinase XerD M5005_Spy_0309 scpB NE 316591 317292 233 + 3572598 COG1386K segregation and condensation protein A M5005_Spy_0310 rluB NE 317289 317840 183 + 3572590 COG1386K segregation and condensation protein B M5005_Spy_0310 rluB NE 317939 318685 248 + 3572600 COG11871 ribosomal large subunit pseudouridine synthase B	
M5005_Spy_0307 xerD NE 315845 316591 248 + 3572597 COG4974L site-specific tyrosine recombinase XerD M5005_Spy_0308 scpA NE 316591 317292 233 + 3572598 COG1354S segregation and condensation protein A M5005_Spy_0309 scpB NE 317289 317840 183 + 3572599 COG1386K segregation and condensation protein B M5005_Spy_0310 rluB NE 317939 318685 248 + 3572600 COG1187J ribosomal large subunit pseudouridine synthase B	
M5005_Spy_0308 scpA NE 316591 317292 233 + 3572598 COG1354S segregation and condensation protein A M5005_Spy_0309 scpB NE 317289 317840 183 + 3572599 COG1386K segregation and condensation protein B M5005_Spy_0310 rluB NE 317939 318685 248 + 3572600 COG1187J ribosomal large subunit pseudouridine synthase B	
M5005_Spy_0309 scpB NE 317289 317840 183 + <u>3572599</u> COG1386K segregation and condensation protein B M5005_Spy_0310 rluB NE 317939 318685 248 + <u>3572600</u> COG1187J ribosomal large subunit pseudouridine synthase B	
M5005_Spy_0310 rluB NE 317939 318685 248 + 3572600 COG1187J ribosomal large subunit pseudouridine synthase B	
M5005 Spy 0311 - NE 210692 210045 97 - 3572601 COC0750S hypothetical protein M5005 Spy 0311	
M5005_Spy_0312 - NE 319123 319671 182 + <u>3572602</u> COG0219J 23S rRNA methyltransferase	
M5005_Spy_0313 - C 319982 320545 187 + <u>3572603</u> COG3601S riboflavin transporter	
M5005_Spy_0314 - NE 320547 321200 217 + <u>3572604</u> COG0671I phosphatidylglycerophosphatase B	
M5005_Spy_0315 - NE 321493 322413 306 + <u>3572605</u> COG1242R Fe-S oxidoreductase	
M5005_Spy_0316 - NE 322452 323006 184 + <u>3572606</u> COG0144J SAM-dependent methyltransferase	
M5005_Spy_0317 hlyX	
M5005_Spy_0318 pflC NE 324479 325342 287 + <u>3572608</u> COG11800 pyruvate formate-lyase activating enzyme	
M5005_Spy_0319 ppaC NC 325473 326408 311 + 3572609 COG1227C manganese-dependent inorganic pyrophosphatasi	ڍ
M5005_Spy_0320 - NE 326484 327137 217 + <u>3572610</u> - hypothetical protein M5005_Spy_0320	
M5005_Spy_0321c fhuG NE 327182 328108 308 - 3572572 COG0609P ferrichrome transporter permease	
M5005_Spy_0322c fhuB NE 328180 329232 350 - <u>3572573</u> COG0609P ferrichrome transporter permease	
M5005_Spy_0323c fhuD NE 329222 330154 310 - <u>3572574</u> COG0614P ferrichrome-binding protein	
M5005_Spy_0324c fhuA NE 330180 330962 260 - 3572575 COG1120PH ferrichrome ABC transporter ATP-binding protein	
M5005_Spy_0325c murE E 331208 332653 481 - <u>3572576</u> COG0769M ligase	
M5005_Spy_0326 - E 332741 334375 544 + <u>3572577</u> COG2244R export protein for polysaccharides and teichoic ac	ids
M5005_Spy_0327 upp NE 334543 335172 209 + <u>3572578</u> COG0035F uracil phosphoribosyltransferase	
M5005_Spy_0328 clpP C 335396 335986 196 + <u>3572579</u> COG07400U ATP-dependent Clp protease proteolytic subunit	
M5005_Spy_0329 - NE 336478 336753 91 + 3572580 COG4471S hypothetical protein M5005_Spy_0329	
M5005_Spy_0330 tmk E 337002 337637 211 + 3572581 COG0125F thymidylate kinase	
M5005_Spy_0331 dnaX E 337655 338530 291 + 3572582 COG0470L DNA polymerase III subunit delta\'	
M5005_Spy_0332 - NE 338549 338788 79 + <u>3572583</u> - tpl protein	
M5005_Spy_0333 - NC 338877 339038 53 + 3572584 COG1774S signal peptidase-like protein	
M5005_Spy_0334 - NC 339193 339516 107 + 3572585 COG4467S DNA replication initiation control protein YabA	
M5005_Spy_0335 - NE 339521 340384 287 + <u>3572586</u> COG0313R corrin/porphyrin methyltransferase	
M5005_Spy_0336 - NE 340411 340803 130 + <u>3572587</u> - hypothetical protein M5005_Spy_0336	
M5005_Spy_0337c cutC NE 340850 341479 209 - 3572588 COG3142P copper homeostasis protein	
M5005_5py_0338 - NE 341778 342134 118 + 3572589 COG1393P arsenate reductase	
M5005_Spy_0339c exoA NC 342208 343119 303 - <u>3572590</u> COG0708L exodeoxyribonuclease III	
- · · · - · · · · · · · · · · · · · · ·	
113003_5py_0310 119003_5py_0310 119003_5py_0310	_
M5005_Spy_0347 nrdF NE 353869 354882 337 + <u>3572558</u> COG0208F ribonucleotide-diphosphate reductase subunit bet	

M5005_Spy_0348	nrdI	NE	354886	355374	162	+	3572559 COG1780F	ribonucleotide reductase stimulatory protein	
M5005_Spy_0349	nrdE.1	NE	355341	357521	726	+	3572560 COG0209F	ribonucleotide-diphosphate reductase subunit alpha	
M5005_Spy_0350	-	NC	357500	357718	720	+	3572561 -	hypothetical protein M5005_Spy_0350	
M5005_Spy_0351c	spyA	NE	357724	358476	250	-	3572562 COG5585T	C3 family ADP-ribosyltransferase	_
M5005_Spy_0351C	эрун	NE	358935	359471	178	+	3572563 -	hypothetical protein M5005_Spy_0352	
M5005_Spy_0353							3572564 -	hypothetical protein M5005_Spy_0352	_
M5005_Spy_0354c	-	NE	359613	359996	127	+	3572565 -	hypothetical protein M5005_Spy_0353	_
	-	NE	360090	360722	210	-			
M5005_Spy_0355		NE	361401	361721	106	+	<u>3572566</u> -	hypothetical protein M5005_Spy_0355	_
M5005_Spy_0356c	speJ	NE	362034	362732	232	-	<u>3572567</u> -	exotoxin type J	
M5005_Spy_0357c	-	NE	362980	363594	204	-	<u>3572568</u> -	hypothetical protein M5005_Spy_0357	_
M5005_Spy_0358	-	NE	363955	364191	78	+	<u>3572569</u> -	hypothetical protein M5005_Spy_0358	
M5005_Spy_0359	fabG	NE	364175	364882	235	+	3572570 COG1028IQR	3-ketoacyl-ACP reductase	
M5005_Spy_0360		NE	364928	365917	329	+	3572571 COG0673R	NAD-dependent oxidoreductase	
M5005_Spy_0361	glpT	NE	366250	367587	445	+	3572533 COG2271G	phosphoglycerate transporter protein	
M5005_Spy_0362	glmU	E	367760	369142	460	+	3572534 COG1207M	uridyltransferase/glucosamine-1-phosphate	
M5005_Spy_0363	-	NE	369173	369727	184	+	3572535 COG0494LR	phosphohydrolase	
M5005_Spy_0364	-	NC	369727	369978	83	+	<u>3572536</u> -	hypothetical protein M5005_Spy_0364	
M5005_Spy_0365	pfs	E	369998	370693	231	+	3572537 COG0775F	nucleosidase	
M5005_Spy_0366	-	NE	370844	371185	113	+	<u>3572538</u> -	hypothetical protein M5005_Spy_0366	
M5005_Spy_0367c	mtsR	NC	371286	371933	215	-	3572539 COG1321K	iron-dependent repressor	
M5005_Spy_0368	mtsA	NE	372091	373011	306	+	3572540 COG0803P	manganese-binding protein	
M5005_Spy_0369	mtsB	NE	373075	373800	241	+	3572541 COG1121P	manganese transporter ATP-binding protein	
M5005_Spy_0370	mtsC	NE	373801	374655	284	+	3572542 COG1108P	manganese transporter membrane protein	
M5005_Spy_0371c	cypB	NE	374803	375609	268	-	3572543 COG0652O	peptidyl-prolyl cis-trans isomerase	
M5005_Spy_0372	ftsK	E	375826	378231	801	+	3572544 COG1674D	cell division protein	_
M5005_Spy_0373c	-	NE	378301	378654	117	-	3572545 -	hypothetical protein M5005_Spy_0373	
M5005_Spy_0374	rplK	NC	378898	379323	141	+	3572546 COG0080J	50S ribosomal protein L11	_
M5005_Spy_0375	rpIA	E	379429	380118	229	+	3572547 COG0081J	50S ribosomal protein L1	
M5005_Spy_0376	·-	NE	380469	381602	377	+	3572548 COG5433L	transposase	_
M5005_Spy_0377	pyrH	E	381767	381937	56	+	3572549 COG0528F	uridylate kinase	
M5005_Spy_0380	frr	E	382524	383081	185	+	3572513 COG0233J	ribosome recycling factor	
M5005_Spy_0381	-	NE	383190	384047	285	+	3572514 COG2996S	S1 RNA-binding domain-containing protein	_
M5005_Spy_0382	msrA.2	NE	384120	384629	169	+	3572515 COG02250	methionine sulfoxide reductase A	_
M5005_Spy_0383	-	NE	384626	384841	71	+	3572516 COG4479S	hypothetical protein M5005_Spy_0383	
M5005_Spy_0384	-	NE	384997	386166	389	+	3572517 -	surface antigen	_
M5005_Spy_0385	_	NE	386441	388252	603	+	3572518 COG4716S	hypothetical protein M5005_Spy_0385	_
M5005_Spy_0386	phoH	NE	388411	389463	350	+	3572519 COG1702T	phoH protein	-
M5005_Spy_0387		NE	389509	390084	191	+	3572520 COG1573L	uracil DNA glycosylase	_
M5005_Spy_0388	_	E	390192	390740	182	+	3572521 COG0319R	metalloprotease	_
M5005_Spy_0389	dgk	E	390721	391128	135	+	3572522 COG0818M	diacylglycerol kinase	
M5005_Spy_0390	era	c	391248	392144	298	+	3572523 COG1159R	GTP-binding protein Era	-
M5005_Spy_0391	-	NE	392128	392640	170	+	3572524 COG1051F	phosphohydrolase	
M5005_Spy_0392c	_	NE	392945	393199	84		3572525 -	hypothetical protein M5005_Spy_0392	_
M5005_Spy_03920	_	NE	393597	393842	81	+	3572526 -	hypothetical protein M5005_Spy_0393	
M5005_Spy_0394	_	NE	393857	394039	60	+	3572527 -	hypothetical protein M5005_Spy_0394	
M5005_Spy_0395c	_	NE	394230	394409	59		3572528 -	transposase	
M5005_Spy_0396c	_	NC	394348	394497	49	-	3572529 COG3328L	transposase	
M5005_Spy_0390c	_	NE	394346	394916	140	-	3572530 COG3328L	transposase	
M5005_Spy_0398						+	3572530 COG3328L 3572531 -	bacteriocin	_
M5005_Spy_0398	=	NE NE	395189	395398	69	+	3572532 -	hypothetical protein M5005 Spy 0399	
M5005_Spy_0399 M5005_Spy_0400	silD		395463	395663	66 64	+	3572532 - 3572494 -	hypothetical protein M5005_Spy_0399	-
M5005_Spy_0400 M5005_Spy_0401c	SIID	NE	395957	396151		+	<u>3572494</u> - 3572495 -	hypothetical protein M5005_Spy_0400 hypothetical protein M5005_Spy_0401	
	-	NC	396344	396460	38	-	<u>3572495</u> - 3572496 -	7	
M5005_Spy_0402	-	NE	396644	397639	331	+	3572496 - 3572497 -	hypothetical protein M5005_Spy_0402	
M5005_Spy_0403	-	NE	397684	398130	148	+		hypothetical protein M5005_Spy_0403	_
M5005_Spy_0404c	-	NE	398478	398747	89	-	<u>3572498</u> -	hypothetical protein M5005_Spy_0404	
M5005_Spy_0405	-	NC	398948	399055	35	+	<u>3572499</u> -	hypothetical protein M5005_Spy_0405	
M5005_Spy_0406c	-	NE	399269	399511	80	-	<u>3572500</u> -	hypothetical protein M5005_Spy_0406	
M5005_Spy_0407	mutR	NE	399818	400684	288	+	<u>3572501</u> -	transcriptional regulator	_
M5005_Spy_0408	fpg	NE	400856	401683	275	+	3572502 COG0266L	formamidopyrimidine-DNA glycosylase	

	_	_					2572522 2222271	
M5005_Spy_0409	coaE	E	401593	402273	226	+	3572503 COG0237H	dephospho-CoA kinase
M5005_Spy_0410	-	NE	402463	403965	500	+	3572504 COG0433R	ATPase
M5005_Spy_0411	-	NE	404087	405280	397	+	3572505 COG2814G	multidrug resistance protein B
M5005_Spy_0412	rpmG	NC	405277	405423	48	+	3572506 COG0267J	50S ribosomal protein L33
M5005_Spy_0413	secG	E	405469	405705	78	+	3572507 COG1314U	preprotein translocase subunit SecG
M5005_Spy_0414	-	NE	405802	408132	776	+	3572508 COG0557K	exoribonuclease II
M5005_Spy_0415	smpB	NC	408135	408602	155	+	3572509 COG06910	SsrA-binding protein
M5005_Spy_0416	-	NE	408617	409327	236	+	3572510 COG38230	glutaminyl-peptide cyclotransferase
M5005_Spy_0417c	рср	NE	409443	410090	215	-	3572511 COG20390	pyrrolidone-carboxylate peptidase
M5005_Spy_0418c	-	NE	410140	411066	308	-	3572512 COG3817S	permease
M5005_Spy_0419c	-	NE	411066	411749	227	-	3572474 COG3819S	permease
M5005_Spy_0420c	-	NE	411960	412886	308	-	3572475 COG0463M	glucosyltransferase
M5005_Spy_0421c	gloA	NE	413031	413408	125	-	3572476 COG0346E	lactoylglutathione lyase
M5005_Spy_0422c	-	NE	413419	414084	221	-	3572477 COG0778C	NAD(P)H-dependent quinone reductase
M5005_Spy_0423c	pepQ	NE	414133	415218	361	-	3572478 COG0006E	Xaa-Pro dipeptidase
M5005_Spy_0424	ссрА	NC	415392	416393	333	+	3572479 COG1609K	catabolite control protein A
M5005_Spy_0425	-	С	416524	417522	332	+	3572480 COG0438M	glycosyltransferase
M5005 Spy 0426	-	E	417524	418858	444	+	3572481 COG0438M	1,2-diacylglycerol 3-glucosyltransferase
M5005 Spy 0427	thrS	E	419280	421223	647	+	3572482 COG0441J	threonyl-tRNA synthetase
M5005 Spy 0428	drrA/tagH	NE	421364	422356	330	+	3572483 COG4586R	daunorubicin resistance ATP-binding protein
M5005_Spy_0429	-	NE	422358	423176	272	+	3572484 COG4587R	daunorubicin resistance transmembrane protein
M5005_Spy_0430	-	NE	423178	423963	261	+	3572485 COG3694R	ABC transporter permease
M5005_Spy_0431	_	NC	424164	424313	49	+	3572486 -	dihydroxyacetone kinase
M5005_Spy_0432	_	NE	424708	425856	382	+	3572487 COG0183I	acetyl-CoA acetyltransferase
M5005_Spy_0433	_	NE	425813	427060	415	+	3572488 COG0318IQ	long-chain-fatty-acidCoA ligase
M5005_Spy_0434	_	NE	427116	428150	344	+	3572489 -	hypothetical protein M5005_Spy_0434
M5005_Spy_0435	vicR	E	428312	429022	236	+	3572490 COG0745TK	two-component response regulator
M5005_Spy_0135	vicK	NE	429015	430367	450	+	3572491 COG5002T	two-component sensor histidine kinase
M5005_Spy_0437	vicX	NE	430371	431180	269	+	3572492 COG1235R	Zn-dependent hydrolase
M5005_Spy_0438	rnc	C	431624	432316	230	+	3572493 COG0571K	ribonuclease III
M5005_Spy_0439	smc	NE NE	432317	435856	1179	+	3572455 COG1196D	chromosome partition protein
M5005_Spy_0440c	-	NE	436109	436960	283	т.	3572456 -	transcriptional regulator
M5005_Spy_0441	aroE	NE	437234	438106	290	+	3572450 3572457 COG0169E	shikimate 5-dehydrogenase
M5005_Spy_0442	-	NE	437234	438939	244	+	3572458 COG1082G	hypothetical protein M5005_Spy_0442
M5005_Spy_0443	_	NE	438941	439675	244	+	3572459 COG1478S	hypothetical protein M5005_Spy_0442
M5005_Spy_0445	_	NE	439668	440654	328	+	3572460 COG0673R	hypothetical protein M5005_3py_0445
M5005_Spy_0445	metK1	NE	440664	441863	399	+	3572461 COG1812E	S-adenosylmethionine synthetase
M5005_Spy_0446	-	NE	441847	441803	322		3572462 COG1493T	hypothetical protein M5005_Spy_0446
M5005_Spy_0440	-				322	+	3572463 COG0463M	cell wall biosynthesis glycosyltransferase
M5005_Spy_0447 M5005_Spy_0448	_	NE	442870	443859		+	3572464 -	hypothetical protein M5005 Spy 0448
M5005_Spy_0448 M5005_Spy_0449	hasB.2	NC	444385	444528	47	+	3572464 - 3572465 COG1004M	UDP-glucose 6-dehydrogenase
M5005_Spy_0449 M5005_Spy_0450	mefE	NE NE	444552 445794	445709	385 402	+	3572465 COG1004M 3572466 COG2270R	macrolide-efflux protein
M5005_Spy_0450 M5005_Spy_0451c	illeic	NE NE		447002	402 69	-	3572466 COG2270K 3572467 COG3655K	transcriptional regulator
M5005_Spy_0451C M5005_Spy_0452c	-	NE NE	447105	447314		-	3572467 COG3633K	chromosome segregation ATPase
M5005_Spy_0452c	-	NE NE	447304	448149	281 242	-	3572466 - 3572469 -	chromosome segregation ATPase
M5005_Spy_0453c	-		448234	448962				hypothetical protein M5005 Spy 0454
M5005_Spy_0454c	-	NE	448953	449177	74	-	<u>3572470</u> -	hypothetical protein M5005_Spy_0454
M5005_Spy_04550	-	NE	449177	450271	364	-	<u>3572471</u> -	plasmid stabilization system antitoxin protein
	-	NC	450317	450619	100	+	3572472 COG3077L	, , , , , , , , , , , , , , , , , , , ,
M5005_Spy_0457	-	NE	450619	450924	101	+	3572473 COG3668R	plasmid stabilization system protein
M5005_Spy_0458	-	NE	450943	451215	90	+	<u>3572435</u> -	hypothetical protein M5005_Spy_0458
M5005_Spy_0459	-	NE	451320	451772	150	+	3572436 COG4695S	portal protein
M5005_Spy_0460	-	NE	451838	452152	104	+	3572437 -	hypothetical protein M5005_Spy_0460
M5005_Spy_0461		NE	452569	452907	112	+	3572438 COG3177S	hypothetical protein M5005_Spy_0461
M5005_Spy_0462	-	NE	452931	453755	274	+	3572439 COG0017J	asparagine synthetase A
M5005_Spy_0463	- 	NE	453769	455016	415	+	3572440 COG0439I	hypothetical protein M5005_Spy_0463
M5005_Spy_0464	mccF	NE	455244	455960	238	+	3572441 COG1619V	microcin C7 self-immunity protein
M5005_Spy_0465	-	NE	455973	456173	66	+	<u>3572442</u> -	hypothetical protein M5005_Spy_0465
M5005_Spy_0466	-	NE	456293	457192	299	+	3572443 COG0124J	hypothetical protein M5005_Spy_0466
M5005_Spy_0467c	-	NE	457645	458358	237	-	3572444 COG2801L	transposase

M5005_Spy_0468c	-	NE	458406	458681	91	-	3572445 COG2963L	transposase
M5005_Spy_0469	-	NE	458701	458919	72	+	<u>3572446</u> -	hypothetical protein M5005_Spy_0469
M5005_Spy_0470	-	NE	458986	459783	265	+	3572447 COG0561R	HAD superfamily hydrolase
M5005_Spy_0471	-	NE	459787	460611	274	+	3572448 COG0561R	HAD superfamily hydrolase
M5005_Spy_0472	ftsY	E	460611	462161	516	+	3572449 COG0552U	cell division protein
M5005_Spy_0473c		NE	462215	463582	455	-	3572450 COG2814G	multidrug resistance protein B
M5005_Spy_0474	licT/bglG	NE	463910	464752	280	+	3572451 COG3711K	BigG family transcription antiterminator
M5005_Spy_0475		NE	464916	466616	566	+	3572452 COG1263G	subunit IIABC
M5005_Spy_0476	bglA	NE	466635	468059	474	+	3572453 COG2723G	6-phospho-beta-glucosidase
M5005_Spy_0477c	-	NE	468158	468973	271	-	3572454 COG3689S	hypothetical protein M5005_Spy_0477
M5005_Spy_0478c	-	NE	468973	469875	300	-	3572416 COG0701R	hypothetical protein M5005_Spy_0478
M5005_Spy_0479	-	NE	470009	470206	65	+	3572417 -	hypothetical protein M5005_Spy_0479
M5005_Spy_0480	-	NE	470304	470432	42	-	3572419 COG2183K	transcription accessory protein
M5005_Spy_0481c	-	NC	470412	472544	710	+	3572418 -	hypothetical protein M5005_Spy_0481
M5005_Spy_0482	-	NE	472486	472968	160	+	3572420 COG3091S	hypothetical protein M5005_Spy_0482
M5005_Spy_0483		NE	473032	473304	90	+	3572421 COG1983KT	stress-responsive transcriptional regulator
M5005_Spy_0484	ptsK	E	473609	474601	330	+	3572422 COG1493T	HPr kinase/phosphorylase
M5005_Spy_0485	lgt	NE	474598	475377	259	+	3572423 COG0682M	prolipoprotein diacylglyceryl transferase
M5005_Spy_0486	-	NE	475399	475806	135	+	3572424 COG4768R	hypothetical protein M5005_Spy_0486
M5005_Spy_0487	-	NE	475799	476227	142	+	<u>3572425</u> -	hypothetical protein M5005_Spy_0487
M5005_Spy_0488c	-	NE	476386	476670	94	-	<u>3572426</u> -	hypothetical protein M5005_Spy_0488
M5005_Spy_0489	-	NE	476869	477237	122	+	3572427 COG08260	U32 family peptidase
M5005_Spy_0491	-	NE	477887	479173	428	+	3572429 COG08260	U32 family peptidase
M5005_Spy_0492c	-	NC	479186	479314	42	-	<u>3572430</u> -	hypothetical protein M5005_Spy_0492
M5005_Spy_0493	-	NE	479383	479595	70	+	3572431 COG4443S	hypothetical protein M5005_Spy_0493
M5005_Spy_0494c	-	NC	479692	479832	46	-	<u>3572432</u> -	hypothetical protein M5005_Spy_0494
M5005_Spy_0495c	lysS	E	479968	481461	497	-	3572433 COG1190J	lysyl-tRNA synthetase
M5005_Spy_0496	-	NE	481635	482537	300	+	3572434 COG1011R	HAD superfamily hydrolase
M5005_Spy_0497c	-	NE	482645	483268	207	-	3572396 COG0406G	phosphoglycerate mutase
M5005_Spy_0498c	-	NE	483609	484088	159	-	3572397 COG2606S	transcriptional regulator
M5005_Spy_0499c	-	NE	484179	484742	187	-	3572398 COG3859S	thiamine transporter
M5005_Spy_0500c	-	C	485011	485859	282	-	3572399 COG3757M	N-acetylmuramoyl-L-alanine amidase
M5005_Spy_0501	-	NE	486184	486687	167	+	<u>3572400</u> - 3572401 -	hypothetical protein M5005_Spy_0501
M5005_Spy_0502	-	NE	486671	487057	128	+		hypothetical protein M5005_Spy_0502
M5005_Spy_0503c		NE	487103	487582	159	-	3572402 COG03860	glutathione peroxidase
M5005_Spy_0504c	pepF	NE	487575	489374	599	-	3572403 COG1164E	oligoendopeptidase F
M5005_Spy_0505	ppc ftsW	NE	489518	492331	937	+	3572404 COG2352C	phosphoenolpyruvate carboxylase cell division protein
M5005_Spy_0506	ILSVV	E	492501	493775	424	+	3572405 COG0772D	•
M5005_Spy_0507c	- tuf	NC	493792	493932	46	-	3572406 - 3572407 COG0050J	hypothetical protein M5005_Spy_0507
M5005_Spy_0508		E	494129	495325	398	+		elongation factor Tu
M5005_Spy_0509	tpiA	C	495566	496324	252	+	3572408 COG0149G	triosephosphate isomerase
M5005_Spy_0510c M5005_Spy_0511c	murN murM	E	496423	497658	411 408	-	3572409 COG2348V 3572410 COG2348V	resistance alanyltransferase/UDP-N-
M5005_Spy_0511c M5005_Spy_0512c	murm	E	497645	498871		-	3572410 COG2348V 3572411 COG0561R	HAD superfamily hydrolase
M5005_Spy_0512c	-	NE	498871	499680	269	-	3572411 COGUSTIR 3572412 -	hypothetical protein M5005_Spy_0513
M5005_Spy_0513c M5005_Spy_0514c	-	NC	499831	500064	77	-	3572412 - 3572413 COG1078R	dGTP triphosphohydrolase
M5005_Spy_0514c M5005_Spy_0515	-	NE	500136	501437	433	+	3572413 COG1076K 3572414 COG4506S	hypothetical protein M5005_Spy_0515
M5005_Spy_0515 M5005_Spy_0516	pacL	NE	501519 502136	501905	128	+	3572414 COG43003 3572415 COG0474P	calcium-transporting ATPase
M5005_Spy_0516 M5005_Spy_0517c	regR	E NE	502136	504817 505896	893	+	3572377 COG1609K	LacI family transcriptional regulator
M5005_Spy_0517c	-	NE NE	505960	507867	331 635	-	3572378 -	oligohyaluronate lyase
M5005_Spy_0518c	agaD	NE		508775	273	-	3572378 - 3572379 COG3716G	transporter subunit IID
M5005_Spy_0519C M5005_Spy_0520c	agaD	NE	507954 508762	508775	260	-	3572379 COG3716G 3572380 COG3715G	transporter subunit IIC
M5005_Spy_0520c M5005_Spy_0521c	agaV	NE	508762	510051	162	-	3572380 COG3713G 3572381 COG3444G	transporter subunit IIB
M5005_Spy_0521c	ugl	NE	510087	511286	399	-	3572382 COG4225R	unsaturated glucuronyl hydrolase
M5005_Spy_05220 M5005_Spy_0523	ugi -	NE NE	511353	511286	176	+	3572383 -	hypothetical protein M5005_Spy_0523
M5005_Spy_0524	idnO	NE NE	511353	511883		+	3572384 COG1028IQR	gluconate 5-dehydrogenase
M5005_Spy_0525	-	NE NE	512059	512853	264	+	3572385 COG10281QK	hypothetical protein M5005_Spy_0525
M5005_Spy_0526	- kdgK	NE NE	512878	513519	213 333	+	3572386 COG0524G	2-dehydro-3-deoxygluconokinase
M5005_Spy_0526 M5005_Spy_0527	kgdA	NE NE	513548	514549	211	+	3572387 COG0800G	phosphogluconate aldolase
1-12002_2py_032/	kyuA	INE	314354	313189	211	+	3372307 COG0000G	phosphoglaconate aldoldse

M5005 Spy 0528	_	NE	515485	516135	216	+	3572388 COG0637R	phosphodismutase
M5005_Spy_0529	_	NE	516776	517951	391	+	3572389 COG1600C	(Fe-S)-binding protein
M5005_Spy_0530	prfB	E	518105	519118	337	+	3572390 COG1186J	peptide chain release factor 2
M5005_Spy_0530	ftsE	NC	519137	519829	230	+	3572391 COG2884D	cell division ATP-binding protein
M5005_Spy_0531	ftsX	C	519822	520751	309	+	3572392 COG2177D	cell division protein
M5005_Spy_0532c	-	NE NE	521061	521696	211	-	3572393 COG0491R	hydroxyacylglutathione hydrolase
M5005_Spy_05330	_	NE				+	3572394 COG1028IQR	acetoin reductase
M5005_Spy_0535	-		521927	522541	204		3572395 COG1028IQR	acetoin reductase acetoin dehydrogenase, partial
M5005_Spy_0536		NC	522545	522691	48	+	3572358 COG1199KL	polymerase III subunit epsilon
M5005_Spy_0536 M5005_Spy_0537	dinG	NE	522841	525300	819	+	3572359 COG1199KL 3572359 COG0436E	
	aspC	NE	525635	526828	397	+		aspartate aminotransferase
M5005_Spy_0538	asnC	E	526849	528195	448	+	3572360 COG0017J	asparaginyl-tRNA synthetase
M5005_Spy_0539	-	NE	528609	529499	296	+	3572361 COG1660R	hypothetical protein M5005_Spy_0539
M5005_Spy_0540	-	NE	529496	530473	325	+	3572362 COG0391S	transporter
M5005_Spy_0541		NE	530470	531381	303	+	3572363 COG1481S	hypothetical protein M5005_Spy_0541
M5005_Spy_0542	pepD	NE	531514	532911	465	+	3572364 COG4690E	dipeptidase
M5005_Spy_0543	adcA	NE	533063	534610	515	+	3572365 COG3443R	high-affinity zinc uptake system protein znuA
M5005_Spy_0544		NE	534758	535480	240	+	3572366 COG2188K	GntR family transcriptional regulator
M5005_Spy_0545	agaS	NE	535499	536698	399	+	3572367 COG2222M	galactosamine-6-phosphate deaminase
M5005_Spy_0546c	rpmE2	С	536795	537055	86	-	3572368 COG0254J	50S ribosomal protein L31
M5005_Spy_0547c	-	NC	537170	538111	313	-	3572369 COG0618R	phosphoesterase, DHH family protein
M5005_Spy_0548	flaV	С	538505	538954	149	+	3572370 COG0716C	flavodoxin
M5005_Spy_0549	-	NE	539130	539414	94	+	3572371 COG1605E	hypothetical protein M5005_Spy_0549
M5005_Spy_0550	-	NE	539407	540669	420	+	3572372 COG0038P	chloride channel protein
M5005_Spy_0551	rpIS	NC	540784	541131	115	+	3572373 COG0335J	50S ribosomal protein L19
M5005_Spy_0552	-	NE	542134	542703	189	+	3572375 COG0546R	DNA gyrase
M5005_Spy_0553	gyrB	E	542704	544656	650	+	3572376 COG0187L	DNA gyrase subunit B
M5005_Spy_0554	ezrA	E	545024	546748	574	+	3572339 COG4477D	septation ring formation regulator EzrA
M5005_Spy_0555c	-	NE	546880	547338	152	-	3572340 COG5506S	hypothetical protein M5005_Spy_0555
M5005_Spy_0556	eno	E	547565	548872	435	+	3572341 COG0148G	phosphopyruvate hydratase
M5005_Spy_0557c	-	NE	549398	549988	196	-	3572342 COG3547L	transposase
M5005_Spy_0558c	-	NE	550037	550288	83	-	<u>3572343</u> -	transposase
M5005_Spy_0559c	-	NE	550650	551306	218	-	<u>3572344</u> -	transcriptional regulator
M5005_Spy_0560c	-	NE	551303	552190	295	-	<u>3572345</u> -	transcriptional regulator
M5005_Spy_0561	epf	NE	552662	558841	2059	+	3572346 COG5271R	extracellular matrix binding protein
M5005_Spy_0562	sagA	NE	559706	559867	53	+	<u>3572347</u> -	streptolysin S
M5005_Spy_0563	sagB	NE	560089	561039	316	+	3572348 COG0778C	streptolysin S biosynthesis protein
M5005_Spy_0564	sagC	NE	561036	562094	352	+	<u>3572349</u> -	streptolysin S biosynthesis protein
M5005_Spy_0565	sagD	NE	562114	563472	452	+	3572350 COG1944S	streptolysin S biosynthesis protein
M5005_Spy_0566	sagE	NE	563447	564118	223	+	3572351 COG1266R	streptolysin S self-immunity protein
M5005_Spy_0567	sagF	NE	564115	564798	227	+	3572352 -	streptolysin S biosynthesis protein
M5005_Spy_0568	sagG	NE	564821	565744	307	+	3572353 COG1131V	streptolysin S export ATP-binding protein
M5005_Spy_0569	sagH	NE	565753	566880	375	+	3572354 COG1668CP	streptolysin S export transmembrane protein
M5005_Spy_0570	sagI	NE	566877	567995	372	+	3572355 COG0842V	streptolysin S export transmembrane protein
M5005_Spy_0571	-	NE	568566	571298	910	+	3572356 COG2374R	hypothetical protein M5005_Spy_0571
M5005_Spy_0572	-	NE	571576	572076	166	+	3572357 COG4708S	hypothetical protein M5005_Spy_0572
M5005_Spy_0573	ligA	E	572270	574228	652	+	3572319 COG0272L	NAD-dependent DNA ligase LigA
M5005_Spy_0574	-	E	574242	575264	340	+	3572320 COG1597IR	lipid kinase
M5005_Spy_0575	atpE	NC	575657	575854	65	+	3572321 COG0636C	ATP synthase F0F1 subunit C
M5005_Spy_0576	atpB	NC	575889	576605	238	+	3572322 COG0356C	ATP synthase F0F1 subunit A
M5005 Spy 0577	atpF	E	576623	577117	164	+	3572323 COG0711C	ATP synthase F0F1 subunit B
M5005 Spy 0578	atpH	E	577117	577653	178	+	3572324 COG0712C	ATP synthase F0F1 subunit delta
M5005_Spy_0579	atpA	E	577669	579177	502	+	3572325 COG0056C	ATP synthase F0F1 subunit alpha
M5005_Spy_0579	atpG	E	579193	580068	291	+	3572326 COG0224C	ATP synthase F0F1 subunit gamma
M5005_Spy_0581	atpD	E	580230	581636	468	+	3572327 COG0055C	ATP synthase F0F1 subunit beta
M5005_Spy_0581	atpC	NC	581649	582065	138	+	3572328 COG0355C	ATP synthase F0F1 subunit epsilon
M5005_Spy_0582 M5005_Spy_0583	- -	NE NE	581649	582588	138 85	+	3572329 -	hypothetical protein M5005 Spy 0583
M5005_Spy_0584	murA	NE NE			85 369	+	3572330 COG0766M	UDP-N-acetylglucosamine 1-carboxyvinyltransferase
M5005_Spy_0584 M5005_Spy_0585	epuA	NE NE	582815 583928	583924 584116	62		3572330 COG0766M	epuA protein
M5005_Spy_0586	endA	NE NE	583928 584152	584691	179	+	<u>3572331</u> - <u>3572332</u> -	DNA-entry nuclease
113303_3py_0300	enua	INL	304132	304031	1/3	т	33,2332	Divi Chay hadease

M5005_Spy_0587	pheS	E	584974	586017	347	+	3572333 COG0016J	phenylalanyl-tRNA synthetase subunit alpha
M5005_Spy_0588	pheT	E	586212	588632	806	+	3572334 COG0072J	phenylalanyl-tRNA synthetase subunit beta
M5005_Spy_0589	-	NE	588742	589119	125	+	3572335 COG17650	salt-stress induced protein
M5005_Spy_0590	-	NE	589112	589498	128	+	3572336 COG3272S	hypothetical protein M5005_Spy_0590
M5005_Spy_0591	-	NE	589571	590647	358	+	3572337 COG0577V	ABC transporter permease
M5005_Spy_0592	-	NE	590657	591325	222	+	3572338 COG1136V	ABC transporter ATP-binding protein
M5005_Spy_0593c	-	NE	591427	592344	305	-	3572300 COG2321R	neutral zinc metallopeptidase
M5005_Spy_0594	rexB	NC	592495	595710	1071	+	3572301 COG3857L	ATP-dependent nuclease subunit B
M5005_Spy_0595	rexA	С	595671	599339	1222	+	3572302 COG1074L	ATP-dependent nuclease subunit A
M5005_Spy_0596	-	NE	599479	600291	270	+	3572303 COG0834ET	arginine-binding protein
M5005_Spy_0597	rpsU	E	600432	600608	58	+	<u>3572304</u> -	30S ribosomal protein S21
M5005_Spy_0598c	mscL	NE	600736	601098	120	-	3572305 COG1970M	large-conductance mechanosensitive channel
M5005_Spy_0599	dnaG	E	601229	603043	604	+	3572306 COG0358L	DNA primase
M5005_Spy_0600	rpoD	E	603052	604161	369	+	3572307 COG0568K	RNA polymerase sigma factor RpoD
M5005_Spy_0601	-	NE	604397	604735	112	+	3572308 COG2151R	hypothetical protein M5005_Spy_0601
M5005_Spy_0602	rmID	E	604873	605727	284	+	3572309 COG1091M	dTDP-4-dehydrorhamnose reductase
M5005_Spy_0603	rgpAc	E	605846	607000	384	+	3572310 COG0438M	alpha-(1,2)-rhamnosyltransferase
M5005_Spy_0604	rgpBc	E	606990	607922	310	+	3572311 COG0463M	alpha-L-Rha alpha-1,3-L-rhamnosyltransferase
M5005_Spy_0605	rgpCc	E	607925	608728	267	+	3572312 COG1682GM	polysaccharide export ABC transporter permease
M5005_Spy_0606	rgpDc	E	608728	609933	401	+	3572313 COG1134GM	polysaccharide export ATP-binding protein
M5005_Spy_0607	rgpEc	E	609958	610965	335	+	3572314 COG0463M	glycosyltransferase
M5005_Spy_0608	rgpFc	E	610962	612707	581	+	3572315 COG3754M	alpha-L-Rha alpha-1,3-L-rhamnosyltransferase
M5005_Spy_0609	-	NE	612704	615178	824	+	3572316 COG1368M	phosphoglycerol transferase
M5005_Spy_0610	-	NE	615357	616052	231	+	3572317 COG0463M	glycosyltransferase
M5005_Spy_0611	-	NE	616054	616395	113	+	<u>3572318</u> -	hypothetical protein M5005_Spy_0611
M5005_Spy_0612	amrA	С	616388	617674	428	+	3572280 COG2244R	transcriptional activator
M5005_Spy_0613	-	E	617655	619151	498	+	3572281 COG4713S	hypothetical protein M5005_Spy_0613
M5005_Spy_0614	pepT	NE	619245	620468	407	+	3572282 COG2195E	peptidase T
M5005_Spy_0615	ebsA	NE	620509	620997	162	+	<u>3572283</u> -	pore forming protein
M5005_Spy_0616c	-	NE	620984	621181	65	-	3572284 COG1141C	ferredoxin
M5005_Spy_0617	-	NC	621230	621706	158	+	<u>3572285</u> -	hypothetical protein M5005_Spy_0617
M5005_Spy_0618	cmk	С	621721	622401	226	+	3572286 COG0283F	cytidylate kinase
M5005_Spy_0619	infC	С	622563	623093	176	+	3572287 COG0290J	translation initiation factor IF-3
M5005_Spy_0620	rpmI	С	623135	623332	65	+	3572288 COG0291J	50S ribosomal protein L35
M5005_Spy_0621	rplT	NC	623391	623750	119	+	3572289 COG0292J	50S ribosomal protein L20
M5005_Spy_0622c	-	E	624041	626212	723	-	3572290 COG1368M	phosphoglycerol transferase
M5005_Spy_0623	-	NE	626359	627522	387	+	3572291 COG1092R	methyltransferase
M5005_Spy_0624	aroD	NE	627519	628205	228	+	3572292 COG0710E	3-dehydroquinate dehydratase
M5005_Spy_0625	aroF	NE	628299	629465	388	+	3572293 COG0082E	chorismate synthase
M5005_Spy_0626	-	NE	629526	629867	113	+	3572294 COG3679S	hypothetical protein M5005_Spy_0626
M5005_Spy_0627	gor	NE	630088	631440	450	+	3572295 COG1249C	glutathione reductase
M5005_Spy_0628c	folC.2	NE	631528	632796	422	-	3572296 COG0285H	folylpolyglutamate synthase/dihydrofolate synthase
M5005_Spy_0629c	-	NE	632826	633266	146	-	<u>3572297</u> -	hypothetical protein M5005_Spy_0629
M5005_Spy_0630	nifS1	NE	633501	634643	380	+	3572298 COG1104E	cysteine desulfhydrase
M5005_Spy_0631	thiI	NE	634655	635869	404	+	3572299 COG0301H	thiamine biosynthesis protein ThiI
M5005_Spy_0632	capA	NE	635907	637199	430	+	3572261 COG2843M	capsule biosynthesis protein
M5005_Spy_0633	rplU	NC	637413	637727	104	+	3572262 COG0261J	50S ribosomal protein L21
M5005_Spy_0634	-	NC	637739	638065	108	+	3572263 COG2868J	hypothetical protein M5005_Spy_0634
M5005_Spy_0635	rpmA	NC	638093	638386	97	+	3572264 COG0211J	50S ribosomal protein L27
M5005_Spy_0636	-	NE	638734	639648	304	+	3572265 COG0583K	LysR family transcriptional regulator
M5005_Spy_0637	Isp	NE	639645	640103	152	+	3572266 COG0597MU	lipoprotein signal peptidase
M5005_Spy_0638	-	NE	640093	640983	296	+	3572267 COG0564J	ribosomal large subunit pseudouridine synthase D
M5005_Spy_0639	pyrR	NE	641379	641900	173	+	3572268 COG2065F	phosphoribosyltransferase
M5005_Spy_0640	pyrP	NE	641916	643175	419	+	3572269 COG2233F	uracil permease
M5005_Spy_0641	pyrB	NE	643236	644171	311	+	3572270 COG0540F	aspartate carbamoyltransferase
M5005_Spy_0642	carA	NE	644215	645297	360	+	3572271 COG0505EF	carbamoyl phosphate synthase small subunit
M5005_Spy_0643	carB	NE	645523	648699	1058	+	3572272 COG0458EF	carbamoyl phosphate synthase large subunit
M5005_Spy_0644	-	NE	648999	650177	392	+	3572273 COG0845M	periplasmic protein of efflux system
M5005_Spy_0645	-	NE	650177	650887	236	+	3572274 COG1136V	ABC transporter ATP-binding protein

ME00E C 0646			C=0000	650440	100		2572275 60605771	ADC harmon days and a second		
M5005_Spy_0646	-	NE	650899	652119	406	+	3572275 COG0577V	ABC transporter permease	_	*
M5005_Spy_0647	- 	NE	652373	654106	577	+	3572276 COG4781C	glycerophosphoryl diester phosphodiesterase	_	*
M5005_Spy_0648	rpsP	NE	654233	654505	90	+	3572277 COG0228J	30S ribosomal protein S16		
M5005_Spy_0649	-	NE	654515	654754	79	+	3572278 COG1837R	RNA binding protein		
M5005_Spy_0650	-	NC	654763	654870	35	+	<u>3572279</u> -	hypothetical protein M5005_Spy_0650		
M5005_Spy_0651	-	NE	655665	658691	1008	+	<u>3572241</u> -	cell surface protein		*
M5005_Spy_0652	-	NE	658711	659112	133	+	3572242 COG3576R	hypothetical protein M5005_Spy_0652		*
M5005_Spy_0653c	czcD	NE	659292	660167	291	-	3572243 COG1230P	cobalt-zinc-cadmium resistance protein		*
M5005_Spy_0654	-	NE	660303	660824	173	+	3572244 COG1309K	TetR family transcriptional regulator		*
M5005_Spy_0655	rimM	NE	661039	661557	172	+	3572245 COG0806J	16S rRNA-processing protein RimM		*
M5005_Spy_0656	trmD	E	661547	662278	243	+	3572246 COG0336J	tRNA (guanine-N(1)-)-methyltransferase		*
M5005_Spy_0657	trxB	NE	662278	663270	330	+	3572247 COG04920	thioredoxin reductase		*
M5005_Spy_0658	-	NE	663448	664506	352	+	3572248 COG3641R	regulatory protein		*
M5005_Spy_0659	apbA	NE	664519	665442	307	+	3572249 COG1893H	2-dehydropantoate 2-reductase		*
M5005_Spy_0660	fruR	NE	665698	666411	237	+	3572250 COG1349KG	fructose repressor		*
M5005_Spy_0661	fruB	NE	666408	667319	303	+	3572251 COG1105G	1-phosphofructokinase		*
M5005_Spy_0662	fruA	NE	667316	669262	648	+	3572252 COG1299G	IIABC		*
M5005_Spy_0663	mur1.1	NE	669361	669954	197	+	3572253 COG1705NU	autolysin		*
M5005_Spy_0664	mur1.2	NE	670106	670813	235	+	3572254 COG1705NU	autolysin		*
M5005_Spy_0665c	-	NE	670870	671088	72	-	3572255 COG2801L	transposase		
M5005_Spy_0666c	-	NC	671291	671410	39	-	3572256 -	hypothetical protein M5005_Spy_0666		
M5005_Spy_0667c	-	NC	671385	671594	69	-	3572257 -	exotoxin type C		
M5005_Spy_0668c	mac	NE	671769	672788	339	_	3572258 -	IgG-degrading protease	_	
M5005_Spy_0669	-	NC	672944	673063	39	+	3572259 -	phage protein		
M5005_Spy_0670	-	NE	673287	673463	58	+	3572260 COG0105F	nucleoside diphosphate kinase	_	
M5005_Spy_0671	-	NE	673691	674071	126	+	3572222 COG4835S	transposase	_	*
M5005_Spy_0672	_	NE	674071	674919	282	+	3572223 COG1307S	degV family protein		*
M5005_Spy_0673	papS	E	675044	676252	402	+	3572224 COG0617J	tRNA CCA-pyrophosphorylase	_	*
M5005_Spy_0674	-	NE	676249	678126	625	+	3572225 COG0488R	ABC transporter ATP-binding protein		*
M5005_Spy_0675	_	NC	678383	678535	50	+	3572226 -	hypothetical protein M5005_Spy_0675	_	
M5005_Spy_0676	_	NE	678544	678762	72	+	3572227 -	hypothetical protein M5005_Spy_0676		
M5005_Spy_0677	fms	NE	679018	679428	136	+	3572228 COG0242J	peptide deformylase	_	*
M5005_Spy_0678c	-	NE	679510	681522	670		3572229 COG0737F	5\'-nucleotidase	_	*
M5005_Spy_0679	_	NE	681742	682392	216	+	3572230 COG2357S	GTP pyrophosphokinase	_	*
M5005_Spy_0680	_	NE	682395	683063	222	+	3572231 COG0745TK	two-component response regulator		*
M5005_Spy_0681	_	NE	683072	684304	410	+	3572232 COG0642T	two-component system histidine kinase		*
M5005_Spy_0682	mvaK1	E	684583	685476	297	+	3572233 COG1577I	mevalonate kinase	_	*
M5005_Spy_0683	mvaD	E	685458	686402	314	+	3572234 COG3407I	diphosphomevalonate decarboxylase		*
M5005_Spy_0684	mvaK2	NC	686395	687402	335	+	3572235 COG1577I	phosphomevalonate kinase		*
M5005_Spy_0685	-	E	687395	688384	329	+	3572236 COG1304C	isopentenyl pyrophosphate isomerase		*
M5005_Spy_0686c	_	C	688614	689891	425	T .	3572237 COG1257I	3-hydroxy-3-methylglutaryl-CoA reductase	_	*
M5005_Spy_0687c	mvaS.1	E	689878	691053	391		3572238 COG3425I	hydroxymethylglutaryl-CoA synthase		*
M5005_Spy_0688	thyA	NC	691262	692101	279	+	3572239 COG0207F	thymidylate synthase		*
M5005_Spy_0689	dyr	E	692181	692678	165	+	3572240 COG0262H	dihydrofolate reductase	-	*
M5005_Spy_0690	-	NE	692698	692868	56	+	3572202 -	hypothetical protein M5005_Spy_0690		
M5005_Spy_0691	clpX	NE	692998	694227	409	+	3572203 COG12190	ATP-dependent protease ATP-binding subunit ClpX	_	*
M5005_Spy_0692	engB	E	694237	694836	199	+	3572204 COG0218R	ribosome biogenesis GTP-binding protein YsxC		*
M5005_Spy_0693	engb	NE	694984	695727	247	+	3572205 -	hypothetical protein M5005_Spy_0693	_	
M5005_Spy_0694c	clpL	NE		697884	699	-	3572205 3572206 COG05420	ATP-dependent protease ATP-binding subunit	_	
M5005_Spy_0094c	rpiA	C	695785			+	3572200 COG03420 3572207 COG0120G	ribose-5-phosphate isomerase A	_	*
	deoB	NE NE	698263	698946	227	+	3572207 COG0120G 3572208 COG1015G	phosphopentomutase		*
M5005_Spy_0696 M5005 Spy 0697			699023	700234	403		3572208 COG1015G 3572209 COG1393P			*
	arsC	NE	700253	700693	146	+	3572209 COG1393P 3572210 COG0005F	arsenate reductase		*
M5005_Spy_0698	punA	NC	700677	701486	269	+	3572210 COG0005F 3572211 COG0813F	purine nucleoside phosphorylase	_	*
M5005_Spy_0699	deoD	NE	702149	702862	237	+	3572211 COG0813F 3572212 -	purine nucleoside phosphorylase		*
M5005_Spy_0700	cpsX	NE	702855	703643	262	+		LytR family transcriptional regulator		
M5005_Spy_0701c	cpsY	NE	703722	704576	284	-	3572213 COG0583K	LysR family transcriptional regulator	_	*
M5005_Spy_0702		NE	704849	705385	178	+	3572214 -	hypothetical protein M5005_Spy_0702	_	*
M5005_Spy_0703	pyrF	NE	705662	706354	230	+	3572215 COG0284F	orotidine 5\'-phosphate decarboxylase		*
M5005_Spy_0704	pyrE	NE	706412	707041	209	+	3572216 COG0461F	orotate phosphoribosyltransferase		*

M5005_Spy_0705	amiC	NE	707238	708692	484	+	3572217 COG0154J	amidase
M5005_Spy_0706	-	NE	708810	709673	287	+	3572218 COG0834ET	cystine-binding protein
M5005_Spy_0707	-	NE	709702	710352	216	+	3572219 COG0765E	cystine transporter permease
M5005_Spy_0708	ung	NE	710485	711138	217	+	3572220 COG0692L	uracil-DNA glycosylase
M5005_Spy_0709	pyrC	NE	711270	712538	422	+	3572221 COG0044F	dihydroorotase
M5005_Spy_0710c	-	E	712596	713237	213	-	3572186 COG0344S	glycerol-3-phosphate acyltransferase
M5005_Spy_0711	parE	E	713372	715321	649	+	3572187 COG0187L	DNA topoisomerase IV subunit B
M5005_Spy_0712	parC	E	715412	717871	819	+	3572188 COG0188L	DNA topoisomerase IV subunit A
M5005_Spy_0713	bcaT	NE	717994	719016	340	+	3572189 COG0115EH	branched-chain amino acid aminotransferase
M5005_Spy_0714	-	NC	719080	719310	76	+	<u>3572190</u> -	hypothetical protein M5005_Spy_0714
M5005_Spy_0715	rpsA	E	719701	720906	401	+	3572193 COG0539J	30S ribosomal protein S1
M5005_Spy_0716c	-	NE	721453	721755	100	-	3572195 -	hypothetical protein M5005_Spy_0716
M5005_Spy_0717	-	NE	721954	722940	328	+	3572196 COG1054R	hypothetical protein M5005_Spy_0717
M5005_Spy_0718	-	NE	723011	723202	63	+	3572197 -	hypothetical protein M5005_Spy_0718
M5005 Spy 0719	-	NE	723251	723670	139	+	3572198 COG06250	glutathione S-transferase
M5005 Spy 0720	_	NE	723907	724815	302	+	3572199 COG1275P	exfoliative toxin
M5005 Spy 0721c	_	NC	724933	725109	58		3572200 -	hypothetical protein M5005 Spy 0721
M5005 Spy 0722	miaA	NE	725243	726142	299	+	3572201 COG0324J	tRNA delta(2)-isopentenylpyrophosphate transferase
M5005_Spy_0723	hflX	NE	726215	727453	412	+	3572166 COG2262R	GTP-binding protein
M5005_Spy_0724	-	NE	727446	728081	211	+	3572167 COG4468G	hypothetical protein M5005 Spy 0724
M5005_Spy_0725	elaC	E	727440	729025	309	+	3572168 COG1234R	ribonuclease Z
M5005_Spy_0726	-	NE	729025	729789	254	+	3572169 COG0300R	short chain dehydrogenase
M5005_Spy_0720 M5005_Spy_0727	recJ					+	3572170 COG0608L	single-stranded-DNA-specific exonuclease
		NE	729786	731996	736		3572170 COG0608L 3572171 COG0503F	= '
M5005_Spy_0728 M5005_Spy_0729	apt dnaD	NE	732147	732665	172	+	3572171 COG0303F 3572172 COG3935L	adenine phosphoribosyltransferase
		NC	732746	733429	227	+		DNA replication protein
M5005_Spy_0730	nth	NE	733426	734082	218	+	3572173 COG0177L	endonuclease III
M5005_Spy_0731	-	E	734154	734738	194	+	3572174 COG2384R	I/anthranilate synthase component I
M5005_Spy_0732	-	NE	734829	735617	262	+	3572175 COG0327S	NIF3-related protein
M5005_Spy_0733	-	NE	735657	736763	368	+	3572176 COG0665E	glycine/D-amino acid oxidase
M5005_Spy_0734	cpsFO/rmIA	E	736821	737690	289	+	3572177 COG1209M	glucose-1-phosphate thymidylyltransferase
M5005_Spy_0735	cpsFP/rmIC	NC	737690	738283	197	+	3572178 COG1898M	dTDP-4-dehydrorhamnose 3,5-epimerase
M5005_Spy_0736	cpsFQ/rmIB	E	738527	739567	346	+	3572179 COG1088M	dTDP-glucose 4,6-dehydratase
M5005_Spy_0737	mutX	NE	739788	740264	158	+	3572180 COG1051F	7,8-dihydro-8-oxoguanine-triphosphatase
M5005_Spy_0738	-	NE	740322	741503	393	+	3572181 COG0628R	hypothetical protein M5005_Spy_0738
M5005_Spy_0739	-	NE	741493	742740	415	+	3572182 COG2956G	hypothetical protein M5005_Spy_0739
M5005_Spy_0740c	fbp	NE	742799	744085	428	-	3572183 COG1293K	fibronectin-binding protein
M5005_Spy_0742	-	NC	744497	744622	41	+	<u>3572185</u> -	hypothetical protein M5005_Spy_0742
M5005_Spy_0743	-	NE	744804	745802	332	+	3572147 COG2984R	ABC transporter substrate-binding protein
M5005_Spy_0744	-	NC	745792	745971	59	+	<u>3572148</u> -	hypothetical protein M5005_Spy_0744
M5005_Spy_0745	-	NE	746148	747017	289	+	3572149 COG4120R	ABC transporter permease
M5005_Spy_0746	-	NE	747014	747772	252	+	3572150 COG1101R	ABC transporter ATP-binding protein
M5005_Spy_0747	-	E	747976	749637	553	+	3572151 COG0595R	Zn-dependent hydrolase
M5005_Spy_0748	estA	NE	749770	750555	261	+	3572152 COG0627R	acetyl esterase
M5005_Spy_0749	-	NE	750585	750911	108	+	<u>3572153</u> -	hypothetical protein M5005_Spy_0749
M5005_Spy_0750	-	NE	750957	752864	635	+	3572154 COG0488R	ABC transporter ATP-binding protein
M5005_Spy_0751	acoA	NE	753149	754117	322	+	3572155 COG1071C	alpha
M5005_Spy_0752	acoB	NE	754173	755174	333	+	3572156 COG0022C	pyruvate dehydrogenase E1 component subunit beta
M5005_Spy_0753	acoC	NE	755359	756768	469	+	3572157 COG0508C	subunit E2
M5005_Spy_0754c	-	NE	756823	757062	79	_	3572158 -	hypothetical protein M5005_Spy_0754
M5005_Spy_0755	acoL	NE	757095	758858	587	+	3572159 COG1249C	dihydrolipoamide dehydrogenase
M5005_Spy_0756c	-	NE	758874	759086	70	-	3572160 -	hypothetical protein M5005_Spy_0756
M5005_Spy_0757c	hylA	NE	759532	761949	805	_	3572161 -	hyaluronate lyase
M5005_Spy_0758	lplB	NE	762182	763171	329	+	3572162 COG0095H	lipoate-protein ligase A
M5005_Spy_0759c	cobQ	E	763280	764071	263	-	3572163 COG3442R	hypothetical protein M5005_Spy_0759
M5005_Spy_0760c	murC2	E	764071	765414	447	_	3572164 COG0769M	diaminopimelate ligase
M5005_Spy_07600 M5005_Spy_0761	-	E	765521	766372	283	+	3572165 COG1624S	hypothetical protein M5005_Spy_0761
M5005_Spy_0761 M5005_Spy_0762	_	NE	765321	767325	318	+	3572105 COG10243 3572127 COG4856S	hypothetical protein M5005_Spy_0761
M5005_Spy_0762 M5005_Spy_0763	glmM	E	767379	767325 768734	451	+	3572127 COG46303 3572128 COG1109G	phosphoglucosamine mutase
M5005_Spy_0763 M5005_Spy_0764	giiii•i -	NE	767379	769509	213	+	3572128 COG1109G	hypothetical protein M5005_Spy_0764
113003_3py_0764	-	INE	/08808	709509	213	+	2212122 -	hypothetical protein M3003_3py_0704

M5005_Spy_0765	hemN	NE	769506	770702	398	+	3572130 COG0635H	coproporphyrinogen III oxidase	
M5005_Spy_0766	-	С	770712	771464	250	+	3572131 COG3884I	acyl-ACP thioesterase	
M5005_Spy_0767	-	NE	771464	772228	254	+	3572132 COG0647G	4-nitrophenylphosphatase	
M5005_Spy_0768	-	NE	772228	772860	210	+	3572133 COG4478S	hypothetical protein M5005_Spy_0768	
M5005_Spy_0769	cas9	NE	773340	777446	1368	+	3572134 COG3513S	hypothetical protein M5005_Spy_0769	
M5005_Spy_0770	cas1	NE	777446	778315	289	+	3572135 COG1518L	hypothetical protein M5005_Spy_0770	
M5005_Spy_0771	cas2	NE	778312	778653	113	+	3572136 COG3512S	hypothetical protein M5005_Spy_0771	
M5005_Spy_0772	csn2	NE	778643	779305	220	+	3572137 -	hypothetical protein M5005_Spy_0772	
M5005_Spy_0773c	-	NE	779352	779639	95	-	3572138 -	hypothetical protein M5005_Spy_0773	
M5005_Spy_0774	-	NE	779772	779951	59	+	3572139 -	nucleoside diphosphate kinase	_
M5005_Spy_0775	-	NC	780015	780161	48	+	3572140 COG0105F	nucleoside diphosphate kinase	
M5005_Spy_0776	lepA	NE	780285	782117	610	+	3572141 COG0481M	GTP-binding protein LepA	
M5005_Spy_0777	sclB	NE	782375	783256	293	+	3572142 -	hypothetical protein M5005_Spy_0777	_
M5005_Spy_0778	msrB/crsA	NE	783442	783879	145	+	3572143 COG02290	methionine sulfoxide reductase B	
M5005_Spy_0779	-	NE	783994	785013	339	+	3572144 COG2855S	hypothetical protein M5005_Spy_0779	
M5005 Spy 0780	_	NE	785220	785645	141	+	3572145 COG2893G	subunit IIA	-
M5005 Spy 0781	ptsB	NE	785664	786155	163	+	3572146 COG3444G	subunit IIB	
M5005_Spy_0782	ptsC	NE	786172	786981	269	+	3572108 COG3715G	subunit IIC	
M5005_Spy_0783	ptsD	NE	786978	787805	275	+	3572109 COG3716G	subunit IID	
M5005_Spy_0784	-	NE	787941	789590	549	+	3572100 COG2972T	two-component sensor kinase	-
M5005_Spy_0785	_	NE	789594	790382	262	+	3572110 COG25721 3572111 COG4753T	two-component response regulator	-
M5005_Spy_0786	_	NE	790376	790362	348	+	3572111 COG1840P	iron(III)-binding protein	_
M5005_Spy_0780 M5005_Spy_0787	_	NE NE				+	3572112 COG1640F 3572113 COG0727R	hypothetical protein M5005_Spy_0787	
M5005_Spy_0787 M5005_Spy_0788	_		791519	791866	115		3572113 COG0727R 3572114 COG0110R	acetyltransferase	_
	-	NE	792201	792767	188	+	3572114 COG0110R 3572115 COG1011R	·	
M5005_Spy_0789		NE	792783	793472	229	+	3572115 COG1011R 3572116 COG1012C	HAD superfamily hydrolase	_
M5005_Spy_0790	gabD	NE	793567	794964	465	+		succinate-semialdehyde dehydrogenase	_
M5005_Spy_0791	uvrC -	NE	795066	796862	598	+	3572117 COG0322L	excinuclease ABC subunit C	_
M5005_Spy_0792	-	NE	797047	797649	200	+	3572118 COG0778C	NAD(P)H-dependent quinone reductase	_
M5005_Spy_0793		NE	797774	799183	469	+	3572119 COG0624E	dipeptidase PepV	_
M5005_Spy_0794c	trmE	С	799251	800627	458	-	3572120 COG0486R	tRNA modification GTPase TrmE	_
M5005_Spy_0795	rpl]	NE	800960	801460	166	+	3572121 COG0244J	50S ribosomal protein L10 50S ribosomal protein L7/L12	
M5005_Spy_0796	rplL	NE	801525	801890	121	+	3572122 COG0222J	• •	_
M5005_Spy_0797	-	NC	802286	802426	46	+	<u>3572123</u> -	hypothetical protein M5005_Spy_0797	
M5005_Spy_0798	-	NE	802420	802788	122	+	<u>3572124</u> -	IFN-response binding factor 1	
M5005_Spy_0799	-	NC	802767	802904	45	+	<u>3572125</u> -	hypothetical protein M5005_Spy_0799	_
M5005_Spy_0800	-	NE	802963	803286	107	+	3572126 COG0270L	DNA-cytosine methyltransferase	_
M5005_Spy_0801	-	NC	803344	803466	40	+	<u>3572088</u> -	relaxase	_
M5005_Spy_0802	-	NE	803599	803811	70	+	<u>3572089</u> -	relaxase	
M5005_Spy_0803	srtI	NE	804076	804771	231	+	<u>3572090</u> -	lantibiotic production protein	
M5005_Spy_0804	srtR	NE	804922	805608	228	+	3572091 COG0745TK	nisin biosynthesis two-component response regulator	
M5005_Spy_0805	srtK	NE	805601	806947	448	+	3572092 COG0642T	nisin biosynthesis sensor protein	
M5005_Spy_0806	srtA	NC	807095	807235	46	+	<u>3572093</u> -	lantibiotic protein	
M5005_Spy_0807	srtT	NE	807350	807967	205	+	3572094 COG1132V	lantibiotic ABC transporter ATP-binding protein	
M5005_Spy_0808	srtF	NE	808049	808738	229	+	3572095 COG1131V	lantibiotic ABC transporter ATP-binding protein	
M5005_Spy_0809	srtE	NE	808744	809493	249	+	<u>3572096</u> -	lantibiotic transport permease	
M5005_Spy_0810	srtG	NE	809496	810218	240	+	3572097 COG4200S	lantibiotic transport permease	
M5005_Spy_0811	-	NE	810410	810628	72	+	3572098 COG1396K	Cro/CI family transcriptional regulator	
M5005_Spy_0812c	-	NE	810737	810952	71	-	<u>3572099</u> -	hypothetical protein M5005_Spy_0812	
M5005_Spy_0817	dacA1	NE	812371	813699	442	+	3572104 COG1686M	D-alanyl-D-alanine carboxypeptidase	
M5005_Spy_0818c	-	NE	813816	814778	320	-	3572105 COG0726G	polysaccharide deacetylase	
M5005_Spy_0819	-	NC	814866	815021	51	+	<u>3572106</u> -	hypothetical protein M5005_Spy_0819	
M5005_Spy_0820	folC.1	E	815110	816387	425	+	3572107 COG0285H	folylpolyglutamate synthase/dihydrofolate synthase	
M5005_Spy_0821	folE	NE	816434	817000	188	+	3572069 COG0302H	GTP cyclohydrolase I	
M5005_Spy_0822	folP	С	817009	817809	266	+	3572070 COG0294H	dihydropteroate synthase	
M5005_Spy_0823	folQ	NE	817816	818175	119	+	3572071 COG1539H	dihydroneopterin aldolase	
M5005_Spy_0824	folK	NC	818172	818672	166	+	3572072 COG0801H	hydroxymethyldihydropteridine pyrophosphokinase	
M5005_Spy_0825	murB	E	818822	819709	295	+	3572073 COG0812M	UDP-N-acetylenolpyruvoylglucosamine reductase	
M5005_Spy_0826	potA	NE	819755	820909	384	+	3572074 COG3842E	protein	
M5005_Spy_0827	potB	NE	820893	821687	264	+	3572075 COG1176E	spermidine/putrescine transporter permease	
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M5005_Spy_0828	potC	NE	821684	822460	258	+	3572076 COG1177E	spermidine/putrescine transporter permease
M5005_Spy_0829	potD	NE	822453	823526	357	+	3572077 COG0687E	spermidine/putrescine-binding protein
M5005_Spy_0830c	dpiA	NE	823581	824246	221	-	3572078 COG4565KT	transcriptional regulatory protein
M5005_Spy_0831c	dpiB	NE	824227	825768	513	-	3572079 COG3290T	sensor kinase
M5005_Spy_0832	malP	NE	825929	827260	443	+	3572080 COG3493C	malate-sodium symport
M5005_Spy_0833	-	NE	827291	828457	388	+	3572081 COG0281C	NAD-dependent malic enzyme
M5005_Spy_0834c	-	NE	828540	829631	363	-	3572082 COG1063ER	dehydrogenase
M5005_Spy_0835	aphA	NE	829825	830187	120	+	3572083 COG3700R	class B acid phosphatase
M5005_Spy_0837	-	NE	830733	832265	510	+	3572085 COG0038P	chloride channel protein
M5005_Spy_0838	-	NE	832428	833042	204	+	3572086 COG2755E	lipase/acylhydrolase
M5005_Spy_0839	-	NE	833222	834349	375	+	3572087 COG0628R	hypothetical protein M5005_Spy_0839
M5005_Spy_0840	radC	NE	834398	835078	226	+	3572049 COG2003L	DNA repair protein RadC
M5005_Spy_0841c	-	NE	835080	835775	231	-	3572050 COG2071R	glutamine amidotransferase, class I
M5005_Spy_0842c	-	NE	835785	836429	214	-	3572051 COG2344R	redox-sensing transcriptional repressor Rex
M5005_Spy_0843c	-	NE	836681	837028	115	-	<u>3572052</u> -	hypothetical protein M5005_Spy_0843
M5005_Spy_0844c	nifS2	E	837018	838145	375	-	3572053 COG1104E	cysteine desulfhydrase
M5005_Spy_0845c	prs	NE	838142	839122	326	-	3572054 COG0462FE	ribose-phosphate pyrophosphokinase
M5005_Spy_0846c	-	NE	839262	839840	192	-	3572055 COG4116S	adenylate cyclase
M5005_Spy_0847	-	NE	839928	840599	223	+	3572056 COG2357S	GTP pyrophosphokinase
M5005_Spy_0848	ppnK	E	840574	841410	278	+	3572057 COG0061G	inorganic polyphosphate/ATP-NAD kinase
M5005_Spy_0849	rluD	NE	841407	842312	301	+	3572058 COG0564J	ribosomal large subunit pseudouridine synthase D
M5005_Spy_0851	pta/eutD	NE	842489	843310	273	+	3572060 COG0280C	phosphotransacetylase
M5005_Spy_0852	-	NE	843437	844054	205	+	3572061 COG4221R	short chain dehydrogenase
M5005_Spy_0853	-	NC	844051	844209	52	+	3572062 COG4221R	short chain dehydrogenase
M5005_Spy_0854c	-	NE	844403	845092	229	-	<u>3572063</u> -	Na+ driven multidrug efflux pump
M5005_Spy_0855	proV	NE	845512	846240	242	+	3572064 COG1125E	glycine betaine transport ATP-binding protein
M5005_Spy_0856	proX	NE	846233	847759	508	+	3572065 COG1732M	glycine betaine transporter permease
M5005_Spy_0857	guaC	NE	848037	849020	327	+	3572066 COG0516F	guanosine 5\'-monophosphate oxidoreductase
M5005_Spy_0858	xpt	NE	849325	849906	193	+	3572067 COG0503F	xanthine phosphoribosyltransferase
M5005_Spy_0859	-	NE	849906	851189	427	+	3572068 COG2233F	xanthine permease
M5005_Spy_0860c	apbE	NE	851253	852191	312	-	3572030 COG1477H	thiamine biosynthesis lipoprotein
M5005_Spy_0861c	-	NE	852244	852429	61	-	3572031 COG1942R	4-oxalocrotonate tautomerase
M5005_Spy_0862	tdk2	NE	852567	853136	189	+	3572032 COG1435F	thymidine kinase
M5005_Spy_0863	prfA	E	853171	854250	359	+	3572033 COG0216J	peptide chain release factor 1
M5005_Spy_0864	hemK	NE	854250	855089	279	+	3572034 COG2890J	methyltransferase
M5005_Spy_0865	-	NC	855073	855663	196	+	3572035 COG0009J	SUA5 protein
M5005_Spy_0866	-	NE	855681	856133	150	+	3572036 COG0456R	phosphinothricin N-acetyltransferase
M5005_Spy_0867	glyA	NE	856123	857379	418	+	3572037 COG0112E	serine hydroxymethyltransferase
M5005_Spy_0868	-	NE	857386	858363	325	+	<u>3572038</u> -	hypothetical protein M5005_Spy_0868
M5005_Spy_0869	-	NE	858364	858963	199	+	3572039 COG0741M	hypothetical protein M5005_Spy_0869
M5005_Spy_0870	-	NE	858973	860697	574	+	3572040 COG1132V	protein/permease
M5005_Spy_0871	-	NE	860694	862421	575	+	3572041 COG1132V	protein/permease
M5005_Spy_0872	nox	NE	862962	864032	356	+	3572042 COG0446R	NADH oxidase H2O-forming
M5005_Spy_0873c	ldh	NE	864191	865174	327	-	3572043 COG0039C	L-lactate dehydrogenase
M5005_Spy_0874	gyrA	E	865365	867851	828	+	3572044 COG0188L	DNA gyrase subunit A
M5005_Spy_0875	-	E	867871	868620	249	+	3572045 COG3764M	sortase
M5005_Spy_0876	-	NE	868700	869116	138	+	3572046 COG0346E	lactoylglutathione lyase
M5005_Spy_0877	-	NC	869603	869722	39	+	<u>3572047</u> -	hypothetical protein M5005_Spy_0877
M5005_Spy_0878	-	NE	869730	870098	122	+	<u>3572048</u> -	hypothetical protein M5005_Spy_0878
M5005_Spy_0879c	-	NE	870148	871059	303	-	3572010 COG1597IR	hypothetical protein M5005_Spy_0879
M5005_Spy_0880c	hlyIII	С	871176	871826	216	-	3572011 COG1272R	hypothetical protein M5005_Spy_0880
M5005_Spy_0881c	-	NE	871823	872263	146	-	3572012 -	hypothetical protein M5005_Spy_0881
M5005_Spy_0882	rbgA	E	872482	873330	282	+	3572013 COG1161R	ribosomal biogenesis GTPase
M5005_Spy_0883	rnhB	NE	873320	874111	263	+	3572014 COG0164L	ribonuclease HII
M5005_Spy_0884	smf	NE	874176	875012	278	+	3572015 COG0758LU	hypothetical protein M5005_Spy_0884
M5005_Spy_0885	topA	С	875119	877248	709	+	3572016 COG0550L	DNA topoisomerase I
M5005_Spy_0886c	-	NE	877323	877805	160	-	3572017 -	LysR family transcriptional regulator
M5005_Spy_0887c	-	NC	877812	877934	40	-	3572018 -	LysR family transcriptional regulator
M5005_Spy_0888c	-	NC	878080	878205	41	-	3572019 COG0583K	LysR family transcriptional regulator
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M5005_Spy_0889	-	NE	878218	878763	181	+	3572020 COG3641R	regulatory protein (pfoS/R)
M5005_Spy_0890	ddh	NE	878778	879770	330	+	3572021 COG1052CHR	D-lactate dehydrogenase
M5005_Spy_0891	satD	E	879875	880540	221	+	<u>3572022</u> -	hypothetical protein M5005_Spy_0891
M5005_Spy_0892	satE	NE	880533	881249	238	+	<u>3572023</u> -	hypothetical protein M5005_Spy_0892
M5005_Spy_0893	gid	NC	881400	882746	448	+	3572024 COG1206J	tRNA (uracil-5-)-methyltransferase Gid
M5005_Spy_0894	oadA2	NE	882899	884305	468	+	3572025 COG5016C	oxaloacetate decarboxylase
M5005_Spy_0895	-	NE	884348	884662	104	+	<u>3572026</u> -	hypothetical protein M5005_Spy_0895
M5005_Spy_0896	-	NE	884662	885012	116	+	3572027 COG4770I	decarboxylase
M5005_Spy_0897	-	NE	885022	886152	376	+	3572028 COG1883C	oxaloacetate decarboxylase subunit beta
M5005_Spy_0898c	-	NE	886352	887236	294	-	3572029 COG1767H	A synthase
M5005_Spy_0899c	citG	NE	887229	887924	231	-	3571991 COG1802K	GntR family transcriptional regulator
M5005_Spy_0900c	-	NE	888082	889488	468	-	3571992 COG2851C	Mg2+/citrate complex secondary transporter
M5005_Spy_0901	-	NE	889865	890188	107	+	<u>3571993</u> -	hypothetical protein M5005_Spy_0901
M5005_Spy_0902	-	NE	890242	890640	132	+	3571994 COG0511I	protein subunit
M5005_Spy_0903	oadB	NE	890685	891806	373	+	3571995 COG1883C	oxaloacetate decarboxylase subunit beta
M5005_Spy_0904	-	NC	891824	891958	44	+	<u>3571996</u> -	hypothetical protein M5005_Spy_0904
M5005_Spy_0905	citD	NE	891994	892302	102	+	3571997 COG3052C	citrate lyase subunit gamma
M5005_Spy_0906	citE	NE	892320	893177	285	+	3571998 COG2301G	citrate lyase subunit beta/citryl-CoA lyase subunit
M5005_Spy_0907	citF	NC	893180	894712	510	+	3571999 COG3051C	citrate lyase subunit alpha/citrate CoA-transferase
M5005_Spy_0908	citX	NE	894642	895283	213	+	3572000 COG3697HI	A synthase
M5005_Spy_0909	oadA1	NE	895298	896692	464	+	3572001 COG5016C	oxaloacetate decarboxylase
M5005_Spy_0910c	citC	NE	896802	897854	350	-	3572002 COG3053C	(citrate (pro-3S)-lyase) ligase
M5005_Spy_0911c	-	NE	897943	898425	160	_	3572003 -	hypothetical protein M5005_Spy_0911
M5005_Spy_0912	-	NC	898910	899014	34	+	3572004 -	hypothetical protein M5005_Spy_0912
M5005_Spy_0913c	xerS	С	899125	900039	304	_	3572005 COG4974L	site-specific tyrosine recombinase XerS
M5005_Spy_0914	-	NE	900733	901362	209	+	3572006 COG2932K	phage transcriptional repressor
M5005_Spy_0915c	ffh	E	901479	903041	520	_	3572007 COG0541U	signal recognition particle subunit FFH/SRP54
M5005_Spy_0916c	ylxM	c	903056	903397	113	_	3572008 COG2739S	DNA-binding protein
M5005_Spy_0917c	-	Č	903486	904184	232	_	3572009 COG2188K	GntR family transcriptional regulator
M5005_Spy_0918c	_	NE	904267	905700	477	_	3571971 -	hypothetical protein M5005_Spy_0918
M5005_Spy_0919	guaA	C	905867	907429	520	+	3571972 COG0519F	GMP synthase
M5005_Spy_0920c	murM2	NE	907471	908694	407	-	3571973 COG2348V	alanyltransferase
M5005 Spy 0921c	-	NE	909059	910603	514	_	3571974 COG0488R	ABC transporter ATP-binding protein
M5005_Spy_0922c	pdxK	NE	910737	911294	185	_	3571975 COG4720S	hypothetical protein M5005_Spy_0922
M5005_Spy_0923c	-	NE	911272	912138	288	_	3571976 COG2240H	pyridoxamine kinase
M5005_Spy_0924	_	NE	912228	913496	422	+	3571977 COG1167KE	GntR family transcriptional regulator
M5005_Spy_0925c	rnhB	NE	913894	914250	118	-	3571978 COG1328F	anaerobic ribonucleoside-triphosphate reductase
M5005_Spy_0926c	-	NC	914572	916149	525	_	3571979 COG1502I	cardiolipin synthetase
M5005_Spy_0927c	fhs.1	E	916234	917904	556	_	3571980 COG2759F	formatetetrahydrofolate ligase
M5005_Spy_0928c	lpIA	NE	918032	919051	339	_	3571981 COG0095H	lipoate-protein ligase A
M5005_Spy_0929c	-	NE	919098	919979	293	_	3571982 COG0846K	SIR2 family protein
M5005_Spy_0930c	_	NE	919972	920784	270	_	3571983 COG2110R	hypothetical protein M5005_Spy_0930
M5005_Spy_0931c	_	NE	920777	921109	110	_	3571984 COG0509E	glycine cleavage system protein H
M5005_Spy_0931c	_	NE	921151	922149	332	_	3571985 COG2141C	luciferase-like monooxygenase
M5005_Spy_0933c	-	NE NE	921151	922149	332 399	-	3571985 COG2141C 3571986 COG1902C	NADH-dependent flavin oxidoreductase
M5005_Spy_0934c	_	NE	923342	923343	278	_	3571987 COG0095H	lipoate-protein ligase A
M5005_Spy_0935	dpfB	C	923342	925066	230	+	3571988 COG0452H	phosphopantothenatecysteine ligase
M5005_Spy_0936	dfp	E	925059	925604	181	+	3571989 COG0452H	phosphopantothenoylcysteine decarboxylase
M5005_Spy_0937	uip -	NE			189	+	3571990 COG4684S	transporter
M5005_Spy_0938	pgmA	E	925662 926407	926231 928125	572	+	3571952 COG1109G	phosphoglucomutase/phosphomannomutase
M5005_Spy_0939c	pgiliA				318	-	3571953 COG1079R	nucleoside transporter permease
M5005_Spy_0939C M5005_Spy_0940c	-	NE	928338	929294		-	3571953 COG1079R 3571954 COG4603R	nucleoside transporter permease
M5005_Spy_0941c		NE	929296	930360	354		3571954 COG4603R 3571955 COG3845R	nucleoside transporter permease nucleoside transport ATP-binding protein
M5005_Spy_0941c M5005_Spy_0942c	-	NE	930353	931903	516	-	3571955 COG3845R 3571956 COG1744R	nucleoside transport ATP-binding protein
	- cdd	NE	932024	933076	350	-	3571956 COG1744R 3571957 COG0295F	ş ·
M5005_Spy_0943c	caa -	NE	933170	933559	129	-		cytidine deaminase
M5005_Spy_0944c		NE	934218	934805	195	-	3571958 COG2813J	16S rRNA m(2)G 1207 methyltransferase
M5005_Spy_0945	coaA	E	935073	935993	306	+	3571959 COG1072H	pantothenate kinase
M5005_Spy_0946	rpsT	NE	936062	936295	77 426	+	3571960 COG0268J	30S ribosomal protein S20
M5005_Spy_0947c	ciaH	NE	936420	937730	436	-	3571961 COG2205T	sensor protein

M5005_Spy_0948c	ciaR	NE	937723	938397	224	-	3571962 COG0745TK	transcriptional regulatory protein
M5005_Spy_0949c	pepN	NE	938743	941280	845	-	3571963 COG0308E	lysyl aminopeptidase/alanine aminopeptidase
M5005_Spy_0950c	phoU	NC	941485	942138	217	-	3571964 COG0704P	phosphate transporter protein
M5005_Spy_0951c	pstB	NE	942206	942964	252	-	3571965 COG1117P	phosphate transporter ATP-binding protein
M5005_Spy_0952c	pstB2	NE	942977	943780	267	-	3571966 COG1117P	phosphate transporter ATP-binding protein
M5005_Spy_0953c	pstA	NE	943796	944683	295	-	3571967 COG0581P	phosphate transporter permease
M5005_Spy_0954c	pstC	NC	944673	945491	272	-	3571968 COG0573P	phosphate transporter permease
M5005_Spy_0955c	pstS	NE	945618	946484	288	-	3571969 COG0226P	phosphate-binding protein
M5005_Spy_0956c	-	E	946623	947933	436	-	3571970 COG0144J	16S rRNA m(5)C 967 methyltransferase
M5005_Spy_0957c	-	NE	947936	948724	262	-	3571932 COG0483G	myo-inositol-1(or 4)-monophosphatase
M5005_Spy_0958c	-	NE	948714	948992	92	-	3571933 COG4476S	hypothetical protein M5005_Spy_0958
M5005_Spy_0959c	spxA	NE	948994	949398	134	-	3571934 COG1393P	Spx family transcriptional regulator
M5005_Spy_0960c	mreA	E	949441	950373	310	-	3571935 COG0196H	adenylyltransferase
M5005_Spy_0961c	truB	NE	950402	951286	294	-	3571936 COG0130J	tRNA pseudouridine synthase B
M5005_Spy_0962c	-	NE	951402	952742	446	-	3571937 COG4487S	hypothetical protein M5005_Spy_0962
M5005_Spy_0963c	-	NE	952839	953795	318	-	3571938 COG4129S	hypothetical protein M5005_Spy_0963
M5005_Spy_0964c	-	NE	953806	954402	198	-	3571939 COG0732V	subunit
M5005_Spy_0965c	-	NE	954494	955669	391	-	3571940 COG0577V	ABC transporter permease
M5005_Spy_0967c	-	NE	957146	957847	233	-	3571942 COG1136V	ABC transporter ATP-binding protein
M5005_Spy_0968	-	NE	957965	958507	180	+	3571943 COG1309K	TetR family transcriptional regulator
M5005_Spy_0969c	-	NC	958504	958647	47	-	<u>3571944</u> -	hypothetical protein M5005_Spy_0969
M5005_Spy_0970c	-	NE	958650	959291	213	-	3571945 COG0490P	component
M5005_Spy_0971c	-	NE	959454	959942	162	-	3571946 COG1302S	Gls24 family general stress protein
M5005_Spy_0972c	-	NE	959953	960153	66	-	3571947 COG3237S	hypothetical protein M5005_Spy_0972
M5005_Spy_0973c	-	NE	960194	960733	179	-	3571948 COG1302S	Gls24 family general stress protein
M5005_Spy_0974c	-	NC	960746	960934	62	-	3571949 COG5547S	small integral membrane protein
M5005_Spy_0975c	-	NE	960945	961532	195	-	<u>3571950</u> -	hypothetical protein M5005_Spy_0975
M5005_Spy_0976c	-	NE	961593	961799	68	-	3571951 COG2261S	hypothetical protein M5005_Spy_0976
M5005_Spy_0977c	pcrA	С	962205	964523	772	-	3571913 COG0210L	DNA helicase II
M5005_Spy_0978	-	NC	964891	965061	56	-	3571915 COG1115E	Na(+)-linked D-alanine glycine permease
M5005_Spy_0979c	-	С	965052	966374	440	+	<u>3571914</u> -	hypothetical protein M5005_Spy_0979
M5005_Spy_0980	-	NE	966494	967729	411	+	3571916 COG0053P	cobalt-zinc-cadmium resistance protein
M5005_Spy_0981c	cfa	NE	968098	968871	257	-	<u>3571917</u> -	cAMP factor
M5005_Spy_0982c	-	NE	969241	970077	278	-	3571918 COG0834ET	histidine-binding protein
M5005_Spy_0983c	-	NC	970093	970722	209	-	3571919 COG1126E	histidine transport ATP-binding protein
M5005_Spy_0984c	-	NE	970732	971373	213	-	3571920 COG0765E	histidine transporter permease
M5005_Spy_0985c	-	NE	971479	971814	111	-	3571921 COG2824P	phnA protein
M5005_Spy_0986c	glmS	E	972010	973824	604	-	3571922 COG0449M	aminotransferase
M5005_Spy_0987c	sipC	NE	974000	974557	185	-	3571923 COG0681U	signal peptidase I
M5005_Spy_0988c	pyk	E	974775	976277	500	-	3571924 COG0469G	pyruvate kinase
M5005_Spy_0989c	pfkA	E	976340	977353	337	-	3571925 COG0205G	6-phosphofructokinase
M5005_Spy_0990c	dnaE	E	977433	980543	1036	-	3571926 COG0587L	DNA polymerase III DnaE
M5005_Spy_0991	-	NC	980728	981099	123	+	3571927 COG1725K	GntR family transcriptional regulator
M5005_Spy_0992	-	NE	981099	981797	232	+	3571928 COG1131V	ABC transporter ATP-binding protein
M5005_Spy_0993	-	NE	981807	982592	261	+	<u>3571929</u> -	ABC transporter permease
M5005_Spy_0994c	-	С	982719	983333	204	-	3571930 COG0398S	membrane-associated alkaline phosphatase
M5005_Spy_0995c	-	NE	983924	984112	62	-	<u>3571931</u> -	phage protein
M5005_Spy_0996	speA2	NE	984332	985087	251	+	<u>3571893</u> -	enterotoxin
M5005_Spy_0997c	-	NE	985209	985868	219	-	<u>3571894</u> -	phage protein
M5005_Spy_0998c	-	NE	985868	986089	73	-	<u>3571895</u> -	phage protein
M5005_Spy_0999c	-	NE	986099	986872	257	-	<u>3571896</u> -	phage protein
M5005_Spy_1000c	-	NE	986883	987485	200	-	<u>3571897</u> -	phage protein
M5005_Spy_1001c	-	NE	987497	988261	254	-	<u>3571898</u> -	phage-associated cell wall hydrolase
M5005_Spy_1002c	-	NE	988263	988595	110	-	<u>3571899</u> -	N-acetylmuramoyl-L-alanine amidase
M5005_Spy_1003c	-	NE	988595	988963	122	-	<u>3571900</u> -	phage protein
M5005_Spy_1004c	-	NC	988932	989096	54	-	<u>3571901</u> -	phage protein
M5005_Spy_1005c	-	NE	989068	989415	115	-	<u>3571902</u> -	phage protein
M5005_Spy_1006c	-	NE	989426	991177	583	-	3571903 COG4675S	phage structural protein
M5005_Spy_1007c	-	NE	991293	994733	1146	-	3571904 COG1705NU	phage protein

M5005_Spy_1008c	-	NE	994734	996218	494	-	3571905 COG4722S	hypothetical protein M5005_Spy_1008
M5005_Spy_1009c	-	NE	996219	998024	601	-	3571906 COG5412S	phage protein
M5005_Spy_1010c	-	NC	998017	998475	152	-	<u>3571907</u> -	phage protein
M5005_Spy_1011c	-	NE	998448	998765	105	-	<u>3571908</u> -	phage protein
M5005_Spy_1012c	-	NE	998778	999284	168	-	3571909 COG5437S	antigen A
M5005_Spy_1013c	-	NE	999296	999706	136	-	<u>3571910</u> -	antigen B
M5005_Spy_1014c	-	NE	999708	1000103	131	-	<u>3571911</u> -	antigen C
M5005_Spy_1015c	-	NE	1000100	1000411	103	-	<u>3571912</u> -	phage protein
M5005_Spy_1016c	-	NE	1000408	1000752	114	-	<u>3571874</u> -	phage protein
M5005_Spy_1017c	-	NE	1000766	1001059	97	-	<u>3571875</u> -	phage protein
M5005_Spy_1018c	-	NE	1001072	1001962	296	-	<u>3571876</u> -	phage protein
M5005_Spy_1019c	-	NE	1001981	1002550	189	-	<u>3571877</u> -	phage scaffold protein
M5005_Spy_1020c	-	NE	1002795	1003064	89	-	<u>3571878</u> -	phage protein
M5005_Spy_1021c	-	NE	1003071	1003979	302	-	3571879 COG5585T	phage protein
M5005_Spy_1022c	-	NE	1003948	1005273	441	-	<u>3571880</u> -	portal protein
M5005_Spy_1023c	-	NE	1005273	1006547	424	-	3571881 COG1783R	terminase large subunit
M5005_Spy_1024c	-	NE	1006537	1006917	126	-	<u>3571882</u> -	phage protein
M5005_Spy_1025c	-	NE	1007527	1007961	144	-	<u>3571883</u> -	ArpU family phage encoded transcriptional regulator
M5005_Spy_1026c	-	NE	1008247	1008513	88	-	<u>3571884</u> -	phage protein
M5005_Spy_1027c	-	NE	1008510	1009034	174	-	<u>3571885</u> -	phage protein
M5005_Spy_1028c	-	NE	1009037	1009669	210	-	3571886 COG0286V	phage protein
M5005_Spy_1029c	-	NE	1009671	1009955	94	-	<u>3571887</u> -	phage protein
M5005_Spy_1030c	-	NE	1009952	1010146	64	-	<u>3571888</u> -	phage protein
M5005_Spy_1031c	-	NE	1010119	1010358	79	-	<u>3571889</u> -	phage protein
M5005_Spy_1032c	-	NE	1010355	1010600	81	-	<u>3571890</u> -	phage protein
M5005_Spy_1033c	-	NE	1010597	1010953	118	-	<u>3571891</u> -	phage protein
M5005_Spy_1034c	-	NE	1010950	1011390	146	-	3571892 COG4570L	phage protein
M5005_Spy_1035c	-	NE	1011390	1011593	67	-	<u>3571854</u> -	phage protein
M5005_Spy_1036c	ssb2	NE	1011599	1012024	141	-	3571855 COG0629L	phage single-strand DNA binding protein
M5005_Spy_1037c	ssb1	NE	1012017	1012691	224	-	<u>3571856</u> -	phage single-strand DNA binding protein
M5005_Spy_1038c	-	NE	1012692	1013174	160	-	<u>3571857</u> -	phage protein
M5005_Spy_1039c	-	NE	1013196	1013450	84	-	<u>3571858</u> -	phage protein
M5005_Spy_1040c	-	NE	1013431	1013784	117	-	<u>3571859</u> -	phage protein
M5005_Spy_1041c	-	NC	1013797	1013934	45	-	<u>3571860</u> -	phage protein
M5005_Spy_1042c	-	NC	1013925	1014707	260	-	3571861 COG1484L	phage replication protein
M5005_Spy_1043c	-	NE	1014694	1015524	276	-	3571862 COG3935L	phage protein
M5005_Spy_1044	-	NE	1015738	1016199	153	+	<u>3571863</u> -	phage protein
M5005_Spy_1045c	-	NC	1016649	1016849	66	-	3571864 COG1396K	transcriptional regulator
M5005_Spy_1046	-	NE	1016923	1017309	128	+	<u>3571865</u> -	phage protein
M5005_Spy_1047c	-	NE	1017298	1017507	69	-	<u>3571866</u> -	phage protein
M5005_Spy_1048	-	NE	1017561	1018160	199	+	<u>3571867</u> -	phage protein
M5005_Spy_1049c	-	NC	1018190	1018348	52	-	3571868 -	phage protein
M5005_Spy_1050	-	C	1018705	1019529	274	+	3571869 COG2932K 3571870 -	phage transcriptional repressor
M5005_Spy_1051 M5005_Spy_1052	int.1	NE NE	1019565 1020579	1020458 1021667	297 362	+	3571870 - 3571871 COG4974L	phage protein integrase
M5005_Spy_1053		NC	1020579	1021667	302	+	3571872 -	hypothetical protein M5005_Spy_1053
M5005_Spy_1054	_	NE NE	1021799	1021912	206	+	3571873 -	integrase hypothetical protein M5005_Spy_1053 hypothetical protein M5005_Spy_1054
M5005_Spy_1055c	glgP	NE NE	1022030	1022650	754	-	3571875 COG0058G	glycogen phosphorylase
M5005_Spy_1056c	malM	NE	1022907	1025171	734 497	-	3571836 COG1640G	4-alpha-glucanotransferase
M5005_Spy_1050c	malR	NE NE	1025206	1026699	339	-	3571837 COG1609K	LacI family transcriptional regulator
M5005_Spy_10576	malE	NE	1020814	1027833	483	+	3571838 COG2182G	
M5005_Spy_1056 M5005_Spy_1059	malF	NE	1027874	1029325	483 376	+	3571839 COG2182G	maltose/maltodextrin-binding protein maltose ABC transporter permease
M5005_Spy_1060	malG	NE NE	1029830	1030960	278	+	3571840 COG3833G	maltose ABC transporter permease
M5005_Spy_1060 M5005_Spy_1061	-	NE NE			278 266	+	3571840 COG3633G 3571841 COG1609K	LacI family transcriptional regulator
M5005_Spy_1061 M5005_Spy_1062c	- malA	NE NE	1031951 1032867	1032751 1033682	266 271	+	3571841 COG1609K 3571842 COG5521S	maltodextrose utilization protein
M5005_Spy_1062c M5005_Spy_1063c	malD	NE NE	1032867	1033682	271	-	3571843 COG3833G	maltodextriose diffization protein
M5005_Spy_1063c	malC	NE NE	1033704	1034564	286 435	-	3571844 COG1175G	maltose ABC transporter permease
M5005_Spy_1004c	amyA	NE NE	1034561	1035868	435 711	-	3571845 COG0366G	alpha-amylase
M5005_Spy_1066c	amyB	NE	1033943	1038078	567	-	3571846 COG0366G	alpha-amylase
	uniyo	IVL	1030104	1033007	307		<u>55, 10 10</u> COG05000	angular anny acc

M5005_Spy_1067c	malX	NE	1039973	1041232	419	_	3571847 COG2182G	maltose/maltodextrin-binding protein
M5005_Spy_1068	-	NE	1039373	1041232	74	+	3571848 -	transposase
M5005_Spy_1069c	_	NE	1041338	1041782	327	-	3571849 COG0657I	esterase
M5005_Spy_1009C	dltD	NE	1041847	1042830	416	-	3571850 COG3966M	hypothetical protein M5005_Spy_1070
M5005_Spy_1070c M5005_Spy_1071c	dltC	NE				-	3571851 COG0236IQ	D-alaninepoly(phosphoribitol) ligase subunit 2
M5005_Spy_1071c	dltB		1044104	1044343	79		3571852 COG1696M	protein DItB
		NE	1044361	1045617	418	-		•
M5005_Spy_1073c	dltA	NE	1045614	1047152	512	-	3571853 COG1020Q	D-alaninepoly(phosphoribitol) ligase subunit 1
M5005_Spy_1074c	-	NC	1047164	1047307	47	-	<u>3571815</u> -	hypothetical protein M5005_Spy_1074
M5005_Spy_1075c	uvrB	NE	1047571	1049562	663	-	3571816 COG0556L	excinuclease ABC subunit B
M5005_Spy_1076	glnH	E	1049755	1051929	724	+	3571817 COG0765E	transporter
M5005_Spy_1077	glnQ.2	NC	1051929	1052669	246	+	3571818 COG1126E	glutamine ABC transporter ATP-binding protein
M5005_Spy_1078c	-	NC	1052817	1052969	50	-	3571819 -	hypothetical protein M5005_Spy_1078
M5005_Spy_1079c	-	NE	1052966	1054345	459	-	3571820 COG1455G	IIC
M5005_Spy_1080c	-	NE	1054523	1054972	149	-	<u>3571821</u> -	hypothetical protein M5005_Spy_1080
M5005_Spy_1081c	-	NE	1054969	1055304	111	-	3571822 COG1447G	IIA
M5005_Spy_1082c	-	NE	1055307	1055618	103	-	3571823 COG1440G	IIB
M5005_Spy_1083c	-	NC	1055641	1057635	664	-	3571824 COG3711K	component
M5005_Spy_1084c	-	NE	1057741	1058835	364	-	3571825 COG3589S	outer surface protein
M5005_Spy_1085c	bglA.2	NE	1058844	1060244	466	-	3571826 COG2723G	beta-glucosidase
M5005_Spy_1086	-	NE	1060469	1061164	231	+	3571827 COG3201H	nicotinamide mononucleotide transporter
M5005_Spy_1087c	-	NC	1061169	1061327	52	-	<u>3571828</u> -	hypothetical protein M5005_Spy_1087
M5005_Spy_1088c	obgE	E	1061396	1062703	435	-	3571829 COG0536R	GTPase ObgE
M5005_Spy_1089c	-	NC	1062766	1062894	42	-	<u>3571830</u> -	hypothetical protein M5005_Spy_1089
M5005_Spy_1090	-	NE	1063136	1063651	171	+	3571831 COG2963L	transposase
M5005_Spy_1091	-	NE	1063824	1064480	218	+	3571832 COG2801L	transposase
M5005_Spy_1092c	rsuA	NE	1064529	1065263	244	-	3571833 COG1187J	ribosomal small subunit pseudouridine synthase A
M5005_Spy_1093	-	NE	1065375	1065740	121	+	3571834 COG5496R	hypothetical protein M5005_Spy_1093
M5005_Spy_1094c	-	NE	1065860	1067080	406	-	3571796 COG2814G	major facilitator transporter
M5005_Spy_1095	-	NE	1067382	1068938	518	+	3571797 COG4868S	hypothetical protein M5005_Spy_1095
M5005_Spy_1096c	-	NE	1069045	1069446	133	-	3571798 COG2050Q	thioesterase
M5005_Spy_1097c	-	NE	1069531	1070043	170	-	3571799 COG2820F	phosphorylase Pnp/Udp family protein
M5005_Spy_1098c	-	NE	1070348	1071703	451	-	3571800 COG2265J	tRNA (uracil-5-)-methyltransferase
M5005_Spy_1099c	psr	NE	1071785	1073236	483	-	3571801 COG1316K	LytR family transcriptional regulator
M5005_Spy_1100c	aroK	NE	1073444	1073935	163	-	3571802 COG0703E	shikimate kinase
M5005_Spy_1101c	aroA1	NE	1073928	1075220	430	_	3571803 COG0128E	3-phosphoshikimate 1-carboxyvinyltransferase
M5005_Spy_1102c	-	NE	1075322	1076287	321	_	3571804 COG1295S	ribonuclease BN
M5005_Spy_1103c	map	E	1076289	1077149	286	_	3571805 COG0024J	methionine aminopeptidase
M5005_Spy_1104c	- '	NE	1077165	1078448	427	_	3571806 COG4109K	hypothetical protein M5005_Spy_1104
M5005_Spy_1105c	-	NE	1078457	1078999	180	_	3571807 COG1670J	ribosomal-protein-alanine acetyltransferase
M5005_Spy_1106c	grab	NE	1079237	1079890	217	_	3571808 COG2723G	protein G-related alpha 2M-binding protein
M5005_Spy_1107c	murZ	NE	1080248	1081507	419	_	3571809 COG0766M	UDP-N-acetylglucosamine 1-carboxyvinyltransferase
M5005_Spy_1108c	metK2	E	1081681	1082877	398	_	3571810 COG0192H	S-adenosylmethionine synthetase
M5005_Spy_1109c	inlA	NE	1083414	1085792	792	_	3571811 COG4886S	internalin protein
M5005_Spy_1110	birA	E	1085996	1086937	313	+	3571812 COG0340H	biotinprotein ligase
M5005_Spy_1111c	-	NE	1086912	1087220	102	_	3571813 -	hypothetical protein M5005_Spy_1111
M5005_Spy_1112c	dnaX	E	1087210	1088880	556	_	3571814 COG2812L	DNA polymerase III subunits gamma/tau
M5005_Spy_1113c	-	NE	1088880	1089377	165	_	3571776 COG1956T	GAF domain-containing protein
M5005_Spy_1114	-	NE	1089522	1090331	269	+	3571777 COG2339S	hypothetical protein M5005_Spy_1114
M5005_Spy_1115c	-	NE	1090384	1090647	87	_	3571778 COG3326S	hypothetical protein M5005_Spy_1115
M5005_Spy_1116c	udk	NE	1090727	1091353	208	_	3571779 COG0572F	uridine kinase
M5005_Spy_1117	deaD2	NE	1091451	1092536	361	+	3571780 COG0513LKJ	ATP-dependent RNA helicase
M5005_Spy_1118c	-	NE	1092700	1093920	406	_	3571781 COG0726G	peptidoglycan N-acetylglucosamine deacetylase
M5005_Spy_1119c	gapN	E	1094015	1095442	475	_	3571782 COG1012C	dehydrogenase
M5005_Spy_1119c	pstI	C	1094013	1093442	577	_	3571783 COG1080G	phosphoenolpyruvate-protein phosphotransferase
M5005_Spy_1120c M5005_Spy_1121c	ptsH	c	1093627	1097628	87	-	3571784 COG1925G	phosphocarrier protein HPr
M5005_Spy_1121c	nrdH	NE	1097303	1097628	72	+	3571785 COG06950	glutaredoxin
M5005_Spy_1122	nrdE.2	NE	1098021	1100418	719	+	3571786 COG0209F	ribonucleotide-diphosphate reductase subunit alpha
M5005_Spy_1124	nrdF	NE	1100751	1100418	319	+	3571787 COG0208F	ribonucleotide-diphosphate reductase subunit beta
M5005_Spy_1124 M5005_Spy_1125	-	NE	1100731	1101710	437	+	3571788 COG0038P	chloride channel protein
. 13003_3py_1123		IVL	1101003	1102330	737	г	<u>5571700</u> C0000001	anonde chamile process

M5005_Spy_1129c	-	NE	1104384	1105079	231	-	3571792 COG1266R	CAAX amino protease
M5005_Spy_1130c	-	NE	1105098	1105859	253	-	<u>3571793</u> -	hypothetical protein M5005_Spy_1130
M5005_Spy_1131c	-	NC	1105856	1106077	73	-	3571794 COG1476K	Cro/CI family transcriptional regulator
M5005_Spy_1132c	alaS	E	1106432	1109050	872	-	3571795 COG0013J	alanyl-tRNA synthetase
M5005_Spy_1133c	prsA	NE	1109437	1110492	351	-	3571757 COG07600	foldase PrsA
M5005_Spy_1134c	-	NE	1110555	1111262	235	-	3571758 COG4122R	O-methyltransferase
M5005_Spy_1135c	-	NE	1111328	1112524	398	-	3571759 COG2271G	oxalate/formate antiporter
M5005_Spy_1136c	рерВ	NE	1112900	1114705	601	-	3571760 COG1164E	oligoendopeptidase F
M5005_Spy_1137c	-	NE	1114718	1115680	320	-	3571761 COG4469R	competence protein/transcription factor
M5005_Spy_1138c	-	NE	1115975	1116691	238	-	3571762 COG1187J	ribosomal small subunit pseudouridine synthase A
M5005_Spy_1139c	nagB	NE	1116810	1117514	234	-	3571763 COG0363G	glucosamine-6-phosphate isomerase
M5005_Spy_1140	queA	NE	1117716	1118744	342	+	3571764 COG0809J	isomerase
M5005_Spy_1141	-	NE	1118751	1119971	406	+	<u>3571765</u> -	hypothetical protein M5005_Spy_1141
M5005_Spy_1142c	-	NE	1120085	1120675	196	-	3571766 COG1686M	hypothetical protein M5005_Spy_1142
M5005_Spy_1143c	-	NE	1120672	1120920	82	-	<u>3571767</u> -	hypothetical protein M5005_Spy_1143
M5005_Spy_1144c	-	NE	1120905	1121132	75	-	<u>3571768</u> -	hypothetical protein M5005_Spy_1144
M5005_Spy_1145c	sodA	NE	1121299	1121904	201	-	3571769 COG0605P	superoxide dismutase
M5005_Spy_1146c	holA	E	1122001	1123041	346	-	3571770 COG1466L	DNA polymerase III subunit delta
M5005_Spy_1147c	comEC	NE	1123112	1125355	747	-	3571771 COG2333R	competence protein ComE
M5005_Spy_1148c	comE	NE	1125336	1125998	220	-	3571772 COG1555L	competence protein ComE
M5005_Spy_1149c	-	E	1126198	1126938	246	-	3571773 COG0204I	1-acyl-sn-glycerol-3-phosphate acyltransferase
M5005_Spy_1150	-	NE	1127056	1127832	258	+	3571774 COG4123R	methyltransferase
M5005_Spy_1151	-	NE	1127822	1128100	92	+	3571775 COG2827L	hypothetical protein M5005_Spy_1151
M5005_Spy_1152c	kup	NE	1128124	1129107	327	-	3571737 COG3158P	kup system potassium uptake protein, partial
M5005_Spy_1154c	deaD	NE	1130251	1131870	539	-	3571739 COG0513LKJ	ATP-dependent RNA helicase
M5005_Spy_1155c	prfC	NE	1132177	1133721	514	-	3571740 COG4108J	peptide chain release factor 3
M5005_Spy_1156c	-	NE	1133969	1134664	231	-	3571741 COG5522S	hypothetical protein M5005_Spy_1156
M5005_Spy_1157c	murF	E	1134744	1136135	463	-	3571742 COG0770M	alanyl-D-alanine ligase
M5005_Spy_1158c	ddl	E	1136326	1137372	348	-	3571743 COG1181M	D-alanyl-alanine synthetase A
M5005_Spy_1159c	recR	NE	1137473	1138069	198	-	3571744 COG0353L	recombination protein RecR
M5005_Spy_1160c	-	NE	1138116	1138307	63	-	<u>3571745</u> -	penicillin-binding protein
M5005_Spy_1161c	fdhC	NE	1138868	1139647	259	-	3571746 COG2116P	formate transporter
M5005_Spy_1162c	-	NE	1139771	1140313	180	-	<u>3571747</u> -	hypothetical protein M5005_Spy_1162
M5005_Spy_1163c	-	NE	1140474	1140995	173	-	3571748 COG1827R	biotin repressor family transcriptional regulator
M5005_Spy_1164c	gpmA	NC	1141102	1141797	231	-	3571749 COG0588G	phosphoglyceromutase
M5005_Spy_1165	pyrD	NE	1142036	1142971	311	+	3571750 COG0167F	dihydroorotate dehydrogenase 1A
M5005_Spy_1166c	-	NC	1143026	1143199	57	-	<u>3571751</u> -	hypothetical protein M5005_Spy_1166
M5005_Spy_1167c	-	NE	1143271	1145133	620	-	3571752 COG2217P	ATPase
M5005_Spy_1168c	-	NC	1145664	1145846	60	-	<u>3571753</u> -	phage protein
M5005_Spy_1169	spd3	NE	1146085	1146885	266	+	<u>3571754</u> -	streptodornase
M5005_Spy_1170	-	NE	1147096	1147590	164	+	<u>3571755</u> -	hypothetical protein M5005_Spy_1170
M5005_Spy_1171c	-	NE	1147660	1148865	401	-	3571756 COG1705NU	phage-associated cell wall hydrolase
M5005_Spy_1172c	-	NE	1148981	1149208	75	-	3571718 COG5546S	holin
M5005_Spy_1173c	-	NE	1149205	1149480	91	-	<u>3571719</u> -	phage protein
M5005_Spy_1174c	-	NE	1149490	1150107	205	-	<u>3571720</u> -	phage protein
M5005_Spy_1175c	-	NE	1150104	1150541	145	-	<u>3571721</u> -	phage protein
M5005_Spy_1176c	-	NE	1150553	1152421	622	-	3571722 COG4926S	phage infection protein
M5005_Spy_1177c	-	NE	1152418	1153113	231	-	3571723 COG4722S	phage protein
M5005_Spy_1178c	-	NE	1153110	1155467	785	-	3571724 COG5412S	phage protein
M5005_Spy_1179c	-	NE	1155467	1155838	123	-	<u>3571725</u> -	phage protein
M5005_Spy_1180c	-	NE	1155853	1156116	87	-	<u>3571726</u> -	phage protein
M5005_Spy_1181c	-	NE	1156127	1156720	197	-	<u>3571727</u> -	major tail protein
M5005_Spy_1182c	-	NE	1156732	1157067	111	-	<u>3571728</u> -	phage protein
M5005_Spy_1183c	-	NE	1157068	1157304	78	-	<u>3571729</u> -	phage protein
M5005_Spy_1184c	-	NE	1157297	1157635	112	-	<u>3571730</u> -	phage protein
M5005_Spy_1185c	-	NE	1157595	1158017	140	-	<u>3571731</u> -	phage protein
M5005_Spy_1186c	-	NE	1158027	1158227	66	-	<u>3571732</u> -	phage protein
M5005_Spy_1187c	-	NE	1158227	1159138	303	-	<u>3571733</u> -	phage structural protein
M5005_Spy_1188c	-	NE	1159163	1159624	153	-	<u>3571734</u> -	phage protein

M5005_Spy_1189c	-	NE	1159705	1161120	471	-	3571735 COG4626R	phage terminase
M5005_Spy_1190c	-	NE	1161230	1161496	88	-	<u>3571736</u> -	phage protein
M5005_Spy_1191c	-	NE	1161535	1161750	71	-	<u>3571698</u> -	phage protein
M5005_Spy_1192c	-	NE	1161719	1161952	77	-	<u>3571699</u> -	phage protein
M5005_Spy_1193c	-	NE	1161949	1163442	497	-	<u>3571700</u> -	phage protein
M5005_Spy_1194c	-	NE	1163435	1164703	422	-	<u>3571701</u> -	phage protein
M5005_Spy_1195c	-	NE	1164700	1165056	118	-	<u>3571702</u> -	phage protein
M5005_Spy_1196c	-	NE	1165205	1165549	114	-	3571703 COG1403V	HNH endonuclease
M5005_Spy_1197c	-	NE	1165658	1166077	139	-	3571704 -	phage protein
M5005_Spy_1198c	-	NE	1166345	1166980	211	-	3571705 COG0286V	phage protein
M5005_Spy_1199c	-	NE	1166982	1167251	89	-	3571706 -	phage protein
M5005_Spy_1200c	-	NE	1167335	1167847	170	-	3571707 -	phage protein
M5005_Spy_1201c	-	NE	1167844	1168257	137	-	3571708 -	phage protein
M5005_Spy_1202c	-	NC	1168363	1168530	55	-	3571709 -	phage protein
M5005_Spy_1203c	-	NE	1168540	1169337	265	-	3571710 -	phage protein
M5005_Spy_1204c	-	NE	1169334	1170263	309	_	3571711 COG3723L	recT protein
M5005_Spy_1205c	-	NE	1170266	1170595	109	-	3571712 -	phage protein
M5005_Spy_1206c	-	NE	1170651	1170857	68	-	3571713 -	phage protein
M5005_Spy_1207c	-	NC	1170866	1171006	46	-	3571714 -	phage protein
M5005_Spy_1208c	-	NE	1171003	1171236	77	-	3571715 -	phage protein
M5005_Spy_1209c	-	NE	1171217	1171606	129	-	3571716 COG3935L	DNA replication protein
M5005_Spy_1210c	-	NE	1171751	1171990	79	-	3571717 -	phage replication protein
M5005_Spy_1211c	-	NC	1172090	1172275	61	-	3571679 -	phage protein
M5005_Spy_1212c	xis	NE	1172277	1172588	103	-	3571680 -	excisionase
M5005_Spy_1213c	-	NC	1172666	1172851	61	-	3571681 COG3655K	phage protein
M5005_Spy_1214	-	NE	1173018	1173257	79	+	3571682 -	phage protein
M5005_Spy_1215	-	NE	1173399	1174205	268	+	3571683 -	phage protein
M5005_Spy_1216c	-	NE	1174140	1174406	88	-	3571684 -	phage protein
M5005_Spy_1217c	-	NE	1174438	1175154	238	-	3571685 COG3645S	phage antirepressor protein
M5005_Spy_1218c	-	NE	1175166	1175357	63	-	3571686 -	phage protein
M5005_Spy_1219	-	E	1176511	1176858	115	+	3571687 -	Cro/CI family phage transcriptional regulator
M5005_Spy_1220	-	NE	1176862	1177242	126	+	3571688 COG2856E	phage protein
M5005_Spy_1221	-	NE	1177254	1177520	88	+	3571689 -	phage protein
M5005_Spy_1222	int.2	NE	1177644	1178786	380	+	3571690 COG4974L	integrase
M5005_Spy_1223c	-	NC	1178876	1179151	91	-	3571691 COG0776L	DNA-binding protein HU
M5005_Spy_1224c	-	NE	1179250	1179837	195	-	3571692 COG4698S	hypothetical protein M5005_Spy_1224
M5005_Spy_1225c	-	NE	1179815	1180657	280	-	3571693 COG2755E	lipase/acylhydrolase
M5005_Spy_1226c	-	NE	1180650	1181501	283	-	3571694 COG1307S	degV family protein
M5005_Spy_1227c	-	NE	1181717	1182658	313	-	<u>3571695</u> -	hypothetical protein M5005_Spy_1227
M5005_Spy_1228c	recN	NE	1182830	1184491	553	-	3571696 COG0497L	DNA repair protein
M5005_Spy_1229c	argR1	NE	1184513	1184983	156	-	3571697 COG1438K	arginine repressor ArgR
M5005_Spy_1230c	-	NE	1184970	1185797	275	-	3571659 COG1189J	hemolysin
M5005_Spy_1231c	fps	NE	1185790	1186662	290	-	3571660 COG0142H	dimethylallyltransferase/geranyltranstransferase
M5005_Spy_1232c	xseB	NE	1186662	1186877	71	-	3571661 COG1722L	exodeoxyribonuclease VII small subunit
M5005_Spy_1233c	xseA	NE	1186855	1188195	446	-	3571662 COG1570L	exodeoxyribonuclease VII large subunit
M5005_Spy_1234c	foID	С	1188348	1189202	284	-	3571663 COG0190H	dehydrogenase/ 5,10-methylene-tetrahydrofolate
M5005_Spy_1235c	-	NE	1189410	1191113	567	-	3571664 COG1109G	phosphoglucomutase
M5005_Spy_1236c	phr	NE	1191282	1192691	469	-	3571665 COG0415L	deoxyribodipyrimidine photolyase
M5005_Spy_1237c	artP/gtr	NE	1192840	1193574	244	-	3571666 COG1126E	arginine transport ATP-binding protein
M5005_Spy_1238c	artQ	NE	1193574	1194260	228	-	3571667 COG0765E	arginine transporter permease
M5005_Spy_1239c	-	NC	1194387	1194617	76	-	3571668 COG4703S	hypothetical protein M5005_Spy_1239
M5005_Spy_1240	clpE	NE	1194915	1197197	760	+	3571669 COG05420	ATP-dependent Clp protease ATP-binding subunit
M5005_Spy_1241	mutT	NE	1197325	1197780	151	+	3571670 COG0494LR	7,8-dihydro-8-oxoguanine-triphosphatase
M5005_Spy_1242	-	NE	1197831	1198133	100	+	<u>3571671</u> -	hypothetical protein M5005_Spy_1242
M5005_Spy_1243c	ileS	E	1198398	1201199	933	-	3571672 COG0060J	isoleucyl-tRNA synthetase
M5005_Spy_1244c	divIVAS	E	1201472	1202230	252	-	3571673 COG3599D	cell division initiation protein
M5005_Spy_1245c	-	NE	1202240	1203031	263	-	3571674 COG2302S	RNA binding protein
M5005_Spy_1246c	-	NC	1203031	1203285	84	-	3571675 COG0762S	hypothetical protein M5005_Spy_1246
M5005_Spy_1247c	-	NE	1203290	1203958	222	-	3571676 COG1799S	hypothetical protein M5005_Spy_1247

M5005_Spy_1248c	-	NE	1203958	1204629	223	-	3571677 COG0325R	pyridoxal-5\'-phosphate family protein
M5005_Spy_1249c	ftsZ	E	1204632	1205951	439	-	3571678 COG0206D	cell division protein FtsZ
M5005_Spy_1250c	ftsA	E	1205975	1207339	454	-	3571640 COG0849D	cell division protein
M5005_Spy_1251c	divIB/ftsQ	NC	1207551	1208699	382	-	3571641 COG1589M	cell division protein
M5005_Spy_1252c	murG	E	1208700	1209803	367	-	3571642 COG0707M	N- acetylglucosaminyltransferase
M5005_Spy_1253c	murD	E	1209782	1211140	452	-	3571643 COG0771M	synthetase
M5005_Spy_1254c	-	NE	1211510	1211761	83	-	<u>3571644</u> -	hypothetical protein M5005_Spy_1254
M5005_Spy_1255c	typA	NC	1211883	1213724	613	-	3571645 COG1217T	GTP-binding protein
M5005_Spy_1256c	-	NE	1213907	1214296	129	-	3571646 COG0607P	rhodanese-related sulfurtransferase
M5005_Spy_1257c	glcK	NE	1214306	1215277	323	-	3571647 COG1940KG	glucokinase/xylose repressor
M5005_Spy_1258c	-	NE	1215282	1215485	67	-	3571648 COG4483S	hypothetical protein M5005_Spy_1258
M5005_Spy_1259c	dpr	NE	1215627	1216154	175	-	3571649 COG0783P	like antioxidant protein
M5005_Spy_1260	-	NE	1216382	1217008	208	+	3571650 COG2898S	prepilin peptidase
M5005_Spy_1261c	-	NE	1217090	1218169	359	-	3571651 COG0820R	ribosomal RNA large subunit methyltransferase N
M5005_Spy_1262c	-	NE	1218173	1218793	206	-	3571652 COG4470S	transcriptional regulator
M5005_Spy_1263c	-	NC	1219088	1219207	39	-	<u>3571653</u> -	hypothetical protein M5005_Spy_1263
M5005_Spy_1264c	-	NE	1219241	1219942	233	-	3571654 COG1609K	ribose operon repressor, partial
M5005_Spy_1265c	-	NE	1220035	1220265	76	-	3571655 COG1609K	ribose operon repressor, partial
M5005_Spy_1266c	-	NE	1220631	1221668	345	-	3571656 COG3480T	ATP-dependent protease La
M5005_Spy_1267c	coaD	E	1221655	1222146	163	-	3571657 COG0669H	phosphopantetheine adenylyltransferase
M5005_Spy_1268c	-	NE	1222136	1222675	179	-	3571658 COG0742L	methyltransferase
M5005_Spy_1269c	asnA	NE	1222798	1223790	330	-	3571620 COG2502E	asparagine synthetase AsnA
M5005_Spy_1270c	arcC	NE	1224103	1225053	316	-	3571621 COG0549E	carbamate kinase
M5005_Spy_1271c	-	NE	1225073	1226404	443	-	3571622 COG0624E	hypothetical protein M5005_Spy_1271
M5005_Spy_1272c	-	NE	1226421	1227914	497	-	3571623 COG1288S	arginine/ornithine antiporter
M5005_Spy_1273c	arcB	NE	1228084	1229097	337	-	3571624 COG0078E	ornithine carbamoyltransferase
M5005_Spy_1274c	-	NE	1229137	1229565	142	-	3571625 COG2153R	acetyltransferase
M5005_Spy_1275c	arcA	NE	1229665	1230900	411	-	3571626 COG2235E	arginine deiminase
M5005_Spy_1276c	-	NE	1231174	1231854	226	-	3571627 COG0664T	Crp/Fnr family transcriptional regulator
M5005_Spy_1277	ahrC.2/argR	NE	1231996	1232469	157	+	3571628 COG1438K	arginine repressor ArgR
M5005_Spy_1278c	-	NE	1232635	1233351	238	-	3571629 COG3382S	hypothetical protein M5005_Spy_1278
M5005_Spy_1279c	-	NE	1233365	1234444	359	-	3571630 COG2315S	hypothetical protein M5005_Spy_1279
M5005_Spy_1280c	yesM	NC	1234517	1236250	577	-	3571631 COG2972T	two-component sensor kinase
M5005_Spy_1281c	yesN	NE	1236247	1236987	246	-	3571632 COG4753T	two-component response regulator
M5005_Spy_1282c	msrA	NE	1237075	1238181	368	-	3571633 COG02250	bifunctional methionine sulfoxide reductase A/B
M5005_Spy_1283c	tlpA	NE	1238224	1238847	207	-	3571634 COG12250	thiol:disulfide interchange protein
M5005_Spy_1284c	ccdA	NE	1238860	1239570	236	-	3571635 COG07850	cytochrome C biogenesis protein
M5005_Spy_1285c	-	NE	1240173	1240466	97	-	3571636 COG1343L	hypothetical protein M5005_Spy_1285
M5005_Spy_1286c	-	NE	1240477	1241502	341	-	3571637 COG1518L	DNA polymerase
M5005_Spy_1287c	-	NE	1241499	1242173	224	-	3571638 COG1468L	hypothetical protein M5005_Spy_1287
M5005_Spy_1288c	-	NE	1242175	1243023	282	-	3571639 COG3649L	hypothetical protein M5005_Spy_1288
M5005_Spy_1289c	-	NE	1243028	1244923	631	-	<u>3571602</u> -	hypothetical protein M5005_Spy_1289
M5005_Spy_1290c	-	NE	1244923	1245651	242	-	<u>3571603</u> -	hypothetical protein M5005_Spy_1290
M5005_Spy_1291c	-	NE	1245784	1248186	800	-	3571604 COG1203R	ATP-dependent RNA helicase
M5005_Spy_1292c	valS	E	1248346	1250751	801	-	3571605 COG0525J	valyl-tRNA synthetase
M5005_Spy_1293c	-	NE	1250995	1251558	187	-	3571606 COG0563F	hypothetical protein M5005_Spy_1293
M5005_Spy_1294c	-	NC	1251555	1251734	59	-	3571607 COG1670J	ribosomal-protein-serine acetyltransferase
M5005_Spy_1295c	-	NE	1252159	1252554	131	-	<u>3571608</u> -	hypothetical protein M5005_Spy_1295
M5005_Spy_1296c	-	NE	1252572	1252826	84	-	<u>3571609</u> -	hypothetical protein M5005_Spy_1296
M5005_Spy_1297	aroA2	NE	1253305	1254057	250	+	3571611 COG2876E	3-deoxy-7-phosphoheptulonate synthase
M5005_Spy_1298	aroB	NE	1254113	1255186	357	+	3571612 COG0337E	3-dehydroquinate synthase
M5005_Spy_1299c	-	NE	1255455	1255613	52	-	<u>3571613</u> -	hypothetical protein M5005_Spy_1299
M5005_Spy_1300c	-	NE	1255621	1255926	101	-	3571614 COG1917S	hypothetical protein M5005_Spy_1300
M5005_Spy_1301c	-	NE	1255928	1256266	112	-	3571615 COG1917S	hypothetical protein M5005_Spy_1301
M5005_Spy_1302c	-	NE	1256319	1257074	251	-	3571616 COG2226H	SAM-dependent methyltransferase
M5005_Spy_1303c	aroE	NE	1257309	1258187	292	-	3571617 COG0169E	shikimate 5-dehydrogenase
M5005_Spy_1304c	lacZ	NE	1258325	1261741	1138	-	3571618 COG3250G	beta-galactosidase
M5005_Spy_1305c	trxR	NE	1261761	1263245	494	-	3571619 COG4753T	two-component response regulator
M5005_Spy_1306c	trxS	NE	1263245	1264969	574	-	3571583 COG2972T	two-component sensor kinase

M5005_Spy_1307c	trxT	NE	1264959	1265564	201	-	3571584 COG5578S	hypothetical protein M5005_Spy_1307
M5005_Spy_1308c	-	NE	1265870	1267315	481	-	3571585 COG1653G	sugar-binding protein
M5005_Spy_1309c	-	NE	1267396	1268322	308	-	3571586 COG0395G	sugar transporter permease
M5005_Spy_1310c	-	NE	1268332	1269282	316	-	3571587 COG4209G	sugar transporter permease
M5005_Spy_1311	-	NE	1269478	1270356	292	+	3571588 COG1940KG	glucokinase
M5005_Spy_1312	-	NC	1270500	1270622	40	+	<u>3571589</u> -	hypothetical protein M5005_Spy_1312
M5005_Spy_1313c		NE	1270968	1272410	480	-	3571590 COG2723G	beta-glucosidase
M5005_Spy_1314c	hyl	NE	1272434	1274128	564	-	<u>3571591</u> -	hyaluronoglucosaminidase
M5005_Spy_1315c	-	NE	1274179	1275219	346	-	3571592 COG1609K	GntR family transcriptional regulator
M5005_Spy_1316	-	NE	1275352	1276638	428	+	3571593 COG3538S	hypothetical protein M5005_Spy_1316
M5005_Spy_1317	-	NE	1276653	1279358	901	+	3571594 COG0383G 3571595 COG2972T	alpha-mannosidase sensory transduction protein kinase
M5005_Spy_1318c M5005_Spy_1319c	rocA -	NE NE	1279459	1280814	451 451	-	3571595 COG29721 3571596 COG2265J	tRNA (uracil-5-)-methyltransferase
M5005_Spy_13190	recX	NE NE	1281479 1282949	1282834	258		3571597 COG2137R	recombination regulator RecX
M5005_Spy_1321	-	C	1282949	1283725 1284338	258 177	+	3571598 COG3557J	hypothetical protein M5005_Spy_1321
M5005_Spy_1321	_	NC	1284437	1284586	49	+	<u>3571599</u> -	hypothetical protein M5005_Spy_1322
M5005_Spy_1322c	_	NE	1284708	1284986	92	+	3571600 -	transposase
M5005_Spy_1324	_	NC	1291239	1291373	44	+	3571555 -	hypothetical protein M5005_Spy_1324
M5005_Spy_1325c	_	NE	1292030	1292578	182	-	3571556 COG1544J	ribosome-associated factor Y
M5005_Spy_1326c	comFC	NE	1292658	1293323	221	_	3571557 COG1040R	competence protein ComF
M5005_Spy_1327c	comFA	NE	1293295	1294509	404	_	3571558 COG4098L	competence protein ComF
M5005 Spy 1328	-	NE	1294676	1295308	210	+	3571559 COG1739S	Xaa-Pro dipeptidase
M5005 Spy 1329	cysM	NE	1295436	1296377	313	+	3571560 COG0031E	cysteine synthase
M5005 Spy 1330c	-	C	1296395	1296772	125	-	3571561 COG1098J	hypothetical protein M5005 Spy 1330
M5005_Spy_1331c	_	NE	1296772	1298172	466	_	3571562 COG06520	peptidyl-prolyl cis-trans isomerase
M5005_Spy_1332c	yvqC	NC	1298209	1298850	213	_	3571563 COG2197TK	two-component response regulator
M5005_Spy_1333c	yvqE	NE	1298843	1299847	334	_	3571564 COG4585T	two-component sensor protein
M5005_Spy_1334c	yvqF	NE	1299844	1300536	230	-	3571565 COG4758S	transporter
M5005_Spy_1335c	-	E	1300659	1302557	632	-	3571566 COG2815S	serine/threonine protein kinase
M5005_Spy_1336c	pppL	E	1302554	1303294	246	_	3571567 COG0631T	protein phosphatase 2C
M5005_Spy_1337c	sunL	NE	1303332	1304654	440	-	3571568 COG0144J	16S rRNA m(5)C 967 methyltransferase
M5005_Spy_1338c	fmt	E	1304644	1305579	311	-	3571569 COG0223J	methionyl-tRNA formyltransferase
M5005_Spy_1339c	priA	С	1305641	1308025	794	-	3571570 COG1198L	primosome assembly protein PriA
M5005_Spy_1340c	-	NE	1308090	1308407	105	-	3571571 COG1758K	DNA-directed RNA polymerase subunit omega
M5005_Spy_1341c	gmk	E	1308423	1309058	211	-	3571572 COG0194F	guanylate kinase
M5005_Spy_1342c	-	NC	1309168	1310775	535	-	3571535 COG1418R	hypothetical protein M5005_Spy_1342
M5005_Spy_1343c	-	NE	1310905	1311801	298	-	3571536 COG0583K	LysR family transcriptional regulator
M5005_Spy_1344	atoB	NE	1312003	1313190	395	+	3571537 COG0183I	acetyl-CoA acetyltransferase
M5005_Spy_1345	atoD.1	NE	1313214	1313864	216	+	3571538 COG1788I	acetate CoA-transferase subunit alpha
M5005_Spy_1346	atoA	NE	1313866	1314525	219	+	3571539 COG2057I	acetate CoA-transferase subunit beta
M5005_Spy_1347	-	NE	1314558	1315337	259	+	<u>3571540</u> COG1028IQR	3-hydroxybutyrate dehydrogenase
M5005_Spy_1348	-	NE	1315408	1316739	443	+	3571541 COG2610GE	D-beta-hydroxybutyrate permease
M5005_Spy_1349	luxS	NE	1316723	1317295	190	+	3571542 COG1854T	S-ribosylhomocysteinase
M5005_Spy_1350c	-	NE	1317440	1318909	489	-	<u>3571543</u> -	hypothetical protein M5005_Spy_1350
M5005_Spy_1351c	-	NE	1318923	1320077	384	-	3571544 COG0116L	methyltransferase
M5005_Spy_1352c	-	NC	1320522	1320848	108	-	3571545 COG3599D	cell division initiation protein
M5005_Spy_1353c		NE	1320970	1321485	171	-	3571546 COG4474S	hypothetical protein M5005_Spy_1353
M5005_Spy_1354	recU	NE	1321566	1322165	199	+	3571547 COG3331R	Holliday junction-specific endonuclease
M5005_Spy_1355	pbp1A	E	1322152	1324317	721	+	3571548 COG0744M	multimodular transpeptidase-transglycosylase
M5005_Spy_1356c	pepC	NE	1324784	1326121	445	-	3571549 COG3579E	aminopeptidase
M5005_Spy_1357c	nadE	E	1326306	1327130	274	-	3571550 COG0171H	NAD synthetase
M5005_Spy_1358c	nadE -	E	1327132	1328586	484	-	3571551 COG1488H	nicotinate phosphoribosyltransferase
M5005_Spy_1359c	-	NE	1328757	1330136	459	-	3571552 COG1113E	amino acid permease thioredoxin reductase
M5005_Spy_1360c M5005_Spy_1361c		C	1330305	1331222	305	-	3571553 COG04920 3571554 -	hypothetical protein M5005_Spy_1361
M5005_Spy_1361c M5005_Spy_1362c	aapA	E	1331286	1331510	74	-	3571534 - 3571516 COG1126E	transporter
M5005_Spy_1362c M5005_Spy_1363c	-	NE	1331614	1332360	248	-	3571516 COG1126E 3571517 COG0765E	amino acid ABC transporter permease
M5005_Spy_1364c	-	NE E	1332357 1333355	1333160 1334698	267 447	-	3571517 COG0763E 3571518 COG0513LKJ	ATP-dependent RNA helicase
M5005_Spy_1365c	mraY	E	1333355	1334698	336	-	3571518 COG0313LKJ 3571519 COG0472M	transferase
113003_3py_1303C	mai	_	1334636	1333000	330	-	3371313 COGO47211	dunisieruse

M5005_Spy_1366c	ftsI	E	1335868	1338123	751	-	3571520 COG0768M	protein ftsI
M5005_Spy_1367c	ftsL	E	1338127	1338450	107	-	3571521 COG4839D	cell division protein
M5005_Spy_1368c	mraW	С	1338455	1339468	337	-	3571522 COG0275M	S-adenosyl-methyltransferase MraW
M5005_Spy_1369c	-	NC	1339492	1339599	35	-	<u>3571523</u> -	hypothetical protein M5005_Spy_1369
M5005_Spy_1370c	proA	NE	1339942	1341192	416	-	3571524 COG0014E	gamma-glutamyl phosphate reductase
M5005_Spy_1371c	proB	NE	1341185	1342006	273	-	3571525 COG0263E	gamma-glutamyl kinase
M5005_Spy_1372c	proB	NE	1342071	1343699	542	-	3571526 COG1269C	ABC transporter permease
M5005_Spy_1373c	-	NE	1343704	1344438	244	-	3571527 COG1131V	ABC transporter ATP-binding protein
M5005_Spy_1374c	-	NE	1344472	1344738	88	-	<u>3571528</u> -	hypothetical protein M5005_Spy_1374
M5005_Spy_1375c	tkt	NE	1344931	1346916	661	-	3571529 COG0021G	transketolase
M5005_Spy_1376c	tal	NE	1347134	1347778	214	-	3571530 COG0176G	translaldolase
M5005_Spy_1377c	-	NE	1347904	1349403	499	-	3571531 COG3711K	trans-acting positive regulator
M5005_Spy_1378c	npx	NE	1349393	1350739	448	-	3571532 COG0446R	NADH peroxidase
M5005_Spy_1379c	glpF	NE	1350848	1351549	233	-	3571533 COG0580G	glycerol uptake facilitator protein
M5005_Spy_1380c	glpO	NE	1351551	1353389	612	-	3571534 COG0578C	alpha-glycerophosphate oxidase
M5005_Spy_1381c	glpK	NE	1353405	1354931	508	-	3571496 COG0554C	glycerol kinase
M5005_Spy_1382c	-	NE	1355292	1355684	130	-	3571497 COG3212S	hypothetical protein M5005_Spy_1382
M5005_Spy_1383c	-	NC	1355811	1356068	85	-	3571498 COG4224S	hypothetical protein M5005_Spy_1383
M5005_Spy_1384c	glyS	E	1356222	1358261	679	-	3571499 COG0751J	glycyl-tRNA synthetase subunit beta
M5005_Spy_1385c	glyQ	E	1358639	1359556	305	-	3571500 COG0752J	glycyl-tRNA synthetase subunit alpha
M5005_Spy_1386c	-	NE	1359928	1360461	177	-	3571501 COG1755S	hypothetical protein M5005_Spy_1386
M5005_Spy_1387c	-	NE	1360593	1361432	279	-	3571502 COG0656R	aldo/keto reductase
M5005_Spy_1388c	nagA	NE	1361554	1362702	382	-	3571503 COG1820G	N-acetylglucosamine-6-phosphate deacetylase
M5005_Spy_1389c	-	NE	1362820	1364469	549	-	3571504 COG1283P	sodium-dependent phosphate transporter
M5005_Spy_1390	-	NE	1364653	1365375	240	+	3571505 COG0711C	hypothetical protein M5005_Spy_1390
M5005_Spy_1391c	-	NE	1365504	1366346	280	-	3571506 COG1307S	degV family protein
M5005_Spy_1392	-	NE	1366639	1367196	185	+	3571507 COG1309K	TetR family transcriptional regulator
M5005_Spy_1393c	-	NE	1367232	1368056	274	-	3571508 COG0561R	HAD superfamily hydrolase
M5005_Spy_1394c	-	NE	1368058	1368675	205	-	3571509 COG2860S	hypothetical protein M5005_Spy_1394
M5005_Spy_1395c	lacD.1	NE	1368872	1369849	325	-	3571510 COG3684G	tagatose 1,6-diphosphate aldolase
M5005_Spy_1396c	lacC1	NE	1369999	1370349	116	-	3571511 COG1105G	tagatose-6-phosphate kinase
M5005_Spy_1397c	lacB.1	NE	1370359	1370874	171	-	3571512 COG0698G	galactose-6-phosphate isomerase subunit LacB
M5005_Spy_1398c	lacA.1	NE	1370889	1371314	141	-	3571513 COG0698G	galactose-6-phosphate isomerase subunit LacA
M5005_Spy_1399c	-	NE	1371554	1373002	482	-	3571514 COG3775G	IIC
M5005_Spy_1400c	-	NE	1373031	1373336	101	-	3571515 COG3414G	IIB
M5005_Spy_1401c	-	NE	1373329	1373802	157	-	3571477 COG1762GT	IIA
M5005_Spy_1402	lacR.1	NE	1374039	1374809	256	+	3571478 COG1349KG	lactose phosphotransferase system repressor
M5005_Spy_1403c	-	NE	1374836	1375006	56	-	<u>3571479</u> -	copper chaperone
M5005_Spy_1404c	copZ	NE	1375013	1375216	67	-	3571480 COG2608P	copper chaperone
M5005_Spy_1405c	copA	NE	1375230	1377461	743	-	3571481 COG2217P	copper-exporting ATPase
M5005_Spy_1406c	copY	NE	1377461	1377895	144	-	3571482 COG3682K	copAB ATPase metal-fist type repressor
M5005_Spy_1407	-	NE	1378067	1379053	328	+	3571483 COG0657I	esterase
M5005_Spy_1408c	rbfA	С	1379187	1379543	118	-	3571484 COG0858J	ribosome-binding factor A
M5005_Spy_1409c	infB	E	1379742	1382603	953	-	3571485 COG0532J	translation initiation factor IF-2
M5005_Spy_1410c	-	С	1382623	1382925	100	-	3571486 COG1358J	hypothetical protein M5005_Spy_1410
M5005_Spy_1411c	-	С	1382918	1383214	98	-	3571487 COG2740K	hypothetical protein M5005_Spy_1411
M5005_Spy_1412c	nusA	E	1383230	1384387	385	-	3571488 COG0195K	transcription elongation factor NusA
M5005_Spy_1413c	-	NE	1384562	1385098	178	-	3571489 COG0779S	hypothetical protein M5005_Spy_1413
M5005_Spy_1414c		NC	1385343	1385522	59	-	<u>3571490</u> -	phage protein
M5005_Spy_1415c	sdaD2	NE	1385761	1386933	390	+	3571491 -	phage-encoded streptodornase
M5005_Spy_1416c	-	NE	1387049	1388245	398	-	3571492 COG1705NU	phage-associated cell wall hydrolase
M5005_Spy_1417c	-	NE	1388356	1388541	61	-	<u>3571493</u> -	phage protein
M5005_Spy_1418c	-	NE	1388538	1388837	99	-	<u>3571494</u> -	phage protein
M5005_Spy_1419c	-	NE	1388848	1389468	206	-	<u>3571495</u> -	phage protein
M5005_Spy_1420c	-	NC	1389471	1389632	53	-	3571457 -	phage infection protein
M5005_Spy_1421c	-	NE	1389641	1391548	635	-	3571458 COG1322S	phage protein
M5005_Spy_1422c	-	NE	1391559	1392194	211	-	<u>3571459</u> -	phage protein
M5005_Spy_1423c	-	NE	1392194	1393249	351 660	-	3571460 -	hyaluronoglucosaminidase
M5005_Spy_1424c	-	NE	1393246	1395228	UOU	-	<u>3571461</u> COG04660	phage endopeptidase

M5005_Spy_1425c	-	NE	1395238	1396080	280	-	<u>3571462</u> -	phage protein
M5005_Spy_1426c	-	NE	1396092	1400474	1460	-	3571463 COG5412S	phage protein
M5005_Spy_1427c	-	NE	1400489	1400722	77	-	<u>3571464</u> -	phage protein
M5005_Spy_1428c	-	NE	1400797	1401252	151	-	<u>3571465</u> -	phage protein
M5005_Spy_1429c	-	NE	1401306	1401905	199	-	<u>3571466</u> -	phage protein
M5005_Spy_1430c	-	NE	1401917	1402276	119	-	<u>3571467</u> -	phage protein
M5005_Spy_1431c	-	NE	1402280	1402606	108	_	3571468 -	phage protein
M5005_Spy_1432c	-	NE	1402621	1402899	92	_	3571469 -	phage protein
M5005_Spy_1433c	-	NE	1402910	1403266	118	_	3571470 -	phage protein
M5005_Spy_1434c	-	NE	1403278	1404165	295	_	3571471 -	phage protein
M5005_Spy_1435c	-	NE	1404178	1404747	189	_	3571472 -	phage scaffold protein
M5005_Spy_1436c	-	NE	1404903	1405169	88	-	3571473 -	phage protein
M5005_Spy_1437c	-	NE	1405172	1405360	62	-	3571474 -	hypothetical protein M5005_Spy_1437
M5005_Spy_1438c	-	NE	1405391	1406830	479	_	3571475 COG5585T	phage protein
M5005_Spy_1439c	-	NE	1406796	1408328	510	_	3571476 -	portal protein
M5005_Spy_1440c	-	NE	1408344	1409621	425	_	3571438 COG1783R	terminase large subunit
M5005 Spy 1441c	_	NE	1409611	1410105	164	_	3571439 COG3728L	phage terminase small subunit
M5005_Spy_1442c	_	NE	1410153	1410569	138	_	3571440 -	phage transcriptional activator
M5005_Spy_1443c	_	NE	1410566	1410757	63	_	3571441 -	phage protein
M5005_Spy_1444c	_	NE	1410747	1411598	283	_	3571442 COG0863L	adenine-specific methyltransferase
M5005_Spy_1445c	_	NE	1411607	1411873	88	_	3571443 -	phage protein
M5005_Spy_1446c	_	NC	1411870	1412037	55	_	3571444 -	phage protein
M5005_Spy_1447c	_	NE	1411070	1413360	440	-	3571445 COG0553KL	phage-related DNA helicase
M5005_Spy_1447c	_	NE	1412036	1413632	91	-	3571446 -	hypothetical protein M5005_Spy_1448
M5005_Spy_1448c M5005_Spy_1449c	_	NE NE	1413357	1413632	794	-	3571447 COG3378R	DNA primase
M5005_Spy_1450c	_	NE			640	-	3571447 COG3378K 3571448 COG0749L	phage-encoded DNA polymerase
M5005_Spy_1451c	_	NE	1416408	1418330		-	3571449 -	phage protein
M5005_Spy_1451c M5005_Spy_1452c	-	NE NE	1418373	1418930	185 132	-	3571449 - 3571450 -	phage protein
M5005_Spy_1452c M5005_Spy_1453c	-	NE NE	1418941	1419339		-	<u>3571450</u> - <u>3571451</u> -	phage protein
M5005_Spy_1454c	_		1419343	1420497	384	-	3571451 - 3571452 -	
M5005_Spy_1454c M5005_Spy_1455c	-	NE	1420497	1420796	99	-		phage protein
M5005_Spy_1456c	-	NC	1420884	1421087	67		<u>3571453</u> - 3571454 -	phage protein
	-	NC	1421084	1421236	50	-		phage protein
M5005_Spy_1457c	-	NE	1421233	1421619	128	-	<u>3571455</u> -	phage protein
M5005_Spy_1458c	-	NC	1421616	1421819	67	-	<u>3571456</u> -	phage protein
M5005_Spy_1459c		NC	1421812	1421982	56		<u>3571419</u> -	phage protein
M5005_Spy_1460c	-	NC	1421979	1422254	91	-	<u>3571420</u> -	phage protein
M5005_Spy_1461c	-	NE	1422316	1422531	71	-	<u>3571421</u> -	phage protein
M5005_Spy_1462		NE	1422579	1422992	137	+	<u>3571422</u> -	phage protein
M5005_Spy_1463c	-	NC	1422973	1423128	51	-	<u>3571423</u> -	phage protein
M5005_Spy_1464		E	1423403	1423804	133	+	3571424 COG1396K	Cro/CI family phage transcriptional regulator
M5005_Spy_1465	-	NE	1423818	1424201	127	+	<u>3571425</u> -	phage protein
M5005_Spy_1466	-	NE	1424212	1424763	183	+	<u>3571426</u> -	phage protein
M5005_Spy_1467	int.3	NE	1424880	1425959	359	+	3571427 COG4974L	integrase
M5005_Spy_1468c	trmB	NE	1426157	1426792	211	-	3571429 COG0220R	tRNA (guanine-N(7)-)-methyltransferase
M5005_Spy_1469c	-	E	1426792	1427583	263	-	3571430 COG0510M	phosphotransferase
M5005_Spy_1470c	-	NE	1427647	1428681	344	-	3571431 COG4473U	protein ecsB
M5005_Spy_1471c	-	NE	1428684	1429409	241	-	3571432 COG1131V	ABC transporter ATP-binding protein
M5005_Spy_1472	hit	NE	1429481	1429900	139	+	3571433 COG0537FGR	bis(5\'-nucleosyl)-tetraphosphatase (asymmetrical)
M5005_Spy_1473	-	NE	1429897	1430253	118	+	<u>3571434</u> -	hypothetical protein M5005_Spy_1473
M5005_Spy_1474c	lytR	NE	1430364	1431638	424	-	3571435 COG1316K	LytR family transcriptional regulator
M5005_Spy_1475c	-	NE	1431647	1432171	174	-	3571436 COG0456R	acetyltransferase
M5005_Spy_1476c	-	NC	1432146	1432607	153	-	3571437 COG0802R	ATP/GTP hydrolase
M5005_Spy_1477c	-	NE	1432761	1434221	486	-	3571400 COG2252R	guanine-hypoxanthine permease
M5005_Spy_1478		NE	1434485	1435297	270	+	3571401 COG0561R	HAD superfamily hydrolase
M5005_Spy_1479	manL	NE	1435649	1436641	330	+	3571402 COG3444G	IIAB
M5005_Spy_1480	manM	NE	1436730	1437539	269	+	3571403 COG3715G	PTS system mannose-specific transporter subunit IIC
M5005_Spy_1481	manN	NE	1437556	1438467	303	+	3571404 COG3716G	PTS system mannose-specific transporter subunit IID
M5005_Spy_1482	manO	NE	1438581	1438940	119	+	3571405 COG4687S	hypothetical protein M5005_Spy_1482
M5005_Spy_1483	serS	E	1439332	1440609	425	+	3571406 COG0172J	seryl-tRNA synthetase

M5005_Spy_1484c	accD	E	1440831	1441601	256	-	3571407 COG0825I	acetyl-CoA carboxylase subunit alpha	
M5005_Spy_1485c	accA	E	1441598	1442464	288	-	3571408 COG0777I	acetyl-CoA carboxylase subunit beta	
M5005_Spy_1486c	accC	E	1442473	1443837	454	-	3571409 COG0439I	acetyl-CoA carboxylase biotin carboxylase subunit	
M5005_Spy_1487c	fabZ	С	1443869	1444291	140	-	3571410 COG0764I	(3R)-hydroxymyristoyl-ACP dehydratase	
M5005_Spy_1488c	accB	E	1444288	1444788	166	-	3571411 COG0511I	protein subunit	
M5005_Spy_1489c	fabF	E	1444790	1446022	410	-	3571412 COG0304IQ	3-oxoacyl-ACP synthase	
M5005_Spy_1490c	fabG	E	1446037	1446771	244	-	3571413 COG1028IQR	3-ketoacyl-ACP reductase	
M5005_Spy_1491c	fabD	E	1446761	1447699	312	-	3571414 COG0331I	ACP S-malonyltransferase	
M5005_Spy_1492c	fabK	С	1447724	1448695	323	-	3571415 COG2070R	enoyl-ACP reductase	
M5005_Spy_1493c	acpP	E	1448897	1449121	74	_	3571416 COG0236IQ	acyl carrier protein	- 1
M5005_Spy_1494c	fabH	E	1449182	1450156	324	-	3571417 COG0332I	3-oxoacyl-ACP synthase	
M5005_Spy_1495c	-	NC	1450157	1450591	144	-	3571418 COG1846K	MarR family transcriptional regulator	
M5005_Spy_1496c	phaB	E	1450668	1451459	263	-	3571380 COG1024I	enoyl-CoA hydratase	
M5005_Spy_1497c	dnaJ	Ē	1451679	1452836	385	_	3571381 COG04840	molecular chaperone DnaJ	
M5005_Spy_1498c	dnaK	Ē	1453117	1454943	608	_	3571382 COG04430	molecular chaperone DnaK	
M5005_Spy_1499c	grpE	E	1455124	1455657	177	_	3571383 COG05760	heat shock protein GrpE	- 1
M5005_Spy_1500c	hrcA	Č	1455699	1456733	344	_	3571384 COG1420K	heat-inducible transcription repressor	
M5005_Spy_1500c	-	NE	1456868	1457437	189	_	3571385 COG1705NU	N-acetylmuramoyl-L-alanine amidase	- 1
M5005_Spy_1501c	_	NE	1457434	1457437	247	_	3571386 COG1876M	D-alanyl-D-alanine carboxypeptidase	
M5005_Spy_1502c M5005_Spy_1503c	_	NE	1457454	1458177	235	-	3571380 COG1876F	phosphoglycerate mutase	
M5005_Spy_1503c M5005_Spy_1504c	-						3571387 COG0400G 3571388 COG2261S	hypothetical protein M5005_Spy_1504	
M5005_Spy_1505c	_	NE	1459265	1459513	82	-	3571389 -	hypothetical protein M5005_Spy_1505	
		NE	1459723	1459938	71				
M5005_Spy_1506c	gatB	E	1459935	1461374	479	-	3571390 COG0064J	aspartyl/glutamyl-tRNA amidotransferase subunit B	
M5005_Spy_1507c	gatA	E	1461374	1462840	488	-	3571391 COG0154J	aspartyl/glutamyl-tRNA amidotransferase subunit A	
M5005_Spy_1508c	gatC	E	1462840	1463142	100	-	3571392 COG0721J	aspartyl/glutamyl-tRNA amidotransferase subunit C	
M5005_Spy_1509c	-	NE	1463374	1463583	69	-	3571393 COG0574G	pyruvate, phosphate dikinase, partial	
M5005_Spy_1510c	-	NC	1463555	1463671	38	-	<u>3571394</u> -	pyruvate, phosphate dikinase	
M5005_Spy_1511c	-	NE	1464245	1464691	148	-	3571395 COG1335Q	pyrazinamidase/nicotinamidase	Į.
M5005_Spy_1512c	codY	С	1464838	1465620	260	-	3571396 COG4465K	transcriptional repressor CodY	
M5005_Spy_1513c	-	NE	1465838	1467052	404	-	3571397 COG0436E	aminotransferase	┙
M5005_Spy_1514	-	NE	1467283	1467735	150	+	3571398 COG0589T	universal stress protein	
M5005_Spy_1515c	-	NE	1467858	1469135	425	-	3571399 COG4696S	HAD superfamily hydrolase	Ш
M5005_Spy_1516	asnB	NE	1469318	1470283	321	+	3571361 COG0252EJ	L-asparaginase	
M5005_Spy_1517c	-	NE	1470632	1471336	234	-	<u>3571362</u> -	lantibiotic transport permease	
M5005_Spy_1518c	-	NE	1471349	1472251	300	-	3571363 COG1131V	transporter	
M5005_Spy_1519c	recG	NE	1472544	1474559	671	-	3571364 COG1200LK	ATP-dependent DNA helicase RecG	
M5005_Spy_1520	-	NE	1474652	1474852	66	+	<u>3571365</u> -	hypothetical protein M5005_Spy_1520	
M5005_Spy_1521c	-	NE	1474934	1476388	484	-	3571366 COG1122P	cobalt ABC transporter ATP-binding protein	П
M5005_Spy_1522c	-	NE	1476325	1477005	226	-	3571367 COG0619P	cobalt transporter cbiQ	
M5005_Spy_1523c	-	NE	1477002	1477595	197	-	<u>3571368</u> -	permease	
M5005_Spy_1524c	cycC	NE	1477592	1479262	556	-	3571369 COG1132V	ABC transporter ATP-binding protein	
M5005_Spy_1525c	cycD	NE	1479255	1481018	587	-	3571370 COG4988CO	ABC transporter ATP-binding protein	
M5005_Spy_1526c	fhuC	NE	1481015	1481851	278	-	3571371 COG1120PH	ferrichrome ABC transporter ATP-binding protein	
M5005_Spy_1527c	fhuB2	NE	1481848	1482870	340	-	3571372 COG0609P	ferrichrome transporter permease	
M5005_Spy_1528c	fhuD2	NE	1482872	1483756	294	-	3571373 COG0614P	ferrichrome-binding protein	
M5005_Spy_1529c	shp	NE	1483740	1484615	291	-	<u>3571374</u> -	heme binding protein	
M5005_Spy_1530c	-	NE	1484812	1488639	1275	-	3571375 COG4886S	Fe3+-siderophore transporter	- 1
M5005_Spy_1531c	isp2	NE	1489128	1490639	503	-	3571376 COG3942R	hypothetical protein M5005_Spy_1531	- 1
M5005_Spy_1532c	alr	NC	1490726	1491826	366	_	3571377 COG0787M	alanine racemase	
M5005_Spy_1533c	acpS	NC	1491823	1492179	118	-	3571378 COG0736I	4\'-phosphopantetheinyl transferase	
M5005_Spy_1534c	secA	E	1492295	1494814	839	_	3571379 COG0653U	preprotein translocase subunit SecA	- 1
M5005_Spy_1535c	-	NC	1494892	1494996	34	-	3571341 -	hypothetical protein M5005_Spy_1535	
M5005_Spy_1536c	-	NE	1494980	1495495	171	-	3571342 -	transposase	
M5005_Spy_1537c	-	NE	1495398	1496102	234	-	3571343 COG5433L	transposase, partial	
M5005_Spy_1538c	pmi	NE	1496264	1497217	317	-	3571344 COG1482G	mannose-6-phosphate isomerase	
M5005_Spy_1539c	scrK	NE	1497312	1498268	318	_	3571345 COG1940KG	fructokinase	
M5005_Spy_1540c	endoS	NE	1497312	1501447	995	_	3571346 -	endo-beta-N-acetylglucosaminidase F2	
M5005_Spy_1541c	-	NC	1501471	1501447	54	_	3571347 -	hypothetical protein M5005_Spy_1541	
M5005_Spy_1542c	scrA	NE	1501471	1503561	627	_	3571348 COG1263G	IIABC	
			1001070	1555501	02/			-	-

ME00E C 1E42	D		4500000	4505343	470		2571240 60616216	
M5005_Spy_1543 M5005_Spy_1544	scrB scrR	NE	1503803	1505242	479 321	+	3571349 COG1621G 3571350 COG1609K	sucrose-6-phosphate hydrolase sucrose operon repressor
M5005_Spy_1544 M5005_Spy_1545c	nusB	NE C	1505247 1506353	1506212 1506805	150	+	3571350 COG1609K 3571351 COG0781K	transcription antitermination protein NusB
M5005_Spy_1546c	ilusb -					-	3571351 COGU781K 3571352 COG1302S	Gls24 family general stress protein
M5005_Spy_1546C M5005_Spy_1547c	efp	NC	1506798	1507187	129 185	-	3571352 COG13025 3571353 COG0231J	elongation factor P
M5005_Spy_1547c	comEB	NE	1507233	1507790		-	3571354 COG02315 3571354 COG2131F	competence protein ComE
M5005_Spy_1548c M5005_Spy_1549c		NE	1507886	1508347	153	-	3571354 COG2131F 3571355 COG0006E	Xaa-Pro dipeptidase
	pepP uvrA	NE	1508382	1509455	357	-	3571355 COG0006E 3571356 COG0178L	excinuclease ABC subunit A
M5005_Spy_1550c M5005_Spy_1551	corA	NE	1509570	1512428	952		3571356 COG0176L 3571357 COG0598P	
M5005_Spy_1551 M5005_Spy_1552	COTA	E	1512601	1513545	314	+	3571357 COG0398P 3571358 COG4858S	magnesium and cobalt transporter
		NE	1513678	1514334	218	+	3571358 COG46363 3571359 COG0238J	hypothetical protein M5005_Spy_1552 30S ribosomal protein S18
M5005_Spy_1553c M5005_Spy_1554c	rpsR ssb3	NC	1514467	1514706	79 162	-	3571359 COG02381 3571360 COG0629L	single-stranded DNA-binding protein
M5005_Spy_1554c M5005_Spy_1555c	rpsF	NC	1514871	1515362	163		3571360 COG0629L 3571322 COG0360J	30S ribosomal protein S6
M5005_Spy_1556c	1 psi	NC	1515384	1515674	96	-	3571322 COG03003 3571323 -	hypothetical protein M5005_Spy_1556
M5005_Spy_1550C M5005_Spy_1557	mutY	NE	1515847	1516140	97		3571325 - 3571324 COG1194L	A/G-specific adenine glycosylase
M5005_Spy_1557 M5005_Spy_1558	-	NE NE	1516461 1517538	1517462 1518125	333 195	+	3571324 COG1134L 3571325 COG1476K	transcriptional regulator
M5005_Spy_1558 M5005_Spy_1559c	trx	NE NE	1517538	1518125	195	+	3571325 COG1470R 3571326 COG31180	thioredoxin
M5005_Spy_1559C	u x -	NE	1518177	1519075	167	-	3571327 COG0671I	phosphatidylglycerophosphatase B
M5005_Spy_1560c	mutS2	NE	1518572	1521415	779	-	3571327 COG00711 3571328 COG1193L	DNA mismatch repair protein
M5005_Spy_1561c M5005_Spy_1562c	-	NE NE				-	3571328 COG1193L 3571329 COG1286R	colicin V production protein
M5005_Spy_1563c	-	NE NE	1521564	1522109	181 102	-	3571329 COG1266K 3571330 -	hypothetical protein M5005_Spy_1563
M5005_Spy_1564	_	C	1522112	1522420	300	+	3571330 - 3571331 COG1039L	ribonuclease HIII
M5005_Spy_1565	spi	E	1522577 1523490	1523479 1524083	197	+	3571331 COG1039L 3571332 COG0681U	signal peptidase I
M5005_Spy_1566	recD	NE	1525490	1526594	817	+	3571332 COG05010 3571333 COG0507L	exodeoxyribonuclease V subunit alpha
M5005_Spy_1567	-	NE	1526685	1527167	160	+	3571334 -	hypothetical protein M5005_Spy_1567
M5005_Spy_1567 M5005_Spy_1568c	dinP	NE	1527260	1528354	364	-	3571335 3571335 COG0389L	DNA polymerase IV
M5005_Spy_1569	pfl	NE	1528563	1530890	775	+	3571335 COG0303E 3571336 COG1882C	formate acetyltransferase
M5005_Spy_1505	-	NE	1531068	1532018	316		3571337 COG1680V	penicillin-binding protein
M5005_Spy_1570c	сррА	NE	1532003	1532755	250	_	3571338 COG2514R	c3-degrading proteinase
M5005_Spy_1572	-	NE	1533053	1533949	298	+	3571339 COG0730R	hypothetical protein M5005_Spy_1572
M5005_Spy_1573c	glpF.2	C	1534285	1535133	282		3571340 COG0580G	aquaporin
M5005_Spy_1574c	-	NC	1535303	1535133	48	_	3571302 -	universal stress protein
M5005_Spy_1575c	norA	NE	1535635	1536831	398	-	3571303 COG2814G	quinolone resistance protein
M5005_Spy_1576	srv	NE	1536937	1537656	239	+	3571304 COG0664T	Crp/Fnr family transcriptional regulator
M5005_Spy_1577	pepXP	NE	1537678	1539960	760	+	3571305 COG2936R	x-prolyl-dipeptidyl aminopeptidase
M5005_Spy_1578c		NE	1540040	1540261	73	-	3571306 COG1476K	Cro/CI family transcriptional regulator
M5005_Spy_1579	-	NE	1540431	1540805	124	+	3571307 COG1476K	transcriptional regulator
M5005_Spy_1580	-	NE	1540998	1541297	99	+	3571308 COG0718S	hypothetical protein M5005_Spy_1580
M5005_Spy_1581c	-	NE	1541354	1542091	245	-	3571309 COG0789K	MerR family transcriptional regulator
M5005_Spy_1582c	dnaQ	NE	1542240	1542827	195	-	3571310 COG0847L	DNA polymerase III subunit epsilon
M5005_Spy_1583c	-	NE	1542876	1543406	176	-	<u>3571311</u> -	hypothetical protein M5005_Spy_1583
M5005_Spy_1584	-	NE	1543612	1544781	389	+	3571312 COG2081R	NAD(FAD)-utilizing dehydrogenase
M5005_Spy_1585c	deoC	NE	1544876	1545547	223	-	3571313 COG0274F	deoxyribose-phosphate aldolase
M5005_Spy_1586c	nupC	NE	1545577	1546779	400	-	3571314 COG1972F	nucleoside permease
M5005_Spy_1587c	udp	NE	1546800	1547579	259	-	3571315 COG2820F	uridine phosphorylase
M5005_Spy_1588c	-	NC	1547644	1547745	33	-	<u>3571316</u> -	hypothetical protein M5005_Spy_1588
M5005_Spy_1589	crgR	NE	1547819	1548562	247	+	3571317 COG2188K	GntR family transcriptional regulator
M5005_Spy_1590	rpsN	NE	1548798	1549067	89	+	3571318 COG0199J	30S ribosomal protein S14
M5005_Spy_1591c	gcp	E	1549238	1550266	342	-	3571319 COG05330	DNA-binding/iron metalloprotein/AP endonuclease
M5005_Spy_1592c	-	NE	1550256	1550711	151	-	3571320 COG0456R	ribosomal-protein-alanine acetyltransferase
M5005_Spy_1593c	-	С	1550683	1551381	232	-	3571321 COG12140	glycoprotease
M5005_Spy_1594	-	E	1551666	1551896	76	+	3571284 COG5503S	hypothetical protein M5005_Spy_1594
M5005_Spy_1595	-	E	1551898	1553580	560	+	3571285 COG0595R	Zn-dependent hydrolase
M5005_Spy_1596c	glnA	NE	1553807	1555153	448	-	3571286 COG0174E	glutamine synthetase
M5005_Spy_1597c	glnR	NE	1555191	1555562	123	-	3571287 COG0789K	MerR family transcriptional regulator
M5005_Spy_1598c	-	NE	1555629	1556180	183	-	3571288 COG4129S	hypothetical protein M5005_Spy_1598
M5005_Spy_1599c	pgk	E	1556443	1557639	398	-	3571289 COG0126G	phosphoglycerate kinase
M5005_Spy_1600c	IppC	NE	1557832	1558686	284	-	3571290 COG2503R	acid phosphatase
M5005_Spy_1601c	-	NE	1558916	1559806	296	-	3571291 COG03300	membrane protease

M5005_Spy_1602c	-	E	1560043	1561707	554	_	3571292 COG1461R	kinase
M5005_Spy_1603c	asp	NE	1561707	1562072	121	_	3571293 COG1302S	alkaline-shock protein
M5005_Spy_1604c	-	NC	1562097	1562234	45	_	3571294 -	hypothetical protein M5005 Spy 1604
M5005 Spy 1605c	_	NE	1562239	1563372	377	_	3571295 COG5433L	transposase
M5005_Spy_1606c	rpmB	NE	1563550	1563738	62	_	3571296 COG0227J	50S ribosomal protein L28
M5005 Spy 1607c	fba	E	1564120	1565001	293	_	3571297 COG0191G	
M5005 Spy 1608c	-	NE	1565347	1566273	308	_	3571299 COG1073R	fructose-bisphosphate aldolase alpha/beta hydrolase
M5005_Spy_1610c	pyrG	NE	1567892	1568044	50	_	3571301 COG0504F	CTP synthase, partial
M5005_Spy_1611c	rpoE	NE	1568301	1568876	191	_	3571270 COG3343K	DNA-directed RNA polymerase subunit delta
M5005_Spy_1612c	tig/ropA	NE	1569093	1570376	427	_	3571271 COG05440	trigger factor
M5005_Spy_1613	-	NE	1570697	1571542	281	+	3571272 COG0668M	mechanosensitive ion channel MscS
M5005_Spy_1614c	_	NE	1571607	1572167	186		3571273 COG4475S	hypothetical protein M5005_Spy_1614
M5005_Spy_1615c	_	NE	1572181	1572651	156	_	3571274 COG4720S	hypothetical protein M5005_Spy_1615
M5005_Spy_1616c	thiD	NE	1572181	1573405	254	_	3571275 COG0351H	phosphomethylpyrimidine kinase
M5005_Spy_1617c	truA	NE	1573395	1574144	249	_	3571276 COG0101J	tRNA pseudouridine synthase A
M5005_Spy_1618c	comX.2	NE	1574329	1574144	183	-	3571277 -	competence-specific sigma factor
M5005_Spy_1619	-	NC	1580302	1580436	44	+	3571277 3571251 -	hypothetical protein M5005_Spy_1619
M5005_Spy_1619 M5005_Spy_1620c	-	NE	1580502	1581740	380	-	3571251 - 3571252 COG1929G	glycerate kinase
M5005_Spy_16200 M5005_Spy_1621	hsdR	NE	1582022	1585000	992	+	3571252 COG1929G 3571253 COG0610V	subunit
M5005_Spy_1621 M5005_Spy_1622	hsdS	NE NE	1582022	1586212	399	+	3571253 COG0610V 3571254 COG0732V	subunit
M5005_Spy_1622 M5005_Spy_1623	hsdM						3571254 COG0732V 3571255 COG0286V	subunit
M5005_Spy_1623 M5005_Spy_1624c	-	NE	1586225	1587805	526	+	3571255 COG0286V 3571256 -	hypothetical protein M5005 Spy 1624
		NE	1588015	1588206	63	-	3571256 - 3571257 COG2197TK	transcriptional regulatory protein
M5005_Spy_1625c	salR	NE	1588358	1588963	201		3571257 COG21971K 3571258 COG4585T	, , , , , , , , , , , , , , , , , , , ,
M5005_Spy_1626c	salK	NE	1588944	1590506	520	-		sensory transduction protein kinase
M5005_Spy_1627c	salY	NE	1590546	1592453	635	-	3571259 COG3127Q	ABC transporter permease
M5005_Spy_1628c	salX	NE	1592455	1593192	245	-	3571260 COG1136V	ABC transporter ATP-binding protein
M5005_Spy_1629c	salX/salT	NE	1593189	1593650	153	-	3571261 COG2274V	lantibiotic transport ATP-binding protein
M5005_Spy_1630c	salB	NE	1593724	1595349	541	-	3571262 COG4403V	serine (threonine) dehydratase
M5005_Spy_1631c	salA	NC	1595432	1595578	48	-	<u>3571263</u> -	lantibiotic salivaricin A
M5005_Spy_1632c	lacG	NE	1596090	1597496	468	-	3571264 COG2723G	6-phospho-beta-galactosidase
M5005_Spy_1633c	lacE	NE	1597584	1599281	565	-	3571265 COG1455G	PTS system lactose-specific transporter subunit IIBC
M5005_Spy_1634c	lacF	NE	1599281	1599598	105	-	3571266 COG1447G	PTS system lactose-specific transporter subunit IIA
M5005_Spy_1635c	lacD.2	NE	1599622	1600605	327	-	3571267 COG3684G	tagatose 1,6-diphosphate aldolase
M5005_Spy_1636c	lacC.2	NE	1600609	1601538	309	-	3571268 COG1105G	tagatose-6-phosphate kinase
M5005_Spy_1637c	lacB.2	NE	1601586	1602101	171	-	3571269 COG0698G	galactose-6-phosphate isomerase subunit LacB
M5005_Spy_1638c	lacA.2	NE	1602136	1602564	142	-	3571231 COG0698G	galactose-6-phosphate isomerase subunit LacA
M5005_Spy_1639	lacR.2	NE	1603011	1603784	257	+	3571232 COG1349KG	lactose phosphotransferase system repressor DNA-damage-inducible protein J
M5005_Spy_1640	-	NE	1604445	1604732	95	+	<u>3571233</u> -	
M5005_Spy_1641	-	NE	1604722	1605057	111	+	<u>3571234</u> -	hypothetical protein M5005_Spy_1641 DNA integration/recombination/invertion protein DNA integration/recombination/invertion protein
M5005_Spy_1642	-	NE	1605209	1605391	60	+	<u>3571235</u> -	DNA integration/recombination/invertion protein
M5005_Spy_1643	-	NC	1605380	1605565	61	-	<u>3571237</u> -	DNA integration/recombination/invertion protein
M5005_Spy_1644c	-	NC	1605479	1605679	66	+	<u>3571236</u> -	hypothetical protein M5005_Spy_1644
M5005_Spy_1645		NC	1606013	1606162	49	+	<u>3571238</u> -	DNA integration/recombination/invertion protein
M5005_Spy_1646c	rpsI	NC	1606282	1606674	130	-	3571239 COG0103J	30S ribosomal protein S9
M5005_Spy_1647c	rplM	NC	1606695	1607141	148	-	3571240 COG0102J	50S ribosomal protein L13
M5005_Spy_1648c	-	NC	1607359	1607565	68	-	3571241 COG1476K	Cro/CI family transcriptional regulator
M5005_Spy_1649c	-	NE	1607562	1608068	168	-	<u>3571242</u> -	hypothetical protein M5005_Spy_1649
M5005_Spy_1650c	-	NE	1608204	1609064	286	-	3571243 COG1307S	degV family protein
M5005_Spy_1651c	-	NE	1609161	1609679	172	-	3571244 COG3688R	hypothetical protein M5005_Spy_1651
M5005_Spy_1652c	-	NE	1609683	1610429	248	-	3571245 COG0566J	23S rRNA methyltransferase
M5005_Spy_1653c	-	NE	1610476	1611273	265	-	<u>3571246</u> -	hypothetical protein M5005_Spy_1653
M5005_Spy_1654c		NE	1611469	1611882	137	-	3571247 COG1939S	hypothetical protein M5005_Spy_1654
M5005_Spy_1655c	cysS	E	1611875	1613218	447	-	3571248 COG0215J	cysteinyl-tRNA synthetase
M5005_Spy_1656c	-	NE	1613246	1613476	76	-	3571249 -	hypothetical protein M5005_Spy_1656
M5005_Spy_1657c	-	NE	1613489	1613761	90	-	<u>3571250</u> -	hypothetical protein M5005_Spy_1657
M5005_Spy_1658c	cysE	NC	1613955	1614536	193	-	3571212 COG1045E	serine acetyltransferase
M5005_Spy_1659c	-	NE	1614545	1615297	250	-	<u>3571213</u> -	hypothetical protein M5005_Spy_1659
M5005_Spy_1660c	pnp	NE	1615290	1617422	710	-	3571214 COG1185J	polynucleotide phosphorylase
M5005_Spy_1661c	-	NE	1617703	1618431	242	-	3571215 COG0176G	translaldolase

ME00E Co. 1662a		NE	4640507	4640022	444		2571216 60620276	IIC	_	*
M5005_Spy_1662c M5005_Spy_1663c	ulaA	NE NE	1618587 1619849	1619822 1620133	411 94	-	3571216 COG3037S 3571217 COG3414G	PTS system transporter subunit IIB		*
M5005_Spy_1664c	-	NE NE	1620126	1622186	686	-	3571217 COG3414G 3571218 COG3711K	component		*
M5005_Spy_1665c	-	NC			47	-	3571216 COG3711K 3571219 -	hypothetical protein M5005_Spy_1665	_	•
M5005_Spy_1666c	rpsO		1622411	1622554		-	3571219 - 3571220 COG0184J	30S ribosomal protein S15		
M5005_Spy_1667c	i pso	NC	1622538	1622807	89	-	3571221 -	hypothetical protein M5005_Spy_1667	_	
	-	NC	1622965	1623120	51		3571221 - 3571222 -		_	
M5005_Spy_1668	- dof	NE E	1623246	1623515	89	+	3571222 - 3571223 COG0242J	transcriptional regulator peptide deformylase	_	•
M5005_Spy_1669	def -		1623616	1624230	204	+		oxidoreductase		*
M5005_Spy_1670c	-	NE	1624264	1624806	180	-	3571224 COG0431R		_	•
M5005_Spy_1671c		NE	1624937	1625365	142	-	3571225 COG1846K	MarR family transcriptional regulator DNA polymerase III PolC	_	*
M5005_Spy_1672c	polC	E	1625475	1629872	1465	-	3571226 COG2176L 3571227 COG0442J		_	*
M5005_Spy_1673c	proS	E	1630127	1631983	618	-	3571227 COG04423 3571228 COG0750M	prolyl-tRNA synthetase	_	*
M5005_Spy_1674c	eep	NE	1632181	1633440	419	-		pheromone-processing membrane metalloprotease		*
M5005_Spy_1675c	cdsA	E	1633513	1634307	264	-	3571229 COG0575I 3571230 COG0020I	phosphatidate cytidylyltransferase		*
M5005_Spy_1676c	uppS	E	1634320	1635069	249	-		undecaprenyl pyrophosphate synthase	_	*
M5005_Spy_1677c	yajC	NE	1635288	1635653	121	-	3571192 COG1862U	preprotein translocase subunit YajC	_	*
M5005_Spy_1678c	-	NE	1635769	1636116	115	-	3571193 COG0526OC	thioredoxin		*
M5005_Spy_1680c	pulA	NE	1638902	1639783	293	-	<u>3571195</u> -	pullulanase, partial		*
M5005_Spy_1681c	dexB	NE	1639954	1641567	537	-	3571196 COG0366G	glucan 1,6-alpha-glucosidase		*
M5005_Spy_1682c	msmK	NE	1641696	1642829	377	-	3571197 COG3839G	multiple sugar transport ATP-binding protein		*
M5005_Spy_1683c	Irp	NE	1643127	1643975	282	-	3571198 COG2508TQ	hypothetical protein M5005_Spy_1683	_	*
M5005_Spy_1684	ska	NE	1644335	1645657	440	+	<u>3571199</u> -	streptokinase	_	
M5005_Spy_1685c	dtd	NE	1645755	1646198	147	-	3571200 COG1490J	D-tyrosyl-tRNA(Tyr) deacylase		*
M5005_Spy_1686c	relA	E	1646213	1648432	739	-	3571201 COG0317TK	GTP pyrophosphokinase	_	*
M5005_Spy_1687c	scIA	NE	1648684	1648827	47	-	<u>3571202</u> -	hypothetical protein M5005_Spy_1687	_	
M5005_Spy_1690	nrdI2	NE	1650113	1650595	160	+	3571205 COG1780F	flavoprotein NrdI	_	
M5005_Spy_1691c	-	NE	1650989	1651807	272	-	3571206 COG3568R	exodeoxyribonuclease III		*
M5005_Spy_1693c	-	NE	1653782	1654075	97	-	3571208 COG1263G	IIABC		*
M5005_Spy_1694c		NE	1654433	1655182	249	-	3571209 COG1385S	16S ribosomal RNA methyltransferase RsmE		*
M5005_Spy_1695c	prmA	NE	1655182	1656135	317	-	3571210 COG2264J	50S ribosomal protein L11 methyltransferase		*
M5005_Spy_1696c	-	NE	1656206	1656676	156	-	3571211 -	hypothetical protein M5005_Spy_1696	_	*
M5005_Spy_1697	papB	NE	1656876	1658633	585	+	3571174 COG0147EH	amino-4-deoxychorismate lyase		*
M5005_Spy_1698	trpG	NC	1658666	1659232	188	+	3571175 COG0512EH	anthranilate synthase component II		*
M5005_Spy_1699	-	NE	1659265	1660533	422	+	3571176 COG2256L	recombination factor protein RarA	_	*
M5005_Spy_1700	pai1	NE	1661030	1661470	146	+	3571178 COG3153R	acetyltransferase		
M5005_Spy_1701	flaR	NE	1661525	1662031	168	+	3571179 COG0563F	topology modulation protein	_	
M5005_Spy_1702	smeZ	NE	1662280	1662981	233	+	<u>3571180</u> -	mitogenic exotoxin Z	_	
M5005_Spy_1703c	-	NE	1663265	1663531	88	-	3571181 -	hypothetical protein M5005_Spy_1703		
M5005_Spy_1704	dppA	NE	1663710	1665338	542	+	3571182 COG0747E	dipeptide-binding protein	_	*
M5005_Spy_1705	dppB	NE	1665451	1666428	325	+	3571183 COG0601EP	dipeptide transporter permease		*
M5005_Spy_1706	dppC	NE	1666425	1667246	273	+	3571184 COG1173EP	dipeptide transporter permease		*
M5005_Spy_1707	dppD	NE	1667258	1668061	267	+	3571185 COG0444EP	dipeptide transport ATP-binding protein		*
M5005_Spy_1708	dppE	NE	1668045	1668671	208	+	3571186 COG1124EP	dipeptide transport ATP-binding protein		*
M5005_Spy_1709c	-	NE	1668752	1668952	66	-	<u>3571187</u> -	hypothetical protein M5005_Spy_1709	_	*
M5005_Spy_1710c	-	NE	1669121	1671598	825	-	<u>3571188</u> -	histidine triad protein		*
M5005_Spy_1711c	lmb	NE	1671611	1672531	306	-	3571189 COG0803P	laminin binding protein		*
M5005_Spy_1712c	-	NE	1672709	1673842	377	-	3571190 COG5433L	transposase		
M5005_Spy_1713c	-	NC	1673896	1674048	50	-	<u>3571191</u> -	hypothetical protein M5005_Spy_1713		
M5005_Spy_1714c		NE	1674093	1675160	355	-	3571154 COG5373S	cell surface protein		
M5005_Spy_1715c	scpA	NE	1675257	1678751	1164	-	3571155 COG14040	C5A peptidase	_	*
M5005_Spy_1716	-	NE	1679185	1680390	401	+	3571156 COG3666L	transposase		
M5005_Spy_1717	- cic1_01	NC	1680369	1680551	60	+	<u>3571157</u> -	transposase, partial	_	
M5005_Spy_1718c	sic1.01	NE	1680969	1681910	313	-	3571158 -	inhibitor of complement protein	_	
M5005_Spy_1719c	emm1.0	NE	1682099	1683553	484	-	3571159 COG1196D	M protein		
M5005_Spy_1720c	mga	NE	1683738	1685327	529	-	<u>3571160</u> -	trans-acting positive regulator	_	
M5005_Spy_1721	-	NC	1685712	1685897	61	+	<u>3571161</u> -	hypothetical protein M5005_Spy_1721	_	
M5005_Spy_1722c	-	NE	1686003	1686254	83	-	3571162 -	hypothetical protein M5005_Spy_1722		*
M5005_Spy_1723c	isp	NE	1686333	1687934	533	-	3571163 COG3942R	hypothetical protein M5005_Spy_1723	_	*
M5005_Spy_1724c	ihk	NE	1688036	1689424	462	-	3571164 COG0642T	two component system histidine kinase		•

M5005_Spy_1725c	irr	NE	1689421	1690074	217	-	3571165 COG0745TK	two-component response regulator
M5005_Spy_1726c	-	NE	1690168	1691385	405	-	3571166 COG0577V	ABC transporter permease
M5005_Spy_1727c	-	NE	1691398	1692072	224	-	3571167 COG1136V	ABC transporter ATP-binding protein
M5005_Spy_1728c	-	NE	1692059	1693327	422	-	3571168 COG0845M	periplasmic protein of efflux system
M5005_Spy_1729c	-	NE	1693750	1694154	134	-	<u>3571169</u> -	hypothetical protein M5005_Spy_1729
M5005_Spy_1730c	-	NE	1694181	1694477	98	-	<u>3571170</u> -	hypothetical protein M5005_Spy_1730
M5005_Spy_1731	grm	NE	1694721	1694957	78	+	<u>3571171</u> -	hypothetical protein M5005_Spy_1731
M5005_Spy_1732c	prsA	С	1695233	1696162	309	-	3571172 COG07600	foldase PrsA
M5005_Spy_1733c	-	NE	1696218	1696535	105	-	<u>3571173</u> -	hypothetical protein M5005_Spy_1733
M5005_Spy_1734c	-	NE	1696642	1696947	101	-	<u>3571135</u> -	hypothetical protein M5005_Spy_1734
M5005_Spy_1735c	speB	NE	1696949	1698145	398	-	<u>3571136</u> -	exotoxin B
M5005_Spy_1736	-	NC	1698670	1698801	43	+	<u>3571137</u> -	hypothetical protein M5005_Spy_1736
M5005_Spy_1737	rgg	NE	1699085	1699927	280	+	3571138 -	transcriptional regulator
M5005_Spy_1738c	spd	NE	1700168	1700983	271	-	<u>3571139</u> -	phage-associated deoxyribonuclease
M5005_Spy_1739	-	NC	1701067	1701195	42	+	3571140 -	hypothetical protein M5005_Spy_1739
M5005_Spy_1740	-	NE	1701347	1701856	169	+	3571141 COG1267I	low temperature requirement C protein
M5005_Spy_1741c	gldA	NE	1701938	1703026	362	-	3571142 COG0371C	glycerol dehydrogenase
M5005_Spy_1742c	mipB	NE	1703083	1703751	222	-	3571143 COG0176G	fructose-6-phosphate aldolase
M5005_Spy_1743c	pflD	NE	1703764	1706136	790	_	3571144 COG1882C	formate acetyltransferase
M5005_Spy_1744c	· -	NE	1706391	1707695	434	_	3571145 COG1455G	IIC
M5005_Spy_1745c	-	NE	1707705	1708013	102	_	3571146 COG1440G	IIB
M5005_Spy_1746c	-	NE	1708041	1708361	106	_	3571147 COG1447G	IIA
M5005_Spy_1747c	-	NE	1708649	1709629	326	_	3571148 COG2390K	sorbitol operon regulator
M5005_Spy_1748c	-	NE	1709645	1710394	249	_	3571149 COG1349KG	DeoR family transcriptional regulator
M5005_Spy_1749	_	NE	1710517	1711290	257	+	3571150 COG11800	pyruvate formate-lyase activating enzyme
M5005_Spy_1750	_	NE	1711325	1711525	66	+	3571151 -	hypothetical protein M5005_Spy_1750
M5005_Spy_1751c	secE	NC	1711527	1711703	58	_	3571152 COG0690U	preprotein translocase subunit SecE
M5005_Spy_1752c	rpmG	NC	1711717	1711869	50	_	3571153 COG0267J	50S ribosomal protein L33
M5005_Spy_1753c	pbp2A	NE	1711918	1714254	778	_	3571116 COG0744M	multimodular transpeptidase-transglycosylase
M5005_Spy_1754c	-	NE	1711313	1714673	126	_	3571117 COG0251J	translation initiation inhibitor
M5005_Spy_1755	_	NE	1715164	1715355	63	+	3571118 -	hypothetical protein M5005_Spy_1755
M5005_Spy_1756	_	NE	1715249	1716250	333	+	3571119 COG0564J	ribosomal large subunit pseudouridine synthase D
M5005_Spy_1757c	_	NE	1716339	1717979	546	-	3571120 COG4640S	hypothetical protein M5005_Spy_1757
M5005_Spy_1758	_	NE	1718226	1719722	498	+	3571121 COG4690E	dipeptidase B
M5005_Spy_1759c	_	NE	1720207	1720371	54	_	3571122 -	MutR family transcriptional regulator
M5005 Spy 1760c	_	NE	1720350	1720532	60	_	3571123 -	MutR family transcriptional regulator
M5005_Spy_1761c	groEL	E	1720925	1722556	543	_	3571124 COG04590	molecular chaperone GroEL
M5005_Spy_1762c	groES	Ē	1722592	1722882	96	_	3571125 COG02340	co-chaperonin GroES
M5005_Spy_1763c	clpC	NE	1723060	1725504	814	_	3571126 COG05420	negative regulator of genetic competence
M5005_Spy_1764c	ctsR	NE	1725504	1725965	153	_	3571127 COG4463K	transcriptional regulator
M5005_Spy_1765c	csp	NE	1726161	1726370	69	_	3571128 COG1278K	cold shock protein
M5005_Spy_1766c	-	NC	1726507	1726611	34	_	3571129 -	hypothetical protein M5005_Spy_1766
M5005_Spy_1767c	-	NE	1726595	1727728	377	_	3571130 COG5433L	transposase
M5005_Spy_1768	ahpC	NE	1728685	1729245	186	+	3571132 COG04500	peroxiredoxin reductase (NAD(P)H)
M5005_Spy_1769	ahpF	NE	1729266	1730798	510	+	3571133 COG36340	peroxiredoxin reductase (NAD(P)H)
M5005_Spy_1770c	hutI	NE	1730856	1732121	421	_	3571134 COG1228Q	imidazolonepropionase
M5005_Spy_1771	hutU	NE	1732413	1734443	676	+	3571097 COG2987E	urocanate hydratase
M5005_Spy_1772	-	NE	1734532	1735431	299	+	3571098 COG3643E	glutamate formiminotransferase
M5005_Spy_1773	-	NE	1735442	1736068	208	+	3571099 COG3404E	formiminotetrahydrofolate cyclodeaminase
M5005_Spy_1774	fhs.2	NE	1736086	1737759	557	+	3571100 COG2759F	formatetetrahydrofolate ligase
M5005_Spy_1775	-	NE	1737781	1738377	198	+	3571101 COG3758S	hypothetical protein M5005 Spy 1775
M5005_Spy_1776	-	NE	1738597	1739940	447	+	3571102 COG0531E	amino acid permease
M5005_Spy_1777	hutH	NE	1739951	1741492	513	+	3571103 COG2986E	histidine ammonia-lyase
M5005_Spy_1778	hutG	NE	1741678	1742664	328	+	3571104 COG0010E	formimidoylglutamase
M5005_Spy_1779c	-	NE	1742695	1745769	1024	-	3571105 COG3899R	LuxR family transcriptional regulator
M5005_Spy_1780	rpsB	E	1746073	1746840	255	+	3571106 COG0052J	30S ribosomal protein S2
M5005_Spy_1781	tsf	E	1746974	1748014	346	+	3571107 COG0264J	elongation factor Ts
M5005_Spy_1782c	pepO	NE	1748180	1750075	631	-	3571108 COG35900	neutral endopeptidase
M5005_Spy_1783c	dexS	NC	1750283	1751911	542	_	3571109 COG0366G	trehalose-6-phosphate hydrolase
			1.50205	_,,,,,,,,	J			

ME00E Cm. 1704a		NE	4754070	475 4002	674		2571110 00012020	DTC aveter trabalant annific HDC assessed
M5005_Spy_1784c	-	NE	1751978	1754002	674	-	3571110 COG1263G	PTS system, trehalose-specific IIBC component
M5005_Spy_1785	-	NE	1754213	1754926	237	+	3571111 COG2188K	trehalose operon transcriptional repressor
M5005_Spy_1786c	-	NE	1755205	1755372	55	-	3571112 COG1733K	MarR family transcriptional regulator, partial
M5005_Spy_1787	-	NE	1755730	1756587	285	+	3571113 COG2514R	glyoxalase
M5005_Spy_1788	yaaA	NE	1756629	1757360	243	+	3571114 COG3022S	hypothetical protein M5005_Spy_1788
M5005_Spy_1789c	nrdG	NE	1757534	1758148	204	-	3571115 COG06020	activating protein
M5005_Spy_1790c	-	NE	1758148	1758657	169	-	3571077 COG3981R	acetyltransferase
M5005_Spy_1791c	-	NC	1758666	1759601	311	-	3571078 COG0673R	virulence factor
M5005_Spy_1792c		NC	1759630	1759776	48	-	<u>3571079</u> -	hypothetical protein M5005_Spy_1792
M5005_Spy_1793c	nrdD	С	1759958	1762156	732	-	3571080 COG1328F	anaerobic ribonucleoside triphosphate reductase
M5005_Spy_1794c	-	NE	1762253	1763812	519	-	3571081 COG1807M	hypothetical protein M5005_Spy_1794
M5005_Spy_1795c	-	NE	1764225	1764530	101	-	3571082 COG3906S	hypothetical protein M5005_Spy_1795
M5005_Spy_1796c	-	E	1764542	1764961	139	-	3571083 COG0816L	Holliday junction resolvase-like protein
M5005_Spy_1797c	-	NE	1764958	1765227	89	-	3571084 COG4472S	hypothetical protein M5005_Spy_1797
M5005_Spy_1798c	spxA	С	1765340	1765738	132	-	3571085 COG1393P	Spx family transcriptional regulator
M5005_Spy_1799c	recA	NE	1766029	1767165	378	-	3571086 COG0468L	recombinase A
M5005_Spy_1800c	cinA	NE	1767254	1768525	423	-	3571087 COG1058R	competence damage-inducible protein A
M5005_Spy_1801c	tag	NC	1768594	1769154	186	-	3571088 COG2818L	DNA-3-methyladenine glycosylase
M5005_Spy_1802c	ruvA	NC	1769164	1769760	198	-	3571089 COG0632L	Holliday junction DNA helicase RuvA
M5005_Spy_1803c	lmrP	NE	1769762	1770982	406	-	3571090 COG2814G	multidrug resistance protein B
M5005_Spy_1804c	mutL	NC	1770993	1772975	660	-	3571091 COG0323L	DNA mismatch repair protein
M5005_Spy_1805c	mutS	NC	1773104	1775659	851	-	3571092 COG0249L	DNA mismatch repair protein MutS
M5005_Spy_1806c	-	NE	1775646	1775852	68	-	3571093 COG4550S	hypothetical protein M5005_Spy_1806
M5005_Spy_1807c	argR2	NE	1775995	1776432	145	-	3571094 COG1438K	arginine repressor ArgR
M5005_Spy_1808	argS	E	1776723	1778414	563	+	3571095 COG0018J	arginyl-tRNA synthetase
M5005_Spy_1809	uviB	NE	1778502	1778810	102	+	3571096 -	bacteriocin
M5005_Spy_1810c	-	NE	1778837	1779709	290	-	3571058 COG1284S	hypothetical protein M5005_Spy_1810
M5005_Spy_1811c	-	NE	1779752	1780687	311	-	3571059 COG1284S	hypothetical protein M5005_Spy_1811
M5005_Spy_1812c	-	NE	1780650	1781591	313	_	3571060 COG1284S	hypothetical protein M5005_Spy_1812
M5005_Spy_1813c	aspS	E	1781584	1783332	582	_	3571061 COG0173J	aspartyl-tRNA synthetase
M5005_Spy_1814c	hisS	E	1783670	1784950	426	_	3571062 COG0124J	histidyl-tRNA synthetase
M5005_Spy_1815	rpmF	NE	1785170	1785352	60	+	3571063 COG0333J	50S ribosomal protein L32
M5005_Spy_1816	rpmG	NC	1785368	1785517	49	+	3571064 COG0267J	50S ribosomal protein L33
M5005_Spy_1817	cadD	NE	1785810	1786424	204	+	3571065 COG4300P	cadmium resistance protein
M5005_Spy_1818	cadC	NE	1786406	1786774	122	+	3571066 COG0640K	cadmium efflux system accessory protein
M5005 Spy 1819	-	NE	1786825	1787748	307	+	3571067 -	hypothetical protein M5005 Spy 1819
M5005_Spy_1820	-	NE	1787814	1788566	250	+	3571068 COG1674D	DNA translocase FtsK
M5005_Spy_1821	-	NE	1788563	1789165	200	+	3571069 -	hypothetical protein M5005_Spy_1821
M5005_Spy_1822c	_	NE	1789641	1789925	94	-	3571070 -	transcriptional regulator
M5005_Spy_1823	_	NE	1790376	1791218	280	+	3571071 COG2035S	hypothetical protein M5005_Spy_1823
M5005_Spy_1824c	_	NE	1791265	1791906	213	-	3571072 COG1051F	phosphohydrolase
M5005_Spy_1825	_	NE	1792113	1792439	108	+	3571073 COG1695K	PadR family transcriptional regulator
M5005_Spy_1826	_	NE	1792426	1793013	195	+	3571074 COG4709S	hypothetical protein M5005_Spy_1826
M5005_Spy_1827	_	NE	1793010	1794089	359	+	3571075 -	hypothetical protein M5005 Spy 1827
M5005_Spy_1828c	_	NE	1794207	1796075	622	-	3571076 COG1511S	phage infection protein
M5005_Spy_1830	_	NE	1796614	1797147	177	+	3571039 COG1309K	TetR family transcriptional regulator
M5005_Spy_1831c	rpsD	E	1797301	1797912	203	-	3571040 COG0522J	30S ribosomal protein S4
M5005_Spy_1832c	-	NC	1798115	1798219	34	_	3571041 -	hypothetical protein M5005_Spy_1832
M5005_Spy_1833c	_	NE	1798203	1799336	377	_	3571042 COG5433L	transposase
M5005_Spy_1834c	_	NE	1799968	1800240	90	_	3571043 COG4466S	hypothetical protein M5005_Spy_1834
M5005_Spy_1034c	holB/dnaC	E	1800257	1801624	455	_	3571044 COG0305L	replicative DNA helicase
M5005_Spy_1836c	rplI	NE	1800257	1802106	150	-	3571044 COG0303L 3571045 COG0359J	50S ribosomal protein L9
M5005_Spy_1837c		NE	18021034	1804079	658	-	3571045 COG03393 3571046 COG3887T	phosphoesterase, DHH family protein
M5005_Spy_1837c M5005_Spy_1838c	gidA	C	1802103	1804079	632	-	3571040 COG38871 3571047 COG0445D	modification protein GidA
M5005_Spy_1839c	giun -	NE	1804170		105	_	3571047 COG0443D 3571048 COG1051F	phosphohydrolase
M5005_Spy_1839C	mnmA	E	1807286	1806509 1808407	373	-	3571048 COG10311 3571049 COG0482J	tRNA-specific 2-thiouridylase MnmA
M5005_Spy_1841	sdhB	NE	1807286	1808407	223	+	3571050 COG1760E	L-serine dehydratase
M5005_Spy_1842	sdhA	NE	1808705	1810260	223	+	3571050 COG1760E 3571051 COG1760E	L-serine dehydratase
M5005_Spy_1842 M5005_Spy_1843c	SullA	NE NE	1810673	1810260	290	-	3571051 COG1760E 3571052 COG0741M	transglycosylase
112002_2hy_1043C	•	INE	10100/3	101120/	204	-	22/1025 COGO/41M	aanagrycoayidae

M5005_Spy_1844c	cbiQ	С	1811659	1812459	266	-	3571053 COG0619P	cobalt transporter		*	
M5005_Spy_1845c	cbiO	E	1812452	1813294	280	-	3571054 COG1122P	cobalt ABC transporter ATP-binding protein		*	
M5005_Spy_1846c	cbiO	E	1813270	1814160	296	-	3571055 COG1122P	cobalt ABC transporter ATP-binding protein		*	
M5005_Spy_1847c	pgsA	NC	1814111	1814653	180	-	3571056 COG0558I	phosphatidyltransferase		*	
M5005_Spy_1848c	-	NE	1814667	1815692	341	-	3571057 COG1426S	hypothetical protein M5005_Spy_1848		*	
M5005_Spy_1849c	-	NE	1815742	1817031	429	-	3571021 COG0612R	zinc protease		*	
M5005_Spy_1850c	-	NE	1817033	1818277	414	-	3571022 COG0612R	zinc protease		*	
M5005_Spy_1851	hasA	NE	1818708	1819967	419	+	3571023 COG1215M	hyaluronan synthase			
M5005_Spy_1852	hasB	NE	1820003	1821211	402	+	3571024 COG1004M	UDP-glucose 6-dehydrogenase			
M5005_Spy_1853	hasC	NE	1821393	1822307	304	+	3571025 COG1210M	UTP-glucose-1-phosphate uridylyltransferase			
M5005_Spy_1854	-	NE	1822615	1823028	137	+	3571026 COG2501S	hypothetical protein M5005_Spy_1854		*	
M5005_Spy_1855	recF	NE	1823030	1824136	368	+	3571027 COG1195L	recombination protein F		*	
M5005_Spy_1856c	-	NE	1824191	1825024	277	-	3571028 COG4975G	glucose uptake protein		*	
M5005_Spy_1857c	guaB	NE	1825256	1826737	493	-	3571029 COG0516F	inosine 5\'-monophosphate dehydrogenase		*	
M5005_Spy_1858c	trsA	E	1827045	1828067	340	-	3571030 COG0180J	tryptophanyl-tRNA synthetase		*	
M5005_Spy_1859c	-	NC	1828159	1828284	41	-	<u>3571031</u> -	hypothetical protein M5005_Spy_1859			
M5005_Spy_1860	-	NE	1828486	1829358	290	+	3571032 COG1284S	hypothetical protein M5005_Spy_1860		*	
M5005_Spy_1861	-	NE	1829437	1831056	539	+	3571033 COG0488R	ABC transporter ATP-binding protein		*	
M5005_Spy_1862	-	NE	1831139	1833715	858	+	3571034 COG4485S	ABC transporter permease		*	
M5005_Spy_1863c	-	NE	1834881	1835162	93	-	3571037 COG2826L	transposase			
M5005_Spy_1864c	-	NE	1835744	1836223	159	-	3571018 COG1576S	rRNA large subunit methyltransferase		*	
M5005_Spy_1865	htrA	С	1836435	1837658	407	+	3571019 COG02650	protease Do	_	*	
M5005_Spy_1866	parB	NE	1837717	1838523	268	+	3571020 COG1475K	chromosome partitioning protein			

Table S5. Bayesian analysis of Tn-seq datasets for GAS M49 NZ131 grown in vitro.

(a) Spy numbers from GAS NZ131 genome.

(b) When available, gene name is provided.

(b) When available, gene name is prov					Bayesian for T ₀		Bayesia	n for T ₁	Bayesian for T ₂		
Locus Tag(a)	Gene Name(b)	Start	Stop	Length	Z score	Call	Z score	Call	Z score	Call	
5py49_0001	dnaA	232	1587	451	0.9995	Е	1	Е	0.7995	U	
py49_0002	dnaN	1742	2878	378	1	E	0.99975	E	1	Е	
py49_0003	-	2953	3150	65	0	NE	0	NE	0	NE	
py49_0004	-	3480	4595	371	0.00025	NE	0	NE	0	NE	
py49_0005	pth	4665	5234	189	0.9995	E	1	E	1	E	
py49_0006	trcF	5321	8740	1139	0.00025	NE	0	NE	0.00025	NE	
5py49_0008	-	8902	9174	90	0.00025	NE	0	NE	0	NE	
Spy49_0009	divIC	9161	9532	123	0.21775	U	1	E	0.98775	U	
Spy49_0010	-	9667	10953	428	0	NE	0	NE	0	NE	
Spy49_0011	mesJ	10950	12236	428	0.996	E	1	E	1	E	
Spy49_0012	hpt	12241	12783	180	0.00025	NE	0	NE	0.00025	NE	
Spy49_0013	ftsH	12805	14784	659	0.99975	E	1	E	1	E	
py49_0014	-	15041	16501	486	0.00025	NE	0	NE	0	NE	
py49_0015	-	31169	32365	398	0.9945	E	1	E	0.99225	E	
py49_0016	prsA	32618	33580	320	1	E	1	E	1	E	
py49_0017	recO -	33766	34521	251	0.00025	NE	0	NE	0	NE	
Spy49_0018		34624	35631	335	0.04475	U	1	E	1	E	
5py49_0019	acp	35624	35866	80 244	0.99875 0	E NE	0.08725 0	U	0.9965	E	
py49_0020 py49_0021	purC	35987 36798	36721 40571	1257	0.00975	NE	0	NE NE	0.004	NE NE	
Spy49_0021	purL purF	40805	42259	484	0.00975	NE	0	NE NE	0.01125 0.00025	NE	
Spy49_0022 Spy49_0023	purM	42287	43309	340	0	NE	0	NE	0.00025	NE	
Spy49_0023	purN	43477	44031	184	0	NE	0	NE	0.00025	NE	
Spy49_0025	purH	44215	45762	515	0	NE	0	NE	0.00073	NE	
Spy49_0026c	-	45820	46944	374	0	NE	0	NE	0.00025	NE	
py49_00200	purD	47107	48462	451	0	NE	0	NE	0.00025	NE	
py49_0028	purE	48621	49232	203	0	NE	0	NE	0.002	NE	
py49_0029	purK	49216	50292	358	0	NE	0	NE	0.00025	NE	
Spy49_0030	-	50394	51875	493	0	NE	0	NE	0	NE	
Spy49_0031	purB	52048	53340	430	0	NE	0	NE	0.01925	NE	
5py49_0032	-	53471	54391	306	0	NE	0	NE	0	NE	
Spy49_0033	ruvB	54617	55615	332	0.01425	NE	0.90475	U	1	Е	
Spy49_0035	-	55753	56190	145	0	NE	0	NE	0	NE	
Spy49_0036	-	56213	56614	133	0.00025	NE	0.99975	Е	0.99625	Е	
5py49_0037	-	56611	58386	591	0.666	U	1	Ε	1	Ε	
Spy49_0038	adhE	58695	61337	880	0	NE	0	NE	0	NE	
Spy49_0039	adhP	61589	62605	338	0	NE	0	NE	0	NE	
Spy49_0040	norM	62993	64282	429	0	NE	0	NE	0	NE	
Spy49_0044	rpsJ	64481	64789	102	0.9775	U	0.95575	U	0.004	NE	
Spy49_0045	rplC	65037	65663	208	0.998	E	1	Ε	0.995	Е	
Spy49_0046	rplD	65687	66310	207	0.82225	U	1	E	0.0035	NE	
Spy49_0048	rplW	66310	66540	76	0.95125	U	1	E	0.94925	U	
5py49_0049	rplB	66625	67458	277	1	E	1	E	1	E	
py49_0050	rpsS	67597	67875	92	0.0005	NE	0.244	U	0.00075	NE	
py49_0052	rplV	67891	68235	114	0.9925	U	1	E	0.64425	U	
Spy49_0053	rpsC	68275	68901	208	0.987	U	1	E	0.9985	E	
5py49_0054	rplP	68905	69318	137	0.93375	U	0.99975	E	0.9955	E	
py49_0055	rpmC	69328	69534	68	0.8785	U	0.99875	E	0.87975	U	
py49_0056	rpsQ	69560	69820	86	0.9915	U	1	E	0.98825	U	
py49_0057	rplN	69845	70213	122	0.99125	U	1	E	0.99	U	
py49_0058	rplX	70292	70597	101	0.00025	NE	1	E	0.995	E	
py49_0059	rplE	70621	71163	180	0.9995	Ε	1	Ε	0.01425	NE	
py49_0060	rpsN.1	71179	71364	61	0.92125	U	0.13125	U	0.01	NE	
py49_0061	rpsH	71515	71913	132	0.99525	E	1	E	0.98825	U	
5py49_0062	rplF	72116	72652	178	0.994	E	1	E	0.9935	E	
Spy49_0064	rplR	72757	73113	118	0.987	U	1	E	0.98025	U	
Spy49_0065	rpsE	73132	73626	164	0.99425	E	1	E	0.96625	U	
Spy49_0066	rpmD	73641	73823	60 146	0.00025	NE	1	E	0.0005	NE	
Spy49_0067	rplO	74038	74478	146	0.96925	U	0.9995	E	0.96575	U	
Spy49_0068	secY	74495	75799 76597	434	0.00775	E	1	E	0.00075	E	
Spy49_0069	adk	75949 76705	76587	212	0.99775	E	1	E	0.99975	E	
Spy49_0070	infA	76705	76923	72	0.98475	U	1	E	0.03775	NE	

Spy49_0071	rpmJ	76949	77065	38	-1	S	-1	S	-1	S
Spy49_0072	rpsM	77083	77448	121	0.0015	NE	1	E	0.992	E
Spy49_0073	rpsK	77466	77849	127	0.979	U	0.0005	NE	0.94975	U
Spy49_0074	rpoA	77895	78833	312	1	E	1	E	1	E
Spy49_0075	rplQ	78848	79234	128	0.98375	U	0.00575	NE	0.97975	U
Spy49_0078	-	87367	87615	82	0	NE	0	NE	0.0185	NE
Spy49_0079	_	87670	87882	70	0.00175	NE	0	NE	0	NE
Spy49_0080	adrR	87992	88435	147	0.00025	NE	0	NE	0	NE
Spy49_0081	adrC	88439	89158	239	0.00025	NE	0	NE	0.1085	U
–	adrB	89151	89966	271	0.00023	NE	0	NE	0.62175	U
Spy49_0082										
Spy49_0083c	-	90006	90389	127	0	NE	0	NE	0	NE
Spy49_0084	tyrS	90440	91696	418	0.941	U	1	E	1	E
Spy49_0086	pbp1b	91800	94100	766	0.00025	NE	0	NE	0.00075	NE
Spy49_0087	rpoB	94364	97930	1188	1	E	1	E	1	E
Spy49_0088	rpoC	98048	101662	1204	1	E	1	E	1	E
Spy49_0089	-	101814	102179	121	0	NE	0	NE	0	NE
Spy49_0090	comYA	102272	103210	312	0.00025	NE	0	NE	0.00025	NE
Spy49_0091	comYB	103305	104180	291	0.00025	NE	0	NE	0	NE
Spy49_0092	comYC	104182	104508	108	0	NE	0	NE	0	NE
Spy49_0093	-	104483	104911	142	0.00025	NE	0	NE	0.00025	NE
Spy49_0094	-	104868	105152	94	0	NE	0	NE	0	NE
Spy49_0095	comYD	105145	105579	144	0.01125	NE	0	NE	0.00025	NE
Spy49_0096	-	105599	105889	96	0	NE	0	NE	0	NE
Spy49_0097	_	105987	106940	317	0.00025	NE	0	NE	0	NE
	ackA	106999	108195	398	0.00025	NE	0	NE	0.587	U
Spy49_0098	- -					NE	0	NE		NE
Spy49_0099		108381	108623	80	0				0.00025	
Spy49_0100	proC	108772	109542	256	0	NE	0	NE	0	NE
Spy49_0101	рерА	109590	110657	355	0	NE	0	NE	0.0005	NE
Spy49_0103	-	112439	112732	97	0	NE	0	NE	0	NE
Spy49_0104	trx.1	112729	113046	105	0.00025	NE	0	NE	0	NE
Spy49_0105	-	113064	113708	214	0	NE	0	NE	0	NE
Spy49_0107	ssb	113842	114237	131	0	NE	0	NE	0	NE
Spy49_0108c	-	114497	115138	213	0.00025	NE	0	NE	0	NE
Spy49_0109c	-	115158	116135	325	0	NE	0	NE	0.00025	NE
Spy49_0110c	hslO	116122	116994	290	0.00025	NE	0	NE	0	NE
Spy49_0111	nra	117120	118655	511	0.00025	NE	0	NE	0.00025	NE
Spy49_0112	cbp	119085	121319	744	0	NE	0	NE	0.00025	NE
Spy49_0113	lepA-1	121312	121833	173	0	NE	0	NE	0.00025	NE
Spy49_0114	- '	121855	122889	344	0	NE	0	NE	0.00025	NE
Spy49_0116	_	122905	123630	241	0	NE	0	NE	0.00025	NE
Spy49_0117	_	123665	124234	189	0	NE	0	NE	0	NE
Spy49_0118	msmR	124394	125599	401	0	NE	0	NE	0	NE
Spy49_0119	prtF	125984	129466	1160	0	NE	0	NE	0	NE
Spy49_0120c	-	129731	130396	221	0.00025	NE	0	NE	0	NE
–	atoE	130750	132156	468	0.00025	NE	0	NE	0.00025	NE
Spy49_0121	- atoL			303	0.00023	NE	0	NE	0.00023	NE
Spy49_0122c	-	132231	133142				0		0	
Spy49_0123	-	133263	134447	394	0	NE	-	NE		NE
Spy49_0124	atoD.2	134459	135118	219	0	NE	0	NE	0	NE
Spy49_0125	-	135121	135768	215	0	NE	0	NE	0	NE
Spy49_0126c	-	135890	136570	226	0	NE	0	NE	0	NE
Spy49_0127	-	136745	137110	121	0	NE	0	NE	0	NE
Spy49_0128	sloR	137147	138166	339	0	NE	0	NE	0.01125	NE
Spy49_0129	-	138620	138940	106	0	NE	0	NE	0	NE
Spy49_0130	ntpl	138930	140930	666	0	NE	0	NE	0.00025	NE
Spy49_0131	ntpK	140932	141411	159	0	NE	0	NE	0.00025	NE
Spy49_0132	ntpE	141479	142063	194	0.00025	NE	0	NE	0	NE
Spy49_0133	ntpC	142079	143077	332	0	NE	0	NE	0	NE
Spy49_0134	ntpG	143074	143394	106	0	NE	0	NE	0	NE
Spy49_0135	ntpA	143595	145370	591	0	NE	0	NE	0	NE
Spy49_0136	ntpB	145371	146786	471	0	NE	0	NE	0.00075	NE
Spy49_0137	ntpD	146831	147457	208	0	NE	0	NE	0	NE
Spy49_0138c	-	147577	148839	420	0	NE	0	NE	0.00025	NE
Spy49_0139c	-	148852	149730	292	0	NE	0	NE	0.00023	NE
–						NE NE	0	NE NE	0	
Spy49_0141	purA -	150168	151460	430	0.00125					NE NE
Spy49_0142		151787	152830	347	0	NE	0	NE	0	NE
Spy49_0143	nusG	152988	153542	184	0.593	U	0	NE	0.9595	U
Spy49_0144	nga	153917	155272	451	0	NE	0	NE	0.0005	NE
Spy49_0145	-	155277	155762	161	0	NE	0	NE	0.00025	NE

Spy49_0146	slo	155786	157501	571	0	NE	0	NE	0.00025	NE
Spy49_0147	-	157756	158184	142	0.99525	E	0.50925	U	0.00375	NE
Spy49_0148	-	158408	158701	97	0.00025	NE	0.3225	U	0.00025	NE
Spy49_0149c	_	158998	159165	55	0	NE	0	NE	0.00025	NE
Spy49_0150c	_	159350	159676	108	0.99925	E	1	E	0.999	E
–					0.55525		0			
Spy49_0151	metB	159929	161299	456		NE		NE	0	NE
Spy49_0152	leuS	161510	164011	833	1	E	1	Е	1	E
Spy49_0153	-	164318	165751	477	0	NE	0	NE	0	NE
Spy49_0154	-	165822	166100	92	0	NE	0	NE	0	NE
Spy49_0155	-	166223	166708	161	0	NE	0	NE	0	NE
Spy49_0156	ulaD	166799	167461	220	0	NE	0	NE	0.086	U
Spy49_0157	-	167466	168329	287	0	NE	0	NE	0	NE
–	araD	168331	169035	234	0	NE	0	NE	0	NE
Spy49_0158										
Spy49_0159	-	169361	171007	548	0	NE	0	NE	0	NE
Spy49_0160	-	171261	172352	363	0	NE	0	NE	0	NE
Spy49_0161	opuAA	172842	174038	398	0	NE	0	NE	0	NE
Spy49_0162	opuABC	174054	175781	575	0	NE	0	NE	0	NE
Spy49_0163	polA	175912	178554	880	0.00025	NE	1	E	1	E
Spy49_0164	-	178732	179187	151	0	NE	0	NE	0	NE
Spy49_0165	_	179239	179706	155	0	NE	0	NE	0	NE
–	-			99	0	NE	0		0	
Spy49_0166	-	179862	180161					NE		NE
Spy49_0167	-	180383	181717	444	0	NE	0	NE	0	NE
Spy49_0168	-	181710	182090	126	0	NE	0	NE	0	NE
Spy49_0169	-	182234	182443	69	0.0125	NE	0	NE	0	NE
Spy49_0170c	-	182570	182785	71	0	NE	0	NE	0	NE
Spy49_0173c	-	183427	183720	97	0	NE	0	NE	0	NE
Spy49_0176	_	183438	183638	290	0	NE	0	NE	0.00025	NE
Spy49_0178c		185332	186204	148	0	NE	0	NE	0	NE
	-									
Spy49_0180c	-	186865	187311	287	0	NE	0	NE	0	NE
Spy49_0181	-	187933	188796	380	0	NE	0	NE	0	NE
Spy49_0182	tgt	189015	190157	103	0	NE	0	NE	0	NE
Spy49_0183	-	190374	190685	179	0	NE	0	NE	0	NE
Spy49_0184	bioY	190689	191228	259	0	NE	0	NE	0	NE
Spy49_0185	-	191368	192147	171	0	NE	0	NE	0	NE
Spy49_0186c	_	192147	192662	406	0	NE	0	NE	0.00025	NE
–	-									
Spy49_0187	-	193276	194496	234	0.00025	NE	0	NE	0	NE
Spy49_0188	speG	194908	195612	449	1	E	1	E	1	E
Spy49_0189c	pgi	196067	197416	465	0	NE	0	NE	0	NE
Spy49_0190	-	197875	199272	223	0.00025	NE	0	NE	0.00025	NE
Spy49_0191c	-	199964	200635	299	0.96075	U	1	E	1	E
Spy49_0192c	hasC.2	200734	201633	338	0.99975	E	1	E	1	E
Spy49 0193	gpsA	201666	202682	68	0.00025	NE	0	NE	0	NE
Spy49_0194	- 660.	203220	203426	568	0	NE	0	NE	0.62625	U
–	-									
Spy49_0195	-	203419	205125	594	0.00025	NE	0	NE	0.0065	NE
Spy49_0198	-	205128	206912	230	0	NE	0	NE	0	NE
Spy49_0199	-	207105	207797	152	0	NE	0	NE	0	NE
Spy49_0200	dut	207907	208365	464	0.00025	NE	0	NE	0.00025	NE
Spy49_0201	radA	208402	209796	165	0	NE	0.00075	NE	0.674	U
Spy49 0202	-	209985	210482	236	0	NE	0	NE	0	NE
Spy49_0203	_	210613	211323	496	0.99875	E	1	E	1	E
Spy49 0204	gltX	211506	212996	448	0.00025	NE	0	NE	0	NE
	-						0			
Spy49_0205	fasB	213347	214693	427	0.00025	NE		NE	0.1585	U
Spy49_0206	-	214690	215973	246	0	NE	0	NE	0.00025	NE
Spy49_0207	fasA	215977	216717	119	0.988	U	0.0005	NE	0.00025	NE
Spy49_0208	rnpA	217257	217616	269	0	NE	0	NE	0	NE
Spy49_0209	-	217600	218409	304	0.00025	NE	0	NE	0.98625	U
Spy49_0210	-	218421	219335	44	-1	S	-1	S	-1	S
Spy49_0211	rpmH	219650	219784	234	0.00025	NE	0	NE	0	NE
–	-			439		NE	0			
Spy49_0212	-	220058	220762		0			NE	0.00025	NE
Spy49_0213	-	220811	222130	295	0	NE	0	NE	0.00025	NE
Spy49_0214	-	222235	223122	276	0.00025	NE	0	NE	0.03225	NE
Spy49_0215	-	223135	223965	201	0	NE	0	NE	0.00025	NE
Spy49_0216	-	224179	224784	304	0	NE	0	NE	0	NE
Spy49_0217	nanH	224796	225710	312	0	NE	0	NE	0	NE
Spy49_0218c	_	225732	226670	276	0	NE	0	NE	0	NE
Spy49_0219	_	226781	227611	274	0	NE	0	NE	0	NE
	_				0	NE	0			
Spy49_0220	-	227863	228687	196				NE	0.00025	NE
Spy49_0221	-	228659	229249	290	0	NE	0	NE	0.00025	NE

\$\$\text{Symbol}\$											
System S	Spy49_0223	ksgA	229363	230235	290	0	NE	0	NE	0.00025	NE
Spy#0_0225	Spy49_0224	engC	230662	231534	220	0	NE	0.61175	U	0.97475	U
Spy#0_0225	Spv49 0225	rpe	231544	232206	210	0	NE	0	NE	0.00025	NE
Symphology	–	•									
Symbol Quart Qua	–										
Spyrid Q230	–										
Spy49_0231											
Spirks	Spy49_0229	purR	235298	236137	873	0	NE	0	NE	0	NE
Spring Good Spring Goo	Spy49_0230	prgA	236128	238749	134	0.01	NE	1	E	0.96225	U
Spring Good Spring Goo	Spv49 0231	rpsL	238963	239367	156	0.9985	Е	1	Е	0.996	Е
Spyrkg Q235		•									
Spy49 0235c Pir 242651 243661 38	–	•									
Symbol Quart Color Col	–										
Symbol Quart Company	–	•									
Spy49 Q238 - 249451 246447 504 0 NE 0 NE 0 NE 0 O00025 NE NE NP49 Q240 Dack 248637 249476 253 0 NE 0 NE 0 NE 0 D00025 NE NP49 Q241 MCA 248637 249476 2538 0 NE 0 NE 0 NE 0 D00025 NE NP49 Q241 MCA 248637 249476 25383 0.99975 E 1 E 1 E E Spy49 Q241 - 251681 252451 420 0.0025 NE 0 NE 0 NE 0.99875 U D97375 U D97375 U D97375 U D97376 U D97	Spy49_0236c	-	243887	244003	246	0.0035	NE		NE		NE
Spy+9 0,0239 -	Spy49_0237c	-	244145	244885	498	0.00025	NE	0	NE	0.0005	NE
Spy+9 Q0240 bacA	Spy49_0238	-	244951	246447	604	0	NE	0	NE	0.00025	NE
Spy49 0240 bacA	Spy49 0239	-	246645	248459	279	0.00025	NE	0	NE	0.00025	NE
Spy#9 (0.24 rgpG mech 249622 25088 389 0.99975 E 1 E 1 E Spy#9 (0.24) (2.75) (2	–	hacA			253		NF	0	NF		
Spy49 Q242	–										
Spy49 Q243 - 251881 252451 420 0.00025 NE 0 NE 0.4965 E	–										
Spy49 0244 - 25246 253808 408 0 NE 0 NE 0 A695 U	–										
Spy49 Q245 - 23839 255065 159 0 NE 0 NE 0 Q245 U	Spy49_0243	-									
SpyHg 0246 - 255032 255531 472 0.00025 NE 0	Spy49_0244	-	252546	253808	408	0	NE	0	NE	0.4695	U
Spy48 Q 02487 bpt 255524 bpt 255642 bpt 393 bpt 0 NE 0	Spy49_0245	-	253839	255065	159	0	NE	0	NE	0.2945	U
Spy48 Q 02487 bpt 255524 bpt 255694 2882 bpt 393 bpt 0 NE	Spv49 0246		255052	255531	472	0.00025	NE	0	NE	0.8825	U
Spir49 (0.248c) php7 257094 258275 395 0 NE 0 NE 0.00025 NE Spir49 (0.249) dacA 258489 259676 6656 0 NE 0 NE 0 NE Spir49 (0.251) oppB 262042 263544 338 0.00025 NE 0 NE 0 NE Spir49 (0.252) oppD 264479 265549 307 0 NE 0 NE 0 NE Spir49 (0.255) - 266613 266852 161 0 NE 0 NE 0 NE Spir49 (0.256) - 266613 266852 161 0 NE 0 NE 0 NE Spir49 (0.258) - 273839 274423 373 0.9945 E 1 E 1 E 1 E 1 E 1 E 1 E 1 NE 5 5		_									
Spy49_0259 dacA 258489 259676 656 0 NE	–	nhn7									
SpVH9_0250 oppA 26007 251977 500 0 NE 0 NE 0 NE SpVH9_0251 oppB 260022 263344 308 0.00025 NE 0 NE 0 NE SpVH9_0253 oppD 264479 356 0 NE 0 NE 0 NE SpVH9_0256 - 266613 266852 161 0 NE 0 NE 0 NE SpVH9_0257 comX1 272853 273338 194 0.01875 NE 0.905 U 1 E SpVH9_0258 - 2734323 273738 194 0.01875 NE 0 NE 0 NE 0 NE SpVH9_0258 - 273423 2737544 102 0 NE 0 0 NE 0	–	• •									
Spy49_0251 oppB 262042 263544 308 0.00025 NE 0 NE 0 NE Spy49_0252 oppC 263544 264470 355 0 NE 0 NE 0 NE Spy49_0254c oppF 265542 266665 79 0 NE 0 NE 0 NE Spy49_0257 comX1 272833 273338 134 0.01875 NE 0.9105 U 1 E Spy49_0259 c 273839 2734423 373 0.9945 E 1 E 1 E 1 E 1 E 1 E 1 E 1 E 1 E 1 E 1 E 1 E 1 E 1 E 1 E 1 E 1 E 1 E 1 2 1 E 1 2 1 E 1 2	–										
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Spy49/0.253 opp D 264479 265549 307 0 NE 0 NE 0 NE Spy49/0.256 - 266613 266852 161 0 NE 0 NE 0 NE Spy49/0.257 comX1 272833 273338 194 0.01875 NE 0.9105 U 1 E Spy49/0.258 - 273839 274423 373 0.9945 E 1 E 0 NE<	Spy49_0251	оррВ	262042	263544	308	0.00025	NE	0	NE	0	NE
Spy49_0256 oppF 265542 266613 266852 161 0 NE 0 NE 0 NE Spy49_0257 comX1 272853 273338 194 0.01875 NE 0.9105 U 1 E Spy49_0258 - 273839 274423 373 0.9945 E 1 E 1 E Spy49_0259 - 274423 275544 102 0 NE 0 NE 0.00025 NE Spy49_0261 nadD 275569 275877 210 0.02375 NE 1 E 0.79075 U Spy49_0261 nadD 275946 276578 197 0.00075 NE 0 NE 0.00025 NE Spy49_0261 nadD 277168 125 0 NE 0 NE 0 NE 0 NE 59y49_0264 - 277168 125 0 NE 0 NE 59y49_0266 <td>Spy49_0252</td> <td>oppC</td> <td>263544</td> <td>264470</td> <td>356</td> <td>0</td> <td>NE</td> <td>0</td> <td>NE</td> <td>0</td> <td>NE</td>	Spy49_0252	oppC	263544	264470	356	0	NE	0	NE	0	NE
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Spy49_0273c - 286820 287959 224 0.89775 U 1 E 0.99975 E Spy49_0274c - 288014 288688 463 0.89875 U 1 E 1 E Spy49_0276 - 288698 290089 237 0.00025 NE 0 NE 0 NE Spy49_0276 gidB 299158 290871 185 0 NE 0 NE 0.00025 NE Spy49_0277 lemA 291021 291578 298 0 NE 0 NE 0.00025 NE Spy49_0278 htpX 291625 292521 177 0.00025 NE 0	Spy49_0271c	atmE	284394	285086	444	0	NE	0	NE	0	NE
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310083 245 U NE U NE U NE		UXAM									
	3µy49_0293	-	203602	310003	245	U	INE	U	INE	U	INE

Spy49_0294	-	310344	311081	166	0	NE	0	NE	0	NE
Spy49_0295	-	311120	311620	229	0.422	U	0	NE	0.65875	U
Spy49_0296	_	311635	312324	80	0.98775	U	1	Е	0.9805	U
–	_	312502	312744	264	0.99625	E	1	E	1	E
Spy49_0297										
Spy49_0298	glr	312922	313716	328	0.00025	NE	0	NE	0	NE
Spy49_0299	-	313713	314699	173	0.00025	NE	0	NE	0	NE
Spy49_0300	-	314678	315199	153	0.00025	NE	0	NE	0.00025	NE
Spy49_0301	-	315196	315657	248	0.00025	NE	0	NE	0.00025	NE
Spy49 0302	xerD	315654	316400	234	0.00025	NE	0	NE	0.00025	NE
Spy49_0303	scpA	316400	317104	183	0	NE	0	NE	0.0005	NE
–	•									
Spy49_0304	scpB	317101	317652	240	0	NE	0	NE	0	NE
Spy49_0305	rluB	317773	318495	86	0	NE	0	NE	0.0035	NE
Spy49_0306	-	318495	318755	182	0.00025	NE	0	NE	0.00025	NE
Spy49_0307	-	318933	319481	178	0.00025	NE	0.00025	NE	0.00075	NE
Spy49_0308	-	319792	320328	152	0.00025	NE	0	NE	0.00025	NE
Spy49_0309	_	320553	321011	306	0.00025	NE	0	NE	0.00025	NE
–				184		NE	0	NE		NE
Spy49_0310	-	321303	322223		0				0.00025	
Spy49_0311	-	322262	322816	444	0.00025	NE	0	NE	0.00025	NE
Spy49_0312	hlyX	322950	324284	287	0	NE	0	NE	0	NE
Spy49_0313	pfIC	324290	325153	311	1	E	1	E	1	E
Spy49_0314	-	325284	326219	217	0	NE	0	NE	0.00025	NE
Spy49 0315	-	326295	326948	345	0.00025	NE	0	NE	0	NE
Spy49 0316	fhuG	326993	328030	350	0	NE	0	NE	0.00025	NE
Spy49_0317c	fhuB1	327991	329043	310	0	NE	0	NE	0.00025	NE
Spy49_0318	fhuD	329033	329965	260	0	NE	0	NE	0.00025	NE
Spy49_0319c	fhuC1	329991	330773	481	1	E	1	E	1	E
Spy49_0320	murE	331019	332464	544	1	E	1	E	1	E
Spy49_0322	-	332552	334186	209	0	NE	0	NE	0	NE
Spy49 0323	upp	334353	334982	196	0.07225	U	0.99575	E	0.999	E
	* *									
Spy49_0325	clpP	335206	335796	91	0	NE	0	NE	0	NE
Spy49_0326	-	336288	336563	211	0.5155	U	1	E	0.99775	E
Spy49_0327	tmk	336812	337447	291	0.972	U	1	E	1	E
Spy49_0328	-	337465	338340	53	-1	S	-1	S	-1	S
Spy49_0329	-	338688	338849	107	0.00025	NE	0.0405	NE	0.99325	E
Spy49 0330	-	339004	339327	287	0.13275	U	0.00025	NE	1	E
Spy49_0331	_	339332	340195	130	0	NE	0	NE	0	NE
–	-	340222		209		NE	0		0.00025	
Spy49_0332c			340614		0.00025			NE		NE
Spy49_0333	-	340661	341290	118	0.00025	NE	0	NE	0	NE
Spy49_0334c	-	341597	341953	303	0.00025	NE	0	NE	0.00025	NE
Spy49_0335	exoA	342027	342938	393	0.00025	NE	0	NE	0.00025	NE
Spy49 0336	lctO	343088	344269	1621	0	NE	0	NE	0.005	NE
Spy49_0337	prtS	344611	349476	217	0.00025	NE	0	NE	0	NE
Spy49_0338	-	350303	350956	666	1	E	1	E	1	E
–										
Spy49_0339	metS	351196	353196	337	0.00025	NE	0	NE	0.00025	NE
Spy49_0340	nrdF.2	353694	354707	162	0	NE	0	NE	0	NE
Spy49_0341	nrdl	354711	355199	726	0	NE	0	NE	0	NE
Spy49_0342c	nrdE.2	355166	357346	250	0	NE	0	NE	0.00125	NE
Spy49_0343	-	357508	358260	72	-1	S	-1	S	-1	S
Spy49 0344	-	358946	359164	67	-1	S	-1	S	-1	S
Spy49_0345c	_	359112	359315	65	0.0005	NE	0	NE	0	NE
–									0.0005	
Spy49_0346c	-	359568	359765	277	0.00025	NE	0	NE		NE
Spy49_0347	-	360026	360859	89	0	NE	0	NE	0	NE
Spy49_0348	-	361343	361612	134	0	NE	0	NE	0	NE
Spy49_0349c	-	362242	362646	129	0	NE	0	NE	0	NE
Spy49_0350c	-	363232	363621	230	0	NE	0	NE	0	NE
Spy49_0351c	-	364340	365032	60	0	NE	0	NE	0.00075	NE
Spy49_0352c	-	365190	365372	61	0.03075	NE	0	NE	0.00025	NE
Spy49_0353c		365511	365696	122	0.03073	NE	0	NE	0.00025	NE
Spy49_0354c	-	365740	366108	57	-1	S	-1	S	-1	S
Spy49_0355c	-	366083	366256	137	0	NE	0	NE	0	NE
Spy49_0356c	-	366619	367032	168	0	NE	0	NE	0.00025	NE
Spy49_0357c	-	367138	367644	109	0.00025	NE	0	NE	0	NE
Spy49_0358c	-	367681	368010	200	0	NE	0	NE	0.00025	NE
Spy49_0359c	_	368000	368602	88	0	NE	0	NE	0	NE
–	_	368868	369134	57	0	NE	0	NE	0	NE
Spy49_0360c	-									
Spy49_0361c	-	369315	369488	562	0	NE	0	NE	0	NE
Spy49_0362c	-	369776	371464	285	0.00025	NE	0	NE	0.00025	NE
Spy49_0363c	-	371433	372290	92	0.0345	NE	0	NE	0.00025	NE

Spy49_0364c	-	372434	372712	37	-1	S	-1	S	-1	S
Spy49_0365c	-	372715	372828	64	0	NE	0	NE	0	NE
Spy49_0366c		373055	373249	69	0	NE	0	NE	0	NE
–	-									
Spy49_0367c	-	373246	373455	82	0	NE	0	NE	0	NE
Spy49_0368c	-	373980	374228	61	0	NE	0	NE	0	NE
Spy49_0369	-	374244	374429	222	1	E	1	E	1	E
Spy49 0370	-	374597	375265	381	0	NE	0	NE	0	NE
Spy49_0371	-	375347	376492	78	0	NE	0	NE	0	NE
Spy49_0372	-	377362	377598	232	0	NE	0	NE	0.00025	NE
Spy49_0373	fabG	377591	378289	319	0	NE	0	NE	0	NE
Spy49 0374	-	378365	379324	445	0	NE	0	NE	0	NE
Spy49_0375	glpT	379657	380994	460	0.99925	E	1	E	1	E
–										
Spy49_0376	glmU	381167	382549	184	0	NE	0	NE	0	NE
Spy49_0377	-	382580	383134	83	0	NE	0	NE	0	NE
Spy49 0378	-	383134	383385	231	0.85825	U	1	E	0.9835	U
Spy49_0379	pfs	383405	384100	113	0	NE	0	NE	0	NE
–	pis									
Spy49_0380c	-	384251	384592	215	0	NE	0	NE	0.8575	U
Spy49_0381	-	384689	385336	274	0.03475	NE	0	NE	0	NE
Spy49_0382	mtsA	385590	386414	241	0.01325	NE	0	NE	0	NE
Spy49_0383	mtsB	386478	387203	284	0	NE	0	NE	0	NE
–		387204	388058	268	0.00025	NE	0	NE	0.00025	NE
Spy49_0384c	mtsC									
Spy49_0385	сурВ	388206	389012	801	1	E	1	E	1	E
Spy49_0386c	ftsK	389229	391634	116	0.00025	NE	0	NE	0	NE
Spy49_0387	-	391704	392054	141	0.02	NE	0.9995	E	0.982	U
Spy49_0388	rplK	392301	392726	229	1	Е	1	Ε	0.9995	E
–	•									
Spy49_0390	rplA	392832	393521	242	1	E	1	E	1	E
Spy49_0391	pyrH	393843	394571	185	0.44075	U	1	E	0.99725	E
Spy49_0392	frr	394600	395157	285	0	NE	0	NE	0	NE
Spy49_0394	-	395266	396123	169	0	NE	0	NE	0	NE
–						NE	0			
Spy49_0395	mrsA	396196	396705	71	0			NE	0	NE
Spy49_0396	-	396702	396917	389	0	NE	0	NE	0	NE
Spy49_0398	-	397073	398242	603	0	NE	0	NE	0	NE
Spy49_0399	-	398517	400328	350	0	NE	0	NE	0	NE
Spy49_0400	phoH	400487	401539	191	0	NE	0	NE	0	NE
–	•									
Spy49_0401	-	401585	402160	165	0.945	U	1	E	0.996	E
Spy49_0402	-	402319	402816	135	0.99725	E	1	E	0.998	E
Spy49_0403	dgk	402797	403204	298	0.914	U	1	E	1	E
Spy49_0404	era	403324	404220	158	0	NE	0	NE	0	NE
–	-	404241	404717	84	0.00025	NE	0	NE	0.0005	NE
Spy49_0405c										
Spy49_0406	-	405023	405277	60	0	NE	0	NE	0	NE
Spy49_0407c	-	405910	406092	49	-1	S	-1	S	-1	S
Spy49_0408c	-	406430	406579	140	0	NE	0	NE	0	NE
Spy49 0409		406576	406998	75	0	NE	0	NE	0	NE
Spy49_0410	-	407316	407543	86	0	NE	0	NE	0	NE
Spy49_0411	-	408295	408555	123	0	NE	0	NE	0	NE
Spy49_0412	-	408771	409142	355	0.00025	NE	0	NE	0.0795	U
Spy49_0413	-	409427	410494	132	0	NE	0	NE	0.00025	NE
Spy49_0414c		410587	410985	89	0	NE	0	NE	0	NE
–										
Spy49_0415	-	411333	411602	288	0.00025	NE	0	NE	0.00025	NE
Spy49_0416	mutR	412673	413539	275	0	NE	0	NE	0	NE
Spy49_0417	fpg	413711	414538	203	0.9985	E	0.99675	E	0.99975	E
Spy49_0418	coaE	414517	415128	500	0.5455	U	0	NE	0	NE
	-	415318		397	0.5455	NE	0	NE		NE
Spy49_0419	-		416820						0.00025	
Spy49_0420	-	416942	418135	48	-1	S	-1	S	-1	S
Spy49_0421	rpmG	418132	418278	78	0.995	E	1	E	0.989	U
Spy49_0422	secG	418324	418560	777	0.00025	NE	0	NE	0.1865	U
Spy49_0423	vacB	418654	420987	155	0.00025	NE	0.00025	NE	0.98825	U
–										
Spy49_0424	smpB	420990	421457	236	0	NE	0	NE	0.00025	NE
Spy49_0425c	-	421472	422182	215	0	NE	0	NE	0	NE
Spy49_0426c	рср	422300	422947	308	0.00025	NE	0	NE	0	NE
Spy49_0427c	-	422998	423924	227	0.00025	NE	0	NE	0.00025	NE
–										
Spy49_0428c	-	423924	424607	308	0	NE	0	NE	0.00025	NE
Spy49_0429c	-	424818	425744	125	0.00025	NE	0	NE	0	NE
Spy49_0430c	gloA	425889	426266	221	0	NE	0	NE	0	NE
Spy49_0431c	-	426277	426942	361	0	NE	0	NE	0	NE
Spy49_0432	pepQ	426991	428076	333	0.959	U	0.999	E	1	E
–										
Spy49_0433	ссрА	428250	429251	332	0.981	U	1	E	1	E
Spy49_0434	-	429382	430380	444	0.99675	E	1	E	0.99475	E

Spy49_0435	-	430382	431716	647	1	E	1	E	1	E
Spy49_0436	thrS	432138	434081	330	0	NE	0	NE	0.001	NE
–				272	0.00025	NE	0	NE		NE
Spy49_0437	tagH	434222	435214						0.00025	
Spy49_0438	-	435216	436034	261	0	NE	0	NE	0.00025	NE
Spy49_0439	-	436036	436821	49	-1	S	-1	S	-1	S
Spy49_0440	-	437022	437171	382	0	NE	0	NE	0	NE
Spy49 0441	-	437566	438714	415	0.00025	NE	0	NE	0.00025	NE
Spy49_0442	-	438671	439918	344	0	NE	0	NE	0	NE
Spy49_0444	-	439974	441008	236	1	E	1	E	0.9995	E
Spy49_0445	vicR	441170	441880	450	0.00025	NE	0	NE	0	NE
Spy49 0446	vicK	441873	443225	269	0.00025	NE	0	NE	0	NE
		443229	444038	230	0.99775	E	0.444	U	0.99725	E
Spy49_0447	vicX									
Spy49_0448	rnc	444483	445175	1179	0.00025	NE	0	NE	0.15575	U
Spy49_0449c	smc	445176	448715	283	0.00025	NE	0	NE	0.00025	NE
Spy49_0450	-	448963	449814	290	0	NE	0	NE	0.00025	NE
Spy49_0451	aroE	450088	450960	278	0.00025	NE	0	NE	0.01975	NE
–										
Spy49_0453	-	450957	451793	244	0.00025	NE	0	NE	0.9755	U
Spy49_0454	-	451795	452529	328	0	NE	0	NE	0.00025	NE
Spy49_0455	-	452522	453508	399	0	NE	0	NE	0.00025	NE
Spy49_0456		453518	454717	300	0	NE	0	NE	0.00025	NE
–										
Spy49_0457	-	454701	455603	329	0.00025	NE	0	NE	0.00025	NE
Spy49_0458	-	455724	456713	88	0	NE	0	NE	0.00025	NE
Spy49_0459	-	457116	457382	385	0.00025	NE	0	NE	0.00025	NE
Spy49_0460	-	457406	458563	389	0.00025	NE	0	NE	0	NE
–		458648	459817	69	0	NE	0	NE	0	NE
Spy49_0461c	-									
Spy49_0462c	-	459958	460167	552	0	NE	0	NE	0	NE
Spy49_0463c	-	460157	461815	74	0	NE	0	NE	0	NE
Spy49 0464c	-	461806	462030	296	0.00025	NE	0	NE	0	NE
Spy49_0465	_	462034	462924	52	-1	S	-1	S	-1	S
–	_									
Spy49_0466	-	462958	463116	100	0.0145	NE	0	NE	0.033	NE
Spy49_0467	-	463171	463473	58	0.00025	NE	0	NE	0	NE
Spy49_0468	-	463602	463778	150	0	NE	0	NE	0	NE
Spy49_0469	_	464174	464626	102	0	NE	0	NE	0.00025	NE
–		464692	465000	62	0.0005	NE	0	NE	0	NE
Spy49_0470c	-									
Spy49_0471	-	465238	465426	107	0	NE	0	NE	0	NE
Spy49_0473	-	465417	465740	223	0.00025	NE	0	NE	0	NE
Spy49_0474	-	465785	466456	415	0	NE	0	NE	0	NE
Spy49_0475	_	466617	467864	238	0	NE	0	NE	0	NE
–	-									
Spy49_0476	-	468092	468808	319	0.00025	NE	0	NE	0	NE
Spy49_0477c	-	468984	469943	267	0	NE	0	NE	0.00025	NE
Spy49_0478c	-	470313	471116	91	0	NE	0	NE	0	NE
Spy49 0479	_	471164	471439	72	0.0305	NE	0	NE	0.00025	NE
=										
Spy49_0480	-	471459	471677	265	0	NE	0	NE	0	NE
Spy49_0481	-	471744	472541	274	0	NE	0	NE	0.00025	NE
Spy49_0482	-	472545	473369	516	1	E	1	E	1	E
Spy49_0483c	ftsY	473369	474919	455	0	NE	0	NE	0	NE
Spy49_0484	_	474973	476340	280	0.00025	NE	0	NE	0.00025	NE
–	h =10									
Spy49_0485	bglG	476668	477510	620	0	NE	0	NE	0.00025	NE
Spy49_0487	-	477512	479374	474	0	NE	0	NE	0	NE
Spy49_0488c	bgIA	479393	480817	271	0	NE	0	NE	0	NE
Spy49_0489c	-	480916	481731	300	0	NE	0	NE	0	NE
–	_	481731	482633	710	0.00025	NE	0	NE	0.00025	NE
Spy49_0490	-									
Spy49_0491	-	483170	485302	160	0	NE	0	NE	0	NE
Spy49_0493	-	485244	485726	90	0	NE	0	NE	0	NE
Spy49_0494	-	485790	486062	330	0.00025	NE	1	E	1	E
Spy49_0495	ptsK	486367	487359	259	0.00025	NE	0	NE	0.00025	NE
–	•									
Spy49_0496	lgt	487356	488135	135	0.00025	NE	0	NE	0	NE
Spy49_0497	-	488157	488564	142	0	NE	0	NE	0	NE
Spy49_0498	-	488557	488985	89	0	NE	0	NE	0	NE
Spy49_0499	_	489044	489313	308	0.00025	NE	0	NE	0	NE
–										
Spy49_0500	-	489631	490557	428	0	NE	0	NE	0	NE
Spy49_0501	-	490659	491945	75	0	NE	0	NE	0	NE
Spy49_0502c	-	492146	492373	46	-1	S	-1	S	-1	S
Spy49_0503c	-	492470	492610	497	1	E	1	E	1	Ε
–	lvcS	492746	494239	300	0.00025	NE	0	NE	0.00025	NE
Spy49_0504	lysS									
Spy49_0505c	-	494413	495315	207	0	NE	0	NE	0	NE
Spy49_0506c	-	495423	496046	159	0	NE	0	NE	0	NE
Spy49_0507c	-	496387	496866	187	0	NE	0	NE	0	NE

Spy49_0508c	-	496957	497520	282	0	NE	0	NE	0	NE
Spy49_0509	-	497789	498637	167	0	NE	0	NE	0.00025	NE
Spy49 0510	_	498962	499465	128	0	NE	0	NE	0	NE
	_				0.00025	NE	0		0.00025	
Spy49_0511c	-	499449	499835	159				NE		NE
Spy49_0512c	-	499881	500360	599	0	NE	0	NE	0	NE
Spy49_0513	pepF	500353	502152	932	0	NE	0	NE	0	NE
Spy49_0514	ррс	502311	505109	302	1	E	1	E	1	E
–					1	E	1	E	0.9905	U
Spy49_0515	ftsW	505279	506187	398						
Spy49_0516	tufA	506912	508108	252	0.95575	U	1	E	1	E
Spy49_0517c	tpiA	508349	509107	411	1	E	1	E	1	E
Spy49 0518c	murN	509207	510442	408	1	E	1	E	1	E
		510429		269	0.00025	NE	0	NE	0.00025	NE
Spy49_0519c	murM.1		511655							
Spy49_0520c	-	511655	512464	433	0	NE	0	NE	0	NE
Spy49_0521	-	512920	514221	128	0	NE	0	NE	0	NE
Spy49 0522	_	514303	514689	893	0.9995	E	1	E	1	E
	nacl	514920	517601	331	0.00025	NE	0	NE	0	NE
Spy49_0523c	pacL									
Spy49_0524c	regR	517687	518682	635	0.00025	NE	0	NE	0	NE
Spy49_0525c	-	518746	520653	273	0	NE	0	NE	0.44825	U
Spy49_0526c	agaD	520740	521561	260	0.00025	NE	0	NE	0.00025	NE
Spy49_0527c	agaW	521548	522330	162	0.00025	NE	0	NE	0	NE
–	-									
Spy49_0528c	agaV	522349	522837	399	0	NE	0	NE	0.00025	NE
Spy49_0529c	ugl	522873	524072	145	0	NE	0	NE	0	NE
Spy49 0530	agaF	524072	524509	264	0	NE	0	NE	0	NE
Spy49_0531	-	524844	525638	213	0	NE	0	NE	0	NE
Spy49_0532	-	525663	526304	333	0	NE	0	NE	0	NE
Spy49_0533	kdgK	526333	527334	211	0	NE	0	NE	0	NE
Spy49_0534	kdgA	527339	527974	216	0.014	NE	0	NE	0.00025	NE
Spy49_0535	-	528272	528922	374	0	NE	0	NE	0	NE
–										
Spy49_0536	-	529618	530742	326	1	E	1	E	0.99175	E
Spy49_0537	prfB	530928	531908	230	0.00075	NE	0.00025	NE	0.27175	U
Spy49_0538	ftsE	531927	532619	309	0.88575	U	1	E	1	E
Spy49_0539c	ftsX	532612	533541	192	0.00025	NE	0	NE	0	NE
–										
Spy49_0540	-	533851	534429	254	0.00025	NE	0	NE	0	NE
Spy49_0541	-	534718	535482	833	0.00025	NE	0	NE	0	NE
Spy49_0543	dinG	535590	538091	397	0	NE	0	NE	0	NE
Spy49_0544	aspC	538426	539619	448	1	E	1	E	1	E
Spy49_0545	asnC	539640	540986	296	1	E	1	Ε	1	E
–										
Spy49_0546	-	541401	542291	325	0	NE	0	NE	0	NE
Spy49_0547	-	542288	543265	303	0.001	NE	0	NE	0.0035	NE
Spy49_0548	-	543262	544173	465	0	NE	0	NE	0.00025	NE
Spy49_0549	pepD	544306	545703	515	0	NE	0	NE	0.0005	NE
–							0			
Spy49_0550	adcA	545855	547402	240	0	NE		NE	0	NE
Spy49_0551	-	547552	548274	399	0.00025	NE	0	NE	0	NE
Spy49_0552c	agaS	548294	549493	86	0.95875	U	0	NE	0	NE
Spy49_0554c	rpmE2	549590	549850	313	0.00025	NE	0	NE	0.00025	NE
–	-	549965	550906	149	0.00025	NE	0	NE	0	NE
Spy49_0555				94			0			
Spy49_0556	flaV	551300	551749		0.00025	NE		NE	0.0495	U
Spy49_0557	-	551925	552209	420	0.032	NE	0.06425	NE	0.99925	E
Spy49_0558	-	552202	553464	115	0.716	U	1	E	0.0895	U
Spy49 0559	rpIS	553579	553926	189	0	NE	0	NE	0	NE
	•									
Spy49_0560	-	554947	555516	650	1	E	1	E	1	E
Spy49_0561	gyrB	555517	557469	574	1	E	1	E	1	E
Spy49_0562c	ezrA	557837	559561	152	0	NE	0	NE	0	NE
Spy49_0563	-	559693	560151	435	0.99875	E	1	E	1	E
–							0		0	
Spy49_0564c	eno	560384	561691	191	0.00025	NE		NE		NE
Spy49_0565c	-	562280	562855	53	-1	S	-1	S	-1	S
Spy49_0566c	-	562941	563102	513	0	NE	0	NE	0	NE
Spy49_0567	-	563464	565005	1130	0	NE	0	NE	0.2585	U
Spy49_0568	_	565552	568944	53	0.0315	NE	0	NE	0	NE
–										
Spy49_0569	sagA	569809	569970	316	0.00025	NE	0	NE	0	NE
Spy49_0570	sagB	570192	571142	352	0.00025	NE	0	NE	0	NE
Spy49_0572	sagC	571139	572197	452	0	NE	0	NE	0.00025	NE
Spy49_0573	sagD	572217	573575	223	0	NE	0	NE	0	NE
–										
Spy49_0574	sagE	573550	574221	227	0.00025	NE	0	NE	0.00025	NE
Spy49_0575	sagF	574218	574901	307	0.9135	U	0	NE	0.99975	E
Spy49_0576	sagG	574924	575847	375	0	NE	0.99625	E	0.73725	U
Spy49_0577	sagH	575856	576983	372	0.00025	NE	0.00025	NE	0.99375	E
Spy49_0578	sagi	576980	578098	910	0.0005	NE	0	NE	0	NE
56, 15_05/0	~~D.	3,0300	3.0030	310	5.0003	.,_	J	712	J	.12

Spy49_0579	-	578669	581401	166	0	NE	0	NE	0	NE
Spy49_0580	-	581679	582179	652	0.99175	U	1	Ε	1	E
–										
Spy49_0581	ligA	582373	584331	340	1	E	1	E	0.99975	E
Spy49_0582	-	584345	585367	65	0.931	U	1	Е	0.93375	U
Spy49_0583	-	585762	585959	238	1	Ε	1	E	1	E
Spy49_0584	_	585994	586710	164	0.99825	E	0.969	U	0.994	Е
Spy49 0585			587222	178	1	E	1	E	1	E
=	-	586728								
Spy49_0586	-	587222	587758	502	1	E	1	E	1	Е
Spy49_0587	-	587774	589282	291	1	E	1	E	1	E
Spy49_0588	-	589298	590173	468	1	E	1	Е	1	E
Spy49_0589		590335	591741	138	0.97825	U	0	NE	0.9285	U
–	-10									
Spy49_0590	atpC	591754	592170	85	0.00025	NE	0	NE	0	NE
Spy49_0591	-	592436	592693	423	0.00025	NE	0	NE	0.00025	NE
Spy49_0592	murA	592758	594029	62	0.001	NE	0	NE	0	NE
., =	_	594033	594221		0	NE	0	NE	0	NE
	nhaC				0	NE	0		0.00025	
	pheS	595077	596120					NE -		NE
Spy49_0596	pheT	596330	598735	347	1	Е	1	Е	1	Е
Spy49_0597	-	598845	599222	801	1	Ε	1	E	1	Ε
Spy49_0598	_	599215	599601	125	0	NE	0	NE	0	NE
–		599674	600750	128	0	NE	0	NE	0.00025	NE
Spy49_0599	-									
Spy49_0600	-	600760	601428	358	0.00025	NE	0	NE	0	NE
Spy49_0601	-	601532	602449	222	0	NE	0	NE	0.0005	NE
Spy49_0602c	rexB	602600	605815	305	0	NE	0	NE	0	NE
Spy49_0603	rexA	605776	609444	1071	0.006	NE	0	NE	1	Ε
–										
Spy49_0604	-	609584	610204	1222	0.93275	U	1	E	1	E
Spy49_0605	rpsU	610543	610719	206	0	NE	0	NE	0	NE
Spy49_0606	mscL	610847	611209	58	0.955	U	0.9985	E	0.26675	U
Spv49 0607c	dnaG	611339	613153	120	0	NE	0	NE	0	NE
., -	rpoD	613162	614271	604	0.999	E	1	E	1	E
Spy49_0608	•									
Spy49_0609	-	614507	614845	369	1	E	1	E	1	E
Spy49_0610	rmlD	614983	615837	112	0.00025	NE	0	NE	0	NE
Spy49_0611	rgpAc	615956	617110	284	0.99925	E	1	E	1	E
Spy49_0612	rgpBc	617100	618032	384	0.2065	U	1	Е	1	Ε
–										
Spy49_0613	rgpCc	618035	618838	310	0.0595	U	1	E	1	E
Spy49_0614	rgpDc	618838	620058	267	1	E	1	E	1	E
Spy49_0615	rgpEc	620069	621076	406	1	Ε	1	E	1	E
Spy49_0617	rgpFc	621073	622818	335	0.99975	E	1	Е	1	Е
–	-					E		E	1	E
Spy49_0618		622815	625289	581	0.99875		1			
Spy49_0619	-	625468	626163	824	0.00025	NE	0	NE	0	NE
Spy49_0620	-	626165	626506	231	0	NE	0	NE	0	NE
Spy49_0621	-	626499	627785	113	0.00025	NE	0	NE	0	NE
Spy49_0622		627766	629262	428	0.00025	NE	0.99575	Ε	1	Ε
–	- -									
Spy49_0623	рерТ	629356	630579	498	0.00375	NE	1	E	1	Е
Spy49_0624	-	630620	631108	407	0.00025	NE	0	NE	0.00025	NE
Spy49_0625	-	631095	631292	162	0	NE	0	NE	0	NE
Spy49_0626c	_	631341	631817	65	0	NE	0	NE	0	NE
–	cmle			158	0		0	NE	0.00025	NE
Spy49_0627	cmk	631832	632512			NE	-			
Spy49_0628	infC	632674	633204	226	0.00025	NE	0	NE	0.16625	U
Spy49_0629	rpml	633246	633443	176	0.9975	E	1	E	0.99225	E
Spy49 0630	rplT	633502	633861	65	0	NE	0	NE	0	NE
Spy49_0631	-	634152	636362	119	0.02	NE	0.9965	E	0.00075	NE
–										
Spy49_0632c	-	636470	637633	736	1	E	1	E	1	E
Spy49_0633	aroD	637630	638316	387	0.00025	NE	0	NE	0.00025	NE
Spy49_0634	aroF	638410	639576	228	0.00025	NE	0	NE	0	NE
Spy49_0635	-	639637	639978	388	0	NE	0	NE	0	NE
Spy49_0636		640200			0	NE	0		0	NE
	gor		641552	113				NE		
Spy49_0637	folC.2	641640	642908	450	0	NE	0	NE	0.00025	NE
Spy49_0638c	-	642938	643378	422	0	NE	0	NE	0	NE
Spy49_0639c	nifS	643613	644755	146	0	NE	0	NE	0	NE
Spy49_0640	thil	644767	645981	380	0	NE	0	NE	0.00025	NE
–										
Spy49_0641	-	646019	647287	404	0	NE	0	NE	0	NE
Spy49_0642	rplU	647526	647840	422	0.00025	NE	0	NE	0.0005	NE
Spy49_0643	-	647852	648178	104	0.9925	U	0.00075	NE	0.9885	U
Spy49_0644	rpmA	648206	648499	108	0.00275	NE	1	E	0.8775	Ü
–	•									
Spy49_0645	-	648847	649761	97	0.057	U	0	NE	0.923	U
Spy49_0646	lsp	649758	650216	304	0.00025	NE	0	NE	0.00025	NE
Spy49_0647	-	650206	651096	152	0	NE	0	NE	0.00025	NE
Spy49_0648	pyrR	651492	652013	296	0	NE	0	NE	0	NE
	. ,					-	-	-	-	-

6 40 0650		652020	652200	470	•		0		0	NE
Spy49_0650	pyrP	652029	653288	173	0	NE	0	NE	0	NE
Spy49_0651	pyrB	653349	654284	419	0	NE	0	NE	0	NE
Spy49_0652	carA	654328	655410	311	0	NE	0	NE	0	NE
Spy49_0653	carB	655656	658832	360	0	NE	0	NE	0.52125	U
Spy49_0654	-	659041	660312	1058	0	NE	0	NE	0.00025	NE
Spy49 0655	-	660312	661022	423	0	NE	0	NE	0.00025	NE
Spy49_0656	_	661034	662254	236	0	NE	0	NE	0.00025	NE
–	_				0.00025	NE	0	NE		
Spy49_0657		662508	664241	406					0.00025	NE
Spy49_0658	rpsP	664368	664640	577	0.39425	U	0	NE	0.997	E
Spy49_0659	-	664650	664889	90	0.999	E	1	Е	0.99825	E
Spy49_0660	-	665821	668847	79	0.9955	E	0	NE	0.9675	U
Spy49_0661	-	668867	669268	1008	0.00025	NE	0	NE	0.00025	NE
Spy49_0662	czcD	669448	670323	133	0.00025	NE	0	NE	0.00025	NE
Spy49_0663c	_	670459	670980	291	0	NE	0	NE	0	NE
Spy49_0664	rimM	671195	671713	173	0	NE	0	NE	0.00025	NE
–										
Spy49_0665	trmD	671700	672434	172	0.2	U	0.00025	NE	0.00025	NE
Spy49_0667	-	672434	673426	244	0.998	E	1	E	1	E
Spy49_0668	-	673603	674661	330	0.00025	NE	0	NE	0	NE
Spy49_0669	apbA	674674	675597	352	0.00025	NE	0	NE	0	NE
Spy49_0671	fruR	675853	676566	307	0	NE	0	NE	0	NE
Spy49 0672	fruK	676563	677474	237	0	NE	0	NE	0	NE
Spy49 0673	fruA	677471	679417	303	0	NE	0	NE	0	NE
Spy49_0674	-	679516	680109	648	0	NE	0	NE	0.00025	NE
Spy49_0675	-	680261	680968	197	0.00025	NE	0	NE	0.00025	NE
Spy49_0676	-	681025	681243	235	0	NE	0	NE	0	NE
Spy49_0677c	mac	681925	682944	72	0	NE	0	NE	0.00025	NE
	-	683850	684230		0	NE	0	NE	0.00075	NE
Spy49_0679	_	684230	685078	339	0	NE	0	NE	0.00025	NE
Spy49_0680	papS	685252	686412	126	0	NE	0	NE	0.0005	NE
–	-	686409	688286	282	0.00025	NE	0	NE	0.0003	NE
Spy49_0681	-									
Spy49_0682	-	689180	689590	386	1	E	1	E	1	E
Spy49_0683	-	689672	691684	625	0	NE	0	NE	0.00025	NE
Spy49_0684	-	691904	692554	136	0	NE	0	NE	0	NE
Spy49_0686c	-	692557	693225	670	0	NE	0	NE	0.0005	NE
Spy49_0687	-	693234	694466	216	0.00025	NE	0	NE	0.00025	NE
Spy49_0688	mvaK1	694760	695638	222	0.00025	NE	0	NE	0.00025	NE
Spy49_0689	mvaD	695620	696564	410	0	NE	0	NE	0	NE
–					0.0005	NE		E	1	E
Spy49_0690	mvaK2	696557	697570	292			1			
Spy49_0691	-	697557	698546	314	0.977	U	1	E	1	E
Spy49_0692	mvaS1	698776	700053	337	1	E	1	E	1	E
Spy49_0693	mvaS2	700040	701215	329	0.6545	U	1	E	1	E
Spy49_0694c	thyA	701424	702263	425	0.9995	E	1	E	1	E
Spy49_0695c	dyr	702343	702840	391	1	E	1	Е	1	E
Spy49_0696	-	702860	703060	279	0.00025	NE	0	NE	0.99975	Ε
Spy49_0697	clpX	703161	704390	165	0.00025	NE	1	E	1	E
–										
Spy49_0698	engB	704400	704999	66	0	NE	0	NE	0.00525	NE
Spy49_0700	-	705147	705890	409	0.306	U	0	NE	0.80075	U
Spy49_0701	clpL	705948	708047	199	0.0005	NE	1	E	0.9985	E
Spy49_0702	rpiA	708425	709108	247	0	NE	0	NE	0	NE
Spy49_0703c	deoB	709185	710396	699	0.00025	NE	0	NE	0.00025	NE
Spy49_0704	arsC	710415	710855	227	0.00025	NE	0	NE	0.98625	U
Spy49_0705	punA	710839	711648	403	0	NE	0	NE	0	NE
–	-									
Spy49_0706	deoD	712176	712946	146	0	NE	0	NE	0	NE
Spy49_0707	-	712939	713727	269	0	NE	0	NE	0	NE
Spy49_0708	cpsY	713807	714712	256	0	NE	0	NE	0	NE
Spy49_0709	-	714934	715470	262	0	NE	0	NE	0	NE
Spy49_0710c	pyrF	715747	716439	301	0	NE	0	NE	0.00025	NE
Spy49 0711	pyrE	716497	717126	178	0	NE	0	NE	0	NE
Spy49_0712	amiC	717323	718777	230	0	NE	0	NE	0	NE
–		717323								
Spy49_0713	-		719758	209	0	NE	0	NE	0.00025	NE
Spy49_0714	-	719787	720437	484	0	NE	0	NE	0.002	NE
Spy49_0715	ung	720570	721223	287	0.00025	NE	0	NE	0	NE
Spy49_0716	pyrC	721355	722623	216	0.00025	NE	0	NE	0	NE
Spy49_0717	-	722681	723322	217	0	NE	0	NE	0	NE
Spy49_0718	parE	723457	725406	422	0	NE	0	NE	0.00025	NE
Spy49_0719c	parC	725497	727956	213	0.9945	E	1	E	1	E
Spy49_0720	bcaT	728079	727330	649	0.99975	E	1	E	1	E
–								E		
Spy49_0721	-	729165	729395	819	1	E	1	С	1	E

Spy49_0722	rpsA	729786	730991	340	0	NE	0	NE	0	NE
Spy49_0723		731493	731795	76	0.96775	U	0	NE	0.058	U
–		731996	732982	401	0.971	U	1	E		E
Spy49_0724	-								1	
Spy49_0725c	-	733293	733700	100	0	NE	0	NE	0	NE
Spy49_0726	-	733950	734858	328	0.00025	NE	0	NE	0	NE
Spy49_0727	-	734976	735152	135	0	NE	0	NE	0.00025	NE
Spy49_0728	miaA	735286	736185	302	0	NE	0	NE	0	NE
–										
Spy49_0729c	hflX	736258	737496	58	0	NE	0	NE	0	NE
Spy49_0730	-	737489	738124	299	0.00025	NE	0	NE	0.0065	NE
Spy49_0731	-	738139	739068	412	0	NE	0	NE	0	NE
Spy49_0732	_	739228	739833	211	0	NE	0	NE	0.00025	NE
–	rocl			309	1	E	1	E		E
Spy49_0733	recJ	739830	742040						1	
Spy49_0734	apt	742190	742708	201	0	NE	0	NE	0	NE
Spy49_0735	dnaD	742789	743472	736	0.00025	NE	0	NE	0	NE
Spy49 0736	nth	743469	744125	172	0	NE	0	NE	0.00025	NE
Spy49_0737	-	744197	744883	227	1	E	1	E	1	E
–	_									
Spy49_0738	-	744873	745661	218	0	NE	0	NE	0	NE
Spy49_0739	-	745701	746825	228	0.996	E	1	E	0.997	E
Spy49_0740	rmlA	746864	747733	262	0	NE	0	NE	0.01375	NE
Spy49_0741	rmIC	747733	748326	374	0.00025	NE	0	NE	0.00025	NE
–										
Spy49_0742	rmlB	748570	749610	289	1	E	1	E	1	E
Spy49_0744	-	749693	750832	197	0.99125	U	1	E	0.97625	U
Spy49 0745	-	750960	751226	346	0.99925	Ε	1	E	0.99975	E
Spy49 0746c	_	751238	751624	379	0.00025	NE	0	NE	0.00025	NE
Spv49 0747c		751627	751977	88	0	NE	0	NE	0.00075	NE
' ' =	-									
Spy49_0748c	-	752273	752443	128	0	NE	0	NE	0	NE
Spy49_0749c	-	752469	753257	116	0.0185	NE	0.0155	NE	0.99875	E
Spy49 0750	-	753308	753499	56	-1	S	-1	S	-1	S
Spy49_0751c	_	753578	753889	262	0.00025	NE	0	NE	0.935	U
Spy49_0752	-	753891	754061	63	0.00225	NE	0.895	U	0.36025	U
Spy49_0753	-	754054	754257	103	0.00825	NE	0.005	NE	0.42875	U
Spy49_0754	-	754254	754640	56	0.541	U	0	NE	0.93575	U
Spy49_0755	_	754786	754989	67	0.02575	NE	0.00025	NE	0.90725	U
	_				0.02575	NE	0			NE
Spy49_0756		755077	755376	128				NE	0.00025	
Spy49_0757	-	755376	756533	67	0.9885	U	0	NE	0.00325	NE
Spy49_0759	-	756548	757105	99	0.00025	NE	0.0005	NE	0.9705	U
Spy49_0760	_	757148	759070	385	0	NE	0.00025	NE	0.00025	NE
Spy49_0761		759075	761459	185	0.00025	NE	0	NE	0.00025	NE
–	-									
Spy49_0762	-	761827	762120	640	0	NE	0	NE	0.73875	U
Spy49_0763	-	762117	763439	794	0	NE	0	NE	0.988	U
Spy49_0764	-	763603	763875	97	0.402	U	0.9875	U	0.3905	U
Spy49_0765	-	764008	764424	440	0	NE	0	NE	0.9845	U
–										
Spy49_0766	-	764496	764966	90	0	NE	0	NE	0	NE
Spy49_0767	-	764956	766233	138	0	NE	0	NE	0.00025	NE
Spy49_0768	-	766249	767781	156	0	NE	0	NE	0.00025	NE
Spy49_0769	_	767747	769189	425	0	NE	0	NE	0	NE
Spy49_0770	_	769410	769802	510	0	NE	0	NE	0.00025	NE
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Spy49_0771	-	769845	770414	480	0	NE	0	NE	0	NE
Spy49_0772	-	770427	771314	130	0.00025	NE	0	NE	0.00025	NE
Spy49_0773	-	771326	771682	189	0.00025	NE	0	NE	0.127	U
Spy49_0774	_	771693	771971	295	0	NE	0	NE	0.00025	NE
–							0			
Spy49_0775	-	771968	772312	118	0	NE		NE	0	NE
Spy49_0776	-	772316	772675	92	0	NE	0	NE	0.00025	NE
Spy49_0777	-	772687	773286	114	0	NE	0	NE	0.00025	NE
Spy49 0778	-	773393	773794	119	0	NE	0	NE	0.9005	U
Spy49 0779	_	773869	774102	199	0	NE	0	NE	1	E
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Spy49_0780	-	774117	778499	133	0.0195	NE	0	NE	0.19775	U
Spy49_0781	-	778511	779353	77	0	NE	0	NE	0.00025	NE
Spy49_0782	-	779363	781342	1460	0.001	NE	0	NE	0.049	U
Spy49_0783	_	781339	783582	280	0	NE	0	NE	0.0005	NE
–										
Spy49_0784	-	783594	783755	659	0.00025	NE	0	NE	0.26	U
Spy49_0785	-	783758	784369	747	0.00025	NE	0	NE	0.86775	U
Spy49_0786	-	784379	784834	53	-1	S	-1	S	-1	S
Spy49_0788	-	784952	785704	203	0	NE	0	NE	0	NE
–										
Spy49_0789	-	785870	786157	151	0	NE	0	NE	0	NE
Spy49_0790	speH	786363	787073	250	0	NE	0	NE	0	NE
Spy49_0791	mutX	787677	788153	95	0	NE	0	NE	0	NE
Spy49_0792	-	788211	789392	236	0	NE	0	NE	0	NE
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Spy49_0793	-	789382	790629	158	0	NE	0	NE	0	NE
Spy49_0794	-	790688	792340	393	0.00025	NE	0	NE	0.00025	NE
Spy49_0795	-	792694	793692	415	0	NE	0	NE	0	NE
Spy49 0796c	-	793643	793861	550	0	NE	0	NE	0.00025	NE
Spy49 0797	-	794037	794906	332	0.00025	NE	0	NE	0.00025	NE
Spy49_0798	_	794903	795661	72	-1	S	-1	S	-1	S
–	-									
Spy49_0799	-	795865	797526	289	0	NE	0	NE	0	NE
Spy49_0800	estA	797659	798444	252	0	NE	0	NE	0	NE
Spy49_0801	-	798474	798800	553	0.99975	E	1	E	1	E
Spy49_0803	-	798846	800753	261	0	NE	0	NE	0.00025	NE
Spy49_0804	acoA	801026	802006	108	0	NE	0	NE	0.00025	NE
Spy49 0805	асоВ	802062	803063	635	0.0165	NE	0	NE	0	NE
Spy49_0807	acoC	803248	804657	326	0.00025	NE	0	NE	0.00025	NE
–							0			
Spy49_0808	acoL	804984	806747	333	0	NE		NE	0	NE
Spy49_0809	hylA	807422	809839	469	0	NE	0	NE	0	NE
Spy49_0810	-	810072	811061	587	0	NE	0	NE	0.00025	NE
Spy49_0811c	cobQ	811170	811961	805	0	NE	0	NE	0	NE
Spy49_0812	murC2	811961	813304	329	0	NE	0	NE	0.00025	NE
Spy49_0813c	-	813406	814257	263	0.9995	E	1	E	1	Е
Spy49_0814c	-	814254	815210	447	0.99975	Е	1	Е	1	Ε
Spy49_0815	glmM	815264	816616	283	0.8475	Ū	1	E	1	E
	RIIIIIVI						0			
Spy49_0816		816739	817380	318	0	NE -		NE	0.00025	NE
Spy49_0817	hemN	817377	818573	450	1	E	1	E	1	E
Spy49_0818	-	818583	819335	213	0.00025	NE	0	NE	0.00025	NE
Spy49_0819	-	819335	820099	398	0	NE	0	NE	0.00025	NE
Spy49_0820	-	820096	820731	250	0.00025	NE	1	E	1	E
Spy49_0821	-	821210	825316	254	0	NE	0	NE	0.00025	NE
Spy49_0822	_	825316	826185	211	0.00025	NE	0	NE	0.00025	NE
–							0			
Spy49_0823	-	826182	826523	1368	0.00025	NE		NE	0	NE
Spy49_0825	-	826513	827175	289	0.00025	NE	0	NE	0.00025	NE
Spy49_0826	-	827952	828122	113	0	NE	0	NE	0	NE
Spy49_0827	lepA-2	828223	830055	220	0	NE	0	NE	0.00025	NE
Spy49_0828	sclB	830338	831435	56	0	NE	0	NE	0	NE
Spy49_0829	csrA	831620	832057	610	0.00025	NE	0	NE	0	NE
Spy49_0830	-	832187	833206	365	0.05675	U	0	NE	0	NE
Spy49_0831	_	833413	833838	145	0.03073	NE	0	NE	0.00025	NE
–	-									
Spy49_0832	-	833865	834356	339	0	NE	0	NE	0.00025	NE
Spy49_0833	-	834449	835183	141	0	NE	0	NE	0	NE
Spy49_0834	-	835180	836019	163	0	NE	0	NE	0.81775	U
Spy49_0835	-	836144	837793	244	0.00025	NE	0	NE	0.00025	NE
Spy49_0836	-	837797	838585	279	0	NE	0	NE	0	NE
Spy49_0837	-	838579	839625	549	0	NE	0	NE	0.00025	NE
Spy49_0839		839741	841138	262	0.00025	NE	0	NE	0.00025	NE
–	· · · · · · · · · · · · · · · · · · ·				0.00023		0		0.00023	
Spy49_0840	uvrC	841239	843035	348		NE		NE		NE
Spy49_0841	-	843221	843823	465	0	NE	0	NE	0	NE
Spy49_0842	-	843948	845357	598	0.00025	NE	0	NE	0	NE
Spy49_0843	trmE	845425	846801	200	0	NE	0	NE	0	NE
Spy49_0844	rplJ	847136	847636	469	0	NE	0	NE	0	NE
Spy49_0845c	-	847701	847799	458	0.00025	NE	1	E	0.99575	E
Spy49_0846	rplL	847874	848065	166	0.00025	NE	0	NE	0.00025	NE
Spy49 0847	dacA1	848292	849605	32	-1	S	-1	S	-1	S
Spy49_0848	-	849658	850620	63	0.9105	U	0.0035	NE	0.7455	U
	f-101									
Spy49_0849	folC1	850952	852229	437	0.00025	NE	0	NE	0.00025	NE
Spy49_0850c	folE	852264	852848	320	0	NE	0	NE	0	NE
Spy49_0851	folP	852857	853657	425	0.00025	NE	1	E	1	E
Spy49_0852	folQ	853664	854023	194	0	NE	0	NE	0	NE
Spy49_0853	folK	854020	854520	266	0.00025	NE	0	NE	0.43975	U
Spy49_0854	murB	854670	855557	119	0.00025	NE	0	NE	0.00025	NE
Spy49_0855	potA	855603	856757	166	0.00023	NE	0	NE	0.00023	NE
–	•				1	E	1	E	0.99975	E
Spy49_0856	potB	856741	857535	295						
Spy49_0857	potC	857532	858308	384	0.00025	NE	0	NE	0	NE
Spy49_0858	potD	858301	859374	264	0	NE	0	NE	0	NE
Spy49_0859	-	859429	860094	258	0	NE	0	NE	0	NE
Spy49_0860	-	860075	861616	357	0	NE	0	NE	0	NE
Spy49_0861c	malP	861777	863108	221	0.00025	NE	0	NE	0	NE
Spy49_0862c	-	863140	864306	513	0	NE	0	NE	0.00025	NE
Spy49_0863	_	864388	865437	443	0.00025	NE	0	NE	0.00025	NE
–	anh A									
Spy49_0864	aphA	865673	866404	388	0.00025	NE	0	NE	0	NE

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Spy49_0865c	-	866582	868114	349	0	NE	0	NE	0	NE
Spy49_0866	-	868277	868891	243	0	NE	0	NE	0	NE
Spy49_0867	-	869071	870180	510	0	NE	0	NE	0.00025	NE
Spy49_0868	radC	870247	870927	204	0.00025	NE	0	NE	0.00025	NE
Spy49_0869	-	870929	871624	369	0	NE	0	NE	0	NE
Spy49_0870	_	871634	872278	226	0	NE	0	NE	0.00025	NE
–			872877			NE	0			NE
Spy49_0871c	-	872530		231	0			NE	0.00025	
Spy49_0872c	-	872867	873994	214	0	NE	0	NE	0	NE
Spy49_0873c	prs	873991	874971	115	0.00025	NE	0	NE	0	NE
Spy49_0874c	-	875111	875689	375	1	E	1	E	1	E
Spy49_0875c	-	875777	876448	326	0.00025	NE	0	NE	0.00025	NE
Spy49_0876c	ppnK	876423	877259	192	0	NE	0	NE	0.912	U
Spy49_0877	rluD	877256	878161	223	0.00025	NE	0	NE	0.00025	NE
–	eutD	878165	879160	278	1	E	1	E	1	E
Spy49_0878										
Spy49_0879	-	879286	880041	301	0	NE	0	NE	0	NE
Spy49_0880	-	880235	880924	331	0	NE	0	NE	0	NE
Spy49_0881	proV	881350	882078	251	0	NE	0	NE	0.0005	NE
Spy49_0882c	proX	882071	883597	229	0	NE	0	NE	0	NE
Spy49_0883	-	883875	884858	242	0.00025	NE	0	NE	0.00025	NE
Spy49_0884	-	884895	885152	508	0	NE	0	NE	0.00025	NE
Spy49_0885	xpt	885163	885744	327	0	NE	0	NE	0	NE
–	-									
Spy49_0886c	-	885744	887027	85	0	NE	0	NE	0	NE
Spy49_0887	-	887091	888029	193	0.00025	NE	0	NE	0	NE
Spy49_0888	-	888082	888267	427	0	NE	0	NE	0	NE
Spy49_0891c	tdk	888405	888974	312	0	NE	0	NE	0	NE
Spy49_0892c	prfA	889009	890088	61	0	NE	0	NE	0	NE
Spy49_0893	hemK	890088	890927	189	0	NE	0	NE	0	NE
Spy49_0894	-	890911	891501	359	1	E	1	Е	1	Е
–	_	891519	891971	279	0.00025	NE	0	NE	0.06075	Ū
Spy49_0895										
Spy49_0896	glyA	891961	893217	196	0.8395	U	1	E	1	E
Spy49_0897	-	893224	894201	150	0.00025	NE	0	NE	0	NE
Spy49_0898	-	894202	894801	418	0	NE	0	NE	0	NE
Spy49_0899	-	894811	896535	325	0	NE	0	NE	0.0595	U
Spy49_0900	-	896532	898247	199	0.00025	NE	0	NE	0.00025	NE
Spy49_0901	nox1	898500	899870	574	0	NE	0	NE	0.064	U
Spy49_0902	ldh	900029	901012	571	0.00025	NE	0	NE	0.00025	NE
–							0			
Spy49_0903	gyrA	901203	903689	456	0	NE		NE	0	NE
Spy49_0904c	-	903709	904458	327	0.00025	NE	0.00425	NE	1	Е
Spy49_0905	-	904538	904954	828	1	E	1	E	1	E
Spy49_0906	-	905603	906007	249	0.00025	NE	0.80075	U	0.999	E
Spy49_0907	-	906057	906968	138	0.00025	NE	0	NE	0.99625	Ε
Spy49_0908	hlyIII	907220	907735	134	0	NE	0	NE	0	NE
Spy49_0909c	-	907732	908172	303	0.00025	NE	0	NE	0.00025	NE
–		908391	909239	171	0.99975	E	1	E	1	E
Spy49_0910c	rbgA									
Spy49_0911c	rnhB	909229	910020	146	0.00875	NE	0	NE	0	NE
Spy49_0912	smf	910085	910921	282	0.916	U	1	E	1	E
Spy49_0913	topA	911028	913157	263	0	NE	0	NE	0	NE
Spy49_0914	-	913233	913715	278	0	NE	0	NE	0	NE
Spy49_0915	-	913722	913844	709	1	E	1	E	1	Е
Spy49 0916c	-	914130	914696	160	0	NE	0	NE	0	NE
Spy49_0917c	_	914711	915703	40	-1	S	-1	S	-1	S
–										
Spy49_0918	-	915808	916473	188	0	NE	0	NE	0	NE
Spy49_0919	-	916466	917182	330	0.00025	NE	0	NE	0.00025	NE
Spy49_0920	gid	917333	918679	221	0.998	E	1	E	1	E
Spy49_0921	-	918856	920238	238	0	NE	0	NE	0	NE
Spy49_0922	-	920281	920595	448	0	NE	0	NE	0.9835	U
Spy49_0923	-	920595	920945	460	0.00025	NE	0	NE	0.00025	NE
Spy49_0924	-	920955	922085	104	0	NE	0	NE	0.00125	NE
–	citG	922286	923170	116	0.00025	NE	0	NE	0	NE
Spy49_0925										
Spy49_0926	-	923163	923858	376	0	NE	0	NE	0.7035	U
Spy49_0927c	-	924016	925422	294	0	NE	0	NE	0	NE
Spy49_0928c	-	925799	926122	231	0.00025	NE	0	NE	0	NE
Spy49_0929c	-	926611	927732	468	0	NE	0	NE	0	NE
Spy49_0930	citD	927920	928228	107	0	NE	0	NE	0	NE
Spy49_0933	citE	928216	929103	373	0.00175	NE	0	NE	0	NE
–	citF	929106	930638	102	0.00025	NE	0	NE	0	NE
Spy49_0934										
Spy49_0936	citX	930535	931209	295	0.115	U	0	NE	0	NE
Spy49_0937	oadA	931224	932618	510	0	NE	0	NE	0	NE

Spy49_0938	citC	932729	933781	224	0.00025	NE	0	NE	0	NE
Spy49_0939	-	933968	934351	464	0.00025	NE	0	NE	0	NE
Spy49_0940c	xerS	935045	936115	350	0	NE	0	NE	0	NE
Spy49_0942c	-	936585	937283	127	0	NE	0	NE	0	NE
Spy49 0943c	ffh	937400	938962	356	0.0035	NE	0.00025	NE	0.9995	E
Spy49 0944	-	938977	939318	232	0.00025	NE	0	NE	0	NE
	-			520		E	1	E	1	E
Spy49_0945c		939407	940105		1					
Spy49_0946c	-	940188	941477	113	0.99725	E	0.02475	NE	0.00025	NE
Spy49_0947c	guaA	941789	943351	232	0.00025	NE	0	NE	0.00025	NE
Spy49_0948c	murM2	943393	944604	429	0	NE	0	NE	0	NE
Spy49_0949	-	944959	946524	520	0.2225	U	0	NE	0.99675	E
Spy49_0951c	-	946637	947194	403	0	NE	0	NE	0.00025	NE
Spy49 0952c	pdxK	947172	948038	521	0	NE	0	NE	0	NE
Spy49_0953c	-	948128	949396	185	0	NE	0	NE	0	NE
Spy49_0954c	-	949867	950223	288	0	NE	0	NE	0	NE
Spy49_0955	-	950545	952122	422	0	NE	0	NE	0.00025	NE
Spy49_0957c	fhs1	952207	953877	118	0	NE	0	NE	0	NE
Spy49_0958c	lplA	954005	955024	525	0.00025	NE	1	E	0.998	E
Spy49 0959c	-	955071	955952	556	0.97375	U	0.00975	NE	1	E
Spy49 0960c	_	955945	956757	339	0	NE	0	NE	0.00025	NE
Spy49_0961c	_	956750	957082	293	0.00025	NE	0	NE	0.00025	NE
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Spy49_0962c	-	957124	958122	270	0.00025	NE	0	NE	0	NE
Spy49_0963c	-	958119	959318	110	0	NE	0	NE	0	NE
Spy49_0964c	-	959315	960151	332	0.00025	NE	0	NE	0	NE
Spy49_0965c	dpfB	960347	961039	399	0.00025	NE	0	NE	0	NE
Spy49_0966c	dfp	961032	961577	278	0	NE	0	NE	0	NE
Spy49_0967	-	961636	962205	230	0.00025	NE	1	Е	0.99975	E
Spy49 0968	pgmA	962381	964099	181	0.99975	E	1	Е	1	E
	-	964312	965268	189	0.00025	NE	0	NE	1	E
Spy49_0969										
Spy49_0970	-	965270	966334	572	0.998	E	1	E	1	E
Spy49_0971c	-	966327	967859	318	0	NE	0	NE	0	NE
Spy49_0972c	-	967998	969050	354	0	NE	0	NE	0	NE
Spy49_0973c	cdd	969144	969533	510	0	NE	0	NE	0	NE
Spy49 0974c	-	970186	970779	350	0.03775	NE	0	NE	0	NE
Spy49_0975c	coaA	971047	971967	129	0	NE	0	NE	0	NE
Spy49_0976c	rpsT	972036	972269	197	0	NE	0	NE	0	NE
	•					U			1	
Spy49_0977	ciaH	972394	973704	306	0.8445		1	E		E
Spy49_0978	ciaR	973697	974371	77	0.00275	NE	0	NE	0.9535	U
Spy49_0979c	pepN	974718	977255	436	0.00025	NE	0.00075	NE	0.9995	E
Spy49_0980c	phoU	977460	978113	224	0.00025	NE	1	E	1	E
Spy49_0981c	pstB	978182	978940	845	0.00025	NE	0	NE	0.00025	NE
Spy49_0982c	pstB2	978953	979756	217	0.00025	NE	0	NE	0.0005	NE
Spy49_0983c	pstA	979772	980659	252	0.99475	Е	0	NE	0.00025	NE
Spy49_0984c	•	980649	981584	267	0.00025	NE	0	NE	0.99875	E
–	pstC									
Spy49_0985c	pstS	981595	982461	295	0.00025	NE -	0	NE	0.88725	U
Spy49_0986	-	982600	983910	311	0.99925	E	0.00025	NE	0.98675	U
Spy49_0987c	-	983913	984701	288	0.36625	U	0	NE	0.63625	U
Spy49_0988c	-	984691	984969	436	0.99975	E	1	E	1	E
Spy49_0989c	spxA	984971	985375	262	0	NE	0.00025	NE	0.00025	NE
Spy49_0990c	-	985418	986350	92	0.00025	NE	0	NE	0	NE
Spy49_0991c	truB	986340	987263	134	0	NE	0	NE	0.00025	NE
Spy49_0991c	-	987379	988719	310	0.992	U	1	E		E
	-								1	
Spy49_0993c	-	988816	989772	307	0	NE	0	NE	0	NE
Spy49_0994c	-	989783	990379	446	0.00025	NE	0	NE	0.00025	NE
Spy49_0995c	-	990471	993107	318	0	NE	0	NE	0.00025	NE
Spy49_0996c	-	993122	993823	198	0	NE	0	NE	0	NE
Spy49_0997c	-	993941	994483	878	0	NE	0	NE	0.00025	NE
Spy49 0998c	_	994638	995267	233	0	NE	0	NE	0.00025	NE
	_	995430	995918	180	0	NE	0	NE	0.00025	NE
Spy49_0999	-									
Spy49_1000c	-	995929	996129	209	0.00025	NE	0	NE	0.00025	NE
Spy49_1001c	-	996170	996709	162	0	NE	0	NE	0	NE
Spy49_1002c	-	996722	996910	66	0	NE	0	NE	0	NE
Spy49_1003c	-	996921	997508	179	0.00025	NE	0	NE	0	NE
Spy49_1004c	-	997569	997817	62	0.16625	U	0.0005	NE	0.008	NE
Spy49_1005c	pcrA	998180	1000498	195	0.00025	NE	0	NE	0	NE
Spy49_1006c	-	1001027	1000430	82	0.00025	NE	0	NE	0	NE
	-	1001027	1002349	772	0.00025	NE	1	E	1	E
Spy49_1007c										
Spy49_1008	cfa	1004074	1004847	440	0	NE	0	NE	0.24275	U

5 40 4000		4005247	4000050		0.00025			NE	0	
Spy49_1009	-	1005217	1006053	411	0.00025	NE	0	NE	0	NE
Spy49_1010c	-	1006069	1006698	257	0.00025	NE	0	NE	0.00025	NE
Spy49_1011c	-	1006708	1007349	278	0.00025	NE	0	NE	0.00025	NE
Spy49_1012c	-	1007456	1007791	209	0	NE	0	NE	0	NE
Spy49_1013c	glmS	1007987	1009801	213	0.00025	NE	0	NE	0	NE
Spy49_1014c	sipC	1009977	1010534	111	0	NE	0	NE	0	NE
Spy49 1015c	pyk	1010752	1012254	604	1	E	1	Е	1	E
Spy49_1016c	pfk	1012317	1013330	185	0.00025	NE	0	NE	0.0015	NE
Spy49_1017c	dnaE	1012317	1016520	500	1	E	1	E	1	E
–	-			337		E		E		E
Spy49_1018c		1016705	1017076		0.99575		1		1	
Spy49_1019c	-	1017076	1017774	1036	1	E	1	E	1	E
Spy49_1020	-	1017784	1018569	123	0.00025	NE	0	NE	0.00025	NE
Spy49_1021	-	1018706	1019311	232	0.00025	NE	0.0345	NE	0.99975	Е
Spy49_1022	-	1020050	1020670	261	0.08325	U	0.00025	NE	1	E
Spy49_1023c	glgP	1020927	1023191	201	0.00025	NE	1	E	1	E
Spy49_1024	malQ	1023226	1024719	206	0.00025	NE	0	NE	0	NE
Spy49_1025c	malR	1024834	1025853	754	0.00025	NE	0	NE	0.00025	NE
Spy49 1026c	malE	1026097	1027344	497	0.00025	NE	0	NE	0.0005	NE
Spy49_1027c	malF	1027618	1028979	339	0.00025	NE	0.00075	NE	0.00375	NE
–	malG		1028373	415	0.00023	NE	0.00073	NE	0.00373	NE
Spy49_1028		1028979								
Spy49_1029	-	1029996	1030982	453	0.00025	NE	0	NE	0.00025	NE
Spy49_1030	-	1031207	1031431	278	0	NE	0	NE	0.00025	NE
Spy49_1819c	-	1031496	1032479	328	0	NE	0	NE	0	NE
Spy49_1033c	dltD	1032510	1033760	327	0	NE	0	NE	0	NE
Spy49_1034c	dltC	1033753	1033992	416	0.00025	NE	0	NE	0.00025	NE
Spy49_1035c	dltB	1034010	1035266	79	0.00025	NE	0	NE	0	NE
Spy49_1036c	dltA	1035263	1036801	418	0.00025	NE	0	NE	0.13625	U
Spy49 1037c	-	1036813	1036956	512	0.00025	NE	0	NE	0.888	U
Spy49_1038c	uvrB	1037219	1039310	47	-1	S	-1	S	-1	S
Spy49_1038c Spy49_1039c	glnP	1037213	1033210	663	0.00025	NE	0	NE	0.00025	NE
	•									
Spy49_1040	glnQ	1041577	1042317	724	0.00725	NE	0	NE	1	E
Spy49_1041	-	1042465	1042617	246	0.00025	NE	0	NE	0.99975	E
Spy49_1042c	-	1042614	1043993	50	-1	S	-1	S	-1	S
Spy49_1043c	-	1044171	1044620	459	0	NE	0	NE	0.003	NE
Spy49_1044c	-	1044617	1044952	149	0	NE	0	NE	0.00025	NE
Spy49_1045c	-	1044955	1045266	111	0.00025	NE	0	NE	0.00025	NE
Spy49_1046c	-	1045289	1047283	103	0	NE	0	NE	0	NE
Spy49 1047c	-	1047389	1048483	664	0	NE	0	NE	0.775	U
Spy49 1048c	_	1048492	1049892	364	0	NE	0	NE	0.00025	NE
Spy49_1049c	_	1050117	1050812	466	0.00025	NE	0	NE	0.00025	NE
–		1050117	1050812	231	0.00025	NE	0	NE	0.00025	NE
Spy49_1050	- ohaE									
Spy49_1051c	obgE	1051044	1052357	52	-1	S	-1	S	-1	S
Spy49_1053c	-	1052786	1053181	437	0.81525	U	1	E	1	E
Spy49_1054	-	1053321	1054199	131	0	NE	0	NE	0	NE
Spy49_1055	-	1054597	1055097	292	0.00025	NE	0	NE	0.00025	NE
Spy49_1056	-	1055100	1055906	166	0	NE	0	NE	0	NE
Spy49_1057	-	1057303	1058613	268	0.00025	NE	0	NE	0.00025	NE
Spy49_1059	-	1058770	1058985	436	0	NE	0	NE	0	NE
Spy49 1060	-	1059129	1059314	71	0	NE	0	NE	0.18975	U
Spy49_1062	rsuA	1059757	1060488	61	0	NE	0	NE	0.00025	NE
Spy49_1064c	-	1060603	1060968	243	0	NE	0	NE	0.32225	U
Spy49_1065	_	1061088	1062308	121	0	NE	0	NE	0	NE
–				406	0.0005	NE	0	NE	0.00025	NE
Spy49_1066c	-	1062720	1064165							
Spy49_1067	-	1064270	1064671	481	0.00025	NE	0	NE	0.00025	NE
Spy49_1070c	-	1064835	1065269	133	0	NE	0	NE	0	NE
Spy49_1071c	-	1065688	1067046	144	0	NE	0	NE	0	NE
Spy49_1072c	psr	1067128	1068579	452	0	NE	0	NE	0.00025	NE
Spy49_1073c	aroK	1068787	1069278	483	0	NE	0	NE	0	NE
Spy49_1074c	aroA1	1069271	1070554	163	0	NE	0	NE	0.00025	NE
Spy49_1075c	-	1070665	1071630	427	0	NE	0	NE	0.00025	NE
Spy49 1076c	map	1071632	1072492	321	0.01175	NE	0	NE	0	NE
Spy49_1077c	-	1072508	1073791	286	0.042	U	1	E	0.993	E
Spy49_1078c	_	1073800	1074342	427	0	NE	0	NE	0.51825	U
–	arah	1073600	1074342	180	0	NE	0	NE	0.51825	NE
Spy49_1079c	grab									
Spy49_1080c	murZ	1075506	1076765	179	0	NE	0	NE	0	NE
Spy49_1082c	metK	1076939	1078135	419	0	NE	0	NE	0	NE
Spy49_1083c	inlA	1078672	1081050	398	1	E	1	E	1	E
Spy49_1084c	birA	1081425	1082195	792	0.0275	NE	0	NE	0.00025	NE

C40, 400E		4002470	4002272	256	0.00035	NIE	4	-	4	-
Spy49_1085	-	1082170	1082373	256	0.00025	NE	1	E	1	E
Spy49_1086c	dnaX	1082469	1084139	67	0	NE	0	NE	0.00025	NE -
Spy49_1087c	-	1084139	1084636	556	1	E	1	E	1	E
Spy49_1088c		1084842	1085591	165	0	NE	0	NE	0	NE
Spy49_1089	udk	1085989	1086615	249	0	NE	0	NE	0	NE
Spy49_1090c	deaD2	1086713	1087798	208	0	NE	0	NE	0	NE
Spy49_1091	-	1087909	1089183	361	0	NE	0	NE	0	NE
Spy49_1092c	gapN	1089304	1090707	424	0	NE	0	NE	0	NE
Spy49_1093c	ptsl	1090892	1092625	467	1	E	1	E	1	E
Spy49_1094c	ptsH	1092630	1092893	577	0.63275	U	0.00725	NE	1	E
Spy49_1095c	nrdH	1093253	1093504	87	0.959	U	0.11725	U	0.94925	U
Spy49_1096	nrdE1	1093524	1095683	83	0	NE	0	NE	0	NE
Spy49_1097	nrdF1	1095664	1095981	719	0.0005	NE	0	NE	0.003	NE
Spy49_1098	nrdF	1096016	1096975	105	0	NE	0	NE	0	NE
Spy49_1099	_	1096950	1098263	319	0	NE	0	NE	0.00075	NE
Spy49_1100	_	1098401	1098694	437	0.00025	NE	0	NE	0.00025	NE
Spy49_1101	_	1099127	1099297	97	0	NE	0	NE	0.0715	U
Spy49_1101 Spy49_1103	_	1099337	1099558	56	-1	S	-1	S	-1	S
Spy49_1103 Spy49_1104		1099651	1100346	73	0	NE	0	NE	0	NE NE
	-	1100365	1100340	231	0	NE	0	NE	0	NE
Spy49_1105c	-									
Spy49_1106c	- -l-C	1101123	1101353	253	0	NE	0	NE	0	NE
Spy49_1107c	alaS	1101699	1104317	76	0.0235	NE -	0	NE -	0	NE
Spy49_1108c	prsA	1104704	1105759	872	1	E	1	E	1	E
Spy49_1109c	-	1105822	1106529	351	0	NE	0	NE	0	NE
Spy49_1110c	-	1106595	1107791	235	0.00025	NE	0	NE	0	NE
Spy49_1111c	рерВ	1108168	1109973	398	0.00025	NE	0	NE	0.00025	NE
Spy49_1112c	-	1109986	1110948	601	0.00025	NE	0	NE	0.00025	NE
Spy49_1113c	-	1111245	1111961	320	0	NE	0	NE	0.00025	NE
Spy49_1114c	nagB	1112080	1112784	238	0	NE	0	NE	0	NE
Spy49_1115c	queA	1112986	1114014	234	0	NE	0	NE	0	NE
Spy49_1116	-	1114021	1115241	342	0	NE	0	NE	0.00025	NE
Spy49_1117	-	1115355	1115945	406	0	NE	0	NE	0.00025	NE
Spy49_1119c	-	1115942	1116190	196	0	NE	0	NE	0.00025	NE
Spy49_1120c	_	1116175	1116402	82	0	NE	0	NE	0	NE
Spy49_1121c	sodM	1116524	1117168	75	0.57725	U	0	NE	0.96925	U
Spy49_1122c	holA	1117265	1118305	214	0	NE	0	NE	0	NE
Spy49_1123c	comEC	1117203	1120619	346	1	E	1	E	1	E
Spy49_1123c Spy49_1124c	comE	1120600	1121262	747	0	NE	0	NE	0.00025	NE
–					0					
Spy49_1126c	-	1121462	1122202	220		NE	0	NE	0.008	NE
Spy49_1127c	-	1122242	1123096	246	1	E	1	E	1	E
Spy49_1128	-	1123086	1123364	284	0.00025	NE	0	NE	0	NE
Spy49_1129	kup	1123388	1125388	92	0	NE	0	NE	0.00025	NE
Spy49_1130c	deaD1	1125516	1127135	666	0.00025	NE	0	NE	0	NE
Spy49_1132c	prfC	1127442	1128986	539	0	NE	0	NE	0	NE
Spy49_1133c	-	1129234	1129929	514	0	NE	0	NE	0.00025	NE
Spy49_1135c	murF	1130009	1131400	231	0	NE	0	NE	0.00025	NE
Spy49_1136c	ddl	1131591	1132637	463	1	E	1	E	1	E
Spy49_1137c	recR	1132738	1133334	348	1	E	1	E	1	E
Spy49_1138c	-	1133381	1133572	198	0.00725	NE	0	NE	0.99875	E
Spy49_1139c	fdhC	1134132	1134947	63	0	NE	0	NE	0.02225	NE
Spy49_1140c	-	1135034	1135576	271	0	NE	0	NE	0.00025	NE
Spy49_1141c	-	1135737	1136258	180	0.00025	NE	0	NE	0.00025	NE
Spy49_1142c	gpmA	1136365	1137060	173	0.00025	NE	0	NE	0.00025	NE
Spy49_1143c	pyrD	1137357	1138238	231	0.996	E	1	E	0.9925	E
Spy49_1144	-	1138293	1138466	293	0	NE	0	NE	0	NE
Spy49_1145c	cadA	1138233	1140400	57	-1	S	-1	S	-1	S
Spy49_1146c	CauA	1140732	1141007	620	0.00025	NE	0	NE	0.062	U
Spy49_1147c	-	1141106	1141693	91 105	0.00025	NE NE	1	E	0.84025	U
Spy49_1148c	-	1141671	1142513	195	0.00025	NE	0	NE	0.00025	NE
Spy49_1149c	-	1142506	1143357	280	0	NE	0	NE	0.0005	NE
Spy49_1150c	-	1143573	1144529	283	0	NE	0.00025	NE	0.9995	E
Spy49_1151c	recN	1144701	1146362	318	0	NE	0	NE	0	NE
Spy49_1152c	-	1146383	1146853	553	0.00025	NE	0	NE	0	NE
Spy49_1153c	-	1146840	1147667	156	0	NE	0	NE	0	NE
Spy49_1154c	fps	1147867	1148532	275	0	NE	0	NE	0	NE
Spy49_1155c	xseB	1148532	1148747	221	0	NE	0	NE	0	NE
Spy49_1156c	xseA	1148725	1150065	71	0	NE	0	NE	0	NE
Spy49_1157c	folD	1150218	1151072	446	0	NE	0	NE	0	NE

Spy49_1158c	-	1151280	1152974	284	0.00025	NE	0	NE	0.98475	U
Spy49_1159c	phr	1153152	1154561	564	0.00025	NE	0	NE	0	NE
Spy49_1160c	gtr	1154710	1155444	469	0.00025	NE	0	NE	0.00025	NE
–	-									
Spy49_1161c	-	1155444	1156130	244	0	NE	0	NE	0.00025	NE
Spy49_1162c	-	1156257	1156487	228	0.00025	NE	0	NE	0.00025	NE
Spy49_1163c	clpE	1156785	1159067	76	0.8645	U	0.006	NE	0.878	U
Spy49 1164	mutT	1159195	1159650	760	0.00025	NE	0	NE	0.00075	NE
• • =	-									
Spy49_1165		1159701	1160003	151	0	NE	0	NE	0	NE
Spy49_1166	ileS	1160268	1163024	100	0.00025	NE	0	NE	0.00025	NE
Spy49_1167c	divIVA	1163342	1164100	918	1	E	1	E	1	E
Spy49_1168c	_	1164110	1164901	252	0.00025	NE	0	NE	0.204	U
Spy49 1169c	_	1164901	1165155	263	0.00025	NE	0	NE	0	NE
• • =	-									
Spy49_1170c	-	1165160	1165828	84	0	NE	0	NE	0.0005	NE
Spy49_1171c	-	1165828	1166499	222	0.91975	U	0.00025	NE	1	E
Spy49_1172c	ftsZ	1166502	1167821	223	0	NE	0	NE	0	NE
Spy49_1173c	ftsA	1167845	1169209	439	1	Е	1	Е	1	Ε
–										
Spy49_1174c	ftsQ	1169420	1170568	454	1	E	1	E	1	Е
Spy49_1175c	murG	1170569	1171651	382	0.00025	NE	1	E	0.99975	E
Spy49_1176c	murD	1171651	1173009	360	1	E	1	E	1	E
Spy49_1177c	_	1173365	1173616	452	1	E	1	E	1	E
–	_	1173738	1175579	83	0	NE	0	NE	0	NE
Spy49_1178c	-									
Spy49_1179c	-	1175762	1176151	613	0	NE	0	NE	0	NE
Spy49_1180c	-	1176161	1177132	129	0	NE	0	NE	0.00025	NE
Spy49_1181c	-	1177137	1177340	323	0	NE	0	NE	0.00025	NE
Spy49_1182c	_	1177482	1178009	67	0	NE	0	NE	0	NE
–										
Spy49_1183c	-	1178237	1178863	175	0.00025	NE	0	NE	0	NE
Spy49_1184	-	1178945	1180024	208	0	NE	0	NE	0	NE
Spy49 1185c	-	1180028	1180648	359	0.00025	NE	0	NE	0	NE
Spy49_1186c	_	1181096	1182073	206	0	NE	0	NE	0	NE
–					0.00025	NE	0	NE	0.00025	NE
Spy49_1187c	-	1182487	1183524	325						
Spy49_1188c	coaD	1183511	1184002	345	0	NE	0	NE	0	NE
Spy49_1189c	-	1183992	1184531	163	1	E	1	E	1	E
Spy49_1190c	asnA	1184654	1185646	179	0	NE	0	NE	0	NE
Spy49_1191c	arcC	1185959	1186909	330	0	NE	0	NE	0.00025	NE
–										
Spy49_1192c	-	1186929	1188260	316	0	NE	0	NE	0.1035	U
Spy49_1193c	-	1188277	1189578	443	0	NE	0	NE	0	NE
Spy49_1194c	arcB	1189941	1190954	433	0	NE	0	NE	0	NE
Spy49_1195c	_	1190979	1191419	337	0.163	U	0	NE	0	NE
–	a = a A									
Spy49_1196c	arcA	1191519	1192754	146	0	NE	0	NE	0	NE
Spy49_1197c	-	1193028	1193708	411	0	NE	0	NE	0	NE
Spy49_1198c	argR	1193850	1194323	226	0.00025	NE	0	NE	0	NE
Spy49_1199	_	1194490	1195206	157	0	NE	0	NE	0	NE
–		1195220	1196299	238	0	NE	0	NE	0.00025	NE
Spy49_1200c	-									
Spy49_1201c	yesM	1196372	1198105	359	0	NE	0	NE	0.00025	NE
Spy49_1202c	yesN	1198102	1198842	577	0	NE	0	NE	0.00025	NE
Spy49_1203c	msrA1	1198930	1200036	246	0	NE	0	NE	0.00025	NE
Spy49_1204c		1200079	1200702	368	0.00025	NE	0	NE	0.0005	NE
	ccd A						-			
Spy49_1205c	ccdA	1200715	1201404	207	0.00025	NE	0	NE	0.00025	NE
Spy49_1206c	-	1202097	1202390	229	0.00025	NE	0	NE	0	NE
Spy49_1207c	-	1202401	1203426	97	0	NE	0	NE	0	NE
Spy49_1208c	-	1203423	1204097	341	0	NE	0	NE	0.00025	NE
Spy49_1209c	_	1204099	1204947	224	0	NE	0	NE	0.00025	NE
Spy49_1210c	-	1204952	1206847	282	0	NE	0	NE	0	NE
Spy49_1211c	-	1206847	1207575	631	0.12025	U	0	NE	0.721	U
Spy49_1212c	-	1207708	1210110	242	0.00025	NE	0	NE	0.00025	NE
Spy49_1213c	valS	1210270	1212918	800	0.00025	NE	0	NE	0.00025	NE
–										
Spy49_1215c	-	1212920	1213483	882	1	E	1	E	1	E
Spy49_1216c	-	1213480	1213659	187	0	NE	0	NE	0	NE
Spy49_1217c	-	1214086	1214481	59	-1	S	-1	S	-1	S
Spy49_1218c	_	1214499	1214753	131	0.9435	U	0	NE	0	NE
–	aroA2			84	0.00025	NE	0.00325	NE	0.36475	U
Spy49_1219c	aroA2	1215231	1215983							
Spy49_1220	aroB	1216039	1217112	250	0	NE	0	NE	0	NE
Spy49_1221	-	1217548	1217853	357	0	NE	0	NE	0.00025	NE
Spy49_1222c	-	1217855	1218193	101	0	NE	0	NE	0	NE
Spy49_1223c	_	1218246	1219001	112	0	NE	0	NE	0	NE
	araE1									
Spy49_1224c	aroE1	1219236	1220114	251	0	NE	0	NE	0.645	U
Spy49_1225c	-	1220252	1223668	292	0	NE	0	NE	0.00025	NE
Spy49_1226c	-	1223688	1225172	1138	0	NE	0	NE	0.03425	NE
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Spy49_1227c	-	1225172	1226896	494	0	NE	0	NE	0.00025	NE
Spy49_1228c	-	1226886	1227491	574	0	NE	0	NE	0	NE
Spy49_1229c	-	1227797	1229242	201	0	NE	0	NE	0.002	NE
Spy49_1230c	-	1229323	1230249	481	0	NE	0	NE	0.02875	NE
Spy49_1231c		1230259	1231209	308	0.536	U	0	NE	0.00025	NE
–	_									
Spy49_1233c	-	1231405	1232100	316	0	NE	0	NE	0	NE
Spy49_1234	-	1232893	1234335	231	0.00025	NE	0	NE	0	NE
Spy49_1235c	hyl	1234359	1236053	480	0	NE	0	NE	0	NE
Spy49_1236c	-	1236104	1237144	564	0	NE	0	NE	0.03875	U
Spy49_1237c	-	1237277	1238563	346	0.00025	NE	0	NE	0.00025	NE
Spy49_1238	-	1238578	1241283	428	0	NE	0	NE	0.15425	U
Spy49 1239	-	1241384	1242739	901	0	NE	0	NE	0.91675	U
• • =		1243405	1244760	451	0	NE	0	NE	0	NE
Spy49_1240c										
Spy49_1241c	recX	1244875	1245651	451	0.00025	NE	0	NE	0.7135	U
Spy49_1242	-	1245731	1246264	258	0	NE	0	NE	0.00025	NE
Spy49_1243	-	1246634	1246912	177	0.00025	NE	0	NE	0.06475	U
Spy49_1244	-	1246927	1247034	92	0	NE	0	NE	0	NE
Spy49_1245	-	1254000	1254548	35	-1	S	-1	S	-1	S
Spy49_1247c	comF	1254628	1255293	182	0	NE	0	NE	0.00025	NE
Spy49_1248c	-	1255265	1256590	221	0	NE	0	NE	0	NE
–				441	0	NE	0		0	
Spy49_1249c	-	1256646	1257278					NE		NE
Spy49_1250	cysM	1257406	1258347	210	0.00025	NE	0	NE	0	NE
Spy49_1251	-	1258365	1258742	313	0	NE	0	NE	0	NE
Spy49_1252c	-	1258742	1260142	125	0	NE	0	NE	0.993	E
Spy49_1253c	-	1260179	1260820	466	0	NE	0	NE	0.00225	NE
Spy49_1254c	-	1260813	1261817	213	0.00025	NE	1	E	0.99675	E
Spy49_1255c	-	1261814	1262506	334	0	NE	0	NE	0.00025	NE
Spy49_1256c	_	1262629	1264527	230	0	NE	0	NE	0	NE
–	-									
Spy49_1257c	pppL	1264524	1265264	632	0.5185	U	1	E	1	E
Spy49_1259c	sunL	1265302	1266624	246	0.9555	U	1	E	1	E
Spy49_1260c	fmt	1266614	1267549	440	0	NE	0	NE	0	NE
Spy49_1261c	priA	1267611	1269995	311	0.99975	E	1	E	1	E
Spy49_1262c	-	1270060	1270377	794	0.00025	NE	0.00025	NE	1	E
Spy49_1263c	gmk	1270393	1271028	105	0.0435	U	0.00275	NE	0.979	U
Spy49_1265c	-	1271138	1272745	211	1	E	1	E	0.998	E
Spy49_1266c		1272875	1273771	535	0	NE	0	NE	0	NE
–	- ataD									
Spy49_1267c	atoB	1273972	1275159	298	0	NE	0	NE	0	NE
Spy49_1268	atoD1	1275183	1275833	395	0	NE	0	NE	0.22225	U
Spy49_1269	atoA	1275835	1276494	216	0	NE	0	NE	0.00025	NE
Spy49_1270	-	1276527	1277306	219	0	NE	0	NE	0	NE
Spy49_1271	-	1277377	1278708	259	0	NE	0	NE	0.00025	NE
Spy49_1272	luxS	1278782	1279264	443	0	NE	0	NE	0.00025	NE
Spy49_1273	-	1279411	1280880	160	0	NE	0	NE	0	NE
–					0		0			
Spy49_1274c	-	1280894	1282048	489		NE		NE	0.00025	NE
Spy49_1275c	-	1282493	1282819	384	0	NE -	0	NE -	0	NE
Spy49_1276c	-	1282947	1283456	108	0.99925	E	1	E	0.95425	U
Spy49_1277c	recU	1283537	1284145	169	0	NE	0	NE	0.00025	NE
Spy49_1278	pbp1A	1284132	1286297	202	0.9875	U	0.2455	U	0.986	U
Spy49_1279	pepC	1286764	1288101	721	0.95475	U	1	E	1	Е
Spy49 1280c	nadE	1288286	1289134	445	0.00025	NE	0	NE	0	NE
Spy49_1281c	-	1289112	1290566	282	1	E	1	E	0.998	E
	- aapA	1209112		484	0.9995	E	1	E	1	E
Spy49_1282c	•		1292116							
Spy49_1283c	nox2	1292285	1293202	459	0.00025	NE	0	NE	0	NE
Spy49_1284c	-	1293266	1293490	305	0	NE	0	NE	0	NE
Spy49_1285c	-	1293594	1294337	74	0	NE	1	E	0.00125	NE
Spy49_1286c	-	1294337	1295140	247	0.00025	NE	0	NE	0.00025	NE
Spy49_1287c	-	1295335	1296678	267	0.00025	NE	0	NE	0.00025	NE
Spy49 1289c	mraY	1296836	1297846	447	0.9465	U	1	E	1	Е
Spy49_1290c	ftsI	1297848	1300103	336	0.98825	Ü	1	E	1	E
Spy49_1291c	ftsL	1300107	1300430	751	0.99975	E	1	E	1	E
Spy49_1292c	mraW	1300435	1301385	107	0.58975	U	1	E	0.93775	U
Spy49_1293c	-	1301736	1301942	316	0.00025	NE	0	NE	0.00025	NE
Spy49_1294c	proA	1301917	1303167	68	0	NE	0	NE	0	NE
Spy49_1295c	proB	1303160	1303981	416	0	NE	0	NE	0	NE
Spy49_1296c	-	1304045	1305673	273	0	NE	0	NE	0.00025	NE
Spy49_1297c	_	1305678	1306412	542	0	NE	0	NE	0.00025	NE
	_	1306446	1306712	244	0	NE	0	NE	0.00023	NE
Spy49_1298c	+1.+									
Spy49_1299c	tkt	1306904	1308889	88	0	NE	0	NE	0.00025	NE

										_
Spy49_1300c	tal	1309107	1309751	661	0.32125	U	0.00725	NE	1	E
Spy49_1301c	-	1309877	1311376	214	0.00025	NE	0	NE	0	NE
Spy49_1303c	npx	1311366	1312712	499	0	NE	0	NE	0	NE
Spy49 1304c	glpF1	1312821	1313522	448	0	NE	0	NE	0.00025	NE
Spy49_1305c	glpO	1313524	1315362	233	0	NE	0	NE	0.0045	NE
Spy49 1306c	glpK	1315378	1316904	612	0	NE	0	NE	0.00025	NE
	gipit				0.00125	NE	0	NE		NE
Spy49_1307c		1317264	1317656	508					0.00025	
Spy49_1308c	-	1317784	1318041	130	0.00025	NE	0	NE	0	NE
Spy49_1309c	glyS	1318195	1320234	85	0	NE	0	NE	0	NE
Spy49_1310c	glyQ	1320606	1321523	679	1	E	1	E	1	E
Spy49_1311c	-	1321896	1322402	305	1	E	1	E	1	E
Spy49_1312c	-	1322561	1323400	168	0.00025	NE	0	NE	0	NE
Spy49_1313c	nagA	1323522	1324670	279	0	NE	0	NE	0.00025	NE
–	павл	1324787		382	0	NE	0	NE	0.00025	NE
Spy49_1314c	-		1326418							
Spy49_1316c	-	1327469	1328311	543	0.00025	NE	0	NE	0.03675	NE
Spy49_1318c	-	1328604	1329161	280	0	NE	0	NE	0	NE
Spy49_1319	-	1329198	1330022	185	0.00025	NE	0	NE	0.00025	NE
Spy49_1320c	-	1330024	1330641	274	0	NE	0	NE	0	NE
Spy49_1321c	lacD1	1330838	1331815	205	0	NE	0	NE	0.00025	NE
Spy49_1322c	lacC1	1331897	1332160	325	0	NE	0	NE	0	NE
Spy49_1323c	-	1331965	1332315	87	0	NE	0	NE	0	NE
–						S				
Spy49_1324c	lacB	1332325	1332840	116	-1		-1	S	-1	S
Spy49_1325c	lacA	1332855	1333280	171	0	NE	0	NE	0	NE
Spy49_1326c	-	1333538	1334989	141	0	NE	0	NE	0.00025	NE
Spy49_1327c	-	1335015	1335320	483	0	NE	0	NE	0.00025	NE
Spy49_1328c	-	1335313	1335786	101	0	NE	0	NE	0	NE
Spy49_1329c	lacR1	1336023	1336793	157	0.00025	NE	0	NE	0	NE
Spy49_1330	copZ	1336997	1337200	256	0	NE	0	NE	0	NE
–				67	0	NE	0	NE	0	
Spy49_1331c	copA	1337214	1339445							NE
Spy49_1332c	copY	1339445	1339882	743	0	NE	0	NE	0	NE
Spy49_1334c	-	1340045	1341046	145	0	NE	0	NE	0	NE
Spy49_1335	rbfA	1341098	1341448	333	0	NE	0	NE	0	NE
Spy49_1336c	infB	1341654	1344515	116	0.9855	U	1	E	0.98375	U
Spy49_1337c	-	1344535	1344837	953	0.99975	E	1	E	1	Е
Spy49_1338c	_	1344830	1345126	100	0.00025	NE	0	NE	0.00025	NE
Spy49_1339c	nusA	1345142	1346299	98	0.9875	U	1	E	0.9865	U
–										
Spy49_1340c	-	1346474	1347010	385	1	E	1	E	1	E
Spy49_1341c	trmB	1347269	1347904	178	0.00025	NE	0	NE	0.00025	NE
Spy49_1342c	-	1347904	1348695	211	0	NE	0	NE	0	NE
Spy49_1343c	-	1348759	1349793	263	0.38775	U	1	E	1	E
Spy49_1344c	-	1349796	1350521	344	0	NE	0	NE	0.00025	NE
Spy49 1345c	hit	1350593	1351012	241	0	NE	0	NE	0.0005	NE
Spy49_1346	-	1351009	1351365	139	0	NE	0	NE	0	NE
–	-								0	
Spy49_1347	-	1351476	1352759	118	0	NE	0	NE		NE
Spy49_1348c	-	1352768	1353292	427	0	NE	0	NE	0	NE
Spy49_1349c	-	1353267	1353728	174	0	NE	0	NE	0	NE
Spy49_1350c	-	1353882	1355342	153	0.00025	NE	1	E	0.04125	U
Spy49_1351c	-	1355607	1356002	486	0.00025	NE	0	NE	0	NE
Spy49 1352	-	1356019	1356420	131	0	NE	0	NE	0	NE
Spy49_1353	manL	1356772	1357764	133	0.00025	NE	0	NE	0	NE
Spy49_1353	manM	1357853	1358662	330	0.00023	NE	0	NE	0.00025	NE
Spy49_1355	manN	1358679	1359590	269	0	NE	0	NE	0	NE
Spy49_1356	-	1359704	1360063	303	0.00025	NE	0	NE	0	NE
Spy49_1357	serS	1360454	1361731	119	0.00025	NE	0	NE	0	NE
Spy49_1358	accA	1361964	1362734	425	0.99975	E	1	E	1	E
Spy49_1359c	accD	1362731	1363597	256	0.66025	U	1	E	0.97275	U
Spy49_1360c	accC	1363606	1364970	288	1	E	1	Е	1	E
Spy49_1361c	fabZ	1365002	1365424	454	1	E	1	E	1	E
–									0.97425	U
Spy49_1362c	accB	1365421	1365921	140	0.98325	U	0.9985	E		
Spy49_1363c	fabF	1365923	1367155	166	0.6345	U	0.99975	E	0.9875	U
Spy49_1364c	fabG	1367170	1367904	410	1	E	1	E	1	E
Spy49_1365c	fabD	1367894	1368832	244	0.95475	U	1	E	1	E
Spy49_1366c	fabK	1368857	1369828	312	1	E	1	E	0.9965	E
Spy49_1367c	acpP	1370029	1370253	323	0.952	U	1	Е	1	Ε
Spy49_1368c	fabH	1370314	1371288	74	0.724	U	1	E	0.96375	Ū
–	Tabii								0.90373	
Spy49_1369c	- mhaD	1371289	1371723	324	0.73025	U	1	E		E
Spy49_1370c	phaB	1371797	1372588	144	0	NE	0	NE -	0	NE _
Spy49_1371c	dnaJ	1372809	1373945	263	0.99975	E	1	Е	1	Е

Spy40 1272c		1274000	127/217	378	0.00475	_	1	Е	1	E
Spy49_1372c	- dnak	1374008 1374226	1374217	378 69	0.99475	E	1 0	NE NE	1 0.00075	
Spy49_1373	dnaK		1376052		0.60925	U				NE
Spy49_1374c	grpE	1376233	1376805	608	1	E	1	E	1	E
Spy49_1375c	hrcA	1376808	1377851	190	0.92525	U	1	E	0.99075	E
Spy49_1376c	-	1377978	1378547	347	0.00025	NE	0	NE	0.00025	NE
Spy49_1377c	-	1378544	1379287	189	0	NE	0	NE	0	NE
Spy49_1378c	-	1379277	1379984	247	0	NE	0	NE	0	NE
Spy49_1379c	-	1380376	1380615	235	0	NE	0	NE	0	NE
Spy49_1380c	-	1380834	1381049	79	0	NE	0	NE	0	NE
Spy49_1381c	gatB	1381046	1382485	71	0	NE	0	NE	0	NE
Spy49_1382c	gatA	1382485	1383951	479	1	E	1	E	1	E
Spy49_1383c	gatC	1383951	1384253	488	1	E	1	E	1	E
Spy49_1384c	-	1384485	1384733	100	0.96525	U	1	E	0.955	U
Spy49_1385c	- - and V	1385248	1385802	82	0	NE	0	NE	0	NE
Spy49_1386c	codY -	1385949	1386731	184 260	0.00025	NE E	0	NE E	1	NE E
Spy49_1387c	-	1386949 1388395	1388130 1388847	393	1 0	NE NE	1 0	NE NE	0	NE NE
Spy49_1388c	-				0		0		0	
Spy49_1389	asnB	1388970 1390430	1390358 1391395	150 462	0	NE NE	0	NE NE	0.00025	NE NE
Spy49_1390c	d5IID -	1391744	1391393	321	0	NE NE	0	NE NE	0.00025	NE
Spy49_1391	-	1392461	1393363	234	0	NE	0	NE	0.00023	NE
Spy49_1392c Spy49_1393c	recG	1393655	1395670	300	0.00025	NE	0	NE	0.00025	NE
–	reco	1396045	1397499	671	0.00023	NE	0	NE	0.9995	E
Spy49_1394c	-	1397436	1397499	484	0	NE NE	0	NE NE	0.9995	NE NE
Spy49_1395c Spy49_1396c	-	1398113	1398706	226	0.00025	NE	0	NE	0.00025	NE
Spy49_1397c	cycC	1398703	1400373	197	0.00023	NE	0	NE	0.00023	NE
Spy49_1398c	cycD	1400366	1400373	556	0.00025	NE	0	NE	0	NE
Spy49_1400c	fhuC2	1402126	1402962	587	0.00025	NE	0	NE	0	NE
Spy49_1401c	fhuB2	1402959	1403981	278	0.00025	NE	0	NE	0	NE
Spy49_1402c	fhuD2	1403983	1405728	340	0	NE	0	NE	0.00125	NE
Spy49_1403c	-	1405925	1409752	581	0	NE	0	NE	0.00025	NE
Spy49_1405c	isp2	1410242	1411753	1275	0.00025	NE	0	NE	0.00025	NE
Spy49_1407c	alr	1411840	1412940	503	0.00025	NE	0	NE	0	NE
Spy49_1408c	acpS	1412937	1413293	366	1	E	1	Е	1	E
Spy49_1409c	secA	1413409	1415928	118	0.9995	E	1	E	0.9975	E
Spy49_1410c	pmi	1417389	1418342	839	1	E	1	E	1	E
Spy49_1412c	scrK	1418389	1419393	317	0	NE	0	NE	0	NE
Spy49_1413c	endoS	1419562	1422093	334	0	NE	0	NE	0	NE
Spy49_1414c	scrA	1422324	1424207	843	0	NE	0	NE	0	NE
Spy49_1415c	scrB	1424449	1425888	627	0	NE	0	NE	0	NE
Spy49_1416	scrR	1425893	1426858	479	0	NE	0	NE	0.12925	U
Spy49_1417	nusB	1426999	1427451	321	0.00025	NE	0	NE	0.00025	NE
Spy49_1418c	-	1427444	1427833	150	0	NE	0	NE	0	NE
Spy49_1419c	efp	1427879	1428436	129	0.00025	NE	0	NE	0.0005	NE
Spy49_1420c	comEB	1428532	1428993	185 153	0	NE NE	0	NE NE	0 0.00025	NE
Spy49_1421c Spy49_1422c	pepP uvrA	1429028 1430216	1430101 1433074	357	0	NE NE	0	NE NE	0.00025	NE NE
Spy49_1422c Spy49_1423c	UVIA	1433247	1433074	952	0	NE	0	NE	0	NE
Spy49_1424		1434323	1434979	314	0.212	U	0.00025	NE	0.99825	E
Spy49_1425	rpsR	1435112	1435351	218	0	NE	0	NE	0	NE
Spy49_1426c	ssb2	1435516	1436007	79	0.87025	U	0.9515	U	0.02275	NE
Spy49_1427c	rpsF	1436029	1436319	163	0.00175	NE	0.9875	Ü	0.999	E
Spy49 1428c	-	1436492	1436785	96	0.97675	U	0	NE	0.971	U
Spy49_1429c	mutY	1436953	1438107	97	0	NE	0	NE	0.00025	NE
Spy49_1430	-	1438284	1438871	384	0	NE	0	NE	0	NE
Spy49_1431	trx2	1438923	1439237	195	0.00025	NE	0	NE	0.00025	NE
Spy49_1432c	-	1439318	1439713	104	0	NE	0	NE	0.00025	NE
Spy49_1433c	mutS2	1439822	1442161	131	0	NE	0	NE	0	NE
Spy49_1434c	-	1442310	1442855	779	0.00025	NE	0	NE	0	NE
Spy49_1435c	-	1442858	1443166	181	0.00025	NE	0	NE	0	NE
Spy49_1436c	-	1443323	1444225	102	0	NE	0	NE	0	NE
Spy49_1437	spi	1444236	1444829	300	0.9885	U	1	E	1	E
Spy49_1438	recD	1444887	1447340	197	0.009	NE	1	Е	0.99975	E
Spy49_1439	-	1447431	1447913	817	0	NE	0	NE	0.0005	NE
Spy49_1440	dinP	1448006	1449100	160	0	NE	0	NE	0.00025	NE
Spy49_1441c	pfl	1449309	1451636	364	0.06525	U	0	NE	0.0685	U
Spy49_1442	- cnnA	1451724	1452113	775 120	0.00025	NE	0	NE	0.06875	U
Spy49_1443c	сррА	1452098	1452850	129	0	NE	0	NE	0	NE

Spy49_1444c	_	1453112	1454044	250	0	NE	0	NE	0	NE
Spy49_1445	glpF2	1454380	1455327	310	0	NE	0	NE	0	NE
Spy49_1447c	norA	1455730	1456926	315	0	NE	0	NE	0.963	U
Spy49_1449c	-	1457032	1457751	398	0.00025	NE	0	NE	0.505	NE
Spy49_1450	рерХР	1457773	1460055	239	0.00025	NE	0	NE	0	NE
Spy49_1451	-	1460135	1460356	760	0.00025	NE	0	NE	0.00025	NE
Spy49_1452c	_	1460526	1460900	73	0.00025	NE	0	NE	0	NE
Spy49_1453	_	1461245	1461424	124	0	NE	0	NE	0	NE
Spy49_1454c	spd3	1461662	1462462	59	0.00925	NE	0	NE	0	NE
Spy49_1455	-	1462842	1463168	266	0	NE	0	NE	0	NE
Spy49_1456	-	1463218	1464084	108	0	NE	0	NE	0	NE
Spy49_1457c	-	1464072	1464596	288	0	NE	0	NE	0	NE
Spy49_1458c	_	1464736	1465944	174	0	NE	0	NE	0	NE
Spy49 1459c	_	1466060	1466287	402	0	NE	0	NE	0	NE
Spy49_1460c	-	1466284	1466559	75	0	NE	0	NE	0	NE
Spy49_1461c	-	1466569	1467186	91	0	NE	0	NE	0	NE
Spy49_1462c	-	1467189	1467350	205	0	NE	0	NE	0	NE
Spy49 1463c	-	1467364	1469274	53	-1	S	-1	S	-1	S
Spy49_1464c	-	1469290	1470294	636	0.00025	NE	0	NE	0.00025	NE
Spy49_1465c	-	1470291	1472342	334	0.00025	NE	0	NE	0.8635	U
Spy49_1466c	-	1472339	1473118	683	0.00075	NE	0	NE	0.90375	U
Spy49_1467c	-	1473151	1476786	259	0.00025	NE	0	NE	0.06925	U
Spy49_1468c	-	1476801	1477130	1211	0	NE	0	NE	0.00225	NE
Spy49_1470c	-	1477172	1477531	109	0	NE	0	NE	0.0005	NE
Spy49_1471c	-	1477584	1478237	119	0.00025	NE	0	NE	0.00025	NE
Spy49_1472c	-	1478247	1478636	217	0	NE	0	NE	0.00025	NE
Spy49_1474c	-	1478633	1478989	129	0	NE	0	NE	0.00025	NE
Spy49_1475c	-	1478979	1479287	118	0	NE	0	NE	0.00025	NE
Spy49_1476c	-	1479284	1479637	102	0	NE	0	NE	0	NE
Spy49_1477c	-	1479651	1479893	117	0.00025	NE	0	NE	0	NE
Spy49_1478c	-	1479903	1480985	80	0	NE	0	NE	0.007	NE
Spy49_1479c	-	1480988	1481368	360	0	NE	0	NE	0	NE
Spy49_1480c	-	1481378	1481911	126	0.00025	NE	0	NE	0.00025	NE
Spy49_1481c	-	1482055	1482321	177	0	NE	0	NE	0	NE
Spy49_1482c	-	1482324	1482638	88	0	NE	0	NE	0	NE
Spy49_1483c	-	1482708	1482893	104	0	NE	0	NE	0	NE
Spy49_1484c	-	1482897	1484459	61	0	NE	0	NE	0	NE
Spy49_1485c	-	1484440	1485942	520	0	NE	0	NE	0	NE
Spy49_1486c	-	1485954	1487243	500	0	NE	0	NE	0	NE
Spy49_1487c	-	1487221	1487703	429	0	NE	0	NE	0	NE
Spy49_1488c	-	1488535	1488975	160	0.00025	NE	0	NE	0	NE
Spy49_1489c	-	1489415	1489936	146	0	NE	0	NE	0	NE
Spy49_1491c	-	1489933	1490226	173	0	NE	0	NE	0.00025	NE
Spy49_1492c	-	1490223	1490408	97	0	NE	0	NE	0.0005	NE
Spy49_1493c	-	1490506	1490991	61	0.03475	NE	0	NE	0	NE
Spy49_1494c	-	1491276	1491680	161	0	NE	0	NE	0.952	U
Spy49_1496c	-	1491664	1491954	134	0	NE	0	NE	0	NE
Spy49_1497c	-	1492193	1492549	96	0.52275	U	0	NE	0.0015	NE
Spy49_1498c	-	1492625	1492987	118	0	NE	0	NE	0.00975	NE
Spy49_1499c	-	1493196	1493621	120	0	NE	0	NE	0.00025	NE
Spy49_1500c	-	1493614	1494288	141	0	NE	0	NE	0.09725	U
Spy49_1501c	-	1494289	1494435	224	0	NE S	0	NE c	0.00025	NE c
Spy49_1502c	-	1494793	1495047	48	-1		-1	S	-1	S
Spy49_1504c	-	1495034 1495522	1495381	84 115	0	NE	0	NE	0.00025	NE
Spy49_1505c	-		1497093	115	0 00035	NE NE	0 0	NE	0.10075	U
Spy49_1506c	-	1497209	1497652	523 147	0.00025 0	NE	0	NE NE	0.02375	NE NE
Spy49_1507c	_	1498078 1498523	1498350 1498702	147 90	0.00025	NE NE	0	NE NE	0.00025	NE NE
Spy49_1509c Spy49_1510c	-	1498523	1498702 1498967	90 59	0.00025	U	1	NE E	0.0005 0.97825	NE U
Spy49_1510c Spy49_1511c	-	1498833	1498967	59 44	0.9765 -1	S	-1	S	0.97825 -1	S
	_	1499249	1499608	119	0.00025	NE	0	S NE	0	S NE
Spy49_1512c Spy49_1513c	_	1500142	1500483	85	0.00025	NE NE	0	NE NE	0	NE NE
Spy49_1514c	_	1500142	1500465	113	0.00025	NE	0	NE	0.00025	NE
Spy49_1514c Spy49_1516c	_	1500755	1500904	49	-1	S	-1	S	-1	S
Spy49_1516c Spy49_1517c	_	1500936	1501885	242	0	NE	0	S NE	0.00025	S NE
Spy49_1518c	_	1502073	1502255	62	0.00025	NE	0	NE	0.00025	NE
Spy49_1518C Spy49_1520c	_	1502573	1503293	60	-1	S	-1	S	-1	S
Spy49_1521c	_	15033460	1503233	253	0.00025	NE	0	NE NE	0	NE NE
JP7-13_1321C		1303400	1303/32	233	0.00023	112	J	112	J	112

Spy49_1522	-	1504006	1504473	90	0.99225	U	0	NE	0.99525	E
Spy49_1525	-	1504589	1505368	155	0.00025	NE	0	NE	0	NE
–		1505502		259	0.00025	NE	0	NE	0.00025	NE
Spy49_1526	-		1505660							
Spy49_1528c	-	1506024	1506782	52	-1	S	-1	S	-1	S
Spy49_1529	-	1506855	1507277	252	0.00025	NE	1	E	0.93025	U
Spy49_1530	-	1507398	1508534	140	0	NE	0	NE	0	NE
Spy49_1531		1508573	1508893	378	0	NE	0	NE	0	NE
–										
Spy49_1532	-	1508950	1509687	106	0	NE	0	NE	0	NE
Spy49_1533c	dnaQ	1509840	1510427	245	0	NE	0	NE	0.00025	NE
Spy49_1534c	-	1510476	1511057	195	0.00025	NE	0	NE	0.98775	U
Spy49_1535c	_	1511183	1511698	193	0.0005	NE	0	NE	0.836	U
–		1511601			0		0		0	
Spy49_1536c	-		1512305	171		NE		NE		NE
Spy49_1537c	-	1512526	1513695	234	0	NE	0	NE	0.00025	NE
Spy49_1538	deoC	1513790	1514461	389	0.00025	NE	0	NE	0.00025	NE
Spy49 1540c	nupC	1514491	1515693	223	0	NE	0	NE	0	NE
Spy49_1541c	udp	1515714	1516493	400	0	NE	0	NE	0.00025	NE
–	•									
Spy49_1542c	-	1516733	1517491	259	0.00025	NE	0	NE	0	NE
Spy49_1543	rpsN	1517700	1517969	252	0	NE	0	NE	0	NE
Spy49_1544	gcp	1518141	1519169	89	0	NE	0	NE	0	NE
Spy49_1545c	-	1519159	1519614	342	0.4205	U	1	Ε	0.98275	U
–										
Spy49_1546c	-	1519586	1520284	151	0	NE	0	NE	0	NE
Spy49_1547c	-	1520568	1520798	232	0.29175	U	1	E	1	E
Spy49 1548	-	1520800	1522482	76	0	NE	1	E	0.00025	NE
Spy49_1549	glnA	1522710	1524056	560	1	E	1	E	1	E
–	glnR	1524094	1524465	448	0.0005	NE	0	NE	0.00325	NE
Spy49_1550c	giiik									
Spy49_1551c	-	1524532	1525083	123	0	NE	0	NE	0	NE
Spy49_1552c	pgk	1525345	1526541	183	0	NE	0	NE	0.00025	NE
Spy49 1553c	IppC	1526726	1527580	398	0.9995	E	1	E	0.705	U
Spy49_1554c	-	1527820	1528701	284	0	NE	0	NE	0	NE
–										
Spy49_1555c	-	1528938	1530602	293	0	NE	0	NE	0	NE
Spy49_1556c	asp	1530602	1530967	554	0.84	U	1	E	1	E
Spy49_1557c	rpmB	1531119	1531307	121	0.00025	NE	0.00075	NE	0.9865	U
Spy49_1558c	fba	1531689	1532570	62	0	NE	0	NE	0	NE
–	-				1	E		E	1	E
Spy49_1559c		1532916	1533842	293			1			
Spy49_1560c	pyrG	1534010	1535614	308	0.00025	NE	0	NE	0	NE
Spy49_1561c	rpoE	1535871	1536479	534	0.00025	NE	0	NE	0.00025	NE
Spy49_1562c	tig	1536663	1537946	202	0	NE	0	NE	0	NE
Spy49_1563c	-	1538267	1539112	427	0.03825	NE	0	NE	0	NE
–										
Spy49_1564	-	1539177	1539737	281	0.00025	NE	0	NE	0.00125	NE
Spy49_1565c	-	1539751	1540221	186	0	NE	0	NE	0	NE
Spy49_1566c	thiD	1540211	1540975	156	0	NE	0	NE	0	NE
Spy49_1567c	truA	1540965	1541714	254	0	NE	0	NE	0.00025	NE
–										
Spy49_1568c	comX2	1542131	1542388	249	0	NE	0	NE	0	NE
Spy49_1569c	-	1548174	1549316	85	0	NE	0	NE	0	NE
Spy49_1571c	hsdR	1549597	1552575	380	0	NE	0	NE	0	NE
Spy49 1572	hsdS	1552588	1553730	992	0	NE	0	NE	0	NE
	hsdM	1553743	1555323	380	0	NE	0	NE	0.00025	NE
Spy49_1573	HOUIVI						_			
Spy49_1574	-	1555533	1555733	526	0.00025	NE	0	NE	0	NE
Spy49_1575c	salR	1555876	1556481	66	0	NE	0	NE	0	NE
Spy49_1576c	salK	1556462	1557883	201	0	NE	0	NE	0	NE
Spy49_1577c	salY	1558064	1559971	473	0.00025	NE	0	NE	0	NE
–	salX	1559973	1560710	635		NE	0	NE	0	NE
Spy49_1578c					0					
Spy49_1579c	salT	1560707	1561168	245	0	NE	0	NE	0.00025	NE
Spy49_1580c	salB	1561242	1562867	153	0	NE	0	NE	0	NE
Spy49 1582c	salA	1562951	1563097	541	0	NE	0	NE	0.00025	NE
Spy49_1583c	lacG	1563609	1565042	48	-1	S	-1	S	-1	S
–										
Spy49_1584c	lacE	1565103	1566800	477	0	NE	0	NE	0	NE
Spy49_1585c	lacF	1566800	1567117	565	0	NE	0	NE	0	NE
Spy49_1586c	lacD2	1567141	1568124	105	0	NE	0	NE	0	NE
Spy49_1587c	lacC2	1568128	1569057	327	0	NE	0	NE	0	NE
–									0	
Spy49_1588c	lacB2	1569103	1569618	309	0	NE	0	NE		NE
Spy49_1589c	lacA2	1569653	1570081	171	0	NE	0	NE	0.00075	NE
Spy49_1590c	lacR2	1570527	1571300	142	0	NE	0	NE	0	NE
Spy49_1591	-	1572028	1572249	257	0	NE	0	NE	0	NE
–	-	1572239		73	0	NE	0	NE	0	NE
Spy49_1592			1572574							
Spy49_1593	-	1573340	1573660	111	0	NE	0	NE	0	NE
Spy49_1594	rpsl	1573828	1574220	106	0	NE	0	NE	0	NE
Spy49_1595c	rplM	1574241	1574687	130	0.063	U	0.99725	E	0.99175	E
_										

								_	0.010	
Spy49_1596c	-	1574905	1575111	148	0.89875	U	0.99975	E	0.913	U
Spy49_1597c	-	1575108	1575806	68	0.01	NE	0.00025	NE	0.05825	U
Spy49_1598c	-	1575942	1576817	232	0	NE	0	NE	0.00025	NE
Spy49_1599c	-	1576898	1577380	291	0	NE	0	NE	0.3945	U
Spy49_1600c	-	1577419	1578165	160	0	NE	0	NE	0	NE
Spy49_1601c	-	1578212	1579009	248	0	NE	0	NE	0	NE
Spy49_1602c	-	1579205	1579618	265	0	NE	0	NE	0	NE
Spy49_1603c	cysS	1579611	1580954	137	0	NE	0	NE	0	NE
Spy49_1604c	-	1580982	1581212	447	1	E	1	E	1	E
Spy49_1605c	cysE	1581691	1582272	76	0	NE	0	NE	0	NE
Spy49_1606c	-	1582281	1583033	193	0.46375	U	0	NE	0	NE
Spy49_1607c	pnp	1583026	1585158	250	0.00025	NE	0	NE	0	NE
Spy49_1608c	-	1585438	1586166	710	0	NE	0	NE	0.02175	NE
Spy49_1609c	ulaA	1586179	1587558	242	0	NE	0	NE	0	NE
Spy49_1610c	-	1587585	1587869	459	0	NE	0	NE	0.00025	NE
Spy49_1611c	_	1587862	1589922	94	0	NE	0	NE	0.00025	NE
Spy49_1612c	rpsO	1590275	1590544	686	0	NE	0	NE	0	NE
Spy49_1613c	-	1590720	1590920	89	0	NE	0	NE	0.96975	U
Spy49_1614c	def	1591319	1591933	66	0	NE	0	NE	0.90973	NE
–	-	1591967	1591933	204	0	NE	1	E	0.985	U
Spy49_1615	-				0		0			
Spy49_1616c	10	1592640	1593068	180		NE		NE	0	NE
Spy49_1617c	polC	1593178	1597575	142	0	NE	0	NE	0	NE
Spy49_1618c	proS	1597830	1599686	1465	0.99975	E	1	E	1	E
Spy49_1619c	eep	1599884	1601143	618	0.9995	E	1	E	1	E
Spy49_1620c	cdsA	1601216	1602010	419	0	NE	0	NE	0.00025	NE
Spy49_1621c	uppS	1602023	1602772	264	0.84425	U	1	E	1	E
Spy49_1622c	yajC	1602991	1603356	249	0.95275	U	1	E	1	E
Spy49_1624c	-	1603472	1603819	121	0	NE	0	NE	0	NE
Spy49_1625c	pulA	1603961	1607365	115	0	NE	0	NE	0	NE
Spy49_1626c	dexB	1607656	1609269	1134	0	NE	0	NE	0	NE
Spy49_1627c	msmK	1609398	1610531	537	0	NE	0	NE	0	NE
Spy49_1628c	Irp	1610829	1611722	377	0.00025	NE	0	NE	0	NE
Spy49_1629c	ska	1612017	1613339	297	0	NE	0	NE	0	NE
Spy49_1630	dtd	1613437	1613880	440	0	NE	0	NE	0	NE
Spy49_1631c	relA	1613895	1616114	147	0	NE	0	NE	0	NE
Spy49_1632c	scIA	1616358	1617626	739	0.18525	U	0	NE	1	E
Spy49_1633c	nrdI2	1618008	1618490	422	0.00025	NE	0	NE	0.00025	NE
Spy49_1634	-	1618883	1619701	160	0	NE	0	NE	0	NE
Spy49_1635c	_	1619784	1621970	272	0	NE	0	NE	0	NE
Spy49_1636c	_	1622326	1623075	728	0.00025	NE	0	NE	0.0165	NE
Spy49_1637c	nrm A	1623075	1624028	249	0.00023	NE	0	NE	0.004	NE
	prmA									
Spy49_1638c	nudC	1624045	1625127	317	0.00025	NE	0	NE	0.00025	NE
Spy49_1639c	nudB	1625304	1625660	360	0.00025	NE	0	NE	0.00025	NE
Spy49_1640c	nudA	1625688	1626005	118	0	NE	0	NE	0	NE
Spy49_1641c	-	1626019	1626489	105	0	NE	0	NE	0	NE
Spy49_1642c	-	1626554	1626673	156	0	NE	0	NE	0	NE
Spy49_1643c	-	1626954	1627532	39	-1	S	-1	S	-1	S
Spy49_1644c	-	1627693	1627983	192	0.00025	NE	0	NE	0	NE
Spy49_1646c	-	1628038	1628844	96	0	NE	0	NE	0	NE
Spy49_1647c	-	1629499	1629813	268	0	NE	0	NE	0	NE
Spy49_1649c	-	1630202	1630438	104	0	NE	0	NE	0	NE
Spy49_1651	-	1630510	1630704	78	0	NE	0	NE	0	NE
Spy49_1652	рарВ	1630830	1632587	64	0.5285	U	0	NE	0	NE
Spy49_1653	trpG	1632620	1633186	585	0	NE	0	NE	0	NE
Spy49_1654	-	1633219	1634487	188	0	NE	0	NE	0	NE
Spy49_1655	pai1	1634985	1635425	422	0	NE	0	NE	0	NE
Spy49_1656	-	1635460	1635966	146	0	NE	0	NE	0.00025	NE
Spy49 1657	_	1636090	1636425	168	0	NE	0	NE	0	NE
Spy49_1658c	_	1636435	1637079	111	0.00025	NE	0	NE	0.00025	NE
Spy49_1659c	dppA	1638159	1639649	214	0.00023	NE	0	NE	0.00023	NE
		1639762		496	0	NE	0	NE	0	NE
Spy49_1660	dppB		1640739							
Spy49_1661	dppC	1640736	1641557	325	0	NE	0	NE	0.0005	NE
Spy49_1662	dppD	1641569	1642372	273	0	NE	0	NE	0.00025	NE
Spy49_1663	dppF	1642356	1642982	267	0	NE	0	NE	0	NE
Spy49_1664	-	1643064	1643264	208	0	NE	0	NE	0	NE
Spy49_1665c	-	1643433	1645904	66	0	NE	0	NE	0	NE
Spy49_1666c	lmb	1645917	1646837	823	0	NE	0	NE	0.00025	NE
Spy49_1667c	-	1647073	1648410	306	0	NE	0	NE	0.00025	NE

\$\text{\$\text{Symple}\$, 16665 \text{\$\text{\$k\$}} \text{\$\text{\$1.000}} \text{\$\text{\$k\$}} \text{\$\text{\$1.000}} \text{\$\text{\$1.0000}} \text{\$\text{\$1.0000}} \text{\$\text{\$1.0000}} \text{\$\text{\$1.0000}} \text{\$\text{\$1.0000}} \text{\$\text{\$1.0000}} \text{\$\text{\$1.00000}} \text{\$\text{\$1.0000}} \text{\$\text{\$1.0000}} \text{\$\text{\$1.0000}} \text{\$\text{\$1.00000}} \$\text{\$1.000000000000000000000000000000000000											
Symple	Spy49_1668c	scpA	1648661	1652050	445	0	NE	0	NE	0.00025	NE
Symbol 1970	Spy49_1669c	ennX	1652385	1653491	1129	0	NE	0	NE	0.00025	NE
Symbol 1672 mgs 1666527 1659121 415 0 NE	Spy49_1670c	emm49	1653701	1654858	368	0	NE	0	NE	0	NE
Symbol 1672 mgs 1666527 1659121 415 0 NE	–	-	1655083	1656330	385	0.00025	NE	0	NE	0.00025	NE
Symbol 1676 165912 165912 165912 155	–	mga									
Spy49_1676_ Spy4	–	-									
Spy#9_1675c 1660286 1662241 1662881 342 0 NE	–										
Spyr#9_1676c 1662281 1662881 1662881 1662881 166288 166288 166288 166288 166288 166288 166288 166288 166288 166288 166288 166288 166687	–	ishī									
Symbol 1677c 166278 166218 166219 166218 166228 162228 134 0.00025 NE	–	-									
Symbol 1678c - 1664878 1664879 224 0.00025 NE 0 NE 0 NE 0 NE 0 NE 1 166702 1666705 1666729 134 0.00025 NE 0 NE 0 NE 0 NE 0 NE 166703 166702 166703 16	Spy49_1676c	-									
Spy49_16801 - 1666979 1666147 224 0.00025 NE	Spy49_1677c	-	1662988	1664205	217	0	NE	0	NE	0	NE
Symba 1860 - 1666702 1666703 140 0.0025 NE	Spy49_1678c	-	1664218	1664892	405	0	NE	0	NE	0	NE
Spy49 1682 1667400 1667407 1667400 1669395 98 0 NE 0 N	Spy49_1679c	-	1664879	1666147	224	0.00025	NE	0	NE	0	NE
Spy49 1682 1667400 1667407 1667400 1669395 98 0 NE 0 N	Spv49 1680c	-	1666571	1666975	422	0	NE	0	NE	0	NE
Symba 1662 166494 166794 166794 167265 561 0 NE 0 NE 0 NE 0 NE 167393 NE 167393 1673134 1026 0.00025 NE 0 NE 0.00025 NE 167393 1673304 167390 167494 167390 167494		-			134		NE	0	NE	0.00025	
Spy49 1683c Fig.	–	sfhX49									
Spy49 1684c - 1673773 1673314 1026 0.00025 NE 0 NE 0.00025 NE 0 NE 0.00025 NE Spy49 1686c - 1674572 1674589 316 0 NE 0 NE 0.4775 U NE 0.00025	–										
Spired 1686	–										
Spy49 1687c 1674572 1674872 1674879 316 0 NE	–										
Spy49_1688c	–	•									
Spy49 1698c 1697304 1678200 101 0 NE	–	-									
Spy49 1690c rop8 1677441 1678283 398 0 NE	Spy49_1688c	-	1674997	1675302	105		NE		NE		
Spy49 1691	Spy49_1689c	speB	1675304	1676500	101	0	NE	0	NE	0.996	E
Spy49 1592c 1679426 1679554 276 0 NE	Spy49_1690c	ropB	1677441	1678283	398	0	NE	0	NE	0	NE
Spy49 1699c 1679767 1680216 42 -1 S -1 S -1 S Spy49 1698 816 1680285 1681373 1699 0 NE 0 NE 0 NE 0 NE Spy49 1698c mipB 1681430 1682088 362 0 NE 0 NE 0 NE 0 NE Spy49 1696c mipB 1681430 1682088 362 0 NE 0 NE 0 NE 0 NE Spy49 1696c mipB 1681430 1682088 362 0 NE 0 NE 0 NE 0 NE 0 NE Spy49 1696c 1686431 1682088 805 0 NE 0 NE 0 NE 0 NE 0 NE Spy49 1696c -1 16864528 222 0 NE	Spv49 1691	mf1	1678512	1679342	280	0	NE	0	NE	0	NE
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Spy49_1732c rpsB 1724449 1725216 1024 0.00075 NE 0 NE 0 NE Spy49_1733 tsf 1725350 1726390 255 1 E 1 E 0.99925 E Spy49_1734 pepO 1726556 1728451 346 0.65075 U 1 E 0.997 E Spy49_1735c dexS 1728659 1730287 631 0 NE 0 NE 0.1435 U Spy49_1736c - 1730354 1732378 542 1 E 1 E 1 E Spy49_1737c - 1732589 1733302 674 0 NE 0 NE 0.5975 U	Spy49_1730	hutG		1721040							
Spy49_1733 tsf 1725350 1726390 255 1 E 1 E 0.99925 E Spy49_1734 pepO 1726556 1728451 346 0.65075 U 1 E 0.997 E Spy49_1735c dexS 1728659 1730287 631 0 NE 0 NE 0.1435 U Spy49_1736c - 1730354 1732378 542 1 E 1 E 1 E Spy49_1737c - 1732589 1733302 674 0 NE 0 NE 0.5975 U	Spy49_1731	-	1721071	1724145	328	0	NE	0	NE	0	NE
Spy49_1733 tsf 1725350 1726390 255 1 E 1 E 0.99925 E Spy49_1734 pepO 1726556 1728451 346 0.65075 U 1 E 0.997 E Spy49_1735c dexS 1728659 1730287 631 0 NE 0 NE 0.1435 U Spy49_1736c - 1730354 1732378 542 1 E 1 E 1 E Spy49_1737c - 1732589 1733302 674 0 NE 0 NE 0.5975 U	Spy49_1732c	rpsB	1724449	1725216	1024	0.00075	NE	0	NE	0	NE
Spy49_1734 pepO 1726556 1728451 346 0.65075 U 1 E 0.997 E Spy49_1735c dexS 1728659 1730287 631 0 NE 0 NE 0.1435 U Spy49_1736c - 1730354 1732378 542 1 E 1 E 1 E Spy49_1737c - 1732589 1733302 674 0 NE 0 NE 0.5975 U		tsf	1725350	1726390	255	1	E	1	Е	0.99925	E
Spy49_1735c dexS 1728659 1730287 631 0 NE 0 NE 0.1435 U Spy49_1736c - 1730354 1732378 542 1 E 1 E 1 E Spy49_1737c - 1732589 1733302 674 0 NE 0 NE 0.5975 U	–										
Spy49_1736c - 1730354 1732378 542 1 E 1 E 1 E Spy49_1737c - 1732589 1733302 674 0 NE 0 NE 0.5975 U	–										
Spy49_1737c - 1732589 1733302 674 0 NE 0 NE 0.5975 U	–	-									
		_									
3PY45_1/30 - 1/33581 1/3382U 23/ U.UUU25 NE U NE U.UUU5 NE	–	-									
	2h442_1/38	-	1/33381	1/33020	25/	0.00025	INE	U	INE	0.0005	INE

Cm.,40, 1720a		1724105	1724062	70	0	NE	0	NE	0	NIE
Spy49_1739c	-	1734105	1734962	79	0	NE	0	NE	0	NE
Spy49_1740	-	1735004	1735735	285	0.00025	NE	0	NE	0.00025	NE
Spy49_1742	nrdG	1735909	1736523	243	0.00025	NE	0	NE	0	NE
Spy49_1743c	-	1736523	1737032	204	0.00025	NE	0	NE	0.91675	U
Spy49_1744c	-	1737041	1737976	169	0.00025	NE	0	NE	0.00025	NE
Spy49_1745c	-	1738005	1738151	311	0.00025	NE	1	E	1	Е
Spy49_1746c	nrdD	1738333	1740531	48	-1	S	-1	S	-1	S
Spy49_1747c	-	1740628	1742187	732	0.00025	NE	0	NE	0.629	U
Spy49_1748c	_	1742600	1742905	519	0.00025	NE	0	NE	0	NE
Spy49_1749c	_	1742917	1743336	101	0.00023	NE	0	NE	0.00025	NE
–	-			139	0.00025	NE		U		U
Spy49_1750c	- A	1743333	1743602				0.19025		0.98825	
Spy49_1751c	spxA	1743716	1744114	89	0.00025	NE	0	NE	0.00025	NE
Spy49_1752c	recA	1744405	1745541	132	0.0005	NE	0.00075	NE	0.0005	NE
Spy49_1753c	cinA	1745629	1746900	378	0	NE	0	NE	0.984	U
Spy49_1754c	tag	1746969	1747529	423	0	NE	0	NE	0.00025	NE
Spy49_1755c	ruvA	1747539	1748135	186	0	NE	0	NE	0	NE
Spy49_1756c	ImrP	1748137	1749357	198	0.00375	NE	0.92175	U	0.99825	E
Spy49 1757c	mutL	1749368	1751350	406	0	NE	0	NE	0.99275	Е
Spy49_1758c	mutS	1751480	1754035	660	0.32375	U	0	NE	1	Е
Spy49_1759c	-	1754371	1754706	851	0.92175	Ü	0	NE	0.2075	Ū
Spy49_1761c	argS	1755099	1756790	111	0.52175	NE	0	NE	0	NE
–	-			563	1	E	1	E	1	E
Spy49_1762	-	1756878	1757186							
Spy49_1763	-	1757213	1758085	102	0	NE	0	NE	0	NE
Spy49_1764c	-	1758128	1759063	290	0	NE	0	NE	0	NE
Spy49_1765c	-	1759026	1759967	311	0.0005	NE	0	NE	0	NE
Spy49_1767c	aspS	1759960	1761708	313	0.00025	NE	0	NE	0.00025	NE
Spy49_1768c	hisS	1762046	1763326	582	1	E	1	E	1	E
Spy49_1769c	rpmF	1763546	1763728	426	1	E	1	E	1	Е
Spy49_1770	rpmG	1763744	1763893	60	0	NE	0	NE	0	NE
Spy49_1771	-	1763933	1764157	49	-1	S	-1	S	-1	S
Spy49_1772c	cadD	1764186	1764800	74	0.00025	NE	0	NE	0	NE
Spy49_1773	cadX	1764812	1765150	204	0.00025	NE	0	NE	0	NE
–					0.00023				0	
Spy49_1774	-	1765194	1766117	112		NE	0	NE		NE
Spy49_1775	-	1766183	1766935	307	0.00025	NE	0	NE	0.00025	NE
Spy49_1777	-	1766932	1767534	250	0	NE	0	NE	0	NE
Spy49_1778	-	1768745	1769587	200	0.00025	NE	0	NE	0.00075	NE
Spy49_1779	-	1769591	1770274	280	0.00025	NE	0	NE	0.0075	NE
Spy49_1780c	-	1770481	1770807	227	0.00475	NE	0	NE	0.00025	NE
Spy49_1781	-	1770794	1771381	108	0.00025	NE	0	NE	0	NE
Spy49_1782	-	1771378	1772451	195	0	NE	0	NE	0.00025	NE
Spy49_1783	-	1772567	1774861	357	0.00025	NE	0	NE	0.00025	NE
Spy49_1784c	-	1774975	1775511	764	0.00025	NE	0	NE	0.36525	U
Spy49_1785	rpsD	1775661	1776272	178	0	NE	0	NE	0	NE
Spy49_1786c	-	1777001	1777273	203	0.99975	E	1	E	0.99925	E
–		1777290								
Spy49_1787c	dnaC		1778657	90	0.0035	NE	0.00025	NE	0.00125	NE
Spy49_1788c	rpll	1778687	1779139	455	1	E	1	E	1	Ε
Spy49_1789c	-	1779136	1781112	150	0.00025	NE	0	NE	0.04825	U
Spy49_1790c	gidA	1781202	1783100	658	0.98	U	1	E	1	E
Spy49_1791c	-	1783224	1783541	632	0.00275	NE	1	E	1	E
Spy49_1792c	mnmA	1784316	1785437	105	0.00025	NE	0	NE	0	NE
Spy49_1793c	sdhB	1785735	1786406	373	0.9795	U	1	E	1	E
Spy49_1794	sdhA	1786418	1787290	223	0.00025	NE	0	NE	0	NE
Spy49 1795	-	1787704	1788318	290	0	NE	0	NE	0.00675	NE
Spy49_1796c	_	1788690	1789490	204	0	NE	0	NE	0	NE
Spy49_1797c	cbiO	1789483	1790325	266	0.9985	E	1	E	1	E
–	cbiO	1790301	1791191	280	0.9845	Ü	1	E	1	E
Spy49_1798c		1790301					0.99375	E	0.99975	
Spy49_1799c	pgsA		1791684	296	0.99975	E				E
Spy49_1800c	-	1791698	1792723	180	0.99975	E	1	E	1	E
Spy49_1801c	-	1792773	1794062	341	0	NE	0	NE	0	NE
Spy49_1802c	-	1794064	1795308	429	0	NE	0	NE	0	NE
Spy49_1803c	hasA	1795670	1797007	414	0	NE	0	NE	0	NE
Spy49_1804	hasB	1797043	1798251	445	0.00025	NE	0	NE	0	NE
Spy49_1806	hasC	1798433	1799347	402	0.00025	NE	0	NE	0	NE
Spy49_1808	-	1799655	1800068	304	0.0005	NE	0	NE	0.00125	NE
Spy49_1809	recF	1800070	1801176	137	0	NE	0	NE	0	NE
Spy49_1810	-	1801232	1802095	368	0.0005	NE	0	NE	0.67575	U
Spy49_1811c	guaB	1802298	1803779	287	0.0003	NE	0	NE	0.07373	NE
Spy49_1811c	trsA	1804087	1805779	493	0.00025	NE	0	NE	0	NE
3py+3_1012C	u sn	1004007	1003103	+33	0.00023	IVL	0	INL	U	INL

Spy49_1813c	-	1805528	1806400	340	1	E	1	Ε	1	E
Spy49_1814	-	1806479	1808086	290	0	NE	0	NE	0	NE
Spy49_1815	-	1808184	1810760	535	0	NE	0	NE	0	NE
Spy49_1817	-	1813005	1813484	858	0.00225	NE	0.00025	NE	0.017	NE
Spy49_1819c	degP	1813696	1814919		0	NE	0	NE	0.00025	NE
Spy49_1820c	parB	1814978	1815784	159	0	NE	0	NE	0	NE
Spy49_1821				407	0.9795	U	1	Ε	0.99975	E
Spy49_1822				268	0.00025	NE	0	NE	0.00025	NE

Table S6. Integrated gene essentiality determination for GAS M49 NZ131 for all time points. (a) Spy numbers from GAS NZ131 genome.

) Hyperlink to	the NCBI Gene web		ses on 3 tim o://www.nc		ov/gene).			
ocus Tag(a)) Gene Name(b)	Call(c)	Start	Stop	Length				n Protein Function
y49_0001 y49_0002	dnaA dnaN	NC E	232 1742	1587 2878	451 378	+		COG0593L COG0592L	chromosomal replication initiation protein DNA polymerase III subunit beta
y49_0003	-	NE	2953	3150	65	+		COG4481S	hypothetical protein Spy49_0003
y49_0004		NE	3480	4595	371	+		COG0012J	GTP-dependent nucleic acid-binding protein EngD
y49_0005 y49_0006	pth trcF	E NE	4665 5321	5234 8740	189 1139	+		COG0193J COG1197LK	peptidyl-tRNA hydrolase transcription-repair coupling factor
y49_0008	-	NE	8902	9174	90	+	6984522	COG1188J	hypothetical protein Spy49_0008
y49_0009	divIC	NC	9161	9532	123	+		COG2919D	cell division protein
y49_0010 y49_0011	mesJ	NE E	9667 10950	10953 12236	428 428	+		COG2367V COG0037D	hypothetical protein Spy49_0010 tRNA(IIe)-lysidine synthetase
y49_0012	hpt	NE	12241	12783	180	+	6984526	COG0634F	Hypoxanthine-guanine phosphoribosyltransferase
y49_0013	ftsH	E NE	12805 15041	14784 16501	659 486	+		COG04650 COG0531E	cell division protein FtsH
0y49_0014 0y49_0015		E	31169	32365	398	+		COG3331E	amino acid permease secreted protein
y49_0016	prsA	E	32618	33580	320	+	6984564	COG0462FE	ribose-phosphate pyrophosphokinase
0y49_0017 0y49_0018	recO	NE E	33766 34624	34521 35631	251 335	+		COG1381L COG0416I	DNA repair protein RecO glycerol-3-phosphate acyltransferase PlsX
y49_0018 y49_0019	acp	NC	35624	35866	80	+		COG04161 COG0236IQ	acyl carrier protein
y49_0020	purC	NE	35987	36721	244	+		COG0152F	phosphoribosylaminoimidazole-succinocarboxamide synthase
y49_0021 y49_0022	purL purF	NE NE	36798 40805	40571 42259	1257 484	+		COG0046F COG0034F	phosphoribosylformylglycinamidine synthase, synthetase subunit/phosphoribosylformylglycinamidine syn amidophosphoribosyltransferase
y49_0023	purM	NE	42287	43309	340	+		COG0150F	phosphoribosylaminoimidazole synthetase
y49_0024	purN	NE	43477	44031	184	+	6984572	COG0299F	phosphoribosylglycinamide formyltransferase
y49_0025 y49_0026c	purH -	NE	44215 45820	45762	515 374	+		COG0138F	bifunctional phosphoribosylaminoimidazolecarboxamide formyltransferase/IMP cyclohydrolase
y49_0026c y49_0027	- purD	NE NE	45820 47107	46944 48462	451	+		COG3942R COG0151F	Autolysin phosphoribosylamineglycine ligase
y49_0028	purE	NE	48621	49232	203	+	6984576	COG0041F	phosphoribosylaminoimidazole carboxylase catalytic subunit
y49_0029	purK	NE	49216 50394	50292	358 493	+		COG0026F	phosphoribosylaminoimidazole carboxylase ATPase subunit
949_0030 949_0031	- purB	NE NE	50394 52048	51875 53340	493 430	+	6984578 6984579	COG0015F	hypothetical protein Spy49_0030 adenylosuccinate lyase
y49_0032	-	NE	53471	54391	306	+	6984580	-	Cro/CI family transcriptional regulator
y49_0033	ruvB	C	54617	55615	332	+		COG2255L	Holliday junction DNA helicase RuvB
y49_0035 y49_0036	-	NE E	55753 56213	56190 56614	145 133	+		COG0394T COG4642S	protein tyrosine phosphatase hypothetical protein Spy49_0036
y49_0037	-	E	56611	58386	591	+	6984664	COG1835I	acyltransferase
y49_0038	adhE	NE	58695	61337	880	+		COG1454C	bifunctional acetaldehyde-CoA/alcohol dehydrogenase
y49_0039 y49_0040	adhP norM	NE NE	61589 62993	62605 64282	338 429	+		COG1064R COG0534V	alcohol dehydrogenase Na+ driven multidrug efflux pump
y49_0044	rpsJ	NC	64481	64789	102	+		COG0051J	30S ribosomal protein S10
y49_0045	rpIC	E	65037	65663	208	+		COG0087J	50S ribosomal protein L3
y49_0046 y49_0048	rplD rplW	NC NC	65687 66310	66310 66540	207 76	+		COG0088J COG0089J	50S ribosomal protein L4 50S ribosomal protein L23p
y49_0049	rplB	E	66625	67458	277	+		COG0090J	50S ribosomal protein L2
y49_0050	rpsS	NC	67597	67875	92	+		COG0185J	30S ribosomal protein S19
y49_0052 y49_0053	rpIV rpsC	NC E	67891 68275	68235 68901	114 208	+		COG0091J COG0092J	50S ribosomal protein L22 30S ribosomal protein S3
y49_0054	rpIP	E	68905	69318	137	+		COG0197J	50S ribosomal protein L16
y49_0055	rpmC	NC	69328	69534	68	+	6984677	COG0255J	50S ribosomal protein L29
y49_0056	rpsQ	NC NC	69560 69845	69820 70213	86 122	+		COG0186J COG0093J	30S ribosomal protein S17 50S ribosomal protein L14
y49_0057 y49_0058	rplN rplX	E	70292	70597	101	+		COG00933	50S ribosomal protein L14
y49_0059	rplE	NC	70621	71163	180	+	6984681	COG0094J	50S ribosomal protein L5
y49_0060	rpsN.1	NC NC	71179 71515	71364 71913	61 132	+		COG0199J COG0096J	30S ribosomal protein S14p 30S ribosomal protein S8
0y49_0061 0y49_0062	rpsH rplF	E	72116	72652	178	+		COG0097J	50S ribosomal protein S6
y49_0064	rpIR	NC	72757	73113	118	+	6984685	COG0256J	50S ribosomal protein L18
y49_0065	rpsE rpmD	NC NC	73132	73626	164	+		COG0098J	30S ribosomal protein S5
949_0066 949_0067	rpmD rplO	NC NC	73641 74038	73823 74478	60 146	+		COG1841J COG0200J	50S ribosomal protein L30 50S ribosomal protein L15
y49_0068	secY	E	74495	75799	434	+	6984689	COG0201U	preprotein translocase subunit SecY
y49_0069	adk	E NC	75949 76705	76587	212	+		COG0563F	adenylate kinase
0y49_0070 0y49_0071	infA rpmJ	NC NC	76705 76949	76923 77065	72 38	+		COG0361J COG0257J	translation initiation factor IF-1 50S ribosomal protein L36
y49_0072	rpsM	E	77083	77448	121	+	6984693	COG0099J	30S ribosomal protein S13
y49_0073	rpsK	NC	77466	77849	127	+		COG0100J	30S ribosomal protein S11
y49_0074 y49_0075	rpoA rplQ	E NC	77895 78848	78833 79234	312 128	+		COG0202K COG0203J	DNA-directed RNA polymerase subunit alpha 50S ribosomal protein L17
y49_0078	-	NE	87367	87615	82	+	6984713	COG1947I	4-diphosphocytidyl-2-C-methyl-D-erythritol kinase
y49_0079	-	NE	87670	87882	70	+	6984714		4-diphosphocytidyl-2-C-methyl-D-erythritol kinase
y49_0080 y49_0081	adrR adrC	NE NC	87992 88439	88435 89158	147 239	+		COG1846K COG1121P	repressor protein ABC transporter
y49_0081 y49_0082	adrB	NC	89151	89966	271	+		COG1121P	ABC transporter
y49_0083c	-	NE	90006	90389	127	-	6984718	COG0537FGR	histidine triad (HIT) protein
y49_0084 y49_0086	tyrS pbp1b	E NE	90440 91800	91696 94100	418 766	+		COG0162J COG0744M	tyrosyl-tRNA synthetase multimodular transpeptidase-transglycosylase
y49_0087	rpoB	E	94364	97930	1188	+	6984721	COG0744IVI COG0085K	DNA-directed RNA polymerase subunit beta
y49_0088	rpoC	E	98048	101662	1204	+	6984722	COG0086K	DNA-directed RNA polymerase subunit beta\'
y49_0089 y49_0090	- comYA	NE NE	101814 102272	102179 103210	121 312	+		COG4699S COG2804NU	DNA binding protein ABC transporter
y49_0090 y49_0091	comYB	NE	103305	103210	291	+		COG2804NU COG1459NU	competence protein, ABC transporter subunit
y49_0092	comYC	NE	104182	104508	108	+	6984726	COG4537U	competence protein
y49_0093 y49_0094	-	NE NE	104483 104868	104911 105152	142 94	+	6984727 6984728	COG2165NU	Competence protein hypothetical protein Spy49_0094
y49_0094 y49_0095	comYD	NE	104868	105152	144	+		- COG4940U	competence protein
y49_0096	-	NE	105599	105889	96	+	6984730	-	hypothetical protein Spy49_0096
y49_0097	-	NE NC	105987	106940	317 398	+		COG0827L COG0282C	adenine-specific methyltransferase acetate kinase
y49_0098 y49_0099	ackA -	NC NE	106999 108381	108195 108623	398 80	+	6984732	-	acetate kinase hypothetical protein Spy49_0099
y49_0100	proC	NE	108772	109542	256	-	6984734	COG0345E	pyrroline-5-carboxylate reductase
y49_0101	pepA	NE	109590	110657	355	-		COG1363G	glutamyl-aminopeptidase
y49_0103 y49_0104	trx.1	NE NE	112439 112729	112732 113046	97 105	+	6984736 6984737	- COG0526OC	hypothetical protein Spy49_0103 thioredoxin
y49_0104 y49_0105	-	NE	113064	113708	214	+		COG05260C COG0073R	tRNA binding domain-containing protein
y49_0107	ssb	NE	113842	114237	131	+	6984739	COG0629L	single-stranded DNA-binding protein
y49_0108c y49_0109c	-	NE NE	114497 115158	115138 116135	213 325	-		COG1428F COG0042J	deoxyadenosine kinase/deoxyguanosine kinase transcriptional regulator
y49_0109c y49_0110c	hsIO	NE	115158	116135	290	-	6984742	COG00423 COG12810	transcriptional regulator Hsp33-like chaperonin
y49_0111	nra	NE	117120	118655	511	-	6984823		Regulatory protein
y49_0112	cbp	NE	119085	121319	744	+	6984824	- COG4959OU	collagen binding protein
y49_0113	lepA-1	NE	121312	121833	173 344	+	6984825	CUU4939UU	signal peptidase I

Spy49_0116			422005	422520	244		6004027	50545005	NIDOTN
Spy49_0117	-	NE NE	122905 123665	123630 124234	241 189	+	6984828	COG4509S	NPQTN specific sortase B hypothetical protein Spy49 0117
Spy49_0118	msmR	NE	124394	125599	401	-	6984829	COG2207K	AraC family transcriptional regulator
Spy49_0119	prtF	NE	125984	129466	1160	+	6984830	COG4932M	fibronectin binding protein
Spy49_0120c	-	NE	129731	130396	221	-	6984831	-	hypothetical protein Spy49_0120c
Spy49_0121	atoE	NE	130750	132156	468 303	+		COG2031I	short-chain fatty acids transporter
Spy49_0122c Spy49_0123	-	NE NE	132231 133263	133142 134447	394	+	6984833	COG0583K COG0183I	transcriptional regulator acetyl-CoA acetyltransferase
Spy49_0124	atoD.2	NE	134459	135118	219	+	6984835		acetate CoA-transferase subunit alpha
Spy49_0125	-	NE	135121	135768	215	+	6984836		Butyrate-acetoacetate CoA-transferase subunit beta
Spy49_0126c	-	NE	135890	136570	226	-	6984837		transcriptional regulator
Spy49_0127	-	NE	136745	137110	121	+	6984838		translation initiation inhibitor
Spy49_0128	sloR	NE	137147	138166	339	+	6984839	COG1299G	regulatory protein
Spy49_0129 Spy49_0130	ntpl	NE NE	138620 138930	138940 140930	106 666	+	6984840	- COG1269C	hypothetical protein Spy49_0129 V-type ATP synthase subunit I
Spy49_0131	ntpK	NE	140932	141411	159	+	6984842	COG0636C	V-type ATP synthase subunit K
Spy49_0132	ntpE	NE	141479	142063	194	+	6984843	-	V-type Na+-ATPase subunit E
Spy49_0133	ntpC	NE	142079	143077	332	+	6984844	COG1527C	V-type sodium ATP synthase subunit C
Spy49_0134	ntpG	NE	143074	143394	106	+	6984845		V-type ATP synthase subunit F
Spy49_0135	ntpA	NE	143595	145370	591	+		COG1155C	V-type ATP synthase subunit A
Spy49_0136 Spy49_0137	ntpB ntpD	NE NE	145371 146831	146786 147457	471 208	+	6984848	COG1156C COG1394C	V-type ATP synthase subunit B V-type ATP synthase subunit D
Spy49_0138c	-	NE	147577	148839	420	-	6984849		toxic anion resistance protein
Spy49_0139c	-	NE	148852	149730	292	-	6984850	-	hypothetical protein Spy49_0139c
Spy49_0141	purA	NE	150168	151460	430	+		COG0104F	adenylosuccinate synthetase
Spy49_0142	-	NE	151787	152830	347	+	6984852		ABC transporter
Spy49_0143 Spy49_0144	nusG	NC NE	152988 153917	153542 155272	184 451	+	6984853 6984854	COG0250K	transcription antitermination protein NusG Nicotine adenine dinucleotide glycohydrolase (NADGH)
Spy49_0145	nga -	NE	155277	155762	161	+	6984855	-	hypothetical protein Spy49_0145
Spy49_0146	slo	NE	155786	157501	571	+	6984856	-	Thiol-activated cytolysin
Spy49_0147	-	NC	157756	158184	142	+	6984857	-	hypothetical protein Spy49_0147
Spy49_0148	-	NC	158408	158701	97	+	6984858	-	hypothetical protein Spy49_0148
Spy49_0149c Spy49_0150c	-	NE	158998 159350	159165	55	-	6984859	-	hypothetical protein Spy49_0149c hypothetical protein Spy49_0150c
Spy49_01500 Spy49_0151	metB	E NE	159350	159676 161299	108 456	+	6984860	COG0626E	cystathionine beta-lyase
Spy49_0151	leuS	E	161510	164011	833	+	6984862	COG0495J	leucyl-tRNA synthetase
Spy49_0153	-	NE	164318	165751	477	+	6984863		PTS system ascorbate-specific transporter subunit IIC
Spy49_0154	-	NE	165822	166100	92	+		COG3414G	PTS system IIB component
Spy49_0155	- Lin	NE	166223	166708	161	+	6984865		PTS system IIA component
Spy49_0156 Spy49_0157	ulaD	NC NE	166799 167466	167461 168329	220 287	+	6984866 6984867		3-keto-L-gulonate-6-phosphate decarboxylase L-xylulose 5-phosphate 3-epimerase
Spy49_0158	araD	NE	168331	169035	234	+	6984868		L-ribulose-5-phosphate 4-epimerase
Spy49_0159	-	NE	169361	171007	548	+		COG3711K	transcriptional regulator
Spy49_0160	-	NE	171261	172352	363	+		COG2220R	L-ascorbate 6-phosphate lactonase
Spy49_0161	opuAA	NE	172842	174038	398	+		COG4175E	L-proline glycine betaine ABC transport ATP- binding protein proV
Spy49_0162 Spy49_0163	opuABC polA	NE E	174054 175912	175781 178554	575 880	+	6984873	COG4176E COG0749L	glycine/betaine ABC transporter permease DNA polymerase I
Spy49_0164	-	NE	178732	179187	151	+		COG1832R	CoA-binding domain-containing protein
Spy49_0165	-	NE	179239	179706	155	+	6984875	COG0735P	ferric transport regulator protein
Spy49_0166	-	NE	179862	180161	99	+	6984876	-	M protein trans-acting positive regulator-like protein
Spy49_0167 Spy49_0168		NE NE	180383 181710	181717 182090	444 126	+	6984878	COG3969R COG1475K	hypothetical protein Spy49_0167 hypothetical protein Spy49_0168
Spy49_0169	-	NE	182234	182443	69	+	6984879	-	hypothetical protein Spy49_0169
Spy49_0170c	-	NE	182570	182785	71	-		COG2801L	transposase
Spy49_0173c	-	NE	183427	183720	97	-	6984881		hypothetical protein Spy49_0173c
Spy49_0176 Spy49_0178c		NE NE	185332 186865	186204 187311	290 148	+		COG0157H COG2801L	nicotinate-nucleotide pyrophosphorylase transposase, IS861
Spy49_0180c	-	NE	187933	188796	287	-	6984885		hypothetical protein Spy49_0180c
Spy49_0181	tgt	NE	189015	190157	380	+	6984886		queuine tRNA-ribosyltransferase
Spy49_0182	- h:-v	NE	190374	190685	103	+	6984887		hypothetical protein Spy49_0182
Spy49_0183 Spy49_0184	bioY -	NE NE	190689 191368	191228 192147	179 259	+	6984888 6984889	COG1268R COG1234R	Biotin transporter bioY hypothetical protein Spy49_0184
Spy49_0185	-	NE	192147	192662	171	+	6984890	COG0590FJ	cytosine deaminase
Spy49_0186c	-	NE	193276	194496	406	-	6984891	COG5279D	hypothetical protein Spy49_0186c
				195612	234 449	+	6984892 6984893	-	Exotoxin type G
Spy49_0187	speG	NE	194908			+	6984894	COG0166G	glucose-6-phosphate isomerase
Spy49_0188	speG pgi -	NE E	196067	197416		-			
Spy49_0188 Spy49_0189c		NE E NE	196067 197875	197416 199272 200635	465	+	6984895	COG0705R	RofA family transcriptional regulator hypothetical protein Spy49 0190
Spy49_0188		NE E	196067	199272 200635 201633	465 223 299	+	6984896	COG0705R COG1210M	RofA family transcriptional regulator hypothetical protein Spy49_0190 UTPglucose-1-phosphate uridylyltransferase
Spy49_0188 Spy49_0189c Spy49_0190 Spy49_0191c Spy49_0192c	pgi - -	NE E NE NE E	196067 197875 199964 200734 201666	199272 200635 201633 202682	465 223 299 338	-	6984896 6984897	COG1210M	RofA family transcriptional regulator hypothetical protein Spy49_0190 UTP-glucose-1-phosphate uridylyltransferase NAD[P]H-dependent glycerol-3-phosphate dehydrogenase
Spy49_0188 Spy49_0189c Spy49_0190 Spy49_0191c Spy49_0192c Spy49_0193	pgi - - hasC.2	NE E NE NE E E	196067 197875 199964 200734 201666 203220	199272 200635 201633 202682 203426	465 223 299 338 68	- - +	6984896 6984897 6984898	COG1210M COG0240C	Rofa Family transcriptional regulator hypothetical protein Spy49, 19190 UTP-glucose-1-phosphate uridylyltransferase NAD(P)H-dependent glycerol-3-phosphate dehydrogenase Mark Tamily transcriptional regulator, partial
Spy49_0188 Spy49_0189c Spy49_0190 Spy49_0191c Spy49_0192c Spy49_0193 Spy49_0194	pgi - - hasC.2	NE E NE NE E E NE	196067 197875 199964 200734 201666 203220 203419	199272 200635 201633 202682 203426 205125	465 223 299 338 68 568	- + +	6984896 6984897 6984898 6984899	COG1210M COG0240C - COG1132V	RofA family transcriptional regulator hypothetical protein Spy49_0190 UTP-glucose-1-phosphate uridylyltransferase NAD(PJH-dependent glycerol-3-phosphate dehydrogenase Mark family transcriptional regulator, partial ABC transporter ATP-binding protein
Spy49_0188 Spy49_0189c Spy49_0190 Spy49_0191c Spy49_0192c Spy49_0193 Spy49_0194 Spy49_0195	pgi - - hasC.2	NE E NE NE E E	196067 197875 199964 200734 201666 203220	199272 200635 201633 202682 203426	465 223 299 338 68	- - +	6984896 6984897 6984898 6984899	COG1210M COG0240C - COG1132V COG1132V	Rofa Family transcriptional regulator hypothetical protein Spy49, 19190 UTP-glucose-1-phosphate uridylyltransferase NAD(P)H-dependent glycerol-3-phosphate dehydrogenase Mark Tamily transcriptional regulator, partial
Spy49_0188 Spy49_0189c Spy49_0190 Spy49_0191c Spy49_0192c Spy49_0193 Spy49_0194 Spy49_0195 Spy49_0198 Spy49_0199	pgi - - hasC.2	NE E NE E NC NC NE NE	196067 197875 199964 200734 201666 203220 203419 205128 207105 207907	199272 200635 201633 202682 203426 205125 206912 207797 208365	465 223 299 338 68 568 594	- + +	6984896 6984898 6984899 6984900 6984901 6984902	COG1210M COG0240C - COG1132V COG1132V	RofA family transcriptional regulator hypothetical protein Spy49_0190 Hypothetical protein Spy49_0190 Hyp-elgucose-Lphosphate uridylyltransferase NAD(P)H-dependent glycerol-3-phosphate dehydrogenase MarR family transcriptional regulator, partial ABC transporter ATP-binding protein ABC transporter ATP-binding protein/permease
Spy49_0188 Spy49_0189c Spy49_0191c Spy49_0191c Spy49_0192c Spy49_0193 Spy49_0194 Spy49_0195 Spy49_0199 Spy49_0199 Spy49_0200	pgi - - hasC.2 gpsA - -	NE E NE E NE NC NC NE NE NE NE NE NE	196067 197875 199964 200734 201666 203220 203419 205128 207105 207907 208402	199272 200635 201633 202682 203426 205125 206912 207797 208365 209796	465 223 299 338 68 568 594 230 152 464	- + + + + +	6984896 6984898 6984899 6984900 6984901 6984902 6984983	COG1210M COG0240C - COG1132V COG1132V COG1636S COG0756F COG1066O	Rofa family transcriptional regulator hypothetical protein Spy49_0190 UTP-glucose-1-phosphate undylyltransferase NAD(P)H-dependent glycerol-3-phosphate dehydrogenase Mark family transcriptional regulator, partial ABC transporter ATP-binding protein ABC transporter ATP-binding protein/permease hypothetical protein Spy49_0198 deoxyuridine 5\'triphosphate nucleotidohydrolase DNA repair protein RadA
Spy49_0188 Spy49_0189c Spy49_0191c Spy49_0191c Spy49_0192c Spy49_0193 Spy49_0195 Spy49_0198 Spy49_0199 Spy49_0190 Spy49_0200 Spy49_0201	pgi - - hasC.2 gpsA - - - dut	NE E NE E E NC NC NE NC NE NC NC NC NC NC	196067 197875 199964 200734 201666 203220 203419 205128 207105 207907 208402 209985	199272 200635 201633 202682 203426 205125 206912 207797 208365 209796 210482	465 223 299 338 68 568 594 230 152 464 165	- + + + + + +	6984896 6984898 6984899 6984900 6984901 6984902 6984983 6984984	COG1210M COG0240C - COG1132V COG1132V COG1636S COG0756F COG10660 COG0288P	Rofa family transcriptional regulator hypothetical protein Spy49_0190 hypothetical protein Spy49_0190 hypothetical protein Spy49_0190 hypothetical protein Spy49_0190 has based by ADR/PH-dependent glycerol-3-phosphate dehydrogenase Mara family transcriptional regulator, partial ABC transporter ATP-binding protein ABC transporter ATP-binding protein ABC transporter ATP-binding protein/permease hypothetical protein Spy49_0198 deoxyuridine 5\\^\text{-triphosphate nucleotidohydrolase} DNA repair protein RadA carbonic anhydrase
Spy49_0188 Spy49_01890 Spy49_0190 Spy49_0191c Spy49_0192c Spy49_0193 Spy49_0194 Spy49_0195 Spy49_0198 Spy49_0200 Spy49_0201 Spy49_0201 Spy49_0201	pgi - hasC.2 gpsA dut radA -	NE E NE E NE NC NE NC NE	196067 197875 199964 200734 201666 203220 203419 205128 207105 207907 208402 209985 210613	199272 200635 201633 202682 203426 205125 206912 207797 208365 209796 210482 211323	465 223 299 338 68 568 594 230 152 464 165 236	- - + + + + + + +	6984896 6984897 6984898 6984990 6984901 6984902 6984983 6984984	COG1210M COG0240C - COG1132V COG1132V COG1636S COG0756F COG1066O COG0288P COG2013S	Rofa Family transcriptional regulator hypothetical protein Spy49, 0190 UTP-glucose-1-phosphate unidylytransferase NAD(P)H-dependent glycerol-3-phosphate dehydrogenase MAR family transcriptional regulator, partial ABC transporter ATP-binding protein ABC transporter ATP-binding protein/permease hypothetical protein Spy49, 0198 deoxyuridine 5\'-triphosphate nucleotidohydrolase DNA repair protein RadA carbonic anhydrase hypothetical protein Spy49, 0202
Spy49_0188 Spy49_0189c Spy49_0190 Spy49_0191c Spy49_0192c Spy49_0193 Spy49_0194 Spy49_0195 Spy49_0199 Spy49_0200 Spy49_0200 Spy49_0202 Spy49_0202 Spy49_0202 Spy49_0202	pgi - hasC.2 gpsA dut radA - gltX	NE E NE E NE NC NE NC NE NE NC NE	196067 197875 199964 200734 201666 203220 203419 205128 207105 207907 208402 209985 210613 211506	199272 200635 201633 202682 203426 205125 206912 207797 208365 209796 210482	465 223 299 338 68 568 594 230 152 464 165	- + + + + + +	6984896 6984897 6984898 6984990 6984901 6984902 6984983 6984984 6984985 6984986	COG1210M COG0240C - COG1132V COG1132V COG1636S COG0756F COG1066O COG0288P COG2013S COG0008J	Rofa family transcriptional regulator hypothetical protein Spy49_0190 UTP-glucose-1-phosphate uridylyltransferase NAD(P)H-dependent glycerol-3-phosphate dehydrogenase Mark family transcriptional regulator, partial ABC transporter ATP-binding protein ABC transporter ATP-binding protein/permease hypothetical protein Spy49_0198 deoxyuridine 5\\\^triphosphate nucleotidohydrolase DNA repair protein RadA carbonic anhydrase hypothetical protein Spy49_0202 glutamyl-tRNA synthetase
Spy49_0188 Spy49_01890 Spy49_0190 Spy49_0191c Spy49_0192c Spy49_0193 Spy49_0194 Spy49_0195 Spy49_0198 Spy49_0200 Spy49_0201 Spy49_0201 Spy49_0201	pgi - hasC.2 gpsA dut radA -	NE E NE E NE NC NE NC NE	196067 197875 199964 200734 201666 203220 203419 205128 207105 207907 208402 209985 210613	199272 200635 201633 202682 203426 205125 206912 207797 208365 209796 210482 211323 212996	465 223 299 338 68 568 594 230 152 464 165 236 496	- - + + + + + + + +	6984896 6984897 6984898 6984990 6984901 6984902 6984983 6984984	COG1210M COG0240C - COG1132V COG1132V COG1636S COG0756F COG1066O COG0288P COG2013S	Rofa Family transcriptional regulator hypothetical protein Spy49, 0190 UTP-glucose-1-phosphate unidylytransferase NAD(P)H-dependent glycerol-3-phosphate dehydrogenase MAR family transcriptional regulator, partial ABC transporter ATP-binding protein ABC transporter ATP-binding protein/permease hypothetical protein Spy49, 0198 deoxyuridine 5\'-triphosphate nucleotidohydrolase DNA repair protein RadA carbonic anhydrase hypothetical protein Spy49, 0202
Spy49_0188 Spy49_0189c Spy49_0190 Spy49_0191c Spy49_0191c Spy49_0193 Spy49_0195 Spy49_0195 Spy49_0195 Spy49_0200 Spy49_0201 Spy49_0201 Spy49_0203 Spy49_0203 Spy49_0203 Spy49_0204 Spy49_0205 Spy49_0205 Spy49_0205 Spy49_0205 Spy49_0205 Spy49_0205 Spy49_0205 Spy49_0205	pgi hasC.2 gpsA dut radA - gltX fasB	NE E NE E NE NC NE NE NE NE NE NC NE NC NE NC NE NC NE NC NE NC NE	196067 197875 199964 200734 201666 203220 203419 205128 207105 207907 208402 209985 210613 211506 213347 214690 215977	199272 200635 201633 202682 203426 205125 206912 207797 208365 209796 210482 211323 212996 214693 215973 216717	465 223 299 338 68 568 594 230 152 464 165 236 496 448 427 246	- + + + + + + + + + +	6984896 6984897 6984899 6984900 6984901 6984902 6984983 6984984 6984985 6984985 6984987 6984988	COG1210M COG0240C - COG1132V COG1132V COG1636S COG0756F COG10660 COG0288P COG2013S COG0008J COG2972T COG2972T COG3279KT	Rofa family transcriptional regulator hypothetical protein Spy49_0190 UTP-glucose-1-phosphate uridylyltransferase NAD(PlH-dependent glycerol-3-phosphate dehydrogenase MAR family transcriptional regulator, partial ABC transporter ATP-binding protein ABC transporter ATP-binding protein Poptemase hypothetical protein Spy49_0198 deoxyuridine S\'.triphosphate nucleotidohydrolase DNA repair protein RadA carbonic antiydrase hypothetical protein Spy49_0202 glutamyl-RNA synthetase histidine kinase histidine kinase Response regulator FasA
Spy49_0188 Spy49_0189c Spy49_0190 Spy49_0191c Spy49_0192c Spy49_0193 Spy49_0195 Spy49_0195 Spy49_0200	pgi - hasC.2 gpsA	NE E NE E NE NC NE NE NE NE NC NE NC NE NC NE NC NC NC NC NC NC	196067 197875 199964 200734 201666 203220 203419 205128 207105 207907 208402 209985 210613 211506 213347 214690 215977 217257	199272 200635 201633 202682 203426 205125 206912 207797 208365 209796 210482 211323 212996 214693 215973 216717 217616	465 223 299 338 68 568 594 230 152 464 165 236 496 448 427 246 119	- - + + + + + + + + + + +	6984896 6984897 6984899 6984900 6984901 6984902 6984984 6984985 6984986 6984987 6984988 6984989 6984989	COG1210M COG0240C - - COG1132V COG132S COG0756F COG1066O COG0288P COG2013S COG0981 COG2972T COG2972T COG3279KT COG0594J	Rofa Family transcriptional regulator hypothetical protein Spy49_0190 UTP-glucose-1-phosphate undylyltransferase NAD(P)H-dependent glycerol-3-phosphate dehydrogenase MAR family transcriptional regulator, partial ABC transporter ATP-binding protein ABC transporter ATP-binding protein/permease hypothetical protein Spy49_0198 deoxyuridine S\-'triphosphate nucleotidohydrolase DNA repair protein RadA carbonic anhydrase hypothetical protein Spy49_0202 glutamyl-tRNA synthetase histidine kinase histidine kinase Response regulator FasA ribonuclease P
Spy49_0188 Spy49_0189c Spy49_0190 Spy49_0191c Spy49_0191c Spy49_0192c Spy49_0195 Spy49_0195 Spy49_0195 Spy49_0200 Spy49_0200 Spy49_0201 Spy49_0203 Spy49_0203 Spy49_0203 Spy49_0205 Spy49_0205 Spy49_0205 Spy49_0205 Spy49_0205 Spy49_0205 Spy49_0205 Spy49_0205 Spy49_0205 Spy49_0205 Spy49_0205 Spy49_0206 Spy49_0206 Spy49_0206 Spy49_0206 Spy49_0208	pgi hasC.2 gpsA dut radA - gltX fasB	NE E NE E NE	196067 197875 199964 200734 201666 203220 203419 205128 207105 207907 208402 209985 210613 211506 213347 214690 215977 217257 217600	199272 200635 201633 202682 203426 205125 206912 207797 208365 209796 210482 211323 212996 214693 215973 21671 217616 218409	465 223 299 338 68 568 594 230 152 464 165 236 496 448 427 246 119 269	- + + + + + + + + + + + + + + + + + + +	6984896 6984897 6984898 6984890 6984901 6984902 6984983 6984986 6984986 6984986 6984989 6984989 6984990	COG1210M COG0240C COG1132V COG1132V COG1636S COG0756F COG10660 COG028P COG2013S COG0008J COG2972T COG2972T COG3279KT COG0594J COG0766U	Rofa family transcriptional regulator hypothetical protein Spy49_0190 UTP-glucose-1-phosphate uridylyltransferase NAD(P)H-dependent glycerol-3-phosphate dehydrogenase Mark family transcriptional regulator, partial ABC transporter ATP-binding protein ABC transporter ATP-binding protein/permease hypothetical protein Spy49_0198 deoxyuridine 5\\\^triphosphate nucleotidohydrolase DNA repair protein RadA carbonic anhydrase hypothetical protein Spy49_0202 glutamyl-RNA synthetase histdine kinase Response regulator FasA ribonuclease P hypothetical protein Spy49_0208
Spy49_0188 Spy49_0189c Spy49_0190 Spy49_0191c Spy49_0192c Spy49_0193 Spy49_0195 Spy49_0195 Spy49_0200	pgi hasC.2 gpsA dut radA - gltX fasB	NE E NE E NE NC NE NE NE NE NC NE NC NE NC NE NC NC NC NC NC NC	196067 197875 199964 200734 201666 203220 203419 205128 207105 207907 208402 209985 210613 211506 213347 214690 215977 217257	199272 200635 201633 202682 203426 205125 206912 207797 208365 209796 210482 211323 212996 214693 215973 216717 217616	465 223 299 338 68 568 594 230 152 464 165 236 496 448 427 246 119	- - + + + + + + + + + + +	6984896 6984897 6984899 6984900 6984901 6984902 6984984 6984985 6984986 6984987 6984988 6984989 6984989	COG1210M COG0240C - - COG1132V COG132S COG0756F COG1066O COG0288P COG2013S COG0981 COG2972T COG2972T COG3279KT COG0594J	Rofa Family transcriptional regulator hypothetical protein Spy49_0190 UTP-glucose-1-phosphate undylyltransferase NAD(P)H-dependent glycerol-3-phosphate dehydrogenase MAR family transcriptional regulator, partial ABC transporter ATP-binding protein ABC transporter ATP-binding protein/permease hypothetical protein Spy49_0198 deoxyuridine S\-'triphosphate nucleotidohydrolase DNA repair protein RadA carbonic anhydrase hypothetical protein Spy49_0202 glutamyl-tRNA synthetase histidine kinase histidine kinase Response regulator FasA ribonuclease P
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		_	242554	242554	226		C00F01F	00000570	NAP described to sold the de 2 described to the described
Spy49_0234 Spy49_0235c	plr -	E NC	242651 243887	243661 244003	336 38	+	6985016	COG0057G	NAD-dependent glyceraldehyde-3-phosphate dehydrogenase hypothetical protein Spy49_0235c
Spy49_0236c	-	NE	244145	244885	246	-		COG1126E	amino acid ABC transporter ATP-binding protein
Spy49_0237c	-	NE	244951	246447	498	-	6985018	COG0765E	glutamine-binding periplasmic protein
Spy49_0238	-	NE	246645	248459	604	+		COG4907S	hypothetical protein Spy49_0238
Spy49_0239 Spy49_0240	bacA mecA	NE NE	248637 249622	249476 250383	279 253	+		COG1968V COG4862OTN	undecaprenyl pyrophosphate phosphatase adaptor protein
Spy49_0240	rgpG	E	250390	251559	389	+		COG0472M	undecaprenyl-phosphate N-acetylglucosaminyl 1- phosphate transferase
Spy49_0242	-	NC	251681	252451	256	+		COG0396O	iron-sulfur cluster assembly ATPase SufC
Spy49_0243	-	С	252546	253808	420	+		COG07190	iron-sulfur cluster assembly protein SufD
Spy49_0244	-	NC	253839	255065	408	+		COG0520E	cysteine desulfurase
Spy49_0245 Spy49_0246	-	NC NC	255052 255524	255531 256942	159 472	+		COG0822C COG0719O	iron-sulfur cluster assembly scaffold protein IscU iron-sulfur cluster assembly protein SufB
Spy49_0247	pbp7	NE	257094	258275	393			COG1686M	D-alanyl-D-alanine carboxypeptidase
Spy49_0248c	dacA	NE	258489	259676	395			COG1686M	Penicillin-binding protein 7
Spy49_0249	oppA	NE	260007	261977	656	+		COG4166E	peptide ABC transporter substrate-binding protein
Spy49_0250	oppB	NE	262042	263544	500	+		COG0601EP	peptide ABC transporter permease
Spy49_0251	oppC	NE	263544	264470	308	+		COG1173EP COG0444EP	peptide ABC transporter permease
Spy49_0252 Spy49_0253	oppD oppF	NE NE	264479 265542	265549 266465	356 307	+		COG0444EP COG1123R	peptide transport ATP-binding protein oppD peptide transport ATP-binding protein oppF
Spy49_0254c	-	NE	266613	266852	79		6985035	-	transposase
Spy49_0256	comX1	NE	272853	273338	161	+	6985042	-	ComX1 Alternate Sigma Factor
Spy49_0257	-	С	273839	274423	194	+		COG2179R	hypothetical protein Spy49_0257
Spy49_0258	-	E	274423	275544	373	+		COG1161R	GTP-binding protein YqeH
Spy49_0259 Spy49_0260	- nadD	NE NC	275569 275946	275877 276578	102 210	+		COG1534J COG1057H	hypothetical protein Spy49_0259 nicotinic acid mononucleotide adenylyltransferase
Spy49_0261	-	NE	276575	277168	197	+		COG1713H	hypothetical protein Spy49_0261
Spy49_0262	-	NE	277168	277545	125	+		COG0799S	hypothetical protein Spy49_0262
Spy49_0263	-	NE	277593	278336	247	+		COG2226H	ubiquinone/menaquinone biosynthesis methyltransferase UbiE/COQ5
Spy49_0264	-	NE	278558	279664	368	+		COG1323R	hypothetical protein Spy49_0264
Spy49_0265 Spy49_0266	atmA	NE NC	280146 281260	280862 281907	238 215	+		COG0217S COG0834ET	hypothetical protein Spy49_0265 ABC transporter substrate-binding protein
Spy49_0268	atmB	NE	282234	283079	281	+		COG1464P	methionine ABC transporter substrate-binding protein
Spy49_0269	atmD	NE	283329	284393	354	+		COG1135P	ABC transporter
Spy49_0270	atmE	NE	284394	285086	230	+		COG2011P	methionine ABC transporter permease
Spy49_0271c	braB	NE	285140	286474	444	-		COG1114E	branched-chain amino acid ABC transporter
Spy49_0272	-	NE	286820	287959	379	+		COG3633E	serine/threonine transporter SstT
Spy49_0273c Spy49_0274c		E	288014 288698	288688 290089	224 463			COG0569P COG0168P	potassium uptake protein, Trk family V-type Na+-ATPase subunit J
Spy49_0275	gidB	NE	290158	290871	237	-		COG0357M	16S rRNA methyltransferase GidB
Spy49_0276	lemA	NE	291021	291578	185	+		COG1704S	cytoplasmic membrane protein
Spy49_0277	htpX	NE	291625	292521	298	+		COG05010	heat shock protein HtpX
Spy49_0278	-	NE	292755	293288	177	+		COG1399R	hypothetical protein Spy49_0278
Spy49_0279 Spy49_0280	csrR csrS	NC E	293555 294247	294241 295749	228 500	+		COG0745TK COG0642T	Response regulator CsrR transmembrane histidine kinase CsrS
Spy49_0281	nrdR	c	295964	296458	164	+		COG1327K	NrdR family transcriptional regulator
Spy49_0282	dnaB	E	296442	297617	391	+		COG3611L	chromosome replication initiation protein/membrane attachment protein
Spy49_0283	dnal	E	297618	298520	300	+		COG1484L	primosomal protein Dnal
Spy49_0284	engA	E	298583	299893	436	+		COG1160R	GTP-binding protein EngA
Spy49_0285 Spy49_0286	snf	NC NE	300100 303442	303198 304044	1032 200	+	6985150	COG0553KL	SNF helicase hypothetical protein Spy49_0286
Spy49_0286 Spy49_0287	murC	E	304084	305412	442	+		COG0773M	UDP-N-acetylmuramateL-alanine ligase
Spy49_0288	-	NE	305458	305940	160	+		COG0456R	arylalkylamine n-acetyltransferase
Spy49_0289	-	NC	306058	307626	522	+	6985154	COG1559R	aminodeoxychorismate lyase
Spy49_0290	greA	NC	307651	308181	176	+		COG0782K	transcription elongation factor GreA
Spy49_0291	oxaA	E	308800	309723	307	-		COG0706U	OxaA-like protein
Spy49_0292c Spy49_0293	-	NE NE	309805 310344	310083 311081	92 245	+		COG1254C COG0566J	acylphosphatase rRNA methylase
Spy49_0294		NE	311120	311620	166	+		COG1418R	hypothetical protein Spy49_0294
Spy49_0295	-	NC	311635	312324	229	+		COG0670R	hypothetical protein Spy49_0295
Spy49_0296	-	NC	312502	312744	80	+		COG3763S	hypothetical protein Spy49_0296
Spy49_0297	glr	E	312922	313716	264	+		COG0796M	glutamate racemase
Spy49_0298 Spy49_0299		NE NE	313713 314678	314699 315199	328 173	+		COG0127F COG0622R	deoxyribonucleotide triphosphate pyrophosphatase/unknown domain fusion protein hypothetical protein Spy49 0299
Spy49_0300		NE	315196	315657	153	+		COG4109K	CBS domain-containing protein
Spy49_0301	xerD	NE	315654	316400	248	+	6985166	COG4974L	site-specific tyrosine recombinase XerD-like protein
Spy49_0302	scpA	NE	316400	317104	234	+		COG1354S	segregation and condensation protein A
Spy49_0303	scpB	NE	317101	317652	183	+	6985168	COG1386K	
Spy49_0304 Spy49_0305	rluB	NE	317773						segregation and condensation protein B
Spy49_0306		NE		318495	240	+	6985169	COG1187J	ribosomal large subunit pseudouridine synthase
		NE NE	318495	318755	240 86	+ + +	6985169 6985170	COG0759S	ribosomal large subunit pseudouridine synthase hypothetical protein Spy49_0305
Spy49_0307	-	NE NE NE			240	+	6985169 6985170 6985171 6985172	COG0759S COG0219J COG3601S	ribosomal large subunit pseudouridine synthase
Spy49_0308	-	NE NE NE	318495 318933 319792 320553	318755 319481 320328 321011	240 86 182 178 152	+	6985169 6985170 6985171 6985172 6985173	COG0759S COG0219J COG3601S COG0671I	ribosomal large subunit pseudouridine synthase hypothetical protein Spy49_0305 rRNA methylase riboflavin transporter YpaA phosphatase, partial
Spy49_0308 Spy49_0309		NE NE NE NE	318495 318933 319792 320553 321303	318755 319481 320328 321011 322223	240 86 182 178 152 306	+ + + +	6985170 6985171 6985172 6985173 6985174	COG0759S COG0219J COG3601S COG0671I COG1242R	ribosomal large subunit pseudouridine synthase hypothetical protein spyt49_0305 rRNA methylase riboflavin transporter YpaA phosphatase, partial hypothetical protein Spyt49_0309
Spy49_0308 Spy49_0309 Spy49_0310	- - - hlvX	NE NE NE NE	318495 318933 319792 320553 321303 322262	318755 319481 320328 321011 322223 322816	240 86 182 178 152 306 184	+++++++++++++++++++++++++++++++++++++++	6985169 6985170 6985171 6985172 6985173 6985174 6985175	COG0759S COG0219J COG3601S COG0671I COG1242R COG2265J	ribosomal large subunit pseudouridine synthase hypothetical protein Spy49_0305 rRNA methylase riboflavin transporter YpaA phosphatase, partial hypothetical protein Spy49_0309 hypothetical protein Spy49_0310
Spy49_0308 Spy49_0309	- - - - hlyX pfIC	NE NE NE NE	318495 318933 319792 320553 321303	318755 319481 320328 321011 322223	240 86 182 178 152 306	+ + + + +	6985169 6985170 6985171 6985172 6985173 6985174 6985175 6985176	COG0759S COG0219J COG3601S COG0671I COG1242R	ribosomal large subunit pseudouridine synthase hypothetical protein spyt49_0305 rRNA methylase riboflavin transporter YpaA phosphatase, partial hypothetical protein Spyt49_0309
Spy49_0308 Spy49_0309 Spy49_0310 Spy49_0311 Spy49_0312 Spy49_0313		NE NE NE NE NE NE NE NE E	318495 318933 319792 320553 321303 322262 322950 324290 325284	318755 319481 320328 321011 322223 322816 324284 325153 326219	240 86 182 178 152 306 184 444 287 311	+ + + + + + +	6985169 6985170 6985171 6985172 6985173 6985174 6985175 6985176 6985177 6985178	COG0759S COG0219J COG3601S COG0671I COG1242R COG2265J COG1253R	ribosomal large subunit pseudouridine synthase hypothetical protein Spy49_0305 rRNA methylase riboflavin transporter YpaA phosphatase, partial hypothetical protein Spy49_0309 hypothetical protein Spy49_0310 hemolysin pyruvate formate-lyase activating enzyme manganese-dependent inorganic pyrophosphatase
Spy49_0308 Spy49_0309 Spy49_0310 Spy49_0311 Spy49_0312 Spy49_0313 Spy49_0314	pfIC - -	NE	318495 318933 319792 320553 321303 322262 322950 324290 325284 326295	318755 319481 320328 321011 322223 322816 324284 325153 326219 326948	240 86 182 178 152 306 184 444 287 311 217	+ + + + + + +	6985169 6985170 6985171 6985172 6985173 6985174 6985175 6985176 6985177 6985178 6985179	COG0759S COG0219J COG3601S COG0671J COG1242R COG2265J COG1253R COG1180O COG1227C	ribosomal large subunit pseudouridine synthase hypothetical protein Spy49_0305 rRNA methylase riboflavin transporter YpaA phosphatase, partial hypothetical protein Spy49_0309 hypothetical protein Spy49_0310 hemolysin pyruvate formate-lyase activating enzyme manganese-dependent inorganic pyrophosphatase hypothetical protein Spy49_0314
Spy49_0308 Spy49_0309 Spy49_0310 Spy49_0311 Spy49_0312 Spy49_0313 Spy49_0314 Spy49_0315	pfIC - - fhuG	NE N	318495 318933 319792 320553 321303 322262 322950 324290 325284 326295 326993	318755 319481 320328 321011 322223 322816 324284 325153 326219 326948 328030	240 86 182 178 152 306 184 444 287 311 217 345	+ + + + + + +	6985169 6985170 6985171 6985172 6985173 6985174 6985175 6985176 6985177 6985178 6985179 6985180	COG0759S COG0219J COG3601S COG1671I COG1242R COG2265J COG1253R COG1180O COG1227C - COG0609P	ribosomal large subunit pseudouridine synthase hypothetical protein Spy49_0305 rRNA methylase riboflavin transporter YpaA phosphatase, partial hypothetical protein Spy49_0309 hypothetical protein Spy49_0310 hemolysin pyruvate formate-lyase activating enzyme manganese-dependent inorganic pyrophosphatase hypothetical protein Spy49_0314 ferrichrome ABC transporter permease
Spy49_0308 Spy49_0309 Spy49_0310 Spy49_0311 Spy49_0312 Spy49_0313 Spy49_0314 Spy49_0315 Spy49_0316	pfIC - - fhuG fhuB1	NE N	318495 318933 319792 320553 321303 322262 322950 324290 325284 326295 326993 327991	318755 319481 320328 321011 322223 322816 324284 325153 326219 326948 328030 329043	240 86 182 178 152 306 184 444 287 311 217 345 350	+ + + + + + +	6985169 6985170 6985171 6985172 6985173 6985174 6985175 6985176 6985177 6985178 6985179 6985180 6985181	COG0759S COG0219J COG3601S COG0671I COG1242R COG2265J COG1253R COG1180O COG1227C - COG0609P COG0609P	ribosomal large subunit pseudouridine synthase hypothetical protein Spy49_0305 rRNA methylase riboflavin transporter YpaA phosphatase, partial hypothetical protein Spy49_0309 hypothetical protein Spy49_0310 hemolysin pyruvate formate-lyase activating enzyme manganese-dependent inorganic pyrophosphatase hypothetical protein Spy49_0314 ferrichrome ABC transporter permease ferrichrome ABC transporter permease ferrichrome ABC transporter permease
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Spy49_0308 Spy49_0310 Spy49_0311 Spy49_0312 Spy49_0312 Spy49_0314 Spy49_0314 Spy49_0316 Spy49_0316 Spy49_0316 Spy49_0316 Spy49_0322 Spy49_0322 Spy49_0322 Spy49_0325 Spy49_0326 Spy49_0326 Spy49_0327 Spy49_0328 Spy49_0328 Spy49_0328 Spy49_0328 Spy49_0328 Spy49_0328 Spy49_0328 Spy49_0328 Spy49_0333 Spy49_0335 Spy49_0335 Spy49_0335 Spy49_0335 Spy49_0335 Spy49_0335 Spy49_0335 Spy49_0335 Spy49_0335 Spy49_0335 Spy49_0335 Spy49_0335 Spy49_0335 Spy49_0335 Spy49_0335 Spy49_0335 Spy49_0335 Spy49_0335 Spy49_0335 Spy49_0336	pfiC	NE N	318495 318933 319792 320553 321303 322262 322950 324290 325284 326295 326993 327991 329991 332552 334353 335206 334353 335206 336288 336288 336812 337465 338688 339332 340222 340222 340222 340222 34053 35506 35693 35693 35693 35693 36793 36	318755 319481 320328 321011 322223 322816 324284 325153 326948 328030 329043 329043 339773 332464 334182 335796 336563 337447 338340 338349 339327 340195 34	240 86 182 178 86 182 178 152 2306 184 444 287 350 310 217 260 481 291 291 53 310 217 287 339 31621 217 666 337 162 725 250	+ + + + + + + + + + + + + + + + + + + +	9985169 9985171 9985172 9985173 9985173 9985174 9985175 9985178 9985178 9985178 9985181 9985181 9985183 9985184 9985185 9985188 9985189 9985189 9985191 9985191 9985192 9985193 9985194 9985195 9985196 9985196 9985197 9985198	COG0759S COG0759S COG0671I COG0671I COG1242R COG226SJ COG128CR COG128CR COG128CR COG128CR COG1800P COG0609P COG0609P COG0614P COG0609P COG0614P COG0769M COG2244R COG0035F COG0740OU COG0769M COG2244R COG0035F COG0740OU COG1774S COG4471S COG0470L COG1774S COG4675 COG0768L COG0768L COG0768L COG0708L COG1393P COG0708L COG1394C COG1404OC COG1404OC COG1404OC COG1404OC COG1404OC COG3619S COG0143J COG0028F COG01780F	ribosomal large subunit pseudouridine synthase hypothetical protein Spy49_0305 rRNA methylase riboflavin transporter YpaA phosphatase, partial hypothetical protein Spy49_0309 hypothetical protein Spy49_0310 hemolysin pyruvate formate-lyase activating enzyme manganese-dependent inorganic pyrophosphatase hypothetical protein Spy49_0314 ferrichrome ABC transporter permease ferrichrome ABC transporter permease ferrichrome ABC transporter binding protein fmuc UDP-N-acetylmuramoylalanyl-D-glutamate-L-lysine ligase polysaccharide biosynthesis protein uracil phosphoribosyltransferase ATP-dependent Clp protease proteolytic subunit hypothetical protein Spy49_0325 thymidylate kinase DNA polymerase Ill subunit deltal' signal peptidase-like protein DNA replication initiation control protein YabA tetrapyrrole methylase hypothetical protein Spy49_0331 copper homeostasis protein arsenate reductase Jevo deoxyribonuclease lactate oxidase cell envelope proteinase lactate oxidase cell envelope proteinase lactate oxidase cell envelope proteinase linsubunit protein Spy49_0337 methionyl-tRNA synthetase ribonucleotide diphosphate reductase subunit alpha hypothetical protein Spy49_0337 methionyl-tRNA synthetase ribonucleotide reductase stimulatory protein ribonucleotide reductase stimu
Spv49_0308 Spv49_0310 Spv49_0311 Spv49_0312 Spv49_0312 Spv49_0314 Spv49_0315 Spv49_0315 Spv49_0316 Spv49_0319 Spv49_0320 Spv49_0320 Spv49_0320 Spv49_0323 Spv49_0326 Spv49_0326 Spv49_0327 Spv49_0328 Spv49_0328 Spv49_0328 Spv49_0328 Spv49_0328 Spv49_0328 Spv49_0328 Spv49_0328 Spv49_0328 Spv49_0338	pfiC	NE N	318495 318933 319792 320553 321303 322262 325284 326295 326993 327991 329033 329991 331019 332552 334353 334353 335206 336288 336812 337455 336812 337457 340227 34088 340222 340661 351196 351196 351196 35194 355166	318755 319481 320328 321011 322223 322816 324284 325153 326219 326948 328030 329965 330773 332464 334186 335796 336563 337447 338340 339327 340195 340614 341953 34298 344269 34982 353196 353196 353196 353196 353196	240 182 178 366 182 178 306 184 444 444 287 350 260 481 209 211 291 53 107 287 107 287 130 209 118 303 393 393 393 393 393 393 393	+ + + + + + + + + + + + + + + + + + + +	9985169 9985170 9985171 9985172 9985173 9985174 9985175 9985176 9985176 9985176 9985176 9985178 9985181 9985181 9985181 9985188 9985188 9985189 9985189 9985190 9985190 9985190 9985200 9985200 9985200 9985200 9985200	COG0759S COG0759S COG0759S COG0671I COG0671I COG0671I COG1242R COG226SJ COG124R COG1253R COG11800 COG127C COG0609P COG0609P COG0609P COG0609P COG0609P COG070P COG0709M COG2244R COG0709S COG0740OU COG4471S COG078S COG0740OU COG4471S COG0179T COG0179S COG0133R COG0708L COG1304C COG1304C COG170BC COG01780F COG0208F COG1780F COG0209F	ribosomal large subunit pseudouridine synthase hypothetical protein Spy49_0305 rRNA methylase riboflavin transporter YpaA phosphatase, partial hypothetical protein Spy49_0309 hypothetical protein Spy49_0310 hemolysin pyrouste formate-lyase activating enzyme manganese-dependent inorganic pyrophosphatase hypothetical protein Spy49_0314 ferrichrome ABC transporter permease ferrichrome ABC transporter permease ferrichrome ABC transporter substrate-binding protein ferrichrome ABC transporter substrate-binding protein ferrichrome ABC transporter substrate-binding protein fuc UDP-N-acetylmuramoylalanyl-D-glutamate-L-lysine ligase polysaccharide biosynthesis protein uracil phosphoribosyltransferase ATP-dependent Clp protease proteolytic subunit hypothetical protein Spy49_0325 thymidylate kinase USAP polymerase ill subunit delta\'signal peptidase-like protein DNA replication intation control protein YabA tetrapyrrole methylase hypothetical protein Spy49_0331 copper homeostasis protein arsenate reductase 3-exo-deoxynbonuclease lactate oxidase cell envelope proteinase hypothetical protein Spy49_0337 methionyl-tRNA synthetase ribonucleotide diphosphate reductase subunit beta ribonucleotide reductase stimulatory protein ribonucleotide diphosphate reductase subunit alpha

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Snv49 0345c
                                                        359568
                                                                       359765
                                                                                                         6985208 COG3464I
                                                                                                                                             transposase
                                              277
89
134
Spy49_0346c
Spy49_0347
                                                        360026
361343
                                                                       360859
361612
                                                                                                                                              transposase
transposase, ISSmu2
hypothetical protein Spy49_0347
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Spy49 0348
                                                        362242
                                                                       362646
                                                                                                         6985211
                                                                                                                                              hypothetical protein Spy49 0348
                                                                                                                                              hypothetical protein Spy49_0349c
hypothetical protein Spy49_0350c
hypothetical protein Spy49_0351c
Spy49 03490
                                                        363232
                                                                       363621
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                                                                                                         6985212
Spy49_0350c
Spy49_0351c
                                                        364340
365190
                                                                       365032
365372
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                                                                                                          6985213
                                                                                                         6985214
                                                                                      60
61
Spy49 0352c
                                                        365511
                                                                       365696
                                                                                                         6985215
                                                                                                                                              hypothetical protein Spy49 0352d
Spy49_0353c
Spy49_0354c
                                                                       366108
366256
367032
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57
137
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hypothetical protein Spy49_0354c
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                                                        366083
366619
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Spy49 03550
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                                                                                                                                              hypothetical protein Spy49 03550
Spv49_0356c
                                                        367138
                                                                       367644
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                                                                                                         6985219
                                                                                                                                              hypothetical protein Spy49 0356c
Spy49_0357c
Spy49_0358c
                                                        367681
368000
                                                                       368010
368602
                                                                                     109
200
                                                                                                                                              hypothetical protein Spy49_0357c
Prophage ps3 protein 07
                                                                                                         6985220
                                                                                                                                              hypothetical protein Spy49 0359c
Spy49 0359c
                                                        368868
                                                                       369134
                                                                                     88
57
562
285
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Spy49_0360c
Spy49_0361c
Spy49_0362c
                                                                                                                                              phage protein
DNA primase-phage associated
                                                        369315
                                                                       369488
                                                                                                         6985303
                                                        369776
371433
                                                                      371464
372290
                                                                                                          6985304
                                                                                                                       COG3378R
                                                                                                         6985305
                                                                                                                                              replication protein
                                                                                                                                              hypothetical protein Spy49 0363c
Spy49 0363c
                                                        372434
                                                                       372712
                                                                                                         6985306
                                                                                      92
37
64
69
                                                        372715
373055
373246
Spy49_0364c
Spy49_0365c
                                                                                                                                              hypothetical protein Spy49_0364c, partial
hypothetical protein Spy49_0365c
                                                                       372828
                                                                                                         6985307
                                                                      373249
373455
                                                                                                          6985308
                                                                                                         6985309
Spy49 0366c
                                                                                                                                              hypothetical protein Spy49 0366c
Spy49 0367c
                                                        373980
                                                                       374228
                                                                                      82
                                                                                                         6985310
                                                                                                                                              hypothetical protein Spy49 03670
                                                                                     61
222
381
Spy49_0368c
Spy49_0369
                                                        374244
374597
                                                                      374429
375265
                                                                                                         6985311 COG1426S
                                                                                                                                              hypothetical protein Spy45_0368c
phage-associated protein
                                                                                                                       COG1396K
Spy49 0370
                                              375347
                                                                       376492
                                                                                                         6985313
                                                                                                                       COG4974L
                                                                                                                                              integrase
Spy49_0371
Spy49_0372
Spy49_0373
                                                                                     78
232
319
                                                        377362
                                                                       377598
                                                                                                         6985314
                                                                                                                                              hypothetical protein Spy49 0371
                                                        377591
378365
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379324
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6985316
                                                                                                                       COG1028IQR
COG0673R
                                                                                                                                              3-ketoacyl-ACP reductase
hypothetical protein Spy49_0373
                    fabG
Spy49 0374
                    glpT
                                                        379657
                                                                       380994
                                                                                     445
                                                                                                         6985317
                                                                                                                       COG2271G
                                                                                                                                              glycerol-3-phosphate transporter
Spy49_0375
Spy49_0376
Spy49_0377
                                                                                                                                              greeton-spinspinate unapported
infurctional N-acetylglucosamine-1-phosphate uridyltransferase/glucosamine-1-phosphate acetyltransfe...
ADP-ribose pyrophosphatase
hypothetical protein Spy49_0377
                    glmU
                                                                                     460
184
                                                        381167
                                                                       382549
                                                                                                         6985318
                                                                                                                       COG1207M
                                                        382580
                                                                       383134
                                                                                                          6985319
                                                                                                                       COG0494LR
                                                                                      83
                                                        383134
                                                                       383385
                                                                                                         6985320
                                                                                                         6985321 COG0775F
Spv49 0378
                    nfs
                                                        383405
                                                                       384100
                                                                                     231
                                                                                                                                              5\'-methylthioadenosine/S-adenosylhomocysteine nucleosidase
Spy49_0379
Spy49_0380c
                                                        384251
384689
                                                                       384592
385336
                                                                                                                                              hypothetical protein Spy49_0379
metal-dependent transcriptional regulator
                                                                                     113
215
                                                                                                         6985322
                                                                                                                       COG1321K
Spy49 0381
                    mtsA
                                                        385590
                                                                       386414
                                                                                     274
                                                                                                         6985324
                                                                                                                       COG0803P
                                                                                                                                              Metal ABC transporter substrate-binding lipoprotein
Spy49_0382
Spy49_0383
Spy49_0384c
                                                                                     241
284
268
                                                                                                                                              ATP-binding protein MtsB
Integral membrane protein MtsC, ABC transporter
cyclophilin-type protein
                    mtsB
                                                        386478
                                                                       387203
                                                                                                         6985325
                                                                                                                       COG1121P
                                                        387204
388206
                                                                       388058
389012
                                                                                                          6985326
                                                                                                                       COG1108P
                                                                                                         6985327
                                                                                                                       COG0652O
                    cypB
Spy49 0385
                    ftsK
                                                        389229
                                                                       391634
                                                                                     801
                                                                                                         6985328 COG1674D
                                                                                                                                              cell division protein FtsK
Spy49_0386c
Spy49_0387
Spy49_0388
                                                                                                                                              hypothetical protein Spy49_0386c
50S ribosomal protein L11
50S ribosomal protein L1
                                                        391704
                                                                       392054
                                                                                     116
141
                                                                                                         6985329
                                                                                                         6985330 COG0080J
6985331 COG0081J
                    rplK
                                                        392301
                                                                       392726
                    rplA
                                                                       393521
                                                                                     229
                                                        392832
Spy49 0390
                    pyrH
frr
                                                        393843
                                                                       394571
                                                                                     242
                                                                                                         6985332
                                                                                                                       COG0528F
                                                                                                                                              uridylate kinase
Spy49_0391
Spy49_0392
                                                        394600
395266
                                                                       395157
396123
                                                                                                                       COG0233J
COG2996S
                                                                                                                                              ribosome recycling factor
S1 RNA binding domain
                                                                                     185
285
                                                                                                         6985333
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NE
NE
NE
NE
NE
E
                    mrsA
                                                                                     169
Spy49 0394
                                                        396196
                                                                       396705
                                                                                                         6985335
                                                                                                                       COG02250
                                                                                                                                              methionine sulfoxide reductase A
Spy49_0395
Spy49_0396
Spy49_0398
                                                                                     71
389
603
                                                                                                                                              hypothetical protein Spy49_0395
42 kDa protein
myosin-cross-reactive antigen
                                                        396702
                                                                       396917
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                                                                                                                       COG4479S
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398517
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400328
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                                                                                                         6985338
                                                                                                                       COG4716S
Spy49 0399
                    phoH
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Spy49_0400
Spy49_0401
Spy49_0402
                                                                                     191
165
135
                                                                                                                                              hypothetical protein Spy49_0400
metalloprotease
                                                        401585
                                                                       402160
                                                                                                         6985340
                                                                                                                       COG1573L
                                                        402319
                                                                       402816
                                                                                                         6985341
                    dgk
                                                        402797
                                                                       403204
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                                                                                                                       COG0818M
                                                                                                                                              Diacylglycerol kinase
                                                                                                                                              GTP-binding protein Era
hypothetical protein Spy49_0404
hypothetical protein Spy49_0405
Spv49 0403
                    era
                                                        403324
                                                                      404220
                                                                                     298
                                                                                                         6985343 COG1159R
                                                                                     158
84
60
Spy49_0404
Spy49_0405c
                                                        404241
405023
                                                                      404717
405277
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                                                                                                                       COG1051F
                                              Spy49 0406
                                                        405910
                                                                       406092
                                                                                                         6985346
                                                                                                                                              hypothetical protein Spy49 0406
Spy49_0407c
Spy49_0408c
Spy49_0409
                                                                                      49
140
75
                                                        406430
                                                                      406579
                                                                                                         6985347 COG3328I
                                                                                                                                              transposase
                                                        406576
407316
                                                                      406998
407543
                                                                                                          6985348
                                                                                                                       COG3328L
                                                                                                                                              transposase for insertion sequence element IS905
                                                                                                         6985349
                                                                                                                                              bacteriocin
                                                                                                                                              hypothetical protein Spy49 0410
Spy49 0410
                                                        408295
                                                                      408555
                                                                                      86
                                                                                                         6985350
Spy49_0411
Spy49_0412
Spy49_0413
                                                                                      123
355
                                                                                                                                              hypothetical protein Spy49_0411
hypothetical protein Spy49_0412
                                                        408771
                                                                      409142
                                                                                                         6985351
                                                                      410494
410985
                                                                                                         6985352
6985353
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                                                        410587
                                                                                     132
                                                                                                                                              hypothetical protein Spy49 0413
Spy49 0414c
                                                        411333
                                                                      411602
                                                                                      89
                                                                                                         6985354
                                                                                                                                              hypothetical protein Spy49 0414c
Spy49_0415
Spy49_0416
                                                        412673
413711
                                                                      413539
414538
                                                                                     288
275
                                                                                                                                              positive transcriptional regulator
formamidopyrimidine-DNA glycosylase
                                                                                                         6985355
                    mutR
                                                                                                                       COG0266L
                    fpg
Spy49 0417
                    coaE
                                                        414517
                                                                      415128
                                                                                     203
                                                                                                         6985357
                                                                                                                       COG0237H
                                                                                                                                              dephospho-CoA kinase
Spy49_0418
Spy49_0419
Spy49_0420
                                                                                                                                              hypothetical protein Spy49_0418
multidrug resistance efflux pump
50S ribosomal protein L33
                                                        415318
                                                                      416820
                                                                                     500
                                                                                                         6985358
                                                                                                                       COG0433R
                                              NC
NC
NC
NC
NE
NE
NE
NE
NE
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418132
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418278
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48
78
                                                                                                          6985359
                                                                                                                       COG28140
                                                                                                         6985360
                    rpmG
                                                                                                                       COG0267J
                                                                                                                                              preprotein translocase subunit SecG
Spy49 0421
                    secG
                                                        418324
                                                                      418560
                                                                                                         6985361
Spy49_0422
Spy49_0423
Spy49_0424
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420990
421472
                                                                                     777
155
                    vacB
                                                                       420987
                                                                                                         6985362
                                                                                                                       COG0557K
                                                                                                                                              exoribonuclease R
                                                                                                                       COG06910
COG38230
                    smpB
                                                                       421457
                                                                                                          6985363
                                                                                                                                              SsrA-binding protein
                                                                                                         6985364
                                                                                                                                              glutamine cyclotransferase
                                                                       422182
                                                                                     236
                                                                                                                                              pyrrolidone-carboxylate peptidase
hypothetical protein Spy49_0426c
hypothetical protein Spy49_0427c
Spv49 0425c
                    рср
                                                        422300
                                                                      422947
                                                                                     215
                                                                                                         6985365
                                                                                                                       COG2039O
Spy49_0426c
Spy49_0427c
                                                        422998
423924
                                                                      423924
424607
                                                                                     308
227
                                                                                                         6985366
                                                                                                                       COG3817S
COG3819S
Spy49 0428c
                                                        424818
                                                                       425744
                                                                                     308
                                                                                                         6985368 COG0463M
                                                                                                                                              sugar transferase
Spy49_0429c
Spy49_0430c
Spy49_0431c
                                                                                     125
221
361
                    gloA
                                                        425889
                                                                      426266
                                                                                                         6985369
                                                                                                                       COG0346F
                                                                                                                                              lactoylglutathione lyase
NAD(P)H-flavin oxidoreductase
                                                                      426942
428076
                                                                                                                       COG0778C
COG0006E
                                                        426277
                                                                                                          6985370
                                                                                                         6985371
                    pepQ
                                                        426991
                                                                                                                                              Xaa-Pro dipeptidase
Spy49 0432
                    ссрА
                                                        428250
                                                                      429251
                                                                                     333
                                                                                                         6985372
                                                                                                                       COG1609K
                                                                                                                                              Catabolite control protein A
Spy49_0433
Spy49_0434
Spy49_0435
                                                                                     332
444
647
                                                                                                                                              sugar transferase
glucosyl transferase
threonyl-tRNA synthetase
                                                        429382
                                                                       430380
                                                                                                         6985373
                                                                                                                       COG0438M
                                                                                                         6985374 COG0438M
6985375 COG0441J
                                                        430382
                                                                       431716
                    thrS
                                                        432138
                                                                       434081
Spy49 0436
                    tagH
                                                        434222
                                                                      435214
                                                                                     330
                                                                                                         6985376
                                                                                                                       COG45868
                                                                                                                                              Teichoic acid export ATP-binding protein tagH
                                              435216
436036
437022
Spy49_0437
Spy49_0438
                                                                      436034
436821
                                                                                                                       COG4587R
COG3694R
                                                                                                                                              hypothetical protein Spy49_0437
hypothetical protein Spy49_0438
                                                                                     272
261
                                                                                                         6985377
Spy49 0439
                                                                      437171
                                                                                     49
382
                                                                                                         6985379
                                                                                                                                              dihydroxyacetone kinase
Spy49_0440
Spy49_0441
Spy49_0442
                                                                                                                                              acetyl-CoA acetyltransferase
Long-chain-fatty-acid--CoA ligase
hypothetical protein Spy49_0442
                                                        437566
                                                                      438714
                                                                                                         6985380 COG01831
                                                        438671
439974
                                                                      439918
441008
                                                                                     415
344
                                                                                                         6985381
6985382
                                                                                                                       COG0318IQ
                                                                                                         6985463 COG0745TK
Spy49 0444
                    vicR
                                                        441170
                                                                      441880
                                                                                     236
                                                                                                                                              two-component response regulator
Spy49_0445
Spy49_0446
Spy49_0447
                                                                      443225
444038
445175
                                                                                     450
269
230
                    vicK
vicX
                                                        441873
                                                                                                         6985464
                                                                                                                       COG5002T
                                                                                                                                              two-component sensor histidine kinase
Zn-dependent hydrolase
                                                        443229
444483
                                                                                                          6985465
                                                                                                                       COG1235R
                    rnc
                                                                                                         6985466
                                                                                                                       COG0571K
                                                                                                                                              ribonuclease III
Spv49 0448
                    smc
                                                        445176
                                                                      448715
                                                                                     1179
                                                                                                         6985467
                                                                                                                       COG1196D
                                                                                                                                              chromosome segregation SMC
Spy49_0449c
Spy49_0450
                                                        448963
450088
                                                                      449814
450960
                                                                                     283
290
                                                                                                                                              positive regulator
shikimate 5-dehydrogenase
                                                                                                         6985468
                                                                                                                       COG0169E
                    aroE
                                                                                                         6985469
                                                                                                                                              hypothetical protein Spy49_0451
Spy49 0451
                                                        450957
                                                                       451793
                                                                                     278
                                                                                                         6985470
                                                                                                                       COG1082G
Spy49_0453
Spy49_0454
                                                                                                                                              hypothetical protein Spy49_0453
hypothetical protein Spy49_0454
S-adenosylmethionine synthetase
                                                        451795
                                                                       452529
                                                                                     244
                                                                                                         6985471
                                                                                                                       COG1478S
                                                        452522
453518
                                                                      453508
454717
                                                                                                                       COG0673R
COG1812E
                                                                                      328
                                                                                                         6985472
Spy49_0455
                                                                                                         6985473
                                                                                      399
Spy49 0456
                                                        454701
                                                                      455603
                                                                                      300
                                                                                                         6985474 COG1493T
                                                                                                                                              hypothetical protein Spy49 0456
```

Spy49_0457			455724	456743	220		C00E47E		h and and a second of the second
Spy49_0458	-	NE NE	455724 457116	456713 457382	329 88	+	6985476	COG0463M	hypothetical protein Spy49_0457 hypothetical protein Spy49_0458
Spy49_0459	-	NE	457406	458563	385	+		COG1004M	UDP-glucose dehydrogenase
Spy49_0460	-	NE	458648	459817	389	+	6985478	-	efflux protein
Spy49_0461c	-	NE	459958	460167	69	-	6985479	COG3655K	hypothetical protein Spy49_0461c
Spy49_0462c	-	NE	460157	461815	552	-	6985480	-	hypothetical protein Spy49_0462c
Spy49_0463c	-	NE	461806	462030	74	-	6985481	-	hypothetical protein Spy49_0463c
Spy49_0464c Spy49_0465	-	NE NC	462034 462958	462924 463116	296 52	+	6985482 6985483	-	hypothetical protein Spy49_0464c hypothetical protein Spy49_0465
Spy49_0466	-	NE	463171	463473	100	+	6985484	COG3077L	hypothetical protein Spy49_0466
Spy49_0467	-	NE	463602	463778	58	+	6985485	-	hypothetical protein Spy49_0467, partial
Spy49_0468	-	NE	464174	464626	150	+	6985486	COG4695S	Portal protein
Spy49_0469	-	NE	464692	465000	102	+	6985487	-	hypothetical protein Spy49_0469
Spy49_0470c	-	NE	465238	465426	62	-	6985488	-	hypothetical protein Spy49_0470c
Spy49_0471 Spy49_0473	-	NE NE	465417 465785	465740 466456	107 223	+	6985489 6985490		hypothetical protein Spy49_0471 asparagine synthetase A
Spy49_0474	-	NE	466617	467864	415	+	6985491		hypothetical protein Spy49_0474
Spy49_0475	-	NE	468092	468808	238	+	6985492		Microcin C7 self-immunity protein mccF
Spy49_0476	-	NE	468984	469943	319	+	6985493		hypothetical protein Spy49_0476
Spy49_0477c	-	NE	470313	471116	267	-	6985494		transposase
Spy49_0478c Spy49_0479	-	NE	471164	471439	91	+	6985495	COG2963L	transposase OrfA, IS3 family
Spy49_0479 Spy49_0480		NE NE	471459 471744	471677 472541	72 265	+	6985496 6985497	- COG0561R	hypothetical protein Spy49_0479 hypothetical protein Spy49_0480
Spy49_0481		NE	472545	473369	274	+	6985498		hypothetical protein Spy49_0481
Spy49_0482	ftsY	E	473369	474919	516	+	6985499		signal recognition particle receptor protein FtsY subunit alpha
Spy49_0483c	-	NE	474973	476340	455	-		COG2814G	drug resistance protein
Spy49_0484	bglG	NE	476668	477510	280	+	6985501		transcription antiterminator
Spy49_0485	-	NE	477512	479374	620 474	+	6985502 6985503		beta-glucoside permease IIABC component
Spy49_0487 Spy49_0488c	bgIA -	NE NE	479393 480916	480817 481731	271	+	6985504		beta-glucosidase hypothetical protein Spy49_0488c
Spy49_0489c		NE	481731	482633	300	-	6985505		hypothetical protein Spy49_0489c
Spy49_0490	-	NE	483170	485302	710	+	6985506	COG2183K	hypothetical protein Spy49_0490
Spy49_0491	-	NE	485244	485726	160	+	6985507		hypothetical protein Spy49_0491
Spy49_0493	- ntsV	NE	485790	486062	90	+		COG1983KT	hypothetical protein Spy49_0493
Spy49_0494 Spy49_0495	ptsK Igt	E NE	486367 487356	487359 488135	330 259	+	6985509 6985510	COG1493T COG0682M	HPr kinase/phosphorylase prolipoprotein diacylglyceryl transferase
Spy49_0495 Spy49_0496	-	NE	488157	488564	135	+	6985511		hypothetical protein Spy49_0496
Spy49_0497	-	NE	488557	488985	142	+	6985512	-	hypothetical protein Spy49_0497
Spy49_0498	-	NE	489044	489313	89	+	6985513	-	hypothetical protein Spy49_0498
Spy49_0499	-	NE	489631	490557	308	+	6985514		protease
Spy49_0500 Spy49_0501		NE NE	490659 492146	491945 492373	428 75	+	6985515 6985516		protease hypothetical protein Spy49_0501
Spy49_0502c		NC	492470	492610	46	-	6985517	-	hypothetical protein Spy49_0502c
Spy49_0503c	lysS	E	492746	494239	497	-	6985518		lysyl-tRNA synthetase
Spy49_0504	-	NE	494413	495315	300	+	6985519		hypothetical protein Spy49_0504
Spy49_0505c Spy49_0506c	-	NE NE	495423 496387	496046 496866	207 159	-	6985520 6985521		phosphoglycerate mutase transcription regulator
Spy49_0507c	-	NE	496957	497520	187		6985522		thiamin transporter
Spy49_0508c	-	NE	497789	498637	282	-		COG3757M	endolysin, phage associated
Spy49_0509	-	NE	498962	499465	167	+	6985524	-	ABC transporter permease
Spy49_0510	-	NE	499449	499835	128	+	6985525	-	hypothetical protein Spy49_0510
Spy49_0511c Spy49_0512c	pepF	NE NE	499881 500353	500360 502152	159 599	-	6985526 6985527		glutathione peroxidase oligoendopeptidase F
Spy49_0513	ppc	NE	502311	505109	932	+	6985528		phosphoenolpyruvate carboxylase
Spy49_0514	ftsW	E	505279	506187	302	+	6985529		cell division protein FtsW
Spy49_0515	tufA	NC	506912	508108	398	+	6985530		elongation factor Tu
Spy49_0516	tpiA murN	E	508349 509207	509107	252 411	+	6985531 6985532		triosephosphate isomerase peptidoglycan branched peptide synthesis protein, alanine adding enzyme
Spy49_0517c Spy49_0518c	murM.1	E		510442				COG2348V	peptidogrycan branched peptide synthesis protein, alanine adding enzyme
		E	510429	511655	408	-			pentidoglycan branched pentide synthesis protein, serine/alanine adding enzyme
Spy49_0519c	-	E NE	510429 511655	511655 512464	408 269	-	6985533		peptidoglycan branched peptide synthesis protein, serine/alanine adding enzyme hypothetical protein Spy49_0519c
Spy49_0520c	-	NE NE	511655 512920	512464 514221	269 433	-	6985534 6985535	COG0561R COG1078R	hypothetical protein Spy49_0519c HD domain-containing protein
Spy49_0520c Spy49_0521	-	NE NE NE	511655 512920 514303	512464 514221 514689	269 433 128	- - +	6985534 6985535 6985536	COG0561R COG1078R COG4506S	hypothetical protein Spy49_0519c HD domain-containing protein hypothetical protein Spy49_0521
Spy49_0520c Spy49_0521 Spy49_0522	- - - pacL	NE NE NE E	511655 512920 514303 514920	512464 514221 514689 517601	269 433 128 893	-	6985534 6985535 6985536 6985537	COG0561R COG1078R COG4506S COG0474P	hypothetical protein Spy49_0519c HD domain-containing protein hypothetical protein Spy49_0521 calcium-transporting ATPase
Spy49_0520c Spy49_0521	-	NE NE NE	511655 512920 514303	512464 514221 514689	269 433 128	- - + +	6985534 6985535 6985536	COG0561R COG1078R COG4506S COG0474P	hypothetical protein Spy49_0519c HD domain-containing protein hypothetical protein Spy49_0521
Spy49_0520c Spy49_0521 Spy49_0522 Spy49_0523c Spy49_0524c Spy49_0525c	- - - pacL regR - agaD	NE NE NE E NE NE	511655 512920 514303 514920 517687 518746 520740	512464 514221 514689 517601 518682 520653 521561	269 433 128 893 331 635 273	- + +	6985534 6985535 6985536 6985537 6985538 6985539	COG0561R COG1078R COG4506S COG0474P COG1609K - COG3716G	hypothetical protein Spy49_0519c HD domain-containing protein hypothetical protein Spy49_0521 calcium-transporting ATPase transcriptional regulator hypothetical protein Spy49_0524c PTS dependent galactosamine IID component
Spy49_0520c Spy49_0521 Spy49_0522 Spy49_0523c Spy49_0524c Spy49_0525c Spy49_0526c	- - pacL regR - agaD agaW	NE NE E NE NE NE NE NE	511655 512920 514303 514920 517687 518746 520740 521548	512464 514221 514689 517601 518682 520653 521561 522330	269 433 128 893 331 635 273 260	+ +	6985534 6985535 6985536 6985537 6985538 6985539 6985540 6985541	COG0561R COG1078R COG4506S COG0474P COG1609K - COG3716G COG3715G	hypothetical protein Spy49_0519c HD domain-containing protein hypothetical protein Spy49_0521 calcium-transporting ATPase transcriptional regulator hypothetical protein Spy49_0524c PTS dependent galactosamine IID component PTS dependent N-acetyl-galactosamine- IIC component
Spy49_0520c Spy49_0521 Spy49_0522 Spy49_0523c Spy49_0524c Spy49_0525c Spy49_0526c Spy49_0527c	- - pacL regR - - agaD agaW agaV	NE NE E NE NE NE NE NE NC NE	511655 512920 514303 514920 517687 518746 520740 521548 522349	512464 514221 514689 517601 518682 520653 521561 522330 522837	269 433 128 893 331 635 273 260 162	+ +	6985534 6985535 6985536 6985537 6985538 6985539 6985540 6985541 6985542	COG0561R COG1078R COG4506S COG0474P COG1609K - COG3716G COG3715G COG3444G	hypothetical protein Spy49_0519c HD domain-containing protein hypothetical protein Spy49_0521 calcium-transporting ATPase transcriptional regulator hypothetical protein Spy49_0524c PTS dependent galactosamine IID component PTS dependent N-acetyl-galactosamine-IIC component PTS system IIB component
Spy49_0520c Spy49_0521 Spy49_0522 Spy49_0523c Spy49_0524c Spy49_0525c Spy49_0526c	- - pacL regR - agaD agaW agaV ugl	NE NE E NE NE NE NE NE	511655 512920 514303 514920 517687 518746 520740 521548	512464 514221 514689 517601 518682 520653 521561 522330	269 433 128 893 331 635 273 260	+ +	6985534 6985535 6985536 6985537 6985538 6985539 6985540 6985541 6985542 6985543	COG0561R COG1078R COG4506S COG0474P COG1609K - COG3716G COG3715G COG3444G	hypothetical protein Spy49_0519c HD domain-containing protein hypothetical protein Spy49_0521 calcium-transporting ATPase transcriptional regulator hypothetical protein Spy49_0524c PTS dependent galactosamine IID component PTS dependent N-acetyl-galactosamine- IIC component
Spy49_0520c Spy49_0521 Spy49_0523c Spy49_0523c Spy49_0523c Spy49_0525c Spy49_0526c Spy49_0526c Spy49_0528c Spy49_0528c Spy49_0529c Spy49_0530	- - pacL regR - - agaD agaW agaV	NE NE E NE NE NE NE NC NE NE NE NE NE NE NE NE	511655 512920 514303 514920 517687 518746 520740 521548 522349 522873 524072 524844	512464 514221 514689 517601 518682 520653 521561 522330 522837 524072 524509 525638	269 433 128 893 331 635 273 260 162 399 145 264	+ + +	6985534 6985535 6985536 6985537 6985538 6985539 6985540 6985541 6985542 6985543 6985544	COG0561R COG1078R COG4506S COG0474P COG1609K - COG3716G COG3715G COG3444G COG4225R COG2893G COG1028IQR	hypothetical protein Spy49_0519c HD domain-containing protein hypothetical protein Spy49_0521 calcium-transporting AlPase transcriptional regulator hypothetical protein Spy49_0524c PTS dependent galactosamine IID component PTS dependent N-acetyl-galactosamine-IIC component PTS system IIB component glucuronyl hydrolase PTS dependent N-acetyl-galactosamine- and galactosamine IIA component glucuronyl bydrolase
Spy49_0520c Spy49_0521 Spy49_0522 Spy49_0523c Spy49_0524c Spy49_0526c Spy49_0526c Spy49_0527c Spy49_0528c Spy49_0528c Spy49_0530 Spy49_0530	- pacL regR - agaD agaW agaV ugl agaF -	NE NE E NE NE NE NC NE	511655 512920 514303 514920 517687 518746 520740 521548 522349 522873 524072 524844 525663	512464 514221 514689 517601 518682 520653 521561 522330 522837 524072 524509 525638 526304	269 433 128 893 331 635 273 260 162 399 145 264 213	- + + - - - - - - + +	6985534 6985535 6985536 6985537 6985538 6985539 6985540 6985541 6985542 6985543 6985544 6985545	COG0561R COG1078R COG41078R COG4506S COG0474P COG1609K - COG3715G COG3715G COG3444G COG4225R COG4225R COG1028IQR COG0698G	hypothetical protein Spy49_0519c HD domain-containing protein hypothetical protein Spy49_0521 calcium-transporting ATPase transcriptional regulator hypothetical protein Spy49_0524 PTS dependent galactosamine IID component PTS dependent N-acetyl-galactosamine-IIC component PTS system IIB component glucuronyl hydrolase PTS dependent N-acetyl-galactosamine- and galactosamine- IIA component glucuronyl hydrolase PTS dependent N-acetyl-galactosamine- and galactosamine- IIA component glucuronyl hydrolase PTS dependent N-acetyl-galactosamine- and galactosamine- glycuronyl hydrolase PTS dependent N-acetyl-galactosamine- and galactosamine- glycuronyl hydrolase PTS dependent N-acetyl-galactosamine- and galactosamine- IIA component glycuronyl hydrolase
Spy49_0520c Spy49_0521 Spy49_0522 Spy49_0523c Spy49_0524c Spy49_0525c Spy49_0527c Spy49_0527c Spy49_0529c Spy49_0530 Spy49_0531 Spy49_0531	- pacL regR - agaD agaW agaV ugI agaF - kdgK	NE NE E NE NE NC NE	511655 512920 514303 514920 517687 518746 520740 521548 522349 522873 524072 524844 525663 526333	512464 514221 514689 517601 518682 520653 521561 522330 522837 524072 524509 525638 526304 527334	269 433 128 893 331 635 273 260 162 399 145 264 213 333	+ + +	6985534 6985535 6985536 6985537 6985538 6985539 6985541 6985542 6985543 6985544 6985544 6985544 6985545	COG0561R COG1078R COG47078R COG45065 COG0474P COG1609K	hypothetical protein Spy49_0519c HD domain-containing protein hypothetical protein Spy49_0521 calcium-transporting ATPase transcriptional regulator hypothetical protein Spy49_0524c PTS dependent galactosamine IID component PTS dependent N-acetyl-galactosamine- IIC component PTS system IIB component glucuronyl hydrolase PTS dependent N-acetyl-galactosamine- and galactosamine IIA component glucuronyl bydrolase hypothetical protein Spy49_0531 2-dehydro-3-deoxygluconokinase
Spy49_0520c Spy49_0521 Spy49_0522 Spy49_0523c Spy49_0524c Spy49_0526c Spy49_0526c Spy49_0527c Spy49_0528c Spy49_0528c Spy49_0530 Spy49_0530	- pacL regR - agaD agaW agaV ugl agaF -	NE NE E NE NE NE NC NE	511655 512920 514303 514920 517687 518746 520740 521548 522349 522873 524072 524844 525663	512464 514221 514689 517601 518682 520653 521561 522330 522837 524072 524509 525638 526304	269 433 128 893 331 635 273 260 162 399 145 264 213	- + + - - - - - - + +	6985534 6985535 6985536 6985537 6985538 6985539 6985540 6985541 6985542 6985543 6985544 6985545	COG0561R COG4506S COG474P COG4506S COG0474P COG3716G COG3715G COG3715G COG3715G COG3444G COG4225R COG4893G COG1028IQR COG0698C COG0524G COG0800G	hypothetical protein Spy49_0519c HD domain-containing protein hypothetical protein Spy49_0521 calcium-transporting ATPase transcriptional regulator hypothetical protein Spy49_0524 PTS dependent galactosamine IID component PTS dependent N-acetyl-galactosamine-IIC component PTS system IIB component glucuronyl hydrolase PTS dependent N-acetyl-galactosamine- and galactosamine- IIA component glucuronyl hydrolase PTS dependent N-acetyl-galactosamine- and galactosamine- IIA component glucuronyl hydrolase PTS dependent N-acetyl-galactosamine- and galactosamine- glycuronyl hydrolase PTS dependent N-acetyl-galactosamine- and galactosamine- glycuronyl hydrolase PTS dependent N-acetyl-galactosamine- and galactosamine- IIA component glycuronyl hydrolase
Spy49_0520c Spy49_0521 Spy49_0522 Spy49_0522c Spy49_0525c Spy49_0525c Spy49_0525c Spy49_0528c Spy49_0528c Spy49_0531 Spy49_0531 Spy49_0531 Spy49_0534 Spy49_0534 Spy49_0534	- regR - agaD agaW agaV ugi agaF - - kdgK kdgA	NE NE E NE	511655 512920 5143920 514920 517687 518746 520749 521548 522349 522873 524072 524844 525663 526333 52733 528272 528272	512464 514221 514680 517601 518682 520653 521561 522330 522837 524072 524503 525638 526304 527334 527334 527972 530742	269 433 128 893 331 635 273 260 162 399 145 264 213 333 3211 216 374	- + + - - - - + + + + +	6985534 6985535 6985537 6985537 6985538 6985539 6985541 6985542 6985544 6985545 6985545 6985546 6985545 6985546 6985547 6985548 6985548	COGOSGIR COG1078R COG4506S COG0474P COG1609K - COG3716G COG3716G COG3715G COG3444G COG4225R COG1028IQR COG1028IQR COG069524G COG05524G COG0557R COG0657R COG1600C	hypothetical protein Spy49_0519c HD domain-containing protein hypothetical protein Spy49_0521 calcium-transporting AlPase transcriptional regulator hypothetical protein Spy49_0524c HTS dependent galactosamine IID component PTS dependent Reacetyl-galactosamine-IIC component PTS dependent N-acetyl-galactosamine-IIC component glucuroniy hydrolase PTS dependent N-acetyl-galactosamine-and galactosamine IIA component glucuronety-dehydrogenase hypothetical protein Spy49_0531 2-dehydro-3-deoxygluconokinase keto-hydroxyglutarate-aldolase/keto-deoxy-phosphogluconate aldolase hypothetical protein Spy49_0534 hypothetical protein Spy49_0535
Spv49_0520c Spv49_0521 Spv49_0522 Spv49_0523c Spv49_0524c Spv49_0525c Spv49_0527c Spv49_0527c Spv49_0527c Spv49_0530 Spv49_0530 Spv49_0531 Spv49_0533 Spv49_0533 Spv49_0533 Spv49_0533 Spv49_0533 Spv49_0535 Spv49_0535 Spv49_0536	pacL regR agaD agaW agaW ugl agaF - kdgK - prfB	NE N	511655 512920 514902 514902 517687 518768 520740 521548 522347 524072 524844 525633 526333 527339 528272 529618 530928	512464 514221 514680 517601 518682 520653 521561 522330 522837 524072 524072 525388 526304 527334 527974 528922 531908	269 433 128 893 331 635 273 260 162 399 145 264 213 333 211 216 374 326	- + + - - - - + + + + + +	6985534 6985536 6985536 6985537 6985538 6985540 6985541 6985542 6985543 6985544 6985545 6985545 6985546 6985546 6985546 6985549 6985549 6985549 6985549	COGOSGIR COG1078R COG4506S COG0474P COG1609K - COG3716G COG3716G COG3715G COG4225R COG1225R COG1028IQR COG0524C COG0524C COG0524C COG0524C COG0524C COG0537R COG0698C COG0537R COG108C COG0537R COG108C COG0537R COG1186I	hypothetical protein Spy49_0519c HD domain-containing protein hypothetical protein Spy49_0521 calcium-transporting ATPase transcriptional regulator hypothetical protein Spy49_0524 PTS dependent galactosamine IID component PTS dependent N-acetyl-galactosamine-IIC component PTS system IIB component glucronyl hydrolase PTS dependent N-acetyl-galactosamine- and galactosamine- IIA component glucronyl hydrolase PTS dependent N-acetyl-galactosamine- and galactosamine- IIA component glucronyl hydrolase PTS dependent N-acetyl-galactosamine- and galactosamine- IIA component glucronate 5-dehydrogenase hypothetical protein Spy49_0531 2-dehydro-3-deoxygluconokinase keto-hydroxyglutrate-aldolase/keto-deoxy-phosphogluconate aldolase hypothetical protein Spy49_0534 hypothetical protein Spy49_0535 peptide chain release factor 2
Spy49_0520c Spy49_0521 Spy49_0522 Spy49_0524c Spy49_0524c Spy49_0524c Spy49_0526c Spy49_0527c Spy49_0529c Spy49_0530 Spy49_0530 Spy49_0532 Spy49_0534 Spy49_0534 Spy49_0535 Spy49_0535 Spy49_0536 Spy49_0536 Spy49_0536 Spy49_0536	pacL regR agaD agaW agaW ugl agaF - kdgK kdgA -	NE N	511655 512920 514303 514920 517687 518746 520740 521548 522349 522872 524872 524872 52663 527339 528272 529218 530928 531927	512464 514221 514689 517601 518682 520553 521561 522330 522837 524509 525638 526304 527974 528922 530742 531908 531908	269 433 128 893 331 635 273 260 162 399 145 264 213 333 211 216 374 326 230	- - - - - - - - + + + + + + +	985534 6985536 6985536 6985536 6985538 6985538 6985539 6985540 6985542 6985542 6985544 6985544 6985545 6985544 6985546 6985546 6985547 6985546 6985547 6985540 6985541 6985550	COGOSGIR COG4506S COG474P COG1678R - COG3716G COG3716G COG3715G COG374G COG6225R COG6283G COG6088G COG6088G COG6083R COG6083R COG6083R COG6083R COG6188I COG6083R COG6188I COG6083R	hypothetical protein Spy49_0519c HD domain-containing protein hypothetical protein Spy49_0521 calcium-transporting Al Plase transcriptional regulator hypothetical protein Spy49_0524c PTS dependent galactosamine IID component PTS dependent palactosamine IID component PTS system IIB component glucuronyl hydrolase PTS dependent N-acetyl-galactosamine- IIC component glucuronyl hydrolase PTS dependent N-acetyl-galactosamine- and galactosamine IIA component glucurones behydrogenase hypothetical protein Spy49_0531 2-dehydro3-deoxygluconokinase keto-hydroxyglutarate-aldolase/keto-deoxy-phosphogluconate aldolase hypothetical protein Spy49_0534 hypothetical protein Spy49_0535 peptide chain release factor 2 cell division transporter ATP-binding protein ftsE
Spv49_0520c Spv49_0521 Spv49_0522 Spv49_0523c Spv49_0524c Spv49_0525c Spv49_0527c Spv49_0527c Spv49_0527c Spv49_0530 Spv49_0530 Spv49_0531 Spv49_0533 Spv49_0533 Spv49_0533 Spv49_0533 Spv49_0533 Spv49_0535 Spv49_0535 Spv49_0536	pacL regR agaD agaW agaW ugl agaF - kdgK - prfB	NE N	511655 512920 514902 514902 517687 518768 520740 521548 522347 524072 524844 525633 526333 527339 528272 529618 530928	512464 514221 514680 517601 518682 520653 521561 522330 522837 524072 524072 525388 526304 527334 527974 528922 531908	269 433 128 893 331 635 273 260 162 399 145 264 213 333 211 216 374 326	- + + - - - - + + + + + +	6985534 6985536 6985536 6985537 6985538 6985540 6985541 6985542 6985543 6985544 6985545 6985545 6985546 6985546 6985546 6985549 6985549 6985549 6985549	COGOSGIR COG1078R COG4506S COG0474P COG1609K - COG3716G COG3715G COG3215G COG3225R COG10281QR COG0698G COG0524C COG0698G COG0698G COG0698C COG0698C COG0688C COG0688C COG0688C COG0688C COG0688C COG0688C COG0687R COG0688C	hypothetical protein Spy49_0519c HD domain-containing protein hypothetical protein Spy49_0521 calcium-transporting ATPase transcriptional regulator hypothetical protein Spy49_0524 PTS dependent galactosamine IID component PTS dependent N-acetyl-galactosamine-IIC component PTS system IIB component glucronyl hydrolase PTS dependent N-acetyl-galactosamine- and galactosamine- IIA component glucronyl hydrolase PTS dependent N-acetyl-galactosamine- and galactosamine- IIA component glucronyl hydrolase PTS dependent N-acetyl-galactosamine- and galactosamine- IIA component glucronate 5-dehydrogenase hypothetical protein Spy49_0531 2-dehydro-3-deoxygluconokinase keto-hydroxyglutrate-aldolase/keto-deoxy-phosphogluconate aldolase hypothetical protein Spy49_0534 hypothetical protein Spy49_0535 peptide chain release factor 2
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Spy49_0520c Spy49_0521c Spy49_0522 Spy49_0523c Spy49_0524c Spy49_0524c Spy49_0525c Spy49_0526c Spy49_0527c Spy49_0529c Spy49_0531 Spy49_0531 Spy49_0531 Spy49_0534 Spy49_0533 Spy49_0534 Spy49_0534 Spy49_0534 Spy49_0534 Spy49_0536 Spy49_0536 Spy49_0541 Spy49_0545 Spy49_0545 Spy49_0545 Spy49_0545 Spy49_0555 Spy49_0555 Spy49_0555 Spy49_0556 Spy49_0560 Spy49_0561 Spy49_0561	- pacL regR - agaD agaW agaV ugl agaF - kdgK kdgA rfts fts fts fts - dinG aspC aspC aspC aspC	NE N	511655 512920 514303 514920 517687 518746 520740 521548 522349 522873 524072 524844 525663 526333 527339 528272 529618 530928 531927 532612 53851 534718 535590 538416 539640 541401 542288 543265 543265 543265 54525 555217 555517 555517 555637 55693	512464 514261 514689 517601 518682 520653 521561 522330 524072 524509 525638 526304 527334 527974 528925 530742 531908 533641 533641 534429 533541 534629 534565 54505 550906 551749 553266 555516 5507469 559561 560151 561651	269 433 1128 893 311 635 515 515 515 515 515 189 4 420 650 650 650 650 650 650 650 650 650 65		985534 985536 985537 9885537 9885539 9885540 9885541 9885542 9885544 9885546 9885546 9885546 9885546 9885546 9885546 9885546 9885546 9885546 9885546 9885556 9885556 9885556 9885556 9885566 9885566 988566 988566 988566 988566 988566 988567 9885566 9885570 9885571 9885572 9885572 9885573	CGGG561R CGG4506S CGG474P CGG1078R CGG4506S CGGG474P CGG3716G CGG3716G CGG3716G CGG3715G CGG3715G CGG3715G CGG3715G CGG3715G CGG322SR CGG282SR CGG6982G CGG6982G CGG6982G CGG6987R CGG6987R CGG6987R CGG6987R CGG10281GR CGG6987R CGG10281GR CGG1186I CGG2186I CGG2186I CGG10281GR CGG01381G CGG0564GR CGG0564GR CGG0335I CGG0546R CGG0335I CGG0546R CGG0335I CGG0546R CGG0187L CGG64477D CGG5506S	hypothetical protein Spy49_0519c HD domain-containing protein hypothetical protein Spy49_0521 calcium-transporting AlPase transcriptional regulator hypothetical protein Spy49_0524 PTS dependent galactosamine IID component PTS dependent galactosamine IID component PTS dependent galactosamine IID component PTS dependent N-acetyl-galactosamine-IIC component PTS system IIB component glucurony hydrolase PTS dependent N-acetyl-galactosamine- and galactosamine IIA component glucurony hydrolase PTS dependent N-acetyl-galactosamine- and galactosamine IIA component glucurony hydrolase PTS dependent N-acetyl-galactosamine- and galactosamine IIA component glucurony hydrolase hypothetical protein Spy49_0531 2-dehydro-3-deoxygluconokinase keto-hydroxyglutarate-aldolase/keto-deoxy-phosphogluconate aldolase hypothetical protein Spy49_0535 peptide chain release factor 2 cell division transporter ATP-binding protein ftsE cell division protein Spy49_0535 peptide chain release factor 2 cell division transporter ATP-binding protein ftsE cell division protein Spy49_0546 pyothetical protein Spy49_0546 hypothetical protein Spy49_0545 hypothetical protein Spy49_0547 dipeptidase A zinc-binding protein adA Gntk family transcriptional regulator tagatose-6-phosphata aldose/ketose isomerase SOS ribosomal protein I1y pB hypothetical protein Spy49_0556 transmembrane protein SOS ribosomal protein I19 phosphoplycolate phosphatase DNA gyrase subunit B septation ring formation regulator EzrA hypothetical protein fopty49_0562c phosphopyrucate hydratsee
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Spy49_0520c Spy49_0521 Spy49_0521 Spy49_0522 Spy49_0524c Spy49_0526c Spy49_0526c Spy49_0526c Spy49_0526c Spy49_0526c Spy49_0533 Spy49_0533 Spy49_0533 Spy49_0533 Spy49_0533 Spy49_0533 Spy49_0534 Spy49_0534 Spy49_0535 Spy49_0536 Spy49_0540 Spy49_0550 Spy49_0560 Spy49_05661 Spy49_05664 Spy49_05666	- pacL regR - agaD agaW agaV ugl agaF - kdgK kdgA rfts fts fts fts - dinG aspC aspC aspC aspC	NE N	511655 512920 512920 517687 518746 520740 521548 5222873 524072 524844 525663 526333 527339 528272 529618 530928 531927 532612 533816 534718 53590 534718 53590 544201 544208 543262 544306 545855 541927 55450 551925 55450 551925 55202 555517 555202 555517 5556344 56038	512464 514221 514689 517601 518682 520653 521561 522330 522837 524072 524509 525638 526304 527974 528922 530742 531908 532619 533541 534429 533541 534429 535961 534573 547402 548274 549493 54980 551749 552099 553464 5559561 555166 5577469 559561 560151 561661 560151 561661 562855 563102	269 433 1128 893 311 635 626 421 273 266 162 273 264 213 333 333 399 145 226 421 216 225 426 425 426 425 426 425 426 425 426 425 426 426 426 426 426 426 426 426 426 426		985534 985536 985537 985538 985537 985539 985541 985542 985544 985544 985544 985545 985545 985554 985554 985554 985554 985554 985554 985554 985554 985556 985556 985556 985556 985556 985556 985556 985556 985556 985556 985556 985557 985557 985557 985576 985577 985577 985577 985577 985577 985577	CGGG561R CGG4506S CGG474P CGG1078R CGG4506S CGGG474P CGG3716G CGG3716G CGG3716G CGG3715G CGG3715G CGG3715G CGG3715G CGG3715G CGG322SR CGG282SR CGG6982G CGG6982G CGG6982G CGG6987R CGG6987R CGG6987R CGG6987R CGG10281GR CGG6987R CGG10281GR CGG1186I CGG2186I CGG2186I CGG10281GR CGG01381G CGG0564GR CGG0564GR CGG0335I CGG0546R CGG0335I CGG0546R CGG0335I CGG0546R CGG0187L CGG64477D CGG5506S	hypothetical protein Spy49_0519c HD domain-containing protein hypothetical protein Spy49_0521 calcium-transporting AlPase transcriptional regulator hypothetical protein Spy49_0524c FTS dependent galactosamine IID component PTS dependent Racetyl-galactosamine-IIC component PTS dependent N-acetyl-galactosamine-IIC component PTS system IIB component glucuronity Hydrolase PTS dependent N-acetyl-galactosamine- and galactosamine- IIA component glucuronity Hydrolase PTS dependent N-acetyl-galactosamine- and galactosamine- IIA component glucuronity Hydrolase PTS dependent N-acetyl-galactosamine- and galactosamine- IIA component glucuronity Hydrolase - hydrony-3-deoxygluconokinase keto-hydroxyglutarate-aldolase/keto-deoxy-phosphogluconate aldolase hypothetical protein Spy49_0534 hypothetical protein Spy49_0535 peptide chain release factor 2 cell division transporter ATP-binding protein ftsE cell division protein FtsX oxyacyglutathione hydrolase acetoin reductase bifunctional ATP-dependent DNA helicase/DNA polymerase III subunit epsilon aspartate aminotransferase asparaginyl-tRNA synthetase hypothetical protein Spy49_0545 hypothetical protein Spy49_0546 hypothetical protein Spy49_0547 dipeptidase A ainc-binding protein adA offint family transcriptional regulator tagatose-6-phosphate aldose/ketose isomerase SOS ribosomal protein 131 type B hypothetical protein Spy49_0556 transmembrane protein SOS ribosomal protein Spy49_0556 transmembrane protein SOS ribosomal protein Spy49_0556 transmembrane protein SOS ribosomal protein Spy49_0562c hoposhopytwote hydratase transposase transposase transposase transposase transposase transposase transposase

Spy49_0569	sagB	NE	570192	571142	316	+	6985583		streptolysin S biosynthesis protein B SagB
Spy49_0570	sagC	NE	571139	572197	352	+	6985584	-	streptolysin S biosynthesis protein C SagC
Spy49_0572	sagD	NE	572217	573575	452	+	6985585 6985586	COG1944S	streptolysin S biosynthesis protein D SagD
Spy49_0573 Spy49_0574	sagE sagF	NE NE	573550 574218	574221 574901	223 227	+	6985587	-	streptolysin S self-immunity protein SagE streptolysin S biosynthesis protein SagF
Spy49_0575	sagG	С	574924	575847	307	+	6985588	COG1131V	streptolysin S export ATP-binding protein SagG
Spy49_0576	sagH	NC	575856	576983	375	+		COG0842V	streptolysin S export transmembrane protein SagH
Spy49_0577 Spy49_0578	sagl -	C NE	576980 578669	578098 581401	372 910	+		COG0842V COG2374R	streptolysin S export transmembrane protein Sagl endonuclease/exonuclease/phosphatase
Spy49_0579	-	NE	581679	582179	166	+		COG4708S	hypothetical protein Spy49_0579
Spy49_0580	ligA	E	582373	584331	652	+	6985593	COG0272L	NAD-dependent DNA ligase LigA
Spy49_0581	-	E	584345	585367	340	+		COG1597IR	lipid kinase
Spy49_0582 Spy49_0583		NC E	585762 585994	585959 586710	65 238	+		COG0636C COG0356C	F0F1 ATP synthase subunit C F0F1 ATP synthase subunit A
Spy49_0584		NC	586728	587222	164	+		COG0711C	FOF1 ATP synthase subunit B
Spy49_0585	-	E	587222	587758	178	+		COG0712C	F0F1 ATP synthase subunit delta
Spy49_0586	-	E	587774	589282	502 291	+		COG0056C	FOF1 ATP synthase subunit alpha
Spy49_0587 Spy49_0588	-	Ē	589298 590335	590173 591741	468	+		COG0224C COG0055C	F0F1 ATP synthase subunit gamma F0F1 ATP synthase subunit beta
Spy49_0589	atpC	NC	591754	592170	138	+		COG0355C	FOF1 ATP synthase subunit epsilon
Spy49_0590	-	NE	592436	592693	85	+	6985603	-	hypothetical protein Spy49_0590
Spy49_0591 Spy49_0592	murA	NE NE	592758 594033	594029 594221	423 62	+	6985604 6985605	COG0766M	UDP-N-acetylglucosamine 1-carboxyvinyltransferase
Spy49_0596	pheS	E	595077	596120	347	+		COG0016J	hypothetical protein Spy49_0592 phenylalanyl-tRNA synthetase subunit alpha
Spy49_0597	pheT	E	596330	598735	801	+		COG0072J	phenylalanyl-tRNA synthetase subunit beta
Spy49_0598	-	NE	598845	599222	125	+	6985610	-	hypothetical protein Spy49_0598
Spy49_0599 Spy49_0600	-	NE NE	599215 599674	599601 600750	128 358	+	6985612	COG3272S	hypothetical protein Spy49_0599 hypothetical protein Spy49_0600
Spy49_0601	-	NE	600760	601428	222	+		COG1136V	ABC transporter ATP-binding protein
Spy49_0602c	-	NE	601532	602449	305	-		COG2321R	hypothetical protein Spy49_0602c
Spy49_0603	rexB	C E	602600	605815 609444	1071 1222	+		COG3857L	ATP-dependent exonuclease subunit B
Spy49_0604 Spy49_0605	rexA -	NE NE	605776 609584	610204	206	+		COG1074L COG0834ET	ATP-dependent exonuclease subunit A ABC transporter
Spy49_0606	rpsU	NC	610543	610719	58	+	6985618	COG0828J	30S ribosomal protein S21p
Spy49_0607c	mscL	NE	610847	611209	120	-	6985619	COG1970M	large conductance mechanosensitive channel
Spy49_0608 Spy49_0609	dnaG rpoD	E	611339 613162	613153 614271	604 369	+		COG0358L COG0568K	DNA primase RNA polymerase sigma factor RpoD
Spy49_0610	-	NE	614507	614845	112	+		COG2151R	probably aromatic ring hydroxylating enzyme
Spy49_0611	rmID	E	614983	615837	284	+	6985623	COG1091M	dTDP-4-dehydrorhamnose reductase
Spy49_0612	rgpAc	E	615956	617110	384	+		COG0438M	rhamnosyltransferase
Spy49_0613 Spy49_0614	rgpBc rgpCc	E E	617100 618035	618032 618838	310 267	+		COG0463M COG1682GM	Rhamnosyltransferase Teichoic acid translocation permease tagG
Spy49_0615	rgpDc	E	618838	620058	406	+		COG1134GM	Teichoic acid export ATP-binding protein tagH
Spy49_0617	rgpEc	E	620069	621076	335	+		COG0463M	glycosyltransferase
Spy49_0618	rgpFc	E NE	621073	622818	581 824	+		COG3754M COG1368M	RgpFc protein
Spy49_0619 Spy49_0620	-	NE NE	622815 625468	625289 626163	231	+		COG0463M	hypothetical protein Spy49_0619 glycosyl transferase
Spy49_0621	-	NE	626165	626506	113	+	6985632	-	hypothetical protein Spy49_0621
Spy49_0622	-	E	626499	627785	428	+		COG2244R	Heteropolysaccharide repeat unit export protein
Spy49_0623 Spy49_0624	- pepT	E NE	627766 629356	629262 630579	498 407	+		COG4713S COG2195E	hypothetical protein Spy49_0623 peptidase T
Spy49_0625	-	NE	630620	631108	162	+	6985636	-	pore-forming peptide
Spy49_0626c	-	NE	631095	631292	65	-	6985637	COG1141C	ferredoxin
Spy49_0627	-	NE	631341	631817	158	+	6985638	-	hypothetical protein Spy49_0627
Spy49_0628 Spy49_0629	cmk infC	NC E	631832 632674	632512 633204	226 176	+		COG0283F COG0290J	cytidylate kinase translation initiation factor IF-3
Spy49_0630	rpml	NE	633246	633443	65	+		COG0291J	50S ribosomal protein L35
Spy49_0631	rplT	NC	633502	633861	119	+		COG0292J	50S ribosomal protein L20
Spy49_0632c Spy49_0633	-	E NE	634152	636362	736	+		COG1368M COG1092R	phosphoglycerol transferase
Spy49_0634	aroD	NE	636470 637630	637633 638316	387 228	+		COG1032K COG0710E	hypothetical protein Spy49_0633 3-dehydroquinate dehydratase
Spy49_0635	aroF	NE	638410	639576	388	+	6985646	COG0082E	chorismate synthase
Spy49_0636	-	NE	639637	639978	113	+		COG3679S	hypothetical protein Spy49_0636
Spy49_0637 Spy49_0638c	gor folC.2	NE NE	640200 641640	641552 642908	450 422	+		COG1249C COG0285H	glutathione reductase dihydrofolate synthase / Folylpolyglutamate synthase
Spy49_0639c	-	NE	642938	643378	146	-	6985650	-	hypothetical protein Spy49_0639c
Spy49_0640	nifS	NE	643613	644755	380	+		COG1104E	cysteine desulfurase
Spy49_0641 Spy49_0642	thil	NE NE	644767 646019	645981 647287	404 422	+		COG0301H COG2843M	thiamine biosynthesis protein Thil hypothetical protein Spy49_0642
Spy49_0643	rplU	NC	647526	647840	104	+		COG0261J	50S ribosomal protein L21
Spy49_0644	-	NC	647852	648178	108	+	6985655	COG2868J	hypothetical protein Spy49_0644
Spy49_0645	rpmA	NC	648206	648499	97 304	+		COG0211J	50S ribosomal protein L27
Spy49_0646 Spy49_0647	Isp	NE NE	648847 649758	649761 650216	152	+		COG0583K COG0597MU	capsular polysaccharide biosynthesis regulatory protein lipoprotein signal peptidase
Spy49_0648	-	NE	650206	651096	296	+	6985659	COG0564J	ribosomal large subunit pseudouridine synthase
Spy49_0650	pyrR	NE	651492	652013	173	+		COG2065F	bifunctional pyrimidine regulatory protein PyrR uracil phosphoribosyltransferase
Spy49_0651 Spy49_0652	pyrP pyrB	NE NE	652029 653349	653288 654284	419 311	+		COG2233F COG0540F	uracil permease aspartate carbamoyltransferase catalytic subunit
Spy49_0653	carA	NC	654328	655410	360	+	6985663	COG0505EF	carbamoyl phosphate synthase small subunit
Spy49_0654	carB	NE	655656	658832	1058	+	6985664	COG0458EF	carbamoyl phosphate synthase large subunit
Spy49_0655 Spy49_0656	-	NE NE	659041 660312	660312 661022	423 236	+		COG0845M COG1136V	hypothetical protein Spy49_0655 ABC transporter
Spy49_0657	-	NE	661034	662254	406	+		COG0577V	Permease
Spy49_0658	-	С	662508	664241	577	+	6985668	COG4781C	glycerophosphoryl diester phosphodiesterase
Spy49_0659	rpsP	E	664368	664640	90	+		COG0228J	30S ribosomal protein S16
Spy49_0660 Spy49_0661	-	NC NE	664650 665821	664889 668847	79 1008	+	6985671	COG1837R	KH domain-containing protein hypothetical protein Spy49_0661
Spy49_0662	-	NE	668867	669268	133	+	6985672	COG3576R	hypothetical protein Spy49_0662
Spy49_0663c	czcD	NE	669448	670323	291	-		COG1230P	cation-efflux system membrane protein
Spy49_0664 Spy49_0665	- rimM	NE NC	670459 671195	670980 671713	173 172	+	6985674 6985675	- COG0806J	hypothetical protein Spy49_0664 16S rRNA-processing protein RimM
Spy49_0667	trmD	E	671700	672434	244	+		COG0336J	tRNA (guanine-N(1)-)-methyltransferase
Spy49_0668	-	NE	672434	673426	330	+	6985677	COG04920	thioredoxin reductase
Spy49_0669	-	NE	673603	674661	352	+		COG3641R	regulatory protein
Spy49_0671 Spy49_0672	apbA fruR	NE NE	674674 675853	675597 676566	307 237	+		COG1893H COG1349KG	2-dehydropantoate 2-reductase transcriptional repressor
Spy49_0673	fruK	NE	676563	677474	303	+	6985681	COG1105G	tagatose-6-phosphate kinase
Spy49_0674	fruA	NE	677471	679417	648	+		COG1299G	PTS system fructose-specific IIABC component
Spy49_0675 Spy49_0676	-	NE NE	679516 680261	680109 680968	197 235	+		COG1705NU COG1705NU	peptidoglycan hydrolase
Spy49_0676 Spy49_0677c	-	NE NE	681025	681243	72 72	+	6985685	-	peptidoglycan hydrolase transposase, ISSmu1
Spy49_0679	mac	NE	681925	682944	339	-	6985687		Immunoglobulin G-endopeptidase (IdeS) / Mac
Spy49_0680	-	NE NE	683850	684230	126	+		COG4835S	hypothetical protein Spy49_0680
Spy49_0681 Spy49_0682	- papS	NE E	684230 685252	685078 686412	282 386	+		COG1307S COG0617J	DegV family protein tRNA CCA-pyrophosphorylase
Spy49_0683	-	NE	686409	688286	625	+	6985691	COG0488R	ABC transporter
Spy49_0684	-	NE	689180	689590	136	+	6985692	COG0242J	peptide deformylase

Spy49_0686c	-	NE	689672	691684	670	_	6985693	COG0737F	5-nucleotidase
Spy49_0687	-	NE	691904	692554	216	+	6985694	COG2357S	GTP pyrophosphokinase
Spy49_0688	-	NE NE	692557	693225	222 410	+		COG0745TK	DNA-binding response regulator
Spy49_0689 Spy49_0690	mvaK1	E	693234 694760	694466 695638	292	+		COG0642T COG1577I	two-component sensor histidine kinase mevalonate kinase
Spy49_0691	mvaD	E	695620	696564	314	+	6985698	COG3407I	Diphosphomevalonate decarboxylase
Spy49_0692	mvaK2	E	696557	697570	337	+		COG1577I	phosphomevalonate kinase
Spy49_0693 Spy49_0694c	mvaS1	E	697557 698776	698546 700053	329 425	+		COG1304C COG1257I	isopentenyl pyrophosphate isomerase hydroxymethylglutaryl-CoA reductase
Spy49_0695c	mvaS2	E	700040	701215	391	-	6985702	COG3425I	hydroxymethylglutaryl-CoA synthase
Spy49_0696	thyA	C	701424	702263	279	+		COG0207F	thymidylate synthase
Spy49_0697 Spy49_0698	dyr -	E NE	702343 702860	702840 703060	165 66	+	6985705	COG0262H	dihydrofolate reductase hypothetical protein Spy49_0698
Spy49_0700	clpX	NC	703161	704390	409	+		COG12190	ATP-dependent protease ATP-binding protein ClpX
Spy49_0701	engB	E	704400	704999	199	+		COG0218R	ribosome biogenesis GTP-binding protein YsxC
Spy49_0702 Spy49_0703c	- clpL	NE NE	705147 705948	705890 708047	247 699	+	6985708	- COG0542O	hypothetical protein Spy49_0702 ATP-dependent Clp proteinase
Spy49_0704	rpiA	NC	708425	709108	227	+		COG0120G	ribose-5-phosphate isomerase A
Spy49_0705	deoB	NE	709185	710396	403	+		COG1015G	phosphopentomutase
Spy49_0706 Spy49_0707	arsC punA	NE NE	710415 710839	710855 711648	146 269	+		COG1393P COG0005F	arsenate reductase purine nucleoside phosphorylase
Spy49_0708	deoD	NE	712176	711046	256	+		COG0813F	purine nucleoside phosphorylase
Spy49_0709	-	NE	712939	713727	262	+	6985715		histidine protein kinase
Spy49_0710c Spy49_0711	cpsY	NE NE	713807 714934	714712 715470	301 178	+	6985716 6985717	COG0583K	transcriptional regulator hypothetical protein Spy49_0711
Spy49_0711	pyrF	NE	715747	716439	230	+		COG0284F	orotidine 5\'-phosphate decarboxylase
Spy49_0713	pyrE	NE	716497	717126	209	+		COG0461F	orotate phosphoribosyltransferase
Spy49_0714 Spy49_0715	amiC	NE NE	717323 718895	718777 719758	484 287	+		COG0154J COG0834ET	amidase ABC transporter
Spy49_0715 Spy49_0716	-	NE	719787	720437	216	+		COG0765E	amino-acid ABC transporter permease yckA
Spy49_0717	ung	NE	720570	721223	217	+	6985723	COG0692L	uracil-DNA glycosylase
Spy49_0718	pyrC	NE	721355	722623	422	+		COG0044F	dihydroorotase
Spy49_0719c Spy49_0720	parE	E	722681 723457	723322 725406	213 649	+		COG0344S COG0187L	glycerol-3-phosphate acyltransferase PlsY DNA topoisomerase IV subunit B
Spy49_0721	parC	E	725497	727956	819	+		COG0188L	DNA topoisomerase IV subunit A
Spy49_0722	bcaT	NE	728079	729101	340	+		COG0115EH	branched-chain amino acid aminotransferase
Spy49_0723 Spy49_0724	- rpsA	NC E	729165 729786	729395 730991	76 401	+	6985729 6985732	- COG0539J	hypothetical protein Spy49_0723 30S ribosomal protein S1
Spy49_0725c	-	NE	731493	731795	100	-	6985734		hypothetical protein Spy49_0725c
Spy49_0726	-	NE	731996	732982	328	+		COG1054R	hypothetical protein Spy49_0726
Spy49_0727 Spy49_0728	-	NE NE	733293 733950	733700 734858	135 302	+	6985736	- COG1275P	hypothetical protein Spy49_0727 exfoliative toxin
Spy49_0728 Spy49_0729c	-	NE	734976	735152	58	-	6985738		hypothetical protein Spy49_0729c
Spy49_0730	miaA	NE	735286	736185	299	+	6985739	COG0324J	tRNA delta(2)-isopentenylpyrophosphate transferase
Spy49_0731	hflX	NE	736258	737496	412	+		COG2262R	GTP-binding protein HfIX
Spy49_0732 Spy49_0733	-	NE E	737489 738139	738124 739068	211 309	+		COG4468G COG1234R	hypothetical protein Spy49_0732 ribonuclease Z
Spy49_0734	-	NE	739228	739833	201	+		COG0300R	oxidoreductase
Spy49_0735	recJ	NE	739830	742040	736	+		COG0608L	Single-stranded-DNA-specific exonuclease recJ
Spy49_0736 Spy49_0737	apt dnaD	NE E	742190 742789	742708 743472	172 227	+		COG0503F COG3935L	adenine phosphoribosyltransferase DNA replication protein DnaD
Spy49_0738	nth	NE	743469	744125	218	+		COG0177L	endonuclease III
Spy49_0739	-	E	744197	744883	228	+		COG2384R	hypothetical protein Spy49_0739
Spy49_0740 Spy49_0741	-	NE NE	744873 745701	745661 746825	262 374	+		COG0327S COG0665E	hypothetical protein Spy49_0740 oxidoreductase
Spy49_0742	rmIA	E	746864	747733	289	+		COG1209M	glucose-1-phosphate thymidylyltransferase
Spy49_0744	rmIC	NC	747733	748326	197	+	6985752	COG1898M	dTDP-4-dehydrorhamnose 3,5-epimerase
Spy49_0745 Spy49_0746c	rmlB	E NE	748570 749693	749610	346 379	+		COG1088M COG4974L	dTDP-glucose 4,6-dehydratase
Spy49_0746c Spy49_0747c	-	NE	750960	750832 751226	88	-	6985755	-	Prophage ps2 integrase hypothetical protein Spy49_0747c
Spy49_0748c	-	NE	751238	751624	128	-	6985756		phage-associated protein
Spy49_0749c	-	C	751627	751977	116	+		COG1396K	repressor-phage associated
Spy49_0750 Spy49_0751c	-	NC NC	752273 752469	752443 753257	56 262	-	6985758 6985759		hypothetical protein Spy49_0750 hypothetical protein Spy49_0751c
Spy49_0752	-	NC	753308	753499	63	+	6985760	-	antirepressor protein
Spy49_0753	-	NC	753578	753889	103	+	6985761		excisionase
Spy49_0754 Spy49_0755	-	NC NC	753891 754054	754061 754257	56 67	+	6985762 6985763		putative phage associated protein hypothetical protein Spy49_0755
Spy49_0756	-	NE	754254	754640	128	+	6985764		hypothetical protein Spy49_0756
Spy49_0757	-	NC	754786	754989	67	+	6985765		putative phage associated protein
Spy49_0759 Spy49_0760	-	NC NE	755077 755376	755376 756533	99 385	+	6985766 6985767		putative phage associated protein phage-associated protein
Spy49_0761	-	NE	756548	757105	185	+	6985768	-	hypothetical protein Spy49_0761
Spy49_0762	-	NC	757148	759070	640	+		COG0749L	DNA polymerase
Spy49_0763 Spy49_0764	-	NC NC	759075 761827	761459 762120	794 97	+	6985770	COG3378R	DNA primase/helicase-phage associated hypothetical protein Spy49_0764
Spy49_0765	-	NC	762117	763439	440	+		COG0553KL	helicase-phage associated
Spy49_0766	-	NE	763603	763875	90	+	6985773		hypothetical protein Spy49_0766
Spy49_0767 Spy49_0768	-	NE NE	764008 764496	764424 764966	138 156	+	6985774 6985775	- COG3728L	transcriptional activator-phage associated terminase small subunit
Spy49_0769	-	NE	764956	766233	425	+		COG1783R	terminase large subunit
Spy49_0770	-	NE	766249	767781	510	+	6985777		phage-associated protein
Spy49_0771 Spy49_0772	-	NE NE	767747 769410	769189 769802	480 130	+	6985778 6985779	COG5585T	phage-associated protein putative phage associated protein
Spy49_0773	-	NC	769845	770414	189	+	6985780		phage protein
Spy49_0774	-	NE	770427	771314	295	+	6985781	-	major head protein (phage associated)
Spy49_0775 Spy49_0776	-	NE NE	771326 771693	771682	118	+	6985782 6985783		phage protein putative phage associated protein
Spy49_0776 Spy49_0777	-	NE	771968	771971 772312	92 114	+	6985784		hypothetical protein Spy49_0777
Spy49_0778	-	NC	772316	772675	119	+	6985785	-	putative phage associated protein
Spy49_0779	-	C	772687	773286	199	+	6985786		phage protein
Spy49_0780 Spy49_0781	-	NC NE	773393 773869	773794 774102	133 77	+	6985787 6985788		putative phage associated protein putative phage associated protein
Spy49_0782	-	NC	774117	778499	1460	+	6985789	-	hypothetical protein Spy49_0782
Spy49_0783	-	NE	778511	779353	280	+	6985790		putative phage associated protein
Spy49_0784 Spy49_0785	-	NC NC	779363 781339	781342 783582	659 747	+	6985791 6985792		phage protein phage hyaluronidase
Spy49_0786	-	NC	783594	783755	53	+	6985793	-	hypothetical protein Spy49_0786
Spy49_0788	-	NE	783758	784369	203	+	6985794	-	hypothetical protein Spy49_0788
Spy49_0789 Spy49_0790	-	NE NE	784379 784952	784834 785704	151 250	+	6985795 6985796	COG4824R	holin protein-phage associated phage-associated cell wall hydrolase
Spy49_0790 Spy49_0791	-	NE NE	785870	785704 786157	95	+	6985797		hypothetical protein Spy49_0791
Spy49_0792	speH	NE	786363	787073	236	+	6985798	-	streptococcal pyrogenic exotoxin H (SpeH)
Spy49_0793 Spy49_0794	mutX	NE NE	787677 788211	788153	158	+		COG1051F	7,8-dihydro-8-oxoguanine-triphosphatase
Spy49_0794 Spy49_0795	-	NE NE	789382	789392 790629	393 415	+		COG0628R COG3063NU	hypothetical protein Spy49_0794 hypothetical protein Spy49_0795
Spy49_0796c	-	NE	790688	792340	550	-		COG1293K	fibronectin-binding protein-like protein A

Spy49_0797 Spy49_0798	_								
		NE	792694	793692	332	+		COG2984R	ABC transporter substrate-binding protein
	-	NC	793643	793861	72	+	6985804	-	hypothetical protein Spy49_0798
Spy49_0799	-	NE	794037	794906	289	+		COG4120R	ABC transport protein
Spy49_0800	-	NE	794903	795661	252	+	6985806		ABC transporter
Spy49_0801		E	795865	797526	553	+	6985807		hypothetical protein Spy49_0801
Spy49_0803	estA	NE	797659	798444	261	+	6985808	COG0627R	Tributyrin esterase
Spy49_0804	-	NE	798474	798800	108	+	6985809	-	hypothetical protein Spy49_0804
Spy49_0805		NE	798846	800753	635	+		COG0488R	ABC transporter
Spy49_0807	acoA	NE	801026	802006	326	+	6985811		pyruvate dehydrogenase E1 component subunit alpha
Spy49_0808	acoB	NE	802062	803063	333	+		COG0022C COG0508C	pyruvate dehydrogenase E1 component subunit beta
Spy49_0809	acoC acoL	NE NE	803248	804657	469	+			branched-chain alpha-keto acid dehydrogenase subunit E2
Spy49_0810		NE NE	804984	806747	587	+	6985815	COG1249C	dihydrolipoamide dehydrogenase
Spy49_0811c	hylA	NE	807422	809839	805			-	Extracellular hyaluronate lyase
Spy49_0812			810072	811061	329	+		COG0095H COG3442R	Lipoate-protein ligase A
Spy49_0813c	cobQ	E	811170 811961	811961	263 447		6985817	COG0769M	Cobyric acid synthase
Spy49_0814c	murC2	E		813304				COG1624S	UDP-N-acetylmuramyl tripeptide synthetase hypothetical protein Spy49 0815
Spy49_0815	-	E NE	813406	814257	283	+		COG4856S	hypothetical protein Spy49_0816
Spy49_0816			814254	815210 816616	318	+			
Spy49_0817	glmM	E NE	815264 816739	817380	450	+	6985821	00011090	phosphoglucosamine mutase
Spy49_0818	- hN				213		6985822	-	hypothetical protein Spy49_0818
Spy49_0819	hemN	NE	817377	818573	398	+		COG0635H COG3884I	coproporphyrinogen III oxidase
Spy49_0820	-	E	818583	819335	250	+	6985824	COG38841 COG0647G	acyl-ACP thioesterase
Spy49_0821 Spy49_0822	-	NE NE	819335	820099	254	+		COG4478S	phosphatase NagD hypothetical protein Spy49_0822
Spy49_0822 Spy49_0823	-	NE NE	820096	820731	211	+		COG3513S	
Spy49_0825	-	NE NE	821210 825316	825316 826185	1368 289	+		COG1518L	hypothetical protein Spy49_0823 Lipoyl-binding domain-containing protein
Spy49_0826	-	NE	826182	826523	113	+	6985829		hypothetical protein Spy49_0826
Spy49_0827	-	NE	826513	827175	220	+	6985830	00033123	hypothetical protein Spy49_0827
Spy49_0828		NE	827952	828122	56	+		COG0105F	nucleoside diphosphate kinase
Spy49_0829	lepA-2	NE	828223	830055	610	+	6985832		GTP-binding protein LepA
Spy49_0830	sclB	NC	830338	831435	365	+	6985833	-	ScIB protein
Spy49 0831	csrA	NE	831620	832057	145	+		COG02290	methionine sulfoxide reductase B
Spy49_0832	-	NE	832187	833206	339	+	6985835		hypothetical protein Spy49_0832
Spy49 0833		NE	833413	833838	141	+		COG2893G	PTS system IIA component
Spy49_0834	-	NC	833865	834356	163	+		COG3444G	PTS system IIB component
Spy49_0835	-	NE	834449	835183	244	+	6985838		phosphotransferase system (PTS), enzyme II component C
Spy49 0836	-	NE	835180	836019	279	+		COG3716G	phospotransferase system (PTS), enzyme II component D
Spy49_0837	-	NE	836144	837793	549	+	6985840		two-component sensor histidine kinase
Spy49_0839	-	NE	837797	838585	262	+		COG4753T	two-component response regulator
Spy49_0840		NE	838579	839625	348	+		COG1840P	iron ABC transporter iron-binding protein
Spy49_0841	-	NE	839741	841138	465	+		COG1012C	succinate-semialdehyde dehydrogenase NADP+
Spy49_0842	uvrC	NE	841239	843035	598	+		COG0322L	excinuclease ABC subunit C
Spy49 0843		NE	843221	843823	200	+		COG0778C	NADH dehydrogenase
Spy49 0844		NE	843948	845357	469	+		COG0624E	dipeptidase PepV
Spy49_0845c	trmE	E	845425	846801	458	_		COG0486R	tRNA modification GTPase TrmE
Spy49_0846	rplJ	NE	847136	847636	166	+	6985848		50S ribosomal protein L10
Spy49_0847	-	NC	847701	847799	32	+	6985849	-	hypothetical protein Spy49_0847
Spy49_0848	rplL	NC	847874	848065	63	+		COG0222J	50S ribosomal protein L7/L12, partial
Spy49_0849	dacA1	NE	848292	849605	437	+	6985851		Penicillin-binding protein 7
Spy49_0850c	-	NE	849658	850620	320	_		COG0726G	polysaccharide deacetylase
Spy49_0851	folC1	E	850952	852229	425	+	6985853		dihydrofolate synthase
Spy49_0852	folE	NE	852264	852848	194	+	6985854		GTP cyclohydrolase I
Spy49_0853	folP	NC	852857	853657	266	+	6985855		dihydropteroate synthase
Spy49_0854	folQ	NE	853664	854023	119	+	6985856		dihydroneopterin aldolase
Spy49_0855	folK	NE	854020	854520	166	+		COG0801H	2-amino-4-hydroxy-6- hydroxymethyldihydropteridine pyrophosphokinase
Spy49_0856	murB	E	854670	855557	295	+		COG0812M	UDP-N-acetylenolpyruvoylglucosamine reductase
Spy49_0857	potA	NE	855603	856757	384	+	6985859		Spermidine Putrescine transport ATP-binding protein potA
Spy49_0858	potB	NE	856741	857535	264	+	6985860		Spermidine Putrescine ABC transporter permease potB
Spy49_0859	potC	NE	857532	858308	258	+		COG1177E	Spermidine Putrescine ABC transporter permease potC
Spy49_0860	potD	NE	858301	859374	357	+		COG0687E	spermidine/putrescine ABC transporter substrate-binding protein
Spy49_0861c	-	NE	859429	860094	221	-	6985863		two-component response regulator
Spy49_0862c	-	NE	860075	861616	513	-	6985864		two-component sensor histidine kinase
Spy49_0863	malP	NE	861777	863108	443	+		COG3493C	L-malate permease
Spy49_0864	-	NE	863140	864306	388	+		COG0281C	NAD-dependent malic enzyme
Spy49_0865c	-	NE	864388	865437	349	-	6985867	COG1063ER	zinc-containing alcohol dehydrogenase
Spy49_0866	aphA		865673	866404	243	+	6985868	COG3700R	acid phosphatase/phosphotransferase
		NE		868114	510	+	6985869	COG0038P	
Spy49_0867	-	NE NE	866582						voltage-gated chloride channel protein
Spy49_0867 Spy49_0868	-			868891	204	+	6985870	COG2755E	
		NE	866582		204 369	+		COG2755E COG0628R	voltage-gated chloride channel protein
Spy49_0868 Spy49_0869 Spy49_0870	- - radC	NE NE NE NE	866582 868277 869071 870247	868891 870180 870927	369 226	++	6985871 6985872	COG0628R COG2003L	voltage-gated chloride channel protein hypothetical protein Spy49_0868 hypothetical protein Spy49_0869 DNA repair protein RadC
Spy49_0868 Spy49_0869	-	NE NE NE	866582 868277 869071	868891 870180	369	+	6985871 6985872 6985873	COG0628R COG2003L COG2071R	voltage-gated chloride channel protein hypothetical protein Spy49_0868 hypothetical protein Spy49_0869
Spy49_0868 Spy49_0869 Spy49_0870 Spy49_0871c Spy49_0872c	-	NE NE NE NE NE	866582 868277 869071 870247 870929 871634	868891 870180 870927 871624 872278	369 226 231 214	+ -	6985871 6985872 6985873 6985874	COG0628R COG2003L COG2071R COG2344R	voltage-gated chloride channel protein hypothetical protein Spy49_0868 hypothetical protein Spy49_0869 DNA repair protein RadC glutamine amidotransferase, class I redox-sensing transcriptional repressor Rex
Spy49_0868 Spy49_0869 Spy49_0870 Spy49_0871c Spy49_0872c Spy49_0873c	-	NE NE NE NE NE NE	866582 868277 869071 870247 870929 871634 872530	868891 870180 870927 871624 872278 872877	369 226 231 214 115	+ + -	6985871 6985872 6985873 6985874 6985875	COG0628R COG2003L COG2071R COG2344R	voltage-gated chloride channel protein hypothetical protein Spy49_0868 hypothetical protein Spy49_0869 DNA repair protein RadC glutamine amidotransferase, class I redox-sensing transcriptional repressor Rex hypothetical protein Spy49_0873c
Spy49_0868 Spy49_0869 Spy49_0870 Spy49_0871c Spy49_0872c Spy49_0873c Spy49_0874c	- - - radC - -	NE NE NE NE NE NE NE	866582 868277 869071 870247 870929 871634 872530 872867	868891 870180 870927 871624 872278 872877 873994	369 226 231 214 115 375	+ -	6985871 6985872 6985873 6985874 6985875 6985876	COG0628R COG2003L COG2071R COG2344R - COG1104E	voltage-gated chloride channel protein hypothetical protein Spy49_0868 hypothetical protein Spy49_0869 DNA repair protein RadC glutamine amidotransferase, class I redox-sensing transcriptional repressor Rex hypothetical protein Spy49_0873c cysteine desuffurase
Spy49_0868 Spy49_0869 Spy49_0870 Spy49_0871c Spy49_0872c Spy49_0873c Spy49_0874c Spy49_0875c	-	NE	866582 868277 869071 870247 870929 871634 872530 872867 873991	868891 870180 870927 871624 872278 872877 873994 874971	369 226 231 214 115 375 326	+ +	6985871 6985872 6985873 6985874 6985875 6985876 6985877	COG0628R COG2003L COG2071R COG2344R - COG1104E COG0462FE	voltage-gated chloride channel protein hypothetical protein Spy49_0868 hypothetical protein Spy49_0869 DNA repair protein RadC glutamine amidotransferase, class I redox-sensing transcriptional repressor Rex hypothetical protein Spy49_0873c cysteine desulfurase ribose-phosphate pyrophosphokinase
Spy49_0868 Spy49_0869 Spy49_0870 Spy49_0871c Spy49_0872c Spy49_0873c Spy49_0874c Spy49_0875c Spy49_0876c	- - - radC - -	NE NC	866582 868277 869071 870247 870929 871634 872530 872867 873991 875111	868891 870180 870927 871624 872278 872877 873994 874971 875689	369 226 231 214 115 375 326 192	+ +	6985871 6985872 6985873 6985874 6985875 6985876 6985877 6985878	COG0628R COG2003L COG2071R COG2344R - COG1104E COG0462FE COG4116S	voltage-gated chloride channel protein hypothetical protein Spy49_0868 hypothetical protein Spy49_0869 DNA repair protein RadC glutamine amidotransferase, class I redox-sensing transcriptional repressor Rex hypothetical protein Spy49_0873c cysteine desulfurase riboxe-phosphate pyrophosphokinase hypothetical protein Spy49_0876c
Spy49_0868 Spy49_0869 Spy49_0870 Spy49_0871c Spy49_0872c Spy49_0873c Spy49_0874c Spy49_0876c Spy49_0876c Spy49_0877	- - radC - - - - - prs	NE N	866582 868277 869071 870247 870929 871634 872530 872867 873991 875111 875777	868891 870180 870927 871624 872278 872877 873994 874971 875689 876448	369 226 231 214 115 375 326 192 223	+ + +	6985871 6985872 6985873 6985874 6985875 6985876 6985877 6985878 6985879	COG0628R COG2003L COG2071R COG2344R - COG1104E COG0462FE COG4116S COG2357S	voltage-gated chloride channel protein hypothetical protein Spy49_0868 hypothetical protein Spy49_0869 DNA repair protein RadC glutamine amidotransferase, class I redox-sensing transcriptional repressor Rex hypothetical protein Spy49_0873c cysteine desulfurase ribose-phosphate pyrophosphokinase hypothetical protein Spy49_0876c GTP pyrophosphokinase
Spy49_0868 Spy49_0869 Spy49_0870 Spy49_0871c Spy49_0872c Spy49_0873c Spy49_0874c Spy49_0875c Spy49_0876c Spy49_0877 Spy49_0878	radC	NE NE NE NE NE NE NE NE NC NE	866582 868277 869071 870247 870929 871634 872530 872867 873991 875111 875777 876423	868891 870180 870927 871624 872278 872877 873994 874971 875689 876448 877259	369 226 231 214 115 375 326 192 223 278	+ + - - - - + +	6985871 6985872 6985873 6985874 6985875 6985876 6985877 6985878 6985879 6985880	COG0628R COG2003L COG2071R COG2344R - COG1104E COG0462FE COG4116S COG2357S COG0061G	voltage-gated chloride channel protein hypothetical protein Spy49_0868 hypothetical protein Spy49_0869 DNA repair protein RadC glutamine amidotransferase, class I redox-sensing transcriptional repressor Rex hypothetical protein Spy49_0873c cysteine desulfurase ribose-phosphate pyrophosphokinase hypothetical protein Spy49_0876c GTP pyrophosphokinase inorganic polyphosphate/ATP-NAD kinase
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Spy49_0910c									
	hlyIII	E NE	907220 907732	907735 908172	171 146	-	6985910	COG1272R	hemolysin III, partial hypothetical protein Spy49_0911c
Spy49_0911c Spy49_0912	rbgA	E	908391	909239	282	+		COG1161R	ribosomal biogenesis GTPase
Spy49_0913	rnhB	NE	909229	910020	263	+	6985913		ribonuclease HII
Spy49_0914	smf	NE	910085	910921	278	+		COG0758LU	DNA processing protein
Spy49_0915	topA	E	911028	913157	709	+	6985915	COG0550L	DNA topoisomerase I
Spy49_0916c	-	NE	913233	913715	160	-	6985916	-	LysR family transcriptional regulator
Spy49_0917c Spy49_0918	-	NC NE	913722 914130	913844 914696	40 188	+	6985917 6985918	COG3641R	LysR family transcriptional regulator Regulatory protein
Spy49_0919	-	NE	914711	915703	330	+	6985919		D-lactate dehydrogenase
Spy49_0920	-	E	915808	916473	221	+	6985920	-	acid tolerance SatD-like protein
Spy49_0921	-	NE	916466	917182	238	+	6985921	-	hypothetical protein Spy49_0921
Spy49_0922	gid	NC	917333	918679	448	+		COG1206J	tRNA (uracil-5-)-methyltransferase Gid
Spy49_0923	-	NE	918856	920238	460	+	6985923	COG5016C	oxaloacetate decarboxylase
Spy49_0924	-	NE	920281	920595	104	+	6985924	-	hypothetical protein Spy49_0924
Spy49_0925 Spy49_0926	-	NE NC	920595 920955	920945 922085	116 376	+		COG4770I COG1883C	Biotin carboxyl carrier protein of oxaloacetate decarboxylase Oxaloacetate decarboxylase subunit beta
Spy49_0927c	citG	NE	922286	923170	294			COG1767H	2-(5-triphosphoribosyl)-3- dephosphocoenzyme-A synthase
Spy49_0928c	-	NE	923163	923858	231	-		COG1802K	GntR family transcriptional regulator
Spy49_0929c	-	NE	924016	925422	468	-	6985929	COG2851C	citrate transporter
Spy49_0930	-	NE	925799	926122	107	+	6985930	-	hypothetical protein Spy49_0930
Spy49_0933 Spy49_0934	- citD	NE NE	926611 927920	927732 928228	373 102	+	6985931	COG1883C COG3052C	Oxaloacetate decarboxylase subunit beta citrate lyase subunit gamma
Spy49_0936	citE	NC	928216	929103	295	+		COG2301G	citrate lyase subunit gamma
Spy49_0937	citF	NE	929106	930638	510	+		COG3051C	citrate lyase subunit alpha
Spy49_0938	citX	NE	930535	931209	224	+		COG3697HI	2\'-(5\'\'-triphosphoribosyl)-3\'-dephospho-CoA:apo-citrate lyase
Spy49_0939	oadA	NE	931224	932618	464	+		COG5016C	oxaloacetate decarboxylase
Spy49_0940c	citC	NE	932729	933781	350	-	6985937	COG3053C	citrate (pro-3S)-lyase ligase
Spy49_0942c	-	NE	933968	934351	127	-	6985938	-	hypothetical protein Spy49_0942c
Spy49_0943c Spy49_0944	xerS	C NE	935045 936585	936115 937283	356 232	+	6985940	COG4974L COG2932K	site-specific tyrosine recombinase XerS repressor protein
Spy49_0945c	ffh	E	937400	938962	520			COG0541U	signal recognition particle subunit Ffh SRP54
Spy49_0946c	-	NC	938977	939318	113	-		COG2739S	DNA-binding protein
Spy49_0947c	-	NE	939407	940105	232	-	6985943		GntR family transcriptional regulator
Spy49_0948c	-	NE	940188	941477	429	-	6985944	-	hypothetical protein Spy49_0948c
Spy49_0949	guaA	C	941789	943351	520	+		COG0519F	GMP synthase
Spy49_0951c Spy49_0952c	murM2 -	NE NE	943393 944959	944604 946524	403 521		6985946 6985947	COG2348V COG0488R	antimicrobial resistance factor ABC transporter ATP-binding protein
Spy49_0953c	-	NE	944939	940524	185			COG4720S	hypothetical protein Spy49_0953c
Spy49_0954c	pdxK	NE	947172	948038	288	-		COG2240H	pyridoxamine kinase
Spy49_0955	-	NE	948128	949396	422	+		COG1167KE	transcriptional regulator/aminotransferase
Spy49_0957c	-	NE	949867	950223	118	-		COG1328F	anaerobic ribonucleotide reductase
Spy49_0958c	-	E	950545	952122	525	-		COG1502I	Cardiolipin synthetase
Spy49_0959c	fhs1	C	952207	953877	556	-		COG2759F COG0095H	formatetetrahydrofolate ligase
Spy49_0960c Spy49_0961c	lpIA	NE NE	954005 955071	955024 955952	339 293			COG0846K	Lipoate-protein ligase A hypothetical protein Spy49_0961c
Spy49_0962c		NE	955945	956757	270	-		COG2110R	hypothetical protein Spy49_0962c
Spy49_0963c	-	NE	956750	957082	110	-		COG0509E	glycine cleavage system H protein
Spy49_0964c	-	NE	957124	958122	332	-		COG2141C	hypothetical protein Spy49_0964c
Spy49_0965c	-	NE	958119	959318	399	-		COG1902C	trimethylamine dehydrogenase
Spy49_0966c Spy49_0967	-	NE E	959315	960151 961039	278	+		COG0095H COG0452H	Lipoate-protein ligase A
Spy49_0968	dpfB dfp	E	960347 961032	961577	230 181	+		COG0452H	phosphopantothenatecysteine ligase phosphopantothenoylcysteine decarboxylase
Spy49_0969	-	C	961636	962205	189	+		COG4684S	hypothetical protein Spy49_0969
Spy49_0970	pgmA	E	962381	964099	572	+		COG1109G	phosphoglucomutase
Spy49_0971c	-	NE	964312	965268	318	-		COG1079R	sugar ABC transporter
Spy49_0972c Spy49_0973c	-	NE	965270	966334	354	-		COG4603R COG3845R	sugar ABC transporter
Spy49_0974c	-	NE NE	966327 967998	967859 969050	510 350			COG1744R	sugar ABC transporter lipoprotein
Spy49_0975c	cdd	NE	969144	969533	129	-		COG0295F	cytidine deaminase
Spy49_0976c	-	NE	970186	970779	197	-		COG2813J	hypothetical protein Spy49_0976c
Spy49_0977	coaA	E	971047	971967	306	+		COG1072H COG0268J	pantothenate kinase
Spy49_0978 Spy49_0979c	rpsT ciaH	NC C	972036 972394	972269 973704	77 436	-		COG2205T	30S ribosomal protein S20 histidine kinase
Spy49_0980c	ciaR		973697	974371	224	-		COG0745TK	CiaR family transcriptional regulator
		E			845	-		COG0308E	lysyl-aminopeptidase
Spy49_0981c	pepN	E NE	974718	977255	043		6985976		iysyi-ammopeptidase
Spy49_0982c	pepN phoU	NE NE	977460	978113	217	-			phosphate uptake regulatory protein
Spy49_0982c Spy49_0983c	pepN phoU pstB	NE NE NC	977460 978182	978113 978940	217 252	-		COG1117P	phosphate uptake regulatory protein phosphate transporter ATP-binding protein
Spy49_0982c Spy49_0983c Spy49_0984c	pepN phoU pstB pstB2	NE NC C	977460 978182 978953	978113 978940 979756	217 252 267	-	6985978	COG1117P COG1117P	phosphate uptake regulatory protein phosphate transporter ATP-binding protein phosphate transporter ATP-binding protein
Spy49_0982c Spy49_0983c Spy49_0984c Spy49_0985c	pepN phoU pstB pstB2 pstA	NE NC C NC	977460 978182 978953 979772	978113 978940 979756 980659	217 252 267 295		6985978 6985979	COG1117P COG1117P COG0581P	phosphate uptake regulatory protein phosphate transporter ATP-binding protein phosphate transporter ATP-binding protein phosphate ABC transporter permease
Spy49_0982c Spy49_0983c Spy49_0984c Spy49_0985c Spy49_0986	pepN phoU pstB pstB2 pstA pstC	NE NC C NC	977460 978182 978953 979772 980649	978113 978940 979756 980659 981584	217 252 267 295 311		6985978 6985979 6985980	COG1117P COG1117P COG0581P COG0573P	phosphate uptake regulatory protein phosphate transporter ATP-binding protein phosphate transporter ATP-binding protein phosphate ABC transporter permease phosphate ABC transporter permease
Spy49_0982c Spy49_0983c Spy49_0984c Spy49_0985c Spy49_0986 Spy49_0987c Spy49_0988c	pepN phoU pstB pstB2 pstA	NE NC C NC NC NC E	977460 978182 978953 979772 980649 981595 982600	978113 978940 979756 980659 981584 982461 983910	217 252 267 295 311 288 436		6985978 6985979 6985980 6985981 6985982	COG1117P COG1117P COG0581P COG0573P COG0226P COG0144J	phosphate uptake regulatory protein phosphate transporter ATP-binding protein phosphate transporter ATP-binding protein phosphate ransporter ATP-binding protein phosphate ABC transporter permease phosphate ABC transporter permease phosphate ABC transporter periplasmic phosphate-binding protein pstS nucleolar protein
Spy49_0982c Spy49_0983c Spy49_0984c Spy49_0985c Spy49_0986 Spy49_0987c Spy49_0988c Spy49_0989c	pepN phoU pstB pstB2 pstA pstC	NE NC C NC NC NC NC NC NC	977460 978182 978953 979772 980649 981595 982600 983913	978113 978940 979756 980659 981584 982461 983910 984701	217 252 267 295 311 288 436 262		6985978 6985979 6985980 6985981 6985982 6985983	COG1117P COG1117P COG0581P COG0573P COG0226P COG0144J COG0483G	phosphate uptake regulatory protein phosphate transporter ATP-binding protein phosphate transporter ATP-binding protein phosphate ABC transporter permease phosphate ABC transporter permease phosphate ABC transporter permease phosphate ABC transporter periplasmic phosphate-binding protein pstS nudeolar protein Myo-inositol-1(or 4)-monophosphatase
Spy49_0982c Spy49_0983c Spy49_0984c Spy49_0985c Spy49_0985c Spy49_0987c Spy49_0988c Spy49_0989c Spy49_0990c	pepN phoU pstB pstB2 pstA pstC pstS	NE NC C NC	977460 978182 978953 979772 980649 981595 982600 983913 984691	978113 978940 979756 980659 981584 982461 983910 984701 984969	217 252 267 295 311 288 436 262 92		6985978 6985979 6985980 6985981 6985982 6985983 6985984	COG1117P COG1117P COG0581P COG0573P COG0226P COG0144J COG0483G COG4476S	phosphate uptake regulatory protein phosphate transporter ATP-binding protein phosphate transporter ATP-binding protein phosphate transporter ATP-binding protein phosphate ABC transporter permease phosphate ABC transporter permease phosphate ABC transporter periplasmic phosphate-binding protein pstS nucleolar protein Myo-inositol-1(or 4)-monophosphatase hypothetical protein Spv49_0990C
Spy49_0982c Spy49_0983c Spy49_0985c Spy49_0985c Spy49_0986 Spy49_0987c Spy49_0988c Spy49_0980c Spy49_0990c Spy49_0991c	pepN phoU pstB pstB2 pstA pstC	NE NC C NC N	977460 978182 978953 979772 980649 981595 982600 983913 984691 984971	978113 978940 979756 980659 981584 982461 983910 984701 984969 985375	217 252 267 295 311 288 436 262 92		6985978 6985979 6985980 6985981 6985982 6985983 6985984 6985985	COG1117P COG1117P COG0581P COG0573P COG0226P COG0144J COG0483G COG4476S COG1393P	phosphate uptake regulatory protein phosphate transporter ATP-binding protein phosphate transporter ATP-binding protein phosphate ABC transporter permease phosphate ABC transporter permease phosphate ABC transporter permease phosphate ABC transporter periplasmic phosphate-binding protein pstS nucleolar protein Myo-inositol-1(or 4)-monophosphatase hypothetical protein Spy49_0990c transcriptional regulator Spx
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Spy49_0832 Spy49_0834 Spy49_0836 Spy49_0836 Spy49_0836 Spy49_0896 Spy49_0896 Spy49_0990 Spy49_0990 Spy49_0990 Spy49_0996 Spy49_0996 Spy49_0997 Spy49_0996 Spy49_0996 Spy49_0996 Spy49_0996 Spy49_0996 Spy49_10006 Spy49_10006 Spy49_10006 Spy49_10006 Spy49_10006 Spy49_10006 Spy49_10006 Spy49_1006 Spy49_1006 Spy49_1006 Spy49_1006 Spy49_1006 Spy49_1006 Spy49_1006 Spy49_1006 Spy49_1006 Spy49_1006 Spy49_1006 Spy49_1006 Spy49_1016 Spy49_1016 Spy49_1016 Spy49_1016 Spy49_1016 Spy49_1016 Spy49_1017 Spy49_1016 Spy49_1016 Spy49_1017	pepN phoU pstB pstB2 pstA2 pstC pstS spxA truB	NE NE NC C NC N	977460 978182 978953 979772 980649 981595 982600 983913 984971 985418 986340 987379 988816 989783 990471 993122 993911 993122 993910 994638 995429 996722 996921 997599 996722 996921 1002469 1004745 1005217 1006069 1006708 1007456 1007456 1007987 100752 1007456 1007987 100752 10107977 1010752 10123117 10113410 1016705	978113 978940 979756 980659 981584 982461 983910 984701 984701 9847701 984707 996379 997508 997508 997508 997508 997508 997508 1000498 1002349 1004847 10046053 1006698 1007791 1009801 1007501 1007501	217 295 252 267 295 3111 288 436 262 2134 4310 307 446 878 223 3180 92 195 82 209 162 266 179 278 440 411 257 278 209 213 111 604 112 550 500 337 1036 123 232 232 232	+ + + +	6985978 6985929 6985980 6985981 6985982 6985983 6985984 6985985 6985991 6985992 6985991 6985992 6985991 6985992 6985993 6985991 6986902 6986002 6986004 6986004 6986005 6986006 6986006 6986006 6986007 6986008 6986001 6986011 6986011 6986011 6986011	COG1117P COG0581P COG0581P COG0573P COG0573P COG026P COG014J COG0476S COG1393P COG01301 COG01301 COG4129S COG0732V COG0577V COG1136V COG01302S COG0577V COG1309S COG0567V COG1309S COG0567V COG1309S COG0567V COG0577V COG1126C COG0577V COG0567V COG0	phosphate uptake regulatory protein phosphate transporter ATP-binding protein phosphate transporter ATP-binding protein phosphate ABC transporter permease phosphate ABC transporter permease phosphate ABC transporter permease phosphate ABC transporter periplasmic phosphate-binding protein pstS nucleolar protein Myo-inositol-1(or 4)-monophosphatase hypothetical protein Spy49_0990c transcriptional regulator Spx bifunctional riboflavin kinase/FMN adenylyitransferase tRNA pseudouridine synthase B hypothetical protein Spy49_0994c hypothetical protein Spy49_0995c hypothetical protein Spy49_0995c ABC transporter permease ABC transporter permease ABC transporter permease ABC transporter permease hypothetical protein Spy49_1001c hypothetical protein Spy49_1002c hypothetical protein Spy49_1002c hypothetical protein Spy49_1003c hypothetical protein Spy49_1004c hypothetical protein Spy49_1005c hypothetical protein Spy49_1006c ATP-dependent DNA helicase amino acid ABC transporter substrate-binding protein amino acid ABC transporter permease PhNA protein glucosamine—fructose-6-phosphate aminotransferase signal peptidase I pyruvate kinase ENABC transporter CHBC TRANSPORTER BY ABC TR
Spy49_0882c Spy49_0884c Spy49_0886 Spy49_0886 Spy49_0886 Spy49_0896 Spy49_0896 Spy49_0991c Spy49_0991c Spy49_0992c Spy49_0993c Spy49_0993c Spy49_0994c Spy49_0996 Spy49_0996 Spy49_0996 Spy49_0996 Spy49_0996 Spy49_1000c Spy49_1001c Spy49_1001c Spy49_1006 Spy49_1007 Spy49_1008 Spy49_1009 Spy49_1009 Spy49_1010 Spy49_1010 Spy49_1010 Spy49_1010 Spy49_1011 Spy49_101	pepN phoU pstB pstB2 pstA2 pstC pstS spxA truB	NE NC C NC E NE NE E NE	977460 978182 978182 978953 979772 980649 981595 982600 983913 984691 985418 986340 987379 988163 990471 993122 993941 995403 995722 996170 996722 996217 1002469 1004074 1005069 1004074 1005069 1007987 1007987 1007987 1007987 1007987 1007987 1007987 1007987 100977 1001752 1011317 10113410 1016705	978113 978940 979756 980659 981584 982461 983910 984701 984969 985375 986350 987263 988719 990379 993107 993823 994483 995267 995918 996709 996910 995918 1002349 1003704 1004887 1006498 1007349 1007791 1004881 1007349 1007349 1007349 1010534 1010534 10102544 1013330 1016520	217 252 267 295 311 288 436 262 92 134 310 307 446 318 878 233 180 66 61 279 62 213 411 257 278 440 411 257 278 209 213 111 1036 604 185 500 337 1036 604 185 500 337 1036 604 185 500 337 1036 604 123 1036 123 1037 1038 1038 1038 1038 1038 1038 1038 1038	+ +	9985978 998598 998598 998598 998598 998598 998598 998598 998599 998599 998599 998599 998599 998599 998599 998599 998600 998599 998600	COG1117P COG0581P COG0581P COG0573P COG0573P COG0256P COG01441 COG0483G COG4476S COG1393P COG0196H COG0130P COG04887 COG4129S COG4129S COG0577V COG0577V COG1309K COG0490P COG0490P COG0490P COG0577V COG1309K COG0577V COG1309K COG0577V COG1309K COG0577V COG1309K COG0577V COG1309K COG0577V COG1309K COG06957V COG1309K COG0597 - COG0681U COG0681U COG0681U COG0681U COG0687C COG0687C COG0687C COG0687C COG06957C COG0687C COG06957C COG0695C COG	phosphate uptake regulatory protein phosphate transporter ATP-binding protein phosphate transporter ATP-binding protein phosphate ABC transporter permease phosphate ABC transporter permease phosphate ABC transporter permease phosphate ABC transporter periplasmic phosphate-binding protein pstS nucleolar protein Myo-inositol-1(or 4)-monophosphatase hypothetical protein Spy49_0990 transcriptional regulator Syx bifunctional riboflavin kinase/FMN adenylyltransferase tRNA pseudouridine synthase B hypothetical protein Spy49_0994c hypothetical protein Spy49_0995c hypothetical protein Spy49_0996c ABC transporter TetR family transcriptional regulator transcriptional regulator transcriptional regulator transcriptional regulator hypothetical protein Spy49_1001c hypothetical protein Spy49_1002c hypothetical protein Spy49_1002c hypothetical protein Spy49_1005c

Spy49 1023c		E	1018706	1019311	201		6986017	COG0398S	hypothetical protein Spy49_1023c
Spy49_1024	-	NE	1020050	1020670	206	+	6986019	-	hypothetical protein Spy49_1024
Spy49_1025c	glgP	NE	1020927	1023191	754	-		COG0058G	glycogen phosphorylase
Spy49_1026c	malQ	NE	1023226	1024719	497	-		COG1640G	4-alpha-glucanotransferase
Spy49_1027c Spy49_1028	malR malE	NE NE	1024834 1026097	1025853 1027344	339 415	+		COG1609K COG2182G	maltose operon transcriptional repressor maltose maltodextrin ABC transporter substrate binding periplasmic protein malE
Spy49_1029	malF	NE	1020037	1027344	453	+		COG2182G COG1175G	maltose ABC transporter permease
Spy49_1030	malG	NE	1028979	1029815	278	+		COG3833G	maltose AVC transporter permease
Spy49_1032	-	NE	1031207	1031431	74	+	6986027	-	transposase for insertion-like sequence element IS1161
Spy49_1033c	-	NE	1031496	1032479	327	-		COG0657I	esterase
Spy49_1034c	dltD dltC	NE	1032510	1033760	416	-		COG3966M	Protein dltD
Spy49_1035c Spy49_1036c	dltB	NE NC	1033753 1034010	1033992 1035266	79 418	-		COG0236IQ COG1696M	D-alaninepoly(phosphoribitol) ligase subunit 2 hypothetical protein Spy49_1036c
Spy49_1030c	dltA	NC	1035263	1036801	512	-		COG1030W	D-alaninepoly(phosphoribitol) ligase subunit 1
Spy49_1038c	-	NC	1036813	1036956	47	-	6986033		hypothetical protein Spy49_1038c
Spy49_1039c	uvrB	NE	1037219	1039210	663	-		COG0556L	excinuclease ABC subunit B
Spy49_1040	glnP	С	1039403	1041577	724	+		COG0765E	glutamine ABC transporter glutamine-binding protein/permease
Spy49_1041 Spy49_1042c	glnQ	C NC	1041577 1042465	1042317 1042617	246 50	+	6986036	COG1126E	glutamine transport ATP-binding protein glnQ hypothetical protein Spy49_1042c
Spy49_1043c	-	NE	1042403	1042017	459	-		COG1455G	PTS system IIC component
Spy49_1044c	-	NE	1044171	1044620	149	-	6986039	-	hypothetical protein Spy49_1044c
Spy49_1045c	-	NE	1044617	1044952	111	-	6986040	COG1447G	PTS enzyme III
Spy49_1046c	-	NE	1044955	1045266	103	-		COG1440G	PTS system enzyme II
Spy49_1047c	-	NC	1045289	1047283	664	-		COG3711K	transcriptional antiterminator
Spy49_1048c Spy49_1049c	-	NE NE	1047389 1048492	1048483 1049892	364 466	-		COG3589S COG2723G	hypothetical protein Spy49_1048c beta-glucosidase
Spy49_1050	-	NE	1050117	1050812	231	+		COG3201H	ribosyl nicotinamide transporter
Spy49_1051c	-	NC	1050817	1050975	52	-	6986046	-	hypothetical protein Spy49_1051c
Spy49_1053c	obgE	E	1051044	1052357	437	-		COG0536R	GTPase ObgE
Spy49_1054	-	NE	1052786	1053181	131	+		COG2963L	hypothetical protein Spy49_1054
Spy49_1055	-	NE	1053321	1054199	292	+		COG2801L	transposase, IS861
Spy49_1056 Spy49_1057	-	NE NE	1054597 1055100	1055097 1055906	166 268	+		COG2963L COG2801L	hypothetical protein Spy49_1056 transposase, IS861
Spy49_1059	-	NE	1057303	1058613	436	+		COG0471P	integral membrane protein
Spy49_1060	-	NC	1058770	1058985	71	+	6986053	-	hypothetical protein Spy49_1060
Spy49_1062	-	NE	1059129	1059314	61	+	6986054	-	Insertion element iso-IS904 coding for a transposase
Spy49_1064c	rsuA	NC	1059757	1060488	243	-		COG1187J	16S pseudouridylate synthase
Spy49_1065	-	NE	1060603	1060968	121 406	+		COG5496R COG2814G	hypothetical protein Spy49_1065 hypothetical protein Spy49_1066c
Spy49_1066c Spy49_1067	-	NE NE	1061088 1062720	1062308 1064165	481	+		COG2814G COG4868S	hypothetical protein Spy49_1067
Spy49_1070c	-	NE	1064270	1064671	133	-		COG2050Q	phenylacetic acid degradation protein Paal
Spy49_1071c	-	NE	1064835	1065269	144	-		COG2820F	Uridine phosphorylase
Spy49_1072c	-	NE	1065688	1067046	452	-		COG2265J	RNA methyltransferase
Spy49_1073c	psr	NE	1067128	1068579	483	-		COG1316K	PBP 5 synthesis repressor
Spy49_1074c Spy49_1075c	aroK aroA1	NE NE	1068787 1069271	1069278 1070554	163 427	-		COG0703E COG0128E	shikimate kinase 3-phosphoshikimate 1-carboxyvinyltransferase
Spy49_1076c	-	NE	1070665	1071630	321	-		COG1295S	ribonuclease BN
Spy49_1077c	map	E	1071632	1072492	286	-		COG0024J	methionine aminopeptidase
Spy49_1078c	-	NC	1072508	1073791	427	-		COG4109K	hypothetical protein Spy49_1078c
Spy49_1079c	-	NE	1073800	1074342	180	-		COG1670J	acetyl transferase
Spy49_1080c	grab murZ	NE	1074609	1075148	179	-	6986069	-	Protein G-related alpha 2 macroglobulin-binding protein (GRAB)
Spy49_1082c Spy49_1083c	metK	NE E	1075506 1076939	1076765 1078135	419 398	-		COG0766M COG0192H	UDP-N-acetylglucosamine 1-carboxyvinyltransferase S-adenosylmethionine synthetase
Spy49_1084c	inIA	NE	1078672	1081050	792	-		COG4886S	internalin
Spy49_1085	birA	E	1081425	1082195	256	+	6986073	COG0340H	Biotin-protein ligase / Biotin operon repressor
Spy49_1086c	-	NE	1082170	1082373	67	-	6986074	-	hypothetical protein Spy49_1086c
Spy49_1087c	dnaX	E	1082469	1084139	556	-		COG2812L	DNA polymerase III subunits gamma/tau
Spy49_1088c Spy49_1089	-	NE NE	1084139 1084842	1084636 1085591	165 249	+		COG1956T COG2339S	hypothetical protein Spy49_1088c hypothetical protein Spy49_1089
Spy49_1090c	udk	NE	1085989	1085551	208	-		COG0572F	uridine kinase
Spy49_1091	deaD2	NE	1086713	1087798	361	+		COG0513LKJ	RNA helicase
Spy49_1092c	-	NE	1087909	1089183	424	-	6986080	COG0726G	polysaccharide deacetylase
Spy49_1093c	gapN	E	1089304	1090707	467	-		COG1012C	glyceraldehyde-3-phosphate dehydrogenase (NADP)
Spy49_1094c	ptsl	C	1090892	1092625	577	-		COG1080G	phosphoenolpyruvate-protein phosphotransferase of PTS system
Spy49_1095c Spy49_1096	ptsH nrdH	NC NE	1092630 1093253	1092893 1093504	87 83	+		COG1925G COG0695O	phosphocarrier protein HPr glutaredoxin
Spy49_1097	nrdE1	NE	1093524	1095683	719	+		COG0209F	ribonucleotide-diphosphate reductase subunit alpha
Spy49_1098	nrdF1	NE	1095664	1095981	105	+	6986086	-	hypothetical protein Spy49_1098
Spy49_1099	nrdF	NE	1096016	1096975	319	+		COG0208F	ribonucleotide-diphosphate reductase subunit beta
Spy49_1100	-	NE	1096950	1098263	437	+		COG0038P	chloride channel protein
Spy49_1101	-	NC	1098401	1098694	97	+	6986089	COG2963L	hypothetical protein Spy49_1101
Spy49_1103 Spy49_1104	-	NC NE	1099127 1099337	1099297 1099558	56 73	+		- COG2801L	transposase transposase
Spy49_1105c	-	NE	1099651	1100346	231	-		COG1266R	hypothetical protein Spy49_1105c
Spy49_1106c	-	NE	1100365	1101126	253	-	6986093	-	hypothetical protein Spy49_1106c
Spy49_1107c	- 1-6	NE	1101123	1101353	76	-		COG1476K	Cro/CI family transcriptional regulator
Spy49_1108c	alaS	E NE	1101699 1104704	1104317	872 351	-	6986095 6986096		alanyl-tRNA synthetase
Spy49_1109c Spy49_1110c	prsA -	NE NE	1104/04	1105759 1106529	351 235	-	6986095		foldase PrsA methyltransferase
Spy49_1110c Spy49_1111c	-	NE	1105622	1100323	398	-		COG2814G	oxalate:formate antiporter
Spy49_1112c	рерВ	NE	1108168	1109973	601	-	6986099	COG1164E	oligopeptidase PepB
Spy49_1113c	-	NE	1109986	1110948	320	-		COG4469R	transcription factor
Spy49_1114c		NE	1111245	1111961	238	-		COG1187J	16S pseudouridylate synthetase
Spy49_1115c Spy49_1116	nagB queA	NE NE	1112080 1112986	1112784 1114014	234 342	+		COG0363G COG0809J	glucosamine-6-phosphate deaminase S-adenosylmethionine:tRNA ribosyltransferase-isomerase
Spy49_1117	-	NE	1114021	1115241	406	+	6986104	-	hypothetical protein Spy49 1117
Spy49_1119c	-	NE	1115355	1115945	196	-		COG1686M	hypothetical protein Spy49_1119c
Spy49_1120c	-	NE	1115942	1116190	82	-	6984358	-	hypothetical protein Spy49_1120c
Spy49_1121c	-	NC	1116175	1116402	75	-	6984359	-	hypothetical protein Spy49_1121c
Spy49_1122c Spy49_1123c	sodM holA	NE E	1116524 1117265	1117168 1118305	214 346	-	6984360 6984361	COG0605P COG1466L	superoxide dismutase DNA polymerase III subunit delta
Spy49_1123c Spy49_1124c	comEC	NE.	1117265	1118305	747	-		COG2333R	DNA polymerase III subunit delta DNA internalization-related competence protein ComEC/Rec2
Spy49_1126c	comE	NE	1120600	1121262	220	-		COG1555L	competence protein
Spy49_1127c	-	E	1121462	1122202	246	-	6984364	COG0204I	1-acyl-sn-glycerol-3-phosphate acyltransferase
	-	NE	1122242	1123096	284	+		COG4123R	hypothetical protein Spy49_1128
Spy49_1128	-	NE	1123086	1123364	92	+		COG2827L	hypothetical protein Spy49_1129
Spy49_1129		NE	1123388 1125516	1125388 1127135	666 539			COG3158P COG0513LKJ	potassium uptake protein ATP-dependent RNA helicase
Spy49_1129 Spy49_1130c	kup deaD1				514	-		COG0513LKJ	peptide chain release factor 3
Spy49_1129 Spy49_1130c Spy49_1132c	deaD1	NE		1128986				COG5522S	hypothetical protein Spy49_1135c
Spy49_1129 Spy49_1130c			1127442 1129234	1128986 1129929	231	-	0904370		hypothetical protein spy45_1155c
Spy49_1129 Spy49_1130c Spy49_1132c Spy49_1133c Spy49_1135c Spy49_1136c	deaD1 prfC - murF	NE NE NE E	1127442 1129234 1130009	1129929 1131400	463	-	6984371	COG0770M	UDP-N-acetylmuramoyl-tripeptide-D-alanyl-D-alanine ligase
Spy49_1129 Spy49_1130c Spy49_1132c Spy49_1133c Spy49_1135c Spy49_1136c Spy49_1137c	deaD1 prfC - murF ddl	NE NE NE E	1127442 1129234 1130009 1131591	1129929 1131400 1132637	463 348	-	6984371 6984372	COG0770M COG1181M	UDP-N-acetylmuramoyl-tripeptide-D-alanyl-D-alanine ligase D-alanyl-alanine synthetase A
Spy49_1129 Spy49_1130c Spy49_1132c Spy49_1133c Spy49_1135c Spy49_1136c Spy49_1137c Spy49_1138c	deaD1 prfC - murF	NE NE NE E C	1127442 1129234 1130009 1131591 1132738	1129929 1131400 1132637 1133334	463 348 198	-	6984371 6984372 6984373	COG0770M	UDP-N-acetylmuramoyl-tripeptide-D-alanyl-D-alanine ligase D-alanyl-alanine synthetase A recombination protein RecR
Spy49_1129 Spy49_1130c Spy49_1132c Spy49_1133c Spy49_1135c Spy49_1136c Spy49_1137c Spy49_1138c Spy49_1139c	deaD1 prfC - murF ddl recR -	NE NE NE E C	1127442 1129234 1130009 1131591 1132738 1133381	1129929 1131400 1132637 1133334 1133572	463 348 198 63	-	6984371 6984372 6984373 6984374	COG0770M COG1181M COG0353L	UDP-N-acetylmuramoyl-tripeptide-D-alanyl-D-alanine ligase D-alanyl-alanine synthetase A recombination protein RecR hypothetical protein Spy49_1139c
Spy49_1129 Spy49_1130c Spy49_1132c Spy49_1133c Spy49_1135c Spy49_1136c Spy49_1137c Spy49_1138c	deaD1 prfC - murF ddl	NE NE NE E C	1127442 1129234 1130009 1131591 1132738	1129929 1131400 1132637 1133334	463 348 198	-	6984371 6984372 6984373 6984374	COG0770M COG1181M	UDP-N-acetylmuramoyl-tripeptide-D-alanyl-D-alanine ligase D-alanyl-alanine synthetase A recombination protein RecR
Spy49_1129 Spy49_1130c Spy49_1132c Spy49_1133c Spy49_1135c Spy49_1136c Spy49_1137c Spy49_1138c Spy49_1139c Spy49_1140c	deaD1 prfC - murF ddl recR -	NE NE E C NE	1127442 1129234 1130009 1131591 1132738 1133381 1134132	1129929 1131400 1132637 1133334 1133572 1134947	463 348 198 63 271	-	6984371 6984372 6984373 6984374 6984375 6984376	COG0770M COG1181M COG0353L	UDP-N-acetylmuramoyl-tripeptide-D-alanyl-D-alanine ligase D-alanyl-alanine synthetase A recombination protein RecR hypothetical protein Spy49_1139c formate/nitrie transporter family member

Spy49 1143c	gpmA	E	1136365	1137060	231		6984378	COG0588G	phosphoglyceromutase
Spy49_1143c	pyrD	NE	1137357	1138238	293	+	6984379	COG0167F	dihydroorotate dehydrogenase 1A
Spy49_1145c	-	NC	1138293	1138466	57	-	6984380	-	hypothetical protein Spy49_1145c
Spy49_1146c	cadA	NC	1138538	1140400	620	-	6984381	COG2217P	heavy metal-transporting ATPase
Spy49_1147c	-	NC	1140732	1141007	91	-	6984382	COG0776L	DNA-binding protein HU
Spy49_1148c	-	NE	1141106	1141693	195	-	6984383		hypothetical protein Spy49_1148c
Spy49_1149c	-	NE	1141671	1142513	280	-	6984384	COG2755E	Lipase/acylhydrolase
Spy49_1150c	-	С	1142506	1143357	283	-	6984385	COG1307S	DegV family protein
Spy49_1151c		NE	1143573	1144529	318	-	6984386	-	hypothetical protein Spy49_1151c
Spy49_1152c	recN	NE	1144701	1146362 1146853	553 156	-	6984388	COG0497L COG1438K	DNA repair and genetic recombination protein
Spy49_1153c Spy49_1154c	-	NE NE	1146383 1146840	1140853	275		6984389		repressor protein hemolysin
Spy49_1155c	fps	NE	1147867	1148532	221	-	6984390		Octaprenyl-diphosphate synthase / Dimethylallyltransferase / Geranyltranstransferase / Geranylgerany
Spy49_1156c	xseB	NE	1148532	1148747	71	-	6984391		exodeoxyribonuclease VII small subunit
Spy49_1157c	xseA	NE	1148725	1150065	446	-		COG1570L	exodeoxyribonuclease VII large subunit
Spy49_1158c	folD	NC	1150218	1151072	284	-		COG0190H	bifunctional 5,10-methylene-tetrahydrofolate dehydrogenase/ 5,10-methylene-tetrahydrofolate cyclohyd
Spy49_1159c	-	NE	1151280	1152974	564	-		COG1109G	phosphoglucomutase/phosphomannomutase
Spy49_1160c	phr	NE	1153152	1154561	469	-	6984395	COG0415L	deoxyribodipyrimidine photolyase
Spy49_1161c	gtr	NE	1154710	1155444	244	-		COG1126E	amino acid ABC transporter
Spy49_1162c	-	NE	1155444	1156130	228	-		COG0765E	amino acid ABC transporter
Spy49_1163c	-	NC	1156257	1156487	76	-	6984398		hypothetical protein Spy49_1163c
Spy49_1164	clpE	NE	1156785	1159067	760	+	6984399		ATP-dependent protease
Spy49_1165 Spy49_1166	mutT	NE NE	1159195 1159701	1159650 1160003	151 100	+	6984400 6984401	COG0494LR	MutT/nudix family protein hypothetical protein Spy49_1166
Spy49_1166 Spy49_1167c	ileS	E	1160268	1163024	918			COG0060J	isoleucyl-tRNA synthetase
Spy49_1168c	divIVA	NC	1163342	1164100	252	-	6984403		cell-division initiation protein
Spy49_1169c	-	NE	1164110	1164901	263	-		COG2302S	hypothetical protein Spy49_1169c
Spy49_1170c	-	NE	1164901	1165155	84	-	6984405		YGGT family protein
Spy49_1171c	-	С	1165160	1165828	222	-	6984406		hypothetical protein Spy49_1171c
Spy49_1172c	-	NE	1165828	1166499	223	-	6984407		hypothetical protein Spy49_1172c
Spy49_1173c	ftsZ	E	1166502	1167821	439	-	6984408		cell division protein FtsZ
Spy49_1174c	ftsA	E	1167845	1169209	454	-	6984409		cell division protein FtsA
Spy49_1175c	ftsQ	E	1169420	1170568	382	-	6984410		cell division protein FtsQ
Spy49_1176c Spy49_1177c	murG murD	E	1170569	1171651 1173009	360 452	-	6984411 6984412		undecaprenyldiphospho-muramoylpentapeptide beta-N- acetylglucosaminyltransferase
Spy49_1177c Spy49_1178c	ur <i>D</i>	E NE	1171651 1173365	1173009 1173616	452 83		6984413	- COGO//IM	UDP-N-acetylmuramoyl-L-alanyl-D-glutamate synthetase hypothetical protein Spy49_1178c
Spy49_1178c Spy49_1179c	-	NE NE	1173738	1175579	613			- COG1217T	nypotnetical protein Spy49_1178c GTP-binding protein TypA/BipA
Spy49_1180c	-	NE	1175762	1176151	129	-	6984415		hypothetical protein Spy49_1180c
Spy49_1181c	-	NE	1176161	1177132	323	-	6984416		glucokinase
Spy49_1182c	-	NE	1177137	1177340	67	-	6984417		hypothetical protein Spy49_1182c
Spy49_1183c	-	NE	1177482	1178009	175	-	6984418	COG0783P	peroxide resistance protein
Spy49_1184	-	NE	1178237	1178863	208	+	6984419	-	Type IV prepilin peptidase-like protein
Spy49_1185c	-	NE	1178945	1180024	359	-		COG0820R	ribosomal RNA large subunit methyltransferase N
Spy49_1186c	-	NE	1180028	1180648	206	-	6984421		hypothetical protein Spy49_1186c
Spy49_1187c	-	NE	1181096	1182073	325	-	6984422		ribose operon repressor
Spy49_1188c	- D	NE	1182487 1183511	1183524 1184002	345	-		COG3480T	ATP-dependent protease La
Spy49_1189c Spy49_1190c	coaD	E NE	1183992	1184531	163 179		6984425	COG0669H COG0742L	phosphopantetheine adenylyltransferase hypothetical protein Spy49_1190c
Spy49_1191c	asnA	NE	1184654	1185646	330	-		COG2502E	asparagine synthetase AsnA
Spy49_1192c	arcC	NC	1185959	1186909	316	-		COG0549E	carbamate kinase
Spy49_1193c	-	NE	1186929	1188260	443	-		COG0624E	hypothetical protein Spy49_1193c
Spy49_1194c	-	NE	1188277	1189578	433	-		COG1288S	hypothetical protein Spy49_1194c
Spy49_1195c	arcB	NC	1189941	1190954	337	-	6984430		ornithine carbamoyltransferase
Spy49_1196c	-	NE	1190979	1191419	146	-	6984431		hypothetical protein Spy49_1196c
Spy49_1197c	arcA	NE	1191519	1192754	411	-	6984432		arginine deiminase
Spy49_1198c	-	NE	1193028	1193708	226	-		COG0664T	Crp/Fnr family transcriptional regulator
Spy49_1199	argR	NE	1193850	1194323	157	+		COG1438K	arginine repressor
Spy49_1200c	-	NE	1194490 1195220	1195206 1196299	238 359	-	6984435	COG3382S COG2315S	hypothetical protein Spy49_1200c
Spy49_1201c Spy49_1202c	vesM	NE NE	1195220	1198299	577		6984437		hypothetical protein Spy49_1201c two-component sensor histidine kinase
Spy49_1202c Spy49_1203c	yesN	NE	1190372	1198842	246	-	6984438		two-component response regulator
Spy49_1204c	msrA1	NE	1198930	1200036	368	-	6984439		peptide methionine sulfoxide reductase msrA/msrB
Spy49_1205c	-	NE	1200079	1200702	207	-	6984440		hypothetical protein Spy49_1205c
Spy49_1206c	ccdA	NE	1200715	1201404	229	-	6984441		cytochrome C biogenesis protein
Spy49_1207c	-	NE	1202097	1202390	97	-	6984442		hypothetical protein Spy49_1207c
Spy49_1208c	-	NE	1202401	1203426	341	-	6984443	COG1518L	hypothetical protein Spy49_1208c
Spy49_1209c	-	NE	1203423	1204097	224	-	6984444	COG1468L	hypothetical protein Spy49_1209c
Spy49_1210c	-	NE	1204099	1204947	282	-	6984445	COG3649L	hypothetical protein Spy49_1210c
Spy49_1211c	-	NC	1204952	1206847	631	-	6984446	-	hypothetical protein Spy49_1211c
Spy49_1212c	-	NE	1206847	1207575	242	-	6984447	-	hypothetical protein Spy49_1212c
Spy49_1213c	-	NE	1207708	1210110	800	-		COG1203R	ATP-dependent RNA helicase SrmB
Spy49_1215c	valS	E NE	1210270 1212920	1212918 1213483	882 187	-	6984449 6984450	COG0525J	valyl-tRNA synthetase
Spy49_1216c Spy49_1217c		NC NC	1212920	1213483	187 59		6984451	- COG1670J	hypothetical protein Spy49_1216c hypothetical protein Spy49_1217c
Spy49_1218c	-	NC	1213480	1213033	131		6984452	-	hypothetical protein Spy49_1217c
Spy49_1219c	-	NC	1214499	1214753	84	-	6984453	-	hypothetical protein Spy49_1219c
Spy49_1220	aroA2	NE	1215231	1215983	250	+		COG2876E	3-deoxy-7-phosphoheptulonate synthase
Spy49_1221	aroB	NE	1216039	1217112	357	+	6984456		3-dehydroquinate synthase
Spy49_1222c	-	NE	1217548	1217853	101	-	6984457		acetate kinase
Spy49_1223c	-	NE	1217855	1218193	112	-	6984458		hypothetical protein Spy49_1223c
Spy49_1224c	-	NC	1218246	1219001	251	-	6984459		ubiquinone/menaquinone biosynthesis methyltransferase UbiE/COQ5
Spy49_1225c	aroE1	NE NE	1219236 1220252	1220114 1223668	292 1138	-	6984460 6984461		Shikimate 5-dehydrogenase beta-galactosidase
Spy49_1226c Spy49_1227c	-	NE NE	1220252	1223668	494		6984462		two-component sensor response regulator
Spy49_1228c		NE NE	1225172	1225172	574			COG2972T	two-component sensor response regulator two-component sensor histidine kinase
Spy49_1229c	-	NE	1226886	1227491	201	-		COG5578S	hypothetical protein Spy49_1229c
Spy49_1230c	-	NE	1227797	1229242	481	-		COG1653G	ABC transporter substrate-binding protein
Spy49_1231c	-	NC	1229323	1230249	308	-	6984466	COG0395G	ABC transporter permease
Spy49_1233c	-	NE	1230259	1231209	316	-	6984467	COG4209G	sugar-binding transport protein
Spy49_1234	-	NE	1231405	1232100	231	+		COG1940KG	transcriptional regulator
Spy49_1235c	-	NE	1232893	1234335	480	-	6984469	COG2723G	beta-glucosidase
Spy49_1236c	hyl	NC	1234359	1236053	564	-	6984470	-	hyaluronidase transcription regulator
Spy49_1237c		NE NC	1236104	1237144	346 428	-		COG1609K	transcription regulator
Spy49_1238 Spy49_1239	-	NC NC	1237277 1238578	1238563 1241283	428 901	+		COG3538S COG0383G	hypothetical protein Spy49_1238 Alpha-mannosidase
Spy49_1240c	-	NE NE	1238578	1241283	901 451	+		COG2972T	histidine kinase
Spy49_1240c Spy49_1241c	_	NC	1241364	1242739	451	-		COG2265J	TrmA family RNA methyltransferase
Spy49_1242	recX	NE	1244875	1245651	258	+		COG2137R	recombination regulator RecX
Spy49_1243	-	NC	1245731	1246264	177	+	6984477	COG3557J	hypothetical protein Spy49_1243
Spy49_1244	-	NE	1246634	1246912	92	+	6984478	-	hypothetical protein Spy49_1244
Spy49_1245	-	С	1246927	1247034	35	+	6984479	-	hypothetical protein Spy49_1245
Spy49_1247c	-	NE	1254000	1254548	182	-		COG1544J	ribosomal subunit Interface protein
Spy49_1248c	comF	NE	1254628	1255293	221	-	6984491		late competence protein
Spy49_1249c	-	NE	1255265	1256590	441	-	6984492		late competence protein required for DNA uptake
Spy49_1250	-	NE	1256646	1257278	210 313	+	6984493		hypothetical protein Spy49_1250
Spy49_1251 Spy49_1252c	cysM -	NE C	1257406 1258365	1258347 1258742	313 125	+		COG0031E COG1098J	cysteine synthase A hypothetical protein Spy49_1252c
JP777_1232C			1230303	1230742	123	-		20020000	

Spy49_1253c	-	NE	1258742	1260142	466	-	6984496	COG0652O	Hydrolase, haloacid dehalogenase family/peptidyl-prolyl cis-trans isomerase, cyclophilin type
Spy49_1254c	-	E	1260179	1260820	213	-		COG2197TK	two-component response regulator
Spy49_1255c	-	NE	1260813	1261817	334	-		COG4585T	two-component sensor histidine kinase
Spy49_1256c	-	NE	1261814	1262506	230	-		COG4758S	hypothetical protein Spy49_1256c
Spy49_1257c Spy49_1259c	pppL	E E	1262629 1264524	1264527 1265264	632 246	-		COG2815S COG0631T	Serine/threonine protein kinase phosphoprotein phosphatase
Spy49_1260c	sunL	NE	1265302	1266624	440	-		COG0144J	RNA-binding Sun protein
Spy49_1261c	fmt	E	1266614	1267549	311	-		COG0223J	methionyl-tRNA formyltransferase
Spy49_1262c	priA	С	1267611	1269995	794	-		COG1198L	primosome assembly protein PriA
Spy49_1263c Spy49_1265c	- gmk	NC E	1270060 1270393	1270377 1271028	105 211	-		COG1758K COG0194F	DNA-directed RNA polymerase subunit omega guanylate kinase
Spy49_1266c	- gilik	NE	1271138	1272745	535	-		COG0194F COG1418R	hypothetical protein Spy49_1266c
Spy49_1267c	-	NE	1272875	1273771	298	-		COG0583K	transcriptional regulator
Spy49_1268	atoB	NC	1273972	1275159	395	+		COG0183I	acetyl-CoA acetyltransferase
Spy49_1269	atoD1	NE	1275183	1275833	216	+		COG1788I	acetyl-CoA:acetoacetyl-CoA transferase A subunit
Spy49_1270 Spy49_1271	atoA	NE NE	1275835 1276527	1276494 1277306	219 259	+		COG2057I COG1028IQR	acetyl-CoA:acetoacetyl-CoA transferase b subunit 3-hydroxybutyrate dehydrogenase
Spy49_1272		NE	1277377	1278708	443	+		COG2610GE	permease
Spy49_1273	luxS	NE	1278782	1279264	160	+	6984514	COG1854T	S-ribosylhomocysteinase
Spy49_1274c	-	NE	1279411	1280880	489	-	6984515	-	hypothetical protein Spy49_1274c
Spy49_1275c	-	NE	1280894 1282493	1282048 1282819	384 108	-		COG0116L	hypothetical protein Spy49_1275c
Spy49_1276c Spy49_1277c	-	NC NE	1282947	1283456	169			COG3599D COG4474S	hypothetical protein Spy49_1276c hypothetical protein Spy49_1277c
Spy49_1278	recU	NC	1283537	1284145	202	+		COG3331R	Holliday junction-specific endonuclease
Spy49_1279	pbp1A	E	1284132	1286297	721	+		COG0744M	multimodular transpeptidase-transglycosylase
Spy49_1280c	pepC	NE	1286764	1288101	445	-		COG3579E	aminopeptidase C
Spy49_1281c Spy49_1282c	nadE	E E	1288286 1289112	1289134 1290566	282 484			COG0171H COG1488H	NAD synthetase nicotinate phosphoribosyltransferase
Spy49_1283c	aapA	NE	1290737	1292116	459	-		COG1488H	amino acid permease
Spy49_1284c	nox2	NE	1292285	1293202	305	-		COG04920	thioredoxin reductase
Spy49_1285c	-	NC	1293266	1293490	74	-	6984592	-	hypothetical protein Spy49_1285c
Spy49_1286c Spy49_1287c	-	NE NE	1293594 1294337	1294337 1295140	247 267	-		COG1126E COG0765E	amino acid ABC transporter ATP-binding protein amino acid ABC transporter
Spy49_1287c Spy49_1289c	-	NE E	1294337	1295140	447	_		COG0765E COG0513LKJ	ATP-dependent RNA helicase
Spy49_1290c	mraY	E	1296836	1297846	336	-		COG0472M	phospho-N-acetylmuramoyl-pentapeptide-transferase
Spy49_1291c	ftsI	E	1297848	1300103	751	-		COG0768M	cell division protein Ftsl
Spy49_1292c	ftsL	NC	1300107	1300430	107	-		COG4839D	cell division protein FtsL
Spy49_1293c Spy49_1294c	mraW -	NE NE	1300435 1301736	1301385 1301942	316 68	-	6984599 6984600	COG0275M	S-adenosyl-methyltransferase MraW hypothetical protein Spy49 1294c
Spy49_1295c	proA	NE	1301730	1303167	416	-		COG0014E	gamma-glutamyl phosphate reductase
Spy49_1296c	proB	NE	1303160	1303981	273	-			gamma-glutamyl kinase
Spy49_1297c	-	NE	1304045	1305673	542	-	6984603	-	hypothetical protein Spy49_1297c
Spy49_1298c	-	NE	1305678 1306446	1306412	244	-		COG1131V	ABC transporter
Spy49_1299c Spy49_1300c	tkt	NE C	1306904	1306712 1308889	88 661	-	6984605 6984606	COG0021G	hypothetical protein Spy49_1299c transketolase
Spy49_1301c	tal	NE	1309107	1309751	214	-		COG0176G	translaldolase
Spy49_1303c	-	NE	1309877	1311376	499	-	6984608	-	transcriptional regulatory protein
Spy49_1304c	npx	NE	1311366	1312712	448	-		COG0446R	NADH peroxidase
Spy49_1305c Spy49_1306c	glpF1 glpO	NE NE	1312821 1313524	1313522 1315362	233 612	-		COG0580G COG0578C	glycerol uptake facilitator protein aerobic glycerol-3-phosphate dehydrogenase
Spy49_1307c	glpK	NE	1315378	1316904	508	-		COG0554C	glycerol kinase
Spy49_1308c	-	NE	1317264	1317656	130	-		COG3212S	hypothetical protein Spy49_1308c
Spy49_1309c	-	NE	1317784	1318041	85	-		COG4224S	hypothetical protein Spy49_1309c
Spy49_1310c Spy49_1311c	glyS glyQ	E E	1318195 1320606	1320234 1321523	679 305	-		COG0751J COG0752J	glycyl-tRNA synthetase subunit beta glycyl-tRNA synthetase subunit alpha
Spy49_1312c	giyQ -	NE	1321896	1322402	168	-		COG1755S	hypothetical protein Spy49_1312c
Spy49_1313c	-	NE	1322561	1323400	279	-		COG0656R	2,5-diketo-D-gluconic acid reductase
Spy49_1314c	nagA	NE	1323522	1324670	382	-		COG1820G	N-acetylglucosamine-6-phosphate deacetylase
Spy49_1316c	-	NE	1324787	1326418	543	-		COG1283P	Sodium-dependent phosphate transporter
Spy49_1318c Spy49_1319	-	NE NE	1327469 1328604	1328311 1329161	280 185	+		COG1307S COG1309K	hypothetical protein Spy49_1318c TetR family transcriptional regulator
Spy49_1320c	-	NE	1329198	1330022	274	-		COG0561R	hypothetical protein Spy49_1320c
Spy49_1321c	-	NE	1330024	1330641	205	-		COG2860S	hypothetical protein Spy49_1321c
Spy49_1322c	lacD1	NE	1330838	1331815	325	-		COG3684G	tagatose 1,6-diphosphate aldolase
Spy49_1323c Spy49_1324c	lacC1	NE NC	1331897 1331965	1332160 1332315	87 116			COG1105G COG1105G	Tagatose-6-phosphate kinase / 1- phosphofructokinase Tagatose-6-phosphate kinase / 1- phosphofructokinase
Spy49_1325c	lacB	NE	1332325	1332840	171	-		COG0698G	galactose-6-phosphate isomerase subunit LacB
Spy49_1326c	lacA	NE	1332855	1333280	141	-		COG0698G	galactose-6-phosphate isomerase subunit LacA
Spy49_1327c	-	NE	1333538	1334989	483	-		COG3775G	PTS system enzyme IIC component
Spy49_1328c Spy49_1329c	-	NE NE	1335015 1335313	1335320 1335786	101 157			COG3414G COG1762GT	PTS system IIB component PTS system enzyme IIA component
Spy49_1330	lacR1	NE	1336023	1336793	256	+		COG1349KG	lactose phosphotransferase system repressor
Spy49_1331c	copZ	NE	1336997	1337200	67	-	6984634	COG2608P	copper chaperone-copper transport operon
Spy49_1332c	copA	NE	1337214	1339445	743	-		COG2217P	copper-transporting ATPase
Spy49_1334c Spy49_1335	copY	NE NE	1339445 1340045	1339882 1341046	145 333	+		COG3682K COG0657I	Negative transcriptional regulator, CopY esterase
Spy49_1336c	rbfA	NC	1341098	1341448	116	-		COG0858J	ribosome-binding factor A
Spy49_1337c	infB	E	1341654	1344515	953	-	6984639	COG0532J	translation initiation factor IF-2
Spy49_1338c	-	NE	1344535	1344837	100	-		COG1358J	hypothetical protein Spy49_1338c
Spy49_1339c Spy49_1340c	- nusA	NC E	1344830 1345142	1345126 1346299	98 385	-		COG2740K COG0195K	Predicted nucleic-acid-binding protein transcription elongation factor NusA
Spy49_1340c Spy49_1341c	-	NE NE	1345142	1346299	385 178	-		COG0195K COG0779S	hypothetical protein Spy49_1341c
Spy49_1342c	trmB	NE	1347269	1347904	211	-	6984645	COG0220R	tRNA (guanine-N(7)-)-methyltransferase
Spy49_1343c	-	E	1347904	1348695	263	-		COG0510M	hypothetical protein Spy49_1343c
Spy49_1344c	-	NE	1348759	1349793	344	-		COG4473U	ABC transporter
Spy49_1345c Spy49_1346	hit	NE NE	1349796 1350593	1350521 1351012	241 139	+		COG1131V COG0537FGR	ABC transporter ATP-binding protein cell-cycle regulation histidine triad (HIT) protein
Spy49_1347	-	NE	1351009	1351365	118	+	6984650	-	hypothetical protein Spy49_1347
Spy49_1348c	-	NE	1351476	1352759	427	-		COG1316K	transcription regulator
Spy49_1349c	-	NE	1352768	1353292	174	-		COG0456R	histone acetyltransferase
Spy49_1350c Spy49_1351c	-	NC NE	1353267 1353882	1353728 1355342	153 486			COG0802R COG2252R	hypothetical protein Spy49_1350c hypothetical protein Spy49_1351c
Spy49_13510 Spy49_1352	-	NE	1355607	1356002	131	+		COG2252R COG0561R	hypothetical protein Spy49_1351c hypothetical protein Spy49_1352
Spy49_1353	-	NE	1356019	1356420	133	+	6984656	COG0561R	hypothetical protein Spy49_1353, partial
Spy49_1354	manL	NE	1356772	1357764	330	+		COG3444G	mannose-specific phosphotransferase system component IIAB
Spy49_1355	manM	NE	1357853	1358662	269	+		COG3715G	PTS system mannose-specific transporter subunit IIC
Spy49_1356 Spy49_1357	manN -	NE NE	1358679 1359704	1359590 1360063	303 119	+		COG3716G COG4687S	mannose-specific phosphotransferase system component IID hypothetical protein Spy49_1357
Spy49_1358	serS	E	1360454	1361731	425	+		COG40873	seryl-tRNA synthetase
Spy49_1359c	accA	NC	1361964	1362734	256	-	6984662	COG0825I	acetyl-CoA carboxylase subunit alpha
Spy49_1360c	accD	E	1362731	1363597	288	-		COG0777I	acetyl-CoA carboxylase subunit beta
Spy49_1361c Spy49_1362c	accC fabZ	E NC	1363606 1365002	1364970 1365424	454 140	-		COG0439I COG0764I	acetyl-CoA carboxylase biotin carboxylase subunit (3R)-hydroxymyristoyl-ACP dehydratase
Spy49_1363c	accB	NC	1365421	1365921	166	-		COG07641 COG0511I	acetyl-CoA carboxylase biotin carboxyl carrier protein subunit
Spy49_1364c	fabF	E	1365923	1367155	410	-	6984747	COG0304IQ	3-oxoacyl-ACP synthase II
Spy49_1365c	fabG	E	1367170	1367904	244	-	6984748	COG1028IQR	3-ketoacyl-ACP reductase
Spy49_1366c	fabD	E	1367894	1368832	312	-	6984749	COG0331I	Malonyl CoA-ACP transacylase

Spy49_1367c	fabK	E	1368857	1369828	323		6984750	COG2070R	Enoyl-ACP reductase (FMN)
Spy49_1368c	acpP	NC	1370029	1370253	74	-		COG0236IQ	acyl carrier protein
Spy49_1369c	fabH	E	1370314	1371288	324	-	6984752	COG0332I	3-oxoacyl-ACP synthase III
Spy49_1370c	-	NE	1371289	1371723	144	-		COG1846K	transcriptional regulator
Spy49_1371c	phaB	E	1371797	1372588	263	-		COG1024I	enoyl-CoA hydratase
Spy49_1372c Spy49_1373	dnaJ -	E NC	1372809 1374008	1373945 1374217	378 69	+	6984756	COG04840	molecular chaperone DnaJ hypothetical protein Spy49_1373
Spy49_1374c	dnaK	E	1374226	1376052	608	-		COG04430	molecular chaperone DnaK
Spy49_1375c	grpE	E	1376233	1376805	190	-	6984758	COG0576O	heat shock protein GrpE
Spy49_1376c	hrcA	NE	1376808	1377851	347	-		COG1420K	heat-inducible transcription repressor
Spy49_1377c	-	NE NE	1377978	1378547	189	-		COG1705NU	N-acetyl-muramidase
Spy49_1378c Spy49_1379c		NE	1378544 1379277	1379287 1379984	247 235			COG1876M COG0406G	D-alanyl-D-alanine carboxypeptidase phosphoglycerate mutase family
Spy49_1380c	-	NE	1380376	1380615	79	-		COG2261S	hypothetical protein Spy49_1380c
Spy49_1381c	-	NE	1380834	1381049	71	-	6984764	-	hypothetical protein Spy49_1381c
Spy49_1382c	gatB	E	1381046	1382485	479	-		COG0064J	aspartyl/glutamyl-tRNA amidotransferase subunit B
Spy49_1383c	gatA	E	1382485	1383951	488	-		COG0154J	aspartyl/glutamyl-tRNA amidotransferase subunit A
Spy49_1384c	gatC	NC NE	1383951 1384485	1384253 1384733	100 82			COG0721J COG0574G	aspartyl/glutamyl-tRNA amidotransferase subunit C
Spy49_1385c Spy49_1386c		NE	1385248	1385802	184			COG1335Q	pyruvate,phosphate dikinase Nicotinamidase
Spy49_1387c	codY	E	1385949	1386731	260	-		COG4465K	transcriptional repressor CodY
Spy49_1388c	-	NE	1386949	1388130	393	-	6984771	COG0436E	aminotransferase AlaT
Spy49_1389	-	NE	1388395	1388847	150	+		COG0589T	hypothetical protein Spy49_1389
Spy49_1390c	- D	NE	1388970	1390358	462	-		COG4696S	hypothetical protein Spy49_1390c
Spy49_1391 Spy49_1392c	asnB	NE NE	1390430 1391744	1391395 1392448	321 234	+	6984775	COG0252EJ	L-asparaginase hypothetical protein Spy49_1392c
Spy49_1393c		NE	1392461	1393363	300			COG1131V	ABC transporter
Spy49_1394c	recG	С	1393655	1395670	671	-		COG1200LK	ATP-dependent DNA helicase RecG
Spy49_1395c	-	NE	1396045	1397499	484	-		COG1122P	cobalt ABC transporter ATPase
Spy49_1396c	-	NE	1397436	1398116	226	-		COG0619P	cobalt ABC transporter permease
Spy49_1397c Spy49_1398c	-	NE NE	1398113	1398706 1400373	197 556	-	6984780	- COG1132V	ABC transporter permease
Spy49_1400c	cycC cycD	NE	1398703 1400366	1400373	587			COG4988CO	ABC transporter ABC transporter
Spy49_1401c	fhuC2	NE	1402126	1402962	278	-		COG1120PH	ferrichrome transport ATP-binding protein fhuC
Spy49_1402c	fhuB2	NE	1402959	1403981	340	-	6984784	COG0609P	ferrichrome ABC transporter permease
Spy49_1403c	fhuD2	NE	1403983	1405728	581	-		COG0614P	ferrichrome ABC transporter substrate-binding protein
Spy49_1405c	-	NE	1405925	1409752	1275	-		COG4886S COG3942R	Fe3+-siderophore transport protein
Spy49_1407c Spy49_1408c	isp2 alr	NE E	1410242 1411840	1411753 1412940	503 366			COG3942R COG0787M	Immunogenic secreted protein alanine racemase
Spy49_1409c	acpS	E	1412937	1413293	118	-		COG073711	4\'-phosphopantetheinyl transferase
Spy49_1410c	secA	E	1413409	1415928	839	-		COG0653U	preprotein translocase subunit SecA
Spy49_1412c	pmi	NE	1417389	1418342	317	-		COG1482G	mannose-6-phosphate isomerase
Spy49_1413c	scrK	NE	1418389	1419393	334	-		COG1940KG	Fructokinase
Spy49_1414c	endoS scrA	NE NE	1419562 1422324	1422093 1424207	843 627	-		COG3469G COG1263G	endo-beta-N-acetylglucosaminidase
Spy49_1415c Spy49_1416	scrB	NC	1424449	1425888	479	+		COG1621G	sucrose-specific PTS permease, enzyme II Sucrose-6-phosphate hydrolase
Spy49_1417	scrR	NE	1425893	1426858	321	+		COG1609K	sucrose operon repressor
Spy49_1418c	nusB	NE	1426999	1427451	150	-		COG0781K	transcription antitermination protein NusB
Spy49_1419c	-	NE	1427444	1427833	129	-		COG1302S	hypothetical protein Spy49_1419c
Spy49_1420c	efp comEB	NE NE	1427879 1428532	1428436 1428993	185 153	-		COG0231J COG2131F	elongation factor P
Spy49_1421c Spy49_1422c	pepP	NE	1429028	1430101	357			COG0006E	late competence protein required for DNA binding aminopeptidase YpdF
Spy49_1423c	uvrA	NE	1430216	1433074	952	-		COG0178L	excinuclease ABC subunit A
Spy49_1424	-	С	1433247	1434191	314	+		COG0598P	divalent cation transport protein, magnesium transporter CorA family
Spy49_1425		NE	1434323	1434979	218	+		COG4858S	hypothetical protein Spy49_1425
Spy49_1426c	rpsR ssb2	NC C	1435112 1435516	1435351 1436007	79 163	-		COG0238J COG0629L	30S ribosomal protein S18 single-stranded DNA-binding protein
Spy49_1427c Spy49_1428c	rpsF	NC	1436029	1436319	96			COG0360J	30S ribosomal protein S6
Spy49_1429c	-	NE	1436492	1436785	97	-	6984808	-	hypothetical protein Spy49_1429c
Spy49_1430	mutY	NE	1436953	1438107	384	+	6984809	COG1194L	A/G-specific adenine glycosylase
Spy49_1431	-	NE	1438284	1438871	195	+		COG1476K	Cro/CI family transcriptional regulator
					104	-		COG31180	
Spy49_1432c	trx2	NE	1438923	1439237					thioredoxin reductase
Spy49_1433c	-	NE	1439318	1439713	131	-	6984812 6984813	-	PAP2 family protein, partial
Spy49_1433c Spy49_1434c	trx2 - mutS2 -		1439318 1439822	1439713 1442161		-	6984813	COG1193L COG1286R	PAP2 family protein, partial DNA mismatch repair protein
Spy49_1433c	- mutS2	NE NE	1439318	1439713	131 779		6984813	- COG1193L	PAP2 family protein, partial
Spy49_1433c Spy49_1434c Spy49_1435c Spy49_1436c Spy49_1437	- mutS2 - -	NE NE NE NE	1439318 1439822 1442310 1442858 1443323	1439713 1442161 1442855 1443166 1444225	131 779 181 102 300	- - +	6984813 6984814 6984815 6984816	- COG1193L COG1286R - COG1039L	PAP2 family protein, partial DNA mismatch repair protein hypothetical protein Spy49_1435c hypothetical protein Spy49_1436c ribonuclesse Hill
Spy49_1433c Spy49_1434c Spy49_1435c Spy49_1436c Spy49_1437 Spy49_1438	- mutS2 - - - spi	NE NE NE NE E	1439318 1439822 1442310 1442858 1443323 1444236	1439713 1442161 1442855 1443166 1444225 1444829	131 779 181 102 300 197	- - +	6984813 6984814 6984815 6984816 6984817	- COG1193L COG1286R - COG1039L COG0681U	PAP2 family protein, partial DNA mismatch repair protein hypothetical protein Spy49_1435c hypothetical protein Spy49_1436c ribonuclease Hill signal peptidase I
Spy49_1433c Spy49_1434c Spy49_1435c Spy49_1436c Spy49_1437 Spy49_1438 Spy49_1439	- mutS2 - -	NE NE NE E E	1439318 1439822 1442310 1442858 1443323 1444236 1444887	1439713 1442161 1442855 1443166 1444225 1444829 1447340	131 779 181 102 300 197 817	- + +	6984813 6984814 6984815 6984816 6984817 6984818	- COG1193L COG1286R - COG1039L	PAP2 family protein, partial DNA mismatch repair protein hypothetical protein Spy49_1435c hypothetical protein Spy49_1436c ribonuclease Hill signal peptidase I Exodeoxyribonuclease V subunit alpha
Spy49_1433c Spy49_1434c Spy49_1435c Spy49_1436c Spy49_1437 Spy49_1438 Spy49_1439 Spy49_1440	mutS2 spi recD	NE NE NE E E NE NE	1439318 1439822 1442310 1442858 1443323 1444236 1444887 1447431	1439713 1442161 1442855 1443166 1444225 1444829 1447340 1447913	131 779 181 102 300 197 817 160	- - +	6984813 6984814 6984815 6984816 6984817 6984818 6984819	- COG1193L COG1286R - COG1039L COG0681U COG0507L	PAP2 family protein, partial DNA mismatch repair protein hypothetical protein Spy49_1435c hypothetical protein Spy49_1436c ribonuclease HIIII signal peptidase I Exodeoxyribonuclease V subunit alpha hypothetical protein Spy49_1440
Spy49_1433c Spy49_1434c Spy49_1435c Spy49_1436c Spy49_1437 Spy49_1438 Spy49_1439	- mutS2 - - - spi	NE NE NE E E	1439318 1439822 1442310 1442858 1443323 1444236 1444887	1439713 1442161 1442855 1443166 1444225 1444829 1447340	131 779 181 102 300 197 817	- + +	6984813 6984814 6984815 6984816 6984817 6984818 6984819 6984820	- COG1193L COG1286R - COG1039L COG0681U	PAP2 family protein, partial DNA mismatch repair protein hypothetical protein Spy49_1435c hypothetical protein Spy49_1436c ribonuclease Hill signal peptidase I Exodeoxyribonuclease V subunit alpha
Spy49_1433c Spy49_1435c Spy49_1436c Spy49_1436c Spy49_1437 Spy49_1438 Spy49_1439 Spy49_1440 Spy49_1441c Spy49_1441c Spy49_1442	mutS2 spi recD - dinP pfl	NE NE NE E NE NC NC NC	1439318 1439822 1442310 1442858 1443323 1444236 1444887 1447431 1448006 1449309 1451724	1439713 1442161 1442855 1443166 1444225 1444829 1447340 1447913 1449100 1451636 1452113	131 779 181 102 300 197 817 160 364 775 129	- + + +	6984813 6984814 6984815 6984816 6984817 6984818 6984819 6984820 6984821 6984822	- COG1193L COG1286R - COG1039L COG0681U COG0507L - COG0389L	PAP2 family protein, partial DNA mismatch repair protein hypothetical protein Spy49_1435c hypothetical protein Spy49_1436c ribonuclease HIII signal peptidase I Exodeoxyribonuclease V subunit alpha hypothetical protein Spy49_1440 DNA polymerase IV pyruvate formate-lyase esterase
Spy49_1433c Spy49_1434c Spy49_1436c Spy49_1436c Spy49_1437 Spy49_1438 Spy49_1449 Spy49_1441c Spy49_1441c Spy49_1441c Spy49_1442c Spy49_1444c	- mutS2 - - - spi recD - dinP	NE NE NE E E NE NE NC NC NC NE	1439318 1439822 1442310 1442858 1443323 1444236 1444887 1447431 1448006 1449309 1451724 1452098	1439713 1442161 1442855 1443166 1444225 14474829 1447740 1447913 1449100 1451636 1452113 1452850	131 779 181 102 300 197 817 160 364 775 129 250	- + + + - -	6984813 6984814 6984815 6984816 6984817 6984818 6984819 6984820 6984821 6984822 6984903	- COG1193L COG1286R - COG1039L COG0681U COG0507L - COG0389L COG1882C	PAP2 family protein, partial DNA mismatch repair protein hypothetical protein Spy49_1435c hypothetical protein Spy49_1436c ribonuclease Hill signal peptidase I Exodeoxyribonuclease V subunit alpha hypothetical protein Spy49_1440 DNA polymerase IV pyruvate formate-lyase esterase C3-degranding proteinase
Spy49_1433c Spy49_1434c Spy49_1435c Spy49_1435c Spy49_1437 Spy49_1437 Spy49_1439 Spy49_1440 Spy49_1441c Spy49_1442 Spy49_1442 Spy49_1444c Spy49_1444c Spy49_1444c	mutS2 spi recD - dinP pfl - cppA	NE NE NE E E NE NE NE NE NE NE NC NC NC NE NE	1439318 1439822 1442310 1442858 1443323 1444236 1444887 1447431 1448006 1449309 1451724 1452098 1453112	1439713 1442161 1442855 1443166 1444225 1447340 1447913 1449100 1451636 1452113 1452850 1454044	131 779 181 102 300 197 817 160 364 775 129 250 310	- + + +	6984813 6984814 6984815 6984816 6984817 6984819 6984819 6984820 6984821 6984822 6984903 6984904	COG1193L COG1286R - COG1039L COG0507L - COG0389L COG1882C COG1680V	PAP2 family protein, partial DNA mismatch repair protein hypothetical protein Spy49_1435c hypothetical protein Spy49_1436c ribonuclease Hill signal peptidase I Exodeoxyribonuclease V subunit alpha hypothetical protein Spy49_1440 DNA polymerase IV pryruvate formate-lyase esterase C3-degrading proteinase hypothetical protein Spy49_1445
Spy49_1433c Spy49_1434c Spy49_1435c Spy49_1436c Spy49_1438 Spy49_1438 Spy49_1439 Spy49_1441c Spy49_1441c Spy49_1442 Spy49_1445c Spy49_1445 Spy49_1445	mutS2 spi recD - dinP pfl	NE NE NE E E NE NE NC NC NC NE	1439318 1439822 1442310 1442858 1443323 1444236 1444887 1447431 1448006 1449309 1451724 1452098	1439713 1442161 1442855 1443166 1444225 14474829 1447740 1447913 1449100 1451636 1452113 1452850	131 779 181 102 300 197 817 160 364 775 129 250	- + + + + - - +	6984813 6984814 6984815 6984816 6984817 6984818 6984819 6984820 6984821 6984903 6984904 6984904	- COG1193L COG1286R - COG1039L COG0681U COG0507L - COG0389L COG1882C	PAP2 family protein, partial DNA mismatch repair protein hypothetical protein Spy49_1435c hypothetical protein Spy49_1436c ribonuclease Hill signal peptidase I Exodeoxyribonuclease V subunit alpha hypothetical protein Spy49_1440 DNA polymerase IV pyruvate formate-lyase esterase C3-degrading proteinase Hypothetical protein Spy49_1445 glycerol uptake facilitator protein
Spy49_1433c Spy49_1434c Spy49_1435c Spy49_1435c Spy49_1437 Spy49_1437 Spy49_1439 Spy49_1440 Spy49_1441c Spy49_1442 Spy49_1442 Spy49_1444c Spy49_1444c Spy49_1444c	- mutS2 Spi recD - dinP pfl - cppA - glpF2	NE NE NE E E NE NC NC NC NC NE NE NE NE NC	1439318 1439822 1442310 1442858 1443323 1444236 1444887 1447431 1448006 1449309 1451724 1452098 1453112 1454380	1439713 1442161 1442855 1443166 1444225 1444829 1447340 1447913 1449100 1451636 1452113 1452850 1454044 1455327	131 779 181 102 300 197 817 160 364 775 129 250 310 315	- + + + + - - +	6984813 6984814 6984815 6984816 6984817 6984819 6984820 6984821 6984822 6984903 6984903 6984904 6984905	COG1193L COG1286R - COG1039L COG0681U COG0507L - COG0389L COG188CV - COG1680V	PAP2 family protein, partial DNA mismatch repair protein hypothetical protein Spy49_1435c hypothetical protein Spy49_1436c ribonuclease Hill signal peptidase I Exodeoxyribonuclease V subunit alpha hypothetical protein Spy49_1440 DNA polymerase IV pryruvate formate-lyase esterase C3-degrading proteinase hypothetical protein Spy49_1445
Spy49_1433c Spy49_1435c Spy49_1435c Spy49_1436c Spy49_1437 Spy49_1438 Spy49_1440 Spy49_1441c Spy49_1441c Spy49_1441c Spy49_1441c Spy49_1442c Spy49_1445c Spy49_1445c Spy49_1445c Spy49_1450 Spy49_1450 Spy49_1450 Spy49_1450	- mutS2 Spi recD - dinP pfl - cppA - glpF2	NE NE NE E E NE NC NC NC NC NE NE NE NE NE NE NE NE NC NC NE NE NC	1439318 1439822 1442310 1442858 1443323 1444236 1447431 1447431 1447431 1445006 1445309 1451724 1452098 1453112 1454380 14557032 14577032 1457773	1439713 1442161 1442855 1443166 1444225 14478429 1447943 1447913 1449100 1451636 1452113 1452850 1454044 1455327 1456926 1457751 1460055	131 779 181 102 300 197 817 160 364 775 129 250 310 315 398 239 760	+ + + - + +	6984813 6984814 6984816 6984816 6984817 6984818 6984819 6984821 6984821 6984903 6984904 6984905 6984905 6984908	COG1193L COG1286R - COG1039L COG0581U COG0507L - COG0389L COG1882C COG1680V - - COG0580G COG2814G	PAP2 family protein, partial DNA mismatch repair protein hypothetical protein Spy49_1435c hypothetical protein Spy49_1436c ribonuclease Hill signal peptidase I Exodeoxyribonuclease V subunit alpha hypothetical protein Spy49_1440 DNA polymerase IV pyruvate formate-lyase esterase C3-degrading proteinase hypothetical protein Spy49_1445 glycerol uptake facilitator protein antibiotic resistance protein NorA Crp/Fnr family transcriptional regulator x-prolyt-ilepetidy aminopeptidase
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Spy49_1482c Spy49_1483c									
	-	NE	1482055	1482321	88 104	-	6984937 6984938	-	putative phage associated protein
	-	NE	1482324	1482638		-	6984939	-	hypothetical protein Spy49_1483c hypothetical protein Spy49_1484c
Spy49_1484c Spy49_1485c	-	NE NE	1482708 1482897	1482893 1484459	61 520	-	6984940	COG5585T	hypothetical protein Spy49_1484c
Spy49_1486c		NE	1484440	1485942	500	_	6984941	-	hypothetical protein Spy49_1486c
Spy49_1487c	-	NE	1485954	1487243	429	_	6984942	COG1783R	Large terminase
Spy49_1488c		NE	1487221	1487703	160	-	6984943	COG3728L	Small terminase
Spy49 1489c		NE	1488535	1488975	146	-	6984944	-	hypothetical protein Spy49_1489c
Spy49_1491c	-	NE	1489415	1489936	173	-	6984945	-	phage protein
Spy49_1492c	-	NE	1489933	1490226	97	-	6984946	-	hypothetical protein Spy49_1492c
Spy49_1493c	-	NE	1490223	1490408	61	-	6984947	-	putative phage associated protein
Spy49_1494c	-	NC	1490506	1490991	161	-	6984948	COG2226H	DNA N-4 cytosine methyltransferase M.NgoMXV
Spy49_1496c	-	NE	1491276	1491680	134	-	6984949	-	phage protein
Spy49_1497c	-	NC	1491664	1491954	96	-	6984950	-	hypothetical protein Spy49_1497c
Spy49_1498c	-	NE	1492193	1492549	118	-	6984951	-	putative phage associated protein
Spy49_1499c	-	NE	1492625	1492987	120	-	6984952	COG4570L	hypothetical protein Spy49_1499c
Spy49_1500c	-	NC	1493196	1493621	141	-	6984953	COG0629L	Single-strand binding protein 3
Spy49_1501c	-	NE	1493614	1494288	224	-	6984954	-	Recombination protein
Spy49_1502c	-	NC	1494289	1494435	48	-	6984955	-	hypothetical protein Spy49_1502c
Spy49_1504c	-	NE	1494793	1495047	84	-	6984956	-	hypothetical protein Spy49_1504c
Spy49_1505c	-	NC	1495034	1495381	115	-	6984957	·	hypothetical protein Spy49_1505c
Spy49_1506c	-	NE	1495522	1497093	523	-	6984958	COG1484L	DNA replication protein DnaC
Spy49_1507c	-	NE	1497209	1497652	147	-	6984959	-	hypothetical protein Spy49_1507c
Spy49_1509c	-	NE	1498078	1498350	90 59	-	6984960 6984961	-	hypothetical protein Spy49_1509c
Spy49_1510c Spy49_1511c	-	NC NC	1498523 1498833	1498702 1498967	44	-	6984962	-	hypothetical protein Spy49_1510c putative phage associated protein
Spy49_1511c	•	NE	1499249	1499608	119		6984963	•	hypothetical protein Spy49_1512c
Spy49_1513c		NE	1499682	1499939	85		6984964		hypothetical protein Spy49_1513c
Spy49_1514c		NE	1500142	1500483	113	-	6984965		hypothetical protein Spy49_1513c
Spy49_1516c		NC	1500755	1500904	49		6984966	-	putative phage associated protein
Spy49_1517c	-	NE	1500735	1501664	242		6984967	COG3645S	P1-type antirepressor-phage associated
Spy49 1518c		NE	1501697	1501885	62	-	6984968	-	cro protein
Spy49_1520c	-	NC	1502073	1502255	60	-	6984969	-	hypothetical protein Spy49_1520c
Spy49_1521c	-	NE	1502532	1503293	253	-	6984970	COG3617K	Antirepressor
Spy49_1522	-	С	1503460	1503732	90	+	6984971	-	hypothetical protein Spy49_1522
Spy49_1525	-	NE	1504006	1504473	155	+	6984972	-	hypothetical protein Spy49_1525
Spy49_1526	-	NE	1504589	1505368	259	+	6984973	-	hypothetical protein Spy49_1526
Spy49_1528c	-	NC	1505502	1505660	52	-	6984974	-	hypothetical protein Spy49_1528c
Spy49_1529	-	NC	1506024	1506782	252	+	6984975	COG2932K	Repressor protein
Spy49_1530	-	NE	1506855	1507277	140	+	6984976	-	Lj965 prophage superinfection immunity protein
Spy49_1531	-	NE	1507398	1508534	378	+	6984977	COG4974L	Prophage NZ131.3 integrase
Spy49_1532	-	NE	1508573	1508893	106	+	6984978	COG0718S	hypothetical protein Spy49_1532
Spy49_1533c		NE	1508950	1509687	245	-	6984979	COG0789K	MerR family transcriptional regulator
Spy49_1534c	dnaQ	NC	1509840	1510427	195	-	6984980	COG0847L	DNA polymerase III subunit epsilon
Spy49_1535c	-	NC	1510476	1511057	193	-	6984981	-	hypothetical protein Spy49_1535c
Spy49_1536c	-	NE	1511183	1511698	171	-	6984982	-	transposase-IS1548
Spy49_1537c	-	NE	1511601	1512305	234	-	6985063	COG5433L	transposase-IS1548
Spy49_1538	-	NE	1512526	1513695	389	+	6985064	COG2081R	hypothetical protein Spy49_1538
Spy49_1540c Spy49_1541c	deoC nupC	NE NE	1513790 1514491	1514461 1515693	223 400	-	6985065 6985066	COG0274F COG1972F	deoxyribose-phosphate aldolase nucleoside permease nupC
Spy49_1542c	udp	NE	1515714	1516493	259		6985067	COG2820F	Uridine phosphorylase
Spy49_1543	- -	NE	1516733	1517491	252	+	6985068	COG2188K	GntR family transcriptional regulator
Spy49_1544	rpsN	NE	1517700	1517969	89	+	6985069	COG0199J	30S ribosomal protein S14
Spy49_1545c	gcp	NC	1518141	1519169	342	-		COG05330	DNA-binding/iron metalloprotein/AP endonuclease
Spy49_1546c	-	NE	1519159	1519614	151	-	6985071	COG0456R	ribosomal-protein-S18p-alanine acetyltransferase
Spy49_1547c	-	E	1519586	1520284	232	-	6985072	COG12140	molecular chaperone
Spy49_1548	-	NC	1520568	1520798	76	+	6985073	COG5503S	hypothetical protein Spy49_1548
Spy49_1549	-	E	1520800	1522482	560	+		COG0595R	hypothetical protein Spy49_1549
Spy49_1550c	glnA	NE	1522710	1524056	448	-	6985075	COG0174E	glutamine synthetase
Spy49_1551c	glnR	NE	1524094	1524465	123	-	<u>6985076</u>	COG0789K	transcriptional regulator
Spy49_1552c	-	NE	1524532	1525083	183	-	6985077	COG4129S	hypothetical protein Spy49_1552c
Spy49_1553c	pgk	NC	1525345	1526541	398	-	<u>6985078</u>	COG0126G	phosphoglycerate kinase
	1		1526726						
Spy49_1554c	IppC	NE		1527580	284	-	6985079	COG2503R	acid phosphatase
Spy49_1555c	IppC -	NE NE	1527820	1527580 1528701	293	-	<u>6985080</u>	COG03300	hypersensitive- induced response protein-like protein
Spy49_1555c Spy49_1556c	-	NE NE E	1527820 1528938	1527580 1528701 1530602	293 554		6985080 6985081	COG03300 COG1461R	hypersensitive- induced response protein-like protein DAK2 domain-containing protein
Spy49_1555c Spy49_1556c Spy49_1557c	- asp	NE NE E NC	1527820 1528938 1530602	1527580 1528701 1530602 1530967	293 554 121		6985080 6985081 6985082	COG03300 COG1461R COG1302S	hypersensitive- induced response protein-like protein DAK2 domain-containing protein alkaline-shock protein
Spy49_1555c Spy49_1556c Spy49_1557c Spy49_1558c	- - asp rpmB	NE NE E NC NE	1527820 1528938 1530602 1531119	1527580 1528701 1530602 1530967 1531307	293 554 121 62	-	6985080 6985081 6985082 6985083	COG03300 COG1461R COG1302S COG0227J	hypersensitive- induced response protein-like protein DAK2 domain-containing protein alkaline-shock protein 50S ribosomal protein L28
Spy49_1555c Spy49_1556c Spy49_1557c Spy49_1558c Spy49_1559c	- asp	NE NE E NC NE E	1527820 1528938 1530602 1531119 1531689	1527580 1528701 1530602 1530967 1531307 1532570	293 554 121	-	6985080 6985081 6985082 6985083 6985084	COG03300 COG1461R COG1302S COG0227J COG0191G	hypersensitive- induced response protein-like protein DAK2 domain-containing protein alkaline-shock protein 505 ribosomal protein L28 fructose-bisphosphate aldolase
Spy49_1555c Spy49_1556c Spy49_1557c Spy49_1558c	- - asp rpmB	NE NE E NC NE	1527820 1528938 1530602 1531119	1527580 1528701 1530602 1530967 1531307	293 554 121 62 293		6985080 6985081 6985082 6985083	COG03300 COG1461R COG1302S COG0227J	hypersensitive- induced response protein-like protein DAK2 domain-containing protein alkaline-shock protein 50S ribosomal protein L28
Spy49_1555c Spy49_1556c Spy49_1557c Spy49_1558c Spy49_1559c Spy49_1560c	- - asp rpmB fba -	NE NE E NC NE E	1527820 1528938 1530602 1531119 1531689 1532916	1527580 1528701 1530602 1530967 1531307 1532570 1533842	293 554 121 62 293 308	-	6985080 6985081 6985082 6985083 6985084 6985086	COG03300 COG1461R COG1302S COG0227J COG0191G COG1073R	hypersensitive induced response protein-like protein DAK2 domain-containing protein alkaline-shock protein 50S ribosomal protein L28 fructose-bisphosphate aldolase hypothetical protein Spy49_1560c
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Spy49_1601c	-	NE	1577419	1578165	248	-		COG0566J	23S rRNA methyltransferase
Spy49_1602c	-	NE	1578212	1579009	265	-	6985132	-	hypothetical protein Spy49_1602c
Spy49_1603c	-	NE	1579205	1579618	137	-		COG1939S	hypothetical protein Spy49_1603c
Spy49_1604c	cysS	E	1579611	1580954	447	-	6985135	COG0215J	cysteinyl-tRNA synthetase
Spy49_1605c		NE	1580982	1581212	76	-			hypothetical protein Spy49_1605c
Spy49_1606c	cysE	NC	1581691 1582281	1582272 1583033	193 250	-	6985137	COG1045E	Serine acetyltransferase cysE
Spy49_1607c Spy49_1608c	pnp	NE NE	1583026	1585158	710	-		COG1185J	hypothetical protein Spy49_1607c polynucleotide phosphorylase/polyadenylase
Spy49_1609c	bub	NE	1585438	1586166	242	-		COG0176G	translaldolase
Spy49_1610c	ulaA	NE	1586179	1587558	459	•		COG3037S	PTS system ascorbate-specific transporter subunit IIC
Spy49_1611c	-	NE	1587585	1587869	94			COG3414G	PTS system IIB component
Spy49_1612c		NE	1587862	1589922	686			COG3711K	transcriptional regulator
Spy49_1613c	rpsO	NE	1590275	1590544	89			COG0184J	30S ribosomal protein S15
Spy49_1614c	-	NE	1590720	1590920	66		6985224	-	hypothetical protein Spy49_1614c
Spy49_1615	def	c	1591319	1591933	204	+		COG0242J	peptide deformylase
Spy49_1616c	-	NE	1591967	1592509	180	-		COG0431R	hypothetical protein Spy49_1616c
Spy49_1617c		NE	1592640	1593068	142			COG1846K	MarR family transcriptional regulator
Spy49_1618c	polC	E	1593178	1597575	1465			COG2176L	DNA polymerase III PolC
Spy49_1619c	proS	E	1597830	1599686	618	-		COG0442J	prolyl-tRNA synthetase
Spy49_1620c	eep	NE	1599884	1601143	419	-		COG0750M	hypothetical protein Spy49_1620c
Spy49_1621c	cdsA	E	1601216	1602010	264	-		COG0575I	phosphatidate cytidylyltransferase
Spy49_1622c	uppS	E	1602023	1602772	249	-	6985232	COG0020I	undecaprenyl pyrophosphate synthase
Spy49_1624c	yajC	NE	1602991	1603356	121	-	6985233	COG1862U	preprotein translocase subunit YajC
Spy49_1625c	-	NE	1603472	1603819	115	-	6985234	COG0526OC	bacterocin transport accessory protein, Bta
Spy49_1626c	pulA	NE	1603961	1607365	1134	-	6985235	COG1523G	pullulanase
Spy49_1627c	dexB	NE	1607656	1609269	537	-		COG0366G	glucan 1,6-alpha-glucosidase
Spy49_1628c	msmK	NE	1609398	1610531	377	-		COG3839G	sugar ABC transporter ATP-binding protein
Spy49_1629c	Irp	NE	1610829	1611722	297	-		COG2508TQ	hypothetical protein Spy49_1629c
Spy49_1630	ska	NE	1612017	1613339	440	+	6985239		streptokinase
Spy49_1631c	dtd	NE	1613437	1613880	147	-		COG1490J	D-tyrosyl-tRNA(Tyr) deacylase
Spy49_1632c	relA	С	1613895	1616114	739	-		COG0317TK	GTP pyrophosphokinase / Guanosine- 3,5-bis(Diphosphate) 3-pyrophosphohydrolase
Spy49_1633c	scIA	NE	1616358	1617626	422	-	6985242	-	Collagen-like surface protein
Spy49_1634	nrdI2	NE	1618008	1618490	160	+		COG1780F	flavoprotein Nrdl
Spy49_1635c	-	NE	1618883	1619701	272	-		COG3568R	hypothetical protein Spy49_1635c
Spy49_1636c	-	NE	1619784	1621970	728	-		COG1263G	PTS system glucose-specific IIBC component
Spy49_1637c	- nrmA	NE	1622326	1623075 1624028	249	-		COG1385S	16S ribosomal RNA methyltransferase RsmE
Spy49_1638c	prmA nudC	NE NE	1623075		317			COG2264J	ribosomal protein L11 methyltransferase
Spy49_1639c Spy49_1640c	nudC nudB	NE NE	1624045 1625304	1625127 1625660	360 118		6985248 6985249	- COG1051F	hypothetical protein Spy49_1639c MutT/nudix family protein
Spy49_1641c	nudA	NE	1625688	1626005	105	•		COG4043S	hypothetical protein Spy49_1641c
Spy49_1642c	HuuA	NE	1626019	1626489	156	•	6985251	COG40433	hypothetical protein Spy49_1642c
Spy49_1643c		NC	1626554	1626673	39		6985252		hypothetical protein Spy49_1643c
Spy49_1644c		NE	1626954	1627532	192	-		COG2801L	transposase
Spy49_1646c		NE	1627693	1627983	96		6985254	-	transposase
Spy49_1647c		NE	1628038	1628844	268			COG2801L	transposase, IS861
Spy49_1649c		NE	1629499	1629813	104	-	6985256	-	hypothetical protein Spy49 1649c
Spy49 1651	-	NE	1630202	1630438	78	+	6985257	-	hypothetical protein Spy49_1651
Spy49_1652	-	NC	1630510	1630704	64	+	6985258	-	hypothetical protein Spy49_1652
Spy49_1653	papB	NE	1630830	1632587	585	+	6985259	COG0147EH	Para-aminobenzoate synthase, aminase component / aminodeoxychorismate lyase
Spy49_1654	trpG	NE	1632620	1633186	188	+	6985260	COG0512EH	anthranilate synthase component II
Spy49_1655	-	NE	1633219	1634487	422	+	6985261	COG2256L	recombination factor protein RarA
Spy49_1656	pai1	NE	1634985	1635425	146	+	6985263	COG3153R	Pai1 protein
Spy49_1657	-	NE	1635460	1635966	168	+	6985264	COG0563F	topology modulation protein
Spy49_1658c	-	NE	1636090	1636425	111	-	6985265	-	hypothetical protein Spy49_1658c
Spy49_1659c	-	NE	1636435	1637079	214	-	6985266		hypothetical protein Spy49_1659c
Spy49_1660	dppA	NE	1638159	1639649	496	+		COG0747E	peptide ABC transporter substrate-binding protein
Spy49_1661	dppB	NE	1639762	1640739	325	+		COG0601EP	peptide ABC transporter permease
Spy49_1662	dppC	NE	1640736	1641557	273	+		COG1173EP	peptide ABC transporter permease
Spy49_1663	dppD	NE	1641569	1642372	267	+		COG0444EP	peptide ABC transporter ATP-binding protein
Spy49_1664	dppF	NE	1642356	1642982	208	+		COG1124EP	peptide ABC transporter ATP-binding protein dppF
Spy49_1665c	-	NE	1643064	1643264	66	-	6985272	-	hypothetical protein Spy49_1665c
Spy49_1666c	-	NE	1643433	1645904	823	-	6985273		hypothetical protein Spy49_1666c
Spy49_1667c	lmb	NE	1645917	1646837	306	-		COG0803P	laminin-binding surface protein
Spy49_1668c	-	NE	1647073	1648410	445	-	6985275	-	cell surface/fibronectin-binding protein
Spy49_1669c	scpA	NE	1648661	1652050	1129	-		COG14040	C5a peptidase
Spy49_1670c Spy49_1671c	ennX emm49	NE NE	1652385 1653701	1653491 1654858	368 385	-	6985278	COG1196D	EnnX protein Antiphagocytic M protein
Spy49_1672c	emmas	NE	1655083	1656330	415	•		COG1196D	Fc-gamma receptor
Spy49_1673c	mga	NE	1656520	1658121	533	-	6985280		M protein trans-acting positive regulator (Mga)
Spy49_1674c	-	NE	1658797	1659048	83		6985281		hypothetical protein Spy49_1674c
Spy49_1675c	isp1	NE	1659126	1660754	542	-		COG3942R	Immunogenic secreted protein
Spy49_1676c	-	NE	1660856	1662244	462	-		COG0642T	two-component system histidine kinase
Spy49_1677c	-	NE	1662241	1662894	217	-		COG0745TK	two-component system response regulator
Spy49_1678c	-	NE	1662988	1664205	405	-	6985285	COG0577V	ABC transporter
Spy49_1679c	-	NE	1664218	1664892	224	-		COG1136V	ABC transporter ATP-binding protein
Spy49_1680c	-	NE	1664879	1666147	422	-		COG0845M	ATP-binding cassette transporter protein
Spy49_1681c	-	NE	1666571	1666975	134	-	6985288	-	hypothetical protein Spy49_1681c
Spy49_1682c	-	NE	1667002	1667298	98	-	6985289	-	hypothetical protein Spy49_1682c
Spy49_1683c	sfbX49	NE	1667440	1669395	651	-	6985290	-	fibronectin-binding protein
Spy49_1684c	sof	NE	1669575	1672655	1026	-	6985291	-	Serum opacity factor
Spy49_1686	- ronA	NE	1673078	1673314	78 216	+	6985292 6985293	-	hypothetical protein Spy49_1686 foldase PrsA
Spy49_1687c Spy49_1688c	ropA	NE NE	1673590 1674572	1674540 1674889	316 105		6985293	_	hypothetical protein Spy49_1688c
Spy49_1688c Spy49_1689c	_	C	1674997	1675302	105	_	6985295	_	nypotnetical protein Spy49_1688c Spi SpeB protease inhibitor
Spy49_1690c	speB	NE	1675304	1676500	398		6985296	-	strepotococcal cysteine protease (streptopain) / streptococcal pyrogenic exotoxin B (SpeB)
Spy49_1691	ropB	NE	1677441	1678283	280	+	6985297	-	RooB
Spy49_1692c	mf1	NE	1678512	1679342	276	-	6985298	-	streptodornase B / Mitogenic factor 1
Spy49_1693	-	NC	1679426	1679554	42	+	6985299	-	hypothetical protein Spy49_1693
Spy49_1694	-	NE	1679707	1680216	169	+		COG1267I	low temperature requirement C protein
Spy49_1695c	gldA	NE	1680285	1681373	362	-		COG0371C	glycerol dehydrogenase
Spy49_1696c	mipB	NE	1681430	1682098	222	-		COG0176G	fructose-6-phosphate aldolase
Spy49_1697c	pfID	NE	1682111	1684528	805	-	6985383	COG1882C	pyruvate formate lyase 3
Spy49_1698c	-	NE	1684739	1686043	434	-	6985384	COG1455G	PTS system cellobiose-specific IIC component
Spy49_1699c	-	NE	1686053	1686361	102	-		COG1440G	PTS system cellobiose-specific IIB component
Spy49_1700c	-	NE	1686389	1686709	106	-		COG1447G	PTS system enzyme III
Spy49_1701c	-	NE	1686996	1687976	326	-		COG2390K	transcriptional regulator
Spy49_1702c	-	NE	1687992	1688741	249	-		COG1349KG	DeoR family transcriptional regulator
Spy49_1703	-	NE	1688864	1689637	257	+		COG11800	pyruvate formate-lyase activating enzyme
Spy49_1704c	secE	NC	1689873	1690049	58	-		COG0690U	preprotein translocase subunit SecE
Spy49_1705c	rpmG	NC	1690063	1690215	50	-		COG0267J	50S ribosomal protein L33
Spy49_1706c	pbp2A	NC	1690264	1692600	778	-		COG0744M	multimodular transpeptidase-transglycosylase
Spy49_1707c	-	NE	1692639	1693019	126	-		COG0251J	translation initiation inhibitor
Spy49_1708	-	NE	1693510	1693701	63	+	6985394	-	hypothetical protein Spy49_1708
Spy49_1709	-	NE	1693595	1694596	333	+		COG0564J	ribosomal large subunit pseudouridine synthase
Spy49_1710c Spy49_1713	-	NE NE	1694685	1696409 1698071	574 499	+		COG4640S COG4690E	hypothetical protein Spy49_1710c
Spy49_1713 Spy49_1714c	-	NE NE	1696572 1698783	16980/1	499 115	-		COG4690E COG1395K	dipeptidase transcriptional regulator
3p1-3_1/14C		.42	1030/03	1055130				-501555K	

Speek 1,777										
Symph 1715 Cold 1915							-			
Symphy 1795							-			
Symph 1792 19							-			
Sympt 1772 wide wide 1765							-			
Symph 1772 May 1797 M		csp					-			,
Sympt 1722 ms ms 1791-96 1791-97 ms ms ms ms ms ms ms m		-					-			
Syet 1725 which with 179222 71925 which with 179222 register 17922 which with which							+			
Symple 1772							+			
Sprekg 1772							-			
Symple 175		hutU					+			
Symph 1752 m	Spy49_1725	-	NE	1712907	1713806	299	+	6985410	COG3643E	glutamate formiminotransferase
Symph 1792	Spy49_1726	-	NE	1713817	1714443	208	+	6985411	COG3404E	formiminotetrahydrofolate cyclodeaminase
Symple 1792	Spy49_1727	fhs2	NE	1714461	1716134	557	+	6985412	COG2759F	formatetetrahydrofolate ligase
Symph 1741	Spy49_1728	-	NE	1716155	1716751	198	+	6985413	COG3758S	hypothetical protein Spy49_1728
Symple 17-32 Mode	Spy49_1729		NE	1716971	1718314	447	+	6985414	COG0531E	cationic amino acid transporter protein
Symple 1782	Spy49_1730	hutH	NE	1718326	1719867	513	+	6985415	COG2986E	histidine ammonia-lyase
Symple 1774	Spy49 1731	hutG	NE	1720054	1721040	328	+	6985416	COG0010E	formimidoylglutamase
Symbol 1744	Spy49 1732c	-	NE	1721071	1724145	1024	-	6985417	COG3899R	regulatory protein
Spyte 1756 Per Pe		rpsB					+			
Symbol 1756 etc.							+			
Symbol 17956							-			
Spying 1775		dexS		1728659			-	6985421	COG0366G	trehalose-6-phosphate hydrolase
Spying 1798 No. No. 179389 179380 237 w 6005522 CO02328 Controlled protein prote		-			1732378		-			PTS system enzyme II
Sympl_1796 No. 173586 753580		-					+			trehalose operon transcriptional repressor
Symple 1746										
Symbol 1742							+			
Symbol 1745 mol										
Symbol 1746c Fig. 1740c Fig.		nrdG					-			
Symbol 1765 No. 1782005 178181 48 5805520 Control 1782005 178181 48 5805520 Control 1782005										
Symbol 1746 No. 178805 178815 48 6885530 178815		-					-			
Symbol 1746							-		-	
Spy89_1748c No. 1746605 1746505 174505 101		nrdD					-		COG1328F	
Spy#9 17762 No. 1742697 174281 1742919 174291 174291 174291 174291 174291 174291 17429							_			
Sympsol 17302 No. 174917 174333 17490 Septembroom Septembroom Symptops							_		COG3906S	
Spy8g 17352 cpc										
Spy89_1752c Spx89_1756c Col. 1746455 1746592 1757592 186 Spx99_1756c Col. 1746455 1746592 1757592 186 Spx99_1756c Col. 1746455 1757592 186 Spx99_1756c Col. 1746592 1757593 Col. 174659										
Spy#9_1756		snyΔ								
Spy#9 1755 In										
Spy#9_1756 Image: Common										
Symple 1756										
Syy49 1758; mtd										
Symple 1798 muts									-	
Symple 1795 Page									COG03231	
Spy49_1765										
Symple 1762 arg c		-								
Sympo		aroS								
Sympo		-							-	
SyM9_1756 NE									COG1284S	
Syy49_1767c Syy49_1767c Syy49_1767c Syy49_1767c Syy49_1767c Syy49_1767c Syy49_1767c Syy49_1777c										
Symple 1768c Symple 1769c Symple 1779c Symple Symple Symple Symple Symple Symple Symple Symple										
Fig. Fig. Bis Fig. Tis T		asnS								
Spy49, 1770 rpm6 NE 1763546 1763728 60 4 98285432 (GOG0333) 505 ribosomal protein 132 Spy49, 1771 rpm6 NC 176344 1763893 1764157 74 4 69285453 (GOG0333) 505 ribosomal protein 133 Spy49, 1773 cadb NE 176186 1764800 20 4 69285455 (GOG0334) COG0334 (GOG040) Spy49, 1773 cadb NE 176181 1765150 112 cadb Forest (GOG040) Coddition of the 175 cadd of the 176481 cadd o										
Syy49 1771							+			
Syy49 1773										
Syy49 1773 CadD NE 1764186 1764800 204										
Syy49 1778 CadX NE 1764812 1765150 112		cadD					+		COG4300P	
Syy49 1775 NE 1765194 1766117 307										
Spy49 1777 Ne		-					+		-	
Syy49 1778 NE		-	NE	1766183	1766935	250	+	6985458	COG1674D	
Spy49 1779 Ne		-	NE	1766932	1767534	200	+	6985459	-	
Spy49 1780 Ne	Spy49_1779	-	NE	1768745	1769587	280	+	6985460	COG2035S	
Spy49_1781 -	Spy49_1780c	-	NE	1769591	1770274	227	-	6985461	COG1051F	
Spy49_1782 -	Spy49_1781		NE	1770481	1770807	108	+	6985462	COG1695K	hypothetical protein Spy49_1781
Spy49_1788 -	Spy49_1782		NE	1770794	1771381	195	+	6986105	COG4709S	hypothetical protein Spy49_1782
Spy49 1784c NC 1772567 1774861 764 - 6986107 Colf-15115 phage infection protein Spy49 1786 Fsp49 1786 Fsp49 1786 Fsp49 1786 Fsp49 1786 Fsp49 1787 NE 1777501 178 Ssp49 1786 Fsp49 1787 NE 1777501 1777273 90 - 6986109 Cold-4666 hypothetical protein Spy49 1787 Fsp49 1788 Grad	Spy49_1783	-	NE	1771378	1772451	357	+	6986106	COG0572F	
Spy49_1787c	Spy49_1784c	-	NC	1772567	1774861	764	-	6986107	COG1511S	
Spy49_1786c		-					+			
Spy49_1787c NE 1777001 1777273 90 - 6986110 CoG4466S hypothetical protein Spy49_1787c Spy49_1788c dnaC E 1777290 1778657 455 6986112 CoG0359 505 ribosomal protein L9	Spy49_1786c	rpsD	E	1775661	1776272	203	-	6986109	COG0522J	30S ribosomal protein S4
Spy49_1788c		-		1777001			-	6986110	COG4466S	
Spy49_1790c Fig. NC 178687 179139 150 - 6986112 CoG03591 Co		dnaC					-	6986111	COG0305L	
Spy49_1791c gldA							-			
Spy49_1792c		-		1779136			-	6986113	COG3887T	DHH family protein
Spy49_1793c	Spy49_1791c	gidA	E	1781202	1783100	632	-	6986114	COG0445D	tRNA uridine 5-carboxymethylaminomethyl modification protein GidA
Spy49_1796	Spy49_1792c	-	NE	1783224	1783541	105	-	6986115	COG1051F	hypothetical protein Spy49_1792c
Spy49_1796							-			
Spy49_1796c Ne										
Spy49_1798c Chi		sdhA					+		COG1760E	
Spy49_1800		-					-		-	
Spy49_1800c PigsA Fe 17910d 1791191 296 - 6986122 Colos1122P Cobalt transporter ATP-binding protein		-								
Spy49_1800c PSA										
Spy49_1801c -										
Spy49_1802c - NE		pgsA								
Spy49_1803c NE 1794064 1795308 414 - 6986126 COG0612R hypothetical protein Spy49_1803c Spy49_1806 has8 NE 1797043 1798251 402 + 5986128 COG10218M UDP-glucose de-dehydrogenase Spy49_1808 hasC NE 1799633 1799347 304 + 6986122 COG1210M UDP-glucose de-dehydrogenase Spy49_1809 - NE 1799655 1800068 137 6986132 COG1210M UDP-glucose pyrophosphorylase Spy49_1810 recF NE 1800070 1801176 368 + 5986131 COG1191 UPP-glucose pyrophosphorylase Spy49_1810 recF NE 1800070 1801176 368 + 5986131 COG1180 recombination protein Spy49_1809 Spy49_1811 - NE 1802298 1803779 439 - 5986132 COG4975G hypothetical protein Spy49_1811c Spy49_1814 - NE 1802298 180379 430 - 6986134 COG01801 tryptophanyl-tRNA synthetase II		-								
Spy49_1806 hasA NE 1795670 1797007 445 + 6986122 CoG1215M hyaluronan synthase Spy49_1806 hasB NE 1797043 1798251 402 + 6986128 CoG1215M UDP-glucose 6-dehydrogenase Spy49_1808 hasC NE 1798433 1799347 304 + 5986129 CoG1210M UDP-glucose pyrophosphorylase Spy49_1810 recF NE 1800070 1801176 368 + 5986131 CoG125015 Spy649_1810 recF NE 1800070 1801176 368 + 5986131 CoG125015 Spy649_1810 recF NE 1800070 1801176 368 + 5986131 CoG125015 Spy649_1810 recP NE 1800070 1801176 368 + 5986131 CoG125015 Spy649_1811 recP NE 1800279 180179 343 - 6986132 CoG4975G Spy49_1813c trsA E 1804087 1805109 340 - 5986132 CoG01516F Spy49_1813 resA E 1804087 1805109 340 - 5986134 CoG1180 Tryptophanyl-tRNA synthetase Spy49_1814 - NE 1805258 1806400 290 + 5986135 CoG02884 Spy649_1815 recP NE 1806479 180806 535 + 5986136 CoG04885 ABC transporter ATP-binding protein Spy49_1817 - NE 1808184 1810760 858 + 5986132 CoG44855 ABC transporter ATP-binding protein Spy49_1810 recP NE 1813005 1814919 407 + 5986142 CoG01250 rendopeptidase degP F 1813696 1814919 407 + 5986142 CoG01250 rendopeptidase degP F 1813696 1814919 407 + 5986142 CoG01250 rendopeptidase degP F 1813696 F F F F F F F F F		-								
Spy49_1806 hasB NE 1797043 1798251 402 + 6986128 (OG1004M) UDP-glucose 6-dehydrogenase Spy49_1808 hasC NE 1798633 1799347 304 + 6986128 (OG1210M) UDP-glucose 6-dehydrogenase Spy49_1809 NE 1800076 1800068 137 + 5986132 (OG25015 hypothetical protein Spy49_1809 Spy49_1810 recF NE 1800070 1801176 368 + 6986131 (OG0516F) recombination protein F Spy49_1811c ne NE 1801232 1803779 493 - 5986133 (OG0516F) hypothetical protein Spy49_1811c Spy49_1812c guaB NE 1804087 1805109 340 - 6986133 (OG0516F) inosine SV-monophosphate dehydrogenase Spy49_1814 - NE 1805528 1806400 290 + 6986132 (OG0180) tryptophanyl-tRNA synthetase II tryptophanyl-tRNA synthetase II Spy49_1817 - NE 1805528 1806400 290 + 6986132 (OG		-								
Spy49_1808 hasC NE 1798433 1799947 304 + 6986129 (G02120M UDP-glucose pyrophosphorylase Spy49_1810 recf NE 1800070 1801176 368 + 5986131 (G011951 Hopethetical protein Spy49_1809 Spy49_18110 NE 1801232 1802095 287 - 6986132 (G064975G Hypothetical protein Spy49_1811c Spy49_1812 VBA NE 1802298 1803779 493 - 6986133 (G065164 C0G01801 Hypothetical protein Spy49_1811c Spy49_1813c VBA NE 1805298 1805109 340 - 6986134 (G061801) C0G01801 tryptophanyl-tRNA synthetase II Spy49_1814 NE NE 1806479 1808086 53 5986135 (G064885) ARC transporter ATP-binding protein Spy49_1817 NE 1806479 1808086 53 5986132 (G064885) ARC transporter ATP-binding protein Spy49_1817 NE 1806479 1808086 53 5986133 (G064856) C06044855 ARC transporter ATP-binding pro										
Spy49_1810 -										
Spy49_1810 recF NE 1800070 1801176 368 + 6986131 begin for some for										
Spy49_1811c NE 1801232 1802095 287 - 6986132 CoG4975G hypothetical protein Spy49_1811c Spy49_1813c trsA E 1804087 1805109 340 - 5986134 CoG01806 tryptophanyl-tRNA synthetase Tryptophanyl-tRNA synthetase Spy49_1814 - NE 1805528 1806400 290 + 6986135 CoG12845 Spy49_1815 - NE 1806479 1808086 535 + 6986136 CoG04886 ABC transporter AFP-binding protein Spy49_1817 NE 1808184 1810760 858 + 6986137 CoG4855 ABC transporter AFP-binding protein Spy49_1817 Spy49_1817 NE 1813005 1813484 1810760 858 + 6986137 CoG4855 ABC transporter permease										
Spy49_1812c guaB NE 1802298 1803779 493 - 6986133 (OG0516F inosine 5\'-monophosphate dehydrogenase inosi		recr								
Spy49_1813c trsA E 1804087 1805109 340 - 6986134 C0G0180J tryptophanyl-tRNA synthetase II Spy49_1814 - NE 1805528 1806400 290 + 6986135 C0G1284s hypbothetical protein Syn49_1814 Spy49_1815 - NE 1806479 1806086 535 + 6986136 C0G04888 ABC transporter ATP-binding protein Spy49_1817 - NE 1803184 1810760 858 + 6986137 C0G44855 ABC transporter permease Spy49_1820 - NE 1813005 1813484 159 - 6986142 C0G15765 rRNA large subunit methyltransferase Spy49_1821 degP E 1813995 1814919 407 + 6986142 C0G02650 endopeptidase degP		guaR								
Spy49_1814 - NE 1805528 1806400 290 + 6986135 COG1284S hypothetical protein Spy49_1814 Spy49_1815 - NE 1806479 1808086 535 + 6986136 COG488R ABC transporter ATP-linding protein Spy49_1817 - NE 1808184 1810760 858 + 6986137 COG488S ABC transporter permease Spy49_1820c - NE 1813805 1813484 159 - 6986141 COG15765 rRNA large subunit methyltransferase Spy49_1821 degP E 1813696 1814919 407 + 6986142 COG02650 endopeptidase degP										
Spy49_1815 - NE 1806479 1808086 535 + 6986136 COG0488R ABC transporter ATP-binding protein Spy49_1817 - NE 1808184 1810760 858 + 5986137 COG44855 ABC transporter ATP-binding protein Spy49_1820c - NE 1813005 1813484 159 - 5986141 COG1765 ARC transporter ATP-binding protein Spy49_1820c - NE 1813005 1813484 159 - 5986141 COG12650 FixNA large subunit methyltransferase Spy49_1821 degP E 1813695 1814919 407 + 6986142 COG02650 endopeptidase degP		-								
Spy49_1817 NE 1808184 1810760 858 + 6986137 COG4485S ABC transporter permease Spy49_1820 - NE 1813005 1813484 159 - 6986141 COG15765 rRNA large subunit methyltransferase Spy49_1821 degP E 1813696 1814919 407 + 5986142 COG02550 endopeptidase degP		_								
Spy49_1820c - NE 1813005 1813484 159 - 6986141 COG1576S rRNA large subunit methyltransferase Spy49_1821 degP E 1813696 1814919 407 + 6986142 COG0265O endopeptidase degP										
Spy49_1821 degP E 1813696 1814919 407 + <u>6986142</u> COG02650 endopeptidase degP										
		degP								
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Table S7. Conserved GAS essential genes identified in both M1T1 5448 and M49 NZ131 compared to the predicted GAS core genome.

(a) Spy numbers from MGAS5005 genome.

(b) Hyperlink to the NCBI Gene website (http://www.ncbi.nlm.nih.gov/gene).

(c) Call integrating data from Bayesian analyses on 3 time points.

(d) Spy numbers from GAS NZ131 genome.

(e) When available, gene name is provided.

(f) Asteriks refer to genes found in the GAS core genome.

(g) S. Songuing's ortholog found essential

Essential or Critical in one GAS strain, but not the other

Critical for both GAS strains or Critical for one and Essential for the other

S. peumoniae ortholo GAS M1T1		ential.								
		sential.	GAS	M49 NZ131		Gene	GAS Core	Found essential	in other Strep. species	
	Gene ID(b)		Locus Tag(d)	Gene ID (b)		Name(e)	Genome(f)	S. sanguinis(g)	S. pneumoniae(h)	Protein Function
	3571011	E	Spy49_0001	6986144	NC	dnaA	*	SSA_0001	SP_0001	chromosome replication initiator DnaA
	3571012 3571013	E	Spy49_0002	6984517 6984518	E	dnaN	*	SSA_0002	SP_0002	DNA polymerase III subunit beta hypothetical protein M5005_Spy_0003
	3571013	NE NE	Spy49_0003 Spy49_0004	6984519	NE NE	ychF	*			GTP-dependent nucleic acid-binding protein EngD
	3571015	NC	Spy49_0005	6984520	E	pth	*	SSA_0006		peptidyl-tRNA hydrolase
	3571016	NE	Spy49 0006	6984521	NE	trcF	*			transcription-repair coupling factor
	3572946	NE	Spy49_0008	6984522	NE	-	*			heat shock protein 15
M5005_Spy_0008	3572947	NE	Spy49_0009	6984523	NC	divIC	*			cell division protein
	3572948	NC				-				hypothetical protein M5005_Spy_0009
	3572949	NE	Spy49_0010	6984524	NE		*			beta-lactamase
	3572950	E	Spy49_0011	6984525	E	tilS/mesJ	*	SSA_0013	SP_0011	tRNA(Ile)-lysidine synthetase
	3572951	NC	Spy49_0012	6984526	NE	hpt				hypoxanthine-guanine phosphoribosyltransferase
	3572952	E	Spy49_0013	6984527	E	ftsH	*		SP_0013	cell division protein
	3572953 3572954	NE	Spy49_0014	6984528	NE	-	*			amino acid permease hypothetical protein M5005_Spy_0015
	3572901	NC E	Spy49 0015	6984563	Е	sibA	*		SP_2216	secreted protein
	3572902	E	Spy49_0016	6984564	E	prsA.2	*		51_2235	ribose-phosphate pyrophosphokinase
	3572903	NE	Spy49_0017	6984565	NE	recO	*			DNA repair protein RecO
	3572904	E	Spy49_0018	6984566	E	plsX	*		SP_0027	glycerol-3-phosphate acyltransferase
5005_Spy_0021	3572905	NC	Spy49_0019	6984567	NC	acpP.2				acyl carrier protein
	3572906	NC	Spy49_0020	6984568	NE	purC				phosphoribosylaminoimidazole-succinocarboxamide synthase
	3572907	NE	Spy49_0021	6984569	NE	purL	*			phosphoribosylformylglycinamidine synthase
	3572908	NE	Spy49_0022	6984570	NE	purF	*			amidophosphoribosyltransferase
	3572909	NE	Spy49_0023	6984571	NE	purM	*			phosphoribosylaminoimidazole synthetase
5005_Spy_0026	3572910	NE	Spy49_0024	6984572	NE	purN	*			phosphoribosylglycinamide formyltransferase
5005_Spy_0027	3572911	NE	Spy49_0025	6984573	NE	purH				bifunctional phosphoribosylaminoimidazolecarboxamide formyltransferas cyclohydrolase
	3572912	NE	Spy49_0026c		NE	-	*			autolysin
	3572913	NE	Spy49_0027	6984575	NE	purD	*			phosphoribosylamineglycine ligase
	3572914	NE	Spy49_0028	6984576	NE	purE	*			phosphoribosylaminoimidazole carboxylase catalytic subunit
5005_Spy_0031	3572915	NE	Spy49_0029	6984577	NE	purK	*			phosphoribosylaminoimidazole carboxylase ATPase subunit
	3572916	NE	Spy49_0030	6984578	NE	-				hypothetical protein M5005_Spy_0032
	3572917	NE	Spy49_0031	6984579	NE	purB	*			adenylosuccinate lyase
	3572880	NE	Spy49_0032	6984580	NE	-				transcriptional regulator
	3572881	NE	Spy49_0033	6984581	C	ruvB	*		SP_0259	Holliday junction DNA helicase RuvB
	3572882	NE	Spy49_0035	6984582	NE	-	*			protein tyrosine phosphatase
	3572883 3572884	NC	Spy49_0036	6984663 6984664	E E	-				hypothetical protein M5005_Spy_0037 acyltransferase
	3572885	E NE	Spy49_0037 Spy49_0038	6984665	NE.	adh2/adhE	-			bifunctional acetaldehyde-CoA/alcohol dehydrogenase
	3572886	NE	Spy49_0039	6984666	NE	adhA/adhP	*			alcohol dehydrogenase
	3572887	NE	Spy49_0040	6984667	NE	norM	*			Na+ driven multidrug efflux pump
	3572889	E	Spy49_0044	6984668	NC	rpsJ	*	SSA_0106	SP_0208	30S ribosomal protein S10
15005_Spy_0044	3572890	E	Spy49_0045	6984669	E	rpIC	*	SSA_0107	SP_0209	50S ribosomal protein L3
5005_Spy_0045	3572891	E	Spy49_0046	6984670	NC	rpID	*	SSA_0108	SP_0210	50S ribosomal protein L4
	3572892	NE	Spy49_0048	6984671	NC	rplW	*		SP_0211	50S ribosomal protein L23
	<u>3572893</u>	E	Spy49_0049	6984672	E	rpIB	*	SSA_0110	SP_0212	50S ribosomal protein L2
	3572894	С	Spy49_0050	6984673	NC	rpsS	*	SSA_0111	SP_0213	30S ribosomal protein S19
	3572895	E	Spy49_0052	6984674	NC	rplV	*	SSA_0112	SP_0214	50S ribosomal protein L22
	3572896 3572897	E E	Spy49_0053 Spy49_0054	6984675 6984676	E E	rpsC rpIP	*	SSA_0113 SSA_0114	SP_0215 SP_0216	30S ribosomal protein S3 50S ribosomal protein L16
	3572898	NE	Spy49_0055	6984677	NC	rpmC		33A_0114	3F_0210	50S ribosomal protein L29
	3572899	NC	Spy49_0056	6984678	NC	rpsQ				30S ribosomal protein S17
	3572861	c	Spy49_0057	6984679	NC	rpIN	*	SSA_0117	SP_0219	50S ribosomal protein L14
	3572862	NC	Spy49_0058	6984680	E	rpIX	*	_	SP_0220	50S ribosomal protein L24
	3572863	NC	Spy49_0059	6984681	NC	rpIE	*			50S ribosomal protein L5
5005_Spy_0057	3572864	NC	Spy49_0060	6984682	NC	rpsN				30S ribosomal protein S14
	3572865	NC	Spy49_0061	6984683	NC	rpsH	*			30S ribosomal protein S8
	3572866	E	Spy49_0062	6984684	E	rplF	*	SSA_0122	SP_0225	50S ribosomal protein L6
	3572867	NC	Spy49_0064	6984685	NC	rpIR	*		66 666	50S ribosomal protein L18
	3572868	E	Spy49_0065	6984686	NC	rpsE	*	SSA_0124	SP_0227	30S ribosomal protein S5
	3572869	E	Spy49_0066	6984687	NC	rpmD rplO			SP_0228	50S ribosomal protein L30 50S ribosomal protein L15
	3572870 3572871	NE F	Spy49_0067	6984688 6984689	NC F		*	SSA 0127		•
	3572871 3572872	E NC	Spy49_0068 Spy49_0069	6984689 6984690	E E	secY adk	*	SSA_0127 SSA_0128	SP_0231	preprotein translocase subunit SecY adenylate kinase
	3572873	NC E	Spy49_0069 Spy49_0070	6984691	NC	infA	-	SSA_0128 SSA_0129	SP_0231 SP_0232	translation initiation factor IF-1
5005_Spy_0067		NC	Spy49_0070	6984692	NC	rpmJ		333123	55252	50S ribosomal protein L36
5005_Spy_0068		E	Spy49_0072	6984693	E	rpsM			SP_0234	30S ribosomal protein S13
	3572876	E	Spy49_0073	6984694	NC	rpsK	*	SSA_0131	SP_0235	30S ribosomal protein S11
	3572877	E	Spy49_0074	6984695	E	rpoA	*	SSA_0132	SP_0236	DNA-directed RNA polymerase subunit alpha
	3572878	E	Spy49_0075	6984696	NC	rplQ	*	SSA_0133	SP_0237	50S ribosomal protein L17
	3572879	NC				-				hypothetical protein M5005_Spy_0072
5005_Spy_0073	<u>3572845</u>	NC				-				hypothetical protein M5005_Spy_0073
	3572846	NC				-				4-diphosphocytidyl-2-C-methyl-D-erythritol kinase
	3572847	NC	Spy49_0078	6984713	NE	-				4-diphosphocytidyl 2 C methyl D pythritol kinase, partial
	3572848	NC	Spy49_0079	6984714 6984715	NE	adcR				4-diphosphocytidyl-2-C-methyl-D-erythritol kinase MarR family transcriptional regulator
	3572849 3572850	NE NE	Spy49_0080 Spy49_0081	6984715	NE NC	adck adcC	*			high-affinity zinc uptake system ATP-binding protein
	3572819	NE NE	Spy49_0081 Spy49_0082	6984717	NC	adcB	*			high-affinity zinc uptake system membrane protein
	3572820	NE	Spy49_0083c		NE	-				bis(5\'-nucleosyl)-tetraphosphatase (asymmetrical)
	3572821	E	Spy49_0083C	6984719	E	tyrS	*	SSA 0174	SP_2100	tyrosyl-tRNA synthetase
	3572822	NE	Spy49_0086	6984720	NE	pbp1b	*			multimodular transpeptidase-transglycosylase PBP 1B
5005_Spy 0082	3572823	E	Spy49_0087	6984721	E	rpoB	*	SSA_0176	SP_1961	DNA-directed RNA polymerase subunit beta
	3572824	E	Spy49_0088	6984722	E	rpoC	*	SSA_0177	SP_1960	DNA-directed RNA polymerase subunit beta\'
15005_Spy_0083	3572825	NE	Spy49_0089	6984723	NE	-	*			DNA binding protein
5005_Spy_0083 5005_Spy_0084	3372023	NE	Spy49_0090	6984724	NE	comYA	*			competence protein ComG
5005_Spy_0083 5005_Spy_0084 5005_Spy_0085	3572826					comYB	*			competence protein ComG
5005_Spy_0083 5005_Spy_0084 5005_Spy_0085 5005_Spy_0086 5005_Spy_0087	3572826 3572827	NE	Spy49_0091	6984725	NE					
15005_Spy_0083 15005_Spy_0084 15005_Spy_0085 15005_Spy_0086 15005_Spy_0087 15005_Spy_0088	3572826		Spy49_0091 Spy49_0092	6984725 6984726	NE	comYC	*			competence protein ComG
5005_Spy_0083 5005_Spy_0084 5005_Spy_0085 5005_Spy_0086 5005_Spy_0087 5005_Spy_0088 5005_Spy_0089	3572826 3572827 3572828 3572829	NE NE NE	Spy49_0092 Spy49_0093	6984726 6984727	NE NE		*			competence protein ComG competence protein ComG
5005_Spy_0083 5005_Spy_0084 5005_Spy_0085 5005_Spy_0086 5005_Spy_0087 5005_Spy_0088 5005_Spy_0089 5005_Spy_0090	3572826 3572827 3572828	NE NE	Spy49_0092	6984726	NE	comYC	*			competence protein ComG

M5005_Spy_0093										
	3572833	NE	Spy49_0097	6984731	NE	-	*			adenine-specific methyltransferase
M5005_Spy_0094	3572834	NE	Spy49_0098	6984732	NC	ackA	*			acetate kinase
M5005_Spy_0095	3572835	NE	Spy49_0099	6984733	NE	-				hypothetical protein M5005_Spy_0095
M5005_Spy_0096c		NE	Spy49_0100	6984734	NE	proC	*			pyrroline-5-carboxylate reductase
M5005_Spy_0097c		NE	Spy49_0101	6984735	NE	pepA	*			glutamyl aminopeptidase
M5005_Spy_0098	3572838	NC	Spy49_0103	6984736	NE	-				hypothetical protein M5005_Spy_0098
M5005_Spy_0099	3572800	NE		6004727			*			hypothetical protein M5005_Spy_0099
M5005_Spy_0100	3572801	NE	Spy49_0104	6984737	NE	trx.1				thioredoxin
M5005_Spy_0101	3572802	NE	Spy49_0105	6984738	NE	-				tRNA-binding domain-containing protein
M5005_Spy_0102	3572803	NE	Spy49_0107	6984739	NE	ssb				single-stranded DNA-binding protein
M5005_Spy_0103c M5005_Spy_0104c		NE	Spy49_0108c	6984740	NE	-				deoxyadenosine kinase/deoxyguanosine kinase tRNA-dihydrouridine synthase
		NE	Spy49_0109c	6984741	NE	hslO				· · · · · · · · · · · · · · · · · · ·
M5005_Spy_0105c		NE	Spy49_0110c	6984742	NE		*			heat shock protein 33
M5005_Spy_0106c M5005_Spy_0107	3572807 3572808	NE NE	Spy49_0111 Spy49_0112	6984823 6984824	NE NE	rofA/nra cbp				transcriptional regulator fibronectin-binding protein
M5005_Spy_0107	3572809	NE	Spy49_0112 Spy49_0113	6984825	NE	lepA-1				signal peptidase I
M5005_Spy_0100	3572810	NE	Spy49_0114	6984826	NE	prtF				fibronectin-binding protein
M5005_Spy_0109	3572811	NE	Spy49_0116	6984827	NE	eftLSL.B				hypothetical protein M5005_Spy_0110
M5005_Spy_0110	3572812	NE	Spy49_0110	6984828	NE	-				hypothetical protein M5005_Spy_0110
M5005_Spy_0111		NE	3py45_0117	0304020	INL	-				transposase
M5005 Spy 0113c		NE				_				transposase
M5005_Spy_0114		NE				-				sortase
			Spy49_0118	6984829	NE	msmR				
			Spy49_0119	6984830	NE	prtF				
			Spy49_0120c	6984831	NE					
M5005_Spy_0115c	3572816	NE	., _			-	*			hypothetical protein M5005_Spy_0115
M5005_Spy_0116	3572817	NE	Spy49_0121	6984832	NE	atoE	*			short-chain fatty acids transporter
M5005_Spy_0117c	3572818	NE				-				LysR family transcriptional regulator
M5005_Spy_0118c	3572780	NE	Spy49_0122c	6984833	NE	-				LysR family transcriptional regulator
M5005_Spy_0119	3572781	NE	Spy49_0123	6984834	NE	-				acetyl-CoA acetyltransferase
M5005_Spy_0120	3572782	NE	Spy49_0124	6984835	NE	atoD.2				acetate CoA-transferase subunit alpha
M5005_Spy_0121		NE	Spy49_0125	6984836	NE	-	*			acetyl-CoA:acetoacetyl-CoA transferase subunit beta
M5005_Spy_0122c		NE	Spy49_0126c	6984837	NE	-	*			DNA-binding protein
M5005_Spy_0123	3572785	NE	Spy49_0127	6984838	NE	-	*			translation initiation inhibitor
M5005_Spy_0124	3572786	NE	Spy49_0128	6984839	NE	sloR	*			transcriptional regulator
M5005_Spy_0125	3572787	NE	Spy49_0129	6984840	NE	-	*			hypothetical protein M5005_Spy_0125
M5005_Spy_0126	3572788	NE	Spy49_0130	6984841	NE	ntpI	*			V-type ATP synthase subunit I
M5005_Spy_0127	3572789	NE	Spy49_0131	6984842	NE	ntpK	*			V-type ATP synthase subunit K
M5005_Spy_0128	3572790	NE	Spy49_0132	6984843	NE	ntpE	*			V-type sodium ATP synthase subunit E
M5005_Spy_0129	3572791	NE	Spy49_0133	6984844	NE	ntpC	*			V-type ATP synthase subunit C
M5005_Spy_0130	3572792	NE	Spy49_0134	6984845	NE	ntpF				V-type ATP synthase subunit F
M5005_Spy_0131	3572793	NE	Spy49_0135	6984846	NE	ntpA	*			V-type ATP synthase subunit A
M5005_Spy_0132	3572794	NE	Spy49_0136	6984847	NE	ntpB	*			V-type ATP synthase subunit B
M5005_Spy_0133	3572795 3572796	NE	Spy49_0137	6984848 6984849	NE	ntpD				V-type ATP synthase subunit D tellurite resistance protein
M5005_Spy_0134c M5005_Spy_0135c		NE NE	Spy49_0138c Spy49_0139c	6984850	NE NE	-				hypothetical protein M5005_Spy_0135
M5005_Spy_01336	3572798	NE	Spy49_0139C Spy49_0141	6984851	NE	purA				adenylosuccinate synthetase
M5005_Spy_0130	3572799	NE	Spy49_0141 Spy49_0142		NE	puiA	*			nucleoside-binding protein
M5005_Spy_0137	3572761	C	Spy49_0142 Spy49_0143	6984852 6984853	NC	nusG			SP_2007	transcription antitermination protein NusG
M5005_Spy_0130	3572762	NE	Spy49_0143	6984854	NE	nga	*		3F_2007	NAD glycohydrolase
M5005_Spy_0140	3572763	NE	Spy49_0145	6984855	NE	-	-			hypothetical protein M5005_Spy_0140
M5005_Spy_0141	3572764	NE	Spy49_0146	6984856	NE	slo	*			streptolysin O
M5005_Spy_0112	3572765	NE	Spy49_0147	6984857	NC	-				hypothetical protein M5005_Spy_0142
M5005_Spy_0143c		NE	Spy49_0148	6984858	NC	-				hypothetical protein M5005_Spy_0143
M5005_Spy_0143c		NC	Spy49_0148	6984859	NE	-				hypothetical protein M5005_Spy_0143
M5005_Spy_0145c		NE	Spy49_0150c	6984860	E	-				hypothetical protein M5005_Spy_0145
M5005_Spy_0146	3572769	NE	Spy49_0151	6984861	NE	metB				cystathionine beta-lyase
M5005_Spy_0147	3572770	E	Spy49_0152	6984862	E	leuS	*	SSA_0289	SP_0254	leucyl-tRNA synthetase
M5005_Spy_0148	3572771	NC	Spy49_0153	6984863	NE	ulaA	*	55/1_0205	50254	PTS system ascorbate-specific transporter subunit IIC
M5005_Spy_0149	3572772	NE	Spy49 0154	6984864	NE	-	*			PTS system 3-keto-L-gulonate specific transporter subunit IIB
M5005_Spy_0150	3572773	NE	Spy49_0155	6984865	NE	-	*			PTS system 3-keto-L-gulonate specific transporter subunit IIA
M5005_Spy_0151	3572774	NE	Spy49_0156	6984866	NC	ulaD	*			3-keto-L-gulonate-6-phosphate decarboxylase
M5005_Spy_0152	3572775	NE	Spy49_0157	6984867	NE	-	*			L-xylulose 5-phosphate 3-epimerase
M5005_Spy_0153	3572776	NE		6984868	NE	araD	*			L-ribulose-5-phosphate 4-epimerase
	3572777		Spy49_0158							
M5005_Spy_0154		NC	Spy49_0158			-				hypothetical protein M5005_Spy_0154
	3572778		Spy49_0158 Spy49_0159	6984869	NE	-	*			hypothetical protein M5005_Spy_0154 BigG family transcription antiterminator
M5005_Spy_0154	3572778 3572779	NC			NE NE	- - -	*			
M5005_Spy_0154 M5005_Spy_0155 M5005_Spy_0156 M5005_Spy_0157		NC NE	Spy49_0159	6984869		- - - opuAA	* *			BigG family transcription antiterminator L-ascorbate 6-phosphate lactonase glycine betaine transport ATP-binding protein
M5005_Spy_0154 M5005_Spy_0155 M5005_Spy_0156 M5005_Spy_0157 M5005_Spy_0158	3572779 3572741 3572742	NC NE NE	Spy49_0159 Spy49_0160 Spy49_0161 Spy49_0162	6984869 6984870 6984871 6984872	NE	opuABC	* * *			BigG family transcription antiterminator L-ascorbate 6-phosphate lactonase glycine betaine transport ATP-binding protein glycine betaine-binding protein/glycine betaine transporter permease
M5005_Spy_0154 M5005_Spy_0155 M5005_Spy_0156 M5005_Spy_0157	3572779 3572741	NC NE NE NE	Spy49_0159 Spy49_0160 Spy49_0161	6984869 6984870 6984871	NE NE		* * * *	SSA_0100	SP_0032	BigG family transcription antiterminator L-ascorbate 6-phosphate lactonase glycine betaine transport ATP-binding protein
M5005_Spy_0154 M5005_Spy_0155 M5005_Spy_0156 M5005_Spy_0157 M5005_Spy_0158 M5005_Spy_0159 M5005_Spy_0160	3572779 3572741 3572742 3572743 3572744	NC NE NE NE E NE	Spy49_0159 Spy49_0160 Spy49_0161 Spy49_0162 Spy49_0163 Spy49_0164	6984869 6984870 6984871 6984872 6984873	NE NE NE E NE	opuABC polA	* * * * *	SSA_0100	SP_0032	BigG family transcription antiterminator L-ascorbate 6-phosphate lactonase glycine betaine transport ATP-binding protein glycine betaine-binding protein/glycine betaine transporter permease DNA polymerase I CoA binding protein
M5005_Spy_0154 M5005_Spy_0155 M5005_Spy_0156 M5005_Spy_0157 M5005_Spy_0158 M5005_Spy_0159 M5005_Spy_0160 M5005_Spy_0160	3572779 3572741 3572742 3572743 3572744 3572745	NC NE NE NE E NE	Spy49_0159 Spy49_0160 Spy49_0161 Spy49_0162 Spy49_0163 Spy49_0164 Spy49_0165	6984869 6984870 6984871 6984872 6984873 6984874 6984875	NE NE NE E NE	opuABC polA perR	* * * * * * *	SSA_0100	SP_0032	BigG family transcription antiterminator L-ascorbate 6-phosphate lactonase glycine betaine transport ATP-binding protein glycine betaine-binding protein/glycine betaine transporter permease DNA polymerase I CoA binding protein ferric uptake regulation protein
M5005_Spy_0154 M5005_Spy_0155 M5005_Spy_0156 M5005_Spy_0157 M5005_Spy_0158 M5005_Spy_0159 M5005_Spy_0160 M5005_Spy_0161 M5005_Spy_0161	3572779 3572741 3572742 3572743 3572744 3572745 3572746	NC NE NE NE E NE NE NE	Spy49_0159 Spy49_0160 Spy49_0161 Spy49_0162 Spy49_0163 Spy49_0164 Spy49_0165 Spy49_0166	6984869 6984870 6984871 6984872 6984873 6984874 6984875 6984876	NE NE NE E NE NE	opuABC polA	* * * * * * *	SSA_0100	SP_0032	BigG family transcription antiterminator L-ascorbate 6-phosphate lactonase glycine betaine transport ATP-binding protein glycine betaine-binding protein/glycine betaine transporter permease DNA polymerase I CoA binding protein ferric uptake regulation protein trans-acting positive regulator Mry
M5005_Spy_0154 M5005_Spy_0155 M5005_Spy_0156 M5005_Spy_0157 M5005_Spy_0159 M5005_Spy_0159 M5005_Spy_0160 M5005_Spy_0161 M5005_Spy_0162 M5005_Spy_0162	3572779 3572741 3572742 3572743 3572744 3572745 3572746 3572747	NC NE NE NE E NE NE NE	Spy49_0159 Spy49_0160 Spy49_0161 Spy49_0162 Spy49_0163 Spy49_0164 Spy49_0165 Spy49_0166 Spy49_0167	6984869 6984870 6984871 6984872 6984873 6984874 6984875 6984876 6984877	NE NE E NE NE NE NE	opuABC polA perR	* * * * *	SSA_0100	SP_0032	BigG family transcription antiterminator L-ascorbate 6-phosphate lactonase glycine betaine transport ATP-binding protein glycine betaine-binding protein/glycine betaine transporter permease DNA polymerase I CoA binding protein ferric uptake regulation protein trans-acting positive regulator Mry 3\'-phosphoadenosine S\'-phosphosulfate sulfotransferase
M5005_Spy_0154 M5005_Spy_0155 M5005_Spy_0156 M5005_Spy_0157 M5005_Spy_0158 M5005_Spy_0159 M5005_Spy_0160 M5005_Spy_0161 M5005_Spy_0162 M5005_Spy_0163 M5005_Spy_0163 M5005_Spy_0163	3572779 3572741 3572742 3572743 3572744 3572745 3572746 3572747 3572748	NC NE	Spy49_0159 Spy49_0160 Spy49_0161 Spy49_0162 Spy49_0163 Spy49_0164 Spy49_0165 Spy49_0166 Spy49_0167 Spy49_0168	6984869 6984870 6984871 6984872 6984873 6984874 6984875 6984876 6984877 6984878	NE NE E NE NE NE NE NE NE NE	opuABC polA perR	* * * * * *	SSA_0100	SP_0032	BigG family transcription antiterminator L-ascorbate 6-phosphate lactonase glycine betaine transport ATP-binding protein glycine betaine-binding protein/glycine betaine transporter permease DNA polymerase I CoA binding protein ferric uptake regulation protein trans-acting positive regulator Mry 3\-phosphoadenosine 5\-phosphosulfate sulfotransferase parB-like nuclease
M5005_Spy_0154 M5005_Spy_0156 M5005_Spy_0156 M5005_Spy_0157 M5005_Spy_0159 M5005_Spy_0160 M5005_Spy_0160 M5005_Spy_0162 M5005_Spy_0164 M5005_Spy_0164 M5005_Spy_0164 M5005_Spy_0164	3572779 3572741 3572742 3572743 3572744 3572745 3572746 3572747 3572748 3572749	NC NE NE NE E NE NE NE NE NE NE NE NE NE N	Spy49_0159 Spy49_0160 Spy49_0161 Spy49_0162 Spy49_0163 Spy49_0165 Spy49_0166 Spy49_0166 Spy49_0167 Spy49_0168 Spy49_0169	6984869 6984870 6984871 6984872 6984873 6984874 6984875 6984875 6984877 6984878	NE NE E NE NE NE NE NE NE NE NE	opuABC polA perR	* * * * *	SSA_0100	SP_0032	BigG family transcription antiterminator L-ascorbate 6-phosphate lactonase glycine betaine transport ATP-binding protein glycine betaine-binding protein/glycine betaine transporter permease DNA polymerase I CoA binding protein ferric uptake regulation protein trans-acting positive regulator Mry 3'-phosphoadenosine 5\-phosphosulfate sulfotransferase parB-like nuclease
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M5005_Spy_0154 M5005_Spy_0155 M5005_Spy_0157 M5005_Spy_0157 M5005_Spy_0158 M5005_Spy_0163 M5005_Spy_0161 M5005_Spy_0162 M5005_Spy_0162 M5005_Spy_0164 M5005_Spy_0164 M5005_Spy_0164 M5005_Spy_0165 M5005_Spy_0165 M5005_Spy_0166 M5005_Spy_0166	3572779 3572741 3572742 3572743 3572744 3572745 3572746 3572747 3572748 3572749 3572750 3572751	NC NE	Spy49_0159 Spy49_0160 Spy49_0161 Spy49_0163 Spy49_0164 Spy49_0165 Spy49_0165 Spy49_0167 Spy49_0168 Spy49_0169 Spy49_0170c	6984869 6984870 6984871 6984872 6984873 6984874 6984875 6984876 6984876 6984878 6984879 6984880	NE NE E NE	opuABC polA - perR vlg	* * * * * *	SSA_0100	SP_0032	BigG family transcription antiterminator L-ascorbate 6-phosphate lactonase glycine betaine transport ATP-binding protein glycine betaine-binding protein/glycine betaine transporter permease DNA polymerase I CoA binding protein ferric uptake regulation protein trans-acting positive regulation Mry 3\'-phosphoadenosine 5\'-phosphosulfate sulfotransferase parB-like nuclease transposase transposase transposase
M5005_Spy_0154 M5005_Spy_0156 M5005_Spy_0157 M5005_Spy_0157 M5005_Spy_0158 M5005_Spy_0159 M5005_Spy_0160 M5005_Spy_0162 M5005_Spy_0162 M5005_Spy_0164 M5005_Spy_0164 M5005_Spy_0166 M5005_Spy_0166 M5005_Spy_0166 M5005_Spy_0166 M5005_Spy_0166 M5005_Spy_0165 M5005_Spy_0166 M5005_Spy_0166	3572779 3572741 3572742 3572743 3572744 3572745 3572746 3572747 3572748 3572749 3572750 3572750 3572751	NC NE	Spy49_0159 Spy49_0160 Spy49_0161 Spy49_0162 Spy49_0163 Spy49_0165 Spy49_0166 Spy49_0166 Spy49_0167 Spy49_0168 Spy49_0169	6984869 6984870 6984871 6984872 6984873 6984874 6984875 6984875 6984877 6984878	NE NE E NE NE NE NE NE NE NE NE	opuABC polA perR	* * * * * *	SSA_0100	SP_0032	BigG family transcription antiterminator L-ascorbate 6-phosphate lactonase glycine betaine transport ATP-binding protein glycine betaine-binding protein/glycine betaine transporter permease DNA polymerase I CoA binding protein ferric uptake regulation protein frans-acting positive regulation Mry 3\'-phosphoadenosine 5\'-phosphosulfate sulfotransferase parB-like nuclease transposase transposase transposase transposase transposase transposase
MS005_Spy_0154 MS005_Spy_0155 MS005_Spy_0157 MS005_Spy_0157 MS005_Spy_0159 MS005_Spy_0159 MS005_Spy_0169 MS005_Spy_0161 MS005_Spy_0162 MS005_Spy_0164 MS005_Spy_0166 MS005_Spy_0166 MS005_Spy_0166 MS005_Spy_0166 MS005_Spy_0166 MS005_Spy_0166 MS005_Spy_0166 MS005_Spy_0166 MS005_Spy_01666 MS005_Spy_01666 MS005_Spy_01666 MS005_Spy_01666	3572779 3572741 3572742 3572743 3572744 3572745 3572746 3572747 3572748 3572749 3572750 3572751 3572751 3572752 3572752	NC NE NE NE E NE NE NE NE NE NE NE NE NE N	Spy49_0159 Spy49_0160 Spy49_0161 Spy49_0163 Spy49_0163 Spy49_0164 Spy49_0166 Spy49_0167 Spy49_0169 Spy49_0169 Spy49_0169 Spy49_0170c	6984869 6984870 6984871 6984872 6984873 6984874 6984875 6984876 6984876 6984878 6984879 6984880	NE NE E NE	opuABC polA perR vlg - - - - - - - - - - - - -	* * * * * *	SSA_0100	SP_0032	BigG family transcription antiterminator L-ascorbate 6-phosphate lactonase glycine betaine transport ATP-binding protein glycine betaine-binding protein/glycine betaine transporter permease DNA polymerase I COA binding protein ferric uptake regulation protein trans-acting positive regulator Mry 3'\-phosphoadenosine 5\'-phosphosulfate sulfotransferase parB-like nuclease transposase transposase transposase transposase transposase transposase transposase transposase transposase
M5005_Spy_0154 M5005_Spy_0156 M5005_Spy_0157 M5005_Spy_0157 M5005_Spy_0157 M5005_Spy_0159 M5005_Spy_0169 M5005_Spy_0161 M5005_Spy_0162 M5005_Spy_0164 M5005_Spy_0165c	3572779 3572741 3572742 3572743 3572744 3572745 3572746 3572747 3572748 3572749 3572750 3572751 3572752 3572752	NC NE	Spy49_0159 Spy49_0160 Spy49_0161 Spy49_0162 Spy49_0163 Spy49_0165 Spy49_0166 Spy49_0166 Spy49_0169 Spy49_0170c Spy49_0170c Spy49_0173c	6984869 6984870 6984871 6984872 6984873 6984873 6984875 6984876 6984877 6984879 6984880 6984881	NE N	opuABC polA - perR vlg	* * * * * *	SSA_0100	SP_0032	BigG family transcription antiterminator L-ascorbate 6-phosphate lactonase glycine betaine transport ATP-binding protein glycine betaine-binding protein/glycine betaine transporter permease DNA polymerase I CoA binding protein ferric uptake regulation protein trans-acting positive regulator Mry 3'\-phosphoadenosine 5\'-phosphosulfate sulfotransferase parB-like nuclease transposase transposase transposase transposase transposase malonate permease micotinate-nucleotide pyrophosphorylase
MS005_Spy_0154 MS005_Spy_0155 MS005_Spy_0157 MS005_Spy_0158 MS005_Spy_0158 MS005_Spy_0159 MS005_Spy_0160 MS005_Spy_0161 MS005_Spy_0161 MS005_Spy_0163 MS005_Spy_0163 MS005_Spy_0164 MS005_Spy_0166 MS005_Spy_0166 MS005_Spy_0166 MS005_Spy_0168 MS005_Spy_0169 MS005_Spy_0170	3572779 3572741 3572742 3572743 3572744 3572745 3572746 3572748 3572748 3572749 3572750 3572751 3572752 3572752 3572753	NC NE	Spy49_0159 Spy49_0160 Spy49_0161 Spy49_0163 Spy49_0163 Spy49_0164 Spy49_0166 Spy49_0167 Spy49_0169 Spy49_0169 Spy49_0169 Spy49_0170c	6984869 6984870 6984871 6984872 6984873 6984874 6984875 6984876 6984876 6984878 6984879 6984880	NE NE E NE	opuABC polA perR vlg - - - - - - - - - - - - -	* * * * * *	SSA_0100	SP_0032	BigG family transcription antiterminator L-ascorbate 6-phosphate lactonase glycine betaine transport ATP-binding protein glycine betaine-binding protein/glycine betaine transporter permease DNA polymerase I CoA binding protein ferric uptake regulation protein frans-acting positive regulator Mry 3\'-phosphoadenosine 5\'-phosphosulfate sulfotransferase parB-like nuclease transposase transposase transposase transposase malonate permease micotinate-nucleotide pyrophosphorylase transposase
M5005_Spy_0154 M5005_Spy_0155 M5005_Spy_0156 M5005_Spy_0156 M5005_Spy_0158 M5005_Spy_0159 M5005_Spy_0169 M5005_Spy_0161 M5005_Spy_0161 M5005_Spy_0164 M5005_Spy_0166 M5005_Spy_0166 M5005_Spy_0166 M5005_Spy_0166 M5005_Spy_01690 M5005_Spy_01690 M5005_Spy_01690 M5005_Spy_01690 M5005_Spy_01690 M5005_Spy_01690 M5005_Spy_01690 M5005_Spy_01690 M5005_Spy_01720 M5005_Spy_01720	3572779 3572741 3572742 3572743 3572744 3572745 3572746 3572747 3572750 3572750 3572751 3572752 3572752 3572753 3572753	NC NE	Spy49_0159 Spy49_0160 Spy49_0161 Spy49_0163 Spy49_0163 Spy49_0165 Spy49_0165 Spy49_0166 Spy49_0168 Spy49_0170c Spy49_0170c Spy49_0173c Spy49_0173c Spy49_0178c	6984869 6984870 6984871 6984872 6984873 6984873 6984875 6984876 6984876 6984876 6984880 6984881 6984883	NE NE E NE	opuABC polA perR vlg - - - - - - - - - - - - -	*	SSA_0100	SP_0032	BigG family transcription antiterminator L-ascorbate 6-phosphate lactonase glycine betaine transport ATP-binding protein glycine betaine-binding protein/glycine betaine transporter permease DNA polymerase I CoA binding protein ferric uptake regulation protein trans-acting positive regulation Mry 3\'-phosphoadenosine 5\'-phosphosulfate sulfotransferase parB-like nuclease transposase transposase transposase transposase transposase transposase transposase transposase incotinate-nucleotide pyrophosphorylase transposase transposase
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M5005_Spy_0192c M5005_Spy_0194c M5005_Spy_0195										
	3572737	NC	Spy49_0191c	6984896	E	hasC.2	*	SSA_2169	SP_2092	UTP-glucose-1-phosphate uridylyltransferase
M5005 Spv 0195	3572739	E	Spy49_0192c	6984897	E	gpsA	*		SP_2091	glycerol-3-phosphate dehydrogenase, partial
	3572740	NE	Spy49_0193	6984898	NE	-	*		_	MarR family transcriptional regulator
M5005_Spy_0196	3572702	NE	Spy49_0194	6984899	NC	-	*			multidrug resistance ABC transporter ATP-binding protein/permease
M5005_Spy_0197	3572703	NE	Spy49_0195	6984900	NE	_	*			multidrug resistance ABC transporter ATP-binding protein/permease
M5005_Spy_0198	3572704	NE	Spy49_0198	6984901	NE	_	*			hypothetical protein M5005_Spy_0198
M5005_Spy_0199	3572705	NE		6984902	NE	dut				deoxyuridine 5\'-triphosphate nucleotidohydrolase
			Spy49_0199				•			
M5005_Spy_0200	3572706	NE	Spy49_0200	6984983	NE	radA	*			DNA repair protein RadA
M5005_Spy_0201	3572707	C	Spy49_0201	6984984	NC	-	*			carbonic anhydrase
M5005_Spy_0202	3572708	NE	Spy49_0202	6984985	NE	-	*			hypothetical protein M5005_Spy_0202
M5005_Spy_0203	3572709	E	Spy49_0203	6984986	E	gltX	*	SSA_2144	SP_2069	glutamyl-tRNA synthetase
M5005_Spy_0204	3572710	NE	Spy49_0204	6984987	NE	fasB	*			sensory transduction protein kinase
M5005_Spy_0205	3572711			6984988	NC	fasC				sensory transduction protein kinase
		NE	Spy49_0205							
M5005_Spy_0206	3572712	NE	Spy49_0206	6984989	NE	fasA	*			response regulator
M5005_Spy_0207	3572713	C	Spy49_0207	6984990	NC	rnpA	*	SSA_2140	SP_2042	ribonuclease P
M5005_Spy_0208	3572714	NE	Spy49_0208	6984991	NE	-	*			hypothetical protein M5005_Spy_0208
M5005 Spy 0209	3572715	NE	Spy49 0209	6984992	NC	-	*			jag protein
M5005_Spy_0210	3572716	NC	.,,			_				hypothetical protein M5005_Spy_0210
	3572717		Cm.,40, 0210	6004002	NC	rpmH				50S ribosomal protein L34
M5005_Spy_0211		NC	Spy49_0210	6984993	NC	rpilin				
M5005_Spy_0212	3572718	NE	Spy49_0211	6984994	NE	-	*			N-acetylmannosamine-6-phosphate 2-epimerase
M5005_Spy_0213	3572719	NE	Spy49_0212	6984995	NE	-	*			N-acetylneuraminate-binding protein
M5005_Spy_0214	3572720	NE	Spy49_0213	6984996	NE	-	*			N-acetylneuraminate transporter permease
M5005_Spy_0215	3572721	NE	Spy49_0214	6984997	NE	-	*			N-acetylneuraminate transporter permease
M5005_Spy_0216	3572683	NE	Spy49_0215	6984998	NE	-	*			hypothetical protein M5005_Spy_0216
M5005_Spy_0217	3572684	NE	Spy49_0216	6984999	NE	nanH	*			N-acetylneuraminate lyase
M5005_Spy_0218	3572685	NE	Spy49_0217	6985000	NE	-	*			N-acetylmannosamine kinase
							*			
M5005_Spy_0219c	3572686	NE	Spy49_0218c	6985001	NE		•			RpiR family transcriptional regulator
M5005_Spy_0220	3572687	NE	Spy49_0219	6985002	NE	tatD	*			sec-independent protein translocase
M5005_Spy_0221	3572688	NE	Spy49_0220	6985003	NE	-	*			ribonuclease M5
M5005_Spy_0222	3572689	NE	Spy49_0221	6985004	NE	ksgA	*			dimethyladenosine transferase
M5005_Spy_0223	3572690	E	Spy49 0223	6985005	NE	engC	*		SP_1984	ribosome-associated GTPase
M5005_Spy_0224	3572691	С	Spy49_0224	6985006	NC	rpe	*			ribulose-phosphate 3-epimerase
M5005_Spy_0225	3572692	NE	Spy49 0225	6985007	NE					thiamin pyrophosphokinase
M5005_Spy_0226	3572693	NE	Spy49_0226	6985008	NE		*			rmuC family protein
M5005_Spy_0227	3572694	NE	Spy49_0227	6985009	NE	cbf	*			CMP-binding factor
M5005_Spy_0228	3572695	NE	Spy49_0228	6985010	NE	purR	*			pur operon repressor
M5005_Spy_0229	3572696	NE	Spy49_0229	6985011	NE	prgA	*			surface exclusion protein
M5005_Spy_0230	3572697	Ε	Spy49_0230	6985012	NC	rpsL	*	SSA_2111	SP_0271	30S ribosomal protein S12
M5005_Spy_0231	3572698	E	Spy49 0231	6985013	E	rpsG	*	SSA_2110	SP_0272	30S ribosomal protein S7
						fus	*			elongation factor G
M5005_Spy_0232	3572699	E	Spy49_0233	6985014	E			SSA_2109	SP_0273	•
M5005_Spy_0233	3572700	E	Spy49_0234	6985015	E	plr	*	SSA_2108	SP_2012	glyceraldehyde-3-phosphate dehydrogenase
M5005_Spy_0234c	3572701	NC	Spy49_0235c	6985016	NC	-				hypothetical protein M5005_Spy_0234
M5005_Spy_0235c	3572663	E	Spy49_0236c	6985017	NE	-	*		SP_1460	amino acid transport ATP-binding protein
M5005_Spy_0236c	3572664	E	Spy49_0237c	6985018	NE	-	*		SP_1461	amino acid ABC transporter permease
M5005_Spy_0237	3572665	NE	Spy49_0238	6985019	NE	-	*			hypothetical protein M5005_Spy_0237
M5005_Spy_0238	3572666	NE	Spy49_0239	6985020	NE	uppP/bacA	*			undecaprenyl pyrophosphate phosphatase
						mecA	*			
M5005_Spy_0239	3572667	NE	Spy49_0240	6985021	NE					adaptor protein
M5005_Spy_0240	3572668	E	Spy49_0241	6985022	E	rgpG	*	SSA_1870	SP_0337	undecaprenyl-phosphate alpha-N-acetylglucosaminephosphotransferase
M5005_Spy_0241	3572669	NC				rgpG				hypothetical protein M5005_Spy_0241
M5005_Spy_0242	3572670	C	Spy49_0242	6985023	NC	-	*		SP_1541	ABC transporter ATP-binding protein
M5005_Spy_0243	3572671	C	Spy49_0243	6985024	С	-	*		SP_0868	ABC transporter
M5005_Spy_0244	3572672	С	Spy49_0244	6985025	NC	nifS3	*		SP_0869	cysteine desulfhydrase
M5005_Spy_0245	3572673	C	Spy49_0245	6985026	NC	nifU	*		SP_0870	iscU protein
M5005_Spy_0246	3572674	c	Spy49_0246	6985027		11110				ABC transporter
					NC	7	-		SP_0871	
M5005_Spy_0247c	3572675	NE	Spy49_0247	6985028	NE	pbp7				D-alanyl-D-alanine carboxypeptidase
M5005_Spy_0248c	3572676	NE	Spy49_0248c	6985029	NE	dacA2	*			D-alanyl-D-alanine carboxypeptidase
M5005_Spy_0249	3572677	NE	Spy49_0249	6985030	NE	oppA				oligopeptide-binding protein
M5005_Spy_0250	3572678	NE	Spy49_0250	6985031	NE	oppB	*			oligopeptide transporter permease
M5005_Spy_0251	3572679	NE	Spy49_0251	6985032	NE	oppC	*			oligopeptide transporter permease
M5005_Spy_0252	3572680	NE	Spy49_0252	6985033	NE	oppD	*			oligopeptide transport ATP-binding protein
M5005_Spy_0253	3572681	NE	Spy49_0253	6985034	NE	oppF	*			oligopeptide transport ATP-binding protein
M5005_Spy_0254c			3py45_0233	6985035	NE	оррі				
M3003_Spy_0234C	3572682	NC	C40 0354-							
			Spy49_0254c							transposase
M5005_Spy_0255c	3572650	NC	Spy49_0254c Spy49_0256	6985042	NE	-				transposase hypothetical protein M5005_Spy_0255
M5005_Spy_0256	3572657	NC NE				comX1.1				transposase
						comX1.1				transposase hypothetical protein M5005_Spy_0255
M5005_Spy_0256	3572657	NE NE				comX1.1				transposase hypothetical protein M5005_Spy_0255 competence-specific sigma factor
M5005_Spy_0256 M5005_Spy_0257 M5005_Spy_0258	3572657 3572658 3572659	NE NE NE				comX1.1				transposase hypothetical protein M5005_Spy_0255 competence-specific sigma factor transposase, partial transposase
M5005_Spy_0256 M5005_Spy_0257 M5005_Spy_0258 M5005_Spy_0259	3572657 3572658 3572659 3572660	NE NE NE	Spy49_0256	<u>6985042</u>	NE	comX1.1	*	SSA 0575	SP 1750	transposase hypothetical protein M5005_Spy_0255 competence-specific sigma factor transposase, partial transposase hypothetical protein M5005_Spy_0259
M5005_Spy_0256 M5005_Spy_0257 M5005_Spy_0258 M5005_Spy_0259 M5005_Spy_0260	3572657 3572658 3572659 3572660 3572661	NE NE NC E	Spy49_0256 Spy49_0257	6985042 6985043	NE C	comX1.1	*	SSA_0575 SSA_1180	SP_1750	transposase hypothetical protein M5005_Spy_0255 competence-specific sigma factor transposase, partial transposase hypothetical protein M5005_Spy_0259 lipase
M5005_Spy_0256 M5005_Spy_0257 M5005_Spy_0258 M5005_Spy_0259 M5005_Spy_0260 M5005_Spy_0261	3572657 3572658 3572659 3572660 3572661 3572662	NE NE NC E C	Spy49_0256 Spy49_0257 Spy49_0258	6985042 6985043 6985044	NE C E	comX1.1	*	SSA_0575 SSA_1189	SP_1750 SP_1749	transposase hypothetical protein M5005_Spy_0255 competence-specific sigma factor transposase, partial transposase hypothetical protein M5005_Spy_0259 lipase GTP-binding protein YqeH
M5005_Spy_0256 M5005_Spy_0257 M5005_Spy_0258 M5005_Spy_0259 M5005_Spy_0260 M5005_Spy_0261 M5005_Spy_0261	3572657 3572658 3572659 3572660 3572661	NE NE NC E C	Spy49_0256 Spy49_0257 Spy49_0258 Spy49_0259	6985042 6985043 6985044 6985045	C E NE	- - - -	* *			transposase hypothetical protein M5005_Spy_0255 competence-specific sigma factor transposase, partial transposase hypothetical protein M5005_Spy_0259 lipase GTP-binding protein YqeH RNA-binding protein
M5005_Spy_0256 M5005_Spy_0257 M5005_Spy_0258 M5005_Spy_0259 M5005_Spy_0260 M5005_Spy_0261 M5005_Spy_0262 M5005_Spy_0263	3572657 3572658 3572659 3572660 3572661 3572662 3572630 3572631	NE NE NC E C NE E	Spy49_0256 Spy49_0257 Spy49_0258 Spy49_0259 Spy49_0260	6985043 6985044 6985045 6985046	C E NE NC	comX1.1	* *			transposase hypothetical protein M5005_Spy_0255 competence-specific sigma factor transposase, partial transposase hypothetical protein M5005_Spy_0259 lipase GTP-binding protein YgeH RNA-binding protein nicotinic acid mononucleotide adenylyltransferase
M5005_Spy_0256 M5005_Spy_0257 M5005_Spy_0258 M5005_Spy_0259 M5005_Spy_0260 M5005_Spy_0261 M5005_Spy_0262 M5005_Spy_0263 M5005_Spy_0263	3572657 3572658 3572659 3572660 3572661 3572662 3572630 3572631 3572632	NE NE NC E C NE E NE	Spy49_0256 Spy49_0257 Spy49_0258 Spy49_0259 Spy49_0260 Spy49_0261	6985043 6985044 6985045 6985046 6985047	C E NE NC NE	- - - -	* * *			transposase hypothetical protein M5005_Spy_0255 competence-specific sigma factor transposase, partial transposase hypothetical protein M5005_Spy_0259 lipase GTP-binding protein YqeH RNA-binding protein nicotinic acid monoucleotide adenylyltransferase HAD superfamily hydrolase
M5005_Spy_0256 M5005_Spy_0257 M5005_Spy_0258 M5005_Spy_0259 M5005_Spy_0260 M5005_Spy_0261 M5005_Spy_0262 M5005_Spy_0264 M5005_Spy_0264 M5005_Spy_0264	3572657 3572658 3572659 3572660 3572661 3572662 3572630 3572631 3572632 3572633	NE NE NC E C NE E	Spy49_0256 Spy49_0257 Spy49_0258 Spy49_0259 Spy49_0260	6985043 6985044 6985045 6985046	C E NE NC	- - - -	* * * *			transposase hypothetical protein M5005_Spy_0255 competence-specific sigma factor transposase, partial transposase hypothetical protein M5005_Spy_0259 lipase GTP-binding protein YgeH RNA-binding protein nicotinic acid mononucleotide adenylyltransferase
M5005_Spy_0256 M5005_Spy_0257 M5005_Spy_0258 M5005_Spy_0259 M5005_Spy_0260 M5005_Spy_0261 M5005_Spy_0262 M5005_Spy_0263 M5005_Spy_0263	3572657 3572658 3572659 3572660 3572661 3572662 3572630 3572631 3572632	NE NE NC E C NE E NE	Spy49_0256 Spy49_0257 Spy49_0258 Spy49_0259 Spy49_0260 Spy49_0261 Spy49_0262	6985043 6985044 6985045 6985046 6985047	C E NE NC NE	- - - -	* * * * * *			transposase hypothetical protein M5005_Spy_0255 competence-specific sigma factor transposase, partial transposase hypothetical protein M5005_Spy_0259 lipase GTP-binding protein YqeH RNA-binding protein nicotinic acid monoucleotide adenylyltransferase HAD superfamily hydrolase
M5005_Spy_0256 M5005_Spy_0257 M5005_Spy_0258 M5005_Spy_0259 M5005_Spy_0260 M5005_Spy_0261 M5005_Spy_0262 M5005_Spy_0264 M5005_Spy_0264 M5005_Spy_0264	3572657 3572658 3572659 3572660 3572661 3572662 3572630 3572631 3572632 3572633	NE NE NC E C NE E NE NE NE NE NE	Spy49_0256 Spy49_0257 Spy49_0258 Spy49_0260 Spy49_0260 Spy49_0262 Spy49_0262 Spy49_0263	6985042 6985043 6985044 6985045 6985046 6985047 6985048	C E NE NC NE NE	- - - -	* * * * * * * * *			transposase hypothetical protein M5005_Spy_0255 competence-specific sigma factor transposase, partial transposase hypothetical protein M5005_Spy_0259 lipase GTP-binding protein YqeH RNA-binding protein nicotinic acid mononucleotide adenylyltransferase HAD superfamily hydrolase iojap superfamily protein
M5005_Spy_0256 M5005_Spy_0258 M5005_Spy_0259 M5005_Spy_0269 M5005_Spy_0260 M5005_Spy_0261 M5005_Spy_0263 M5005_Spy_0264 M5005_Spy_0264 M5005_Spy_0266 M5005_Spy_0266 M5005_Spy_0266 M5005_Spy_0265 M5005_Spy_0265	3572657 3572658 3572659 3572660 3572661 3572662 3572630 3572631 3572632 3572633 3572634 3572634	NE NE NC E C NE E NE NE NE NE NE NE	Spy49_0256 Spy49_0257 Spy49_0258 Spy49_0259 Spy49_0260 Spy49_0261 Spy49_0262	6985042 6985043 6985044 6985045 6985046 6985047 6985048 6985049	C E NE NC NE NE NE NE	- - - -	:			transposase hypothetical protein M5005_Spy_0255 competence-specific sigma factor transposase, partial transposase hypothetical protein M5005_Spy_0259 lipase GTP-binding protein YqeH RNA-binding protein nicotinic acid mononucleotide adenylyltransferase HAD superfamily hyforlase iojap superfamily protein methyltransferase hypothetical protein M5005_Spy_0267
M5005_Spv_0256 M5005_Spv_0257 M5005_Spv_0259 M5005_Spv_0259 M5005_Spv_0260 M5005_Spv_0261 M5005_Spv_0263 M5005_Spv_0263 M5005_Spv_0264 M5005_Spv_0266 M5005_Spv_0266 M5005_Spv_0266 M5005_Spv_0266 M5005_Spv_0266 M5005_Spv_0266	3572657 3572658 3572659 3572660 3572661 3572662 3572630 3572631 3572632 3572633 3572634 3572634 3572636	NE NE NC E C NE E NE N	Spy49_0256 Spy49_0257 Spy49_0258 Spy49_0259 Spy49_0261 Spy49_0261 Spy49_0262 Spy49_0263 Spy49_0264	6985043 6985044 6985045 6985046 6985047 6985048 6985049 6985050	C E NE NC NE NE NE NE	- - - -	* * * * * * * * * * * * * * * * * * * *			transposase hypothetical protein M5005_Spy_0255 competence-specific sigma factor transposase, partial transposase hypothetical protein M5005_Spy_0259 lipase GTP-binding protein YgeH RNA-binding protein nicotinic acid mononucleotide adenylyltransferase HAD superfamily hydrolase iojap superfamily protein methyltransferase hypothetical protein M5005_Spy_0267 hypothetical protein M5005_Spy_0268
M5005_Spv_0256 M5005_Spv_0257 M5005_Spv_0259 M5005_Spv_0259 M5005_Spv_0260 M5005_Spv_0261 M5005_Spv_0261 M5005_Spv_0264 M5005_Spv_0264 M5005_Spv_0266 M5005_Spv_0266 M5005_Spv_0266 M5005_Spv_0266 M5005_Spv_0266 M5005_Spv_0268 M5005_Spv_0268	3572657 3572658 3572659 3572660 3572661 3572662 3572631 3572632 3572633 3572634 3572634 3572635 3572636 3572637	NE NE NC E C NE E NE N	Spy49_0256 Spy49_0257 Spy49_0258 Spy49_0259 Spy49_0260 Spy49_0261 Spy49_0263 Spy49_0264 Spy49_0264	6985043 6985044 6985045 6985046 6985047 6985048 6985049 6985050	C E NE NC NE NE NE NE NE	- - - - - - nadD - - - - -	*			transposase hypothetical protein M5005_Spy_0255 competence-specific sigma factor transposase, partial transposase hypothetical protein M5005_Spy_0259 lipase GTP-binding protein YqeH RNA-binding protein nicotinic acid mononucleotide adenylyltransferase HAD superfamily hydrolase iojap superfamily protein methyltransferase hypothetical protein M5005_Spy_0267 hypothetical protein M5005_Spy_0268 hypothetical protein M5005_Spy_0269
M5005_Spy_0256 M5005_Spy_0258 M5005_Spy_0259 M5005_Spy_0269 M5005_Spy_0261 M5005_Spy_0261 M5005_Spy_0264 M5005_Spy_0264 M5005_Spy_0264 M5005_Spy_0264 M5005_Spy_0266 M5005_Spy_0266 M5005_Spy_0266 M5005_Spy_0266 M5005_Spy_0266 M5005_Spy_0267 M5005_Spy_0267 M5005_Spy_0269 M5005_Spy_0269	3572657 3572658 3572659 3572660 3572661 3572662 3572630 3572631 3572632 3572634 3572634 3572635 3572636 3572636 3572636	NE NE NC E C NE E NE N	Spy49_0256 Spy49_0257 Spy49_0258 Spy49_0250 Spy49_0261 Spy49_0261 Spy49_0263 Spy49_0264 Spy49_0264 Spy49_0265 Spy49_0265	6985042 6985043 6985044 6985045 6985046 6985049 6985049 6985050 6985051 6985052	C E NE NC NE NE NE NE NE	- - - nadD - - - - - - - - - - - - - - - - - - -	*			transposase hypothetical protein M5005_Spy_0255 competence-specific sigma factor transposase, partial transposase hypothetical protein M5005_Spy_0259 lipase GTP-binding protein YqeH RNA-binding protein nicotinic acid mononucleotide adenylyltransferase HAD superfamily hydrolase iojap superfamily protein methyltransferase hypothetical protein M5005_Spy_0267 hypothetical protein M5005_Spy_0268 hypothetical protein M5005_Spy_0269 ABC transporter substrate-binding protein
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M5005_Spy_0256 M5005_Spy_0258 M5005_Spy_0259 M5005_Spy_0269 M5005_Spy_0261 M5005_Spy_0261 M5005_Spy_0264 M5005_Spy_0264 M5005_Spy_0264 M5005_Spy_0264 M5005_Spy_0266 M5005_Spy_0266 M5005_Spy_0266 M5005_Spy_0266 M5005_Spy_0266 M5005_Spy_0267 M5005_Spy_0267 M5005_Spy_0269 M5005_Spy_0269	3572657 3572658 3572659 3572660 3572661 3572662 3572630 3572631 3572632 3572634 3572634 3572635 3572636 3572636 3572636	NE NE NC E C NE E NE N	Spy49_0256 Spy49_0257 Spy49_0258 Spy49_0250 Spy49_0261 Spy49_0261 Spy49_0263 Spy49_0264 Spy49_0264 Spy49_0265 Spy49_0265	6985042 6985043 6985044 6985045 6985046 6985049 6985049 6985050 6985051 6985052	C E NE NC NE NE NE NE NE	- - - nadD - - - - - - - - - - - - - - - - - - -	*			transposase hypothetical protein M5005_Spy_0255 competence-specific sigma factor transposase, partial transposase hypothetical protein M5005_Spy_0259 lipase GTP-binding protein YqeH RNA-binding protein nicotinic acid mononucleotide adenylyltransferase HAD superfamily hydrolase iojap superfamily protein methyltransferase hypothetical protein M5005_Spy_0267 hypothetical protein M5005_Spy_0268 hypothetical protein M5005_Spy_0269 ABC transporter substrate-binding protein
M5005_Spv_0256 M5005_Spv_0257 M5005_Spv_0259 M5005_Spv_0259 M5005_Spv_0261 M5005_Spv_0261 M5005_Spv_0263 M5005_Spv_0264 M5005_Spv_0264 M5005_Spv_0265 M5005_Spv_0266 M5005_Spv_0268 M5005_Spv_0268 M5005_Spv_0269 M5005_Spv_0269 M5005_Spv_0269 M5005_Spv_0269 M5005_Spv_0269 M5005_Spv_0269 M5005_Spv_0270 M5005_Spv_0270	3572657 3572658 3572659 3572659 3572661 3572661 3572631 3572631 3572632 3572633 3572635 3572636 3572636 3572636 3572637 3572638	NE NE NC E C NE E NE N	Spy49_0256 Spy49_0257 Spy49_0258 Spy49_0260 Spy49_0260 Spy49_0263 Spy49_0263 Spy49_0264 Spy49_0265 Spy49_0266 Spy49_0266	6985042 6985043 6985044 6985045 6985046 6985047 6985048 6985049 6985050 6985051 6985052 6985053	C E NE NC NE NE NE NE NE NC NE	nadD	* *			transposase hypothetical protein M5005_Spy_0255 competence-specific sigma factor transposase, partial transposase hypothetical protein M5005_Spy_0259 lipase GTP-binding protein YqeH RNA-binding protein nicotinic acid mononucleotide adenylyltransferase HAD superfamily hydrolase iojap superfamily protein methyltransferase hypothetical protein M5005_Spy_0267 hypothetical protein M5005_Spy_0268 hypothetical protein M5005_Spy_0269 ABC transporter substrate-binding protein ABC transporter substrate-binding protein
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M5005_Spv_0256 M5005_Spv_0258 M5005_Spv_0259 M5005_Spv_0259 M5005_Spv_0260 M5005_Spv_0261 M5005_Spv_0261 M5005_Spv_0263 M5005_Spv_0264 M5005_Spv_0264 M5005_Spv_0268 M5005_Spv_0268 M5005_Spv_0268 M5005_Spv_0269 M5005_Spv_0269 M5005_Spv_0273 M5005_Spv_0273 M5005_Spv_0273 M5005_Spv_0273 M5005_Spv_0274 M5005_Spv_0274 M5005_Spv_0278 M5005_Spv_0280 M5005_Spv_0280 M5005_Spv_0280 M5005_Spv_0280 M5005_Spv_0288	3572652 3572658 3572659 3572661 3572661 3572661 3572633 3572631 3572633 3572633 3572633 3572633 3572634 3572634 3572642 3572644 3572642 3572644 3572644 3572642 3572643 3572641 3572641 3572641 3572641 3572641 3572641 3572641 3572641 3572641 3572641 3572641 3572641 3572611 3572611	NE NE C NE E NE NE NE NE C NE E E E E E	Spy49_0256 Spy49_0257 Spy49_0258 Spy49_0260 Spy49_0261 Spy49_0262 Spy49_0263 Spy49_0266 Spy49_0266 Spy49_0270 Spy49_0270 Spy49_0272 Spy49_0272 Spy49_0272 Spy49_0273 Spy49_0274 Spy49_0274 Spy49_0276 Spy49_0276 Spy49_0278 Spy49_0280 Spy49_0280 Spy49_0280 Spy49_0280 Spy49_0280 Spy49_0286 Spy49_0286 Spy49_0286 Spy49_0286 Spy49_0286 Spy49_0286 Spy49_0286	6985042 6985043 6985044 6985045 6985045 6985046 6985050 6985051 6985051 6985051 6985052 6985053 6985056	C E NE N	nadD nadD atmA atmB atmB braB gidB lemA htpX - covR covS nrdR dnaI engA snf murC	* * * * * *	SSA_1806 SSA_1805 SSA_1803	SP_1713 SP_1712 SP_1711 SP_1709 SP_1521	transposase hypothetical protein M5005_Spy_0255 competence-specific sigma factor transposase, partial transposase hypothetical protein M5005_Spy_0259 lipase GTP-binding protein YqeH RNA-binding protein ricotinic acid mononucleotide adenylyltransferase HAD superfamily hyrotolase iojap superfamily protein methyltransferase hypothetical protein M5005_Spy_0267 hypothetical protein M5005_Spy_0268 hypothetical protein M5005_Spy_0268 hypothetical protein M5005_Spy_0269 ABC transporter substrate-binding protein ABC transporter substrate-binding protein ABC transporter aTP-binding protein ABC transporter Fare-binding protein ABC transporter permease branched-chain amino acid transporter carrier protein senine/threonine transporter SstT potassium uptake protein 16S rRNA methyltransferase GidB hypothetical protein M5005_Spy_0279 heat shock protein HtpX hypothetical protein M5005_Spy_0281 response regulator transmembrane histidine kinase NrdR family transcriptional regulator replicative DNA helicase primosomal protein DnaI GTP-binding protein EngA SWF/SNF family helicase hypothetical protein M5005_Spy_0289 UDP-N-acetylmuramateL-alanine ligase acetyltransferase
M5005_Spy_0256 M5005_Spy_0258 M5005_Spy_0259 M5005_Spy_0259 M5005_Spy_0261 M5005_Spy_0261 M5005_Spy_0263 M5005_Spy_0263 M5005_Spy_0264 M5005_Spy_0265 M5005_Spy_0266 M5005_Spy_0266 M5005_Spy_0266 M5005_Spy_0266 M5005_Spy_0268 M5005_Spy_0269 M5005_Spy_0271 M5005_Spy_0271 M5005_Spy_0271 M5005_Spy_0274 M5005_Spy_0274 M5005_Spy_0274 M5005_Spy_0276 M5005_Spy_0276 M5005_Spy_0276 M5005_Spy_0276 M5005_Spy_0276 M5005_Spy_0276 M5005_Spy_0276 M5005_Spy_0279 M5005_Spy_0278 M5005_Spy_0278 M5005_Spy_0278 M5005_Spy_0278 M5005_Spy_0278 M5005_Spy_0284 M5005_Spy_0284 M5005_Spy_0284 M5005_Spy_0284 M5005_Spy_0284 M5005_Spy_0284 M5005_Spy_0284 M5005_Spy_0284 M5005_Spy_0284 M5005_Spy_0288 M5005_Spy_0288 M5005_Spy_0288 M5005_Spy_0288 M5005_Spy_0288 M5005_Spy_0288 M5005_Spy_0288 M5005_Spy_0288 M5005_Spy_0289 M5005_Spy_0289 M5005_Spy_0289 M5005_Spy_0289	3572652 3572658 3572659 3572660 3572661 3572661 3572632 3572633 3572633 3572634 3572635 3572636 3572636 3572636 3572640 3572644 3572644 3572644 3572645 3572649 3572641 3572645 3572641 3572645 3572641 3572645 3572646 3572646 3572646 3572646 3572646 3572645 3572646	NE NE C NE E NE NE NE NE NE C NE E NE E	Spy49_0256 Spy49_0258 Spy49_0258 Spy49_0260 Spy49_0261 Spy49_0262 Spy49_0264 Spy49_0264 Spy49_0266 Spy49_0276 Spy49_0271c Spy49_0271c Spy49_0271c Spy49_0272 Spy49_0273 Spy49_0276 Spy49_0276 Spy49_0278 Spy49_0278 Spy49_0278 Spy49_0278 Spy49_0278 Spy49_0278 Spy49_0278 Spy49_0278 Spy49_0278 Spy49_0278 Spy49_0278 Spy49_0278 Spy49_0278 Spy49_0278 Spy49_0278 Spy49_0280	6985042 6985043 6985044 6985045 6985045 6985047 6985047 6985052 6985051 6985052 6985053 6985055 6985055 6985056 6985056 6985056 6985056 6985056 6985056 6985056 6985056 6985057 6985060 698506	C E NE N	atmA atmB atmD atmE braB gidB lemA htpX covS nrdR dnaB dnaI engA snf murC	* * * * * *	SSA_1806 SSA_1805 SSA_1803	SP_1713 SP_1712 SP_1711 SP_1709 SP_1521	transposase hypothetical protein M5005_Spy_0255 competence-specific sigma factor transposase, partial transposase hypothetical protein M5005_Spy_0259 lipase GTP-binding protein YqeH RNA-binding protein ricotinic acid monoucleotide adenylyltransferase HAD superfamily hydrolase iojap superfamily protein methyltransferase hypothetical protein M5005_Spy_0267 hypothetical protein M5005_Spy_0268 hypothetical protein M5005_Spy_0268 hypothetical protein M5005_Spy_0269 ABC transporter substrate-binding protein ABC transporter sporter sets branched-chain amino acid transporter carrier protein serine/threonine transporter SstT potassium uptake protein 165 rRNA methyltransferase GidB hypothetical protein M5005_Spy_0279 heat shock protein HtpX hypothetical protein M5005_Spy_0281 response regulator transmembrane histidine kinase NrdR family transcriptional regulator replicative DNA helicase primosomal protein DnaI GTP-binding protein EngA SWF/SNF family helicase hypothetical protein M5005_Spy_0289 UDP-N-acetylmuramateL-alanine ligase acetyltransferase aminodeoxychorismate lyase
M5005_Spy_0256 M5005_Spy_0258 M5005_Spy_0259 M5005_Spy_0259 M5005_Spy_0259 M5005_Spy_0260 M5005_Spy_0260 M5005_Spy_0261 M5005_Spy_0262 M5005_Spy_0262 M5005_Spy_0263 M5005_Spy_0265 M5005_Spy_0267 M5005_Spy_0267 M5005_Spy_0267 M5005_Spy_0267 M5005_Spy_0273 M5005_Spy_0273 M5005_Spy_0273 M5005_Spy_0273 M5005_Spy_0274 M5005_Spy_0278 M5005_Spy_0283 M5005_Spy_0283 M5005_Spy_0284 M5005_Spy_0285	3572652 3572658 3572659 3572660 3572661 3572661 3572631 3572632 3572633 3572633 3572636 3572636 3572636 3572636 3572636 3572640 3572642 3572642 3572644 3572645 3572644 3572646 3572641 3572641 3572641 3572641 3572641 3572641 3572641 3572641 3572641 3572643 3572641 3572643 3572641 3572643 3572641 3572613 3572611 3572616 3572616 3572616 3572618 3572618	NE NEC O NE E NE NE NE NE NE C NE E E E E NE E E NE C NE E NE E NE C NE NE NE E E E	Spy49_0256 Spy49_0258 Spy49_0258 Spy49_0260 Spy49_0261 Spy49_0262 Spy49_0264 Spy49_0264 Spy49_0266 Spy49_0276 Spy49_0271c Spy49_0271c Spy49_0271c Spy49_0272 Spy49_0273 Spy49_0276 Spy49_0276 Spy49_0278 Spy49_0278 Spy49_0278 Spy49_0278 Spy49_0278 Spy49_0278 Spy49_0278 Spy49_0278 Spy49_0278 Spy49_0278 Spy49_0278 Spy49_0278 Spy49_0278 Spy49_0278 Spy49_0278 Spy49_0280	6985042 6985043 6985044 6985045 6985045 6985047 6985047 6985052 6985051 6985052 6985053 6985055 6985055 6985056 6985056 6985056 6985056 6985056 6985056 6985056 6985056 6985057 6985060 698506	C E NE N	atmA atmB atmD atmE braB gidB lemA htpX covS nrdR dnaB dnaI engA snf murC	* * * * * *	SSA_1806 SSA_1805 SSA_1803	SP_1713 SP_1712 SP_1711 SP_1709 SP_1521	transposase hypothetical protein M5005_Spy_0255 competence-specific sigma factor transposase, partial transposase hypothetical protein M5005_Spy_0259 lipase GTP-binding protein YqeH RNA-binding protein nicotinic acid mononucleotide adenylyltransferase HAD superfamily hydrolase iojap superfamily protein methyltransferase hypothetical protein M5005_Spy_0267 hypothetical protein M5005_Spy_0268 hypothetical protein M5005_Spy_0269 ABC transporter substrate-binding protein ABC transporter substrate-binding protein ABC transporter ATP-binding protein ABC transporter substrate-binding protein ABC transporter and cid transporter carrier protein serine/threonine transporter SstT potassium uptake protein potassium uptake protein 165 rRNA methyltransferase GidB hypothetical protein M5005_Spy_0279 heat shock protein M5005_Spy_0279 heat shock protein M5005_Spy_0281 response regulator transmembrane histidine kinase NrdR family transcriptional regulator replicative DNA helicase primosomal protein Dnal GTP-binding protein EngA SWF/SNF family helicase hypothetical protein M5005_Spy_0289 UDP-N-acetylmuramateL-alanine ligase acetyltransferase aminodeoxychorismate lyase transcription elongation factor GreA

M5005_Spy_0295c	3572624	E	Spy49_0291	6985156	Е	oxaA	*		SP_1975	OxaA-like protein precursor
M5005_Spy_0296c		NE	Spy49_0292c	6985157	NE	-	*			acylphosphatase
M5005_Spy_0297c		NE				-				transposase transposase
M5005_Spy_0298c M5005_Spy_0299	3572627 3572628	NE NE	Spy49_0293	6985158	NE	-	*			23S rRNA methyltransferase
M5005_Spy_0300	3572629	NE	Spy49_0294	6985159	NE	-	*			HAD superfamily hydrolase
M5005_Spy_0301	3572591	NE	Spy49_0295	6985160	NC	-	*			hypothetical protein M5005_Spy_0301
M5005_Spy_0302	3572592 3572593	C	Spy49_0296	6985161 6985162	NC	- ale	*	CCA 1704	CD 1001	hypothetical protein M5005_Spy_0302 glutamate racemase
M5005_Spy_0303	3372333	E	Spy49_0297	0503102	E	glr	-	SSA_1784	SP_1881	deoxyribonucleotide triphosphate pyrophosphatase/unknown domain fusion
M5005_Spy_0304	3572594	NE	Spy49_0298	6985163	NE	-	*			protein
M5005_Spy_0305 M5005_Spy_0306	3572595 3572596	NE	Spy49_0299	6985164 6985165	NE	-	*			phosphoesterase hypothetical protein M5005_Spy_0306
M5005_Spy_0307	3572597	NE NE	Spy49_0300 Spy49_0301	6985166	NE NE	xerD	*			site-specific tyrosine recombinase XerD
M5005_Spy_0308	3572598	NE	Spy49_0302	6985167	NE	scpA	*			segregation and condensation protein A
M5005_Spy_0309	3572599	NE	Spy49_0303	6985168	NE	scpB	*			segregation and condensation protein B
M5005_Spy_0310 M5005_Spy_0311	3572600 3572601	NE NE	Spy49_0304 Spy49_0305	6985169 6985170	NE NE	rluB	*			ribosomal large subunit pseudouridine synthase B hypothetical protein M5005_Spy_0311
M5005_Spy_0312	3572602	NE	Spy49_0306	6985171	NE	-	*			23S rRNA methyltransferase
M5005_Spy_0313	3572603	С	Spy49_0307	6985172	NE	-	*			riboflavin transporter
M5005_Spy_0314	3572604	NE	Spy49_0308	6985173	NE	-	*			phosphatidylglycerophosphatase B
M5005_Spy_0315 M5005_Spy_0316	3572605 3572606	NE NE	Spy49_0309 Spy49_0310	6985174 6985175	NE NE	-	*			Fe-S oxidoreductase SAM-dependent methyltransferase
M5005_Spy_0317	3572607	NE	Spy49_0311	6985176	NE	hlyX	*			hemolysin
M5005_Spy_0318	3572608	NE	Spy49_0312	6985177	NE	pfIC	*			pyruvate formate-lyase activating enzyme
M5005_Spy_0319	3572609	NC	Spy49_0313	6985178	E	ppaC	*	SSA_1748	SP_1534	manganese-dependent inorganic pyrophosphatase
M5005_Spy_0320 M5005_Spy_0321c	3572610 3572572	NE NE	Spy49_0314 Spy49_0315	6985179 6985180	NE NE	fhuG	*			hypothetical protein M5005_Spy_0320 ferrichrome transporter permease
M5005_Spy_0322c		NE	Spy49_0316	6985181	NE	fhuB	*			ferrichrome transporter permease
M5005_Spy_0323c		NE	Spy49_0317c	6985182	NE	fhuD	*			ferrichrome-binding protein
M5005_Spy_0324c M5005_Spy_0325c		NE	Spy49_0318	6985183 6985184	NE	fhuA murE	*	CCA 1720	CD 1530	ferrichrome ABC transporter ATP-binding protein UDP-N-acetylmuramoylalanyl-D-glutamateL-lysine ligase
M5005_Spy_0326	3572577	E E	Spy49_0319c Spy49_0320	6985185	E E	-	*	SSA_1739 SSA_1738	SP_1530 SP_1529	export protein for polysaccharides and teichoic acids
M5005_Spy_0327	3572578	NE	Spy49_0322	6985186	NE	upp	*		o	uracil phosphoribosyltransferase
M5005_Spy_0328	3572579	С	Spy49_0323	6985187	E	clpP	*			ATP-dependent Clp protease proteolytic subunit
M5005_Spy_0329 M5005_Spy_0330	3572580 3572581	NE E	Spy49_0325	6985188 6985189	NE E	tmk	*	CCA 1722	CD 002F	hypothetical protein M5005_Spy_0329 thymidylate kinase
M5005_Spy_0330	3572582	E	Spy49_0326 Spy49_0327	6985190	E	dnaX	*	SSA_1722 SSA_1721	SP_0935	DNA polymerase III subunit delta\'
M5005_Spy_0332	3572583	NE	367.13_0327		-	-		55/(_1/21		tpl protein
M5005_Spy_0333	3572584	NC	Spy49_0328	6985191	NC	-				signal peptidase-like protein
M5005_Spy_0334 M5005_Spy_0335	3572585 3572586	NC	Spy49_0329	6985192 6985193	C C	-	*		SP_0937	DNA replication intiation control protein YabA corrin/porphyrin methyltransferase
M5005_Spy_0336	3572587	NE NE	Spy49_0330 Spy49_0331	6985194	NE	-	*			hypothetical protein M5005_Spy_0336
M5005_Spy_0337c		NE	Spy49_0332c	6985195	NE	cutC	*			copper homeostasis protein
M5005_Spy_0338	3572589	NE	Spy49_0333	6985196	NE	-	*			arsenate reductase
M5005_Spy_0339c M5005_Spy_0340	3572590 3572552	NC NE	Spy49_0334c	6985197 6985198	NE NE	exoA lctO	*			exodeoxyribonuclease III L-lactate oxidase
M5005_Spy_0340	3572553	NE	Spy49_0335 Spy49_0336	6985199	NE	prtS	*			lactocepin
M5005_Spy_0343	3572554	NE				-				hypothetical protein M5005_Spy_0343
M5005_Spy_0344	3572555	NE	Spy49_0337	6985200	NE	-	*			permease
M5005_Spy_0345 M5005_Spy_0346	3572556 3572557	E NC	Spy49_0338	6985201	Е	metG	*	SSA_1703	SP_0788	methionyl-tRNA synthetase hypothetical protein M5005_Spy_0346
M5005_Spy_0347	3572558	NE	Spy49_0339	6985202	NE	nrdF	*			ribonucleotide-diphosphate reductase subunit beta
M5005_Spy_0348	3572559	NE	Spy49_0340	6985203	NE	nrdI	*			ribonucleotide reductase stimulatory protein
M5005_Spy_0349	3572560	NE	Spy49_0341	6985204	NE	nrdE.1	*			ribonucleotide-diphosphate reductase subunit alpha
M5005_Spy_0350 M5005_Spy_0351c	3572561 3572562	NC NE	Spy49_0342c	6985205	NE	spyA	*			hypothetical protein M5005_Spy_0350 C3 family ADP-ribosyltransferase
M5005_Spy_0351c	3572563	NE	Spy49_03420 Spy49_0343	6985206	NC	-				hypothetical protein M5005_Spy_0352
M5005_Spy_0353	3572564	NE	Spy49_0344	6985207	NC	-				hypothetical protein M5005_Spy_0353
M5005_Spy_0354c		NE	Spy49_0345c	6985208	NE	-				hypothetical protein M5005_Spy_0354 hypothetical protein M5005_Spy_0355
M5005_Spy_0355 M5005_Spy_0356c	3572566 3572567	NE NE	Spy49_0346c Spy49_0347	6985209 6985210	NE NE	speJ				exotoxin type J
M5005_Spy_0357c		NE	Spy49_0348	6985211	NE	-				hypothetical protein M5005_Spy_0357
M5005_Spy_0358		NE	Spy49_0349c	6985212	NE	-				hypothetical protein M5005_Spy_0358
			Spy49_0350c	6985213	NE					
			Spy49_0351c Spy49_0352c	6985214 6985215	NE NE					
			Spy49_0353c	6985216	NE					
			Spy49_0354c		NC					
			Spy49_0355c	6985218	NE					
			Spy49_0356c Spy49_0357c	6985219 6985220	NE NE					
			Spy49_0358c	6985221	NE					
			Spy49_0359c	6985222	NE					
			Spy49_0360c Spy49_0361c	6985303 6985304	NE NE					
			Spy49_0362c	6985305	NE					
			Spy49_0363c	6985306	NE					
			Spy49_0364c	6985307	NC					
			Spy49_0365c	6985308 6985309	NE					
			Spy49_0366c Spy49_0367c	6985310	NE NE					
			Spy49_0368c	6985311	NE					
			Spy49_0369	6985312	Е					
			Spy49_0370	6985313 6985314	NE NE					
M5005_Spy_0359	3572570	NE	Spy49_0371 Spy49_0372	6985314	NE NE	fabG	*			3-ketoacyl-ACP reductase
M5005_Spy_0360	3572571	NE	Spy49_0373	6985316	NE	-	*			NAD-dependent oxidoreductase
M5005_Spy_0361	3572533	NE	Spy49_0374	6985317	NE	glpT	*			phosphoglycerate transporter protein
M5005_Spy_0362	3572534	Е	Spy49_0375	6985318	Е	glmU	*	SSA_1642	SP_0988	bifunctional N-acetylglucosamine-1-phosphate uridyltransferase/glucosamine- 1-phosphate acetyltransfe
M5005_Spy_0363	3572535	NE	Spy49_0376	6985319	NE	-	*			phosphohydrolase
M5005_Spy_0364	3572536	NC	Spy49_0377	6985320	NE					hypothetical protein M5005_Spy_0364
M5005_Spy_0365 M5005_Spy_0366	3572537 3572538	E NE	Spy49_0378	6985321 6985322	NC NE	pfs	*		SP_0991	5\'-methylthioadenosine/S-adenosylhomocysteine nucleosidase hypothetical protein M5005_Spy_0366
M5005_Spy_0367c		NC	Spy49_0379 Spy49_0380c	6985323	NC	mtsR	*			iron-dependent repressor
M5005_Spy_0368	3572540	NE	Spy49_0381	6985324	NE	mtsA	*			manganese-binding protein
M5005_Spy_0369	3572541	NE	Spy49_0382	6985325	NE	mtsB	*			manganese transporter ATP-binding protein
M5005_Spy_0370 M5005_Spy_0371c	3572542 3572543	NE NE	Spy49_0383 Spy49_0384c	6985326 6985327	NE NE	mtsC cypB	*			manganese transporter membrane protein peptidyl-prolyl cis-trans isomerase
M5005_Spy_03710	3572544	E E	Spy49_0384c Spy49_0385	6985328	E	ftsK	*		SP_0878	cell division protein
M5005_Spy_0373c	3572545	NE	Spy49_0386c	6985329	NE	-				hypothetical protein M5005_Spy_0373
M5005_Spy_0374	3572546	NC	Spy49_0387	6985330	NC	rplK	*			50S ribosomal protein L11

M5005_Spy_0375	3572547	E	Spy49_0388	6985331	E	rpIA	*	SSA_1622		50S ribosomal protein L1
M5005_Spy_0376	3572548	NE				-				transposase
M5005_Spy_0377	3572549	E	Spy49_0390	6985332	E	pyrH	*	SSA_1620	SP_0944	uridylate kinase
M5005_Spy_0380	3572513	E	Spy49_0391	6985333	E	frr	*	SSA_1619	SP_0945	ribosome recycling factor
M5005_Spy_0381	3572514	NE	Spy49_0392	6985334	NE	-	*			S1 RNA-binding domain-containing protein
M5005_Spy_0382	3572515	NE	Spy49_0394	6985335	NE	msrA.2	*			methionine sulfoxide reductase A
M5005_Spy_0383	3572516	NE	Spy49_0395	6985336	NE	-				hypothetical protein M5005_Spy_0383
M5005_Spy_0384	3572517	NE	Spy49_0396	6985337	NE	-	*			surface antigen
M5005_Spy_0385	3572518	NE	Spy49_0398	6985338	NE	-				hypothetical protein M5005_Spy_0385
M5005_Spy_0386	3572519	NE	Spy49_0399	6985339	NE	phoH	*			phoH protein
M5005_Spy_0387	3572520	NE	Spy49_0400	6985340	NE	-	*			uracil DNA glycosylase
M5005_Spy_0388	3572521	E	Spy49_0401	6985341	E	-	*		SP_0967	metalloprotease
M5005_Spy_0389	3572522	E	Spy49_0402	6985342	E	dgk	*		SP_0968	diacylglycerol kinase
M5005_Spy_0390	3572523	С	Spy49_0403	6985343	E	era	*			GTP-binding protein Era
M5005_Spy_0391	3572524	NE	Spy49_0404	6985344	NE	-	*			phosphohydrolase
M5005_Spy_0392c	3572525	NE	Spy49_0405c	6985345	NE	-				hypothetical protein M5005_Spy_0392
M5005_Spy_0393	3572526	NE	Spy49_0406	6985346	NE	-				hypothetical protein M5005_Spy_0393
M5005_Spy_0394	3572527	NE				-				hypothetical protein M5005_Spy_0394
M5005_Spy_0395c	3572528	NE				-				transposase
M5005_Spy_0396c	3572529	NC	Spy49_0407c		NC	-				transposase
M5005_Spy_0397c	3572530	NE	Spy49_0408c	6985348	NE	-				transposase
M5005_Spy_0398	3572531	NE	Spy49_0409	6985349	NE	-				bacteriocin
M5005_Spy_0399	3572532	NE	Spy49_0410	6985350	NE	-				hypothetical protein M5005_Spy_0399
M5005_Spy_0400	3572494	NE	Spy49_0411	6985351	NE	silD				hypothetical protein M5005_Spy_0400
M5005_Spy_0401c	3572495	NC	Spy49_0412	6985352	NC	-				hypothetical protein M5005_Spy_0401
M5005_Spy_0402	3572496	NE	Spy49_0413	6985353	NE	-				hypothetical protein M5005_Spy_0402
M5005_Spy_0403	3572497	NE	Spy49_0414c	6985354	NE	-				hypothetical protein M5005_Spy_0403
M5005_Spy_0404c	3572498	NE				-				hypothetical protein M5005_Spy_0404 hypothetical protein M5005_Spy_0405
M5005_Spy_0405 M5005_Spy_0406c	3572499 3572500	NC				-				hypothetical protein M5005_Spy_0405
M5005_Spy_0400C	3572501	NE NE	Spy49 0415	6985355	NE	mutR				transcriptional regulator
M5005_Spy_0407	3572502	NE	Spy49_0415 Spy49_0416	6985356	NE	fpg				formamidopyrimidine-DNA glycosylase
M5005_Spy_0409	3572503	E	Spy49_0417	6985357	E	coaE	*	CCA 1606	SP_0971	dephospho-CoA kinase
M5005_Spy_0409	3572504		Spy49_0418	6985358		- COUL	*	SSA_1606	3F_03/1	ATPase
M5005_Spy_0410	3572505	NE NE	Spy49_0418	6985359	NC NE		*			multidrug resistance protein B
M5005_Spy_0411	3572506	NC	Spy49_0420	6985360	NC	rpmG				50S ribosomal protein L33
M5005_Spy_0412	3572507	E	Spy49_0421	6985361	NC	secG		SSA_1604		preprotein translocase subunit SecG
M5005_Spy_0414	3572508	NE	Spy49_0422	6985362	NC	vacB	*	33A_1004		exoribonuclease II
M5005_Spy_0415	3572509	NC	Spy49_0423	6985363	NC	smpB	*			SsrA-binding protein
M5005_Spy_0416	3572510	NE	Spy49_0424	6985364	NE	- -	*			glutaminyl-peptide cyclotransferase
M5005_Spy_0417c	3572511	NE	Spy49_0425c	6985365	NE	рср	*			pyrrolidone-carboxylate peptidase
M5005_Spy_0418c	3572512	NE	Spy49_0426c	6985366	NE	-	*			permease
M5005 Spy 0419c		NE	Spy49_0427c	6985367	NE	_	*			permease
M5005_Spy_0420c	3572475	NE	Spy49_0428c	6985368	NE	-	*			glucosyltransferase
M5005_Spy_0421c	3572476	NE	Spy49_0429c	6985369	NE	gloA	*			lactoylglutathione lyase
M5005_Spy_0422c	3572477	NE	Spy49_0430c	6985370	NE	-	*			NAD(P)H-dependent quinone reductase
M5005_Spy_0423c	3572478	NE	Spy49_0431c	6985371	NE	pepQ	*			Xaa-Pro dipeptidase
M5005_Spy_0424	3572479	NC	Spy49_0432	6985372	E	ссрА	*			catabolite control protein A
M5005_Spy_0425	3572480	С	Spy49_0433	6985373	E	-	*		SP_1075	glycosyltransferase
M5005_Spy_0426	3572481	E	Spy49_0434	6985374	E	-	*			1,2-diacylglycerol 3-glucosyltransferase
M5005_Spy_0427	3572482	E	Spy49_0435	6985375	E	thrS	*	SSA_1571	SP_1631	threonyl-tRNA synthetase
M5005_Spy_0428	3572483	NE	Spy49_0436	6985376	NE	drrA/tagH	*			daunorubicin resistance ATP-binding protein
M5005_Spy_0429	3572484	NE	Spy49_0437	6985377	NE	-	*			daunorubicin resistance transmembrane protein
M5005_Spy_0430	3572485	NE	Spy49_0438	6985378	NE	-	*			ABC transporter permease
M5005_Spy_0431	3572486	NC	Spy49_0439	6985379	NC	-				dihydroxyacetone kinase
M5005_Spy_0432	3572487	NE	Spy49_0440	6985380	NE	-	*			acetyl-CoA acetyltransferase
M5005_Spy_0433	3572488	NE	Spy49_0441	6985381	NE	-	*			long-chain-fatty-acidCoA ligase
M5005_Spy_0434	3572489	NE	Spy49_0442	6985382	NE	-	*			hypothetical protein M5005_Spy_0434
M5005_Spy_0435	3572490	E	Spy49_0444	6985463	E	vicR	*	SSA_1565	SP_1227	two-component response regulator
M5005_Spy_0436	3572491	NE	Spy49_0445	6985464	NE	vicK	*			two-component sensor histidine kinase
M5005_Spy_0437 M5005_Spy_0438	3572492	NE	Spy49_0446	6985465	NE	vicX	*		CD 4240	Zn-dependent hydrolase ribonuclease III
M5005_Spy_0438 M5005_Spy_0439	3572493 3572455	C	Spy49_0447	6985466	NC	rnc smc			SP_1248	chromosome partition protein
M5005_Spy_0439	3572456 3572456	NE	Spy49_0448	6985467	NC NE	SHIC	*			transcriptional regulator
M5005_Spy_04400	3572457	NE NE	Spy49_0449c Spy49_0450	6985468 6985469	NE	aroE	*			shikimate 5-dehydrogenase
M5005_Spy_0442	3572458	NE	Spy49_0451	6985470	NE	-	*			
M5005_Spy_0443	3572459	NE	Spy49_0453	6985471	NC	-	*			hynothetical protein M5005 Spy 0442
M5005_Spy_0444	3572460	NE	Spy49_0454	6985472						hypothetical protein M5005_Spy_0442
M5005_Spy_0445	3572461	NE				_	*			hypothetical protein M5005_Spy_0443
M5005_Spy_0446	3572462		SDV49 (1455		NE NF	- metK1	*			hypothetical protein M5005_Spy_0443 hypothetical protein M5005_Spy_0444
		NE	Spy49_0455 Spy49_0456	6985473	NE	metK1	*			hypothetical protein M5005_Spy_0443 hypothetical protein M5005_Spy_0444 S-adenosylmethionine synthetase
M5005_Spy_0447	3572463	NE NE	Spy49_0456			metK1 -	* * *			hypothetical protein M5005_Spy_0443 hypothetical protein M5005_Spy_0444
		NE NC		6985473 6985474	NE NE	- metK1 - -	* * *			hypothetical protein M5005_Spy_0443 hypothetical protein M5005_Spy_0444 5-adenosylmethionine synthetase hypothetical protein M5005_Spy_0446
M5005_Spy_0447	3572463	NE	Spy49_0456 Spy49_0457	6985473 6985474 6985475	NE NE NE	-	* * *			hypothetical protein M5005_Spy_0443 hypothetical protein M5005_Spy_0444 S-adenosylmethionine synthetase hypothetical protein M5005_Spy_0446 cell wall biosynthesis glycosyltransferase
M5005_Spy_0447 M5005_Spy_0448	3572463 3572464	NE NC	Spy49_0456 Spy49_0457 Spy49_0458	6985473 6985474 6985475 6985476	NE NE NE NE	- - -	* * *			hypothetical protein M5005_Spy_0443 hypothetical protein M5005_Spy_0444 S-adenosylmethionine synthetase hypothetical protein M5005_Spy_0446 cell wall biosynthesis glycosyltransferase hypothetical protein M5005_Spy_0448
M5005_Spy_0447 M5005_Spy_0448 M5005_Spy_0449 M5005_Spy_0450	3572463 3572464 3572465 3572466	NE NC NE	Spy49_0456 Spy49_0457 Spy49_0458 Spy49_0459	6985473 6985474 6985475 6985476 6985477	NE NE NE NE	- - - hasB.2	* * *			hypothetical protein M5005_Spy_0443 hypothetical protein M5005_Spy_0444 S-adenosylmethionine synthetase hypothetical protein M5005_Spy_0446 cell wall biosynthesis glycosyltransferase hypothetical protein M5005_Spy_0448 UDP-glucose 6-dehydrogenase
M5005_Spy_0447 M5005_Spy_0448 M5005_Spy_0449 M5005_Spy_0450	3572463 3572464 3572465 3572466	NE NC NE NE	Spy49_0456 Spy49_0457 Spy49_0458 Spy49_0459 Spy49_0460	6985474 6985475 6985476 6985477 6985478	NE NE NE NE NE	- - - hasB.2	* * * *			hypothetical protein M5005_Spy_0443 hypothetical protein M5005_Spy_0444 S-adenosylmethionine synthetase hypothetical protein M5005_Spy_0446 cell wall biosynthesis glycosyltransferase hypothetical protein M5005_Spy_0448 UDP-glucose 6-dehydrogenase macrolide-efflux protein
M5005_Spy_0447 M5005_Spy_0448 M5005_Spy_0449 M5005_Spy_0450 M5005_Spy_0451c M5005_Spy_0452c M5005_Spy_0453c	3572464 3572465 3572466 3572467 3572468 3572469	NE NC NE NE NE	Spy49_0456 Spy49_0457 Spy49_0458 Spy49_0459 Spy49_0460 Spy49_0461c Spy49_0462c Spy49_0463c	6985473 6985474 6985475 6985476 6985477 6985478 6985479 6985480 6985481	NE NE NE NE NE NE	- - - hasB.2	* * * * *			hypothetical protein M5005_Spy_0443 hypothetical protein M5005_Spy_0444 S-adenosylmethionine synthetase hypothetical protein M5005_Spy_0446 cell wall biosynthesis glycosyltransferase hypothetical protein M5005_Spy_0448 UDP-glucose 6-dehydrogenase macrolide-efflux protein transcriptional regulator chromosome segregation ATPase chromosome segregation ATPase
M5005_Spy_0447 M5005_Spy_0448 M5005_Spy_0449 M5005_Spy_0450 M5005_Spy_0451c M5005_Spy_0452c	3572464 3572465 3572466 3572467 3572468 3572469	NE NC NE NE NE	Spy49_0456 Spy49_0457 Spy49_0458 Spy49_0459 Spy49_0460 Spy49_0461c Spy49_0462c	6985473 6985474 6985475 6985476 6985477 6985478 6985479 6985480	NE NE NE NE NE NE NE	- - - hasB.2	* * * * *			hypothetical protein M5005_Spy_0443 hypothetical protein M5005_Spy_0444 S-adenos/jmethionine synthetase hypothetical protein M5005_Spy_0446 cell wall biosynthesis glycosyltransferase hypothetical protein M5005_Spy_0448 UDP-glucose 6-dehydrogenase macrolide-efflux protein transcriptional regulator chromosome segregation ATPase chromosome segregation ATPase hypothetical protein M5005_Spy_0454
M5005_Spy_0447 M5005_Spy_0448 M5005_Spy_0449 M5005_Spy_0451c M5005_Spy_0451c M5005_Spy_0452c M5005_Spy_0453c M5005_Spy_0454c M5005_Spy_0455c	3572464 3572465 3572466 3572467 3572468 3572469	NE NE NE NE NE NE	Spy49_0456 Spy49_0457 Spy49_0458 Spy49_0459 Spy49_0460 Spy49_0461c Spy49_0462c Spy49_0463c	6985473 6985474 6985475 6985476 6985477 6985478 6985479 6985480 6985481	NE	- - - hasB.2	* * * * * * * * * * * * * * * * * * * *			hypothetical protein M5005_Spy_0443 hypothetical protein M5005_Spy_0444 S-adenosylmethionine synthetase hypothetical protein M5005_Spy_0446 cell wall biosynthesis glycosyltransferase hypothetical protein M5005_Spy_0448 UDP-glucose 6-dehydrogenase macrolide-efflux protein transcriptional regulator chromosome segregation ATPase chromosome segregation ATPase
M5005_Spy_0447 M5005_Spy_0448 M5005_Spy_0449 M5005_Spy_0450 M5005_Spy_0451c M5005_Spy_0452c M5005_Spy_0453c M5005_Spy_0455c M5005_Spy_0455c	3572463 3572464 3572465 3572466 3572467 3572468 3572469 3572470 3572471 3572472	NE NC NE	Spy49_0456 Spy49_0457 Spy49_0458 Spy49_0459 Spy49_0461c Spy49_0462c Spy49_0463c Spy49_0463c Spy49_0464c	6985473 6985474 6985475 6985476 6985477 6985478 6985479 6985480 6985481 6985482	NE	- - - hasB.2				hypothetical protein M5005_Spy_0443 hypothetical protein M5005_Spy_0444 S-adenosylmethionine synthetase hypothetical protein M5005_Spy_0446 cell wall biosynthesis glycosyltransferase hypothetical protein M5005_Spy_0448 UDP-glucose 6-dehydrogenase macrolide-efflux protein transcriptional regulator chromosome segregation ATPase hypothetical protein M5005_Spy_0454 hypothetical protein M5005_Spy_0455 plasmid stabilization system antitoxin protein
M5005_Spy_0447 M5005_Spy_0449 M5005_Spy_0450 M5005_Spy_0450 M5005_Spy_0452c M5005_Spy_0452c M5005_Spy_0452c M5005_Spy_0454c M5005_Spy_0456 M5005_Spy_0456 M5005_Spy_0456	3572463 3572464 3572465 3572466 3572467 3572468 3572469 3572470 3572471 3572472 3572473	NE NC NE NC NE	Spy49_0456 Spy49_0457 Spy49_0458 Spy49_0469 Spy49_0460 Spy49_0462c Spy49_0463c Spy49_0463c Spy49_0464c Spy49_0465 Spy49_0466	6985473 6985474 6985475 6985476 6985477 6985478 6985479 6985480 6985481 6985482 6985483 6985484	NE N	- - - hasB.2	*			hypothetical protein M5005_Spy_0443 hypothetical protein M5005_Spy_0444 S-adenosylmethionine synthetase hypothetical protein M5005_Spy_0446 cell wall biosynthesis glycosyltransferase hypothetical protein M5005_Spy_0448 UDP-glucose 6-dehydrogenase macrolide-efflux protein transcriptional regulator chromosome segregation ATPase chromosome segregation ATPase hypothetical protein M5005_Spy_0454 hypothetical protein M5005_Spy_0455 plasmid stabilization system antitoxin protein plasmid stabilization system protein
M5005_Spy_0447 M5005_Spy_0448 M5005_Spy_0449 M5005_Spy_0450 M5005_Spy_0452c M5005_Spy_0452c M5005_Spy_0452c M5005_Spy_0452c M5005_Spy_0456c M5005_Spy_0456c M5005_Spy_0457c M5005_Spy_0457c M5005_Spy_0457c M5005_Spy_0457c	3572463 3572464 3572465 3572466 3572467 3572469 3572470 3572471 3572472 3572473 3572473	NE NC NE NC NE	Spy49_0456 Spy49_0457 Spy49_0459 Spy49_0459 Spy49_0461c Spy49_0463c Spy49_0463c Spy49_0463c Spy49_0464c Spy49_0466 Spy49_0466 Spy49_0466	6985473 6985474 6985475 6985475 6985477 6985478 6985479 6985480 6985481 6985482 6985483 6985484	NE N	- - - hasB.2	*			hypothetical protein M5005_Spy_0443 hypothetical protein M5005_Spy_0444 S-adenosylmethionine synthetase hypothetical protein M5005_Spy_0446 cell wall biosynthesis glycosyltransferase hypothetical protein M5005_Spy_0488 UDP-glucose 6-dehydrogenase macrolide-efflux protein transcriptional regulator chromosome segregation ATPase chromosome segregation ATPase hypothetical protein M5005_Spy_0454 hypothetical protein M5005_Spy_0455 plasmid stabilization system antitoxin protein plasmid stabilization system protein hypothetical protein M5005_Spy_0458
M5005_Spy_0447 M5005_Spy_0448 M5005_Spy_0450 M5005_Spy_0451 M5005_Spy_04512 M5005_Spy_04522 M5005_Spy_04522 M5005_Spy_04542 M5005_Spy_04542 M5005_Spy_0456 M5005_Spy_0457 M5005_Spy_0458 M5005_Spy_0458 M5005_Spy_0458	3572463 3572464 3572465 3572466 3572467 3572468 3572470 3572471 3572472 3572473 3572435 3572436	NE NC NE NE NE NE NE NE NE NE NE NC NE NC NE NE NE	Spy49_0456 Spy49_0457 Spy49_0459 Spy49_0460 Spy49_0461c Spy49_0462c Spy49_0463c Spy49_0463c Spy49_0464c Spy49_0465 Spy49_0466 Spy49_0466	6985473 6985474 6985475 6985476 6985477 6985478 6985479 6985480 6985481 6985482 6985483 6985484	NE NC NE NE NE	- - - hasB.2	*			hypothetical protein M5005_Spy_0443 hypothetical protein M5005_Spy_0444 S-adenosylmethionine synthetase hypothetical protein M5005_Spy_0446 cell wall biosynthesis glycosyltransferase hypothetical protein M5005_Spy_0448 UDP-glucose 6-dehydrogenase macrolide-efflux protein transcriptional regulator chromosome segregation ATPase chromosome segregation ATPase hypothetical protein M5005_Spy_0454 hypothetical protein M5005_Spy_0455 plasmid stabilization system antitoxin protein plasmid stabilization system antitoxin protein hypothetical protein M5005_Spy_0458 portal protein
M5005_Spy_0447 M5005_Spy_0448 M5005_Spy_0449 M5005_Spy_0450 M5005_Spy_0452c M5005_Spy_0452c M5005_Spy_0452c M5005_Spy_0452c M5005_Spy_0456c M5005_Spy_0456c M5005_Spy_0457c M5005_Spy_0457c M5005_Spy_0457c M5005_Spy_0457c	3572463 3572464 3572465 3572466 3572467 3572469 3572470 3572471 3572472 3572473 3572473	NE NC NE NC NE	Spy49_0456 Spy49_0457 Spy49_0458 Spy49_0460 Spy49_0461c Spy49_0462c Spy49_0463c Spy49_0464c Spy49_0466 Spy49_0466 Spy49_0466 Spy49_0466	6985473 6985474 6985475 6985476 6985477 6985477 6985479 6985480 6985481 6985482 6985483 6985484 6985483 6985484	NE N	- - - hasB.2	*			hypothetical protein M5005_Spy_0443 hypothetical protein M5005_Spy_0444 S-adenosylmethionine synthetase hypothetical protein M5005_Spy_0446 cell wall biosynthesis glycosyltransferase hypothetical protein M5005_Spy_0488 UDP-glucose 6-dehydrogenase macrolide-efflux protein transcriptional regulator chromosome segregation ATPase chromosome segregation ATPase hypothetical protein M5005_Spy_0454 hypothetical protein M5005_Spy_0455 plasmid stabilization system antitoxin protein plasmid stabilization system protein hypothetical protein M5005_Spy_0458
M5005_Spy_0447 M5005_Spy_0448 M5005_Spy_0450 M5005_Spy_0450 M5005_Spy_0452c M5005_Spy_0452c M5005_Spy_0452c M5005_Spy_0452c M5005_Spy_04566 M5005_Spy_04566 M5005_Spy_0457 M5005_Spy_0458 M5005_Spy_0458 M5005_Spy_0458 M5005_Spy_0459 M5005_Spy_0459 M5005_Spy_0459	3572463 3572464 3572465 3572466 3572468 3572469 3572470 3572471 3572472 3572473 3572435 3572436	NE NC NE NE NE NE NE NE NE NE NE NC NE NE NE NE NE NE	Spy49_0456 Spy49_0457 Spy49_0459 Spy49_04616 Spy49_0461c Spy49_0462c Spy49_0463c Spy49_0466 Spy49_0466 Spy49_0466 Spy49_0466 Spy49_0466 Spy49_0466 Spy49_0466 Spy49_0466 Spy49_0468	6985473 6985474 6985475 6985476 6985476 6985476 6985478 6985480 6985481 6985482 6985483 6985483 6985485 6985485	NE N	- - - hasB.2	*			hypothetical protein M5005_Spy_0443 hypothetical protein M5005_Spy_0444 S-adenosylmethionine synthetase hypothetical protein M5005_Spy_0446 cell wall biosynthesis glycosyltransferase hypothetical protein M5005_Spy_0488 UDP-glucose 6-dehydrogenase macrolide-efflux protein transcriptional regulator chromosome segregation ATPase chromosome segregation ATPase hypothetical protein M5005_Spy_0454 hypothetical protein M5005_Spy_0455 plasmid stabilization system antitoxin protein plasmid stabilization system protein hypothetical protein M5005_Spy_0458 portal protein hypothetical protein M5005_Spy_0460
M5005_Spy_0447 M5005_Spy_0448 M5005_Spy_0450 M5005_Spy_0451e M5005_Spy_0451e M5005_Spy_0452e M5005_Spy_0452e M5005_Spy_0458e M5005_Spy_0458e M5005_Spy_0458e M5005_Spy_0458e M5005_Spy_0458 M5005_Spy_0458 M5005_Spy_0450 M5005_Spy_0450 M5005_Spy_0450 M5005_Spy_0450	3572463 3572464 3572465 3572466 3572467 3572469 3572470 3572471 3572472 3572473 3572435 3572435 3572437	NE NC NE NE NE NE NE NE NE NE NC NE	Spy49_0456 Spy49_0457 Spy49_0458 Spy49_0460 Spy49_0461c Spy49_0462c Spy49_0464c Spy49_0466 Spy49_0466 Spy49_0466 Spy49_0466 Spy49_0467 Spy49_0469 Spy49_0470 Spy49_0470	\$\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\	NE N		*			hypothetical protein M5005_Spy_0443 hypothetical protein M5005_Spy_0444 S-adenos/jmethionine synthetase hypothetical protein M5005_Spy_0446 cell wall biosynthesis glycosyltransferase hypothetical protein M5005_Spy_0448 UDP-glucose 6-dehydrogenase macrolide-efflux protein transcriptional regulator chromosome segregation ATPase chromosome segregation ATPase hypothetical protein M5005_Spy_0454 hypothetical protein M5005_Spy_0455 plasmid stabilization system antitoxin protein plasmid stabilization system protein hypothetical protein M5005_Spy_0458 portal protein hypothetical protein M5005_Spy_0460 hypothetical protein M5005_Spy_0460 hypothetical protein M5005_Spy_0461
M5005_Spy_0447 M5005_Spy_0489 M5005_Spy_0450 M5005_Spy_0450 M5005_Spy_0452c M5005_Spy_0452c M5005_Spy_0452c M5005_Spy_0454c M5005_Spy_0454c M5005_Spy_0456 M5005_Spy_0456 M5005_Spy_0457 M5005_Spy_0459 M5005_Spy_0459 M5005_Spy_0460	3572463 3572465 3572465 3572466 3572466 3572468 3572469 3572470 3572471 3572472 3572473 3572435 3572435 3572435	NE NC NE NE NE NE NE NC NE NC NE	Spy49_0456 Spy49_0457 Spy49_0458 Spy49_0460 Spy49_04610 Spy49_04620 Spy49_04630 Spy49_04640 Spy49_04640 Spy49_04640 Spy49_04660 Spy49_0467 Spy49_0467 Spy49_0469 Spy49_0470 Spy49_0470 Spy49_0470 Spy49_0470	6985473 6985474 6985475 6985475 6985475 6985476 6985480 6985480 6985481 6985481 6985483 6985484 6985484 6985485 6985485 6985485 6985485 6985485 6985485	NE NC NE NC NE	- - - hasB.2	*			hypothetical protein M5005_Spy_0443 hypothetical protein M5005_Spy_0444 S-adenosylmethionine synthetase hypothetical protein M5005_Spy_0446 cell wall biosynthesis glycosyltransferase hypothetical protein M5005_Spy_0488 UDP-glucose 6-dehydrogenase macrolide-efflux protein transcriptional regulator chromosome segregation ATPase chromosome segregation ATPase hypothetical protein M5005_Spy_0454 hypothetical protein M5005_Spy_0455 plasmid stabilization system antitoxin protein plasmid stabilization system protein hypothetical protein M5005_Spy_0458 portal protein hypothetical protein M5005_Spy_0460 hypothetical protein M5005_Spy_0461 asparagine synthetase A
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M5005_Spy_0447 M5005_Spy_0448 M5005_Spy_0450 M5005_Spy_04512 M5005_Spy_04522 M5005_Spy_04522 M5005_Spy_04524 M5005_Spy_04546 M5005_Spy_0456 M5005_Spy_0457 M5005_Spy_0457 M5005_Spy_0457 M5005_Spy_0457 M5005_Spy_0459 M5005_Spy_0459 M5005_Spy_0460	3572463 3572465 3572465 3572466 3572469 3572469 3572470 3572471 3572472 3572473 3572436 3572436 3572436 3572436 3572436 3572436 3572441 3572441 3572441 3572442 3572443 3572444 3572444 3572444 3572444 3572444 3572444 3572444	NE N	Spy49_0456 Spy49_0457 Spy49_0458 Spy49_0461c Spy49_0461c Spy49_0463c Spy49_0463c Spy49_0464c Spy49_0466 Spy49_0466 Spy49_0466 Spy49_0466 Spy49_0466 Spy49_0466 Spy49_0470 Spy49_0470 Spy49_0470 Spy49_0470 Spy49_0473 Spy49_0473 Spy49_0476 Spy49_0476 Spy49_0476 Spy49_0477 Spy49_0477 Spy49_0477 Spy49_0478 Spy49_0478 Spy49_0478 Spy49_0478 Spy49_0478 Spy49_0478 Spy49_0478 Spy49_0478 Spy49_0481	6985473 6985474 6985475 6985476 6985477 6985477 6985478 6985479 6985482 6985482 6985483 6985484 6985484 6985484 6985485 6985487 6985487 6985487 6985487 6985489 6985490 6985490 6985492 6985492 6985494 6985494 6985494 6985495 6985495 6985494 6985495 6985495 6985496 6985497 6985497	NE N	hasB.2 mefE - - - - - - - - - - - - - - - - - - -	*	SSA 1557	SP 1244	hypothetical protein M5005_Spy_0443 hypothetical protein M5005_Spy_0444 S-adenosylmethionine synthetase hypothetical protein M5005_Spy_0446 cell wall biosynthesis glycosyltransferase hypothetical protein M5005_Spy_0448 UDP-glucose 6-dehydrogenase macrolide-efflux protein transcriptional regulator chromosome segregation ATPase chromosome segregation ATPase hypothetical protein M5005_Spy_0454 hypothetical protein M5005_Spy_0455 plasmid stabilization system antitoxin protein plasmid stabilization system protein hypothetical protein M5005_Spy_0458 portal protein hypothetical protein M5005_Spy_0460 hypothetical protein M5005_Spy_0460 hypothetical protein M5005_Spy_0461 asparagine synthetase A hypothetical protein M5005_Spy_0463 microcin C7 self-immunity protein hypothetical protein M5005_Spy_0465 hypothetical protein M5005_Spy_0469 HAD superfamily hydrolase
M5005_Spy_0447 M5005_Spy_0450 M5005_Spy_0450 M5005_Spy_04510 M5005_Spy_04510 M5005_Spy_04520 M5005_Spy_04640 M5005_Spy_04640 M5005_Spy_04640 M5005_Spy_04660 M5005_Spy_04660 M5005_Spy_04660 M5005_Spy_04660 M5005_Spy_04660 M5005_Spy_04660 M5005_Spy_04660 M5005_Spy_04670 M5005_Spy_0472	3572463 3572464 3572465 3572466 3572469 3572470 3572471 3572471 3572472 3572473 3572436 3572436 3572432 3572432 3572432 3572432 3572432 3572432 3572440 3572442 3572442 3572442 3572444 3572445 3572444 3572444	NE N	Spy49_0456 Spy49_0457 Spy49_0458 Spy49_0458 Spy49_04610 Spy49_0462 Spy49_04636 Spy49_04666 Spy49_0466 Spy49_0466 Spy49_0466 Spy49_0466 Spy49_0467 Spy49_0470 Spy49_0470 Spy49_0471 Spy49_0477 Spy49_0478 Spy49_0476 Spy49_0476 Spy49_0476 Spy49_0479 Spy49_0479 Spy49_0478 Spy49_0479 Spy49_0478 Spy49_0479 Spy49_0478 Spy49_0479 Spy49_04	6985473 6985474 6985475 6985476 6985477 6985477 6985477 6985480 6985480 6985481 6985483 6985484 6985485 6985485 6985485 6985485 6985485 6985485 6985485 6985489 6985490 6985490 6985491 6985490 6985491	NE N	hasB.2 mefE - - - - - - - - - -	*	SSA_1557	SP_1244	hypothetical protein M5005_Spy_0443 hypothetical protein M5005_Spy_0444 S-adenosylmethionine synthetase hypothetical protein M5005_Spy_0446 cell wall biosynthesis glycosyltransferase hypothetical protein M5005_Spy_0484 UDP-glucose 6-dehydrogenase macrolide-efflux protein transcriptional regulator chromosome segregation ATPase chromosome segregation ATPase hypothetical protein M5005_Spy_0454 hypothetical protein M5005_Spy_0455 plasmid stabilization system antitoxin protein plasmid stabilization system protein hypothetical protein M5005_Spy_0458 portal protein hypothetical protein M5005_Spy_0460 hypothetical protein M5005_Spy_0461 asparagine synthetase A hypothetical protein M5005_Spy_0463 microcin C7 self-immunity protein hypothetical protein M5005_Spy_0465 hypothetical protein M5005_Spy_0465 hypothetical protein M5005_Spy_0466 transposase transposase transposase transposase hypothetical protein M5005_Spy_0469 HAD superfamily hydrolase HAD superfamily hydrolase cell division protein
M5005_Spy_0447 M5005_Spy_0448 M5005_Spy_0450 M5005_Spy_0451 M5005_Spy_0451 M5005_Spy_0452 M5005_Spy_0452 M5005_Spy_0456 M5005_Spy_0456 M5005_Spy_0456 M5005_Spy_0459 M5005_Spy_0459 M5005_Spy_0459 M5005_Spy_0460 M5005_Spy_0460 M5005_Spy_0460 M5005_Spy_0460 M5005_Spy_0466 M5005_Spy_0470 M5005_Spy_0470 M5005_Spy_0471 M5005_Spy_0473	3572463 3572464 3572465 3572465 3572469 3572470 3572471 3572472 3572473 3572473 3572433 3572433 3572432 3572434 3572443 3572441 3572441 3572441 3572442 3572443 3572443 3572443 3572444 3572444 3572444 3572444 3572446 3572446	NE N	Spy49_0456 Spy49_0457 Spy49_0458 Spy49_0461c Spy49_0461c Spy49_0463c Spy49_0463c Spy49_0463c Spy49_0464 Spy49_0466 Spy49_0466 Spy49_0466 Spy49_0466 Spy49_0466 Spy49_0466 Spy49_0467 Spy49_0470 Spy49_0471 Spy49_0473 Spy49_0475 Spy49_0475 Spy49_0475 Spy49_0476 Spy49_	6985473 6985474 6985475 6985475 6985477 6985477 6985477 6985480 6985480 6985481 6985481 6985482 6985486 6985486 6985486 6985486 6985486 6985496 6985490 6985497 6985497 6985497 6985497 6985497 6985497 6985497 6985497 6985497 6985497 6985498	NE N	hasb.2 meffe 	*	SSA_1557	SP_1244	hypothetical protein M5005_Spy_0443 hypothetical protein M5005_Spy_0444 S-adenosylmethionine synthetase hypothetical protein M5005_Spy_0446 cell wall biosynthesis glycosyltransferase hypothetical protein M5005_Spy_0448 UDP-glucose 6-dehydrogenase macrolide-efflux protein transcriptional regulator chromosome segregation ATPase chromosome segregation ATPase hypothetical protein M5005_Spy_0454 hypothetical protein M5005_Spy_0455 plasmid stabilization system antitoxin protein plasmid stabilization system protein hypothetical protein M5005_Spy_0458 portal protein hypothetical protein M5005_Spy_0460 hypothetical protein M5005_Spy_0460 hypothetical protein M5005_Spy_0461 asparagine synthetase A hypothetical protein M5005_Spy_0463 microcin C7 self-immunity protein hypothetical protein M5005_Spy_0465 hypothetical protein M5005_Spy_0469 HAD superfamily hydrolase
M5005_Spy_0447 M5005_Spy_0450 M5005_Spy_0450 M5005_Spy_04510 M5005_Spy_04510 M5005_Spy_04520 M5005_Spy_04640 M5005_Spy_04640 M5005_Spy_04640 M5005_Spy_04660 M5005_Spy_04660 M5005_Spy_04660 M5005_Spy_04660 M5005_Spy_04660 M5005_Spy_04660 M5005_Spy_04660 M5005_Spy_04670 M5005_Spy_0472	3572463 3572464 3572465 3572466 3572469 3572470 3572471 3572471 3572472 3572473 3572436 3572436 3572432 3572432 3572432 3572432 3572432 3572432 3572440 3572442 3572442 3572442 3572444 3572445 3572444 3572444	NE N	Spy49_0456 Spy49_0457 Spy49_0458 Spy49_0458 Spy49_04610 Spy49_0462 Spy49_04636 Spy49_04666 Spy49_0466 Spy49_0466 Spy49_0466 Spy49_0466 Spy49_0467 Spy49_0470 Spy49_0470 Spy49_0471 Spy49_0477 Spy49_0478 Spy49_0476 Spy49_0476 Spy49_0476 Spy49_0479 Spy49_0479 Spy49_0478 Spy49_0479 Spy49_0478 Spy49_0479 Spy49_0478 Spy49_0479 Spy49_04	6985473 6985474 6985475 6985476 6985477 6985477 6985477 6985480 6985480 6985481 6985483 6985484 6985485 6985485 6985485 6985485 6985485 6985485 6985485 6985489 6985490 6985490 6985491 6985490 6985491	NE N	hasB.2 mefE - - - - - - - - - - - - - - - - - - -		SSA_1557	SP_1244	hypothetical protein M5005_Spy_0443 hypothetical protein M5005_Spy_0444 S-adenosylmethionine synthetase hypothetical protein M5005_Spy_0446 cell wall biosynthesis glycosyltransferase hypothetical protein M5005_Spy_0488 UDP-glucose 6-dehydrogenase macrolide-efflux protein transcriptional regulator chromosome segregation ATPase chromosome segregation ATPase hypothetical protein M5005_Spy_0454 hypothetical protein M5005_Spy_0455 plasmid stabilization system antitoxin protein plasmid stabilization system protein hypothetical protein M5005_Spy_0458 portal protein hypothetical protein M5005_Spy_0460 hypothetical protein M5005_Spy_0460 hypothetical protein M5005_Spy_0461 asparagine synthetase A hypothetical protein M5005_Spy_0463 microcin C7 self-immunity protein hypothetical protein M5005_Spy_0465 hypothetical protein M5005_Spy_0466 transposase transposase hypothetical protein M5005_Spy_0469 HAD superfamily hydrolase HAD superfamily hydrolase cell division protein multidrug resistance protein B
M5005_Spy_0447 M5005_Spy_0448 M5005_Spy_0450 M5005_Spy_04512 M5005_Spy_04522 M5005_Spy_04522 M5005_Spy_04526 M5005_Spy_04526 M5005_Spy_04546 M5005_Spy_04546 M5005_Spy_0456 M5005_Spy_0460 M5005_Spy_0470 M5005_Spy_0470 M5005_Spy_0473	3572463 3572465 3572465 3572466 3572469 3572469 3572470 3572471 3572472 3572473 3572436 3572436 3572436 3572437 3572438 3572438 3572439 3572443 3572441 3572442 3572442 3572444 3572445 3572445 3572445 3572445 3572445	NE NC NE	Spy49_0456 Spy49_0457 Spy49_0458 Spy49_0461c Spy49_0461c Spy49_0461c Spy49_0463c Spy49_0463c Spy49_0463c Spy49_0466 Spy49_0466 Spy49_0466 Spy49_0466 Spy49_0466 Spy49_0467 Spy49_0470 Spy49_0470 Spy49_0470 Spy49_0470 Spy49_0470 Spy49_0470 Spy49_0470 Spy49_0476 Spy49_0478 Spy49_0478 Spy49_0478 Spy49_0478 Spy49_0478 Spy49_0478 Spy49_0482 Spy49_0482 Spy49_0482 Spy49_0488	6985473 6985474 6985475 6985475 6985477 6985477 6985479 6985480 6985481 6985482 6985484 6985484 6985484 6985488 6985488 6985488 6985488 6985488 6985489 6985490 6985590 6985590 6985590	NE N	hasb.2 meffe 		SSA_1557	SP_1244	hypothetical protein M5005_Spy_0443 hypothetical protein M5005_Spy_0444 S-adenosylmethionine synthetase hypothetical protein M5005_Spy_0446 cell wall biosynthesis glycosyltransferase hypothetical protein M5005_Spy_0448 UDP-glucose 6-dehydrogenase macrolide-efflux protein transcriptional regulator chromosome segregation ATPase chromosome segregation ATPase hypothetical protein M5005_Spy_0454 hypothetical protein M5005_Spy_0455 plasmid stabilization system antitoxin protein plasmid stabilization system protein hypothetical protein M5005_Spy_0458 portal protein M5005_Spy_0458 portal protein M5005_Spy_0460 hypothetical protein M5005_Spy_0460 hypothetical protein M5005_Spy_0461 asparagine synthetase A hypothetical protein M5005_Spy_0463 microcin C7 self-immunity protein hypothetical protein M5005_Spy_0465 hypothetical protein M5005_Spy_0466 transposase transposase transposase hypothetical protein M5005_Spy_0469 HAD superfamily hydrolase cell division protein multidrug resistance protein B BigG family transcription antiterminator
M5005_Spy_0447 M5005_Spy_0450 M5005_Spy_0450 M5005_Spy_04510 M5005_Spy_04510 M5005_Spy_04520 M5005_Spy_04520 M5005_Spy_04520 M5005_Spy_04520 M5005_Spy_04520 M5005_Spy_04520 M5005_Spy_04520 M5005_Spy_04520 M5005_Spy_04520 M5005_Spy_0460 M5005_Spy_0470 M5005_Spy_0470 M5005_Spy_0470 M5005_Spy_0470 M5005_Spy_0474 M5005_Spy_04744 M5005_Spy_047474 M5005_Spy_04744	3572463 3572465 3572465 3572466 3572469 3572469 3572470 3572472 3572472 3572473 3572436 3572436 3572436 3572436 3572436 3572437 3572443 3572444 3572441 3572442 3572443 3572445 3572445 3572445 3572445 3572445 3572445 3572445	NE N	Spy49_0456 Spy49_0457 Spy49_0458 Spy49_0461c Spy49_0461c Spy49_0463c Spy49_0463c Spy49_0464c Spy49_0466 Spy49_0466 Spy49_0466 Spy49_0466 Spy49_0466 Spy49_0466 Spy49_0467 Spy49_0470 Spy49_0470 Spy49_0470 Spy49_0470 Spy49_0470 Spy49_0470 Spy49_0476 Spy49_0476 Spy49_0476 Spy49_0476 Spy49_0476 Spy49_0478 Spy49_0479 Spy49_0478 Spy49_0478 Spy49_0478 Spy49_0480 Spy49_0480 Spy49_0481 Spy49_0483 Spy49_0483 Spy49_0483 Spy49_0483 Spy49_0483	6985473 6985474 6985475 6985475 6985477 6985477 6985477 6985480 6985480 6985481 6985481 6985483 6985484 6985485 6985486 6985486 6985486 6985490 6985491 6985491 6985493 6985493 6985493 6985493 6985493 6985493 6985493 6985493 6985493 6985493 6985493 6985493 6985493 6985493 6985493 6985493 6985493 6985493 6985493 6985593 6985593 6985593 6985593 6985593 6985593 6985593 6985593 6985593 6985593 6985593 6985593 6985593 6985593 6985593 6985593	NE N	hasb.2 mefE		SSA_1557	SP_1244	hypothetical protein M5005_Spy_0443 hypothetical protein M5005_Spy_0444 S-adenosylmethionine synthetase hypothetical protein M5005_Spy_0446 cell wall biosynthesis glycosyltransferase hypothetical protein M5005_Spy_0488 UDP-glucose 6-dehydrogenase macrolide-efflux protein transcriptional regulator chromosome segregation ATPase chromosome segregation ATPase hypothetical protein M5005_Spy_0454 hypothetical protein M5005_Spy_0455 plasmid stabilization system antitoxin protein plasmid stabilization system protein hypothetical protein M5005_Spy_0458 portal protein hypothetical protein M5005_Spy_0460 hypothetical protein M5005_Spy_0460 hypothetical protein M5005_Spy_0461 asparagine synthetase A hypothetical protein M5005_Spy_0461 hypothetical protein M5005_Spy_0465 hypothetical protein M5005_Spy_0465 hypothetical protein M5005_Spy_0465 hypothetical protein M5005_Spy_0466 transposase transposase transposase hypothetical protein M5005_Spy_0469 HAD superfamily hydrolase tAD superfamily hydrolase cell division protein multidrug resistance protein B BigG family transcription antiterminator PTS system beta-glucoside-specific transporter subunit IIABC

M5005_Spy_0478c	3572416	NE	Spy49_0489c	6985505	NE	-	*			hypothetical protein M5005_Spy_0478
M5005_Spy_0479	3572417	NE				-				hypothetical protein M5005_Spy_0479
M5005_Spy_0480	3572419	NE	Spy49_0490	6985506	NE	-	*			transcription accessory protein
M5005_Spy_0481c	3572418	NC				-				hypothetical protein M5005_Spy_0481
M5005_Spy_0482	3572420	NE	Spy49_0491	6985507	NE	-				hypothetical protein M5005_Spy_0482
M5005_Spy_0483	3572421	NE	Spy49_0493	6985508	NE	-				stress-responsive transcriptional regulator
M5005_Spy_0484	3572422	E	Spy49_0494	6985509	Е	ptsK	*		SP_1413	HPr kinase/phosphorylase
M5005_Spy_0485	3572423	NE	Spy49_0495	6985510	NE	lgt	*			prolipoprotein diacylglyceryl transferase
M5005_Spy_0486	3572424	NE	Spy49_0496	6985511	NE	-	*			hypothetical protein M5005_Spy_0486
M5005_Spy_0487	3572425	NE	Spy49_0497	6985512	NE	-	*			hypothetical protein M5005_Spy_0487
M5005_Spy_0488c	3572426	NE	Spy49_0498	6985513	NE	-				hypothetical protein M5005_Spy_0488
M5005_Spy_0489	3572427	NE	Spy49_0499	6985514	NE	-	*			U32 family peptidase
M5005_Spy_0491	3572429	NE	Spy49_0500	6985515	NE	-	*			U32 family peptidase
M5005_Spy_0492c	3572430	NC				-				hypothetical protein M5005_Spy_0492
M5005_Spy_0493	3572431	NE	Spy49_0501	6985516	NE	-	*			hypothetical protein M5005_Spy_0493
M5005_Spy_0494c	3572432	NC	Spy49_0502c	6985517	NC	-				hypothetical protein M5005_Spy_0494
M5005_Spy_0495c	3572433	E	Spy49_0503c	6985518	E	lysS	*	SSA_1529	SP_0713	lysyl-tRNA synthetase
M5005_Spy_0496	3572434	NE	Spy49_0504	6985519	NE	-	*			HAD superfamily hydrolase
M5005_Spy_0497c	3572396	NE	Spy49_0505c	6985520	NE	-				phosphoglycerate mutase
M5005_Spy_0498c	3572397	NE	Spy49_0506c	6985521	NE	-	*			transcriptional regulator
M5005_Spy_0499c		NE	Spy49_0507c	6985522	NE	-	*			thiamine transporter
M5005_Spy_0500c	3572399	С	Spy49_0508c	6985523	NE	-	*			N-acetylmuramoyl-L-alanine amidase
M5005_Spy_0501	3572400	NE	Spy49_0509	6985524	NE	-	*			hypothetical protein M5005_Spy_0501
M5005_Spy_0502	3572401	NE	Spy49_0510	6985525	NE	-	*			hypothetical protein M5005_Spy_0502
M5005_Spy_0503c	3572402	NE	Spy49_0511c	6985526	NE	-	*			glutathione peroxidase
M5005_Spy_0504c	3572403	NE	Spy49_0512c	6985527	NE	pepF	*			oligoendopeptidase F
M5005_Spy_0505	3572404	NE	Spy49_0513	6985528	NE	ppc	*			phosphoenolpyruvate carboxylase
M5005_Spy_0506	3572405	E	Spy49_0514	6985529	E	ftsW	*	SSA_1522	SP_0803	cell division protein
M5005_Spy_0507c	3572406	NC				-				hypothetical protein M5005_Spy_0507
M5005_Spy_0508	3572407	E	Spy49_0515	6985530	NC	tuf	*	SSA_1520	SP_1489	elongation factor Tu
M5005_Spy_0509	3572408	С	Spy49_0516	6985531	E	tpiA	*	SSA_0859	SP_1574	triosephosphate isomerase
M5005_Spy_0510c	3572409	Е	Spy49_0517c	6985532	E	murN	*		SP_0616	factor essential for expression of methicillin resistance
										UDP-N-acetylmuramoylpentapeptide-lysine N(6)-alanyltransferase/UDP-N-
M5005_Spy_0511c		E	Spy49_0518c	6985533	Е	murM	*	SSA_0862		acetylmuramoylpentapeptide-lysi
M5005_Spy_0512c		NE	Spy49_0519c	6985534	NE	-	*			HAD superfamily hydrolase
M5005_Spy_0513c		NC				-				hypothetical protein M5005_Spy_0513
M5005_Spy_0514c		NE	Spy49_0520c		NE	-	*			dGTP triphosphohydrolase
M5005_Spy_0515	3572414	NE	Spy49_0521	6985536	NE	-	*			hypothetical protein M5005_Spy_0515
M5005_Spy_0516	3572415	E	Spy49_0522	6985537	Е	pacL	*		SP_1551	calcium-transporting ATPase
M5005_Spy_0517c		NE	Spy49_0523c	6985538	NE	regR	*			LacI family transcriptional regulator
M5005_Spy_0518c		NE	Spy49_0524c	6985539	NE	-	*			oligohyaluronate lyase
M5005_Spy_0519c		NE	Spy49_0525c	6985540	NC	agaD	*			PTS system N-acetylgalactosamine-specific transporter subunit IID
M5005_Spy_0520c		NE	Spy49_0526c	6985541	NE	agaW	*			PTS system N-acetylgalactosamine-specific transporter subunit IIC
M5005_Spy_0521c		NE	Spy49_0527c	6985542	NE	agaV	*			PTS system N-acetylgalactosamine-specific transporter subunit IIB
M5005_Spy_0522c		NE	Spy49_0528c	6985543	NE	ugl				unsaturated glucuronyl hydrolase
M5005_Spy_0523	3572383	NE	Spy49_0529c	6985544	NE	agaF	*			hypothetical protein M5005_Spy_0523
M5005_Spy_0524	3572384	NE	Spy49_0530	6985545	NE	idnO	*			gluconate 5-dehydrogenase
M5005_Spy_0525	3572385		Spy49_0531	6985546						
M5005_Spy_0526		NE			NE		*			hypothetical protein M5005_Spy_0525
	3572386	NE	Spy49_0532	6985547	NE	kdgK	*			2-dehydro-3-deoxygluconokinase
M5005_Spy_0527	3572387	NE NE	Spy49_0532 Spy49_0533	6985547 6985548	NE NE	kdgK kgdA	* *			2-dehydro-3-deoxygluconokinase keto-hydroxyglutarate-aldolase/keto-deoxy-phosphogluconate aldolase
M5005_Spy_0527 M5005_Spy_0528	3572387 3572388	NE NE NE	Spy49_0532 Spy49_0533 Spy49_0534	6985547 6985548 6985549	NE NE NE		* * *			2-dehydro-3-deoxygluconokinase keto-hydroxyglutarate-aldolase/keto-deoxy-phosphogluconate aldolase beta-phosphoglucomutase/glucose-1-phosphate phosphodismutase
M5005_Spy_0527 M5005_Spy_0528 M5005_Spy_0529	3572387 3572388 3572389	NE NE NE NE	Spy49_0532 Spy49_0533 Spy49_0534 Spy49_0535	6985548 6985549 6985550	NE NE NE NE	kgdA - -	* * *			2-dehydro-3-deoxygluconokinase keto-hydroxyglutarate-aldolase/keto-deoxy-phosphogluconate aldolase beta-phosphoglucomutase/glucose-1-phosphate phosphodismutase (Fe-S)-binding protein
M5005_Spy_0527 M5005_Spy_0528 M5005_Spy_0529 M5005_Spy_0530	3572387 3572388 3572389 3572390	NE NE NE NE E	Spy49_0532 Spy49_0533 Spy49_0534 Spy49_0535 Spy49_0536	6985548 6985549 6985550 6985551	NE NE NE NE E	kgdA - - prfB	* * * *	SSA_0869	SP_0755	2-dehydro-3-deoxygluconokinase keto-hydroxyglutarate-aldolase/keto-deoxy-phosphogluconate aldolase beta-phosphoglucomutase/glucose-1-phosphate phosphodismutase (Fe-S)-binding protein peptide chain release factor 2
M5005_Spy_0527 M5005_Spy_0528 M5005_Spy_0529 M5005_Spy_0530 M5005_Spy_0531	3572387 3572388 3572389 3572390 3572391	NE NE NE NE E NC	Spy49_0532 Spy49_0533 Spy49_0534 Spy49_0535 Spy49_0536 Spy49_0537	6985547 6985548 6985549 6985550 6985551 6985552	NE NE NE NE E NC	kgdA - - prfB ftsE	*	_	_	2-dehydro-3-deoxygluconokinase keto-hydroxyglutarate-aldolase/keto-deoxy-phosphogluconate aldolase beta-phosphoglucomutase/glucose-1-phosphate phosphodismutase (Fe-S)-binding protein peptide chain release factor 2 cell division ATP-binding protein
M5005_Spy_0527 M5005_Spy_0528 M5005_Spy_0529 M5005_Spy_0530 M5005_Spy_0531 M5005_Spy_0532	3572387 3572388 3572389 3572390 3572391 3572392	NE NE NE E NC	Spy49_0532 Spy49_0533 Spy49_0534 Spy49_0535 Spy49_0536 Spy49_0537 Spy49_0538	6985547 6985548 6985549 6985550 6985551 6985552 6985553	NE NE NE NE E NC	kgdA - - prfB	* * * * *	SSA_0869 SSA_0871	SP_0755 SP_0757	2-dehydro-3-deoxygluconokinase keto-hydroxyglutarate-aldolase/keto-deoxy-phosphogluconate aldolase beta-phosphoglucomutase/glucose-1-phosphate phosphodismutase (Fe-S)-binding protein peptide chain release factor 2 cell division ATP-binding protein cell division protein
M5005_Spy_0527 M5005_Spy_0528 M5005_Spy_0529 M5005_Spy_0530 M5005_Spy_0531 M5005_Spy_0533 M5005_Spy_0533c	3572387 3572388 3572389 3572390 3572391 3572392 3572393	NE NE NE E NC C	Spy49_0532 Spy49_0533 Spy49_0534 Spy49_0535 Spy49_0536 Spy49_0537 Spy49_0538 Spy49_0539c	6985547 6985548 6985549 6985550 6985551 6985552 6985553 6985554	NE NE NE E NC E NE	kgdA - - prfB ftsE	*	_	_	2-dehydro-3-deoxygluconokinase keto-hydroxyglutarate-aldolase/keto-deoxy-phosphogluconate aldolase beta-phosphoglucomutase/glucose-1-phosphate phosphodismutase (Fe-S)-binding protein peptide chain release factor 2 cell division ATP-binding protein cell division protein hydroxyacylglutathione hydrolase
M5005_Spy_0527 M5005_Spy_0528 M5005_Spy_0529 M5005_Spy_0530 M5005_Spy_0531 M5005_Spy_0532 M5005_Spy_0533c M5005_Spy_0534	3572387 3572388 3572389 3572390 3572391 3572392 3572393 3572394	NE NE NE E NC C NE NE	Spy49_0532 Spy49_0533 Spy49_0534 Spy49_0535 Spy49_0536 Spy49_0537 Spy49_0538	6985547 6985548 6985549 6985550 6985551 6985552 6985553	NE NE NE NE E NC	kgdA - - prfB ftsE	*	_	_	2-dehydro-3-deoxygluconokinase keto-hydroxyglutarate-aldolase/keto-deoxy-phosphogluconate aldolase beta-phosphoglucomutase/glucose-1-phosphate phosphodismutase (Fe-S)-binding protein peptide chain release factor 2 cell division ATP-binding protein cell division protein hydroxyacy/glutathione hydrolase acetoin reductase
M5005_Spy_0527 M5005_Spy_0528 M5005_Spy_0529 M5005_Spy_0531 M5005_Spy_0531 M5005_Spy_0532 M5005_Spy_05334 M5005_Spy_0534 M5005_Spy_0535	3572387 3572388 3572389 3572390 3572391 3572392 3572393 3572394 3572395	NE NE NE C NC C NE NE	Spy49_0532 Spy49_0533 Spy49_0534 Spy49_0535 Spy49_0536 Spy49_0537 Spy49_0538 Spy49_0539c Spy49_0540	6985547 6985548 6985549 6985550 6985551 6985552 6985553 6985554 6985555	NE NE NE E NC E NE NE	kgdA prfB ftsE ftsX	*	_	_	2-dehydro-3-deoxygluconokinase keto-hydroxyglutare-aldolase/keto-deoxy-phosphogluconate aldolase kete-phosphoglucomutase/glucose-1-phosphate phosphodismutase (Fe-S)-binding protein peptide chain release factor 2 cell division ATP-binding protein cell division protein hydroxyacy[glutathione hydrolase acetoin reductase acetoin reductase acetoin dehydrogenase, partial
M5005_Spy_0527 M5005_Spy_0528 M5005_Spy_0529 M5005_Spy_0530 M5005_Spy_0531 M5005_Spy_0532 M5005_Spy_0533c M5005_Spy_0534 M5005_Spy_0534 M5005_Spy_0536	3572387 3572388 3572389 3572390 3572391 3572392 3572393 3572394 3572395 3572358	NE NE NE E NC C NE NE NE NE NE	Spy49_0532 Spy49_0533 Spy49_0534 Spy49_0535 Spy49_0536 Spy49_0537 Spy49_0539 Spy49_0540 Spy49_0540	6985547 6985548 6985549 6985550 6985551 6985552 6985553 6985554 6985555	NE NE NE E NC E NE NE NE	kgdA prfB ftsE ftsX dinG	* * *	_	_	2-dehydro-3-deoxygluconokinase keto-hydroxyglutarate-aldolase/keto-deoxy-phosphogluconate aldolase beta-phosphoglucomutase/glucose-1-phosphate phosphodismutase (Fe-S)-binding protein peptide chain release factor 2 cell division ATP-binding protein cell division protein hydroxyacylglutathione hydrolase acetoin reductase acetoin dehydrogenase, partial bifunctional ATP-dependent DNA helicase/DNA polymerase III subunit epsilon
M5005_Spy_0527 M5005_Spy_0528 M5005_Spy_0529 M5005_Spy_0530 M5005_Spy_0531 M5005_Spy_0532 M5005_Spy_0534 M5005_Spy_0534 M5005_Spy_0536 M5005_Spy_0536	3572387 3572388 3572389 3572390 3572391 3572392 3572393 3572394 3572395 3572358 3572359	NE NE NE E NC C NE NE NE NC	Spy49_0532 Spy49_0533 Spy49_0534 Spy49_0535 Spy49_0536 Spy49_0537 Spy49_0538 Spy49_05390 Spy49_0540	6985547 6985548 6985549 6985550 6985551 6985552 6985553 6985554 6985555 6985556 6985557	NE NE NE E NC E NE NE NE NE	kgdA prfB ftsE ftsX dinG aspC	*	_	SP_0757	2-dehydro-3-deoxygluconokinase keto-hydroxyglucarate-aldolase/keto-deoxy-phosphogluconate aldolase beta-phosphoglucomutase/glucose-1-phosphate phosphodismutase (Fe-S)-binding protein peptide chain release factor 2 cell division ATP-binding protein cell division protein hydroxyacylglutathione hydrolase acetoin reductase acetoin reductase acetoin in dehydrogenase, partial bifunctional ATP-dependent DNA helicase/DNA polymerase III subunit epsilon aspartate aminotransferase
M5005_Spy_0527 M5005_Spy_0528 M5005_Spy_0529 M5005_Spy_0531 M5005_Spy_0531 M5005_Spy_0532 M5005_Spy_0534 M5005_Spy_0534 M5005_Spy_0534 M5005_Spy_0535 M5005_Spy_0536	3572387 3572388 3572389 3572390 3572391 3572392 3572393 3572394 3572395 3572358 3572359 3572359	NE NE NE E NC C NE NE NC NE NC NE NC NE NC NE NC NE NE NE NE NE	Spy49_0532 Spy49_0533 Spy49_0534 Spy49_0535 Spy49_0536 Spy49_0537 Spy49_0538 Spy49_0539c Spy49_0540 Spy49_0543 Spy49_0543 Spy49_0543	6985547 6985548 6985549 6985550 6985551 6985552 6985553 6985554 6985555 6985555 6985557 6985557	NE NE NE E NC E NE NE NE NE NE E	kgdA prfB ftsE ftsX dinG	* * * * * *	_	_	2-dehydro-3-deoxygluconokinase keto-hydroxyglutarate-aldolase/keto-deoxy-phosphogluconate aldolase beta-phosphoglucomutase/glucose-1-phosphate phosphodismutase (Fe-5)-binding protein peptide chain release factor 2 cell division ATP-binding protein cell division protein hydroxyacylglutathione hydrolase acetoin reductase acetoin reductase acetoin dehydrogenase, partial bifunctional ATP-dependent DNA helicase/DNA polymerase III subunit epsilon aspartate aminotransferase asparaginyl-tRNA synthetase
M5005_Spy_0527 M5005_Spy_0528 M5005_Spy_0529 M5005_Spy_0531 M5005_Spy_0531 M5005_Spy_0533 M5005_Spy_0533 M5005_Spy_0536 M5005_Spy_0536 M5005_Spy_0537 M5005_Spy_0538 M5005_Spy_0538 M5005_Spy_0538	3572387 3572388 3572389 3572390 3572391 3572392 3572393 3572394 3572358 3572358 3572359 3572360 3572361	NE NE NE NE C NE NE NC NE NC NE NC NE NC NE NC NE NE NE NE	Spy49_0532 Spy49_0533 Spy49_0534 Spy49_0535 Spy49_0535 Spy49_0537 Spy49_0538 Spy49_0539 Spy49_0540 Spy49_0541 Spy49_0544 Spy49_0544 Spy49_0544	6985547 6985548 6985549 6985550 6985551 6985552 6985554 6985555 6985556 6985557 6985558 6985559	NE NE NE E NC E NE NE NE NE E E E E E E	kgdA prfB ftsE ftsX dinG aspC	* * *	_	SP_0757	2-dehydro-3-deoxygluconokinase keto-hydroxyglucarate-aldolase/keto-deoxy-phosphogluconate aldolase beta-phosphoglucomutase/glucose-1-phosphate phosphodismutase (Fe-S)-binding protein peptide chain release factor 2 cell division ATP-binding protein cell division protein hydroxyacyfglutathione hydrolase acetoin reductase acetoin reductase acetoin dehydrogenase, partial bifunctional ATP-dependent DNA helicase/DNA polymerase III subunit epsilon aspartate aminotransferase asparaginyl-tRNA synthetase hypothetical protein M5005_Spy_0539
M5005_Spy_0527 M5005_Spy_0528 M5005_Spy_0529 M5005_Spy_0531 M5005_Spy_0531 M5005_Spy_0532 M5005_Spy_0534 M5005_Spy_0535 M5005_Spy_0537 M5005_Spy_0537 M5005_Spy_0538 M5005_Spy_0538 M5005_Spy_0539 M5005_Spy_0539 M5005_Spy_0539 M5005_Spy_0539	3572387 3572388 3572389 3572390 3572391 3572392 3572393 3572394 3572395 3572358 3572359 3572360 3572361 3572362	NE NE NE E NC C NE NC NE NE NE	Spy49_0532 Spy49_0533 Spy49_0534 Spy49_0535 Spy49_0535 Spy49_0538 Spy49_0538 Spy49_0539c Spy49_0540 Spy49_0541 Spy49_0543 Spy49_0545 Spy49_0545	6985547 6985548 6985549 6985550 6985551 6985552 6985553 6985554 6985555 6985556 6985557 6985558 6985559 6985559	NE NE NE E NC E NE NE NE E NE NE NE NE NE NE NE NE NE	kgdA prfB ftsE ftsX dinG aspC	* * * * * *	_	SP_0757	2-dehydro-3-deoxygluconokinase keto-hydroxyglucarate-aldolase/keto-deoxy-phosphogluconate aldolase beta-phosphoglucomutase/glucose-1-phosphate phosphodismutase (Fe-S)-binding protein peptide chain release factor 2 cell division ATP-binding protein cell division protein hydroxyacylglutathione hydrolase acetoin reductase acetoin reductase acetoin dehydrogenase, partial bifunctional ATP-dependent DNA helicase/DNA polymerase III subunit epsilon aspartate aminotransferase asparaginyl-tRNA synthetase hypothetical protein M5005_Spy_0539 transporter
M5005_Spy_0527 M5005_Spy_0528 M5005_Spy_0529 M5005_Spy_0530 M5005_Spy_0531 M5005_Spy_0531 M5005_Spy_0532 M5005_Spy_0534 M5005_Spy_0534 M5005_Spy_0534 M5005_Spy_0537 M5005_Spy_0537 M5005_Spy_0537 M5005_Spy_0537 M5005_Spy_0538 M5005_Spy_0539 M5005_Spy_0530 M5005_Spy_0530	3572387 3572388 3572389 3572390 3572391 3572392 3572393 3572394 3572358 3572358 3572359 3572360 3572361 3572362 3572363	NE NE NE E NC C NE NC NE NE NE NE	Spy49_0532 Spy49_0533 Spy49_0534 Spy49_0535 Spy49_0535 Spy49_0537 Spy49_0538 Spy49_0540 Spy49_0541 Spy49_0543 Spy49_0544 Spy49_0545 Spy49_0544 Spy49_0545	6985547 6985548 6985550 6985551 6985552 6985553 6985554 6985555 6985555 6985557 6985558 6985559 6985560 6985560	NE NE NE E NC E NE N	kgdA prfB ftsE ftsX dinG aspC asnC	* * * * * *	_	SP_0757	2-dehydro-3-deoxygluconokinase keto-hydroxyglucarate-aldolase/keto-deoxy-phosphogluconate aldolase beta-phosphoglucomutase/glucose-1-phosphate phosphodismutase (Fe-S)-binding protein peptide chain release factor 2 cell division ATP-binding protein cell division protein hydroxyacylglutathione hydrolase acetoin reductase acetoin reductase acetoin dehydrogenase, partial bifunctional ATP-dependent DNA helicase/DNA polymerase III subunit epsilon asparatate aminotransferase asparaginyl-tRNA synthetase hypothetical protein M5005_Spy_0539 transporter hypothetical protein M5005_Spy_0541
M5005_Spy_0527 M5005_Spy_0528 M5005_Spy_0530 M5005_Spy_0531 M5005_Spy_0531 M5005_Spy_0534 M5005_Spy_0534 M5005_Spy_0536 M5005_Spy_0536 M5005_Spy_0537 M5005_Spy_0537 M5005_Spy_0539 M5005_Spy_0530 M5005_Spy_0530 M5005_Spy_0530 M5005_Spy_0530 M5005_Spy_0530 M5005_Spy_0530 M5005_Spy_0530	3572387 3572388 3572389 3572390 3572391 3572392 3572393 3572394 3572358 3572358 3572360 3572361 3572362 3572363 3572363	NE NE NE C C NE NC NE NC NE NC NE NC NE	Spy49_0532 Spy49_0533 Spy49_0534 Spy49_0536 Spy49_0536 Spy49_0537 Spy49_0539 Spy49_0540 Spy49_0541 Spy49_0543 Spy49_0545 Spy49_0545 Spy49_0545 Spy49_0545 Spy49_0545	6985547 6985548 6985549 6985550 6985551 6985552 6985553 6985555 6985556 6985556 6985556 6985556 6985560 6985560 6985560 6985560	NE NE NE E NC E NE N	kgdA - prfB ftsE ftsX - dinG aspC asnC - pepD	* * * * * *	_	SP_0757	2-dehydro-3-deoxygluconokinase keto-hydroxyglucarate-aldolase/keto-deoxy-phosphogluconate aldolase beta-phosphoglucomutase/glucose-1-phosphate phosphodismutase (Fe-S)-binding protein peptide chain release factor 2 cell division ATP-binding protein cell division protein hydroxyacyfglutathione hydrolase acetoin reductase acetoin reductase acetoin dehydrogenase, partial bifunctional ATP-dependent DNA helicase/DNA polymerase III subunit epsilon aspartate aminotransferase asparaginyl-tRNA synthetase hypothetical protein M5005_Spy_0539 transporter hypothetical protein M5005_Spy_0541 dipeptidase
M5005_Spy_0527 M5005_Spy_0528 M5005_Spy_0529 M5005_Spy_0530 M5005_Spy_0531 M5005_Spy_0531 M5005_Spy_0534 M5005_Spy_0535 M5005_Spy_0534 M5005_Spy_0535 M5005_Spy_0536 M5005_Spy_0537 M5005_Spy_0537 M5005_Spy_0530 M5005_Spy_0530 M5005_Spy_0530 M5005_Spy_0530 M5005_Spy_0540 M5005_Spy_0540	3572387 3572388 3572389 3572399 3572391 3572392 3572395 3572395 3572358 3572350 3572360 3572361 3572362 3572364 3572364 3572364	NE NE E NC C NE NE NE NC NE NC NE NC NE NC NE NC NE NE NC NE	Spv49_0532 Spv49_0533 Spv49_0534 Spv49_0535 Spv49_0536 Spv49_0537 Spv49_0538 Spv49_0540 Spv49_0540 Spv49_0541 Spv49_0544 Spv49_0545 Spv49_0545 Spv49_0545 Spv49_0545 Spv49_0545	6985547 6985548 6985549 6985550 6985551 6985552 6985553 6985553 6985555 6985556 6985556 6985558 6985558 6985558 6985556 6985560 6985560 6985561 6985561	NE NE E NC E NE N	kgdA prfB ftsE ftsX dinG aspC asnC	* * * * * *	_	SP_0757	2-dehydro-3-deoxygluconokinase keto-hydroxyglucarate-aldolase/keto-deoxy-phosphogluconate aldolase beta-phosphoglucomutase/glucose-1-phosphate phosphodismutase (Fe-S)-binding protein peptide chain release factor 2 cell division ATP-binding protein cell division protein hydroxyacylglutathione hydrolase acetoin reductase acetoin reductase acetoin dehydrogenase, partial bifunctional ATP-dependent DNA helicase/DNA polymerase III subunit epsilon aspartate aminotransferase asparaginyl-tRNA synthetase hypothetical protein M5005_Spy_0539 transporter hypothetical protein M5005_Spy_0541 dipeptidase high-affinity zinc uptake system protein znuA
M5005_Spy_0527 M5005_Spy_0528 M5005_Spy_0529 M5005_Spy_0530 M5005_Spy_0531 M5005_Spy_0531 M5005_Spy_0533 M5005_Spy_0534 M5005_Spy_0536 M5005_Spy_0536 M5005_Spy_0537 M5005_Spy_0538 M5005_Spy_0538 M5005_Spy_0538 M5005_Spy_0538 M5005_Spy_0539 M5005_Spy_0540 M5005_Spy_0543 M5005_Spy_0543	3572387 3572388 3572389 3572390 3572391 3572392 3572394 3572395 3572356 3572360 3572362 3572362 3572363 3572363 3572364 3572364 3572364	NE NE E NC C NE NE NC NE NC NE NC NE	Spy49_0532 Spy49_0533 Spy49_0534 Spy49_0535 Spy49_0536 Spy49_0537 Spy49_0539 Spy49_0540 Spy49_0540 Spy49_0544 Spy49_0544 Spy49_0545 Spy49_0545 Spy49_0545 Spy49_0545 Spy49_0545 Spy49_0545	6985547 6985548 6985549 6985550 6985551 6985552 6985553 6985554 6985555 6985556 6985556 6985556 6985560 6985561 6985561 6985562 6985562 6985563	NE NE NE NC E NE N	kgdA	* * * * * *	_	SP_0757	2-dehydro-3-deoxygluconokinase keto-hydroxyglucarate-aldolase/keto-deoxy-phosphogluconate aldolase beta-phosphoglucomutase/glucose-1-phosphate phosphodismutase (Fe-S)-binding protein peptide chain release factor 2 cell division ATP-binding protein cell division protein hydroxyacylglutathione hydrolase acetoin reductase acetoin reductase acetoin reductase hydroxyacylglutathione hydrolase acetoin dehydrogenase, partial bifunctional ATP-dependent DNA helicase/DNA polymerase III subunit epsilon aspartate aminotransferase asparaginyl-RNA synthetase hypothetical protein M5005_Spy_0539 transporter hypothetical protein M5005_Spy_0541 dipeptidase high-affinity zinc uptake system protein znuA GntR family transcriptional regulator
M5005_Spy_0527 M5005_Spy_0528 M5005_Spy_0529 M5005_Spy_0530 M5005_Spy_0531 M5005_Spy_0531 M5005_Spy_0532 M5005_Spy_0533 M5005_Spy_0533 M5005_Spy_0534 M5005_Spy_0536 M5005_Spy_0536 M5005_Spy_0537 M5005_Spy_0530 M5005_Spy_0540 M5005_Spy_0540 M5005_Spy_0540 M5005_Spy_0544 M5005_Spy_0544	3572387 3572388 3572389 3572399 3572392 3572392 3572393 3572395 3572356 3572356 3572361 3572362 3572364 3572365 3572365 3572365 3572365	NE NE E NC C NE	Spy49_0532 Spy49_0533 Spy49_0534 Spy49_0535 Spy49_0536 Spy49_0537 Spy49_0539 Spy49_0540 Spy49_0541 Spy49_0543 Spy49_0545 Spy49_0545 Spy49_0545 Spy49_0545 Spy49_0545 Spy49_0545 Spy49_0545 Spy49_0545 Spy49_0545 Spy49_0545 Spy49_0545 Spy49_0545	6985547 6985548 6985549 6985550 6985555 6985553 6985555 6985555 6985556 6985556 6985556 6985560 6985560 6985560 6985560 6985562 6985564 6985564 6985564 6985564 6985564	NE NE E NC E NE N	kgdA prfB ftsE ftsX dinG aspC - asnC - pepD adcA - agaS	* * * * * *	_	SP_0757 SP_1542	2-dehydro-3-deoxygluconokinase keto-hydroxyglucarate-aldolase/keto-deoxy-phosphogluconate aldolase beta-phosphoglucomutase/glucose-1-phosphate phosphodismutase (Fe-S)-binding protein peptide chain release factor 2 cell division ATP-binding protein cell division protein hydroxyacylglutathione hydrolase acetoin reductase acetoin dehydrogenase, partial bifunctional ATP-dependent DNA helicase/DNA polymerase III subunit epsilon aspartate aminotransferase asparaginyl-tRNA synthetase hypothetical protein M5005_Spy_0539 transporter hypothetical protein M5005_Spy_0541 dipeptidase high-affinity zinc uptake system protein znuA GntR family transcriptional regulator galactosamine-6-phosphate deaminase
M5005_Spy_0527 M5005_Spy_0528 M5005_Spy_0528 M5005_Spy_0530 M5005_Spy_0531 M5005_Spy_0531 M5005_Spy_0534 M5005_Spy_0534 M5005_Spy_0534 M5005_Spy_0538 M5005_Spy_0538 M5005_Spy_0538 M5005_Spy_0538 M5005_Spy_0539 M5005_Spy_0540 M5005_Spy_0544 M5005_Spy_0544 M5005_Spy_0544 M5005_Spy_0545	3572387 3572388 3572389 3572399 3572392 3572393 3572394 3572395 3572365 3572361 3572362 3572362 3572363 3572363 3572365 3572365 3572365	NE NE E NC C NE	Spv49_0532 Spv49_0533 Spv49_0534 Spv49_0535 Spv49_0536 Spv49_0539 Spv49_0539 Spv49_0540 Spv49_0540 Spv49_0544 Spv49_0544 Spv49_0545 Spv49_0545 Spv49_0545 Spv49_0545 Spv49_0545 Spv49_0545 Spv49_0545 Spv49_0545 Spv49_05525	6985547 6985548 6985549 6985550 6985552 6985552 6985553 6985554 6985555 6985556 6985556 6985556 6985556 6985556 6985556 6985556 6985566 6985566 6985566	NE NE E NC E NE N	kgdA	* * * * * *	_	SP_0757	2-dehydro-3-deoxygluconokinase keto-hydroxyglucarate-aldolase/keto-deoxy-phosphogluconate aldolase beta-phosphoglucomutase/glucose-1-phosphate phosphodismutase (Fe-S)-binding protein peptide chain release factor 2 cell division ATP-binding protein cell division protein hydroxyacylglutathione hydrolase acetoin reductase acetoin reductase acetoin reduvdrogenase, partial bifunctional ATP-dependent DNA helicase/DNA polymerase III subunit epsilon aspartate aminotransferase asparaginyl-HRNA synthetase hypothetical protein M5005_Spy_0539 transporter hypothetical protein M5005_Spy_0541 dipeptidase high-affinity zinc uptake system protein znuA GRR family transcriptional regulator galactosamine-6-phosphate deaminase 505 ribosomal protein L31
M5005_Spy_0527 M5005_Spy_0528 M5005_Spy_0528 M5005_Spy_0532 M5005_Spy_0531 M5005_Spy_0531 M5005_Spy_0534 M5005_Spy_0536 M5005_Spy_0536 M5005_Spy_0536 M5005_Spy_0537 M5005_Spy_0537 M5005_Spy_0537 M5005_Spy_0538 M5005_Spy_0542 M5005_Spy_0544 M5005_Spy_0548 M5005_Spy_0546 M5005_Spy_0546 M5005_Spy_0547 M5005_Spy_0546 M5005_Spy_0547 M5005_Spy_0546 M5005_Spy_0546 M5005_Spy_0546 M5005_Spy_0546 M5005_Spy_0546 M5005_Spy_0546	3572387 3572388 3572389 3572399 3572392 3572393 3572394 3572395 3572365 3572361 3572362 3572362 3572363 3572363 3572365 3572365 3572365	NE NE NE NC C NE NC NE NC NE NC NE	Spv49_0532 Spv49_0533 Spv49_0533 Spv49_0535 Spv49_0537 Spv49_0538 Spv49_0539 Spv49_0540 Spv49_0540 Spv49_0541 Spv49_0545 Spv49_0545 Spv49_0545 Spv49_0545 Spv49_0545 Spv49_0550 Spv49_0550 Spv49_0550 Spv49_0550 Spv49_0552	6985547 6985548 6985549 6985550 6985551 6985552 6985553 6985555 6985556 6985556 6985561 6985561 6985562 6985563 6985563 6985563 6985563 6985563 6985565	NE NE NE NC E NC NE	kgdA prfB ftsE ftsX dinG aspC pepD adcA - agaS rpmE2	* * * * * *	_	SP_1542 SP_1299	2-dehydro-3-deoxygluconokinase keto-hydroxyglucarate-aldolase/keto-deoxy-phosphogluconate aldolase beta-phosphoglucomutase/glucose-1-phosphate phosphodismutase (Fe-S)-binding protein peptide chain release factor 2 cell division ATP-binding protein cell division protein hydroxyacylglutathione hydrolase acetoin reductase acetoin dehydrogenase, partial bifunctional ATP-dependent DNA helicase/DNA polymerase III subunit epsilon aspartate aminotransferase asparaginyl-tRNA synthetase hypothetical protein M5005_Spy_0539 transporter hypothetical protein M5005_Spy_0541 dipeptidase high-affinity zinc uptake system protein znuA GntR family transcriptional regulator galactosamine-6-phosphate deaminase
M5005_Spy_0527 M5005_Spy_0528 M5005_Spy_0530 M5005_Spy_0531 M5005_Spy_0531 M5005_Spy_0531 M5005_Spy_0532 M5005_Spy_0533 M5005_Spy_0533 M5005_Spy_0534 M5005_Spy_0534 M5005_Spy_0539 M5005_Spy_0539 M5005_Spy_0540 M5005_Spy_0540 M5005_Spy_0540 M5005_Spy_0540 M5005_Spy_0543 M5005_Spy_0543 M5005_Spy_0546 M5005_Spy_0545 M5005_Spy_0545 M5005_Spy_0545 M5005_Spy_0545 M5005_Spy_0545 M5005_Spy_0545	3572387 3572388 3572388 3572398 3572391 3572392 3572393 3572395 3572359 3572356 3572360 3572362 3572363 3572365 3572365 3572365 3572365 3572366 3572366 3572366 3572366 3572368	NE NE NE NE C NE	Spv49_0532 Spv49_0533 Spv49_0533 Spv49_0536 Spv49_0536 Spv49_0539 Spv49_0540 Spv49_0541 Spv49_0541 Spv49_0544 Spv49_0545 Spv49_0545 Spv49_0546 Spv49_0546 Spv49_0545 Spv49_0545 Spv49_0545 Spv49_0545 Spv49_0555 Spv49_05552 Spv49_05552 Spv49_05552	6985547 6985548 6985548 6985550 6985555 6985552 6985553 6985553 6985556 6985556 6985556 6985556 69856 698	NE NE NE NE NC NE	kgdA prfB ftsE ftsX dinG aspC - asnC - pepD adcA - agaS	* * * * * *	_	SP_0757 SP_1542	2-dehydro-3-deoxygluconokinase keto-hydroxyglucarate-aldolase/keto-deoxy-phosphogluconate aldolase beta-phosphoglucomutase/glucose-1-phosphate phosphodismutase (Fe-S)-binding protein peptide chain release factor 2 cell division ATP-binding protein cell division protein hydroxyacylglutathione hydrolase acetoin dehydrogenase, partial bifunctional ATP-dependent DNA helicase/DNA polymerase III subunit epsilon aspartate aminotransferase asparaginyl-tRNA synthetase hypothetical protein M5005_Spy_0539 transporter hypothetical protein M5005_Spy_0541 dipeptidase high-affinity zinc uptake system protein znuA GnRt family transcriptional regulator galactosamine-6-phosphate deaminase 50S ribosomal protein L31 phosphoesterase, DHH family protein flavodoxin
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M5005_Spy_0527 M5005_Spy_0528 M5005_Spy_0530 M5005_Spy_0531 M5005_Spy_0531 M5005_Spy_0531 M5005_Spy_0534 M5005_Spy_0536 M5005_Spy_0536 M5005_Spy_0536 M5005_Spy_0537 M5005_Spy_0538 M5005_Spy_0538 M5005_Spy_0530 M5005_Spy_0540 M5005_Spy_0540 M5005_Spy_0540 M5005_Spy_0546 M5005_Spy_0548 M5005_Spy_0548 M5005_Spy_0548 M5005_Spy_0548 M5005_Spy_0548 M5005_Spy_0548 M5005_Spy_0549 M5005_Spy_0549 M5005_Spy_0549 M5005_Spy_0549 M5005_Spy_0549 M5005_Spy_0545 M5005_Spy_0545	3572387 3572388 3572389 3572399 3572391 3572392 3572394 3572395 3572356 3572356 3572356 3572362 3572363 3572363 3572363 3572363 3572363 3572369 3572369 3572369 3572369 3572369 3572370 3572370	NE NE NE NE C NE	Spy49_0532 Spy49_0533 Spy49_0534 Spy49_0536 Spy49_0536 Spy49_0539 Spy49_0540 Spy49_0541 Spy49_0543 Spy49_0544 Spy49_0545 Spy49_0545 Spy49_0545 Spy49_0545 Spy49_0550 Spy49_0550 Spy49_0555 Spy49_0555 Spy49_0555 Spy49_0555 Spy49_0555 Spy49_0555 Spy49_0555 Spy49_0555 Spy49_0555 Spy49_0555 Spy49_0555 Spy49_0555 Spy49_0555	6985547 6985548 6985548 6985559 6985551 6985552 6985553 6985556 6985556 6985556 6985561 6985562 6985562 6985562 6985563 6985563 6985563 6985564 6985564 6985565 6985566 6985566 6985566 6985566 6985566 6985566 6985566 6985566	NE N	kgdA - prfB ftsE ftsX - dinG aspC asnC - pepD adcA - gasS rpmE2 - flaV	* * * * * *	_	SP_1542 SP_1299	2-dehydro-3-deoxygluconokinase keto-hydroxyglucarate-aldolase/keto-deoxy-phosphogluconate aldolase beta-phosphoglucomutase/glucose-1-phosphate phosphodismutase (Fe-S)-binding protein peptide chain release factor 2 cell division ATP-binding protein cell division protein hydroxyacylglutathione hydrolase acetoin reductase acetoin reductase acetoin dehydrogenase, partial bifunctional ATP-dependent DNA helicase/DNA polymerase III subunit epsilon aspartate aminotransferase assparaginyl-tRNA synthetase hypothetical protein M5005_Spy_0539 transporter hypothetical protein M5005_Spy_0541 dipeptidase high-affinity zinc uptake system protein znuA GntR family transcriptional regulator galactosamine-6-phosphate deaminase 505 ribosomal protein L31 phosphoesterase, DHH family protein flavodoxin hypothetical protein M5005_Spy_0549 chloride channel protein
M5005_Spy_0527 M5005_Spy_0528 M5005_Spy_0530 M5005_Spy_0531 M5005_Spy_0531 M5005_Spy_0531 M5005_Spy_0534 M5005_Spy_0535 M5005_Spy_0534 M5005_Spy_0537 M5005_Spy_0538 M5005_Spy_0538 M5005_Spy_0539 M5005_Spy_0540	3572387 3572388 3572388 3572399 3572399 3572392 3572393 3572395 3572359 3572359 3572356 3572362 3572363 3572365 3572365 3572365 3572366 3572366 3572366 3572367 3572367 3572368 3572369 3572369 3572369 3572372 3572372	NE NE NE NC C NE NC NE NC NE NC NE	Spv49_0532 Spv49_0533 Spv49_0533 Spv49_0536 Spv49_0536 Spv49_0539 Spv49_0539 Spv49_0540 Spv49_0541 Spv49_0544 Spv49_0544 Spv49_0545 Spv49_0546 Spv49_0546 Spv49_0547 Spv49_0555 Spv49_0555 Spv49_0555 Spv49_0555 Spv49_0555 Spv49_0555 Spv49_0555 Spv49_0555 Spv49_0555 Spv49_0555 Spv49_0556 Spv49_0556 Spv49_0556 Spv49_0556 Spv49_0556 Spv49_0556 Spv49_0556 Spv49_0556 Spv49_0556	6985547 6985548 6985549 6985550 6985551 6985551 6985552 6985555 6985556 6985556 6985560 6985561 6985562 6985562 6985566 6985566 6985566 6985566 6985566 6985567 6985566 6985567 6985567 6985567 6985567 6985567 6985567 6985567	NE N	kgdA	* * * * * *	_	SP_1542 SP_1299	2-dehydro-3-deoxygluconokinase keto-hydroxyglucarate-aldolase/keto-deoxy-phosphogluconate aldolase beta-phosphoglucomutase/glucose-1-phosphate phosphodismutase (Fe-S)-binding protein peptide chain release factor 2 cell division ATP-binding protein cell division ATP-binding protein cell division protein hydroxyacylglutathione hydrolase acetoin reductase acetoin dehydrogenase, partial bifunctional ATP-dependent DNA helicase/DNA polymerase III subunit epsilon aspartate aminotransferase saparaginyl-HRNA synthetase hypothetical protein M5005_Spy_0539 transporter hypothetical protein M5005_Spy_0541 dipeptidase high-affinity zinc uptake system protein znuA GnR family transcriptional regulator galactosamine-6-phosphate deaminase SOS ribosomal protein L31 phosphoesterase, DHH family protein flavodoxin hypothetical protein M5005_Spy_0549 chloride channel protein L19
M5005_Spy_0527 M5005_Spy_0528 M5005_Spy_0529 M5005_Spy_0531 M5005_Spy_0531 M5005_Spy_0531 M5005_Spy_0534 M5005_Spy_0536 M5005_Spy_0536 M5005_Spy_0536 M5005_Spy_0537 M5005_Spy_0537 M5005_Spy_0537 M5005_Spy_0540 M5005_Spy_0540 M5005_Spy_0540 M5005_Spy_0540 M5005_Spy_0540 M5005_Spy_0546	3572387 3572388 3572389 3572399 3572391 3572392 3572393 3572394 3572356 3572356 3572356 3572356 3572366 3572366 3572365 3572365 3572365 3572365 3572365 3572365 3572367 3572367 3572367 3572367 3572373 3572373	NE NE NE NC C NE NC NC NE NE NE NC	Spy49_0532 Spy49_0533 Spy49_0534 Spy49_0535 Spy49_0537 Spy49_0539 Spy49_0540 Spy49_0540 Spy49_0541 Spy49_0545 Spy49_0545 Spy49_0545 Spy49_0545 Spy49_0545 Spy49_0545 Spy49_0550 Spy49_0550 Spy49_0550 Spy49_05550 Spy49_05550 Spy49_05550 Spy49_05555 Spy49_05555 Spy49_05555 Spy49_05555 Spy49_05555 Spy49_05555 Spy49_05555 Spy49_05555	6985547 6985548 6985549 6985550 6985551 6985552 6985553 6985555 6985556 6985561 6985561 6985562 6985562 6985563 6985566 6985564 6985566 6985566 6985566 6985567 6985569 6985570 6985570 6985571	NE NE NE NC E NE N	kgdA prfB ftsE ftsX dinG aspC asnC pepD adcA - pepD adcA flaV - flaV - rplS	* * * * * *	SSA_0871	SP_1542 SP_1299 SP_1297	2-dehydro-3-deoxygluconokinase keto-hydroxyglucarate-aldolase/keto-deoxy-phosphogluconate aldolase beta-phosphoglucomutase/glucose-1-phosphate phosphodismutase (Fe-S)-binding protein peptide chain release factor 2 cell division ATP-binding protein cell division protein hydroxyacylglutathione hydrolase acetoin reductase acetoin reductase acetoin reductase acetoin reductase acatein al-P-dependent DNA helicase/DNA polymerase III subunit epsilon aspartate aminotransferase asparaginyl-tRNA synthetase hypothetical protein M5005_Spy_0539 transporter hypothetical protein M5005_Spy_0541 dipeptidase high-affinity zinc uptake system protein znuA GnRt family transcriptional regulator galactosamine-6-phosphate deaminase 50S ribosomal protein L11 phosphoesterase, DHH family protein flavodoxin hypothetical protein M5005_Spy_0549 chloride channel protein L19 DNA gyrase
M5005_Spy_0527 M5005_Spy_0528 M5005_Spy_0530 M5005_Spy_0531 M5005_Spy_0531 M5005_Spy_0531 M5005_Spy_0533 M5005_Spy_0533 M5005_Spy_0533 M5005_Spy_0534 M5005_Spy_0534 M5005_Spy_0534 M5005_Spy_0540 M5005_Spy_0540 M5005_Spy_0540 M5005_Spy_0548 M5005_Spy_0553 M5005_Spy_0558	3572387 3572388 3572398 3572399 3572391 3572392 3572393 3572395 3572358 3572356 3572364 3572364 3572365 3572365 3572366 3572366 3572366 3572366 3572366 3572367 3572373 3572373	NE NE NE NC C NE NC NE NC NE NC NE NC NE NC NE	Spv49_0532 Spv49_0533 Spv49_0533 Spv49_0536 Spv49_0536 Spv49_0539 Spv49_0540 Spv49_0541 Spv49_0544 Spv49_0544 Spv49_0544 Spv49_0545 Spv49_0546 Spv49_0547 Spv49_0549 Spv49_0549 Spv49_0549 Spv49_0549 Spv49_0549 Spv49_0549 Spv49_0555 Spv49_0555 Spv49_0555 Spv49_0555 Spv49_0555 Spv49_0555 Spv49_0555 Spv49_0555 Spv49_0558 Spv49_0558 Spv49_0558 Spv49_0558 Spv49_0558 Spv49_0558 Spv49_0558 Spv49_0558 Spv49_0558 Spv49_0558 Spv49_0558	6985547 6985548 6985549 6985551 6985551 6985552 6985553 6985556 6985556 6985556 698557 69857 69857 6	NE NE NE NC E NC E NE N	kgdA prfB ftsE ftsX dinG aspC - asnC pepD adcA - agaS rpmE2 - flaV - rpIS - gyrB		_	SP_1542 SP_1299 SP_1297 SP_0806	2-dehydro-3-deoxygluconokinase keto-hydroxyglucarate-aldolase/keto-deoxy-phosphogluconate aldolase beta-phosphoglucomutase/glucose-1-phosphate phosphodismutase (Fe-S)-binding protein peptide chain release factor 2 cell division ATP-binding protein cell division protein hydroxyacylglutathione hydrolase acetoin edwydrogenase, partial bifunctional ATP-dependent DNA helicase/DNA polymerase III subunit epsilon aspartate aminotransferase asparaginyl-tRNA synthetase hypothetical protein M5005_Spy_0539 transporter hypothetical protein M5005_Spy_0541 dipeptidase high-affinity zinc uptake system protein znuA GnRt family transcriptional regulator galactosamine-6-phosphate deaminase 50S ribosomal protein L31 phosphoesterase, DHH family protein flavodoxin hypothetical protein M5005_Spy_0549 chloride channel protein 50S ribosomal protein L19 DNA gyrase DNA gyrases ubunit B
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M5005_SPy_0528 M5005_SPy_0529 M5005_SPy_0529 M5005_SPy_0530 M5005_SPy_0531 M5005_SPy_0531 M5005_SPy_0531 M5005_SPy_0533 M5005_SPy_0533 M5005_SPy_0533 M5005_SPy_0534 M5005_SPy_0539 M5005_SPy_0539 M5005_SPy_0544 M5005_SPy_0544 M5005_SPy_0546 M5005_SPy_0546 M5005_SPy_0549 M5005_SPy_0546 M5005_SPy_0549 M5005_SPy_0549 M5005_SPy_0549 M5005_SPy_0549 M5005_SPy_0549 M5005_SPy_0549 M5005_SPy_0549 M5005_SPy_0549 M5005_SPy_0559 M5005_SPy_0569	3572382 3572388 3572389 3572390 3572391 3572392 3572393 3572395 3572363 3572363 3572364 3572364 3572366 3572366 3572366 3572366 3572366 3572366 3572366 3572367 3572368 3572369 3572370 357237	NE NE NE NC C NE	Spv49_0532 Spv49_0533 Spv49_0533 Spv49_0533 Spv49_0533 Spv49_0539 Spv49_0540 Spv49_0541 Spv49_0543 Spv49_0544 Spv49_0544 Spv49_0545 Spv49_0545 Spv49_0545 Spv49_0547 Spv49_0545 Spv49_0545 Spv49_0555 Spv49_0555 Spv49_0555 Spv49_0555 Spv49_0556 Spv49_0558 Spv49_0575 Spv49_0575 Spv49_0578 Spv49_0578 Spv49_0578 Spv49_0578 Spv49_0578 Spv49_0578 Spv49_0578 Spv49_0578 Spv49_0578 Spv49_0578 Spv49_0578 Spv49_0578 Spv49_0578 Spv49_0578 Spv49_0578 Spv49_0578 Spv49_0578 Spv49_0578	6985547 6985548 6985549 6985549 6985550 6985551 6985555 6985556 6985556 6985556 6985566 6985566 6985566 6985566 6985567 6985567 6985567 6985568 6985568 6985569 6985569 6985578 6985589 6985589	NE NE NE E E NE NE NE NE NE NE NE NE NE	kgdA		SSA_0871 SSA_0878 SSA_0886	SP_0757 SP_1542 SP_1299 SP_1297 SP_0806 SP_0807	2-dehydro-3-deoxygluconokinase keto-hydroxyglutarate-aldolase/keto-deoxy-phosphogluconate aldolase beta-phosphoglucomutase/glucose-1-phosphate phosphodismutase (Fe-S)-binding protein peptide chain release factor 2 cell division ATP-binding protein cell division protein hydroxyacylglutathione hydrolase acetoin dehydrogenase, partial birunctional ATP-dependent DNA helicase/DNA polymerase III subunit epsilon aspartate aminotransferase asparaginyl-tRNA synthetase hypothetical protein M5005_Spy_0539 transporter hypothetical protein M5005_Spy_0541 dipeptidase high-affinity zinc uptake system protein znuA GntR family transcriptional regulator galactosamine-6-phosphate deaminase 505 ribosomal protein L13 lphosphoesterase, DHH family protein flavodoxin hypothetical protein M5005_Spy_0549 chloride channel protein 505 ribosomal protein L19 DNA gyrase DNA gyrase subunit B septation ring formation regulator EzrA hypothetical protein M5005_Spy_0555 phosphopyruvate hydratase transcriptional regulator transcriptional regulator transcriptional regulator transcriptional regulator transcriptional regulator transcriptional regulator transcriptional spissip protein streptolysin S biosynthesis protein streptolysin S biosynthesis protein streptolysin S sept-immunity protein streptolysin S export transmembrane protein
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M5005_SPy_0528 M5005_SPy_0528 M5005_SPy_0529 M5005_SPy_0530 M5005_SPy_0531 M5005_SPy_0531 M5005_SPy_0533 M5005_SPy_0533 M5005_SPy_0533 M5005_SPy_0533 M5005_SPy_0538 M5005_SPy_0538 M5005_SPy_0538 M5005_SPy_0538 M5005_SPy_0544 M5005_SPy_0544 M5005_SPy_0546 M5005_SPy_0548 M5005_SPy_0548 M5005_SPy_0548 M5005_SPy_0549 M5005_SPy_0559 M5005_SPy_0569 M5005_SPy_0569 M5005_SPy_0569 M5005_SPy_0569 M5005_SPy_0567 M5005_SPy_0567 M5005_SPy_0575 M5005_SPy_0575 M5005_SPy_0575 M5005_SPy_0575	3572387 3572388 3572398 3572399 3572391 3572392 3572393 3572356 3572356 3572356 3572362 3572363 3572363 3572363 3572363 3572364 3572366 3572366 3572367 3572367 3572367 3572367 3572367 3572368 3572367 3572367 3572367 3572367 3572367 3572367 3572367 3572367 3572367 357237 37237 37237 37237 37237 37237 37237 37237 37237 37237 37237	NE NE NE E NC C NE E E NE	Spv49_0532 Spv49_0533 Spv49_0533 Spv49_0533 Spv49_0533 Spv49_0539 Spv49_0540 Spv49_0541 Spv49_0543 Spv49_0544 Spv49_0544 Spv49_0545 Spv49_0545 Spv49_0545 Spv49_0547 Spv49_0545 Spv49_0545 Spv49_0555 Spv49_0555 Spv49_0555 Spv49_0555 Spv49_0556 Spv49_0558 Spv49_0575 Spv49_0575 Spv49_0578 Spv49_0578 Spv49_0578 Spv49_0578 Spv49_0578 Spv49_0578 Spv49_0578 Spv49_0578 Spv49_0578 Spv49_0578 Spv49_0578 Spv49_0578 Spv49_0578 Spv49_0578 Spv49_0578 Spv49_0578 Spv49_0578 Spv49_0578	6985547 6985548 6985549 6985549 6985550 6985551 6985555 6985556 6985556 6985556 6985556 6985566 6985566 6985566 6985567 6985567 6985568 6985568 6985569 6985569 6985569 6985570 6985570 6985571 6985572 6985573 6985573 6985573 6985573 6985573 6985573 6985574 6985575 6985575 6985575 6985575 6985575 6985575 6985575 6985577 6985578 6985578 6985579 6985589 6985589	NE NE NE E E NE NE NE NE NE NE NE NE NE	kgdA prfB ftsE ftsX dinG aspC asnC pepD adcA - agaS rpmE2 - flaV flav epf sagA sagB sagC sagD sagB sagC sagD sagE sagF sagG sagH sagI - tigA - tigB -		SSA_0871 SSA_0878 SSA_0886 SSA_1484 SSA_0783	SP_0757 SP_0757 SP_1542 SP_1299 SP_1297 SP_0806 SP_0807 SP_1128	2-dehydro-3-deoxygluconokinase keto-hydroxyglutarate-aldolase/keto-deoxy-phosphogluconate aldolase beta-phosphoglucomutase/glucose-1-phosphate phosphodismutase (Fe-S)-binding protein peptide chain release factor 2 cell division ATP-binding protein cell division protein hydroxyacylglutathion hydrolase acetoin dehydrogenase, partial bifunctional ATP-dependent DNA helicase/DNA polymerase III subunit epsilon aspartate aminotransferase saparaginyl-HRNA synthetase hypothetical protein M5005_Spy_0539 transporter hypothetical protein M5005_Spy_0541 dipeptidase high-affinity zinc uptake system protein znuA GntR family transcriptional regulator galactosamine-6-phosphate deaminase SOS ribosomal protein L13 phosphoesterase, DHH family protein flavodoxin hypothetical protein M5005_Spy_0549 chloride channel protein SOS ribosomal protein L19 DNA gyrase DNA gyrase subunit B septation ring formation regulator EzrA hypothetical protein M5005_Spy_0555 phosphopyruvate hydratase transposase transcriptional regulator transcriptional regulator transcriptional regulator transcriptional regulator transcriptional regulator transcriptional solicymthesis protein streptolysin S biosynthesis protein streptolysin S export transmembrane protein streptolysin S potein transmembrane protein streptolysin S export transmembrane protein streptolysin S export transmembrane protein streptolysin S potein transmembrane protein streptolysin S export

M5005_Spy_0580	2577276	_	Cmu40 0007	6005600	_	atnG		CCA 0707	CD 1500	ATP synthase F0F1 subunit gamma
M5005_Spy_0580 M5005_Spy_0581	3572326 3572327	E E	Spy49_0587 Spy49_0588	6985600 6985601	E E	atpG atpD	*	SSA_0787 SSA_0788	SP_1509 SP_1508	ATP synthase F0F1 subunit gamma ATP synthase F0F1 subunit beta
M5005_Spy_0582	3572328	NC	Spy49_0589	6985602	NC	atpC	*		*	ATP synthase F0F1 subunit epsilon
M5005_Spy_0583	3572329	NE	Spy49_0590	6985603	NE					hypothetical protein M5005_Spy_0583
M5005_Spy_0584	3572330	NE	Spy49_0591	6985604	NE	murA	*			UDP-N-acetylglucosamine 1-carboxyvinyltransferase
M5005_Spy_0585 M5005_Spy_0586	3572331 3572332	NE NE				epuA endA				epuA protein DNA-entry nuclease
,			Spy49_0592	6985605	NE					,
M5005_Spy_0587	3572333	Е	Spy49_0596	6985608	Ε	pheS	*	SSA_0912	SP_0579	phenylalanyl-tRNA synthetase subunit alpha
M5005_Spy_0588	3572334 3572335	E	Spy49_0597	6985609	E	pheT	*	SSA_0914	SP_0581	phenylalanyl-tRNA synthetase subunit beta salt-stress induced protein
M5005_Spy_0589	33/2333	NE	Spy49_0598	6985610	NE	-	*			sait-stress induced protein
M5005_Spy_0590	3572336	NE	Spy49_0599	6985611	NE	-	*			hypothetical protein M5005_Spy_0590
M5005_Spy_0591	3572337	NE	Spy49_0600	6985612	NE	-	*			ABC transporter permease
M5005_Spy_0592	3572338	NE	Spy49_0601	6985613	NE	-	*			ABC transporter ATP-binding protein
M5005_Spy_0593c M5005_Spy_0594	3572300 3572301	NE NC	Spy49_0602c Spy49_0603	6985614 6985615	NE C	rexB	*	SSA_1452	SP_1151	neutral zinc metallopeptidase ATP-dependent nuclease subunit B
M5005_Spy_0595	3572302	C	Spy49_0604	6985616	E	rexA	*	33A_1432	SP_1151	ATP-dependent nuclease subunit A
M5005_Spy_0596	3572303	NE	Spy49_0605	6985617	NE	-	*			arginine-binding protein
M5005_Spy_0597	3572304	Е	Spy49_0606	6985618	NC	rpsU				30S ribosomal protein S21
M5005_Spy_0598c M5005_Spy_0599	3572305 3572306	NE E	Spy49_0607c Spy49_0608	6985619 6985620	NE E	mscL dnaG	*	SSA_0824	SP_1072	large-conductance mechanosensitive channel DNA primase
M5005_Spy_0600	3572307	E	Spy49_0609	6985621	E	rpoD	*	SSA_0825	SP_1073	RNA polymerase sigma factor RpoD
M5005_Spy_0601	3572308	NE	Spy49_0610	6985622	NE	-	*			hypothetical protein M5005_Spy_0601
M5005_Spy_0602	3572309	Е	Spy49_0611	6985623	Ε	rmID				dTDP-4-dehydrorhamnose reductase
M5005_Spy_0603 M5005_Spy_0604	3572310 3572311	E E	Spy49_0612 Spy49_0613	6985624 6985625	E E	rgpAc rgpBc	*		SP_1366 SP_1365	alpha-(1,2)-rhamnosyltransferase alpha-L-Rha alpha-1,3-L-rhamnosyltransferase
M5005_Spy_0605	3572312	E	Spy49_0614	6985626	E	rgpCc	*		3F_1303	polysaccharide export ABC transporter permease
M5005_Spy_0606	3572313	E	Spy49_0615	6985627	E	rgpDc	*			polysaccharide export ATP-binding protein
M5005_Spy_0607	3572314	E	Spy49_0617	6985628	E	rgpEc	*			glycosyltransferase
M5005_Spy_0608 M5005_Spy_0609	3572315 3572316	E NE	Spy49_0618	6985629 6985630	E NE	rgpFc	*			alpha-L-Rha alpha-1,3-L-rhamnosyltransferase phosphoglycerol transferase
M5005_Spy_0610	3572317	NE	Spy49_0619 Spy49_0620	6985631	NE	-	*			glycosyltransferase
M5005_Spy_0611	3572318	NE	Spy49_0621	6985632	NE	-	*			hypothetical protein M5005_Spy_0611
M5005_Spy_0612	3572280	С	Spy49_0622	6985633	E	amrA	*	SSA_1738		transcriptional activator
M5005_Spy_0613	3572281 3572282	E	Spy49_0623	6985634 6985635	E	pepT	*			hypothetical protein M5005_Spy_0613
M5005_Spy_0614 M5005_Spy_0615	3572283	NE NE	Spy49_0624 Spy49_0625	6985636	NE NE	ebsA	*			peptidase T pore forming protein
M5005_Spy_0616c		NE	Spy49_0626c	6985637	NE	-				ferredoxin
M5005_Spy_0617	3572285	NC	Spy49_0627	6985638	NE	-	*			hypothetical protein M5005_Spy_0617
M5005_Spy_0618	3572286	C	Spy49_0628	6985639	NC	cmk infC	*	CCA 4500	SP_1603	cytidylate kinase translation initiation factor IF-3
M5005_Spy_0619 M5005_Spy_0620	3572287 3572288	c c	Spy49_0629 Spy49_0630	6985640 6985641	E NE	rpmI	*	SSA_1500	SP_0959 SP_0960	50S ribosomal protein L35
M5005_Spy_0621	3572289	NC	Spy49_0631	6985642	NC	rpIT	*		30300	50S ribosomal protein L20
M5005_Spy_0622c	3572290	E	Spy49_0632c	6985643	E	-	*			phosphoglycerol transferase
M5005_Spy_0623	3572291	NE	Spy49_0633	6985644	NE	-	*			methyltransferase
M5005_Spy_0624 M5005_Spy_0625	3572292 3572293	NE NE	Spy49_0634 Spy49_0635	6985645 6985646	NE NE	aroD aroF	*			3-dehydroquinate dehydratase chorismate synthase
M5005_Spy_0626	3572294	NE	Spy49_0636	6985647	NE	-	*			hypothetical protein M5005_Spy_0626
M5005_Spy_0627	3572295	NE	Spy49_0637	6985648	NE	gor	*			glutathione reductase
M5005_Spy_0628c		NE	Spy49_0638c	6985649	NE	folC.2	*			folylpolyglutamate synthase/dihydrofolate synthase
M5005_Spy_0629c M5005_Spy_0630	3572297 3572298	NE	Spy49_0639c Spy49_0640	6985650 6985651	NE	nifS1	*			hypothetical protein M5005_Spy_0629 cysteine desulfhydrase
M5005_Spy_0631	3572299	NE NE	Spy49_0640 Spy49_0641	6985652	NE NE	thiI	*			thiamine biosynthesis protein ThiI
M5005_Spy_0632	3572261	NE	Spy49_0642	6985653	NE	capA	*			capsule biosynthesis protein
M5005_Spy_0633	3572262	NC	Spy49_0643	6985654	NC	rpIU	*			50S ribosomal protein L21
M5005_Spy_0634 M5005_Spy_0635	3572263	NC	Spy49_0644	6985655	NC	rpmA	*			hypothetical protein M5005_Spy_0634 50S ribosomal protein L27
M5005_Spy_0636	3572264 3572265	NC NE	Spy49_0645 Spy49_0646	6985656 6985657	NC NE	-	*			LysR family transcriptional regulator
M5005_Spy_0637	3572266	NE	Spy49_0647	6985658	NE	Isp	*			lipoprotein signal peptidase
M5005_Spy_0638	3572267	NE	Spy49_0648	6985659	NE	-	*			ribosomal large subunit pseudouridine synthase D
M5005_Spy_0639	3572268	NE	Spy49_0650	6985660	NE	pyrR	*			bifunctional pyrimidine regulatory protein PyrR/uracil phosphoribosyltransferase
M5005_Spy_0640	3572269	NE	Spy49_0651	6985661	NE	pyrP	*			uracil permease
M5005_Spy_0641	3572270	NE	Spy49_0652	6985662	NE	pyrB	*			aspartate carbamoyltransferase
M5005_Spy_0642	3572271	NE	Spy49_0653	6985663	NC	carA	*			carbamoyl phosphate synthase small subunit
M5005_Spy_0643 M5005_Spy_0644	3572272 3572273	NE NE	Spy49_0654 Spy49_0655	6985664 6985665	NE NE	carB -	*			carbamoyl phosphate synthase large subunit periplasmic protein of efflux system
M5005_Spy_0645	3572274	NE	Spy49_0656	6985666	NE	-	*			ABC transporter ATP-binding protein
M5005_Spy_0646	3572275	NE	Spy49_0657	6985667	NE	-	*			ABC transporter permease
M5005_Spy_0647	3572276	NE	Spy49_0658	6985668	C	-	*		SP_0994	glycerophosphoryl diester phosphodiesterase
M5005_Spy_0648 M5005_Spy_0649	3572277 3572278	NE NE	Spy49_0659 Spy49_0660	6985669 6985670	E NC	rpsP		SSA_1310	SP_0775	30S ribosomal protein S16 RNA binding protein
M5005_Spy_0650	3572279	NC	Spy49_0661	6985671	NE	-				hypothetical protein M5005_Spy_0650
M5005_Spy_0651	3572241	NE				-	*			cell surface protein
M5005_Spy_0652	3572242	NE	Spy49_0662	6985672	NE		*			hypothetical protein M5005_Spy_0652
M5005_Spy_0653c M5005_Spy_0654	3572243 3572244	NE NE	Spy49_0663c Spy49_0664	6985673 6985674	NE NE	czcD	*			cobalt-zinc-cadmium resistance protein TetR family transcriptional regulator
M5005_Spy_0655	3572245	NE	Spy49_0004 Spy49_0665	6985675	NC	rimM	*			16S rRNA-processing protein RimM
M5005_Spy_0656	3572246	E	Spy49_0667	6985676	E	trmD	*	SSA_1302	SP_0779	tRNA (guanine-N(1)-)-methyltransferase
M5005_Spy_0657	3572247	NE	Spy49_0668	6985677	NE	trxB	*			thioredoxin reductase
M5005_Spy_0658 M5005_Spy_0659	3572248 3572249	NE NE	Spy49_0669 Spy49_0671	6985678 6985679	NE NE	apbA	*			regulatory protein 2-dehydropantoate 2-reductase
M5005_Spy_0660	3572250	NE	Spy49_0671 Spy49_0672	6985680	NE	fruR	*			fructose repressor
M5005_Spy_0661	3572251	NE	Spy49_0673	6985681	NE	fruB	*			1-phosphofructokinase
M5005_Spy_0662	3572252	NE	Spy49_0674	6985682	NE	fruA	*			PTS system fructose-specific transporter subunit IIABC
M5005_Spy_0663 M5005_Spy_0664	3572253 3572254	NE NE	Spy49_0675 Spy49_0676	6985683 6985684	NE NE	mur1.1 mur1.2	*			autolysin autolysin
M5005_Spy_0665c	3572254	NE NE	Spy49_0676 Spy49_0677c	6985685	NE NE	ui 1.2 -	-			transposase
M5005_Spy_0666c	3572256	NC	Spy49_0679	6985687	NE	-				hypothetical protein M5005_Spy_0666
M5005_Spy_0667c		NC				-				exotoxin type C
M5005_Spy_0668c M5005_Spy_0669		NE				mac				IgG-degrading protease
M5005_Spy_0669 M5005_Spy_0670	3572259 3572260	NC NE				-				phage protein nucleoside diphosphate kinase
M5005_Spy_0671	3572222	NE	Spy49_0680	6985688	NE	-	*			transposase
M5005_Spy_0672	3572223	NE	Spy49_0681	6985689	NE	-	*			degV family protein
M5005_Spy_0673 M5005_Spy_0674	3572224 3572225	E NF	Spy49_0682	6985690 6985691	E NE	papS	*	SSA_1086	SP_1554	tRNA CCA-pyrophosphorylase ABC transporter ATP-binding protein
M5005_Spy_0674 M5005_Spy_0675	3572226	NE NC	Spy49_0683	0207031	NE	-	•			hypothetical protein M5005_Spy_0675
M5005_Spy_0676	3572227	NE				-				hypothetical protein M5005_Spy_0676
M5005_Spy_0677	3572228	NE	Spy49_0684	6985692	NE	fms	*			peptide deformylase
M5005_Spy_0678c	3572229	NE	Spy49_0686c	6985693	NE	-	*			5\'-nucleotidase

ME005 C 0670	2572220			C005C04						CTD was about 18 years
	3572230 3572231	NE NE	Spy49_0687 Spy49_0688	6985694 6985695	NE NE	-	*			GTP pyrophosphokinase two-component response regulator
M5005_Spy_0681 3	3572232	NE	Spy49_0689	6985696	NE	-	*			two-component system histidine kinase
	3572233 3572234	E E	Spy49_0690 Spy49_0691	6985697 6985698	E E	mvaK1 mvaD	*	SSA_0333 SSA_0334	SP_0381 SP_0382	mevalonate kinase diphosphomevalonate decarboxylase
M5005_Spy_0684	3572235	NC	Spy49_0692	6985699	E	mvaK2	*	SSA_0335	SP_0383	phosphomevalonate kinase
	3572236 3572237	E	Spy49_0693	6985700 6985701	E	-	*	SSA_0336	SP_0384	isopentenyl pyrophosphate isomerase
	3572238	C E	Spy49_0694c Spy49_0695c	6985702	E E	mvaS1 mvaS2	*	SSA_0337 SSA_0338	SP_1726 SP_1727	3-hydroxy-3-methylglutaryl-CoA reductase hydroxymethylglutaryl-CoA synthase
	3572239	NC	Spy49_0696	6985703	C	thyA	*	SSA_1091	SP_0669	thymidylate synthase
	3572240 3572202	E NE	Spy49_0697 Spy49_0698	6985704 6985705	E NE	dyr -	*	SSA_1092	SP_1571	dihydrofolate reductase hypothetical protein M5005_Spy_0690
M5005_Spy_0691 3	3572203	NE	Spy49_0700	6985706	NC	clpX	*			ATP-dependent protease ATP-binding subunit ClpX
	3572204 3572205	E NE	Spy49_0701 Spy49_0702	6985707 6985708	E NE	engB	*	SSA_1094	SP_1568	ribosome biogenesis GTP-binding protein YsxC hypothetical protein M5005_Spy_0693
	3572206	NE	Spy49_0703c	6985709	NE	clpL	*			ATP-dependent protease ATP-binding subunit
	3572207 3572208	C	Spy49_0704	6985710 6985711	NC	rpiA	*		SP_0828	ribose-5-phosphate isomerase A
	3572208	NE NE	Spy49_0705 Spy49_0706	6985711	NE NE	deoB arsC	*			phosphopentomutase arsenate reductase
	3572210	NC	Spy49_0707	6985713	NE	punA	*			purine nucleoside phosphorylase
	3572211 3572212	NE NE	Spy49_0708 Spy49_0709	6985714 6985715	NE NE	deoD cpsX	*			purine nucleoside phosphorylase LytR family transcriptional regulator
M5005_Spy_0701c 3	3572213	NE	Spy49_0710c	6985716	NE	cpsY	*			LysR family transcriptional regulator
	3572214 3572215	NE NE	Spy49_0711 Spy49_0712	6985717 6985718	NE NE	- pyrF	*			hypothetical protein M5005_Spy_0702 orotidine 5\'-phosphate decarboxylase
	3572216	NE	Spy49_0713	6985719	NE	pyrE	*			orotate phosphoribosyltransferase
	3572217 3572218	NE	Spy49_0714 Spy49_0715	6985720	NE	amiC -	*			amidase
	3572218	NE NE	Spy49_0715 Spy49_0716	6985721 6985722	NE NE	-	*			cystine-binding protein cystine transporter permease
	3572220	NE	Spy49_0717	6985723	NE	ung	*			uracil-DNA glycosylase
	3572221 3572186	NE E	Spy49_0718 Spy49_0719c	6985724 6985725	NE E	pyrC -	*	SSA_1233	SP_0851	dihydroorotase glycerol-3-phosphate acyltransferase
M5005_Spy_0711 3	3572187	E	Spy49_0720	6985726	E	parE	*	SSA_1232	SP_0852	DNA topoisomerase IV subunit B
	3572188 3572189	E NE	Spy49_0721 Spy49_0722	6985727 6985728	E	parC bcaT	*	SSA_1226	SP_0855	DNA topoisomerase IV subunit A branched-chain amino acid aminotransferase
	3572190	NC	Spy49_0722 Spy49_0723	6985729	NE NC	-	*			hypothetical protein M5005_Spy_0714
	3572193	E	Spy49_0724	6985732	E	rpsA	*	SSA_1223	SP_0862	30S ribosomal protein S1
	3572195 3572196	NE NE	Spy49_0725c Spy49_0726	6985734 6985735	NE NE	-	*			hypothetical protein M5005_Spy_0716 hypothetical protein M5005_Spy_0717
M5005_Spy_0718 3	3572197	NE	Spy49_0727	6985736	NE	-				hypothetical protein M5005_Spy_0718
	3572198 3572199	NE NE	Spy49_0728	6985737	NE	-				glutathione S-transferase exfoliative toxin
M5005_Spy_0721c 3		NC	Spy49_0729c	6985738	NE	-				hypothetical protein M5005_Spy_0721
	3572201	NE	Spy49_0730	6985739 6985740	NE	miaA hflX	*			tRNA delta(2)-isopentenylpyrophosphate transferase
	3572166 3572167	NE NE	Spy49_0731 Spy49_0732	6985741	NE NE	-	*			GTP-binding protein hypothetical protein M5005_Spy_0724
	3572168	E	Spy49_0733	6985742	E	elaC	*	SSA_1430	SP_0674	ribonuclease Z
	3572169	NE	Spy49_0734	6985743	NE	-	*			short chain dehydrogenase
		NE	Snv49 0735	6985744		rec1	*			single-stranded-DNA-specific exonuclease
M5005_Spy_0728 3	3572170 3572171	NE NE	Spy49_0735 Spy49_0736	6985744 6985745	NE NE	recJ apt	*			single-stranded-DNA-specific exonuclease adenine phosphoribosyltransferase
M5005_Spy_0728 3 M5005_Spy_0729 3	3572171 3572172	NE NC	Spy49_0736 Spy49_0737	6985745 6985746	NE E	apt dnaD	*	SSA_1419	SP_1575	adenine phosphoribosyltransferase DNA replication protein
M5005_Spy_0728 3 M5005_Spy_0729 3 M5005_Spy_0730 3	3572171 3572172 3572173	NE NC NE	Spy49_0736 Spy49_0737 Spy49_0738	6985745 6985746 6985747	NE E NE	apt	* *	SSA_1419		adenine phosphoribosyltransferase
M5005_Spy_0728 3 M5005_Spy_0729 3 M5005_Spy_0730 3 M5005_Spy_0731 3	3572171 3572172 3572173 3572174	NE NC NE	Spy49_0736 Spy49_0737 Spy49_0738 Spy49_0739	6985745 6985746 6985747 6985748	NE E NE	apt dnaD	* * *	SSA_1419	SP_1575 SP_1610	adenine phosphoribosyltransferase DNA replication protein endonuclease III para-aminobenzoate synthase component I/anthranilate synthase component I
M5005_Spy_0728 3 M5005_Spy_0729 3 M5005_Spy_0730 3 M5005_Spy_0731 3 M5005_Spy_0732 3	3572171 3572172 3572173	NE NC NE	Spy49_0736 Spy49_0737 Spy49_0738	6985745 6985746 6985747	NE E NE	apt dnaD	* *	SSA_1419		adenine phosphoribosyltransferase DNA replication protein endonuclease III
M5005_Spy_0728 3 M5005_Spy_0729 3 M5005_Spy_0730 3 M5005_Spy_0731 3 M5005_Spy_0732 3 M5005_Spy_0733 3 M5005_Spy_0734 3	3572171 3572172 3572173 3572174 3572175 3572176 3572177	NE NC NE E NE NE E	Spy49_0736 Spy49_0737 Spy49_0738 Spy49_0739 Spy49_0740 Spy49_0741 Spy49_0742	6985745 6985746 6985747 6985748 6985749 6985750 6985751	NE E NE E NE NE E	apt dnaD nth cpsFO/rmIA	* * * * *	SSA_1419		adenine phosphoribosyltransferase DNA replication protein endonuclease III para-aminobenzoate synthase component I/anthranilate synthase component I NIF3-related protein glycine/D-amino acid oxidase glucose-1-phosphate thymidylyltransferase
M5005_Spy_0728 3 M5005_Spy_0729 3 M5005_Spy_0730 3 M5005_Spy_0731 3 M5005_Spy_0732 3 M5005_Spy_0733 3 M5005_Spy_0734 3 M5005_Spy_0735 3	3572171 3572172 3572173 3572174 3572175 3572176	NE NC NE E NE	Spy49_0736 Spy49_0737 Spy49_0738 Spy49_0739 Spy49_0740 Spy49_0741 Spy49_0742 Spy49_0744	6985745 6985746 6985747 6985748 6985749 6985750	NE E NE E NE	apt dnaD nth	* * * * *	SSA_1419		adenine phosphoribosyltransferase DNA replication protein endonuclease III para-aminobenzoate synthase component I/anthranilate synthase component I NIF3-related protein glycine/D-amino acid oxidase
M5005_Spy_0728 3 M5005_Spy_0729 3 M5005_Spy_0730 3 M5005_Spy_0731 3 M5005_Spy_0732 3 M5005_Spy_0733 3 M5005_Spy_0733 3 M5005_Spy_0734 3 M5005_Spy_0735 3	3572171 3572172 3572173 3572174 3572175 3572176 3572177 3572177	NE NC NE E NE NE E NC	Spy49_0736 Spy49_0737 Spy49_0738 Spy49_0740 Spy49_0741 Spy49_0742 Spy49_0744 Spy49_0745 Spy49_0745 Spy49_0746c	6985745 6985746 6985747 6985748 6985749 6985750 6985751 6985752 6985753 6985754	NE E NE NE NE E NC E NC	apt dnaD nth cpsFO/rmIA cpsFP/rmIC	* * * * * *	SSA_1419		adenine phosphoribosyltransferase DNA replication protein endonuclease III para-aminobenzoate synthase component I/anthranilate synthase component 1 NIF3-related protein glycine/D-amino acid oxidase glucose-1-phosphate thymidylyltransferase dTDP-4-dehydrorhamnose 3,5-epimerase
M5005_Spy_0728 3 M5005_Spy_0729 3 M5005_Spy_0730 3 M5005_Spy_0731 3 M5005_Spy_0732 3 M5005_Spy_0733 3 M5005_Spy_0733 3 M5005_Spy_0734 3 M5005_Spy_0735 3	3572171 3572172 3572173 3572174 3572175 3572176 3572177 3572177	NE NC NE E NE NE E NC	Spy49_0736 Spy49_0737 Spy49_0738 Spy49_0740 Spy49_0741 Spy49_0742 Spy49_0744 Spy49_0745 Spy49_0745 Spy49_0746c Spy49_0747c	6985745 6985746 6985747 6985748 6985749 6985750 6985751 6985752 6985753 6985754 6985755	NE E NE NE NE E NC E NC E NE NE	apt dnaD nth cpsFO/rmIA cpsFP/rmIC	* * * * * *	SSA_1419		adenine phosphoribosyltransferase DNA replication protein endonuclease III para-aminobenzoate synthase component I/anthranilate synthase component 1 NIF3-related protein glycine/D-amino acid oxidase glucose-1-phosphate thymidylyltransferase dTDP-4-dehydrorhamnose 3,5-epimerase
M5005_Spy_0728 3 M5005_Spy_0729 3 M5005_Spy_0730 3 M5005_Spy_0731 3 M5005_Spy_0732 3 M5005_Spy_0733 3 M5005_Spy_0733 3 M5005_Spy_0734 3 M5005_Spy_0735 3	3572171 3572172 3572173 3572174 3572175 3572176 3572177 3572177	NE NC NE E NE NE E NC	Spy49_0736 Spy49_0737 Spy49_0738 Spy49_0740 Spy49_0741 Spy49_0742 Spy49_0745 Spy49_0745 Spy49_0746c Spy49_0746c Spy49_07478c Spy49_0748c Spy49_0748c	6985745 6985746 6985747 6985748 6985749 6985750 6985751 6985752 6985753 6985754 6985755 6985756	NE E NE NE E NC E NE NE C	apt dnaD nth cpsFO/rmIA cpsFP/rmIC	* * * * * *	SSA_1419		adenine phosphoribosyltransferase DNA replication protein endonuclease III para-aminobenzoate synthase component I/anthranilate synthase component 1 NIF3-related protein glycine/D-amino acid oxidase glucose-1-phosphate thymidylyltransferase dTDP-4-dehydrorhamnose 3,5-epimerase
M5005_Spy_0728 3 M5005_Spy_0729 3 M5005_Spy_0730 3 M5005_Spy_0731 3 M5005_Spy_0732 3 M5005_Spy_0733 3 M5005_Spy_0733 3 M5005_Spy_0734 3 M5005_Spy_0735 3	3572171 3572172 3572173 3572174 3572175 3572176 3572177 3572177	NE NC NE E NE NE E NC	Spy49_0736 Spy49_0737 Spy49_0738 Spy49_0740 Spy49_0741 Spy49_0742 Spy49_0745 Spy49_0746 Spy49_0746c Spy49_0746c Spy49_0746c Spy49_0746c Spy49_0749c Spy49_0749c	6985745 6985746 6985747 6985749 6985750 6985750 6985751 6985752 6985753 6985754 6985755 6985756 6985757 6985757	NE E NE NE E NC E NC E NE NC C NC	apt dnaD nth cpsFO/rmIA cpsFP/rmIC	* * * * * *	SSA_1419		adenine phosphoribosyltransferase DNA replication protein endonuclease III para-aminobenzoate synthase component I/anthranilate synthase component 1 NIF3-related protein glycine/D-amino acid oxidase glucose-1-phosphate thymidylyltransferase dTDP-4-dehydrorhamnose 3,5-epimerase
M5005_Spy_0728 3 M5005_Spy_0729 3 M5005_Spy_0730 3 M5005_Spy_0731 3 M5005_Spy_0732 3 M5005_Spy_0733 3 M5005_Spy_0733 3 M5005_Spy_0734 3 M5005_Spy_0735 3	3572171 3572172 3572173 3572174 3572175 3572176 3572177 3572177	NE NC NE E NE NE E NC	Spv49_0736 Spy49_0737 Spv49_0738 Spv49_0740 Spv49_0741 Spv49_0742 Spv49_0744 Spv49_0746 Spv49_0746 Spv49_0746 Spv49_0746 Spv49_0749 Spv49_0750 Spv49_0750 Spv49_0750	6985745 6985746 6985747 6985748 6985749 6985750 6985751 6985753 6985753 6985755 6985755 6985755 6985756 6985755 6985758 6985758 6985758 6985758 6985758	NE E NE E NE E NC E NE NE NC NC NC NC NC	apt dnaD nth cpsFO/rmIA cpsFP/rmIC	* * * * * *	SSA_1419		adenine phosphoribosyltransferase DNA replication protein endonuclease III para-aminobenzoate synthase component I/anthranilate synthase component 1 NIF3-related protein glycine/D-amino acid oxidase glucose-1-phosphate thymidylyltransferase dTDP-4-dehydrorhamnose 3,5-epimerase
M5005_Spy_0728 3 M5005_Spy_0729 3 M5005_Spy_0730 3 M5005_Spy_0731 3 M5005_Spy_0732 3 M5005_Spy_0733 3 M5005_Spy_0733 3 M5005_Spy_0734 3 M5005_Spy_0735 3	3572171 3572172 3572173 3572174 3572175 3572176 3572177 3572177	NE NC NE E NE NE E NC	Spv49_0736 Spv49_0737 Spv49_0738 Spv49_0740 Spv49_0741 Spv49_0744 Spv49_0744 Spv49_0745 Spv49_0746 Spv49_0746 Spv49_0748 Spv49_0748 Spv49_0748 Spv49_0749 Spv49_0750 Spv49_0751 Spv49_0751	6985745 6985746 6985749 6985749 6985749 6985750 6985751 6985752 6985752 6985754 6985755 6985755 6985757 6985756 6985759 6985759 6985759 6985759 6985759	NE E NE E NC E NE NE NC NC NC NC NC NC	apt dnaD nth cpsFO/rmIA cpsFP/rmIC	* * * * * *	SSA_1419		adenine phosphoribosyltransferase DNA replication protein endonuclease III para-aminobenzoate synthase component I/anthranilate synthase component 1 NIF3-related protein glycine/D-amino acid oxidase glucose-1-phosphate thymidylyltransferase dTDP-4-dehydrorhamnose 3,5-epimerase
M5005_Spy_0728 3 M5005_Spy_0729 3 M5005_Spy_0730 3 M5005_Spy_0731 3 M5005_Spy_0732 3 M5005_Spy_0733 3 M5005_Spy_0733 3 M5005_Spy_0734 3 M5005_Spy_0735 3	3572171 3572172 3572173 3572174 3572175 3572176 3572177 3572177	NE NC NE E NE NE E NC	Spv49_0736 Spy49_0737 Spv49_0738 Spv49_0740 Spv49_0741 Spv49_0742 Spv49_0744 Spv49_0746 Spv49_0746 Spv49_0746 Spv49_0746 Spv49_0749 Spv49_0750 Spv49_0750 Spv49_0750	6985745 6985746 6985747 6985748 6985749 6985750 6985751 6985753 6985753 6985755 6985755 6985755 6985756 6985755 6985758 6985758 6985758 6985758 6985758	NE E NE E NE E NC E NE NE NC NC NC NC NC	apt dnaD nth cpsFO/rmIA cpsFP/rmIC	* * * * * *	SSA_1419		adenine phosphoribosyltransferase DNA replication protein endonuclease III para-aminobenzoate synthase component I/anthranilate synthase component 1 NIF3-related protein glycine/D-amino acid oxidase glucose-1-phosphate thymidylyltransferase dTDP-4-dehydrorhamnose 3,5-epimerase
M5005_Spy_0728 3 M5005_Spy_0729 3 M5005_Spy_0730 3 M5005_Spy_0731 3 M5005_Spy_0732 3 M5005_Spy_0733 3 M5005_Spy_0733 3 M5005_Spy_0734 3 M5005_Spy_0735 3	3572171 3572172 3572173 3572174 3572175 3572176 3572177 3572177	NE NC NE E NE NE E NC	Spy49_0736 Spy49_0737 Spy49_0738 Spy49_0740 Spy49_0741 Spy49_0742 Spy49_0745 Spy49_0745 Spy49_0745 Spy49_0746 Spy49_0746 Spy49_0748c Spy49_0750 Spy49_0751 Spy49_0751 Spy49_0753 Spy49_0755 Spy49_0755 Spy49_0755 Spy49_0755	6985745 6985746 6985747 6985747 6985749 6985750 6985751 6985752 6985753 6985755 6985756 6985756 6985756 6985756 6985756 6985756 6985756 6985762 6985763 6985763	NE E NE E NE NE C NC NC NC NC NC NC NE	apt dnaD nth cpsFO/rmIA cpsFP/rmIC	* * * * * *	SSA_1419		adenine phosphoribosyltransferase DNA replication protein endonuclease III para-aminobenzoate synthase component I/anthranilate synthase component 1 NIF3-related protein glycine/D-amino acid oxidase glucose-1-phosphate thymidylyltransferase dTDP-4-dehydrorhamnose 3,5-epimerase
M5005_Spy_0728 3 M5005_Spy_0729 3 M5005_Spy_0730 3 M5005_Spy_0731 3 M5005_Spy_0732 3 M5005_Spy_0733 3 M5005_Spy_0733 3 M5005_Spy_0734 3 M5005_Spy_0735 3	3572171 3572172 3572173 3572174 3572175 3572176 3572177 3572177	NE NC NE E NE NE E NC	Spv49_0736 Spy49_0737 Spy49_0738 Spy49_0740 Spy49_0741 Spy49_0742 Spy49_0744 Spy49_0746 Spy49_0746c Spy49_0747 Spy49_0748c Spy49_0750 Spy49_0750 Spy49_0752 Spy49_0752 Spy49_0753 Spy49_0753 Spy49_0754	6985745 6985746 6985744 6985749 6985749 6985750 6985751 6985753 6985755 6985755 6985755 6985756 6985759 6985759 6985756 6985756 6985756 6985761 6985761	NE E NE E NE C NC NC NC NC NC NC	apt dnaD nth cpsFO/rmIA cpsFP/rmIC	* * * * * *	SSA_1419		adenine phosphoribosyltransferase DNA replication protein endonuclease III para-aminobenzoate synthase component I/anthranilate synthase component 1 NIF3-related protein glycine/D-amino acid oxidase glucose-1-phosphate thymidylyltransferase dTDP-4-dehydrorhamnose 3,5-epimerase
M5005_Spy_0728 3 M5005_Spy_0729 3 M5005_Spy_0730 3 M5005_Spy_0731 3 M5005_Spy_0732 3 M5005_Spy_0733 3 M5005_Spy_0733 3 M5005_Spy_0734 3 M5005_Spy_0735 3	3572171 3572172 3572173 3572174 3572175 3572176 3572177 3572177	NE NC NE E NE NE E NC	Spy49_0736 Spy49_0737 Spy49_0738 Spy49_0740 Spy49_0741 Spy49_0742 Spy49_0745 Spy49_0745 Spy49_0746c Spy49_0748c Spy49_0748c Spy49_0750 Spy49_0751 Spy49_0752 Spy49_0755 Spy49_0755 Spy49_0755 Spy49_0755 Spy49_0755 Spy49_0755 Spy49_0755 Spy49_0755 Spy49_0755 Spy49_0755 Spy49_0755 Spy49_0755 Spy49_0755 Spy49_0755 Spy49_0755 Spy49_0755 Spy49_0755 Spy49_0755	6985745 6985746 6985748 6985749 6985749 6985750 6985753 6985752 6985752 6985755 6985755 6985756 6985756 6985756 6985760 6985761 6985762 6985762 6985763 6985763 6985763	NE E NE E NE E NE E NE NE NE NE NE NE NE	apt dnaD nth cpsFO/rmIA cpsFP/rmIC	* * * * * *	SSA_1419		adenine phosphoribosyltransferase DNA replication protein endonuclease III para-aminobenzoate synthase component I/anthranilate synthase component 1 NIF3-related protein glycine/D-amino acid oxidase glucose-1-phosphate thymidylyltransferase dTDP-4-dehydrorhamnose 3,5-epimerase
M5005_Spy_0728 3 M5005_Spy_0729 3 M5005_Spy_0730 3 M5005_Spy_0731 3 M5005_Spy_0732 3 M5005_Spy_0733 3 M5005_Spy_0733 3 M5005_Spy_0734 3 M5005_Spy_0735 3	3572171 3572172 3572173 3572174 3572175 3572176 3572177 3572177	NE NC NE E NE NE E NC	Spy49_0736 Spy49_0737 Spy49_0740 Spy49_0740 Spy49_0741 Spy49_0742 Spy49_0745 Spy49_0745 Spy49_0745 Spy49_0745 Spy49_0745 Spy49_0751 Spy49_0755 Spy49_0755 Spy49_0755 Spy49_0755 Spy49_0755 Spy49_0756 Spy49_0755 Spy49_0756 Spy49_0757 Spy49_0756 Spy49_0757 Spy49_0757 Spy49_0757	6985745 6985746 6985747 6985748 6985749 6985750 6985752 6985753 6985755 6985756 6985756 6985756 6985756 6985756 6985761 6985762 6985762 6985764 6985764 6985764 6985765	NE E NE E NE E NE E NE NE C NC N	apt dnaD nth cpsFO/rmIA cpsFP/rmIC	* * * * * *	SSA_1419		adenine phosphoribosyltransferase DNA replication protein endonuclease III para-aminobenzoate synthase component I/anthranilate synthase component 1 NIF3-related protein glycine/D-amino acid oxidase glucose-1-phosphate thymidylyltransferase dTDP-4-dehydrorhamnose 3,5-epimerase
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M5005_Spy_0728 3 M5005_Spy_0729 3 M5005_Spy_0730 3 M5005_Spy_0731 3 M5005_Spy_0732 3 M5005_Spy_0733 3 M5005_Spy_0733 3 M5005_Spy_0734 3 M5005_Spy_0735 3	3572171 3572172 3572173 3572174 3572175 3572176 3572177 3572177	NE NC NE E NE NE E NC	Spy49_0736 Spy49_0739 Spy49_0740 Spy49_0741 Spy49_0742 Spy49_0745 Spy49_0745 Spy49_0745 Spy49_0745 Spy49_0745 Spy49_0755 Spy49_0755 Spy49_0755 Spy49_0755 Spy49_0756 Spy49_0756 Spy49_0756 Spy49_0756 Spy49_0756 Spy49_0756 Spy49_0756 Spy49_0756 Spy49_0756 Spy49_0756 Spy49_0756 Spy49_0756 Spy49_0756 Spy49_0756 Spy49_0756 Spy49_0756 Spy49_0756 Spy49_0756 Spy49_0756 Spy49_0764 Spy49_0766 Spy49_0766 Spy49_0766 Spy49_0767 Spy49_0767 Spy49_0767 Spy49_0768 Spy49_0769 Spy49_0769 Spy49_0775 Spy49_0775 Spy49_0777 Spy49_0775 Spy49_0775 Spy49_0775 Spy49_0775 Spy49_0775 Spy49_0775 Spy49_0775 Spy49_0775 Spy49_0777 Spy49_0778 Spy49_0778 Spy49_0778 Spy49_0778 Spy49_0778 Spy49_0778 Spy49_0778 Spy49_0778 Spy49_0778 Spy49_0778 Spy49_0778 Spy49_0778 Spy49_0778 Spy49_0778 Spy49_0778	9985745 9985746 9985746 9985746 9985747 6985749 9985751 6985752 6985753 6985755 6985756 6985756 6985756 6985756 6985766 6985766 6985766 6985766 6985766 6985767 6985776 6985776 6985776 6985776 6985778 6985789 6985789 6985789	E E E NEE E NC C NC N	apt dnaD nth cpsFO/rmIA cpsFP/rmIC	* * * * * *	SSA_1419		adenine phosphoribosyltransferase DNA replication protein endonuclease III para-aminobenzoate synthase component I/anthranilate synthase component 1 NIF3-related protein glycine/D-amino acid oxidase glucose-1-phosphate thymidylyltransferase dTDP-4-dehydrorhamnose 3,5-epimerase
M5005_Spy_0728 3 M5005_Spy_0729 3 M5005_Spy_0730 3 M5005_Spy_0731 3 M5005_Spy_0732 3 M5005_Spy_0733 3 M5005_Spy_0733 3 M5005_Spy_0734 3 M5005_Spy_0735 3	3572171 3572172 3572173 3572174 3572175 3572176 3572177 3572177	NE NC NE E NE NE E NC	Spy49_0736 Spy49_0739 Spy49_0740 Spy49_0741 Spy49_0742 Spy49_0745 Spy49_0745 Spy49_0745 Spy49_0745 Spy49_0747 Spy49_0748 Spy49_0750 Spy49_0750 Spy49_0750 Spy49_0750 Spy49_0750 Spy49_0750 Spy49_0750 Spy49_0750 Spy49_0750 Spy49_0750 Spy49_0750 Spy49_0750 Spy49_0750 Spy49_0750 Spy49_0750 Spy49_0750 Spy49_0760 Spy49_0770 Spy49_0770 Spy49_0771 Spy49_0772 Spy49_0773 Spy49_0773 Spy49_0778 Spy49_0778 Spy49_0778 Spy49_0778 Spy49_0778 Spy49_0778 Spy49_0778 Spy49_0778 Spy49_0778 Spy49_0778 Spy49_0778 Spy49_0780 Spy49_0781 Spy49_0781 Spy49_0782 Spy49_0784 Spy49_0784 Spy49_0784 Spy49_0784 Spy49_0788	9985745 9985748 9985748 9985749 9985749 9985751 9985752 9985755 9985755 9985756 9985756 9985756 9985756 9985756 9985757 9985761 9985762 9985762 9985764 9985762 9985764 9985762 9985764 9985764 9985766 9985766 9985766 9985766 9985767 9985776 9985776 9985776 9985777 9985777 9985777 9985777 9985777 9985777 9985777 9985778 9985778 9985778 9985778 9985778 9985778 9985778 9985778 9985778 9985778 9985778 9985779 9985788 9985788 9985788 9985788 9985788 9985788 9985788 9985788 9985788 9985788	RE E NE E NC E NE NC C NC C NC	apt dnaD nth cpsFO/rmIA cpsFP/rmIC	* * * * * *	SSA_1419		adenine phosphoribosyltransferase DNA replication protein endonuclease III para-aminobenzoate synthase component I/anthranilate synthase component 1 NIF3-related protein glycine/D-amino acid oxidase glucose-1-phosphate thymidylyltransferase dTDP-4-dehydrorhamnose 3,5-epimerase
M5005_Spy_0728 3 M5005_Spy_0729 3 M5005_Spy_0730 3 M5005_Spy_0731 3 M5005_Spy_0732 3 M5005_Spy_0733 3 M5005_Spy_0733 3 M5005_Spy_0734 3 M5005_Spy_0735 3	3572171 3572172 3572173 3572174 3572175 3572176 3572177 3572177	NE NC NE E NE NE E NC	Spy49_0736 Spy49_0739 Spy49_0740 Spy49_0741 Spy49_0742 Spy49_0745 Spy49_0745 Spy49_0745 Spy49_0745 Spy49_0746 Spy49_0746 Spy49_0750 Spy49_0750 Spy49_0750 Spy49_0751 Spy49_0751 Spy49_0751 Spy49_0751 Spy49_0751 Spy49_0751 Spy49_0751 Spy49_0751 Spy49_0751 Spy49_0751 Spy49_0751 Spy49_0751 Spy49_0751 Spy49_0751 Spy49_0751 Spy49_0751 Spy49_0751 Spy49_0761 Spy49_0761 Spy49_0761 Spy49_0762 Spy49_0763 Spy49_0763 Spy49_0763 Spy49_0763 Spy49_0763 Spy49_0763 Spy49_0763 Spy49_0763 Spy49_0763 Spy49_0778 Spy49_0778 Spy49_0778 Spy49_0778 Spy49_0781 Spy49_0783 Spy49_0783 Spy49_0783 Spy49_0783 Spy49_0783 Spy49_0783	9985745 9985746 9985746 9985746 9985747 6985749 9985751 6985752 6985753 6985755 6985756 6985756 6985756 6985756 6985766 6985766 6985766 6985766 6985766 6985767 6985776 6985776 6985776 6985776 6985778 6985789 6985789 6985789	E E NE E	apt dnaD nth cpsFO/rmIA cpsFP/rmIC	* * * * * *	SSA_1419		adenine phosphoribosyltransferase DNA replication protein endonuclease III para-aminobenzoate synthase component I/anthranilate synthase component 1 NIF3-related protein glycine/D-amino acid oxidase glucose-1-phosphate thymidylyltransferase dTDP-4-dehydrorhamnose 3,5-epimerase
M5005_Spy_0728 3 M5005_Spy_0729 3 M5005_Spy_0730 3 M5005_Spy_0731 3 M5005_Spy_0732 3 M5005_Spy_0733 3 M5005_Spy_0733 3 M5005_Spy_0734 3 M5005_Spy_0735 3	3572171 3572172 3572173 3572174 3572175 3572176 3572177 3572177	NE NC NE E NE NE E NC	Spy49_0736 Spy49_0739 Spy49_0740 Spy49_0741 Spy49_0742 Spy49_0745 Spy49_0745 Spy49_0745 Spy49_0745 Spy49_0745 Spy49_0750 Spy49_0750 Spy49_0751 Spy49_0761 Spy49_0762 Spy49_0763 Spy49_0764 Spy49_0763 Spy49_0763 Spy49_0764 Spy49_0765 Spy49_0767 Spy49_0767 Spy49_0775 Spy49_0775 Spy49_0775 Spy49_0775 Spy49_0777 Spy49_0778 Spy49_0778 Spy49_0778 Spy49_0778 Spy49_0778 Spy49_0778 Spy49_0778 Spy49_0778 Spy49_0778 Spy49_0778 Spy49_0778 Spy49_0780 Spy49_0780 Spy49_0780 Spy49_0782 Spy49_0788 Spy49_0788 Spy49_0788 Spy49_0788 Spy49_0788 Spy49_0788 Spy49_0788 Spy49_0788 Spy49_0788 Spy49_0788 Spy49_0788 Spy49_0788 Spy49_0788 Spy49_0788 Spy49_0788 Spy49_0788	9985745 9985748 9985748 9985749 9985749 9985750 9985751 9985755 9985755 9985756 9985756 9985756 9985756 9985761 9985766 9985766 9985766 9985766 9985766 9985767 9985766 9985767 9985766 9985766 9985767 9985766 9985767 9985776 9985776 9985776 9985776 9985777 9985777 9985777 9985777 9985778 9985778 9985779 9985779 9985780	E E E E E E E E E E E E E E E E E E E	apt dnaD nth cpsFO/rmIA cpsFP/rmIC	* * * * * *	SSA_1419		adenine phosphoribosyltransferase DNA replication protein endonuclease III para-aminobenzoate synthase component I/anthranilate synthase component 1 NIF3-related protein glycine/D-amino acid oxidase glucose-1-phosphate thymidylyltransferase dTDP-4-dehydrorhamnose 3,5-epimerase

			Spy49_0791 Spy49_0792	6985797 6985798	NE NE	speH				
M5005_Spy_0737		NE	Spy49_0793	6985799	NE	mutX	*			7,8-dihydro-8-oxoguanine-triphosphatase
M5005_Spy_0738 M5005_Spy_0739	3572181 3572182	NE NE	Spy49_0794 Spy49_0795	6985800 6985801	NE NE	-	*			hypothetical protein M5005_Spy_0738 hypothetical protein M5005_Spy_0739
M5005_Spy_0740d	3572183	NE	Spy49_0796c	6985802	NE	fbp	*			fibronectin-binding protein
M5005_Spy_0742 M5005_Spy_0743		NC NE	Spy40 0707	6985803	NE	-	*			hypothetical protein M5005_Spy_0742 ABC transporter substrate-binding protein
M5005_Spy_0743	3572148	NC	Spy49_0797 Spy49_0798	6985804	NC	-	-			hypothetical protein M5005_Spy_0744
M5005_Spy_0745		NE	Spy49_0799	6985805	NE	-	*			ABC transporter permease
M5005_Spy_0746 M5005_Spy_0747		NE E	Spy49_0800 Spy49_0801	6985806 6985807	NE E	-	*	SSA_0312	SP_0121	ABC transporter ATP-binding protein Zn-dependent hydrolase
M5005_Spy_0748	3572152	NE	Spy49_0803	6985808	NE	estA	*			acetyl esterase
M5005_Spy_0749 M5005_Spy_0750		NE NE	Spy49_0804 Spy49_0805	6985809 6985810	NE NE	-	*			hypothetical protein M5005_Spy_0749 ABC transporter ATP-binding protein
M5005_Spy_0751	3572155	NE	Spy49_0807	6985811	NE	acoA	*			pyruvate dehydrogenase E1 component subunit alpha
M5005_Spy_0752 M5005_Spy_0753		NE NE	Spy49_0808 Spy49_0809	6985812 6985813	NE NE	acoB acoC	*			pyruvate dehydrogenase E1 component subunit beta branched-chain alpha-keto acid dehydrogenase subunit E2
M5005_Spy_0754c		NE	3py49_0809	0303013	INE	-	-			hypothetical protein M5005_Spy_0754
M5005_Spy_0755		NE	Spy49_0810	6985814	NE	acoL	*			dihydrolipoamide dehydrogenase
M5005_Spy_0756c M5005_Spy_0757c		NE NE	Spy49_0811c	6985815	NE	hylA				hypothetical protein M5005_Spy_0756 hyaluronate lyase
M5005_Spy_0758	3572162	NE	Spy49_0812	6985816	NE	IpIB	*			lipoate-protein ligase A
M5005_Spy_0759c M5005_Spy_0760c		E E	Spy49_0813c Spy49_0814c	6985817 6985818	E E	cobQ murC2	*	SSA_0800 SSA_0801	SP_1590 SP_1589	hypothetical protein M5005_Spy_0759 UDP-N-acetylmuramoylalanyl-D-glutamate2,6-diaminopimelate ligase
M5005_Spy_0761		E	Spy49_0815	6985819	E	-	*	33A_0801	SP_1561	hypothetical protein M5005_Spy_0761
M5005_Spy_0762		NE	Spy49_0816	6985820	NE	-	*			hypothetical protein M5005_Spy_0762
M5005_Spy_0763 M5005_Spy_0764		E NE	Spy49_0817 Spy49_0818	6985821 6985822	E NE	glmM	*	SSA_0804	SP_1559	phosphoglucosamine mutase hypothetical protein M5005_Spy_0764
M5005_Spy_0765	3572130	NE	Spy49_0819	6985823	NE	hemN	*			coproporphyrinogen III oxidase
M5005_Spy_0766 M5005_Spy_0767		C NE	Spy49_0820 Spy49_0821	6985824 6985825	E NE	-	*			acyl-ACP thioesterase 4-nitrophenylphosphatase
M5005_Spy_0768		NE	Spy49_0822	6985826	NE	-				hypothetical protein M5005_Spy_0768
M5005_Spy_0769		NE	Spy49_0823	6985827	NE	cas9				hypothetical protein M5005_Spy_0769
M5005_Spy_0770 M5005_Spy_0771		NE NE	Spy49_0825 Spy49_0826	6985828 6985829	NE NE	cas1 cas2				hypothetical protein M5005_Spy_0770 hypothetical protein M5005_Spy_0771
M5005_Spy_0772	3572137	NE	Spy49_0827	6985830	NE	csn2				hypothetical protein M5005_Spy_0772
M5005_Spy_07730		NE				-				hypothetical protein M5005_Spy_0773 nucleoside diphosphate kinase
M5005_Spy_0774 M5005_Spy_0775		NE NC	Spy49_0828	6985831	NE	-				nucleoside diphosphate kinase nucleoside diphosphate kinase
M5005_Spy_0776	3572141	NE	Spy49_0829	6985832	NE	lepA				GTP-binding protein LepA
M5005_Spy_0777 M5005_Spy_0778		NE	Spy49_0830 Spy49_0831	6985833 6985834	NC NE	sclB msrB/crsA	*			hypothetical protein M5005_Spy_0777 methionine sulfoxide reductase B
M5005_Spy_0770		NE NE	Spy49_0832	6985835	NE	-	*			hypothetical protein M5005_Spy_0779
M5005_Spy_0780		NE	Spy49_0833	6985836	NE	-	*			PTS system mannose/fructose family transporter subunit IIA
M5005_Spy_0781 M5005_Spy_0782		NE NE	Spy49_0834 Spy49_0835	6985837 6985838	NC NE	ptsB ptsC	*			PTS system mannose/fructose family transporter subunit IIB PTS system mannose/fructose family transporter subunit IIC
M5005_Spy_0783	3572109	NE	Spy49_0836	6985839	NE	ptsD	*			PTS system mannose/fructose family transporter subunit IID
M5005_Spy_0784 M5005_Spy_0785		NE NE	Spy49_0837	6985840 6985841	NE NE	-	*			two-component sensor kinase two-component response regulator
M5005_Spy_0786		NE	Spy49_0839 Spy49_0840	6985842	NE	-	*			iron(III)-binding protein
M5005_Spy_0787	3572113	NE	., _			-				hypothetical protein M5005_Spy_0787
M5005_Spy_0788 M5005_Spy_0789		NE NE				-				acetyltransferase HAD superfamily hydrolase
M5005_Spy_0790		NE	Spy49_0841	6985843	NE	gabD	*			succinate-semialdehyde dehydrogenase
M5005_Spy_0791		NE	Spy49_0842	6985844	NE	uvrC	*			excinuclease ABC subunit C
M5005_Spy_0792 M5005_Spy_0793		NE NE	Spy49_0843 Spy49_0844	6985845 6985846	NE NE	-	*			NAD(P)H-dependent quinone reductase dipeptidase PepV
M5005_Spy_07946	3572120	С	Spy49_0845c	6985847	Ε	trmE	*		SP_1016	tRNA modification GTPase TrmE
M5005_Spy_0795	3572121	NE	Spy49_0846 Spy49_0847	6985848 6985849	NE NC	rplJ	*			50S ribosomal protein L10
M5005_Spy_0796		NE	Spy49_0848	6985850	NC	rplL	*			50S ribosomal protein L7/L12
M5005_Spy_0797		NC				-				hypothetical protein M5005_Spy_0797
M5005_Spy_0798 M5005_Spy_0799		NE NC				-				IFN-response binding factor 1 hypothetical protein M5005_Spy_0799
M5005_Spy_0800	3572126	NE				-				DNA-cytosine methyltransferase
M5005_Spy_0801 M5005_Spy_0802		NC NE				-				relaxase relaxase
M5005_Spy_0803		NE				srtI				lantibiotic production protein
M5005_Spy_0804		NE				srtR				nisin biosynthesis two-component response regulator
M5005_Spy_0805 M5005_Spy_0806		NE NC				srtK srtA				nisin biosynthesis sensor protein lantibiotic protein
M5005_Spy_0807	3572094	NE				srtT				lantibiotic ABC transporter ATP-binding protein
M5005_Spy_0808 M5005_Spy_0809		NE NE				srtF srtE				lantibiotic ABC transporter ATP-binding protein lantibiotic transport permease
M5005_Spy_0810		NE				srtG				lantibiotic transport permease
M5005_Spy_0811		NE				-				Cro/CI family transcriptional regulator
M5005_Spy_0812c M5005_Spy_0817		NE NE	Spy49_0849	6985851	NE	dacA1	*			hypothetical protein M5005_Spy_0812 D-alanyl-D-alanine carboxypeptidase
M5005_Spy_0818d	3572105	NE	Spy49_0850c	6985852	NE	-	*			polysaccharide deacetylase
M5005_Spy_0819		NC	540 0054	6005053	_	folC 1		554 0400	CD 0200	hypothetical protein M5005_Spy_0819 folylpolyglutamate synthase/dihydrofolate synthase
M5005_Spy_0820 M5005_Spy_0821		E NE	Spy49_0851 Spy49_0852	6985853 6985854	E NE	folC.1	*	SSA_0198	SP_0290	GTP cyclohydrolase I
M5005_Spy_0822	3572070	С	Spy49_0853	6985855	NC	folP	*	SSA_0197		dihydropteroate synthase
M5005_Spy_0823 M5005_Spy_0824		NE NC	Spy49_0854 Spy49_0855	6985856 6985857	NE NE	folQ folK	*			dihydroneopterin aldolase 2-amino-4-hydroxy-6-hydroxymethyldihydropteridine pyrophosphokinase
M5005_Spy_0825		E	Spy49_0856	6985858	E	murB	*	SSA_1047		UDP-N-acetylenolpyruvoylglucosamine reductase
M5005_Spy_0826		NE	Spy49_0857	6985859	NE	potA	*			spermidine/putrescine transporter ATP-binding protein
M5005_Spy_0827 M5005_Spy_0828	3572075 3572076	NE NE	Spy49_0858 Spy49_0859	6985860 6985861	NE NE	potB potC	*			spermidine/putrescine transporter permease spermidine/putrescine transporter permease
M5005_Spy_0829	3572077	NE	Spy49_0860	6985862	NE	potD	*			spermidine/putrescine-binding protein
M5005_Spy_0830c M5005_Spy_0831c		NE	Spy49_0861c	6985863	NE	dpiA dpiB	*			transcriptional regulatory protein sensor kinase
M5005_Spy_08310		NE NE	Spy49_0862c Spy49_0863	6985864 6985865	NE NE	malP	*			malate-sodium symport
M5005_Spy_0833	3572081	NE	Spy49_0864	6985866	NE	-	*			NAD-dependent malic enzyme
M5005_Spy_0834c M5005_Spy_0835		NE NE	Spy49_0865c Spy49_0866	6985867 6985868	NE NE	- aphA	*			Zn-dependent alcohol dehydrogenase and related dehydrogenase class B acid phosphatase
M5005_Spy_0837	3572085	NE	Spy49_0867	6985869	NE		*			chloride channel protein
M5005_Spy_0838		NE	Spy49_0868	6985870 6985871	NE	-	*			lipase/acylhydrolase
M5005_Spy_0839 M5005_Spy_0840		NE NE	Spy49_0869 Spy49_0870	6985871 6985872	NE NE	radC	*			hypothetical protein M5005_Spy_0839 DNA repair protein RadC
M5005_Spy_0841d		NE	Spy49_0871c	6985873	NE	-	*			glutamine amidotransferase, class I

	3572051	NE	Spy49_0872c	6985874	NE	-	*			redox-sensing transcriptional repressor Rex
	3572052 3572053	NE E	Spy49_0873c Spy49_0874c	6985875 6985876	NE E	nifS2	*	SSA_1213	SP_1094	hypothetical protein M5005_Spy_0843 cysteine desulfhydrase
	3572054	NE	Spy49_0875c	6985877	NE	prs	*	33A_1213	3F_1094	ribose-phosphate pyrophosphokinase
	3572055	NE	Spy49_0876c	6985878	NC	·-	*			adenylate cyclase
	3572056	NE	Spy49_0877	6985879	NE	-	*			GTP pyrophosphokinase
	3572057 3572058	E	Spy49_0878 Spy49_0879	6985880 6985881	E	ppnK rluD	*	SSA_1209	SP_1098	inorganic polyphosphate/ATP-NAD kinase ribosomal large subunit pseudouridine synthase D
	3572060	NE NE	Spy49_0880	6985882	NE NE	pta/eutD	*			phosphotransacetylase
	3572061	NE	Spy49_0881	6985883	NE	-				short chain dehydrogenase
M5005_Spy_0853 3	3572062	NC				-				short chain dehydrogenase
	3572063	NE	Spy49_0882c	6985884	NE		*			Na+ driven multidrug efflux pump
	3572064	NE	Spy49_0883	6985885	NE	proV				glycine betaine transport ATP-binding protein
	3572065 3572066	NE NE	Spy49_0884 Spy49_0885	6985886 6985887	NE NE	proX guaC	*			glycine betaine transporter permease guanosine 5\'-monophosphate oxidoreductase
		INL	Spy49_0886c	6985888	NE	9				5
	3572067	NE	Spy49_0887	6985889	NE	xpt	*			xanthine phosphoribosyltransferase
	3572068	NE	Spy49_0888	6985890	NE	-	*			xanthine permease
	3572030	NE	Spy49_0891c	6985891	NE	apbE	*			thiamine biosynthesis lipoprotein
	3572031 3572032	NE NE	Spy49_0892c Spy49_0893	6985892 6985893	NE NE	tdk2				4-oxalocrotonate tautomerase thymidine kinase
	3572033	E	Spy49_0894	6985894	E	prfA	*	SSA_1152	SP_1020	peptide chain release factor 1
	3572034	NE	Spy49_0895	6985895	NC	hemK	*		**	peptide release factor-glutamine N5-methyltransferase
M5005_Spy_0865 3	3572035	NC	Spy49_0896	6985896	E	-	*		SP_1022	SUA5 protein
	3572036	NE	Spy49_0897	6985897	NE	-	*			phosphinothricin N-acetyltransferase
	3572037	NE	Spy49_0898	6985898	NE	glyA	*			serine hydroxymethyltransferase
	3572038 3572039	NE NE	Spy49_0899	6985899	NC	-	*			hypothetical protein M5005_Spy_0868 hypothetical protein M5005_Spy_0869
113003_5py_0003	337 <u>LU33</u>	INL	Spy49_0900	6985900	NE					nypodredical protein risoos_spy_coos
M5005_Spy_0870 3	3572040	NE	Spy49_0901	6985901	NC	-	*			multidrug resistance ABC transporter ATP-binding protein/permease
	3572041	NE	Spy49_0902	6985902	NE	-	*			multidrug resistance ABC transporter ATP-binding protein/permease
	3572042	NE	Spy49_0903	6985903	NE	nox	*			NADH oxidase H2O-forming
	3572043	NE	Spy49_0904c	6985904 6985905	C	Idh	*	CCA 4220	SP_1220	L-lactate dehydrogenase
	3572044 3572045	E E	Spy49_0905 Spy49_0906	6985906	E C	gyrA	*	SSA_1220	SP_1219	DNA gyrase subunit A sortase
	3572046	NE	Spy49_0907	6985907	c	-	*			lactoylglutathione lyase
	3572047	NC	Spy49_0908	6985908	NE	-				hypothetical protein M5005_Spy_0877
	3572048	NE				-	*			hypothetical protein M5005_Spy_0878
	3572010	NE	Spy49_0909c	6985909	NE	-				hypothetical protein M5005_Spy_0879
	3572011 3572012	C	Spy49_0910c	6985910	E	hlyIII	*			hypothetical protein M5005_Spy_0880
	3572012 3572013	NE E	Spy49_0911c Spy49_0912	6985911 6985912	NE E	rbgA	*	SSA_1189	SP_1155	hypothetical protein M5005_Spy_0881 ribosomal biogenesis GTPase
	3572014	NE	Spy49_0913	6985913	NE	rnhB	*	33A_1109	3F_1133	ribonuclease HII
	3572015	NE	Spy49_0914	6985914	NE	smf	*			hypothetical protein M5005_Spy_0884
M5005_Spy_0885 3	3572016	С	Spy49_0915	6985915	Ε	topA	*	SSA_1184	SP_1263	DNA topoisomerase I
	3572017	NE	Spy49_0916c	6985916	NE	-				LysR family transcriptional regulator
	3572018	NC	Spy49_0917c	6985917	NC	-				LysR family transcriptional regulator
	3572019 3572020	NC NE	Spy49_0918	6985918	NE	-				LysR family transcriptional regulator regulatory protein (pfoS/R)
	3572021	NE	Spy49_0918 Spy49_0919	6985919	NE	ddh				D-lactate dehydrogenase
	3572022	E	Spy49_0920	6985920	E	satD				hypothetical protein M5005_Spy_0891
	3572023	NE	Spy49_0921	6985921	NE	satE				hypothetical protein M5005_Spy_0892
	3572024	NC	Spy49_0922	6985922	NC	gid	*			tRNA (uracil-5-)-methyltransferase Gid
	3572025	NE	Spy49_0923	6985923	NE	oadA2				oxaloacetate decarboxylase
	3572026 3572027	NE NE	Spy49_0924 Spy49_0925	6985924 6985925	NE NE	-				hypothetical protein M5005_Spy_0895 biotin carboxyl carrier protein of oxaloacetate decarboxylase
	3572028	NE	Spy49_0926	6985926	NC	-				oxaloacetate decarboxylase subunit beta
	3572029	NE	Spy49_0927c	6985927	NE	-				2-(5\'\'-triphosphoribosyl)-3\'-dephosphocoenzyme-A synthase
	3571991	NE	Spy49_0928c	6985928	NE	citG				GntR family transcriptional regulator
	3571992	NE	Spy49_0929c	6985929	NE	-				Mg2+/citrate complex secondary transporter
	3571993 3571994	NE NE	Spy49_0930	6985930	NE	-				hypothetical protein M5005_Spy_0901 acetyl-CoA carboxylase biotin carboxyl carrier protein subunit
	3571995	NE	Spy49_0933	6985931	NE	oadB				oxaloacetate decarboxylase subunit beta
	3571996	NC	564.15_0333			-				hypothetical protein M5005_Spy_0904
	3571997	NE	Spy49_0934	6985932	NE	citD				citrate lyase subunit gamma
	3571998	NE	Spy49_0936	6985933	NC	citE				citrate lyase subunit beta/citryl-CoA lyase subunit
	3571999 3572000	NC	Spy49_0937	6985934 6985935	NE	citF				citrate lyase subunit alpha/citrate CoA-transferase 2-(5\'\'-triphosphoribosyl)-3\'-dephosphocoenzyme-A synthase
	3572000 3572001	NE NE	Spy49_0938 Spy49_0939	6985936	NE NE	citX oadA1				oxaloacetate decarboxylase
	3572001	NE	Spy49_0940c	6985937	NE	citC	*			(citrate (pro-3S)-lyase) ligase
M5005_Spy_0911c 3	3572003	NE	Spy49_0942c	6985938	NE	-	*			hypothetical protein M5005_Spy_0911
	3572004	NC				-				hypothetical protein M5005_Spy_0912
	3572005 3572006	C	Spy49_0943c	6985939	C	xerS	*		SP_1159	site-specific tyrosine recombinase XerS phage transcriptional repressor
	3572006 3572007	NE E	Spy49_0944 Spy49_0945c	6985940 6985941	NE E	ffh	*	SSA_1167	SP_1287	signal recognition particle subunit FFH/SRP54
	3572008	C	Spy49_0946c	6985942	NC	ylxM	*	55.1_110/	5120/	DNA-binding protein
M5005_Spy_0917c 3	3572009	c	Spy49_0947c	6985943	NE	-	*			GntR family transcriptional regulator
	3571971	NE	Spy49_0948c	6985944	NE	-	*			hypothetical protein M5005_Spy_0918
	3571972	C	Spy49_0949	6985945 6985946	C	guaA	*		SP_1445	GMP synthase
	3571973 3571974	NE NE	Spy49_0951c Spy49_0952c	6985946	NE NE	murM2	*			UDP-N-acetylmuramoylpentapeptide-lysine N(6)-alanyltransferase ABC transporter ATP-binding protein
	3571975	NE	Spy49_0953c	6985948	NE	pdxK	*			hypothetical protein M5005 Spy 0922
	3571976	NE	Spy49_0954c	6985949	NE	-	*			pyridoxamine kinase
	3571977	NE	Spy49_0955	6985950	NE	-	*			GntR family transcriptional regulator
	3571978	NE	Spy49_0957c	6985951	NE	rnhB	*			anaerobic ribonucleoside-triphosphate reductase
M5005_Spy_0926c 3		NC	Spy49_0958c	6985952	E	fha 1	*			cardiolipin synthetase formatetetrahydrofolate ligase
M5005_Spy_0927c <u>3</u> M5005_Spy_0928c <u>3</u>	3571980 3571981	E NE	Spy49_0959c Spy49_0960c	6985953 6985954	C NE	fhs.1 IpIA	*			lipoate-protein ligase A
	3571981 3571982	NE	Spy49_0960c Spy49_0961c	6985955	NE		*			SIR2 family protein
M5005_Spy_0930c 3	3571983	NE	Spy49_0962c	6985956	NE	-	*			hypothetical protein M5005_Spy_0930
M5005_Spy_0931c 3	3571984	NE	Spy49_0963c	6985957	NE	-	*			glycine cleavage system protein H
	3571985	NE	Spy49_0964c	6985958	NE	-	*			luciferase-like monooxygenase
	3571986	NE	Spy49_0965c	6985959	NE	-	*			NADH-dependent flavin oxidoreductase
	3571987 3571988	NE C	Spy49_0966c Spy49_0967	6985960 6985961	NE E	dpfB	*		SP 1230	lipoate-protein ligase A phosphopantothenatecysteine ligase
	3571989	E	Spy49_0967 Spy49_0968	6985962	E	dfp	*		SP_1230 SP_1231	phosphopantothenoylcysteine decarboxylase
	3571990	NE	Spy49_0969	6985963	c	-	*			transporter
M5005_Spy_0938 3	3571952	E	Spy49_0970	6985964	Ε	pgmA	*		SP_1498	phosphoglucomutase/phosphomannomutase
	3571953	NE	Spy49_0971c	6985965	NE		*			nucleoside transporter permease
	3571954	NE	Spy49_0972c	6985966	NE	-	*			nucleoside transporter permease nucleoside transport ATP-binding protein
	3571955 3571956	NE NE	Spy49_0973c Spy49_0974c	6985967 6985968	NE NE	-	*			nucleoside transport AIP-binding protein nucleoside-binding protein
			30,13_03/40		.42					

M5005_Spy_0943c <u>3571957</u>	NE Spy49_09		NE	cdd	*			cytidine deaminase
M5005_Spy_0944c 3571958	NE Spy49_09		NE	-	*			16S rRNA m(2)G 1207 methyltransferase
M5005_Spy_0945 <u>3571959</u> M5005_Spy_0946 <u>3571960</u>	E Spy49_0		E	coaA	*		SP_0839	pantothenate kinase
M5005_Spy_0946 <u>3571960</u> M5005_Spy_0947c <u>3571961</u>	NE Spy49_09 NE Spy49_09		NC C	rpsT ciaH	*			30S ribosomal protein S20 sensor protein
M5005_Spy_0948c 3571962	NE Spy49_09		E	ciaR	*			transcriptional regulatory protein
M5005_Spy_0949c 3571963	NE Spy49_09		NE	pepN	*			lysyl aminopeptidase/alanine aminopeptidase
M5005_Spy_0950c 3571964	NC Spy49_09		NE	phoU	*			phosphate transporter protein
M5005_Spy_0951c 3571965	NE Spy49_09	3c <u>6985977</u>	NC	pstB	*			phosphate transporter ATP-binding protein
M5005_Spy_0952c 3571966	NE Spy49_09		С	pstB2	*	SSA_0944		phosphate transporter ATP-binding protein
M5005_Spy_0953c <u>3571967</u>	NE Spy49_09		NC	pstA	*			phosphate transporter permease
M5005_Spy_0954c 3571968	NC Spy49_0		NC	pstC	*			phosphate transporter permease
M5005_Spy_0955c 3571969	NE Spy49_09		NC	pstS	*			phosphate-binding protein
M5005_Spy_0956c 3571970	E Spy49_09		Е	-	*			16S rRNA m(5)C 967 methyltransferase
M5005_Spy_0957c 3571932	NE Spy49_09		NE	-	*			myo-inositol-1(or 4)-monophosphatase
M5005_Spy_0958c 3571933 M5005_Spy_0959c 3571934	NE Spy49_09		NE	-	*			hypothetical protein M5005_Spy_0958
M5005_Spy_0959c <u>3571934</u> M5005_Spy_0960c <u>3571935</u>	NE Spy49_09 E Spy49_09		NE	spxA mreA	*	CCA 0026	CD 1110	Spx family transcriptional regulator bifunctional riboflavin kinase/FMN adenylyltransferase
M5005_Spy_0960c 3571936	E Spy49_09 NE Spy49_09		E NE	truB	*	SSA_0936	SP_1110	tRNA pseudouridine synthase B
M5005_Spy_0962c 3571937	NE Spy49_09		NE	-	*			hypothetical protein M5005_Spy_0962
M5005_Spy_0963c 3571938	NE Spy49_09		NE	_	*			hypothetical protein M5005 Spy 0963
M5005_Spy_0964c 3571939	NE Spy49_09		NE	-	*			type I restriction-modification system specificity subunit
M5005_Spy_0965c 3571940	NE Spy49_09		NE	-	*			ABC transporter permease
M5005_Spy_0967c 3571942	NE Spy49_09		NE	-	*			ABC transporter ATP-binding protein
M5005_Spy_0968 3571943	NE Spy49_0	99 6985993	NE	-	*			TetR family transcriptional regulator
M5005_Spy_0969c 3571944	NC			-				hypothetical protein M5005_Spy_0969
M5005_Spy_0970c 3571945		00c <u>6985994</u>	NE	-	*			NAD-dependent K+ or Na+ uptake system component
M5005_Spy_0971c 3571946		1c <u>6985995</u>	NE	-	*			Gls24 family general stress protein
M5005_Spy_0972c <u>3571947</u>		02c <u>6985996</u>	NE	-				hypothetical protein M5005_Spy_0972
M5005_Spy_0973c 3571948	NE Spy49_10		NE	-	*			Gls24 family general stress protein
M5005_Spy_0974c 3571949	NC Spy49_10		NC	-				small integral membrane protein hypothetical protein M5005 Spy 0975
M5005_Spy_0975c 3571950 M5005_Spy_0976c 3571951	NE Spy49_10		NE	-	*			
	NE Spy49_10		NE	norA	*		CD 1007	hypothetical protein M5005_Spy_0976 DNA helicase II
M5005_Spy_0977c <u>3571913</u> M5005_Spy_0978 <u>3571915</u>	C Spy49_10 NC Spy49_10		E NC	pcrA	*		SP_1087	Na(+)-linked D-alanine glycine permease
M5005_Spy_0979c 3571914	C 3py43_1	08 <u>0500002</u>	INC	_	-			hypothetical protein M5005_Spy_0979
M5005_Spy_0980 3571916	NE Spy49_10	09 6986003	NE	_	*			cobalt-zinc-cadmium resistance protein
M5005_Spy_0981c 3571917	NE Spy49_10		NE	cfa				cAMP factor
M5005_Spy_0982c 3571918	NE Spy49_10		NE	-				histidine-binding protein
M5005_Spy_0983c 3571919	NC Spy49_10		NE	-				histidine transport ATP-binding protein
M5005_Spy_0984c 3571920	NE Spy49_10		NE	-				histidine transporter permease
M5005_Spy_0985c 3571921	NE Spy49_10	4c <u>6986008</u>	NE	-				phnA protein
M5005_Spy_0986c 3571922	E Spy49_10	5c <u>6986009</u>	E	glmS		SSA_2107	SP_1087	glucosaminefructose-6-phosphate aminotransferase
M5005_Spy_0987c 3571923	NE Spy49_10		NE	sipC				signal peptidase I
M5005_Spy_0988c <u>3571924</u>	E Spy49_10		E	pyk	*	SSA_0848	SP_0897	pyruvate kinase
M5005_Spy_0989c 3571925	E Spy49_10		E	pfkA	*	SSA_0847	SP_0896	6-phosphofructokinase
M5005_Spy_0990c 3571926	E Spy49_10		E	dnaE	*	SSA_0846	SP_0895	DNA polymerase III DnaE
M5005_Spy_0991 <u>3571927</u>	NC Spy49_10		NE	-	*			GntR family transcriptional regulator
M5005_Spy_0992 <u>3571928</u> M5005_Spy_0993 <u>3571929</u>	NE Spy49_10 NE Spy49_10		C		*			ABC transporter ATP-binding protein ABC transporter permease
M5005_Spy_0994c 3571930	NE Spy49_10 C Spy49_10		C E		*			membrane-associated alkaline phosphatase
M5005_Spy_0995c 3571931	NE Spy45_10	.sc <u>0500017</u>	-	-				phage protein
M5005_Spy_0996 3571893	NE			speA2				enterotoxin
M5005_Spy_0997c 3571894	NE							phage protein
M5005_Spy_0998c 3571895	NE			-				phage protein
M5005_Spy_0999c 3571896	NE			-				phage protein
M5005_Spy_1000c 3571897	NE			-				phage protein
M5005_Spy_1001c 3571898	NE			-				phage-associated cell wall hydrolase
M5005_Spy_1002c 3571899	NE			-				N-acetylmuramoyl-L-alanine amidase
M5005_Spy_1003c <u>3571900</u>	NE			-				phage protein
M5005_Spy_1004c 3571901	NC			-				phage protein
M5005_Spy_1005c 3571902	NE			-				phage protein
M5005_Spy_1006c 3571903 M5005_Spy_1007c 3571904	NE			-				phage structural protein
M5005_Spy_1007c 3571904 M5005_Spy_1008c 3571905	NE NE							phage protein hypothetical protein M5005_Spy_1008
M5005_Spy_1009c 3571906	NE			_				phage protein
M5005_Spy_1010c 3571907	NC			-				phage protein
M5005_Spy_1011c 3571908	NE			-				phage protein
M5005_Spy_1012c 3571909	NE			-				antigen A
M5005_Spy_1013c 3571910	NE			-				antigen B
M5005_Spy_1014c <u>3571911</u>	NE			-				antigen C
M5005_Spy_1015c 3571912	NE			=				phage protein
M5005_Spy_1016c 3571874	NE			-				phage protein
M5005_Spy_1017c 3571875	NE			-				phage protein
M5005_Spy_1018c 3571876 M5005_Spy_1019c 3571877	NE NE			-				phage scaffold protein
M5005_Spy_1019c <u>3571877</u> M5005 Spy 1020c <u>3571878</u>	NE NE			-				phage scaffold protein phage protein
M5005_Spy_1020c 3571879	NE NE			-				phage protein
M5005_Spy_1021c 3571880	NE NE			-				portal protein
M5005_Spy_1023c 3571881	NE			-				terminase large subunit
M5005_Spy_1024c 3571882	NE			-				phage protein
M5005_Spy_1025c 3571883	NE			-				ArpU family phage encoded transcriptional regulator
M5005_Spy_1026c 3571884	NE			-				phage protein
M5005_Spy_1027c <u>3571885</u>	NE			-				phage protein
M5005_Spy_1028c 3571886	NE			-				phage protein
M5005_Spy_1029c 3571887	NE			-				phage protein
M5005_Spy_1030c 3571888	NE			-				phage protein
M5005_Spy_1031c <u>3571889</u> M5005_Spy_1032c <u>3571890</u>	NE			-				phage protein
M5005_Spy_1032c <u>3571890</u> M5005_Spy_1033c <u>3571891</u>	NE NE			-				phage protein phage protein
M5005_Spy_1033c 3571891 M5005_Spy_1034c 3571892				-				phage protein
M5005_Spy_1034c 3571854 M5005_Spy_1035c 3571854	NF			-				phage protein
M5005_Spy_1036c 3571855	NE NE			ssb2				phage single-strand DNA binding protein
	NE			JJJ2				phage single-strand DNA binding protein
	NE NE			ssb1				
M5005_Spy_1037c <u>3571856</u> M5005_Spy_1038c <u>3571857</u>	NE			ssb1				phage protein
M5005_Spy_1037c 3571856	NE NE NE			ssb1 - -				
M5005_Spy_1037c <u>3571856</u> M5005_Spy_1038c <u>3571857</u>	NE NE NE			ssb1 - - -				phage protein
M5005_Spy_1037c 3571856 M5005_Spy_1038c 3571857 M5005_Spy_1039c 3571859 M5005_Spy_1040c 3571859 M5005_Spy_1041c 3571860	NE NE NE NE			ssb1 - - - -				phage protein phage protein
M5005_Spy_1037c 3571856 M5005_Spy_1038c 3571857 M5005_Spy_1039c 3571858 M5005_Spy_1040c 3571859 M5005_Spy_1041c 3571860 M5005_Spy_1042c 3571861	NE NC			ssb1 - - - - -				phage protein phage protein phage protein phage protein phage replication protein
M5005_Spy_1037c 3571856 M5005_Spy_1038c 3571857 M5005_Spy_1039c 3571858 M5005_Spy_1040c 3571859 M5005_Spy_1041c 3571860 M5005_Spy_1042c 3571861 M5005_Spy_1042c 3571861	NE			ssb1				phage protein phage protein phage protein phage protein phage protein phage replication protein phage protein
M5005_Spy_1037c 3271856 M5005_Spy_1038c 3571857 M5005_Spy_1039c 3571858 M5005_Spy_1040c 3571859 M5005_Spy_1041c 3571860 M5005_Spy_1041c 3571860 M5005_Spy_1042c 3571861 M5005_Spy_1043 3571862 M5005_Spy_1044 3571862	NE NE NE NE NE NE NC NC NC			ssb1				phage protein phage protein phage protein phage protein phage protein phage replication protein phage protein phage protein
M5005_Spy_1037c 3571856 M5005_Spy_1038c 3571857 M5005_Spy_1039c 3571858 M5005_Spy_1040c 3571859 M5005_Spy_1041c 3571860 M5005_Spy_1042c 3571861 M5005_Spy_1042c 3571861	NE			ssb1				phage protein phage protein phage protein phage protein phage protein phage replication protein phage protein

Missage Miss	MEANE C. 1016 2571065 NE				allow and the
MODES 1997					
Model Sept. 1985 2015-208 1985-208 1985-209 1		-			
Miles Mile		-			
### Miles Services	M5005_Spy_1050 3571869 C	-			phage transcriptional repressor
1909 1909		-			
Property 1965 2012 1965 19		int.1			
Memory M	M5005_Spy_1053 35/18/2 NC	-			nypotnetical protein M5005_Spy_1053
Memory M	M5005 Spy 1054 3571873 NF	Snv49 1024 6986019 NF -			hypothetical protein M5005 Spy 1054
			*		
Mode Start 1985 1	M5005_Spy_1056c 3571836 NE	Spy49_1026c 6986021 NE malM	*		4-alpha-glucanotransferase
Medical Sept 1982	M5005_Spy_1057c 3571837 NE	Spy49_1027c 6986022 NE malR	*		LacI family transcriptional regulator
Miles Mile			*		
1,000, 3-p. 1,000 2,000 1,000			*		
Medical Section Medical Se		Spy49_1030 <u>6986025</u> NE malG	*		
Model Sept 1866 1871-186		- 			
## MIRAS Sep. 1865. 1523-2522 William France France					
Miles Sept 1985					
Medical Sept 1966 1975 1976					
MODS_Spy_1006, 127-2022 Fig. Spy=1_2012, 127-2022 Fi	M5005_Spy_1067c 3571847 NE	malX			maltose/maltodextrin-binding protein
MRDS_Spy_LONC_ 1971-1972 1971-1976	M5005_Spy_1068 <u>3571848</u> NE	Spy49_1032 <u>6986027</u> NE -			transposase
Mobile Systy 1971; 272,1976			*		
Month Sept 1975 291252 St. Sept 1986 298611 NC			*		
Model S. Spy 1.1076 2211121 K Spy 1.1076					
			*		
## Section 1972 197			•		
1990 5.97 10			*		
			*	SP 1461	
Month Mont			*		
MS005_59_1006 257_1202 MS Sping 1046 2005024 MS MS MS MS MS MS MS M				-	hypothetical protein M5005_Spy_1078
MS005_59_1081_221222 MS999_3046_ 6866554 MS	M5005_Spy_1079c 3571820 NE	Spy49_1043c 6986038 NE -			PTS system cellobiose-specific transporter subunit IIC
Ministry 1975 1971 197			*		
MS005_Sp.1086_Sp.108			*		
MS005_Spy_1084_SPY_1085_SPY_1087_SPY_1086_SPY_			*		
MS905_SP_108			*		
M5905_Sp.1086 3271822 K Symby 1050 6886654 K			*		
March 1955 March 1957 Mar			*		
MS005_Spy_1086 2971292 C Spyel 20104 Spyel 20104 C Spyel 20104			*		
Misson S. Spy. 1090 3271313 M			* SSA 0807	SP 1079	
Section Sect		-			
Spyright	M5005_Spy_1090 3571831 NE	Spy49_1054 6986048 NE -	*		transposase
M5005, Spy, 1092 327,832 NE Spy40, 1095 598,0005 NE	M5005_Spy_1091 <u>3571832</u> NE				transposase
Spy4 1006 9580525 NC Spy4 1006 9580525 NC FIRST Spy4 1007 958					
Spy-1,002 Spy-1,002 Spy-1,006 Sp86055 NE					
MS005_Syn_1096 3271233 N. Syny4_1065 3286055 N. Syny4_1065 Syny4_10					
M5005_Syv_1096 327128 N. Syyky 1,065 5972727 N. Syyky 1,075	M5005 Spv 1092c 3571833 NF		*		ribosomal small subunit pseudouridine synthase A
Mosco Seys 1096 397779 No. Seys 1096 597779 No. Seys 1096 597797 No. Seys 1096 597797 No. Seys 1096 597797 No. Seys 1096			*		
M5005_Spy_1096 3571729 No. Spy49_1076 9986958 No. No. Nyoberhelical protein N5005_Spy_1096 3571729 No. Spy49_1076 9986958 No. No. Nyoberhelical protein N5005_Spy_1096 3571298 No. Spy49_1076 59865958 No. No. Nyoberhelical protein N5005_Spy_1096 3571298 No. Nyoberhelical No. Nyoberhelical Protein N5005_Spy_1096 3571298 No. Nyoberhelical No. Nyoberhelical Protein N5005_Spy_1096 3571298 No. Nyoberhelical Protein N5005_Spy_1096 3571298 No. Nyoberhelical Protein N5005_Spy_1096 No. Nyoberhelical Protein N5005_Spy_1096 Nyoberhe			*		
Mode			*		
Motion M	M5005_Spy_1096c 3571798 NE	Spy49_1070c 6986059 NE -	*		
Most		Spy49_1071c <u>6986060</u> NE -			
Most			*		
Mode			*		
MS00.5 Spv. 1102 3271805 N			*		
Mosco Spv_1104 3271805 E Spv_91 1076 698606 NC			*		
Mosol Spy 1106 3271805 NE Spy4 1078 6986067 NE Spy4 1079 6986068 NE NE New Part			* \$\$A 1/101	SD 1084	
M5005_Spy_1106 2571807 NE Spy49_1076 698608 NE Spy49_1086 698608 NE Spy49_1086 6986072 NE Spy49_1086 Spy49_			*	31_1004	
MS005_Spy_11108_ 3521802 NE Spy49_1084 6986020 NE murZ MS005_Spy_11108_ 3521811 NE Spy49_1084 6986020 E inlA NS005_Spy_11110 3571812 E Spy49_1085 6986020 E inlA NS005_Spy_11110 3571812 Spy49_1085 6986020 E inlA NS005_Spy_11110 Spy49_1085 6986020 NS005_Spy_11110 Spy49_1085 6986020 NS005_Spy_11110 Spy49_1085			*		
MS005 Spy_11196 S371810 NS Syny4 1083 6986072 NE Inin NS Syny4 1084 6986072 NE Inin NS Syny4 1085 Syny4 1085 Syny4 1086	M5005_Spy_1106c 3571808 NE	Spy49_1080c 6986069 NE grab			protein G-related alpha 2M-binding protein
MS005_Spy_11106 S71811 NE Spy49_1086 6986072 NE InitA NE Spy49_1086 6986073 E InitA NE SSA_0999 Initernalin protein MS005_Spy_11112 S71813 NE Spy49_1086 6986073 E InitA NE SSA_0999 Initernalin protein MS005_Spy_1112 S71813 NE Spy49_1086 6986073 E InitA NE SSA_0999 Initernalin protein MS005_Spy_1113 S71813 NE Spy49_1086 6986073 E InitA NE SSA_0999 InitErnalin protein MS005_Spy_1113 S71813 NE Spy49_1086 6986073 NE NE SSA_0997 SP_0865 NE NE SSA_0997 SP_0865 NE NE SPy49_1086 MS005_Spy_1116 S71772 NE Spy49_1086 6986075 NE NE Spy49_1086 MS005_Spy_1116 S71772 NE Spy49_1086 6986075 NE NE Spy49_1086 MS005_Spy_1116 S71772 NE Spy49_1090 G886090 NE NE Spy49_1086 MS005_Spy_1116 S71772 NE Spy49_1092 G886090 NE NE Spy49_1086 MS005_Spy_1116 S71773 NE Spy49_1093 G886090 NE NE Spy49_1086 MS005_Spy_1112 S71773 NE Spy49_1094 G986091 NE Spy49_1086 MS005_Spy_1126 S71773 NE Spy49_1096 G986092 NE Spy49_1086 G986092 NE Spy49_1086 G986093 NE NE Spy49_1086 G986094 NE NR NR Spy49_1086 G986094 NE NR NR Spy49_1086 G986094 NE NR Spy49_1086 G986096 NE NR Spy49_1086 G986098 NE NR Spy49_1086 G986098 NE NR NR Spy49_1086 G986098 NE NR Spy49_1086 G986098 NE NR Spy49_1086 G986094 NE NR Spy49_1086 S986094 NE N			*		
MS005 Spy 1110 3571812 E Spy49 1086 6986074 NE - SSA_0999 SSA_09			* SSA_1495	SP_0762	
MS005_Spy_1111c 327_1812 12 12 12 12 12 12 12			*		
MS005_Spy_1112 S571776 NE		.,,	* SSA_0999		
Mosol Spy 1112 S271776 NE Spy49 1088 6986077 NE - * * * * * * * * *			SSA 0007	CD 006E	
MS005_Spy_1116 3571777 NE			33A_U997	31 _0003	
MS005_Spy_1116 S71778 NE			*		
M5005_Spy_1118 3571780		-			
MS005_Spy_1119c 3571781 Spy49_1093c 6986.081 E G986082 Spy49_1094 G986.081 E G986082 Spy49_1094 G986.081 E G986082 Spy49_1094 G986.081 E G986082 Spy49_1094 G986.081 E G986082 Spy49_1095 Spy49_1095 Spy49_1094 G986.082 Spy49_1095 Spy49_1	M5005_Spy_1116c <u>3571779</u> NE	Spy49_1090c <u>6986078</u> NE udk	*		uridine kinase
MS005_Spy_11126 3571782 E Spy49_10936 6986081 E GapN MS005_Spy_11216 3571783 C Spy49_10946 6986082 C pst * Sp_1176 phosphocarrier protein phosphotransferase MS005_Spy_11212 3571786 NE Spy49_1096 6986082 NE nrdH Spy40_1096 Spy4			*		
MS005_Spy_1120c 3571783			*		
MS005_Spy_11212 3571785					
M5005_Spy_1122 3571785 NE			*		
M5005_Spy_1124 3571786				SP_11//	
M5005_Spy_1124 3571787			*		
M5005_Spy_1124 3571787 NE					
M5005_Spy_1126 Spy	M5005_Spy_1124 3571787 NE		*		ribonucleotide-diphosphate reductase subunit beta
Spy49_1103 Sp86090 NC Spy49_1104 Sp86091 NE Spy49_1105 Sp86091 NE Spy49_1105 Sp86091 NE Spy49_1106 Sp86091 NE Spy49_1106 Sp86092 NE Spy49_1106 Spy			*		chloride channel protein
Spy49_1103 Sp86090 NC Spy49_1104 Sp86091 NE Spy49_1105 Sp86091 NE Spy49_1105 Sp86091 NE Spy49_1106 Sp86091 NE Spy49_1106 Sp86092 NE Spy49_1106 Spy		Spy49_1101 6986089 NC			
MS005_Spy_1130c 3571792 NE Spy49_1105c 6986092 NE Spy49_1105c 6986093 NE Spy49_1105c Spy405_Spy_1130c Spy405_Spy_1130c Spy405_Spy_1130c Spy405_Spy405					
M5005_Spy_1130c 3571793	MEDDE Com 1120				CAAV
MS005_Spy_11312 3571794 NC Spv49_1107 6986.094 NE Spv49_1108 5986.095 E Spv49_1108 5986.095 E Spv49_1108 5986.095 E Spv49_1108			*		
MS005_Spy_1132c 3571795 E Spy49_1108c 6986095 E alaS * SSA_0756 SP_1383 alanyl-tRNA synthetase foldase PrsA MS005_Spy_11375 S571758 NE Spy49_1110c 6986097 NE - * * C- * C- * C- C-			*		
M5005_Spy_1134c 3571758 / Spy135 NE Spy49_1106 6986095 / Spy49_1106 NE Spy49_11106 PrsA * Spy49_1106 * O-methyltransferase M5005_Spy_1135c 3571759 / Spy135c NE Spy49_1110c 6986097 / NE - * * O-methyltransferase × Oaklate/formate antiporter M5005_Spy_1136c 3571760 / Spy135c NE Spy49_1111c 6986099 / NE DepB * Ormethyltransferase M5005_Spy_1136c 3571761 / Spy1316c NE Spy49_1111c 6986100 / NE DepB * Ormethyltransferase M5005_Spy_1136c 3571761 / Spy1316c NE Spy49_1111c 6986100 / NE DepB * Ormethyltransferase M5005_Spy_1137c 3571761 / Spy49_1114c 6986101 / NE DepB * Ormethyltransferase M5005_Spy_1138c 3571761 / Spy49_1114c 6986101 / NE DepB * Ormethyltransferase M5005_Spy_1138c 3571761 / Spy49_1114c 6986101 / NE DepB * Ormethyltransferase M5005_Spy_1138c 3571761 / Spy49_1114c 6986102 / NE DepB * Ormethyltransferase M5005_Spy_1138c 3571761 / Spy49_1114c 6986101 / NE DepB * Ormethyltransferase M5005_Spy_1138c 3571761 / NE Spy49_1114c 6986101 / NE DepB * Ormethyltransferase <td></td> <td></td> <td>*</td> <td>CD 4202</td> <td></td>			*	CD 4202	
MS005_Spy_1136c 3571758 NE Spy49_1110c 6986097 NE - * O-methyltransferase M5005_Spy_1136c 3571750 NE Spy49_1111c 6986098 NE - * oxalate/formate antiporter M5005_Spy_1137c 3571761 NE Spy49_11112 6986100 NE - * competence protein/transcription factor M5005_Spy_1138c 3571761 NE Spy49_1111c 6986101 NE - * competence protein/transcription factor M5005_Spy_1138c 3571762 NE Spy49_1115c 6986101 NE - * competence protein/transcription factor M5005_Spy_1139c 3571762 NE Spy49_1115c 6986102 NE - * competence protein/transcription factor M5005_Spy_1139c 3571763 NE Spy49_1115c 6986102 NE - * competence protein/transcription factor R5005_Spy_1139c 3571765 NE Spy49_1115c 6986102 NE - * comp			* SSA_U/56	25-1383	
M5005_Spy_1136c 3571759 NE Spy49_1111c 6986098 NE - * oxalate/formate antiporter M5005_Spy_1137c 3571761 NE Spy49_1112c 6986099 NE pepB * oligoendopeptidase F M5005_Spy_1137c 3571761 NE Spy49_1111c 6986100 NE - * competence protein/transcription factor M5005_Spy_1138c 3571762 NE Spy49_1111c 6986100 NE - * ribosomal small subunit pseudouridine synthase A M5005_Spy_1138c 3571763 NE Spy49_1115c 6986102 NE nagB * glucosamine-6-phosphate isomerase			*		
M5005_Spy_1136			*		
MS005_Spy_1137c 3571761 NE Spy49_1118c 6986101 NE - * competence protein//transcription factor MS005_Spy_1138c 3571762 NE Spy49_1116 6986101 NE - ribosomal small subunit pseudouridine synthase A MS005_Spy_1139c 3571763 NE Spy49_111b 6986102 NE nagB * glucosamine-6-phosphate isomerase			*		
M5005_Spy_1138c 3571762 NE Spy49_1114c 6986101 NE - ribosomal small subunit pseudouridine synthase A M5005_Spy_1139c 3571763 NE Spy49_1115c 6986102 NE nagB * glucosamine-6-phosphate isomerase			*		
	M5005_Spy_1138c 3571762 NE	Spy49_1114c <u>6986101</u> NE -			ribosomal small subunit pseudouridine synthase A
M5005_Spy_1140 3571764 NE Spy49_1116 6986103 NE queA * S-adenosylmethioninetRNA ribosyltransferase-isomerase			*		
	M5005_Spy_1140 <u>3571764</u> NE	Spy49_1116 <u>6986103</u> NE queA	*		S-adenosylmethioninetRNA ribosyltransferase-isomerase

MEDDE Cour 1141										
M5005_Spy_1141		NE		86104	NE	-	*			hypothetical protein M5005_Spy_1141
M5005_Spy_1142c		NE		84357	NE	-	*			hypothetical protein M5005_Spy_1142
M5005_Spy_1143c		NE		84358	NE	-	*			hypothetical protein M5005_Spy_1143
M5005_Spy_1144c	3571768 3571769	NE		84359 84360	NC	sodA	*			hypothetical protein M5005_Spy_1144 superoxide dismutase
M5005_Spy_1145c M5005_Spy_1146c		NE E		84361	NE E	holA	*	SSA_0720	SP_0765	DNA polymerase III subunit delta
M5005_Spy_1147c		NE		84362	NE	comEC	*	33A_0720	3F_0703	competence protein ComE
M5005_Spy_1148c		NE		84363	NE	comE	*			competence protein ComE
M5005_Spy_1149c		E		84364	E	-	*	SSA_0713		1-acyl-sn-glycerol-3-phosphate acyltransferase
M5005_Spy_1150	3571774	NE		84365	NE	-	*	_		methyltransferase
M5005_Spy_1151	3571775	NE	Spy49_1129 698	84366	NE	-	*			hypothetical protein M5005_Spy_1151
M5005_Spy_1152c	3571737	NE	Spy49_1130c 698	84367	NE	kup	*			kup system potassium uptake protein, partial
M5005_Spy_1154c		NE		84368	NE	deaD	*			ATP-dependent RNA helicase
M5005_Spy_1155c		NE		84369	NE	prfC	*			peptide chain release factor 3
M5005_Spy_1156c	3571741	NE		84370	NE		*			hypothetical protein M5005_Spy_1156
M5005_Spy_1157c		E		84371	E	murF ddl	*	SSA_0692	SP_1670	UDP-N-acetylmuramoylalanine-D-glutamyl-lysineD-alanyl-D-alanine ligase D-alanyl-alanine synthetase A
M5005_Spy_1158c M5005_Spy_1159c		E NE		84372 84372	E C	recR	*	SSA_0691	SP_1671	recombination protein RecR
M5005_Spy_1160c		NE		84373 84374	NE	TECK	*		SP_1672	penicillin-binding protein
M5005_Spy_1161c		NE		84375	NE	fdhC				formate transporter
M5005_Spy_1162c		NE		84376	NE	-	*			hypothetical protein M5005_Spy_1162
M5005_Spy_1163c		NE		84377	NE	-	*			biotin repressor family transcriptional regulator
M5005_Spy_1164c	3571749	NC		84378	E	gpmA	*	SSA_0688	SP_1655	phosphoglyceromutase
M5005_Spy_1165	3571750	NE		84379	NE	pyrD	*			dihydroorotate dehydrogenase 1A
M5005_Spy_1166c	3571751	NC	Spy49_1145c 698	84380	NC	-				hypothetical protein M5005_Spy_1166
M5005_Spy_1167c		NE	Spy49_1146c <u>698</u>	84381	NC	-	*			lead, cadmium, zinc and mercury transporting ATPase
M5005_Spy_1168c		NC				-				phage protein
M5005_Spy_1169	3571754	NE				spd3				streptodornase
M5005_Spy_1170	3571755	NE				-				hypothetical protein M5005_Spy_1170
M5005_Spy_1171c M5005_Spy_1172c		NE NE								phage-associated cell wall hydrolase holin
M5005_Spy_1172c		NE				_				phage protein
M5005_Spy_1174c		NE				-				phage protein
M5005_Spy_1175c		NE				-				phage protein
M5005_Spy_1176c	3571722	NE				-				phage infection protein
M5005_Spy_1177c	3571723	NE				-				phage protein
M5005_Spy_1178c	3571724	NE				-				phage protein
M5005_Spy_1179c	3571725	NE				-				phage protein
M5005_Spy_1180c		NE				-				phage protein
M5005_Spy_1181c		NE				-				major tail protein
M5005_Spy_1182c		NE				-				phage protein
M5005_Spy_1183c		NE				-				phage protein
M5005_Spy_1184c		NE				-				phage protein
M5005_Spy_1185c M5005_Spy_1186c	3571731 3571732	NE NE								phage protein phage protein
M5005_Spy_1187c		NE				-				phage structural protein
M5005_Spy_1188c		NE				-				phage protein
M5005_Spy_1189c		NE				-				phage terminase
M5005_Spy_1190c		NE				-				phage protein
M5005_Spy_1191c	3571698	NE				-				phage protein
M5005_Spy_1192c		NE				-				phage protein
M5005_Spy_1193c		NE				-				phage protein
M5005_Spy_1194c		NE				-				phage protein
M5005_Spy_1195c		NE				-				phage protein
M5005_Spy_1196c	3571703	NE				-				HNH endonuclease
M5005_Spy_1197c M5005_Spy_1198c	3571704 3571705	NE NE				-				phage protein phage protein
M5005_Spy_1198c		NE								phage protein
M5005_Spy_1200c		NE				-				phage protein
M5005_Spy_1201c		NE				-				phage protein
M5005_Spy_1202c		NC				-				phage protein
M5005_Spy_1203c	3571710	NE				-				phage protein
M5005_Spy_1204c	3571711	NE				-				recT protein
		INL				-				
M5005_Spy_1205c	3571712	NE								phage protein
M5005_Spy_1206c	3571713	NE NE				-				phage protein
M5005_Spy_1206c M5005_Spy_1207c	3571713 3571714	NE NE NC				-				phage protein phage protein
M5005_Spy_1206c M5005_Spy_1207c M5005_Spy_1208c	3571713 3571714 3571715	NE NC NE				- - -				phage protein phage protein phage protein
M5005_Spy_1206c M5005_Spy_1207c M5005_Spy_1208c M5005_Spy_1209c	3571713 3571714 3571715 3571716	NE NC NE NE				- - - -				phage protein phage protein phage protein DNA replication protein
M5005_Spy_1206c M5005_Spy_1207c M5005_Spy_1208c M5005_Spy_1209c M5005_Spy_1210c	3571713 3571714 3571715 3571716 3571717	NE NC NE NE NE				- - - - -				phage protein phage protein phage protein DNA replication protein phage replication protein
M5005_Spy_1206c M5005_Spy_1207c M5005_Spy_1208c M5005_Spy_1209c	3571713 3571714 3571715 3571716 3571717 3571679	NE NC NE NE				- - - - - - xis				phage protein phage protein phage protein DNA replication protein
M5005_Spy_1206c M5005_Spy_1207c M5005_Spy_1208c M5005_Spy_1209c M5005_Spy_1210c M5005_Spy_1211c	3571713 3571714 3571715 3571716 3571717 3571679 3571680	NE NC NE NE NE NE				- - - - - - xis				phage protein phage protein phage protein DNA replication protein phage replication protein phage protein phage protein
M5005_Spy_1206c M5005_Spy_1207c M5005_Spy_1208c M5005_Spy_1209c M5005_Spy_1210c M5005_Spy_1211c M5005_Spy_1212c M5005_Spy_1212c M5005_Spy_1213c	3571713 3571714 3571715 3571716 3571717 3571679 3571680 3571681 3571682	NE NC NE NE NE NC NC				- - - - - - xis -				phage protein phage protein phage protein DNA replication protein phage replication protein phage protein excisionase phage protein phage protein phage protein
M5005_Spy_1206c M5005_Spy_1207c M5005_Spy_1208c M5005_Spy_1209c M5005_Spy_1210c M5005_Spy_1210c M5005_Spy_1211c M5005_Spy_1212c M5005_Spy_1213c M5005_Spy_1214 M5005_Spy_1214	3571713 3571714 3571715 3571716 3571717 3571679 3571680 3571681 3571682 3571683	NE NC NE NE NC NE NC NE NC NE NC NE NC NE				- - - - - xis - -				phage protein phage protein phage protein DNA replication protein phage replication protein phage replication protein excisionase phage protein phage protein phage protein phage protein phage protein phage protein
M5005_Spy_1206c M5005_Spy_1207c M5005_Spy_1207c M5005_Spy_1209c M5005_Spy_1210c M5005_Spy_1211c M5005_Spy_1211c M5005_Spy_1212c M5005_Spy_1213c M5005_Spy_1213c M5005_Spy_1214 M5005_Spy_1216	3571713 3571714 3571715 3571716 3571717 3571679 3571680 3571681 3571682 3571683 3571684	NE NE NC NE NE NC NE NC NE NC NE NC NE NC NE NC NE NE NE NE				- - - - - - - - -				phage protein phage protein phage protein DNA replication protein phage replication protein phage replication protein phage protein excisionase phage protein
M5005_Spy_1206c M5005_Spy_1207c M5005_Spy_1208c M5005_Spy_1208c M5005_Spy_1210c M5005_Spy_1211c M5005_Spy_1211c M5005_Spy_1213c M5005_Spy_1213c M5005_Spy_1215 M5005_Spy_1215 M5005_Spy_1216 M5005_Spy_1216 M5005_Spy_1216	3571713 3571714 3571715 3571716 3571717 3571679 3571680 3571681 3571682 3571683 3571684 3571684	NE NE NE NE NC NE NC NE NC NE NC NE NC NE NC NE NE NE NE NE NE				- - - - - - - - - -				phage protein phage protein phage protein DNA replication protein phage replication protein phage protein excisionase phage protein phage antirepressor protein
M5005_Spy_1206c M5005_Spy_1207c M5005_Spy_1208c M5005_Spy_1208c M5005_Spy_1210c M5005_Spy_1210c M5005_Spy_1211c M5005_Spy_1212c M5005_Spy_1213c M5005_Spy_1213c M5005_Spy_1216c M5005_Spy_1216c M5005_Spy_1216c M5005_Spy_1216c M5005_Spy_1217c M5005_Spy_1217c M5005_Spy_1218c	3571713 3571714 3571715 3571716 3571717 3571679 3571680 3571681 3571682 3571682 3571684 3571685 3571685	NE NE NC NE NE NC NE NC NE NC NE NC NE NC NE NE NE NE NE NE NE				xis				phage protein phage protein phage protein DNA replication protein phage replication protein phage replication protein phage protein excisionase phage protein
M5005_Spy_1206c M5005_Spy_1207c M5005_Spy_1208c M5005_Spy_1208c M5005_Spy_1210c M5005_Spy_1211c M5005_Spy_1211c M5005_Spy_1212c M5005_Spy_1212c M5005_Spy_1214 M5005_Spy_1216c M5005_Spy_1216c M5005_Spy_1216c M5005_Spy_1217e M5005_Spy_1218c M5005_Spy_1218c M5005_Spy_1218c M5005_Spy_1218c M5005_Spy_1218c M5005_Spy_1218c M5005_Spy_1218c M5005_Spy_1218c	3571713 3571714 3571715 3571716 3571717 3571679 3571680 3571681 3571682 3571682 3571684 3571684 3571685 3571686	NE NE NE NE NE NC NE NC NE NC NE NC NE				- - - - - - - - - - - -				phage protein phage protein phage protein DNA replication protein phage replication protein phage protein excisionase phage protein phage antirepressor protein phage protein Cro/CI family phage transcriptional regulator
M5005_Spy_1206c M5005_Spy_1207c M5005_Spy_1208c M5005_Spy_1209c M5005_Spy_1210c M5005_Spy_1211c M5005_Spy_1211c M5005_Spy_1213c M5005_Spy_1213 M5005_Spy_1214 M5005_Spy_1216c M5005_Spy_1216c M5005_Spy_1216c M5005_Spy_1218c M5005_Spy_1218c M5005_Spy_1218c M5005_Spy_1218c M5005_Spy_1218c M5005_Spy_1219c M5005_Spy_1219c M5005_Spy_1219c M5005_Spy_1219c	3571713 3571714 3571715 3571715 3571717 3571679 3571680 3571681 3571682 3571683 3571684 3571685 3571686 3571686 3571687	NE NE NC NE NC NE NC NE NC NE NC NE NC NE NE NE NE NE NE NE NE NE								phage protein phage protein phage protein DNA replication protein phage replication protein phage protein excisionase phage protein cro/CI family phage transcriptional regulator phage protein
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M5005_Spy_1243c		E	Spy49_1167c	6984402	E	ileS	*	SSA_0661	SP_1659	isoleucyl-tRNA synthetase
M5005_Spy_1244c		E	Spy49_1168c	6984403	NC	divIVAS	*			cell division initiation protein
M5005_Spy_1245c M5005_Spy_1246c		NE NC	Spy49_1169c Spy49_1170c	6984404 6984405	NE NE	-	*			RNA binding protein hypothetical protein M5005_Spy_1246
M5005_Spy_1247c		NE	Spy49_1170c Spy49_1171c	6984406	C	-	*			hypothetical protein M5005_Spy_1247
M5005_Spy_1248c		NE	Spy49_1171c	6984407	NE	-	*			pyridoxal-5\'-phosphate family protein
M5005_Spy_1249c		E	Spy49_1173c	6984408	E	ftsZ	*	SSA_0656	SP_1666	cell division protein FtsZ
M5005_Spy_1250c	3571640	E	Spy49_1174c	6984409	E	ftsA	*		SP_1667	cell division protein
M5005_Spy_1251c	3571641	NC	Spy49_1175c	6984410	E	divIB/ftsQ	*		SP_0690	cell division protein
M5005_Spy_1252c	3571642	Е	Spy49_1176c	6984411	Е	murG	*	SSA_0653	SP 0689	undecaprenyldiphospho-muramoylpentapeptide beta-N- acetylglucosaminyltransferase
		E	Spy49_1170c Spy49_1177c		E	murD	*	SSA_0652	SP_0688	UDP-N-acetylmuramoyl-L-alanyl-D-glutamate synthetase
		NE	Spy49_1178c	6984413	NE	-		33A_0032	31 _0000	hypothetical protein M5005_Spy_1254
		NC	Spy49_1179c	6984414	NE	typA	*			GTP-binding protein
M5005_Spy_1256c		NE	Spy49_1180c	6984415	NE	-	*			rhodanese-related sulfurtransferase
M5005_Spy_1257c		NE	Spy49_1181c	6984416	NE	glcK	*			glucokinase/xylose repressor
M5005_Spy_1258c	3571648	NE	Spy49_1182c	6984417	NE	-				hypothetical protein M5005_Spy_1258
		NE	Spy49_1183c	6984418	NE	dpr	*			non-specific DNA-binding protein/iron-binding ferritin-like antioxidant protein
M5005_Spy_1260	3571650	NE	Spy49_1184	6984419	NE	-	*			prepilin peptidase
M5005_Spy_1261c	3571651	NE	Spy49_1185c	6984420	NE	-	*			ribosomal RNA large subunit methyltransferase N
M5005_Spy_1262c M5005_Spy_1263c	3571652 3571653	NE NC	Spy49_1186c	6984421	NE	-	•			transcriptional regulator hypothetical protein M5005_Spy_1263
M5005_Spy_1264c		NE	Spy49_1187c	6984422	NE		*			ribose operon repressor, partial
M5005_Spy_1265c		NE	3py43_1107C	OSOTILL	IVE	_	*			ribose operon repressor, partial
M5005_Spy_1266c		NE	Spy49_1188c	6984423	NE	-				ATP-dependent protease La
M5005_Spy_1267c		E	Spy49_1189c	6984424	E	coaD	*	SSA_0625	SP_1968	phosphopantetheine adenylyltransferase
M5005_Spy_1268c	3571658	NE	Spy49_1190c	6984425	NE	-	*	_	_	methyltransferase
M5005_Spy_1269c		NE	Spy49_1191c	6984426	NE	asnA	*			asparagine synthetase AsnA
M5005_Spy_1270c		NE	Spy49_1192c	6984427	NC	arcC	*			carbamate kinase
M5005_Spy_1271c		NE	Spy49_1193c	6984428	NE	-	*			hypothetical protein M5005_Spy_1271
M5005_Spy_1272c		NE	Spy49_1194c	6984429	NE	-	*			arginine/ornithine antiporter
M5005_Spy_1273c		NE	Spy49_1195c	6984430	NC	arcB	*			ornithine carbamoyltransferase acetyltransferase
M5005_Spy_1274c M5005_Spy_1275c		NE NE	Spy49_1196c Spy49_1197c	6984431 6984432	NE NE	arcA	*			arginine deiminase
M5005_Spy_1276c		NE	Spy49_1198c	6984433	NE	-	*			Crp/Fnr family transcriptional regulator
M5005_Spy_1277		NE	Spy49_1199	6984434	NE	ahrC.2/argR	*			arginine repressor ArgR
M5005_Spy_1278c		NE	Spy49_1200c	6984435	NE		*			hypothetical protein M5005_Spy_1278
		NE	Spy49_1201c	6984436	NE	-	*			hypothetical protein M5005_Spy_1279
M5005_Spy_1280c		NC	Spy49_1202c	6984437	NE	yesM				two-component sensor kinase
M5005_Spy_1281c	3571632	NE	Spy49_1203c	6984438	NE	yesN	*			two-component response regulator
M5005_Spy_1282c	3571633	NE	Spy49_1204c	6984439	NE	msrA	*			bifunctional methionine sulfoxide reductase A/B
M5005_Spy_1283c	<u>3571634</u>	NE	Spy49_1205c	6984440	NE	tlpA	*			thiol:disulfide interchange protein
M5005_Spy_1284c		NE	Spy49_1206c	6984441	NE	ccdA	*			cytochrome C biogenesis protein
M5005_Spy_1285c		NE	Spy49_1207c	6984442	NE	-				hypothetical protein M5005_Spy_1285
M5005_Spy_1286c M5005_Spy_1287c		NE NE	Spy49_1208c Spy49_1209c	6984443 6984444	NE NE	-				DNA polymerase hypothetical protein M5005_Spy_1287
M5005_Spy_1288c		NE	Spy49_1210c	6984445	NE	_				hypothetical protein M5005_Spy_1288
		NE	Spy49_1211c	6984446	NC	_				hypothetical protein M5005_Spy_1289
M5005_Spy_1290c		NE	Spy49_1212c	6984447	NE	-				hypothetical protein M5005_Spy_1290
M5005_Spy_1291c		NE	Spy49_1213c	6984448	NE	-				ATP-dependent RNA helicase
M5005_Spy_1292c	3571605	E	Spy49_1215c	6984449	E	valS	*	SSA_1819	SP_0568	valyl-tRNA synthetase
M5005_Spy_1293c		NE	Spy49_1216c	6984450	NE	-	*			hypothetical protein M5005_Spy_1293
M5005_Spy_1294c		NC	Spy49_1217c	6984451	NC	-				ribosomal-protein-serine acetyltransferase
M5005_Spy_1295c		NE	Spy49_1218c	6984452	NC	-	*			hypothetical protein M5005_Spy_1295
M5005_Spy_1296c		NE	Spy49_1219c	6984453	NC		*			hypothetical protein M5005_Spy_1296
M5005_Spy_1297 M5005_Spy_1298	3571611 3571612	NE	Spy49_1220	6984455	NE NE	aroA2 aroB	*			3-deoxy-7-phosphoheptulonate synthase 3-dehydroquinate synthase
		NE NE	Spy49_1221	6984456	INE	a10B	*			hypothetical protein M5005_Spy_1299
M5005_Spy_1200c		NE	Spy49_1222c	6984457	NE	_	*			hypothetical protein M5005_Spy_1299
M5005_Spy_1301c	3571615	NE	Spy49_1223c	6984458	NE	-	*			hypothetical protein M5005_Spy_1301
M5005_Spy_1302c	3571616	NE	Spy49_1224c	6984459	NC	-	*			SAM-dependent methyltransferase
M5005_Spy_1303c	3571617	NE	Spy49_1225c	6984460	NE	aroE	*			shikimate 5-dehydrogenase
M5005_Spy_1304c		NE	Spy49_1226c	6984461	NE	lacZ				beta-galactosidase
M5005_Spy_1305c		NE	Spy49_1227c	6984462	NE	trxR	*			two-component response regulator
M5005_Spy_1306c		NE	Spy49_1228c	6984463	NE	trxS	*			two-component sensor kinase
M5005_Spy_1307c M5005_Spy_1308c		NE	Spy49_1229c	6984464	NE NE	trxT	*			hypothetical protein M5005_Spy_1307 sugar-binding protein
		NE NE	Spy49_1230c Spy49_1231c	6984465 6984466	NC		*			sugar transporter permease
		NE	Spy49_1233c	6984467	NE	_	*			sugar transporter permease
M5005_Spy_1311	3571588	NE	Spy49_1234	6984468	NE	-	*			glucokinase
M5005_Spy_1312	3571589	NC				-				hypothetical protein M5005_Spy_1312
M5005_Spy_1313c	3571590	NE	Spy49_1235c	6984469	NE	-	*			beta-glucosidase
		NE	Spy49_1236c	6984470	NC	hyl	*			hyaluronoglucosaminidase
M5005_Spy_1315c		NE	Spy49_1237c	6984471	NE	-	*			GntR family transcriptional regulator
M5005_Spy_1316	3571593	NE	Spy49_1238	6984472	NC	-	*			hypothetical protein M5005_Spy_1316
M5005_Spy_1317 M5005_Spy_1318c	3571594 3571595	NE NE	Spy49_1239	6984473 6984474	NC	rocA	*			alpha-mannosidase sensory transduction protein kinase
M5005_Spy_1318c M5005_Spy_1319c		NE NE	Spy49_1240c Spy49_1241c	6984474	NE NC	TOLA -	*			tRNA (uracil-5-)-methyltransferase
M5005_Spy_13190	3571597	NE	Spy49_12410 Spy49_1242	6984476	NE	recX	-			recombination regulator RecX
M5005_Spy_1321	3571598	С	Spy49_1243	6984477	NC	-	*		SP_1903	hypothetical protein M5005_Spy_1321
M5005_Spy_1322c		NC	Spy49_1244	6984478	NE	-			-	hypothetical protein M5005_Spy_1322
M5005_Spy_1323	3571600	NE	Spy49_1245	6984479	С	-				transposase
M5005_Spy_1324	3571555	NC				-				hypothetical protein M5005_Spy_1324
M5005_Spy_1325c		NE	Spy49_1247c	6984490	NE	- -	*			ribosome-associated factor Y
M5005_Spy_1326c		NE	Spy49_1248c	6984491	NE	comFC	*			competence protein ComF
M5005_Spy_1327c M5005_Spy_1328	3571558 3571559	NE NE	Spy49_1249c Spy49_1250	6984492 6984493	NE NE	comFA	*			competence protein ComF Xaa-Pro dipeptidase
M5005_Spy_1329	3571560	NE	Spy49_1250 Spy49_1251	6984494	NE	cysM	*			cysteine synthase
		C	Spy49_1252c	6984495	C	- Cysin	*			hypothetical protein M5005_Spy_1330
		NE	Spy49_1253c	6984496	NE	-				peptidyl-prolyl cis-trans isomerase
		NC	Spy49_1254c	6984497	E	yvqC	*			two-component response regulator
		NE	Spy49_1255c	6984498	NE	yvqE	*			two-component sensor protein
M5005_Spy_1334c		NE	Spy49_1256c	6984499	NE	yvqF	*			transporter
M5005_Spy_1335c	3571566	Е	Spy49_1257c	6984500	E	-	*		SP_1732	serine/threonine protein kinase
M5005_Spy_1336c		E	Spy49_1259c	6984501	E	pppL	*		SP_1733	protein phosphatase 2C
M5005_Spy_1337c		NE	Spy49_1260c	6984502	NE	sunL	*		en -===	16S rRNA m(5)C 967 methyltransferase
M5005_Spy_1338c		E	Spy49_1261c		E	fmt	*	SSA_1848	SP_1735	methionyl-tRNA formyltransferase
M5005_Spy_1339c M5005_Spy_1340c		C	Spy49_1262c	6984504 6984505	C	priA -	*		SP_1736	primosome assembly protein PriA DNA-directed RNA polymerase subunit omega
M5005_Spy_1340c M5005_Spy_1341c		NE E	Spy49_1263c Spy49_1265c	6984505	NC E	gmk	*	SSA_1851	SP_1738	guanylate kinase
M5005_Spy_1342c		NC	Spy49_1266c	6984507	NE	-	*	33.1_1031	51/30	hypothetical protein M5005_Spy_1342
M5005_Spy_1343c		NE	Spy49_1267c		NE	-	*			LysR family transcriptional regulator

M5005_Spy_1344	3571537	NE	Spy49_1268	6984509	NC	atoB	*			acetyl-CoA acetyltransferase
M5005_Spy_1345	3571538	NE	Spy49_1269	6984510	NE	atoD.1	*			acetate CoA-transferase subunit alpha
M5005_Spy_1346	3571539	NE	Spy49_1270	6984511	NE	atoA				acetate CoA-transferase subunit beta
M5005_Spy_1347 M5005_Spy_1348	3571540 3571541	NE NE	Spy49_1271 Spy49_1272	6984512 6984513	NE NE	-	*			3-hydroxybutyrate dehydrogenase D-beta-hydroxybutyrate permease
M5005_Spy_1349	3571542	NE	Spy49_1273	6984514	NE	luxS	*			S-ribosylhomocysteinase
M5005_Spy_1350c	3571543	NE	Spy49_1274c		NE	-	*			hypothetical protein M5005_Spy_1350
M5005_Spy_1351c		NE	Spy49_1275c		NE	-	*			methyltransferase
M5005_Spy_1352c	3571545	NC	Spy49_1276c	6984583	NC	-	*			cell division initiation protein
M5005_Spy_1353c	3571546	NE	Spy49_1277c		NE	-	*			hypothetical protein M5005_Spy_1353
M5005_Spy_1354	3571547	NE	Spy49_1278	6984585	NC	recU	*			Holliday junction-specific endonuclease
M5005_Spy_1355	<u>3571548</u>	Е	Spy49_1279	<u>6984586</u>	E	pbp1A	*			multimodular transpeptidase-transglycosylase
M5005_Spy_1356c		NE	Spy49_1280c	6984587	NE	pepC	*			aminopeptidase
M5005_Spy_1357c		E	Spy49_1281c		E	nadE		SSA_1863	SP_1420	NAD synthetase
M5005_Spy_1358c	3571551	E	Spy49_1282c	6984589	E	nadE	*	SSA_1864		nicotinate phosphoribosyltransferase amino acid permease
	3571552 3571553	NE	Spy49_1283c Spy49_1284c	6984590	NE	-	*	CCA 40CF		·
M5005_Spy_1360c M5005_Spy_1361c		C		6984591	NE NC	aapA		SSA_1865		thioredoxin reductase hypothetical protein M5005_Spy_1361
M5005_Spy_1362c	3571516	E NE	Spy49_1285c	6984592 6984593		ааря	*			transporter
M5005_Spy_1363c	3571517	NE	Spy49_1286c Spy49_1287c	6984594	NE NE	-	*			amino acid ABC transporter permease
M5005_Spy_1364c	3571518	E	Spy49_1287c	6984595	E	-	*			ATP-dependent RNA helicase
M5005_Spy_1365c	3571519	Ē	Spy49 1290c	6984596	E	mraY	*	SSA 1870	SP 0337	phospho-N-acetylmuramoyl-pentapeptide-transferase
M5005_Spy_1366c	3571520	E	Spy49_1291c	6984597	E	ftsI	*	SSA_1871	SP_0336	division specific D,D-transpeptidase/cell division protein ftsI
M5005_Spy_1367c	3571521	Ε	Spy49_1292c	6984598	NC	ftsL	*	SSA_1872	SP_0335	cell division protein
M5005_Spy_1368c		С	Spy49_1293c	6984599	NE	mraW	*	_	SP_0334	S-adenosyl-methyltransferase MraW
M5005_Spy_1369c	3571523	NC	Spy49_1294c	6984600	NE	-			_	hypothetical protein M5005_Spy_1369
M5005_Spy_1370c	3571524	NE	Spy49_1295c	6984601	NE	proA				gamma-glutamyl phosphate reductase
M5005_Spy_1371c		NE	Spy49_1296c		NE	proB				gamma-glutamyl kinase
M5005_Spy_1372c		NE	Spy49_1297c		NE	proB	*			ABC transporter permease
M5005_Spy_1373c		NE	Spy49_1298c	6984604	NE	-	*			ABC transporter ATP-binding protein
M5005_Spy_1374c		NE	Spy49_1299c	6984605	NE	-				hypothetical protein M5005_Spy_1374
M5005_Spy_1375c		NE	Spy49_1300c	6984606	C	tkt	*			transketolase
M5005_Spy_1376c		NE	Spy49_1301c	6984607	NE	tal	*			translaldolase
M5005_Spy_1377c		NE	Spy49_1303c	6984608	NE	-				trans-acting positive regulator
M5005_Spy_1378c M5005_Spy_1379c	3571532 3571533	NE NE	Spy49_1304c Spy49_1305c	6984609 6984610	NE NE	npx glpF				NADH peroxidase glycerol uptake facilitator protein
M5005_Spy_1379C	3571534	NE	Spy49_1305c Spy49_1306c		NE	glpO	-			alpha-glycerophosphate oxidase
		NE	Spy49_1300c Spy49_1307c	6984612	NE	glpK	*			glycerol kinase
M5005_Spy_1382c	3571497	NE	Spy49_1307c		NE	gipit -	*			hypothetical protein M5005_Spy_1382
M5005_Spy_1383c	3571498	NC	Spy49_1309c	6984614	NE	-				hypothetical protein M5005_Spy_1383
		E	Spy49_1310c	6984615	E	glyS	*	SSA_1879	SP_1474	glycyl-tRNA synthetase subunit beta
M5005_Spy_1385c	3571500	Ε	Spy49_1311c		Е	glyQ	*	SSA_1880	SP_1475	glycyl-tRNA synthetase subunit alpha
M5005_Spy_1386c	3571501	NE	Spy49_1312c		NE	-	*	_	-	hypothetical protein M5005_Spy_1386
M5005_Spy_1387c	3571502	NE	Spy49_1313c	6984618	NE	-				aldo/keto reductase
M5005_Spy_1388c	3571503	NE	Spy49_1314c	6984619	NE	nagA	*			N-acetylglucosamine-6-phosphate deacetylase
M5005_Spy_1389c	3571504	NE	Spy49_1316c	6984620	NE	-	*			sodium-dependent phosphate transporter
M5005_Spy_1390	3571505	NE				-				hypothetical protein M5005_Spy_1390
M5005_Spy_1391c		NE	Spy49_1318c		NE	-	*			degV family protein
M5005_Spy_1392	3571507	NE	Spy49_1319	6984622	NE	-	*			TetR family transcriptional regulator
		NE	Spy49_1320c		NE	-	*			HAD superfamily hydrolase
M5005_Spy_1394c		NE	Spy49_1321c		NE	leeD 1	*			hypothetical protein M5005_Spy_1394
M5005_Spy_1395c		NE	Spy49_1322c		NE	lacD.1	*			tagatose 1,6-diphosphate aldolase
M5005_Spy_1396c	33/1311	NE	Spy49_1323c	6984626	NE	lacC1				tagatose-6-phosphate kinase
M5005_Spy_1397c	3571512	NE	Spy49_1324c Spy49_1325c	6984627 6984628	NC NE	lacB.1	*			galactose-6-phosphate isomerase subunit LacB
M5005_Spy_1398c	3571513	NE	Spy49_1326c	6984629	NE	lacA.1	*			galactose-6-phosphate isomerase subunit LacA
M5005_Spy_1399c		NE	Spy49_1327c		NE	-	*			PTS system galactose-specific transporter subunit IIC
M5005_Spy_1400c		NE	Spy49_1328c	6984631	NE	_	*			PTS system galactose-specific transporter subunit IIB
M5005_Spy_1401c		NE	Spy49_1329c	6984632	NE	-	*			PTS system galactose-specific transporter subunit IIA
M5005_Spy_1402	3571478	NE	Spy49_1330	6984633	NE	lacR.1	*			lactose phosphotransferase system repressor
M5005_Spy_1403c	3571479	NE				-				copper chaperone
M5005_Spy_1404c		NE	Spy49_1331c	6984634	NE	copZ				copper chaperone
M5005_Spy_1405c		NE	Spy49_1332c	6984635	NE	copA	*			copper-exporting ATPase
		NE	Spy49_1334c	6984636	NE	copY				copAB ATPase metal-fist type repressor
M5005_Spy_1407	3571483	NE	Spy49_1335	6984637	NE	-				esterase
M5005_Spy_1408c	3571484	C	Spy49_1336c	6984638	NC	rbfA	*		SP_0557	ribosome-binding factor A
M5005_Spy_1409c		E	Spy49_1337c		E	infB	*		SP_0556	translation initiation factor IF-2
M5005_Spy_1410c M5005_Spy_1411c		С	Spy49_1338c		NE	-	*		SP_0555	hypothetical protein M5005_Spy_1410 hypothetical protein M5005_Spy_1411
M5005_Spy_1411c		C E	Spy49_1339c Spy49_1340c		NC E	nusA	*		SP_0554 SP_0553	transcription elongation factor NusA
M5005_Spy_1412c		NE	Spy49_1340c Spy49_1341c		NE.		*		31 _0333	hypothetical protein M5005_Spy_1413
M5005_Spy_1414c	3571490	NC	op, 10_10 110			-				phage protein
M5005_Spy_1415c		NE				sdaD2				phage-encoded streptodornase
M5005_Spy_1416c	3571492	NE				-				phage-associated cell wall hydrolase
M5005_Spy_1417c		NE				-				phage protein
M5005_Spy_1418c		NE				-				phage protein
M5005_Spy_1419c		NE				-				phage protein
M5005_Spy_1420c		NC				-				phage protein
M5005_Spy_1421c		NE				-				phage infection protein
M5005_Spy_1422c		NE NE				-				phage protein
M5005_Spy_1423c M5005_Spy_1424c		NE				-				hyaluronoglucosaminidase phage endopeptidase
M5005_Spy_1424c		NE								phage endopephdase phage protein
M5005_Spy_1426c		NE				-				phage protein
M5005_Spy_1427c		NE				-				phage protein
M5005_Spy_1428c	3571464					-				phage protein
		NE								
M5005_Spy_1429c	3571465 3571466					-				phage protein
M5005_Spy_1429c M5005_Spy_1430c	3571465 3571466 3571467	NE				-				phage protein
M5005_Spy_1429c M5005_Spy_1430c M5005_Spy_1431c	3571465 3571466 3571467 3571468	NE NE NE NE				- - -				phage protein phage protein
M5005_Spy_1429c M5005_Spy_1430c M5005_Spy_1431c M5005_Spy_1432c	3571465 3571466 3571467 3571468 3571469	NE NE NE NE				- - -				phage protein phage protein phage protein
M5005_Spy_1429c M5005_Spy_1430c M5005_Spy_1431c M5005_Spy_1432c M5005_Spy_1433c	3571465 3571466 3571467 3571468 3571469 3571470	NE NE NE NE NE				- - - -				phage protein phage protein phage protein phage protein
M5005_Spy_1429c M5005_Spy_1430c M5005_Spy_1431c M5005_Spy_1432c M5005_Spy_1433c M5005_Spy_1434c	3571465 3571466 3571467 3571468 3571469 3571470 3571471	NE NE NE NE NE NE				- - - - -				phage protein phage protein phage protein phage protein phage protein phage protein
M5005_Spy_1429c M5005_Spy_1430c M5005_Spy_1431c M5005_Spy_1432c M5005_Spy_1433c M5005_Spy_1433c M5005_Spy_1435c	3571465 3571466 3571467 3571468 3571469 3571470 3571471 3571472	NE NE NE NE NE NE NE				- - - - -				phage protein phage protein phage protein phage protein phage protein phage protein phage scaffold protein
M5005_Spy_1429c M5005_Spy_1430c M5005_Spy_1431c M5005_Spy_1432c M5005_Spy_1433c M5005_Spy_1433c M5005_Spy_1435c M5005_Spy_1435c	3571465 3571466 3571467 3571468 3571469 3571470 3571471 3571472 3571473	NE NE NE NE NE NE NE NE				-				phage protein phage protein phage protein phage protein phage protein phage protein phage scaffold protein phage protein phage protein
M5005_Spy_1429c M5005_Spy_1430c M5005_Spy_1431c M5005_Spy_1432c M5005_Spy_1433c M5005_Spy_1434c M5005_Spy_1435c M5005_Spy_1435c M5005_Spy_1437c	3571465 3571466 3571467 3571468 3571469 3571470 3571471 3571472 3571473 3571474	NE				-				phage protein phage protein phage protein phage protein phage protein phage protein phage scaffold protein phage protein phage protein phage protein phage protein
M5005_Spy_1429c M5005_Spy_1431c M5005_Spy_1431c M5005_Spy_1432c M5005_Spy_1433c M5005_Spy_1434c M5005_Spy_1436c M5005_Spy_1436c M5005_Spy_1437c M5005_Spy_1438c	3571465 3571466 3571467 3571468 3571470 3571470 3571471 3571472 3571473 3571474 3571475	NE				-				phage protein phage protein phage protein phage protein phage protein phage scaffold protein phage scaffold protein phage protein hypothetical protein M5005_Spy_1437 phage protein
M5005_Spy_1430c M5005_Spy_1430c M5005_Spy_1431c M5005_Spy_1432c M5005_Spy_1433c M5005_Spy_1433c M5005_Spy_1436c M5005_Spy_1436c M5005_Spy_1437c M5005_Spy_1437c M5005_Spy_1437c	3571465 3571466 3571467 3571468 3571470 3571471 3571471 3571472 3571473 3571474 3571475 3571476	NE N				-				phage protein phage protein phage protein phage protein phage protein phage protein phage scaffold protein phage protein hypothetical protein M5005_Spy_1437 phage protein portal protein
M5005_Spy_1429c M5005_Spy_1431c M5005_Spy_1431c M5005_Spy_1432c M5005_Spy_1433c M5005_Spy_1433c M5005_Spy_14346 M5005_Spy_1436c M5005_Spy_1436c M5005_Spy_1437c M5005_Spy_1439c M5005_Spy_1439c M5005_Spy_1439c	3571465 3571466 3571467 3571468 3571469 3571470 3571471 3571472 3571473 3571474 3571475 3571476 3571476	NE N				-				phage protein phage protein phage protein phage protein phage protein phage protein phage scaffold protein phage scaffold protein phage protein hypothetical protein M5005_Spy_1437 phage protein portal protein terminase large subunit
M5005_Spy_1429c M5005_Spy_1431c M5005_Spy_1431c M5005_Spy_1432c M5005_Spy_1433c M5005_Spy_1433c M5005_Spy_1435c M5005_Spy_1436c M5005_Spy_1436c M5005_Spy_1436c M5005_Spy_1436c M5005_Spy_1436c M5005_Spy_1436c M5005_Spy_14346c M5005_Spy_1436c M5005_Spy_1436c M5005_Spy_1436c M5005_Spy_1436c	3571465 3571466 3571467 3571469 3571470 3571471 3571472 3571474 3571474 3571474 3571475 3571476 3571438 3571438	NE N								phage protein phage protein phage protein phage protein phage protein phage scaffold protein phage scaffold protein phage protein hypothetical protein M5005_Spy_1437 phage protein portal protein portal protein terminase large subunit phage terminase small subunit
M5005_Spy_1429c M5005_Spy_1431c M5005_Spy_1431c M5005_Spy_1432c M5005_Spy_1433c M5005_Spy_1433c M5005_Spy_14346 M5005_Spy_1436c M5005_Spy_1436c M5005_Spy_1437c M5005_Spy_1439c M5005_Spy_1439c M5005_Spy_1439c	3571465 3571466 3571468 3571469 3571470 3571471 3571472 3571473 3571474 3571475 3571476 3571438 3571438 3571439 3571440	NE N								phage protein phage protein phage protein phage protein phage protein phage protein phage scaffold protein phage scaffold protein phage protein hypothetical protein M5005_Spy_1437 phage protein portal protein terminase large subunit
M5005_Spy_1429c M5005_Spy_1431c M5005_Spy_1431c M5005_Spy_1432c M5005_Spy_1433c M5005_Spy_14344c M5005_Spy_1436c M5005_Spy_1436c M5005_Spy_1436c M5005_Spy_1436c M5005_Spy_1436c M5005_Spy_1436c M5005_Spy_1436c M5005_Spy_1436c M5005_Spy_1436c M5005_Spy_1446c M5005_Spy_14441c M5005_Spy_14442c	3571465 3571466 3571467 3571469 3571470 3571471 3571472 3571472 3571474 3571475 3571476 3571438 3571439 3571440 3571440	NE N								phage protein phage protein phage protein phage protein phage protein phage protein phage scaffold protein phage scaffold protein phage protein hypothetical protein M5005_Spy_1437 phage protein portal protein terminase large subunit phage terminase small subunit phage terminase small subunit phage terminase small subunit

	NE								phage protein
M5005_Spy_1445c <u>3571443</u> M5005_Spy_1446c <u>3571444</u>	NC				-				phage protein
M5005_Spy_1447c 3571445	NE				-				phage-related DNA helicase
M5005_Spy_1448c 3571446	NE				-				hypothetical protein M5005_Spy_1448
M5005_Spy_1449c <u>3571447</u>	NE				-				DNA primase
M5005_Spy_1450c <u>3571448</u>	NE				-				phage-encoded DNA polymerase
M5005_Spy_1451c 3571449	NE				-				phage protein
M5005_Spy_1452c <u>3571450</u> M5005_Spy_1453c <u>3571451</u>	NE NE								phage protein phage protein
M5005_Spy_1454c 3571452	NE				-				phage protein
M5005_Spy_1455c 3571453	NC				-				phage protein
M5005_Spy_1456c 3571454	NC				-				phage protein
M5005_Spy_1457c 3571455	NE				-				phage protein
M5005_Spy_1458c 3571456	NC				-				phage protein
M5005_Spy_1459c 3571419	NC				-				phage protein
M5005_Spy_1460c 3571420	NC				-				phage protein
M5005_Spy_1461c <u>3571421</u> M5005_Spy_1462 <u>3571422</u>	NE NE								phage protein phage protein
M5005_Spy_1463c 3571423	NC				_				phage protein
M5005_Spy_1464 3571424	E				-				Cro/CI family phage transcriptional regulator
M5005_Spy_1465 3571425	NE				-				phage protein
M5005_Spy_1466 <u>3571426</u>	NE				-				phage protein
M5005_Spy_1467 <u>3571427</u>	NE				int.3				integrase
M5005_Spy_1468c 3571429	NE	Spy49_1342c		NE	trmB	*			tRNA (guanine-N(7)-)-methyltransferase
M5005_Spy_1469c <u>3571430</u> M5005_Spy_1470c <u>3571431</u>	E NE	Spy49_1343c Spy49_1344c	6984646 6984647	E NE	-	*	SSA_1903	SP_0549	phosphotransferase protein ecsB
M5005_Spy_1471c 3571432	NE	Spy49_1345c	6984648	NE	_	*			ABC transporter ATP-binding protein
M5005_Spy_1472 3571433	NE	Spy49_1346	6984649	NE	hit	*			bis(5\'-nucleosyl)-tetraphosphatase (asymmetrical)
M5005_Spy_1473 3571434	NE	Spy49_1347	6984650	NE	-	*			hypothetical protein M5005_Spy_1473
M5005_Spy_1474c 3571435	NE	Spy49_1348c	6984651	NE	lytR	*			LytR family transcriptional regulator
M5005_Spy_1475c 3571436	NE	Spy49_1349c	6984652	NE	-	*			acetyltransferase
M5005_Spy_1476c <u>3571437</u>	NC	Spy49_1350c	6984653	NC	-				ATP/GTP hydrolase
M5005_Spy_1477c 3571400	NE	Spy49_1351c	6984654	NE	-	*			guanine-hypoxanthine permease
M5005_Spy_1478 <u>3571401</u> M5005_Spy_1479 <u>3571402</u>	NE	Spy49_1352 Spy49_1353	6984655 6984656	NE	- manL	*			HAD superfamily hydrolase PTS system mannose-specific transporter subunit IIAB
M5005_Spy_1479 <u>3571402</u> M5005_Spy_1480 <u>3571403</u>	NE NE	Spy49_1353 Spy49_1354	6984657	NE NE	manM	*			PTS system mannose-specific transporter subunit IIC
M5005_Spy_1481 3571404	NE	Spy49_1354 Spy49_1355	6984658	NE	manN	*			PTS system mannose-specific transporter subunit IID
		Spy49_1356	6984659	NE					,
M5005_Spy_1482 3571405	NE	Spy49_1357	6984660	NE	manO	*			hypothetical protein M5005_Spy_1482
M5005_Spy_1483 3571406	E	Spy49_1358	6984661	E	serS	*	SSA_1925	SP_0411	seryl-tRNA synthetase
M5005_Spy_1484c <u>3571407</u>	E	Spy49_1359c	6984662	NC	accD	*	SSA_1930	SP_0427	acetyl-CoA carboxylase subunit alpha
M5005_Spy_1485c <u>3571408</u>	E	Spy49_1360c	6984743	E	accA	*	SSA_1931	SP_0426	acetyl-CoA carboxylase subunit beta
M5005_Spy_1486c <u>3571409</u>	E	Spy49_1361c	6984744	E	accC fabZ	*	SSA_1932	CD 0424	acetyl-CoA carboxylase biotin carboxylase subunit (3R)-hydroxymyristoyl-ACP dehydratase
M5005_Spy_1487c <u>3571410</u> M5005_Spy_1488c <u>3571411</u>	C E	Spy49_1362c Spy49_1363c	6984745 6984746	NC NC	accB	*	SSA_1933 SSA_1934	SP_0424 SP_0423	acetyl-CoA carboxylase biotin carboxyl carrier protein subunit
M5005_Spy_1489c 3571412	E	Spy49_1364c	6984747	E	fabF	*	SSA_1935	SP_0423	3-oxoacyl-ACP synthase
M5005_Spy_1490c 3571413	E	Spy49_1365c	6984748	E	fabG	*	SSA_1936	SP_0421	3-ketoacyl-ACP reductase
M5005_Spy_1491c 3571414	E	Spy49_1366c	6984749	E	fabD	*	SSA_1937	SP_0420	ACP S-malonyltransferase
M5005_Spy_1492c 3571415	С	Spy49_1367c	6984750	E	fabK	*	SSA_1938	SP_0419	enoyl-ACP reductase
M5005_Spy_1493c 3571416	E	Spy49_1368c	6984751	NC	acpP		SSA_1940	SP_0418	acyl carrier protein
M5005_Spy_1494c <u>3571417</u>	E	Spy49_1369c	6984752	Е	fabH	*	SSA_1940	SP_0417	3-oxoacyl-ACP synthase
M5005_Spy_1495c 3571418	NC	Spy49_1370c	6984753	NE		*			MarR family transcriptional regulator
M5005_Spy_1496c 3571380	E E	Spy49_1371c		E E	phaB dnaJ	*	CCA 200F	SP_0415	enoyl-CoA hydratase
M5005_Spy_1497c <u>3571381</u>	E	Spy49_1372c Spy49_1373	6984756	NC	ulias	-	SSA_2005		molecular chaperone DnaJ
M5005_Spy_1498c 3571382	Е	Spy49_1374c	6984757	E	dnaK	*	SSA_2007	SP_0517	molecular chaperone DnaK
M5005_Spy_1499c 3571383	E	Spy49_1375c	6984758	E	grpE	*			heat shock protein GrpE
M5005_Spy_1500c 3571384	С	Spy49_1376c	6984759	NE	hrcA	*			heat-inducible transcription repressor
M5005_Spy_1501c 3571385	NE	Spy49_1377c	6984760	NE	-	*			N-acetylmuramoyl-L-alanine amidase
M5005_Spy_1502c <u>3571386</u>	NE	Spy49_1378c	6984761	NE	-	*			D-alanyl-D-alanine carboxypeptidase
M5005_Spy_1503c 3571387	NE	Spy49_1379c	6984762	NE	-	*			phosphoglycerate mutase
M5005_Spy_1504c <u>3571388</u> M5005_Spy_1505c <u>3571389</u>	NE			NE					
M5005_Spy_1506c 3571390		Spy49_1380c	6984763						hypothetical protein M5005_Spy_1504
	NE	Spy49_1381c	6984764	NE	natR	*	CCA DE71	SD 0426	hypothetical protein M5005_Spy_1505
M5005 Spv 150/c 35/1391	Ε	Spy49_1381c Spy49_1382c	6984764 6984765	NE E	gatB gatA	*	SSA_0571	SP_0436 SP_0437	hypothetical protein M5005_Spy_1505 aspartyl/glutamyl-tRNA amidotransferase subunit B
M5005_Spy_1507c 3571391 M5005_Spy_1508c 3571392	E E	Spy49_1381c	6984764	NE E E	gatA		SSA_0571 SSA_0570 SSA_0569	SP_0437	hypothetical protein M5005_Spy_1505 aspartyl/glutamyl-tRNA amidotransferase subunit B aspartyl/glutamyl-tRNA amidotransferase subunit A
M5005_Spy_1507c 3571391 M5005_Spy_1508c 3571392 M5005_Spy_1509c 3571393	Ε	Spy49_1381c Spy49_1382c Spy49_1383c	6984764 6984765 6984766	NE E			SSA_0570		hypothetical protein M5005_Spy_1505 aspartyl/glutamyl-tRNA amidotransferase subunit B
M5005_Spy_1508c 3571392 M5005_Spy_1509c 3571393 M5005_Spy_1510c 3571394	E E E	Spy49_1381c Spy49_1382c Spy49_1383c Spy49_1384c	6984764 6984765 6984766 6984767	NE E E NC	gatA		SSA_0570	SP_0437	hypothetical protein M5005_Spy_1505 asparty//glutamyl-tRNA amidotransferase subunit B asparty/glutamyl-tRNA amidotransferase subunit A asparty//glutamyl-tRNA amidotransferase subunit C
M5005_Spy_1508c 3571392 M5005_Spy_1509c 3571393 M5005_Spy_1510c 3571394 M5005_Spy_1511c 3571395	E E NE NC NE	Spy49_1381c Spy49_1382c Spy49_1383c Spy49_1384c Spy49_1385c Spy49_1386c	6984764 6984765 6984766 6984767 6984768	NE E E NC NE	gatA gatC - -		SSA_0570	SP_0437 SP_0438	hypothetical protein M5005_Spy_1505 aspartyl/glutamyl-tRNA amidotransferase subunit B aspartyl/glutamyl-tRNA amidotransferase subunit A aspartyl/glutamyl-tRNA amidotransferase subunit C pyruvate, phosphate dikinase, partial pyruvate, phosphate dikinase pyrazinamidase/nicotinamidase
M5005_Spy_1508c 3571392 M5005_Spy_1509c 3571393 M5005_Spy_1510c 3571394 M5005_Spy_1511c 3571395 M5005_Spy_1512c 3571396	E E NE NC NC	Spy49_1381c Spy49_1382c Spy49_1383c Spy49_1384c Spy49_1385c	6984764 6984765 6984766 6984767 6984768 6984769 6984770	NE E NC NE	gatA		SSA_0570	SP_0437	hypothetical protein M5005_Spy_1505 aspartyl/glutamyl-tRNA amidotransferase subunit B aspartyl/glutamyl-tRNA amidotransferase subunit A aspartyl/glutamyl-tRNA amidotransferase subunit C pyruvate, phosphate dikinase, partial pyruvate, phosphate dikinase pyrazinamidase/nicotinamidase transcriptional repressor CodY
M5005_Spy_1508c 3571392 M5005_Spy_1509c 3571393 M5005_Spy_1510c 3571394 M5005_Spy_1511c 3571395 M5005_Spy_1512c 3571396 M5005_Spy_1513c 3571397	E E NE NC NE C NE	Spy49_1381c Spy49_1382c Spy49_1383c Spy49_1384c Spy49_1385c Spy49_1386c Spy49_1387c Spy49_1388c	6984764 6984765 6984766 6984767 6984768 6984769 6984770 6984771	NE E NC NE NE NE	gatA gatC - -		SSA_0570	SP_0437 SP_0438	hypothetical protein M5005_Spy_1505 asparty/glutamyl-tRNA amidotransferase subunit B asparty/glutamyl-tRNA amidotransferase subunit A asparty/glutamyl-tRNA amidotransferase subunit C pyruvate, phosphate dikinase, partial pyruvate, phosphate dikinase pyrazinamidase/nicotinamidase transcriptional repressor CodY aminotransferase
M5005_Spy_1508c 3571392 M5005_Spy_1509c 3571393 M5005_Spy_1510c 3571394 M5005_Spy_1511c 3571395 M5005_Spy_1512c 3571396 M5005_Spy_1513c 3571397 M5005_Spy_1513c 3571398	E E NE NC NE C NE	Spy49_1381c Spy49_1382c Spy49_1383c Spy49_1384c Spy49_1385c Spy49_1386c Spy49_1387c Spy49_1388c Spy49_1389	6984764 6984765 6984766 6984767 6984768 6984769 6984770 6984771 6984772	NE E NC NE NE NE NE	gatA gatC - -		SSA_0570	SP_0437 SP_0438	hypothetical protein M5005_Spy_1505 aspartyl/glutamyl-tRNA amidotransferase subunit B aspartyl/glutamyl-tRNA amidotransferase subunit A aspartyl/glutamyl-tRNA amidotransferase subunit C pyruvate, phosphate dikinase, partial pyruvate, phosphate dikinase pyrazinamidase/nicotinamidase transcriptional repressor CodY aminotransferase universal stress protein
M5005_Spy_1508c 3571392 M5005_Spy_1509c 3571393 M5005_Spy_1510c 3571394 M5005_Spy_1511c 3571395 M5005_Spy_1512c 3571396 M5005_Spy_1513c 3571397 M5005_Spy_1514 3571398 M5005_Spy_1515c 3571398	E E NE NC NE C NE NE	Spy49_1381c Spy49_1382c Spy49_1383c Spy49_1384c Spy49_1385c Spy49_1387c Spy49_1387c Spy49_1388c Spy49_1389c Spy49_1390c	6984764 6984765 6984766 6984767 6984768 6984769 6984770 6984771 6984772 6984773	NE E NC NE NE NE NE NE NE	gatA gatC - - - codY - -		SSA_0570	SP_0437 SP_0438	hypothetical protein M500S_Spy_1505 aspartyl/glutamyl-tRNA amidotransferase subunit B aspartyl/glutamyl-tRNA amidotransferase subunit A aspartyl/glutamyl-tRNA amidotransferase subunit C pyruvate, phosphate dikinase, partial pyruvate, phosphate dikinase pyrazinamidase/nicotinamidase transcriptional repressor Cody aminotransferase universal stress protein HAD superfamily hydrolase
M5005_Spy_1508c 3571392 M5005_Spy_1510c 3571393 M5005_Spy_1511c 3571394 M5005_Spy_1511c 3571395 M5005_Spy_1511c 3571395 M5005_Spy_1514 3571397 M5005_Spy_1515c 3571398 M5005_Spy_1515c 3571398 M5005_Spy_1516 3571398	E E NE NC NE C NE NE NE	Spv49_1381c Spv49_1382c Spv49_1383c Spv49_1384c Spv49_1385c Spv49_1387c Spv49_1388c Spv49_1389 Spv49_1390c Spv49_1391	6984764 6984765 6984766 6984767 6984768 6984769 6984770 6984771 6984772 6984773	NE E E NC NE	gatA gatC - -		SSA_0570	SP_0437 SP_0438	hypothetical protein M5005_Spy_1505 asparty/lglutamyl-tRNA amidotransferase subunit B asparty/lglutamyl-tRNA amidotransferase subunit A asparty/lglutamyl-tRNA amidotransferase subunit C pyruvate, phosphate dikinase, partial pyruvate, phosphate dikinase, partial pyruvate, phosphate dikinase pyrazinamidase/nicotinamidase transcriptional repressor CodY aminotransferase universal stress protein HAD superfamily hydrolase L-asparagimase
M5005_Spy_1508c 3571392 M5005_Spy_1509c 3571393 M5005_Spy_1510c 3571394 M5005_Spy_1511c 3571395 M5005_Spy_1512c 3571396 M5005_Spy_1513c 3571397 M5005_Spy_1514 3571398 M5005_Spy_1515c 3571398	E E NE NC NE C NE NE	Spy49_1381c Spy49_1382c Spy49_1383c Spy49_1384c Spy49_1385c Spy49_1387c Spy49_1387c Spy49_1388c Spy49_1389c Spy49_1390c	6984764 6984765 6984766 6984767 6984768 6984769 6984770 6984771 6984772 6984773	NE E NC NE NE NE NE NE NE	gatA gatC codY asnB		SSA_0570	SP_0437 SP_0438	hypothetical protein M500S_Spy_1505 aspartyl/glutamyl-tRNA amidotransferase subunit B aspartyl/glutamyl-tRNA amidotransferase subunit A aspartyl/glutamyl-tRNA amidotransferase subunit C pyruvate, phosphate dikinase, partial pyruvate, phosphate dikinase pyrazinamidase/nicotinamidase transcriptional repressor Cody aminotransferase universal stress protein HAD superfamily hydrolase
M5005_Spy_1508c 3571392 M5005_Spy_1510c 3571393 M5005_Spy_1511c 3571394 M5005_Spy_1511c 3571395 M5005_Spy_1513c 3571396 M5005_Spy_1513c 3571396 M5005_Spy_1514c 3571398 M5005_Spy_1514c 3571362 M5005_Spy_1514c 3571362 M5005_Spy_1517c 3571362 M5005_Spy_1518c 3571363 M5005_Spy_1518c 3571363 M5005_Spy_1518c 3571363	E E NE NC NE C NE NE NE NE	Spy49_1381c Spy49_1382c Spy49_1383c Spy49_1384c Spy49_1385c Spy49_1386c Spy49_1387c Spy49_1388c Spy49_1389c Spy49_1391c Spy49_1391c	6984764 6984765 6984766 6984767 6984768 6984770 6984771 6984772 6984773 6984774 6984775	NE E NC NE	gatA gatC - - - - codY - - - - asnB	* * * * * * * * * *	SSA_0570	SP_0437 SP_0438	hypothetical protein M5005_Spy_1505 asparty//glutamyl-tRNA amidotransferase subunit B asparty//glutamyl-tRNA amidotransferase subunit A asparty//glutamyl-tRNA amidotransferase subunit C pyruvate, phosphate dikinase, partial pyruvate, phosphate dikinase pyrazinamidase/nicotinamidase transcriptional repressor CodY aminotransferase universal stress protein HAD superfamily hydrolase L-asparaginase lantibiotic transport permease transporter ATP-dependent DNA helicase RecG
MS005_Spy_1508c 3571392 MS005_Spy_1510c 3571393 MS005_Spy_1510c 3571394 MS005_Spy_1511c 3571396 MS005_Spy_1512c 3571396 MS005_Spy_1513c 3571396 MS005_Spy_1515c 3571396 MS005_Spy_1516c 3571396 MS005_Spy_1516c 3571396 MS005_Spy_1516c 3571361 MS005_Spy_1516c 3571363 MS005_Spy_1516c 3571363 MS005_Spy_1516c 3571363 MS005_Spy_1516c 3571363 MS005_Spy_1516c 3571363	E E NE NC NE C NE	Spy49_1381c Spy49_1382c Spy49_1383c Spy49_1384c Spy49_1385c Spy49_1385c Spy49_1386c Spy49_1388c Spy49_1389c Spy49_1390c Spy49_1391c Spy49_1391c Spy49_1391c Spy49_1392c Spy49_1394c	6984764 6984765 6984766 6984767 6984768 6984770 6984771 6984771 6984773 6984774 6984775 6984775	NE E NC NE C	gatA gatC - - - - codY - - - - asnB	* * * * * * * * * * * * * * * * * * * *	SSA_0570	SP_0437 SP_0438	hypothetical protein M500S_Spy_1505 aspartyl/glutamyl-tRNA amidotransferase subunit B aspartyl/glutamyl-tRNA amidotransferase subunit A aspartyl/glutamyl-tRNA amidotransferase subunit C pyruvate, phosphate dikinase, partial pyruvate, phosphate dikinase pyrazinamidase/nicotinamidase transcriptional repressor Cody aminotransferase universal stress protein HAD superfamily hydrolase L-asparaginase lantibiotic transport permease transporter ATP-dependent DNA helicase RecG hypothetical protein M500S_Spy_1520
M5005_Spy_1508c 3571392 M5005_Spy_1510c 3571393 M5005_Spy_15110c 3571394 M5005_Spy_15112c 3571395 M5005_Spy_15112c 3571397 M5005_Spy_15112c 3571397 M5005_Spy_15112c 3571392 M5005_Spy_15112c 3571392 M5005_Spy_15112c 3571361 M5005_Spy_15112c 3571362 M5005_Spy_1518c 3571363 M5005_Spy_1518c 3571364 M5005_Spy_1518c 3571364 M5005_Spy_1519c 3571364 M5005_Spy_1519c 3571364 M5005_Spy_1519c 3571364 M5005_Spy_1519c 3571365	E E NE NC NE C NE	Spy49_1381c Spy49_1382c Spy49_1383c Spy49_1385c Spy49_1385c Spy49_1386c Spy49_1387c Spy49_1388c Spy49_1388c Spy49_1390c Spy49_1391 Spy49_1391 Spy49_1392c Spy49_1393c Spy49_1393c Spy49_1393c	6984764 6984765 6984766 6984767 6984768 6984769 6984770 6984771 6984772 6984774 6984775 6984777 6984777	NE E NC NE	gatA gatC - - - - codY - - - - asnB	* * * * * * * * * * * * * * * * * * * *	SSA_0570	SP_0437 SP_0438	hypothetical protein M5005_Spy_1505 asparty//glutamyl-tRNA amidotransferase subunit B asparty/glutamyl-tRNA amidotransferase subunit A asparty/glutamyl-tRNA amidotransferase subunit C pyruvate, phosphate dikinase, partial pyruvate, phosphate dikinase, partial pyruvate, phosphate dikinase pyrazinamidase/nicotinamidase transcriptional repressor Cody aminotransferase universal stress protein HAD superfamily hydrolase L-asparaginase lantibiotic transport permease transporter ATP-dependent DNA helicase RecG hypothetical protein M5005_Spy_1520 cobalt ABC transporter ATP-binding protein
M5005_Spy_1508c 3571392 M5005_Spy_1510c 3571393 M5005_Spy_1511c 3571394 M5005_Spy_1511c 3571395 M5005_Spy_1513c 3571396 M5005_Spy_1513c 3571396 M5005_Spy_1514c 3571398 M5005_Spy_1516c 3571361 M5005_Spy_1516c 3571362 M5005_Spy_1517c 3571362 M5005_Spy_1518c 3571363 M5005_Spy_1519c 3571364 M5005_Spy_1520c 3571366 M5005_Spy_1521c 3571366 M5005_Spy_1521c 3571366 M5005_Spy_1521c 3571366	E E NE NC NE C NE	Spy49_1381c Spy49_1383c Spy49_1383c Spy49_1384c Spy49_1385c Spy49_1386c Spy49_1387c Spy49_1389c Spy49_1390c Spy49_1391 Spy49_1390c Spy49_1391 Spy49_1391 Spy49_1395c Spy49_1395c Spy49_1395c	6984765 6984765 6984766 6984767 6984768 6984769 6984770 6984772 6984772 6984773 6984774 6984775 6984777 6984775	NE E NC NE	gatA gatC - - - - codY - - - - asnB	* * * * * * * * * * * * * * * * * * * *	SSA_0570	SP_0437 SP_0438	hypothetical protein M500S_Spy_1505 aspartyl/glutamyl-tRNA amidotransferase subunit B aspartyl/glutamyl-tRNA amidotransferase subunit A aspartyl/glutamyl-tRNA amidotransferase subunit C pyruvate, phosphate dikinase, partial pyruvate, phosphate dikinase pyrazinamidase/nicotinamidase transcriptional repressor CodY aminotransferase universal stress protein HAD superfamily hydrolase L-asparaginase lantibiotic transport permease transporter ATP-dependent DNA helicase RecG hypothetical protein M5005_Spy_1520 cobalt ABC transporter ATP-binding protein cobalt transporter cliQ
M5005, Spy, 1508c 3571392 M5005, Spy, 1510c 3571394 M5005, Spy, 1511c 3571394 M5005, Spy, 1512c 3571396 M5005, Spy, 1512c 3571396 M5005, Spy, 1514c 3571396 M5005, Spy, 1515c 3571399 M5005, Spy, 1516c 3571361 M5005, Spy, 1516c 3571361 M5005, Spy, 1516c 3571363 M5005, Spy, 1519c 3571363 M5005, Spy, 1519c 3571363 M5005, Spy, 1520c 3571365 M5005, Spy, 1520c 3571365 M5005, Spy, 1520c 3571365 M5005, Spy, 1521c 3571366 M5005, Spy, 1521c 3571366 M5005, Spy, 1521c 3571365 M5005, Spy, 1521c 3571365	E E R NC NE C NE	Spy49_1381c Spy49_1382c Spy49_1383c Spy49_1383c Spy49_1386c Spy49_1387c Spy49_1387c Spy49_1388c Spy49_1389c Spy49_1390c Spy49_1391 Spy49_1393c Spy49_1393c Spy49_1393c Spy49_1393c Spy49_1393c Spy49_1393c Spy49_1395c Spy49_1395c Spy49_1395c Spy49_1395c Spy49_1395c Spy49_1395c	6984764 6984765 6984766 6984766 6984767 6984769 6984770 6984771 6984773 6984773 6984776 6984777 6984777 6984779 6984779	NE E E NC NE NE E NE N	gatA gatC - - codY - - - asnB - recG	* * * * * * * * * * * * * * * * * * * *	SSA_0570	SP_0437 SP_0438	hypothetical protein M500S_Spy_1505 aspartyl/glutamyl-tRNA amidotransferase subunit B aspartyl/glutamyl-tRNA amidotransferase subunit A aspartyl/glutamyl-tRNA amidotransferase subunit C pyruvate, phosphate dikinase, partial pyruvate, phosphate dikinase, partial pyruvate, phosphate dikinase pyrazinamidase/nicotinamidase transcriptional repressor Cody aminotransferase universal stress protein HAD superfamily hydrolase L-asparaginase lantibiotic transport permease transporter ATP-dependent DNA helicase RecG hypothetical protein M500S_Spy_1520 cobalt ABC transporter ATP-binding protein cobalt transporter cbiQ permease
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MS005, Spy, 1508c 3571392 MS005, Spy, 1510c 3571393 MS005, Spy, 1511c 3571394 MS005, Spy, 1511c 3571395 MS005, Spy, 1512c 3571395 MS005, Spy, 1513c 3571392 MS005, Spy, 1513c 3571392 MS005, Spy, 1515c 3571392 MS005, Spy, 1516c 3571363 MS005, Spy, 1517c 3571362 MS005, Spy, 1519c 3571363 MS005, Spy, 1519c 3571363 MS005, Spy, 1520 3571364 MS005, Spy, 1520 3571363 MS005, Spy, 1520 3571364 MS005, Spy, 1524c 3571367 MS005, Spy, 1524c 3571367 MS005, Spy, 1524c 3571373 MS005, Spy, 1526c 3571373 MS005, Spy, 1526c 3571373 MS005, Spy, 1526c 3571373 MS005, Spy, 1530c 3571373 MS005, Spy, 15310c 3571373 MS005, Spy, 15310c 3571373 MS005, Spy, 1534c 3571373 MS005, Spy, 1534c 3571373 MS005, Spy, 1536c 3571373	E E E NEC NE	Spy49_1381c Spy49_1383c Spy49_1383c Spy49_1385c Spy49_1386c Spy49_1386c Spy49_1386c Spy49_1389c Spy49_1390c Spy49_1390c Spy49_1390c Spy49_1391c Spy49_1391c Spy49_1395c Spy49_1395c Spy49_1396c Spy49_1396c Spy49_1396c Spy49_1396c Spy49_1400c	6984764 6984765 6984765 6984766 6984767 6984770 6984770 6984772 6984772 6984772 6984772 6984773 6984776 6984778 6984784 6984787 6984786 6984787 6984786 6984787 6984787 6984787	NE E NC NE E NE N	gatA gatC		SSA_0570 SSA_0569 SSA_0548 SSA_0547	SP_0437 SP_0438 SP_1584 SP_1698 SP_1699	hypothetical protein M500S_Spy_1505 aspartyl/glutamyl-tRNA amidotransferase subunit B aspartyl/glutamyl-tRNA amidotransferase subunit A aspartyl/glutamyl-tRNA amidotransferase subunit C pyruvate, phosphate dikinase, partial pyruvate, phosphate dikinase pyrazinamidase/nicotinamidase transcriptional repressor CodY aminotransferase universal stress protein HAD superfamily hydrolase L-asparaginase lantibiotic transport permease transporter ATP-dependent DNA helicase RecG hypothetical protein M500S_Spy_1520 cobalt ABC transporter ATP-binding protein cobalt transporter ATP-binding protein ABC transporter ATP-binding protein ABC transporter ATP-binding protein ferrichrome ABC transporter ATP-binding protein ferrichrome transporter permease ferrichrome-binding protein heme binding protein heme binding protein F3+-siderophore transporter hypothetical protein M500S_Spy_1531 alanine racemase 4\'-phosphopantetheinyl transferase preprotein translocase subunit SecA hypothetical protein M500S_Spy_1535 transposase transposase transposase transposase, partial mannose-6-phosphate isomerase fructokinase endo-beta-N-acetylglucosaminidase F2
M5005, Spy, 1508c 3571392 M5005, Spy, 1510c 3571394 M5005, Spy, 1511c 3571394 M5005, Spy, 1511c 3571395 M5005, Spy, 1513c 3571397 M5005, Spy, 1515c 3571396 M5005, Spy, 1515c 3571396 M5005, Spy, 1516c 3571396 M5005, Spy, 1516c 3571362 M5005, Spy, 1517c 3571362 M5005, Spy, 1517c 3571363 M5005, Spy, 1517c 3571363 M5005, Spy, 1520c 3571363 M5005, Spy, 1520c 3571365 M5005, Spy, 1520c 3571366 M5005, Spy, 1520c 3571366 M5005, Spy, 1520c 3571367 M5005, Spy, 1520c 3571367 M5005, Spy, 1520c 3571376 M5005, Spy, 1520c 3571371 M5005, Spy, 1520c 3571372 M5005, Spy, 1530c 3571372 M5005, Spy, 1530c 3571372 M5005, Spy, 1530c 3571373 M5005, Spy, 1530c 3571374 M5005, Spy, 1530c 3571343 M5005, Spy, 1530c 3571343 M5005, Spy, 1530c 3571344 M5005, Spy, 1530c 3571346	E E E NEC NEC NEC NEC NEC NEC NEC NEC NE	Spy49_1381c Spy49_1383c Spy49_1383c Spy49_1386c Spy49_1386c Spy49_1387c Spy49_1388c Spy49_1389c Spy49_1390c Spy49_1390c Spy49_1391c Spy49_1391c Spy49_1391c Spy49_1391c Spy49_1391c Spy49_1391c Spy49_1401c	6984764 6984765 6984766 6984767 6984767 6984770 6984770 6984770 6984772 6984772 6984773 6984773 6984774 6984778 6984778 6984781 6984781 6984781 6984781 6984784 6984785 6984784 6984785 6984784 6984785 6984784 6984785 6984784 6984785 6984784 6984785 6984785 6984784 6984785 6984784 6984785 6984784 6984785 6984784 6984785 6984784 6984785 6984784 6984785 6984784 6984785 6984784 6984785 6984784 6984785 6984784 6984785 6984785 6984784 6984785 6984785 6984784 6984785 6984784 6984785 6984784 6984784 6984784 6984785	NE E NC NE	gatA gatC codY asnB recG cycC cycD fhuC fhuB2 fhuD2 shp - isp2 alr acpS secA pmi scrK endoS -		SSA_0570 SSA_0569 SSA_0548 SSA_0547	SP_0437 SP_0438 SP_1584 SP_1698 SP_1699	hypothetical protein M500S_Spy_150S aspartyl/glutamyl-tRNA amidotransferase subunit B aspartyl/glutamyl-tRNA amidotransferase subunit A aspartyl/glutamyl-tRNA amidotransferase subunit C pyruvate, phosphate dikinase pyrazinamidase/nicotinamidase transcriptional repressor Cody aminotransferase universal stress protein HAD superfamily hydrolase L-asparaginase lantibiotic transport permease transporter ATP-dependent DNA helicase RecG hypothetical protein M500S_Spy_1520 cobalt ABC transporter ATP-binding protein cobalt transporter ChQ permease ABC transporter ATP-binding protein ABC transporter ATP-binding protein ferrichrome ABC transporter ATP-binding protein ferrichrome ABC transporter ATP-binding protein ferrichrome binding protein ferrichrome transporter protein heme binding
M5005, Spy, 1508c 3571392 M5005, Spy, 1510c 3571394 M5005, Spy, 1511c 3571394 M5005, Spy, 1511c 3571395 M5005, Spy, 1513c 3571396 M5005, Spy, 1513c 3571396 M5005, Spy, 1516c 3571361 M5005, Spy, 1516c 3571361 M5005, Spy, 1516c 3571361 M5005, Spy, 1517c 3571362 M5005, Spy, 1518c 3571363 M5005, Spy, 1519c 3571365 M5005, Spy, 1521c 3571365 M5005, Spy, 1521c 3571366 M5005, Spy, 1521c 3571366 M5005, Spy, 1522c 3571367 M5005, Spy, 1523c 3571367 M5005, Spy, 1524c 3571369 M5005, Spy, 1524c 3571367 M5005, Spy, 1524c 3571373 M5005, Spy, 1534c 3571373 M5005, Spy, 1534c 3571373 M5005, Spy, 1534c 3571374 M5005, Spy, 1534c 3571374 M5005, Spy, 1536c 3571341 M5005, Spy, 1536c 3571341 M5005, Spy, 1536c 3571343 M5005, Spy, 1536c 3571344 M5005, Spy, 1536c 3571344 M5005, Spy, 1536c 3571344 M5005, Spy, 1536c 3571344 M5005, Spy, 1536c 3571346 M5005, Spy, 1536c 3571346 M5005, Spy, 1536c 3571346 M5005, Spy, 1536c 3571346	E E E NEC NE	Spy49_1381c Spy49_1383c Spy49_1383c Spy49_1384c Spy49_1385c Spy49_1386c Spy49_1387c Spy49_1389c Spy49_1390c Spy49_1390c Spy49_1390c Spy49_1393c Spy49_1390c Spy49_1390c Spy49_1390c Spy49_1400c Spy49_1410c	6984764 6984765 6984765 6984766 6984766 6984767 6984770 6984772 6984772 6984773 6984773 6984775 6984775 6984776 6984786 6984786 6984786 6984786 6984786 6984786 6984786 6984786 6984786 6984787 6984791	NE E NE	gatA gatC		SSA_0570 SSA_0569 SSA_0548 SSA_0547	SP_0437 SP_0438 SP_1584 SP_1698 SP_1699	hypothetical protein M500S_Spy_1505 aspartyl/glutamyl-tRNA amidotransferase subunit B aspartyl/glutamyl-tRNA amidotransferase subunit A aspartyl/glutamyl-tRNA amidotransferase subunit C pyruvate, phosphate dikinase, partial pyruvate, phosphate dikinase pyrazinamidase/nicotinamidase transcriptional repressor CodY aminotransferase universal stress protein HAD superfamily hydrolase L-asparaginase l-asparaginase lantibiotic transport permease transporter ATP-dependent DNA helicase RecG hypothetical protein M500S_Spy_1520 cobalt ABC transporter ATP-binding protein cobalt transporter ATP-binding protein ABC transporter ATP-binding protein ferrichrome ABC transporter ATP-binding protein ferrichrome transporter permease ferrichrome-binding protein heme binding protein Fe3+-siderophore transporter hypothetical protein M500S_Spy_1531 alanine racemase 4\'\cdot\-phosphopantetheinyl transferase preprotein translocase subunit SecA hypothetical protein M500S_Spy_1535 transposase transposase endo-beta-N-acetylglucosaminidase F2 hypothetical protein M500S_Spy_1541 PTS system sucrose-specific transporter subunit IIABC
MS005, Spy, 1508c 3571392 MS005, Spy, 1510c 3571394 MS005, Spy, 1511c 3571394 MS005, Spy, 1511c 3571395 MS005, Spy, 1513c 3571397 MS005, Spy, 1515c 3571396 MS005, Spy, 1515c 3571396 MS005, Spy, 1516c 3571396 MS005, Spy, 1516c 3571362 MS005, Spy, 1517c 3571362 MS005, Spy, 1517c 3571363 MS005, Spy, 1517c 3571363 MS005, Spy, 1520c 3571363 MS005, Spy, 1520c 3571365 MS005, Spy, 1520c 3571366 MS005, Spy, 1520c 3571366 MS005, Spy, 1520c 3571367 MS005, Spy, 1520c 3571367 MS005, Spy, 1520c 3571376 MS005, Spy, 1520c 3571371 MS005, Spy, 1520c 3571372 MS005, Spy, 1530c 3571372 MS005, Spy, 1530c 3571372 MS005, Spy, 1530c 3571373 MS005, Spy, 1530c 3571374 MS005, Spy, 1530c 3571343 MS005, Spy, 1530c 3571343 MS005, Spy, 1530c 3571344 MS005, Spy, 1530c 3571344 MS005, Spy, 1530c 3571346 MS005, Spy, 1530c 3571346 MS005, Spy, 1530c 3571346 MS005, Spy, 1530c 3571346	E E E NEC NEC NEC NEC NEC NEC NEC NEC NE	Spy49_1381c Spy49_1383c Spy49_1383c Spy49_1386c Spy49_1386c Spy49_1387c Spy49_1388c Spy49_1389c Spy49_1390c Spy49_1390c Spy49_1391c Spy49_1391c Spy49_1391c Spy49_1391c Spy49_1391c Spy49_1391c Spy49_1401c	6984764 6984765 6984766 6984767 6984767 6984770 6984770 6984770 6984772 6984772 6984773 6984773 6984774 6984778 6984778 6984781 6984781 6984781 6984781 6984784 6984785 6984784 6984785 6984784 6984785 6984784 6984785 6984784 6984785 6984784 6984785 6984785 6984784 6984785 6984784 6984785 6984784 6984785 6984784 6984785 6984784 6984785 6984784 6984785 6984784 6984785 6984784 6984785 6984784 6984785 6984784 6984785 6984785 6984784 6984785 6984785 6984784 6984785 6984784 6984785 6984784 6984784 6984784 6984785	NE E NC NE	gatA gatC codY asnB recG cycC cycD fhuC fhuB2 fhuD2 shp - isp2 alr acpS secA pmi scrK endoS -		SSA_0570 SSA_0569 SSA_0548 SSA_0547	SP_0437 SP_0438 SP_1584 SP_1698 SP_1699	hypothetical protein M500S_Spy_150S aspartyl/glutamyl-tRNA amidotransferase subunit B aspartyl/glutamyl-tRNA amidotransferase subunit A aspartyl/glutamyl-tRNA amidotransferase subunit C pyruvate, phosphate dikinase pyrazinamidase/nicotinamidase transcriptional repressor Cody aminotransferase universal stress protein HAD superfamily hydrolase L-asparaginase lantibiotic transport permease transporter ATP-dependent DNA helicase RecG hypothetical protein M500S_Spy_1520 cobalt ABC transporter ATP-binding protein cobalt transporter ChQ permease ABC transporter ATP-binding protein ABC transporter ATP-binding protein ferrichrome ABC transporter ATP-binding protein ferrichrome ABC transporter ATP-binding protein ferrichrome binding protein ferrichrome transporter protein heme binding

M5005_Spy_1545c	3571351	С	Spy49_1418c	6984797	NE	nusB	*		SP_0433	transcription antitermination protein NusB
M5005_Spy_1546c	3571352	NC	Spy49_1419c	6984798	NE	-	*		31_0433	Gls24 family general stress protein
M5005_Spy_1547c M5005_Spy_1548c	3571353 3571354	NE NE	Spy49_1420c Spy49_1421c	6984799 6984800	NE NE	efp comEB	*			elongation factor P competence protein ComE
M5005_Spy_1549c M5005_Spy_1550c	3571355 3571356	NE NE	Spy49_1422c	6984801 6984802	NE NE	pepP uvrA	*			Xaa-Pro dipeptidase excinuclease ABC subunit A
M5005_Spy_1551	3571357	E	Spy49_1423c Spy49_1424	6984803	С	corA	*		SP_0185	magnesium and cobalt transporter
M5005_Spy_1552 M5005_Spy_1553c		NE NC	Spy49_1425 Spy49_1426c	6984804 6984805	NE NC	- rpsR	*			hypothetical protein M5005_Spy_1552 30S ribosomal protein S18
M5005_Spy_1554c	3571360	NC	Spy49_1427c	6984806	С	ssb3	*	SSA_0438	SP_1540	single-stranded DNA-binding protein
M5005_Spy_1555c M5005_Spy_1556c		NC NE	Spy49_1428c Spy49_1429c	6984807 6984808	NC NE	rpsF -	*			30S ribosomal protein S6 hypothetical protein M5005_Spy_1556
M5005_Spy_1557 M5005_Spy_1558	3571324 3571325	NE NE	Spy49_1430 Spy49_1431	6984809 6984810	NE NE	mutY	*			A/G-specific adenine glycosylase transcriptional regulator
M5005_Spy_1559c	3571326	NE	Spy49_1432c	6984811	NE	trx	*			thioredoxin
M5005_Spy_1560c M5005_Spy_1561c		NE NE	Spy49_1433c Spy49_1434c	6984812 6984813	NE NE	mutS2	*			phosphatidylglycerophosphatase B DNA mismatch repair protein
M5005_Spy_1562c M5005_Spy_1563c		NE NE	Spy49_1435c Spy49_1436c	6984814 6984815	NE NE	-	*			colicin V production protein hypothetical protein M5005_Spy_1563
M5005_Spy_1564	3571331	С	Spy49_1437	6984816	Ε	-	*			ribonuclease HIII
M5005_Spy_1565 M5005_Spy_1566	3571332 3571333	E NE	Spy49_1438 Spy49_1439	6984817 6984818	E NE	spi recD	*		SP_0402	signal peptidase I exodeoxyribonuclease V subunit alpha
M5005_Spy_1567 M5005_Spy_1568c	3571334 3571335	NE NE	Spy49_1440 Spy49_1441c	6984819 6984820	NE NC	- dinP	*			hypothetical protein M5005_Spy_1567 DNA polymerase IV
M5005_Spy_1569	3571336	NE	Spy49_1442	6984821	NC	pfl	*			formate acetyltransferase
M5005_Spy_1570c M5005_Spy_1571c		NE NE	Spy49_1443c Spy49_1444c	6984822 6984903	NE NE	- cppA	*			penicillin-binding protein c3-degrading proteinase
M5005_Spy_1572	3571339	NE	Spy49_1445	6984904	NE	-	*		CD 4404	hypothetical protein M5005_Spy_1572
M5005_Spy_1573c M5005_Spy_1574c	3571302	C NC	Spy49_1447c		NC	glpF.2 -			SP_1491	aquaporin universal stress protein
M5005_Spy_1575c M5005_Spy_1576	3571303 3571304	NE NE	Spy49_1449c Spy49_1450	6984906 6984907	NE NE	norA srv	*			quinolone resistance protein Crp/Fnr family transcriptional regulator
M5005_Spy_1577	3571305	NE	Spy49_1451	6984908	NE	pepXP	*			x-prolyl-dipeptidyl aminopeptidase
M5005_Spy_1578c M5005_Spy_1579	3571306 3571307	NE NE	Spy49_1452c Spy49_1453	6984909 6984910	NE NE	-	*			Cro/CI family transcriptional regulator transcriptional regulator
			Spy49_1454c Spy49_1455	6984911 6984912	NE NE					
			Spy49_1456	6984913	NE					
			Spy49_1457c Spy49_1458c	6984914 6984915	NE NE					
			Spy49_1459c Spy49_1460c	6984916 6984917	NE NE					
			Spy49_1461c	6984918 6984919	NE NE					
			Spy49_1462c Spy49_1463c	6984920	NC					
			Spy49_1464c Spy49_1465c	6984921 6984922	NE NC					
			Spy49_1466c Spy49_1467c	6984923 6984924	NC NC					
			Spy49_1468c	6984925	NE					
			Spy49_1470c Spy49_1471c	6984926 6984927	NE NE					
			Spy49_1472c Spy49_1474c	6984928 6984929	NE NE					
			Spy49_1475c	6984930	NE					
			Spy49_1476c Spy49_1477c	6984931 6984932	NE NE					
			Spy49_1478c Spy49_1479c	6984933 6984934	NE NE					
			Spy49_1480c	6984935	NE					
			Spy49_1481c Spy49_1482c	6984936 6984937	NE NE					
			Spy49_1483c Spy49_1484c	6984938 6984939	NE NE					
			Spy49_1485c	6984940	NE					
			Spy49_1486c Spy49_1487c	6984941 6984942	NE NE					
			Spy49_1488c		NE					
			Spy49_1489c Spy49_1491c	6984945	NE NE					
			Spy49_1492c Spy49_1493c	6984946 6984947	NE NE					
			Spy49_1494c Spy49_1496c	6984948	NC NE					
			Spy49_1497c	6984950	NC					
			Spy49_1498c Spy49_1499c		NE NE					
			Spy49_1500c	6984953	NC NE					
			Spy49_1501c Spy49_1502c	6984955	NC					
			Spy49_1504c Spy49_1505c		NE NC					
			Spy49_1506c Spy49_1507c	6984958	NE NE					
			Spy49_1509c	6984960	NE					
			Spy49_1510c Spy49_1511c		NC NC					
			Spy49_1512c Spy49_1513c	6984963	NE NE					
			Spy49_1514c	6984965	NE					
			Spy49_1516c Spy49_1517c		NC NE					
			Spy49_1518c Spy49_1520c	6984968	NE NC					
			Spy49_1521c	6984970	NE					
			Spy49_1522 Spy49_1525	6984971 6984972	C NE					
			Spy49_1526 Spy49_1528c	6984973 6984974	NE NC					
			Spy49_1529	6984975	NC					
			Spy49_1530 Spy49_1531	6984976 6984977	NE NE					
			-							

M5005_Spy_1580 M5005_Spy_1581c	3571308 3571309	NE NE	Spy49_1532	6984978 6984979	NE NE	-	*			hypothetical protein M5005_Spy_1580 MerR family transcriptional regulator
M5005_Spy_1581c		NE	Spy49_1533c Spy49_1534c	6984980	NC	dnaQ	*			DNA polymerase III subunit epsilon
M5005_Spy_1583c		NE	Spy49_1535c	6984981	NC	-	*			hypothetical protein M5005_Spy_1583
,			Spy49 1536c	6984982	NE					77
			Spy49_1537c	6985063	NE					
M5005_Spy_1584	3571312	NE	Spy49_1538	6985064	NE		*			NAD(FAD)-utilizing dehydrogenase
M5005_Spy_1585c	3571313	NE	Spy49_1540c	6985065	NE	deoC	*			deoxyribose-phosphate aldolase
M5005_Spy_1586c M5005_Spy_1587c	3571314 3571315	NE NE	Spy49_1541c Spy49_1542c	6985066 6985067	NE NE	nupC udp	*			nucleoside permease uridine phosphorylase
M5005_Spy_1588c	3571316	NC	3py49_1542C	0303007	INE	-	-			hypothetical protein M5005 Spy 1588
M5005_Spy_1589	3571317	NE	Spy49_1543	6985068	NE	crgR	*			GntR family transcriptional regulator
M5005_Spy_1590	3571318	NE	Spy49_1544	6985069	NE	rpsN	*			30S ribosomal protein S14
M5005_Spy_1591c	3571319	E	Spy49_1545c	6985070	NC	gcp	*		SP_0129	DNA-binding/iron metalloprotein/AP endonuclease
M5005_Spy_1592c	3571320	NE	Spy49_1546c	6985071	NE	-	*			ribosomal-protein-alanine acetyltransferase
M5005_Spy_1593c M5005_Spy_1594	3571321 3571284	C E	Spy49_1547c Spy49_1548	6985072 6985073	E NC	-	*		SP_0122	glycoprotease hypothetical protein M5005_Spy_1594
M5005_Spy_1595	3571285	E	Spy49_1548 Spy49_1549	6985074	E	-	*	SSA_0312	SP_0121	Zn-dependent hydrolase
M5005_Spy_1596c	3571286	NE	Spy49_1550c	6985075	NE	glnA	*	33A_0312	31_0121	glutamine synthetase
M5005_Spy_1597c	3571287	NE	Spy49_1551c	6985076	NE	glnR	*			MerR family transcriptional regulator
M5005_Spy_1598c	3571288	NE	Spy49_1552c	6985077	NE	-	*			hypothetical protein M5005_Spy_1598
M5005_Spy_1599c	3571289	E	Spy49_1553c	6985078	NC	pgk	*	SSA_0302	SP_0499	phosphoglycerate kinase
M5005_Spy_1600c	3571290 3571291	NE	Spy49_1554c	6985079	NE	IppC	*			acid phosphatase
M5005_Spy_1601c M5005_Spy_1602c	3571291	NE E	Spy49_1555c Spy49_1556c	6985080 6985081	NE E	-	*		SP_0443	membrane protease kinase
M5005_Spy_1603c	3571293	NE	Spy49_1557c	6985082	NC	asp	*		3F_0443	alkaline-shock protein
M5005_Spy_1604c	3571294	NC				-				hypothetical protein M5005_Spy_1604
M5005_Spy_1605c	3571295	NE				-				transposase
M5005_Spy_1606c	3571296	NE	Spy49_1558c	6985083	NE	rpmB				50S ribosomal protein L28
M5005_Spy_1607c	3571297	E	Spy49_1559c	6985084	E	fba	*	SSA_1992	SP_0605	fructose-bisphosphate aldolase
M5005_Spy_1608c M5005_Spy_1610c	3571299 3571301	NE NE	Spy49_1560c Spy49_1561c	6985086 6985087	NE NE	pyrG	*			alpha/beta hydrolase CTP synthase, partial
M5005_Spy_1611c		NE	Spy49_1562c	6985088	NE	rpoE	*			DNA-directed RNA polymerase subunit delta
M5005_Spy_1612c		NE	Spy49_1563c	6985089	NE	tig/ropA	*			trigger factor
M5005_Spy_1613	3571272	NE	Spy49_1564	6985090	NE		*			mechanosensitive ion channel MscS
M5005_Spy_1614c	3571273	NE	Spy49_1565c	6985091	NE	-	*			hypothetical protein M5005_Spy_1614
M5005_Spy_1615c	3571274	NE	Spy49_1566c	6985092	NE	-	*			hypothetical protein M5005_Spy_1615
M5005_Spy_1616c	3571275	NE	Spy49_1567c	6985093	NE	thiD	*			phosphomethylpyrimidine kinase
M5005_Spy_1617c M5005_Spy_1618c	3571276 3571277	NE NE	Spy49_1568c Spy49_1569c	6985094 6985095	NE NE	truA comX.2	*			tRNA pseudouridine synthase A competence-specific sigma factor
M5005_Spy_1619	3571251	NC	3py45_1305C	0303033	INL	-				hypothetical protein M5005_Spy_1619
M5005_Spy_1620c	3571252	NE	Spy49_1571c	6985102	NE	-	*			glycerate kinase
M5005_Spy_1621	3571253	NE	Spy49_1572	6985103	NE	hsdR	*			type I restriction-modification system restriction subunit
M5005_Spy_1622	3571254	NE	Spy49_1573	6985104	NE	hsdS				type I restriction-modification system specificity subunit
M5005_Spy_1623	3571255	NE	Spy49_1574	6985105	NE	hsdM	*			type I restriction-modification system methylation subunit
M5005_Spy_1624c M5005_Spy_1625c	3571256 3571257	NE NE	Spy49_1575c	6985106 6985107	NE NE	salR	*			hypothetical protein M5005_Spy_1624 transcriptional regulatory protein
M5005_Spy_1626c	3571258	NE	Spy49_1576c Spy49_1577c	6985108	NE	salK	-			sensory transduction protein kinase
M5005_Spy_1627c	3571259	NE	Spy49_1578c	6985109	NE	salY				ABC transporter permease
M5005_Spy_1628c	3571260	NE	Spy49_1579c	6985110	NE	salX				ABC transporter ATP-binding protein
M5005_Spy_1629c	3571261	NE	Spy49_1580c	6985111	NE	salX/salT				lantibiotic transport ATP-binding protein
M5005_Spy_1630c	3571262	NE	Spy49_1582c	6985112	NE	salB				serine (threonine) dehydratase
M5005_Spy_1631c		NC	Spy49_1583c	6985113	NC	salA lacG				lantibiotic salivaricin A
M5005_Spy_1632c M5005_Spy_1633c	3571265	NE NE	Spy49_1584c Spy49_1585c	6985114 6985115	NE NE	lacE	-			6-phospho-beta-galactosidase PTS system lactose-specific transporter subunit IIBC
M5005_Spy_1634c	3571266	NE	Spy49_1586c	6985116	NE	lacF	*			PTS system lactose-specific transporter subunit IIA
M5005_Spy_1635c	3571267	NE	Spy49_1587c	6985117	NE	lacD.2	*			tagatose 1,6-diphosphate aldolase
M5005_Spy_1636c	3571268	NE	Spy49_1588c	6985118	NE	lacC.2	*			tagatose-6-phosphate kinase
M5005_Spy_1637c	3571269	NE	Spy49_1589c	6985119	NE	lacB.2	*			galactose-6-phosphate isomerase subunit LacB
M5005_Spy_1638c	3571231	NE	Spy49_1590c	6985120	NE	lacA.2	*			galactose-6-phosphate isomerase subunit LacA
M5005_Spy_1639 M5005_Spy_1640	3571232 3571233	NE NE	Spy49_1591 Spy49_1592	6985121 6985122	NE NE	lacR.2	•			lactose phosphotransferase system repressor DNA-damage-inducible protein J
M5005_Spy_1641	3571234	NE	Spy49_1593	6985123	NE	-	*			hypothetical protein M5005 Spy 1641
M5005_Spy_1642	3571235	NE	Spy49_1594	6985124	NE	-				DNA integration/recombination/invertion protein
M5005_Spy_1643	3571237	NC				-				DNA integration/recombination/invertion protein
M5005_Spy_1644c	3571236	NC				-				hypothetical protein M5005_Spy_1644
M5005_Spy_1645	3571238	NC	C40 4505-	6005135	-	T			CD 020F	DNA integration/recombination/invertion protein 30S ribosomal protein S9
M5005_Spy_1646c M5005_Spy_1647c	3571239 3571240	NC NC	Spy49_1595c Spy49_1596c	6985125 6985126	E NC	rpsI rplM	*		SP_0295	50S ribosomal protein S9
M5005_Spy_1648c		NC	Spy49_1597c	6985127	NC					Cro/CI family transcriptional regulator
M5005_Spy_1649c	3571242	NE	Spy49_1598c	6985128	NE	-	*			hypothetical protein M5005_Spy_1649
M5005_Spy_1650c	3571243	NE	Spy49_1599c	6985129	NC	-	*			degV family protein
M5005_Spy_1651c		NE	Spy49_1600c	6985130	NE	-	*			hypothetical protein M5005_Spy_1651
M5005_Spy_1652c		NE	Spy49_1601c	6985131	NE	-	*			23S rRNA methyltransferase
M5005_Spy_1653c M5005_Spy_1654c	3571246 3571247	NE NE	Spy49_1602c Spy49_1603c	6985132 6985133	NE NE	-	*			hypothetical protein M5005_Spy_1653 hypothetical protein M5005_Spy_1654
M5005_Spy_1655c	3571248	E	Spy49_1604c	6985134	E	cysS	*	SSA_2044	SP_0591	cysteinyl-tRNA synthetase
M5005_Spy_1656c	3571249	NE	Spy49_1605c	6985135	NE	-		=		hypothetical protein M5005_Spy_1656
M5005_Spy_1657c	3571250	NE				-				hypothetical protein M5005_Spy_1657
M5005_Spy_1658c	3571212	NC	Spy49_1606c	6985136	NC	cysE	*			serine acetyltransferase
M5005_Spy_1659c	3571213	NE	Spy49_1607c	6985137	NE	-	*			hypothetical protein M5005_Spy_1659
M5005_Spy_1660c M5005_Spy_1661c	3571214 3571215	NE NE	Spy49_1608c Spy49_1609c	6985138 6985139	NE NE	pnp	*			polynucleotide phosphorylase translaldolase
M5005_Spy_1662c	3571216	NE	Spy49_1610c	6985140	NE	ulaA	*			PTS system ascorbate-specific transporter subunit IIC
M5005_Spy_1663c	3571217	NE	Spy49_1611c	6985141	NE	-	*			PTS system transporter subunit IIB
M5005_Spy_1664c	3571218	NE	Spy49_1612c	6985142	NE	-	*			PTS system, mannitol (cryptic)-specific IIA component
M5005_Spy_1665c	3571219	NC								hypothetical protein M5005_Spy_1665
M5005_Spy_1666c	3571220	NC	Spy49_1613c		NE	rpsO				30S ribosomal protein S15
M5005_Spy_1667c M5005_Spy_1668	3571221 3571222	NC NE	Spy49_1614c	6985224	NE	-				hypothetical protein M5005_Spy_1667 transcriptional regulator
M5005_Spy_1669	3571223	E	Spy49_1615	6985225	С	def	*	SSA_2061	SP_1456	peptide deformylase
M5005_Spy_1670c	3571224	NE	Spy49_1616c	6985226	NE	-				oxidoreductase
M5005_Spy_1671c		NE	Spy49_1617c	6985227	NE		*			MarR family transcriptional regulator
M5005_Spy_1672c		E	Spy49_1618c	6985228	E	polC	*	SSA_2066	SP_0274	DNA polymerase III PolC
M5005_Spy_1673c	3571227	E	Spy49_1619c	6985229	E	proS	*	SSA_2069	SP_0264	prolyl-tRNA synthetase
M5005_Spy_1674c M5005_Spy_1675c	3571228 3571229	NE E	Spy49_1620c	6985230 6985231	NE E	eep cdsA	*	CCA 2072	CD 0262	pheromone-processing membrane metalloprotease phosphatidate cytidylyltransferase
M5005_Spy_1676c M5005_Spy_1676c	3571229 3571230	E	Spy49_1621c Spy49_1622c	6985231	E	uppS	*	SSA_2072 SSA_2073	SP_0262 SP_0261	undecaprenyl pyrophosphate synthase
M5005_Spy_1677c	3571192	NE	Spy49_1624c	6985233	NE	yajC	*	JJN_20/J	31_0201	preprotein translocase subunit YajC
M5005_Spy_1678c	3571193	NE	Spy49_1625c	6985234	NE	-	*			thioredoxin
M5005_Spy_1680c	3571195	NE	Spy49_1626c	6985235	NE	pulA	*			pullulanase, partial
M5005_Spy_1681c	3571196	NE	Spy49_1627c	6985236	NE	dexB	*			glucan 1,6-alpha-glucosidase

M5005_Spy_1682c 3571197 N	Spy49_1628c	6985237 NE	msmK	*			multiple sugar transport ATP-binding protein
M5005_Spy_1683c 3571198 N		6985238 NE	Irp	*			hypothetical protein M5005_Spy_1683
M5005_Spy_1684 3571199 NI		6985239 NE	ska				streptokinase
M5005_Spy_1685c <u>3571200</u> NI M5005_Spy_1686c <u>3571201</u> E		6985240 NE 6985241 C	dtd relA	*			D-tyrosyl-tRNA(Tyr) deacylase GTP pyrophosphokinase
M5005_Spy_1687c 3571202 NI		6985242 NE	scIA				hypothetical protein M5005_Spy_1687
M5005_Spy_1690 <u>3571205</u> N		6985243 NE	nrdI2				flavoprotein NrdI
M5005_Spy_1691c 3571206 NI		6985244 NE	-	*			exodeoxyribonuclease III
M5005_Spy_1693c <u>3571208</u> NI M5005_Spy_1694c <u>3571209</u> NI		6985245 NE 6985246 NE	-	*			PTS system glucose-specific transporter subunit IIABC 16S ribosomal RNA methyltransferase RsmE
M5005_Spy_1695c 3571210 N		6985247 NE	prmA	*			50S ribosomal protein L11 methyltransferase
M5005_Spy_1696c <u>3571211</u> N		6985248 NE	-	*			hypothetical protein M5005_Spy_1696
		6985249 NE					
		6985250 NE 6985251 NE					
		6985252 NC					
		6985253 NE					
		6985254 NE					
		6985255 NE					
		6985256 NE 6985257 NE					
		6985258 NC					
ME005 Co., 1607, 3571174		C005350					para-aminobenzoate synthetase component I/4-amino-4-deoxychorismate
M5005_Spy_1697 <u>3571174</u> NI M5005_Spy_1698 <u>3571175</u> NO		6985259 NE 6985260 NE	papB trpG	*			lyase anthranilate synthase component II
M5005_Spy_1699 3571176 N		6985261 NE	-	*			recombination factor protein RarA
M5005_Spy_1700 <u>3571178</u> N		6985263 NE	pai1				acetyltransferase
M5005_Spy_1701 3571179 N		6985264 NE	flaR				topology modulation protein
M5005_Spy_1702 3571180 Ni		6985265 NE	smeZ				mitogenic exotoxin Z
M5005_Spy_1703c <u>3571181</u> NI M5005_Spy_1704 <u>3571182</u> NI		6985266 NE 6985267 NE	dppA	*			hypothetical protein M5005_Spy_1703 dipeptide-binding protein
M5005_Spy_1705 3571183 N		6985268 NE	dppB	*			dipeptide transporter permease
M5005_Spy_1706 3571184 N		6985269 NE	dppC	*			dipeptide transporter permease
M5005_Spy_1707 3571185 N		6985270 NE	dppD	*			dipeptide transport ATP-binding protein
M5005_Spy_1708 <u>3571186</u> NI M5005_Spy_1709c <u>3571187</u> NI		6985271 NE 6985272 NE	dppE	*			dipeptide transport ATP-binding protein hypothetical protein M5005_Spy_1709
M5005_Spy_1710c 3571187 Ni			-	*			histidine triad protein
M5005_Spy_1711c 3571189 N			lmb	*			laminin binding protein
M5005_Spy_1712c 3571190 N			-				transposase
M5005_Spy_1713c 3571191 No			-				hypothetical protein M5005_Spy_1713
M5005_Spy_1714c <u>3571154</u> NI M5005_Spy_1715c <u>3571155</u> NI			scpA				cell surface protein C5A peptidase
M5005_Spy_1715c <u>3571155</u> Ni M5005_Spy_1716 <u>3571156</u> Ni		6985276 NE 6985277 NE	scpA -	•			transposase
M5005_Spy_1717 3571157 No			-				transposase, partial
M5005_Spy_1718c 3571158 N			sic1.01				inhibitor of complement protein
M5005_Spy_1719c 3571159 Ni		6985279 NE	emm1.0				M protein
M5005_Spy_1720c <u>3571160</u> NI M5005_Spy_1721 <u>3571161</u> NO			mga				trans-acting positive regulator hypothetical protein M5005_Spy_1721
M5005_Spy_1721 <u>3571161</u> No M5005_Spy_1722c <u>3571162</u> No		6985281 NE	-				hypothetical protein M5005_Spy_1721 hypothetical protein M5005_Spy_1722
M5005_Spy_1723c 3571163 N		6985282 NE	isp	*			hypothetical protein M5005_Spy_1723
M5005_Spy_1724c 3571164 N		6985283 NE	ihk	*			two component system histidine kinase
M5005_Spy_1725c 3571165 Ni		6985284 NE	irr	*			two-component response regulator
M5005_Spy_1726c <u>3571166</u> NI M5005_Spy_1727c <u>3571167</u> NI		6985285 NE 6985286 NE	-	*			ABC transporter permease ABC transporter ATP-binding protein
M5005_Spy_1728c 3571168 N		6985287 NE	-	*			periplasmic protein of efflux system
M5005_Spy_1729c 3571169 N			-	*			hypothetical protein M5005_Spy_1729
M5005_Spy_1730c <u>3571170</u> N			=	*			hypothetical protein M5005_Spy_1730
M5005_Spy_1731 <u>3571171</u> N			grm				hypothetical protein M5005_Spy_1731
		6985291 NE 6985292 NE					
M5005_Spy_1732c 3571172 C		6985293 NE	prsA	*			foldase PrsA
M5005_Spy_1733c 3571173 N		6985294 NE	-				hypothetical protein M5005_Spy_1733
M5005_Spy_1734c 3571135 NI		6985295 C	- 				hypothetical protein M5005_Spy_1734
M5005_Spy_1735c <u>3571136</u> Ni M5005_Spy_1736 <u>3571137</u> No		6985296 NE	speB -	•			exotoxin B hypothetical protein M5005_Spy_1736
M5005_Spy_1737 3571138 N		6985297 NE	rgg	*			transcriptional regulator
M5005_Spy_1738c 3571139 N		6985298 NE	spd	*			phage-associated deoxyribonuclease
M5005_Spy_1739 3571140 No		6985299 NC	=				hypothetical protein M5005_Spy_1739
M5005_Spy_1740 <u>3571141</u> NI M5005_Spy_1741c <u>3571142</u> NI		6985300 NE 6985301 NE	gldA	*			low temperature requirement C protein glycerol dehydrogenase
M5005_Spy_1741c 3571142 NI M5005_Spy_1742c 3571143 NI	.,,		mipB	*			fructose-6-phosphate aldolase
M5005_Spy_1743c 3571144 N		6985383 NE	pfID	*			formate acetyltransferase
M5005_Spy_1744c 3571145 N	Spy49_1698c	6985384 NE	-	*			PTS system cellobiose-specific transporter subunit IIC
M5005_Spy_1745c <u>3571146</u> NI M5005_Spy_1746c <u>3571147</u> NI		6985385 NE 6985386 NE	-	*			PTS system cellobiose-specific transporter subunit IIB PTS system cellobiose-specific transporter subunit IIA
M5005_Spy_1746C 3571147 Ni M5005_Spy_1747C 3571148 Ni			-	*			sorbitol operon regulator
M5005_Spy_1748c 3571149 N			-	*			DeoR family transcriptional regulator
M5005_Spy_1749 3571150 N		<u>6985389</u> NE	-	*			pyruvate formate-lyase activating enzyme
M5005_Spy_1750 3571151 Ni			-				hypothetical protein M5005_Spy_1750
M5005_Spy_1751c <u>3571152</u> No M5005_Spy_1752c <u>3571153</u> No			secE rpmG				preprotein translocase subunit SecE 50S ribosomal protein L33
M5005_Spy_1752c 3571155 N			pbp2A	*			multimodular transpeptidase-transglycosylase
M5005_Spy_1754c 3571117 N		6985393 NE	-	*			translation initiation inhibitor
M5005_Spy_1755 3571118 N		6985394 NE	-				hypothetical protein M5005_Spy_1755
M5005_Spy_1756 3571119 Ni		6985395 NE	-	*			ribosomal large subunit pseudouridine synthase D hypothetical protein M5005 Spy 1757
M5005_Spy_1757c <u>3571120</u> NI M5005_Spy_1758 <u>3571121</u> NI		6985396 NE 6985397 NE	-	*			dipeptidase B
M5005_Spy_1759c 3571121 Ni		6985398 NE	-				MutR family transcriptional regulator
M5005_Spy_1760c 3571123 N			-				MutR family transcriptional regulator
M5005_Spy_1761c 3571124 E		6985399 E	groEL	*	SSA_0226	SP_1906	molecular chaperone GroEL
M5005_Spy_1762c 3571125 E			groES	*	SSA_0225		co-chaperonin GroES
M5005_Spy_1763c <u>3571126</u> NI M5005_Spy_1764c <u>3571127</u> NI		6985401 NE 6985402 NE	clpC ctsR	*			negative regulator of genetic competence transcriptional regulator
M5005_Spy_1764c 3571127 NI		6985403 NE	csp				cold shock protein
M5005_Spy_1766c 3571129 No			-				hypothetical protein M5005_Spy_1766
M5005_Spy_1767c 3571130 Ni							transposase
M5005_Spy_1768 <u>3571132</u> NI M5005_Spy_1769 <u>3571133</u> NI		6985406 NE 6985407 NE	ahpC ahpF	*			peroxiredoxin reductase (NAD(P)H) peroxiredoxin reductase (NAD(P)H)
M5005_Spy_1769 3571133 NI M5005_Spy_1770c 3571134 NI			hutI	*			imidazolonepropionase
M5005_Spy_1771 <u>3571097</u> N	Spy49_1724	6985409 NE	hutU	*			urocanate hydratase
M5005_Spy_1772 3571098 N		6985410 NE	-	*			glutamate formiminotransferase
M5005_Spy_1773 <u>3571099</u> N	Spy49_1726	6985411 NE	-	*			formiminotetrahydrofolate cyclodeaminase

M5005_Spy_1774 <u>3571100</u> NE							
	Spy49_1727 <u>698</u>	85412 NE	fhs.2	*			formatetetrahydrofolate ligase
M5005_Spy_1775 3571101 NE	Spy49_1728 698	85413 NE	-	*			hypothetical protein M5005_Spy_1775
M5005_Spy_1776 3571102 NE	Spy49_1729 698	85414 NE	-	*			amino acid permease
M5005_Spy_1777 3571103 NE		85415 NE	hutH	*			histidine ammonia-lyase
M5005_Spy_1778 3571104 NE		85416 NE	hutG	*			formimidoylglutamase
M5005_Spy_1779c 3571105 NE		85417 NE		*			LuxR family transcriptional regulator
				*	CCA 2202	CD 2245	
M5005_Spy_1780 <u>3571106</u> E		85418 E	rpsB		SSA_2203	SP_2215	30S ribosomal protein S2
M5005_Spy_1781 <u>3571107</u> E		85419 E	tsf	*	SSA_2202	SP_2214	elongation factor Ts
M5005_Spy_1782c <u>3571108</u> NE		85420 NC	pepO	*			neutral endopeptidase
M5005_Spy_1783c 3571109 NC	Spy49_1736c 698	85421 E	dexS	*		SP_1883	trehalose-6-phosphate hydrolase
M5005_Spy_1784c 3571110 NE	Spy49_1737c 698	85422 NC	-	*			PTS system, trehalose-specific IIBC component
M5005_Spy_1785 3571111 NE	Spy49_1738 698	85423 NE	-	*			trehalose operon transcriptional repressor
M5005_Spy_1786c 3571112 NE		85424 NE	_				MarR family transcriptional regulator, partial
M5005_Spy_1787 3571113 NE		85425 NE					glyoxalase
			vaaA	*			hypothetical protein M5005_Spy_1788
			,	*			
M5005_Spy_1789c 3571115 NE		85427 NC	nrdG				anaerobic ribonucleoside-triphosphate reductase activating protein
M5005_Spy_1790c <u>3571077</u> NE	Spy49_1744c <u>698</u>	85428 NE	-	*			acetyltransferase
M5005_Spy_1791c 3571078 NC	Spy49_1745c 698	85429 E	-	*			virulence factor
M5005_Spy_1792c 3571079 NC	Spy49_1746c 698	85430 NC	-				hypothetical protein M5005_Spy_1792
M5005_Spy_1793c 3571080 C		85431 NC	nrdD	*			anaerobic ribonucleoside triphosphate reductase
M5005_Spy_1794c 3571081 NE		85432 NE	_	*			hypothetical protein M5005_Spy_1794
M5005_Spy_1795c 3571082 NE		85433 NE	_	*			hypothetical protein M5005_Spy_1795
				*			
M5005_Spy_1796c 3571083 E		85434 NC	-	*	SSA_2240		Holliday junction resolvase-like protein
M5005_Spy_1797c <u>3571084</u> NE		85435 NE	-				hypothetical protein M5005_Spy_1797
M5005_Spy_1798c 3571085 C		85436 NE	spxA	*		SP_1405	Spx family transcriptional regulator
M5005_Spy_1799c 3571086 NE	Spy49_1753c 698	85437 NC	recA	*			recombinase A
M5005_Spy_1800c 3571087 NE	Spy49_1754c 698	85438 NE	cinA	*			competence damage-inducible protein A
M5005_Spy_1801c 3571088 NC		85439 NE	tag	*			DNA-3-methyladenine glycosylase
M5005_Spy_1802c 3571089 NC		85440 C	ruvA	*		SP_0179	Holliday junction DNA helicase RuvA
M5005_Spy_1803c 3571090 NE		85441 C	ImrP	*		551/5	multidrug resistance protein B
				*			DNA mismatch repair protein
		85442 C	mutL				
M5005_Spy_1805c 3571092 NC	Spy49_1759c <u>698</u>	85443 NC	mutS	*			DNA mismatch repair protein MutS
M5005_Spy_1806c 3571093 NE			-				hypothetical protein M5005_Spy_1806
M5005_Spy_1807c 3571094 NE		85444 NE	argR2	*			arginine repressor ArgR
M5005_Spy_1808 3571095 E	Spy49_1762 698	85445 E	argS	*	SSA_2262	SP 2078	arginyl-tRNA synthetase
M5005_Spy_1809 3571096 NE		85446 NE	uviB	*	-	_	bacteriocin
M5005_Spy_1810c 3571058 NE		85447 NE	-	*			hypothetical protein M5005_Spy_1810
M5005_Spy_1811c 3571059 NE		85448 NE	_	*			hypothetical protein M5005_Spy_1811
M5005_Spy_1812c 3571060 NE		85449 NE					hypothetical protein M5005_Spy_1812
				*			
M5005_Spy_1813c 3571061 E		85450 E	aspS	*		SP_2114	aspartyl-tRNA synthetase
M5005_Spy_1814c 3571062 E		85451 E	hisS	*	SSA_2284	SP_2121	histidyl-tRNA synthetase
M5005_Spy_1815 <u>3571063</u> NE		85452 NE	rpmF				50S ribosomal protein L32
M5005_Spy_1816 <u>3571064</u> NC	Spy49_1771 <u>698</u>	85453 NC	rpmG				50S ribosomal protein L33
	Spy49_1772c 698	85454 NE					
M5005_Spy_1817 3571065 NE	Spy49_1773 698	85455 NE	cadD	*			cadmium resistance protein
M5005_Spy_1818 3571066 NE		85456 NE	cadC	*			cadmium efflux system accessory protein
M5005_Spy_1819 3571067 NE		85457 NE	-				hypothetical protein M5005_Spy_1819
M5005_Spy_1820 3571068 NE		85458 NE		*			DNA translocase FtsK
			=				
M5005_Spy_1821 3571069 NE	Spy49_1778 <u>698</u>	85459 NE	-	*			hypothetical protein M5005_Spy_1821
M5005_Spy_1822c <u>3571070</u> NE			-				transcriptional regulator
M5005_Spy_1823 3571071 NE	Spy49_1779 <u>698</u>	85460 NE	-	*			hypothetical protein M5005_Spy_1823
M5005_Spy_1824c 3571072 NE	Spy49_1780c 698	85461 NE	-				phosphohydrolase
M5005_Spy_1825 3571073 NE		85462 NE	-	*			DadD family transposintional regulator
M5005 Spv 1826 3571074 NE	Snv49 1782 698	86105 NF	_	*			PadR family transcriptional regulator hypothetical protein M5005, Spy. 1826
M5005_Spy_1826 3571074 NE M5005_Spy_1827 3571075 NE		86105 NE	-	*			hypothetical protein M5005_Spy_1826
M5005_Spy_1827 3571075 NE	Spy49_1783 <u>698</u>	86106 NE	-	*			hypothetical protein M5005_Spy_1826 hypothetical protein M5005_Spy_1827
M5005_Spy_1827 3571075 NE M5005_Spy_1828c 3571076 NE	Spy49_1783 <u>698</u> Spy49_1784c <u>698</u>	86106 NE 86107 NC	-	*			hypothetical protein M5005_Spy_1826 hypothetical protein M5005_Spy_1827 phage infection protein
M5005_Spy_1827 3571075 NE M5005_Spy_1828c 3571076 NE M5005_Spy_1830 3571039 NE	Spy49_1783 <u>698</u> Spy49_1784c <u>698</u> Spy49_1785 <u>698</u>	86106 NE 86107 NC 86108 NE	<u>:</u>	* * *			hypothetical protein M5005_Spy_1826 hypothetical protein M5005_Spy_1827 phage infection protein TetR family transcriptional regulator
M5005_Spy_1827 3571075 NE M5005_Spy_1828c 3571076 NE M5005_Spy_1830 3571039 NE M5005_Spy_1831c 3571040 E	Spy49_1783 <u>698</u> Spy49_1784c <u>698</u> Spy49_1785 <u>698</u>	86106 NE 86107 NC	- - - - rpsD	*	SSA_2350	SP_0085	hypothetical protein M5005_Spy_1826 hypothetical protein M5005_Spy_1827 phage infection protein Tetk family transcriptional regulator 30S ribosomal protein S4
M5005_Spy_1827 3571075 NE M5005_Spy_1828c 3571076 NE M5005_Spy_1830 3571039 NE M5005_Spy_1831c 3571040 E M5005_Spy_1832c 3571041 NC	Spy49_1783 <u>698</u> Spy49_1784c <u>698</u> Spy49_1785 <u>698</u>	86106 NE 86107 NC 86108 NE	rpsD	* * *	SSA_2350	SP_0085	hypothetical protein M5005_Spy_1826 hypothetical protein M5005_Spy_1827 phage infection protein Tetk family transcriptional regulator 30S ribosomal protein S4 hypothetical protein M5005_Spy_1832
M5005_Spy_1827 3571075 NE M5005_Spy_1828c 3571076 NE M5005_Spy_1830 3571039 NE M5005_Spy_1831c 3571040 E	Spy49_1783 <u>698</u> Spy49_1784c <u>698</u> Spy49_1785 <u>698</u>	86106 NE 86107 NC 86108 NE		* * *	SSA_2350	SP_0085	hypothetical protein M5005_Spy_1826 hypothetical protein M5005_Spy_1827 phage infection protein Tetk family transcriptional regulator 30S ribosomal protein S4
M5005_Spy_1827 3571075 NE M5005_Spy_1828c 3571076 NE M5005_Spy_1830 3571039 NE M5005_Spy_1831c 3571049 E M5005_Spy_1832c 3571041 NC	Spy49_1783 698 Spy49_1784c 698 Spy49_1785 698 Spy49_1786c 698	86106 NE 86107 NC 86108 NE		* * *	SSA_2350	SP_0085	hypothetical protein M5005_Spy_1826 hypothetical protein M5005_Spy_1827 phage infection protein Tetk family transcriptional regulator 30S ribosomal protein S4 hypothetical protein M5005_Spy_1832
M5005_Spy_1827 3571075 NE M5005_Spy_1828 3571076 NE M5005_Spy_1830 3571039 NE M5005_Spy_1831c 3571040 E M5005_Spy_1832c 3571041 NC M5005_Spy_1833c 3571042 NE	Spy49_1783 698 Spy49_1784c 699 Spy49_1785 698 Spy49_1786c 698 Spy49_1787c 698	86106 NE 86107 NC 86108 NE 86109 E		* * *	SSA_2350 SSA_2356	SP_0085 SP_2203	hypothetical protein M5005_Spy_1826 hypothetical protein M5005_Spy_1827 phage infection protein TetR family transcriptional regulator 30S ribosomal protein S4 hypothetical protein M5005_Spy_1832 transposase
M5005_Spy_1827 3571075 NE M5005_Spy_1828e 3571039 NE M5005_Spy_1830 3571039 NE M5005_Spy_1831c 3571040 E M5005_Spy_1832c 3571041 NE M5005_Spy_1833c 3571042 NE M5005_Spy_1834c 3571043 NE M5005_Spy_1835c 3571044 NE	Spy49_1783 698 Spy49_1784c 698 Spy49_1785 698 Spy49_1786c 698 Spy49_1787c 698 Spy49_1788c 698	86106 NE 86107 NC 86108 NE 86109 E	holB/dnaC	* * * *	_	_	hypothetical protein M5005_Spy_1826 hypothetical protein M5005_Spy_1827 phage infection protein Tetk family transcriptional regulator 30S ribosomal protein S4 hypothetical protein M5005_Spy_1832 transposase hypothetical protein M5005_Spy_1834 replicative DNA helicase
M5005_Spy_1827 3571075 NE M5005_Spy_1828c 3571039 NE M5005_Spy_1830 3571049 E M5005_Spy_1831c 3571041 NC M5005_Spy_1832c 3571042 NE M5005_Spy_1833c 3571043 NE M5005_Spy_1834c 3571043 NE M5005_Spy_1835c 3571044 NE M5005_Spy_1836c 3571045 NE	Spy49_1783 698 Spy49_1784 698 Spy49_1785 698 Spy49_1786c 698 Spy49_1787c 698 Spy49_1788c 699 Spy49_1788c 699 Spy49_1789c 698	86106 NE 86107 NC 86108 NE 86109 E 86110 NE 86111 E 86112 NC	-	* * * *	_	_	hypothetical protein M5005_Spy_1826 hypothetical protein M5005_Spy_1827 phage infection protein TetR family transcriptional regulator 30S ribosomal protein S4 hypothetical protein M5005_Spy_1832 transposase hypothetical protein M5005_Spy_1834 replicative DNA helicase 50S ribosomal protein L9
M5005_Spy_1827 3571075 NE	Spy49_1783 698 Spy49_1784 698 Spy49_1785 698 Spy49_1786 698 Spy49_1786 698 Spy49_17886 698 Spy49_17896 698 Spy49_17906 698 Spy49_17906 698	86106 NE 86107 NC 86108 NE 86109 E 86110 NE 86111 E 86112 NC 86113 E	holB/dnaC rplI	* * * *	_	SP_2203	hypothetical protein M5005_Spy_1826 hypothetical protein M5005_Spy_1827 phage infection protein Tetk family transcriptional regulator 305 ribosomal protein S4 hypothetical protein M5005_Spy_1832 transposase hypothetical protein M5005_Spy_1834 replicative DNA helicase 505 ribosomal protein L9 phosphoesterase, DHH family protein
M5005_Spy_1827 3571075 NE M5005_Spy_1828c 3571076 NE M5005_Spy_1830 3571039 NE M5005_Spy_1832c 3571041 NC M5005_Spy_1832c 3571042 NE M5005_Spy_1833c 3571042 NE M5005_Spy_1836c 3571044 NE M5005_Spy_1836c 3571045 NE M5005_Spy_1837c 3571046 NE M5005_Spy_1837c 3571046 NE M5005_Spy_1837c 3571047 NE	Spy49_1783 698 Spy49_1784c 698 Spy49_1786c 698 Spy49_1786c 698 Spy49_1787c 698 Spy49_1789c 698 Spy49_1799c 698 Spy49_1791c 698 Spy49_1791c 698	86106 NE 86107 NC 86108 NE 86109 E 86111 E 86111 E 86112 NC 86113 E 86114 E	holB/dnaC	* * * * * * *	_	_	hypothetical protein M5005_Spy_1826 hypothetical protein M5005_Spy_1827 phage infection protein Tetk family transcriptional regulator 30S ribosomal protein S4 hypothetical protein M5005_Spy_1832 transposase hypothetical protein M5005_Spy_1834 replicative DNA helicase 50S ribosomal protein L9 phosphoesterase, DHH family protein tRNA uridine 5-carboxymethylaminomethyl modification protein GidA
M5005_Spy_1827 3571075 NE	Spy49_1783 695 Spy49_1786 695 Spy49_1786 695 Spy49_1786 695 Spy49_1786 695 Spy49_1786 695 Spy49_1789 695 Spy49_1790 695 Spy49_1790 695 Spy49_1790 695 Spy49_1790 695	86106 NE 86107 NC 86108 NE 86109 E 86110 NE 86111 E 86112 NC 86113 E 86114 E 86114 E	holB/dnaC rplI - gidA	* * * * * * * * * * * * * * * * * * * *	SSA_2356	SP_2203 SP_0120	hypothetical protein M5005_Spy_1826 hypothetical protein M5005_Spy_1827 phage infection protein Tett family transcriptional regulator 30S ribosomal protein S4 hypothetical protein M5005_Spy_1832 transposase hypothetical protein M5005_Spy_1834 replicative DNA helicase 50S ribosomal protein L9 phosphoesterase, DHH family protein tRNA uridine 5-carboxymethylaminomethyl modification protein GidA phosphohydrolase
M5005_Spy_1828c 3571075 NE M5005_Spy_1830 3571039 NE M5005_Spy_18310 3571041 NC M5005_Spy_1832c 3571044 NE M5005_Spy_1834c 3571044 NE M5005_Spy_1837c 3571044 NE M5005_Spy_1837c 3571044 NE M5005_Spy_1837c 3571044 NE M5005_Spy_1837c 3571046 NE M5005_Spy_1837c 3571046 NE M5005_Spy_1838c 3571047 C M5005_Spy_1839c 3571048 NE M5005_Spy_1839c 3571048 NE M5005_Spy_1839c 3571048 NE M5005_Spy_1840c 3571049 NE	Spy49_1783 695 Spy49_1784c 695 Spy49_1786c 695 Spy49_1786c 695 Spy49_1787c 695 Spy49_1789c 695 Spy49_1790c 695 Spy49_1791c 695 Spy49_1791c 695 Spy49_1793c 695 Spy49_1793c 695 Spy49_1793c 695	86106 NE 86107 NC 86108 NE 86109 E 86111 E 86111 E 86112 NC 86113 E 86114 E 86114 E 86115 NE 86115 E	holB/dnaC rplI - gidA - mnmA	* * * * * * * * * *	_	SP_2203	hypothetical protein M5005_Spy_1826 hypothetical protein M5005_Spy_1827 phage infection protein Tetk family transcriptional regulator 30S ribosomal protein S4 hypothetical protein M5005_Spy_1832 transposase hypothetical protein M5005_Spy_1834 replicative DNA helicase 50S ribosomal protein L9 phosphoesterase, DHH family protein tRNA uridine 5-carboxymethylaminomethyl modification protein GidA phosphohydrolase tRNA-specific 2-thiouridylase MnmA
M5005_Spy_18282 3571075 NE	Spy49_1783 695 Spy49_1786 695 Spy49_1785 695 Spy49_1786 695 Spy49_1786 695 Spy49_1789 695 Spy49_1799 695 Spy49_1791 695 Spy49_1792 695 Spy49_1793 695 Spy49_1793 695 Spy49_1794 695 Spy49_1794 695	86106 NE 86107 NC 86108 NE 86109 E 86111 E 86111 E 86112 NC 86113 E 86114 E 86115 NE 86116 NE 86117 NE	holB/dnaC rplI - gidA - mnmA sdhB	* * * * * * * * * * * * * * * * * * * *	SSA_2356	SP_2203 SP_0120	hypothetical protein M5005_Spy_1826 hypothetical protein M5005_Spy_1827 phage infection protein TetR family transcriptional regulator 30S ribosomal protein S4 hypothetical protein M5005_Spy_1832 transposase hypothetical protein M5005_Spy_1834 replicative DNA helicase 50S ribosomal protein L9 phosphoesterase, DHH family protein tRNA uridine 5-carboxymethylaminomethyl modification protein GidA phosphohydrolase tRNA-specific 2-thiouridylase MnmA L-serine dehydratase
M5005_Spy_1827 3571075 NE	Spy49_1783 695 Spy49_1786 695 Spy49_1786 695 Spy49_1786 695 Spy49_1786 695 Spy49_1786 695 Spy49_1790 695 Spy49_1790 695 Spy49_1790 695 Spy49_1792 695 Spy49_1792 695 Spy49_1793 695 Spy49_1795 695 Spy49_1795 695	86106 NE 86107 NC 86109 E 86110 NE 86111 E 86112 NC 86113 E 86114 E 86115 NE 86116 E 86115 NE 86116 NE	holB/dnaC rplI - gidA - mnmA	* * * * * * * * * * * * * * * * * * * *	SSA_2356	SP_2203 SP_0120	hypothetical protein M5005_Spy_1826 hypothetical protein M5005_Spy_1827 phage infection protein Tetk family transcriptional regulator 30S ribosomal protein S4 hypothetical protein M5005_Spy_1832 transposase hypothetical protein M5005_Spy_1834 replicative DNA helicase 50S ribosomal protein L9 phosphoesterase, DHH family protein tRNA uridine 5-carboxymethylaminomethyl modification protein GidA phosphohydrolase tRNA-specific 2-thiouridylase MnmA L-serine dehydratase L-serine dehydratase
M5005_Spy_18282 3571075 NE M5005_Spy_1830 3571039 NE M5005_Spy_18310 3571041 NC M5005_Spy_1832c 3571041 NC M5005_Spy_1832c 3571042 NE M5005_Spy_18362 3571044 NE M5005_Spy_1837c 3571044 NE M5005_Spy_1837c 3571046 NE M5005_Spy_1837c 3571047 NE M5005_Spy_1838c 3571047 NE M5005_Spy_1838c 3571047 NE M5005_Spy_1840c 3571049 NE M5005_Spy_1840c 3571049 NE M5005_Spy_1840c 3571049 NE M5005_Spy_1840c 3571049 NE M5005_Spy_1840c 3571050 NE M5005_Spy_1842 3571050 NE M5005_Spy_1842 3571051 NE	Spy49_1783 695 Spy49_1786 695 Spy49_1786 695 Spy49_1786 695 Spy49_1786 695 Spy49_1786 695 Spy49_1790 695 Spy49_1791 695 Spy49_1791 695 Spy49_1793 695 Spy49_1794 695 Spy49_1794 695 Spy49_1794 695 Spy49_1796 695 Spy49_1796 695	86105 NE 86107 NC 86109 E 86110 NE 86111 E 86111 E 86112 NC 86113 E 86114 E 86115 NE 86115 NE 86116 NE 86117 NE	holB/dnaC rplI - gidA - mnmA sdhB sdhA	* * * * * * * * * *	SSA_2356	SP_2203 SP_0120	hypothetical protein M5005_Spy_1826 hypothetical protein M5005_Spy_1827 phage infection protein Tetk family transcriptional regulator 30S ribosomal protein S4 hypothetical protein M5005_Spy_1832 transposase hypothetical protein M5005_Spy_1834 replicative DNA helicase 50S ribosomal protein L9 phosphoesterase, DHH family protein tRNA uridine 5-carboxymethylaminomethyl modification protein GidA phosphohydrolase tRNA-specific 2-thiouridylase MnmA L-serine dehydratase L-serine dehydratase transglycosylase
M5005_Spy_1827 3571075 NE	Spy49_1783 695 Spy49_1786 695 Spy49_1786 695 Spy49_1786 695 Spy49_1786 695 Spy49_1786 695 Spy49_1789 695 Spy49_1791 695 Spy49_1792 695 Spy49_1793 695 Spy49_1794 695 Spy49_1796 695 Spy49_1796 695 Spy49_1796 695	86106 NE 86107 NC 86109 E 86110 NE 86111 E 86111 E 86112 NC 86113 E 86114 E 86115 NE 86115 NE 86116 NE 86118 NE 86118 NE 86119 NE	holB/dnaC rplI - gidA - mnmA sdhB sdhA - cbiQ	* * * * * * * * * * * * * * * * * * * *	SSA_2356	SP_2203 SP_0120	hypothetical protein M5005_Spy_1826 hypothetical protein M5005_Spy_1827 phage infection protein Tett family transcriptional regulator 30S ribosomal protein S4 hypothetical protein M5005_Spy_1832 transposase hypothetical protein M5005_Spy_1834 replicative DNA helicase 50S ribosomal protein L9 phosphoesterase, DHH family protein tRNA uridine 5-carboxymethylaminomethyl modification protein GidA phosphohydrolase tRNA-specific 2-thiouridylase MnmA L-serine dehydratase L-serine dehydratase transglycosylase cobalt transporter
M5005_Spy_18282 3571075 NE M5005_Spy_1830 3571039 NE M5005_Spy_18310 3571041 NC M5005_Spy_1832c 3571041 NC M5005_Spy_1832c 3571042 NE M5005_Spy_18362 3571044 NE M5005_Spy_1837c 3571044 NE M5005_Spy_1837c 3571046 NE M5005_Spy_1837c 3571047 NE M5005_Spy_1838c 3571047 NE M5005_Spy_1838c 3571047 NE M5005_Spy_1840c 3571049 NE M5005_Spy_1840c 3571049 NE M5005_Spy_1840c 3571049 NE M5005_Spy_1840c 3571049 NE M5005_Spy_1840c 3571050 NE M5005_Spy_1842 3571050 NE M5005_Spy_1842 3571051 NE	Spy49_1783 695 Spy49_1785 695 Spy49_1785 695 Spy49_1785 695 Spy49_1785 695 Spy49_1789 695 Spy49_1790 695 Spy49_1790 695 Spy49_1790 695 Spy49_1794 695 Spy49_1794 695 Spy49_1795 695 Spy49_1795 695 Spy49_1796 695 Spy49_1796 695 Spy49_1796 695 Spy49_1796 695 Spy49_1796 695 Spy49_1797 695	86105 NE 86107 NC 86109 E 86110 NE 86111 E 86111 E 86112 NC 86113 E 86114 E 86115 NE 86115 NE 86116 NE 86117 NE	holB/dnaC rplI - gidA - mnmA sdhB sdhA	* * * * * * * * * * * * * * * * * * * *	SSA_2356	SP_2203 SP_0120	hypothetical protein M5005_Spy_1826 hypothetical protein M5005_Spy_1827 phage infection protein Tetk family transcriptional regulator 30S ribosomal protein S4 hypothetical protein M5005_Spy_1832 transposase hypothetical protein M5005_Spy_1834 replicative DNA helicase 50S ribosomal protein L9 phosphoesterase, DHH family protein tRNA uridine 5-carboxymethylaminomethyl modification protein GidA phosphohydrolase tRNA-specific 2-thiouridylase MnmA L-serine dehydratase L-serine dehydratase transglycosylase
M5005_Spy_1827 3571075 NE	Spy49_1783 695 Spy49_1786 695 Spy49_1786 695 Spy49_1787 695 Spy49_17886 695 Spy49_17886 695 Spy49_17986 695 Spy49_1790 695 Spy49_1790 695 Spy49_1793 695 Spy49_1794 695 Spy49_1795 695 Spy49_1796 695	86106 NE 86107 NC 86109 E 86110 NE 86111 E 86111 E 86112 NC 86113 E 86114 E 86115 NE 86115 NE 86116 NE 86118 NE 86118 NE 86119 NE	holB/dnaC rplI - gidA - mnmA sdhB sdhA - cbiQ	* * * * * * * * * * * * * * * * * * * *	SSA_2356	SP_2203 SP_0120	hypothetical protein M5005_Spy_1826 hypothetical protein M5005_Spy_1827 phage infection protein Tett family transcriptional regulator 30S ribosomal protein S4 hypothetical protein M5005_Spy_1832 transposase hypothetical protein M5005_Spy_1834 replicative DNA helicase 50S ribosomal protein L9 phosphoesterase, DHH family protein tRNA uridine 5-carboxymethylaminomethyl modification protein GidA phosphohydrolase tRNA-specific 2-thiouridylase MnmA L-serine dehydratase L-serine dehydratase transglycosylase cobalt transporter
M5005_Spy_1827 3571075 NE M5005_Spy_18328 3571039 NE M5005_Spy_18313 3571039 NE M5005_Spy_18326 3571041 NE M5005_Spy_18326 3571042 NE M5005_Spy_18336 3571042 NE M5005_Spy_18356 3571044 NE M5005_Spy_18356 3571045 NE M5005_Spy_1836 3571046 NE M5005_Spy_18376 3571046 NE M5005_Spy_18406 3571046 NE M5005_Spy_18406 3571047 C M5005_Spy_18406 3571049 NE M5005_Spy_18406 3571049 NE M5005_Spy_18406 3571051 NE M5005_Spy_1841 3571051 NE M5005_Spy_1842 3571051 NE M5005_Spy_18436 3571052 NE M5005_Spy_18446 3571053 C M5005_Spy_18446 3571054 E M5005_Spy_18446 3571054 E	Spy49_1783 695 Spy49_1786 695 Spy49_1786 695 Spy49_1787 695 Spy49_17886 695 Spy49_17886 695 Spy49_17896 695 Spy49_17916 695 Spy49_1792 695 Spy49_1796 695 Spy49_17996 695 Spy49_17996 695 Spy49_17996 695 Spy49_17996 695 Spy49_17996 695 Spy49_17996 695	86106 NE 86107 NC 86108 NE 86109 E 86110 NE 86111 E 86112 NC 86114 E 86115 NE 86116 NE 86117 NE 86118 NE 86110 NE	holB/dnaC rplI gidA - mnmA sdhB sdhA - cbiQ cbiO cbiO	* * * * * * * * * * * * * * * * * * * *	SSA_2356 SSA_2360	SP_2203 SP_0120	hypothetical protein M500S_Spy_1826 hypothetical protein M500S_Spy_1827 phage infection protein Tetk family transcriptional regulator 30S ribosomal protein S4 hypothetical protein M500S_Spy_1832 transposase hypothetical protein M500S_Spy_1834 replicative DNA helicase 50S ribosomal protein L9 phosphoesterase, DHH family protein tRNA uridine 5-carboxymethylaminomethyl modification protein GidA phosphohydrolase tRNA-specific 2-thiouridylase MnmA L-serine dehydratase L-serine dehydratase transglycosylase cobalt transporter cobalt ABC transporter ATP-binding protein cobalt ABC transporter ATP-binding protein
M5005_Spy_1827 3571075 NE	Spy49_1783 695 Spy49_1785 695 Spy49_1786 695 Spy49_1787 695 Spy49_17886 695 Spy49_17896 695 Spy49_17986 695 Spy49_1791 695 Spy49_1792 695 Spy49_1793 695 Spy49_1796 695 Spy49_1796 695 Spy49_1797 695 Spy49_17986 695 Spy49_17986 695 Spy49_17986 695 Spy49_17996 695	86106 NE 86107 NC 86109 E 86110 NE 86110 E 86111 E 86111 E 86112 NC 86113 E 86114 E 86115 NE 86115 NE 86118 NE 86118 NE 86119 NE 86120 E 86121 E	holB/dnaC rplI gidA - mnmA sdhB sdhA - cbiQ cbiO	* * * * * * * * * * * * * * * * * * * *	SSA_2356	SP_2203 SP_0120	hypothetical protein M5005_Spy_1826 hypothetical protein M5005_Spy_1827 phage infection protein Tetk family transcriptional regulator 30S ribosomal protein S4 hypothetical protein M5005_Spy_1832 transposase hypothetical protein M5005_Spy_1832 transposase hypothetical protein M5005_Spy_1834 replicative DNA helicase 50S ribosomal protein L9 phosphoesterase, DHH family protein tRNA uridine 5-carboxymethylaminomethyl modification protein GidA phosphohydrolase tRNA-specific 2-thiouridylase MnmA L-serine dehydratase L-serine dehydratase transplycosylase cobalt transporter cobalt ABC transporter ATP-binding protein cobalt ABC transporter ATP-binding protein CDP-diacylglycerol-glycerol-3-phosphate 3-phosphatidyltransferase
M5005_Spy_1828c 3571075 NE M5005_Spy_1832c 3571041 NE M5005_Spy_1832c 3571043 NE M5005_Spy_1832c 3571044 NE M5005_Spy_1832c 3571044 NE M5005_Spy_1837c 3571044 NE M5005_Spy_1837c 3571044 NE M5005_Spy_1837c 3571047 NE M5005_Spy_1837c 3571047 NE M5005_Spy_1837c 3571047 NE M5005_Spy_1840c 3571047 NE M5005_Spy_1840c 3571047 NE M5005_Spy_1840c 3571049 NE M5005_Spy_1840c 3571050 NE M5005_Spy_1844c 3571050 NE M5005_Spy_1844c 3571051 NE M5005_Spy_1845c 3571052 NE M5005_Spy_1845c 3571055 NE M5005_Spy_18486c 3571055 NC M5005_Spy_1847c 3571057 NC M5005_Spy_1847c 3571	Spy49_1783 695 Spy49_1786 695 Spy49_1786 695 Spy49_1787 695 Spy49_17886 695 Spy49_17896 695 Spy49_17916 695 Spy49_17916 995 Spy49_1792 695 Spy49_1793 695 Spy49_1794 695 Spy49_1795 695 Spy49_1796 695 Spy49_17986 695 Spy49_17986 695 Spy49_18016 695 Spy49_18016 695 Spy49_18016 695	86106 NE 86107 NC 86108 NE 86109 E 86110 NE 86111 E 86112 NC 86114 E 86114 E 86115 NE 86114 NE 86117 NE 86110 NE 86111 E 86112 NE 86112 E 86112 E 86112 E	holB/dnaC rplI gidA - mnmA sdhB sdhA - cbiQ cbiO cbiO	* * * * * * * * * * * * * * * * * * * *	SSA_2356 SSA_2360	SP_2203 SP_0120	hypothetical protein M5005_Spy_1826 hypothetical protein M5005_Spy_1827 phage infection protein Tetk family transcriptional regulator 30S ribosomal protein S4 hypothetical protein M5005_Spy_1832 transposase hypothetical protein M5005_Spy_1834 replicative DNA helicase 50S ribosomal protein L9 phosphoesterase, DHH family protein tRNA uridine 5-carboxymethylaminomethyl modification protein GidA phosphohydrolase tRNA-specific 2-thiouridylase MnmA L-serine dehydratase L-serine dehydratase transglycosylase cobalt transporter cobalt ABC transporter ATP-binding protein cobalt ABC transporter ATP-binding protein cobalt ABC transporter ATP-binding protein CDP-diacylglycerol-glycerol-3-phosphate 3-phosphatidyltransferase hypothetical protein M5005_Spy_1848
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M5005 Spy 1828 M5005 Spy 1830 M5005 Spy 1831 M5005 Spy 1832 M5005 Spy 1832 M5005 Spy 1832 M5005 Spy 1832 M5005 Spy 1836 M5005 Spy 1840 M5005 Spy 1850 M5005 Spy 1860 M500	Spy49_1783 695 Spy49_1786 695 Spy49_1786 695 Spy49_1787 695 Spy49_1787 695 Spy49_17886 695 Spy49_17886 695 Spy49_1790 695 Spy49_1790 695 Spy49_1790 695 Spy49_1791 695 Spy49_1793 695 Spy49_1793 695 Spy49_1796 695 Spy49_1796 695 Spy49_1796 695 Spy49_1796 695 Spy49_1798 695 Spy49_1798 695 Spy49_1798 695 Spy49_1800 695 Spy49_1810 695 Spy49_1810 695 Spy49_1810 695 Spy49_1810 695 Spy49_1810 695 Spy49_18110 695 S	86106 NE 86107 NC 86108 NE 86109 E 86110 NE 86111 E 86111 NE 86111 E 86112 NC 86113 NE 86114 E 86115 NE 86115 NE 86116 E 86115 NE 86116 E 86117 NE 86117 NE 86118 NE 86119 NE 86110 NE 86111 NE	holB/dnaC rplI rplI gldA - mnmA sdhB sdhA - cbiQ cbiO cbiO pgsA hasB hasC recF - guaB trsA htrA		SSA_2356 SSA_2360 SSA_2368	SP_2203 SP_0120 SP_0118	hypothetical protein M5005_Spy_1826 hypothetical protein M5005_Spy_1827 phage infection protein Tetk family transcriptional regulator 30S ribosomal protein S4 hypothetical protein M5005_Spy_1832 transposase hypothetical protein M5005_Spy_1832 transposase hypothetical protein M5005_Spy_1834 replicative DNA helicase 50S ribosomal protein L9 phosphoesterase, DHH family protein tRNA uridine 5-carboxymethylaminomethyl modification protein GidA phosphohydrolase tRNA-specific 2-thiouridylase MnmA L-serine dehydratase t-serine dehydratase t-serine dehydratase transplycosylase cobalt transporter cobalt ABC transporter ATP-binding protein cobalt ABC transporter ATP-binding protein cDP-diacylglycerolglycerol-3-phosphate 3-phosphatidyltransferase hypothetical protein M5005_Spy_1848 zinc protease zinc protease hyaluronan synthase UDP-glucose 6-dehydrogenase UTP-glucose 1-phosphate uridylyltransferase hypothetical protein M5005_Spy_1854 recombination protein F glucose uptake protein inosine S'-monophosphate dehydrogenase tryptophanyl-tRNA synthetase hypothetical protein M5005_Spy_1859 hypothetical protein M5005_Spy_1860 ABC transporter ATP-binding protein

Table S8. Bacterial strains and plasmids.

Strains and plasmids	Description	Reference our source
E. coli strains		
DH5α	hsdR17 recA1 gyrA endA1 relA1	Hanahan and Meselson, 1983
C43[DE3]	F^- ompT gal dcm hsd $S_B(r_B^- m_B^-)$ (DE3)	Miroux and Walker, 1996
S. pyogenes strains		
5448	M1T1	Chatellier et al., 2000
NZ131	M49	Simon and Ferretti, 1991
5448.vicR _{ind}	5448, theophylline-inducible expression of <i>vicR</i> ; Sp ^R	This study
5448.murE _{ind}	5448, theophylline-inducible expression of <i>murE</i> Sp ^R	This study
NZ131.vicR _{ind}	NZ131, theophylline-inducible expression of vicR; Sp ^R	This study
NZ131.murE _{ind}	NZ131, theophylline-inducible expression of <i>murE</i> ; Sp ^R	This study
Plasmids		
pOSKAR	Oskar-delivery plasmid; Sp ^R , Km ^R	Le Breton et al., 2013
pKRMIT	<i>Krmit</i> -delivery plasmid; Sp ^R , Km ^R	This study
pCRS	Temperature-sensitive conditional vector; Sp ^R	Le Breton et al. 2013
pSinS	Suicide plasmid for stable insertional inactivation; Sp ^R	This study
pCRK	Temperature-sensitive conditional vector; Km ^R	Le Breton et al. 2013
pHlpK	Temperature-sensitive conditional helper vector; Km ^R	This study
pEU7742-E	Plasmid containing the fusion of the Psag promoter with the synthetic ribosiwtch E	Topp et al., 2010
pSinMurE	Suicid plasmid for mutagenesis and conditional expression control of murE	This study
pSinVicR	Suicid plasmid for mutagenesis and conditional expression control of vicR	This study

Table S9. Primers used in this study.

Name and main purpose	Sequence (5'3')	Restriction site(s)/Barcode	Target	Role
Construction of the Krmit transpo	oson			
oKrmit1	ccc <u>CTGCAG</u> TAACAG <u>GTTGGA</u> TGATAAGTCCCCGGTCTG	Pstl/Mmel	pOSKAR	Mmel modification of Oskar to create Krmit
Production of Krmit insertion tag	s			
Adapterbarcode501A	TTCCCTACACGACGCTCTTCCGATCT <u>TATAGCCT</u> NN	Adapter501		Mmel Tnseq adapter
Adapterbarcode501B	<u>AGGCTATA</u> AGATCGGAAGAGCGTCGTGTAGGGAAAGAG	Adapter501		Mmel Tnseq adapter
Adapterbarcode502A	TTCCCTACACGACGCTCTTCCGATCT <u>ATAGAGGC</u> NN	Adapter502		Mmel Tnseq adapter
Adapterbarcode502B	<u>GCCTCTAT</u> AGATCGGAAGAGCGTCGTGTAGGGAAAGAG	Adapter502		Mmel Tnseq adapter
Adapterbarcode503A	TTCCCTACACGACGCTCTTCCGATCT <u>CCTATCCT</u> NN	Adapter503		Mmel Tnseq adapter
Adapterbarcode503B	AGGATAGGAGATCGGAAGAGCGTCGTGTAGGGAAAGAG	Adapter503		Mmel Tnseq adapter
Adapterbarcode504A	TTCCCTACACGACGCTCTTCCGATCT <u>GGCTCTGA</u> NN	Adapter504		Mmel Tnseq adapter
Adapterbarcode504B	TCAGAGCCAGATCGGAAGAGCGTCGTGTAGGGAAAGAG	Adapter504		Mmel Tnseq adapter
Adapterbarcode505A	TTCCCTACACGACGCTCTTCCGATCT <u>AGGCGAAG</u> NN	Adapter505		Mmel Tnseq adapter
Adapterbarcode505B	<u>CTTCGCCT</u> AGATCGGAAGAGCGTCGTGTAGGGAAAGAG	Adapter505		Mmel Tnseq adapter
Adapterbarcode506A	TTCCCTACACGACGCTCTTCCGATCT <u>TAATCTTA</u> NN	Adapter506		Mmel Tnseq adapter
Adapterbarcode506B	TAAGATTAAGATCGGAAGAGCGTCGTGTAGGGAAAGAG	Adapter506		Mmel Tnseq adapter
Adapterbarcode507A	TTCCCTACACGACGCTCTTCCGATCT <u>CAGGACGT</u> NN	Adapter507		Mmel Tnseq adapter
Adapterbarcode507B	<u>ACGTCCTG</u> AGATCGGAAGAGCGTCGTGTAGGGAAAGAG	Adapter507		Mmel Tnseq adapter
Adapterbarcode508A	TTCCCTACACGACGCTCTTCCGATCT <u>GTACTGAC</u> NN	Adapter508		Mmel Tnseq adapter
Adapterbarcode508B	<u>GTCAGTAC</u> AGATCGGAAGAGCGTCGTGTAGGGAAAGAG	Adapter508		Mmel Tnseq adapter
oKrmit-Tnseq2	CAAGCAGAAGACGCCATACGAAGCGCCTACGAGGAATTTGTATCG		Krmit	PCR of Krmit insertion tags
oAdapterPCR	AATGATACGGCGACCACCGAGATCACACTCTTTCCCTACACGACGCTCTT	CC	Tnseq adapter	PCR of <i>Krmit</i> insertion tags
Creation of the pSinS/pHlpK syste				
RepAminus1	ccc <u>AGATCT</u> AATCATTAGGAATTGAGTCAGG	<i>Bgl</i> II	pCRS	Deletion of the <i>repA</i> ts gene to create pSinS
RepAminus2	ccc <u>AGATCT</u> GGTTCTTGATGCTGAAACGG	<i>Bgl</i> II	pCRS	Deletion of the <i>repA</i> ts gene to create pSinS
KmR1NotI	ccc <u>GCGGCCGC</u> GATAAACCCAGCGAACCATTTGAGGTG	Notl	pCRK	Deletion of the ColE1 <i>oriR</i> to create pHlpK
OTS2	CCCGCGGCCGCATTAATCGCAACATCAAACCAAA		pCRK	Deletion of the ColE1 <i>oriR</i> to create pHlpK
Theophilline-inducible murE and	vicR mutants			
Psag-RBSWE1	ccc <u>GGATCC</u> ACGGTAAGACAGAAATCGGTC	BamHI	pEU7742-E	Amplification of Psag-riboswitchE
Psag-RBSWE2	CTTGTTGTTACCTCCTTAGCAGGG		pEU7742-E	Amplification of Psag-riboswitchE
oRBSWE-V1	ACCAGCATCGTCTTGATGCC			
oMurE-1	CCCTGCTAAGGAGGTAACAACAAGATGATAACCATTGAACAATTATTAG		murE gene	Amplification of murE fragment for PCR-SOEing with Psag-riboswitchE
oMurE-2	ccc <u>GGATCC</u> ATTTAGGAAAACCCCAACATCG	BamHI	murE gene	Amplification of murE fragment for PCR-SOEing with Psag-riboswitchE
oMurE-3	ATATCAGCTAGGCTAGCACC		murE gene	Verification of correct PCR-SOEing
oVicR-1	CCCTGCTAAGGAGGTAACAACAAGATGAAAAAAAATACTTATTGTGGATG		vicR gene	Amplification of vicR fragment for PCR-SOEing with Psag-riboswitchE
oVicR-2	ccc <u>GGATCC</u> CGCCAAAATAATCATATCCCC	BamHI	vicR gene	Amplification of vicR fragment for PCR-SOEing with Psag-riboswitchE
oVicR-3	CATAAGATTTCATGTAGTACCC		vicR gene	Verification of correct PCR-SOEing

Table S10. Summary of the 20 publicly available GAS genomes.

GAS strain	Serotype	Size	Link to genome sequence
emm Pattern A-C (Throat tropism)		
MGAS5005	M1T1	1,838,554	http://www.ncbi.nlm.nih.gov/nuccore/CP000017.2
SF370	M1	1,852,441	http://www.ncbi.nlm.nih.gov/nuccore/NC_002737.1
A20	M1	1,837,281	http://www.ncbi.nlm.nih.gov/nuccore/CP003901.1
M1-476	M1	1,831,128	http://www.ncbi.nlm.nih.gov/nuccore/AP012491.2
MGAS315	M3	1,900,521	http://www.ncbi.nlm.nih.gov/nuccore/NC_004070.1
SSI-1	M3	1,894,275	http://www.ncbi.nlm.nih.gov/nuccore/NC_004606.1
Manfredo	M5	1,841,271	http://www.ncbi.nlm.nih.gov/nuccore/AM295007.1
MGAS10394	M6	1,899,877	http://www.ncbi.nlm.nih.gov/nuccore/CP000003.1
MGAS8232	M18	1,895,017	http://www.ncbi.nlm.nih.gov/nuccore/AE009949.1
MGAS9429	M12	1,836,467	http://www.ncbi.nlm.nih.gov/nuccore/CP000259.1
MGAS2096	M12	1,860,355	http://www.ncbi.nlm.nih.gov/nuccore/94991497
HKU16	M12	1,908,100	http://www.ncbi.nlm.nih.gov/nuccore/AFRY01000001.1
HSC5	M14	1,818,351	http://www.ncbi.nlm.nih.gov/nuccore/NC_021807.1
emm pattern D (skin tropism)			
Alab49	M53	1,827,308	http://www.ncbi.nlm.nih.gov/nuccore/CP003068.1
emm pattern E (generalists)			
MGAS10270	M2	1,928,252	http://www.ncbi.nlm.nih.gov/nuccore/NC_008022.1
MGAS10750	M4	1,937,111	http://www.ncbi.nlm.nih.gov/nuccore/CP000262.1
MGAS6180	M28	1,897,573	http://www.ncbi.nlm.nih.gov/nuccore/CP000056.1
NZ131	M49	1,815,785	http://www.ncbi.nlm.nih.gov/nuccore/CP000829.1
MGAS1882	M59	1,781,029	http://www.ncbi.nlm.nih.gov/nuccore/NC_017053.1
MGAS15252	M59	1,750,832	http://www.ncbi.nlm.nih.gov/nuccore/CP003116.1