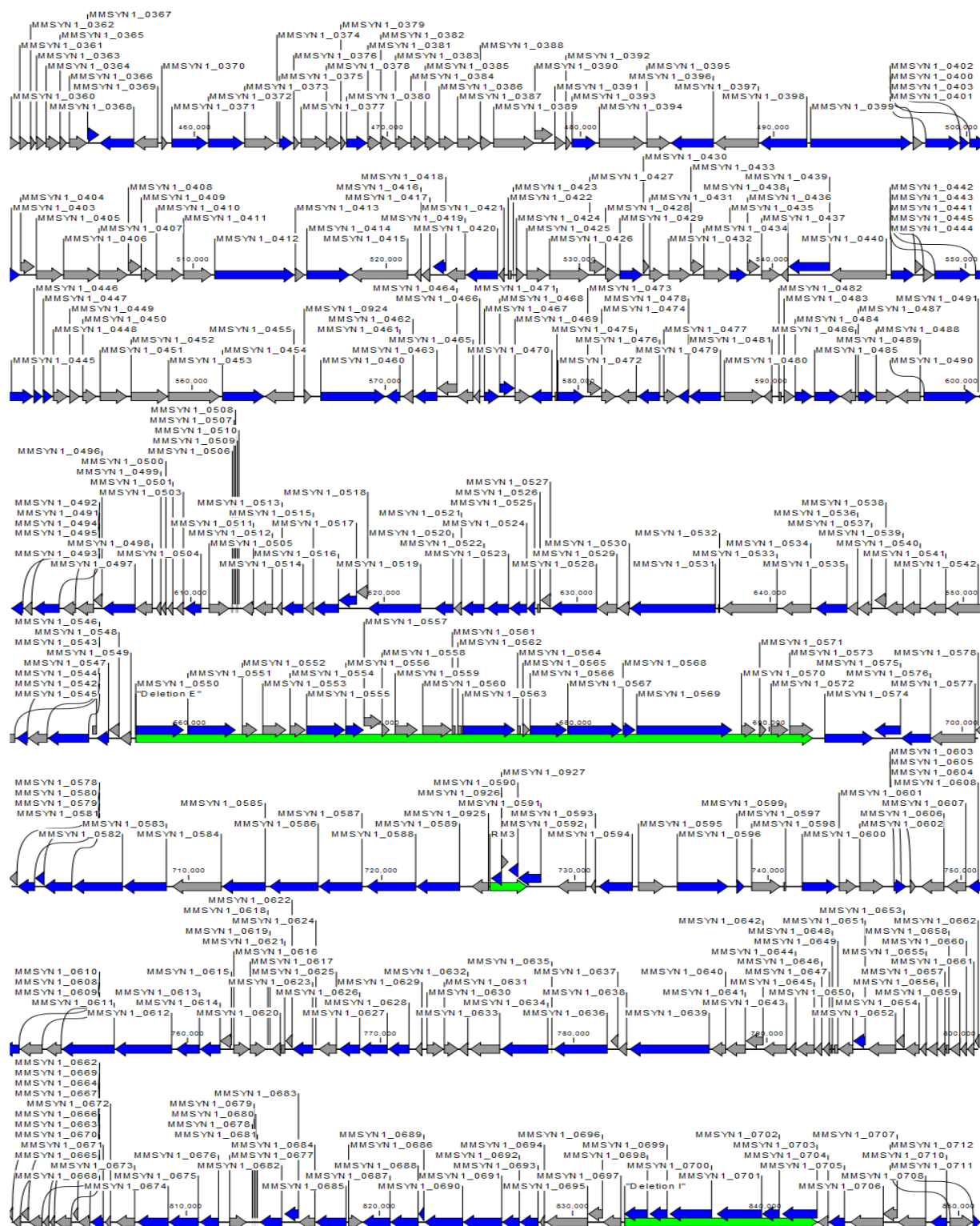


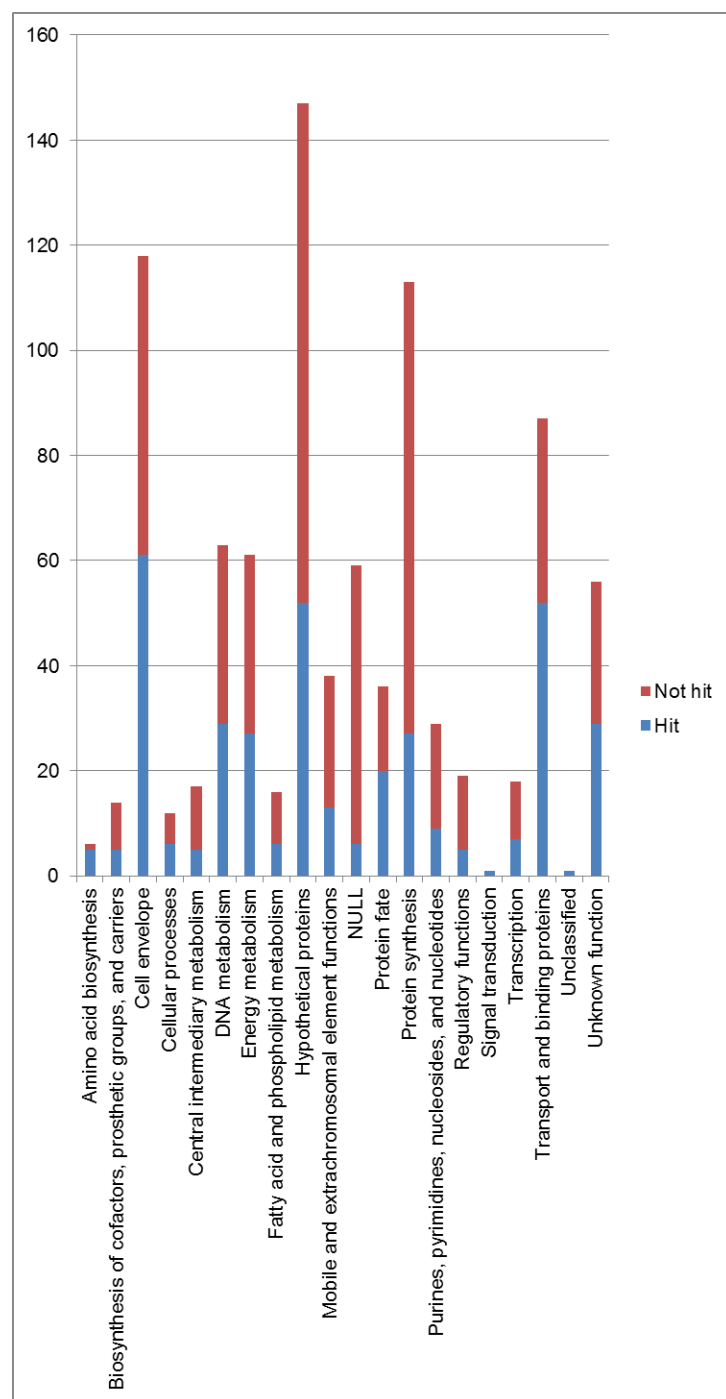
Supplemental Figure S1. The map of the JCVI-syn1.0 genome showing candidate non-essential genes uncovered in the current study (blue) and regions deleted in the seven- and eight-deletion strains (green). The deleted regions include restriction enzyme genes deleted in the JCVI-syn1.0 Δ 1-6 genome.



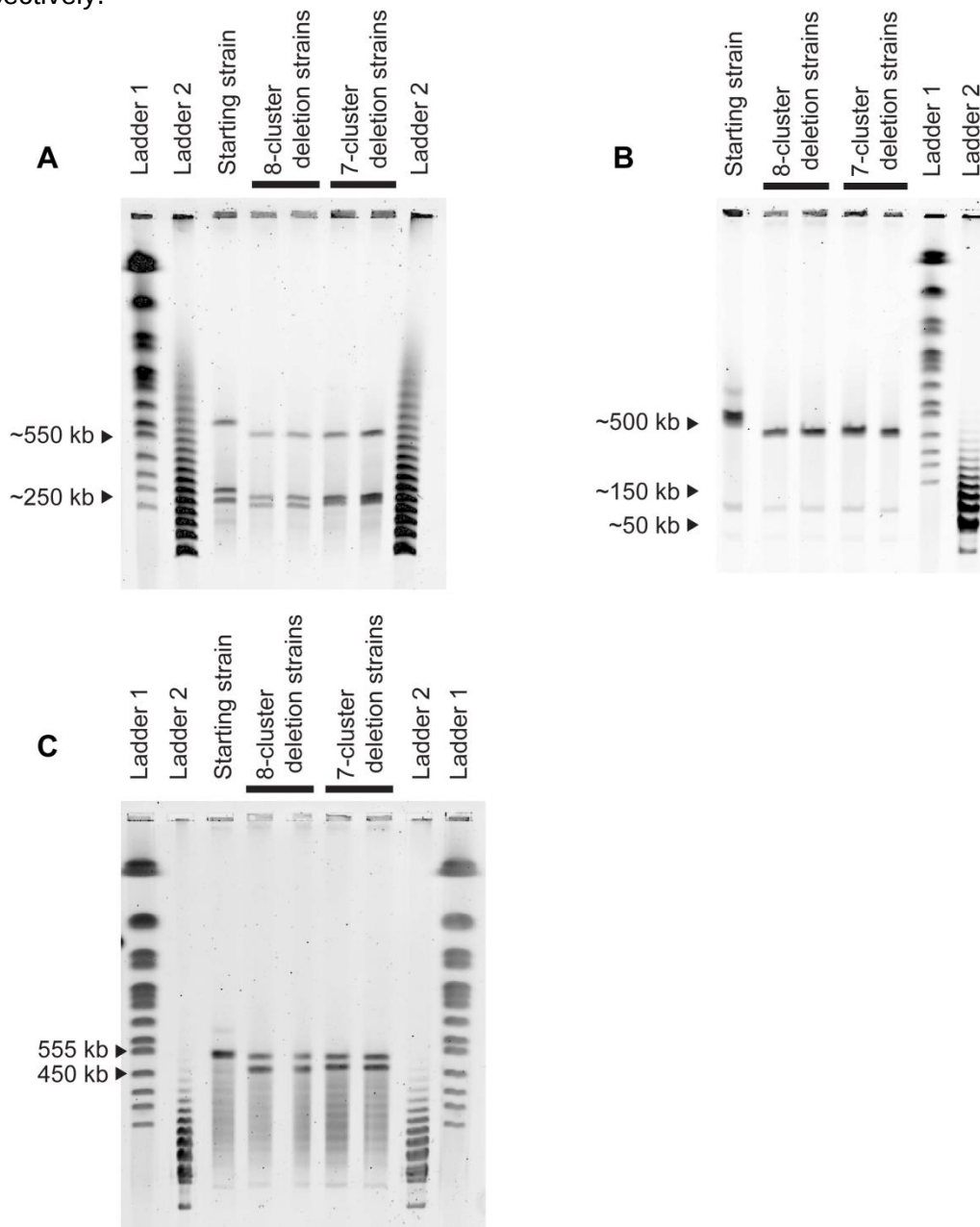




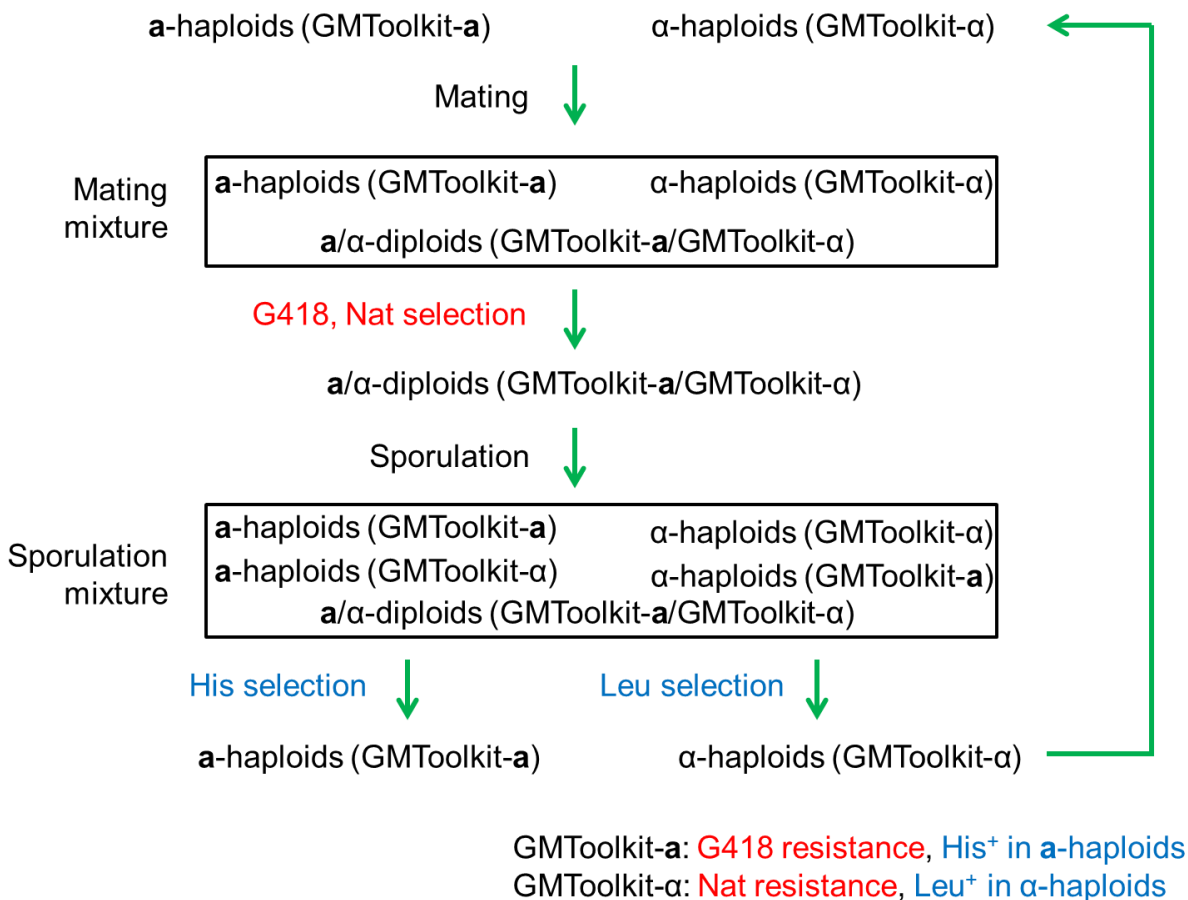
Supplemental Figure S2. Distribution of transposon-hit genes by functional category. The numbers of genes hit by transposons five times or more (“hit”) are shown in blue and those hit less than five times (“not hit”) are shown in red. Only disruptive transposon insertions (see Methods) are included in this analysis. Functional categories are based on a published study (Gibson et al., 2010). The category NULL includes 41 RNA genes and 19 non-conserved hypothetical protein genes. Notably, none of the RNA genes was hit five or more times by transposons (Supplemental Table S2).



Supplemental Figure S3. Pulsed-field gel electrophoresis analysis of reduced genomes. **(A)** XhoI digest. The expected bands were 586 kb, 259 kb, and 217 kb for the starting strain (syn1.0 Δ 1–6 strain), 533 kb, 231 kb, and 198 kb for the eight-cluster deletion strains, and 533 kb, 231 kb, and 210 kb for the seven-cluster deletion strains. The actual result was consistent with the expected result. **(B)** NaeI digest. The expected bands that would be visible in this analysis were 520 kb, 450 kb, 73 kb, and 18 kb for the starting strain, 446 kb, 424 kb, 73 kb, and 18 kb for the eight-cluster deletion strains, and 458 kb, 424 kb, 73 kb, and 18 kb for the seven-cluster deletion strains. The actual result was consistent with the expected result. **(C)** SacII digest. The expected bands were 521 kb, 522 kb, and 20 kb for the starting strain, 447 kb, 496 kb, and 20 kb for the eight-cluster deletion strains, and 459 kb, 496 kb, 20 kb for the seven-cluster deletion strains. The actual result was consistent with the expected result. Ladder 1 and ladder 2 were Yeast Chromosome PFG Marker and Lambda Ladder PFG Marker (New England Biolabs), respectively.

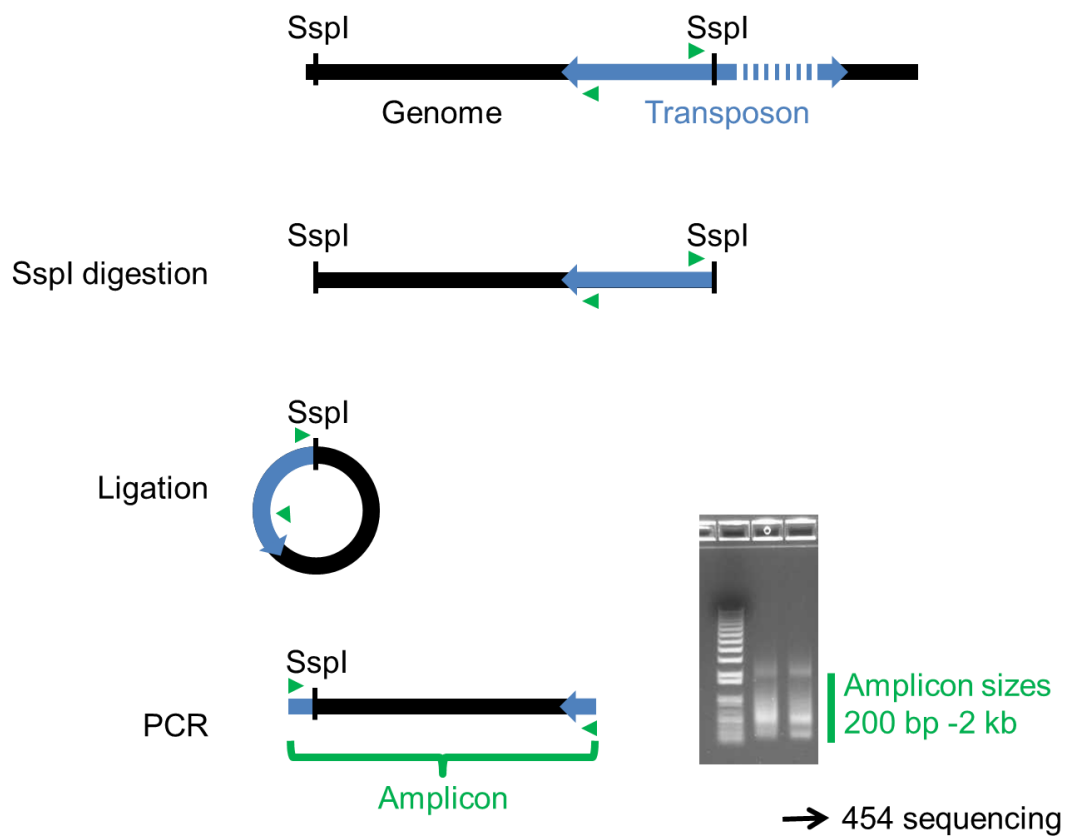


Supplemental Figure S4. The sexual cycling scheme. Haploid- and diploid-selection markers are built into the GMToolkit tools that are integrated into the identical locus (*can1Δ*) in yeast. GMToolkit-a contains the *STE2pr::Sp-his5* marker that is turned on only in mating-type-a haploids and confers the cells the ability to grow in the absence of supplemented histidine (His). It also has a constitutively active G418 resistance marker. Similarly, GMToolkit-α contains the *STE3pr::LEU2* marker that confers the ability to grow in the absence of leucine (Leu) only to α-haploids, as well as a constitutively expressed nourseothricin (Nat) resistance marker. The efficiency of yeast mating is not 100%, but selecting for cells that are resistant to both G418 and Nat enriches for diploids carrying both GMToolkits. Sporulation of diploids results in the indicated mixture of cells, and selection for cells capable of growing in the absence of added histidine and leucine enriches for a-haploids and α-haploids, respectively. These selected haploids are capable of undergoing the sexual cycling process again. The linear mycoplasma genome is marked with a *MET15* marker. During the His or Leu selection, selection for cells also carrying the genome is achieved by using a medium not containing methionine. In an attempt to reduce the copy number of the genome from two or more to one, methionine is added to the pre-mating cultures, to 1% of the standard non-selective concentration. This maximizes the chance of crossover between the genomes brought in by two parental cells, as opposed to crossover between identical genomes brought in by one of the cells. The strains were analyzed using colony PCR twice during the cycle, before mating and after diploid selection, to determine the genotypes of the genomes and whether genomes from two haploid parents are present in the diploids, respectively.

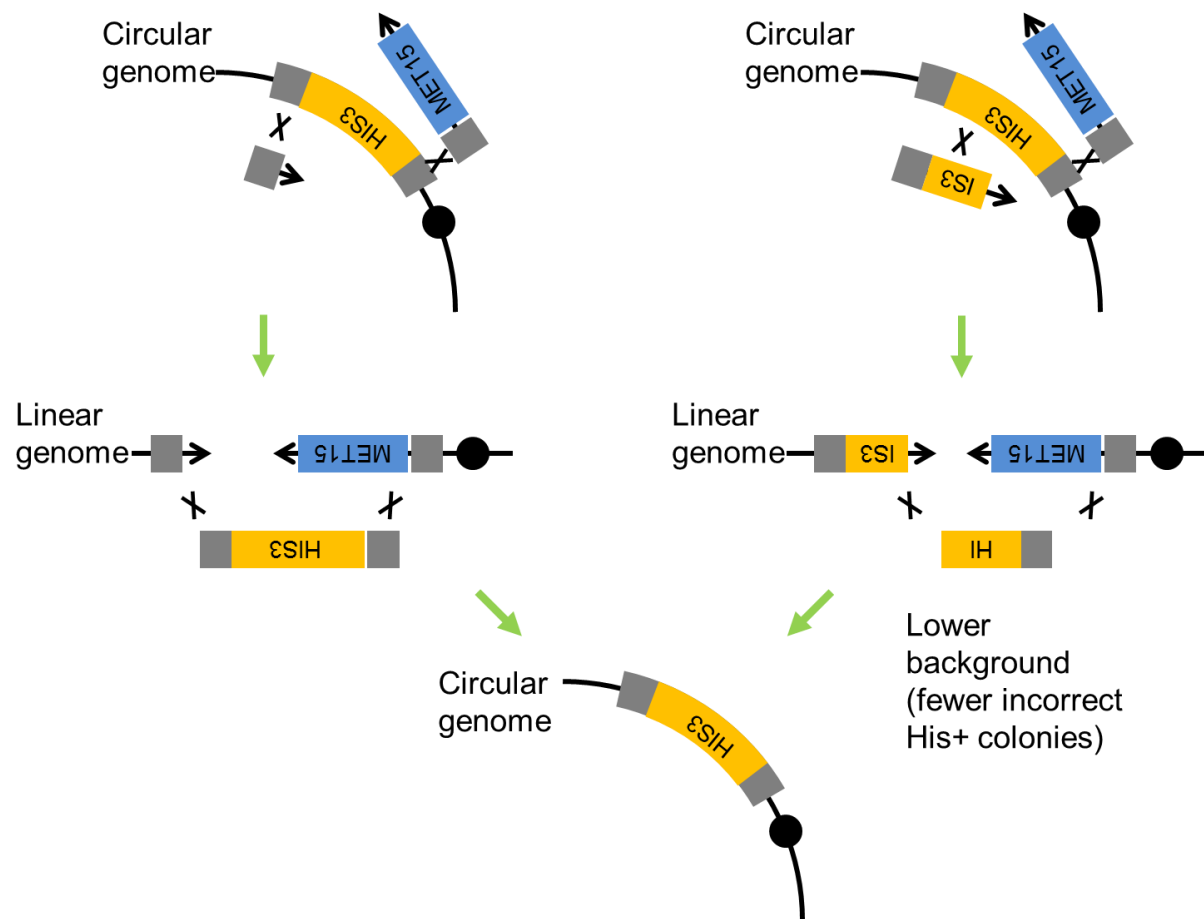


Supplemental Figure S5. Scheme for inverse PCR. The procedure is described in the Methods. The top diagram shows a genomic region containing a transposon (light blue) from one of many transformants pooled for the experiment. A *SspI* site is found roughly every 400 bp in the genome. The region of the transposon from the start to the first *SspI* site is used to capture the genomic sequence upstream of the region. The green arrowheads denote primers used for inverse PCR. The second diagram shows a fragment generated after *SspI* cleavage. The third diagram shows a circular molecule generated after ligation. Both primers now point toward the genomic DNA to be captured. The bottom diagram depicts the PCR product, with the actual samples shown on the right in an agarose gel. Adapter sequences are attached to this and other PCR products in the pool representing numerous transposon insertion sites for 454 sequencing.

Transposon bombardment, pooling of transformants, purification of genomic DNA



Supplemental Figure S6. Schematic diagram of the linearization and recircularization procedures for the JCVI-syn1.0 $\Delta 1-6$ genome in yeast. Two PCR fragments each containing a seed sequence capable of forming a telomere are introduced into a yeast strain containing the circular JCVI-syn1.0 $\Delta 1-6$ genome. One of the fragments contains the *MET15* marker. The *HIS3* marker of the genome is targeted for this engineering. In one of our approaches (left), regions outside of the *HIS3* sequence are used as homologous regions (gray) for integrating the PCR fragments. In the other approach (right), the region extending into the *HIS3* sequence is used as the homologous region for one of the fragments. The expected linearized genomes are shown below. On the right, the linearized genome still keeps part of the *HIS3* sequence (marked as "IS3"). A fragment with homology to both ends of the linearized genome is used to recircularize the genome. On the left, the two ends and the *MET15* marker are replaced with a complete *HIS3* fragment. On the right, the introduced fragment only contains part of the *HIS3* sequence (marked as "HI"), but still contains homology to both ends due to the partial deletion of *HIS3* in the linearization step. The advantage of the strategy on the right is that the fragment for recircularization that does not contain the complete *HIS3* sequence is unlikely to confer the cells the ability to grow in the absence of supplemented histidine unless the fragment lands at the intended site in the mycoplasma genome, thereby contributing to the elimination of background transformants with incorrect engineering.



Supplemental Table S1. List of genes in each deleted gene cluster. When a conventional name is not available for a gene, it is indicated as NULL. Only potentially disruptive insertions defined in Methods and **Supplemental Table S2** are included in the number of transposon hits. Also listed are additional genes deleted in the JCVI-syn1.0 Δ 1-6 background.

Deletion designation	Number of deleted genes	Number of deleted base pairs	Deleted genes			Number of transposon hits
			Systematic name	Conventional name	Product	
A	5	3,688	MMSYN1_0921	tnpA_1	IS1296 transposase protein A	7
			MMSYN1_0922	tnpB_1	IS1296 transposase protein B	15
			MMSYN1_0019	NULL	mannitol-1-phosphate 5-dehydrogenase	26
			MMSYN1_0020	NULL	transcriptional regulator, RpiR family	18
			MMSYN1_0021	NULL	PTS system, mannitol-permease iia component	6
B	5	8,063	MMSYN1_0084	NULL	putative lipoprotein	11
			MMSYN1_0085	NULL	putative lipoprotein	10
			MMSYN1_0086	NULL	putative lipoprotein	7
			MMSYN1_0087	NULL	cell wall anchoring protein	5
			MMSYN1_0088	NULL	conserved hypothetical protein	7
C	7	12,449	MMSYN1_0180	NULL	putative lipoprotein	12
			MMSYN1_0181	NULL	hypothetical protein	11
			MMSYN1_0182	NULL	maltosaccharide ABC transporter, permease, potential pseudogene	6
			MMSYN1_0183	NULL	maltose ABC transporter permease protein	15
			MMSYN1_0184	NULL	multiple sugar-binding transport ATP-binding protein MsmK	13
			MMSYN1_0185	NULL	glycosyl hydrolase, family 65	18
			MMSYN1_0186	NULL	trehalose-6-phosphate hydrolase (Alpha,alpha-phosphotrehalase)	6
D	6	14,716	MMSYN1_0241	ctpA	carboxyl terminal peptidase	13
			MMSYN1_0242	NULL	conserved hypothetical protein	8
			MMSYN1_0243	NULL	putative lipoprotein	7
			MMSYN1_0244	NULL	putative lipoprotein	9
			MMSYN1_0245	NULL	putative membrane protein	10
			MMSYN1_0246	NULL	E1-E2 ATPase subfamily, putative	16
E	24	35,096	MMSYN1_0550	NULL	putative lipoprotein, potential pseudogene	11
			MMSYN1_0551	NULL	putative lipoprotein	18
			MMSYN1_0552	NULL	conserved hypothetical integrative conjugal element protein	0
			MMSYN1_0553	NULL	conserved hypothetical integrative conjugal element protein	3
			MMSYN1_0554	NULL	C-5 cytosine-specific DNA methylase	0
			MMSYN1_0555	NULL	membrane protein, putative (TraD/TraG family)	16
			MMSYN1_0556	NULL	conserved hypothetical integrative conjugal element protein	11

			MMSYN1_0557	NULL	conserved hypothetical integrative conjugal element protein	0
			MMSYN1_0558	NULL	single-strand binding family protein	2
			MMSYN1_0559	NULL	conserved hypothetical integrative conjugal element protein	2
			MMSYN1_0560	NULL	putative lipoprotein	2
			MMSYN1_0561	NULL	conserved hypothetical integrative conjugal element protein	0
			MMSYN1_0562	NULL	conserved hypothetical integrative conjugal element protein	0
			MMSYN1_0563	NULL	putative membrane protein	5
			MMSYN1_0564	NULL	conserved hypothetical integrative conjugal element protein	0
			MMSYN1_0565	NULL	conserved hypothetical integrative conjugal element protein	4
			MMSYN1_0566	NULL	putative membrane protein, potential pseudogene	5
			MMSYN1_0567	NULL	putative membrane protein	7
			MMSYN1_0568	NULL	conserved hypothetical integrative conjugal element protein	6
			MMSYN1_0569	NULL	putative membrane protein	7
			MMSYN1_0570	NULL	conserved hypothetical integrative conjugal element protein	0
			MMSYN1_0571	NULL	conserved hypothetical integrative conjugal element protein	0
			MMSYN1_0572	NULL	CobQ/CobB/MinD/ParA nucleotide binding domain, putative	4
			MMSYN1_0573	NULL	conserved hypothetical integrative conjugal element protein	0
F	5	7,738	MMSYN1_0579	NULL	conserved hypothetical protein	6
			MMSYN1_0580	NULL	conserved hypothetical protein	6
			MMSYN1_0581	NULL	putative membrane protein	8
			MMSYN1_0582	NULL	putative lipoprotein	23
			MMSYN1_0583	NULL	mycoplasma virulence signal region (Myco_arth_vir_N) family	21
G	5	12,324	MMSYN1_0585	NULL	mycoplasma virulence signal region (Myco_arth_vir_N) family	9
			MMSYN1_0586	NULL	putative lipoprotein	11
			MMSYN1_0587	NULL	mycoplasma virulence signal region (Myco_arth_vir_N) family	13
			MMSYN1_0588	NULL	putative lipoprotein	12
			MMSYN1_0589	NULL	mycoplasma virulence signal region (Myco_arth_vir_N) family	18
H	7	9,110	MMSYN1_0687	gatB	glutamyl-tRNA(Gln) amidotransferase, B subunit	7

			MMSYN1_0688	gatA	glutamyl-tRNA(Gln) amidotransferase subunit A (Glu-ADTsubunit A)	6
			MMSYN1_0689	gatC	glutamyl-tRNA(Gln) amidotransferase, C subunit	6
			MMSYN1_0690	ligA	DNA ligase, NAD-dependent	17
			MMSYN1_0691	NULL	putative membrane protein	10
			MMSYN1_0692	NULL	23S rRNA pseudouridine synthase	10
			MMSYN1_0693	NULL	conserved , caax amino protease family	5
I	6	10,014	MMSYN1_0698	NULL	lipoprotein. putative	7
			MMSYN1_0699	msrA/B	peptide methionine sulfoxide reductase MsrA/msrB	8
			MMSYN1_0700	NULL	putative lipoprotein	25
			MMSYN1_0701	NULL	putative lipoprotein	29
			MMSYN1_0702	NULL	transmembrane protein	16
			MMSYN1_0703	NULL	conserved hypothetical protein	25
J	6	8,439	MMSYN1_0741	mmyCIIR	CCTTC-recognizing Type II restriction modification system (MmyCII) endonuclease subunit, potential pseudogene	11
			MMSYN1_0742	mmyCIIM	CCTTC-recognizing Type II restriction modification system (MmyCII) adenine/cytosine DNA methyltransferase subunit	24
			MMSYN1_0743	fruA	PTS system, Fructose specific IIB subunit family	21
			MMSYN1_0744	pfkB	1-phosphofructokinase	14
			MMSYN1_0745	NULL	transcriptional regulator of the fructose operon, DeoR family	8
			MMSYN1_0746	NULL	conserved hypothetical protein	10
K	5	6,656	MMSYN1_0754	mmyCIIM1	GCATC--recognizing Type II restriction modification system (MmyCIII) adenine DNA methyltransferase subunit 1, potential pseudogene	5
			MMSYN1_0755	mmyCIIM2	GCATC--recognizing Type II restriction modification system (MmyCIII) adenine DNA methyltransferase subunit 2	5
			MMSYN1_0756	mmyCIIR	GCATC--recognizing Type II restriction modification system (MmyCIII) endonuclease subunit	7
			MMSYN1_0757	NULL	conserved hypothetical protein	17
			MMSYN1_0758	NULL	beta-glucosidase	14
L	7	14,823	MMSYN1_0840	nusG	transcription antitermination protein nusG	7
			MMSYN1_0841	NULL	hypothetical protein	55
			MMSYN1_0842	NULL	oligopeptide ABC transporter, solute-binding protein	27
			MMSYN1_0843	NULL	oligopeptide ABC transporter, permease component	8
			MMSYN1_0844	NULL	oligopeptide ABC transporter, permease component	8
			MMSYN1_0845	NULL	oligopeptide ABC transporter, ATP-binding component	18

			MMSYN1_0846	NULL	oligopeptide ABC transporter, ATP-binding component	8
M	9	10,037	MMSYN1_0868	NULL	lipoprotein. putative	17
			MMSYN1_0869	NULL	ABC transporter, permease component	8
			MMSYN1_0870	NULL	C4-dicarboxylate anaerobic carrier superfamily	14
			MMSYN1_0871	NULL	zinc metalloprotease	7
			MMSYN1_0872	ychF	GTP-binding protein YchF	14
			MMSYN1_0873	NULL	conserved hypothetical protein	5
			MMSYN1_0874	gidB	16S rRNA methyltransferase GidB	13
			MMSYN1_0875	pgsA	CDP-diacylglycerol--glycerol-3-phosphate 3-phosphatidyltransferase	19
			MMSYN1_0876	NULL	amino acid permease	8
N	16	24,910	MMSYN1_0889	NULL	conserved hypothetical protein, potential pseudogene	5
			MMSYN1_0890	NULL	conserved hypothetical protein	9
			MMSYN1_0891	lppQ	lipoprotein Q, putative (LppQ)	6
			MMSYN1_0892	NULL	putative membrane protein	16
			MMSYN1_0893	NULL	putative membrane protein	12
			MMSYN1_0894	NULL	viral A-type inclusion protein repeat protein	15
			MMSYN1_0895	NULL	conserved hypothetical protein	40
			MMSYN1_0896	NULL	conserved hypothetical protein	8
			MMSYN1_0897	NULL	conserved hypothetical protein	9
			MMSYN1_0898	NULL	conserved hypothetical protein	10
			MMSYN1_0899	NULL	conserved hypothetical protein	7
			MMSYN1_0900	vlcF	lipoprotein, putative (VlcF)	1
			MMSYN1_0901	vlcG	lipoprotein, putative (VlcG)	5
			MMSYN1_0902	vlcH	lipoprotein, putative (VlcH)	4
			MMSYN1_0903	vlcI	lipoprotein (VlcI)	9
			MMSYN1_0904	vlcJ	prolipoprotein, putative (VlcJ)	3
Extra genes deleted in the JCVI-syn1.0 Δ 1-6 genome	15	16626	MMSYN1_0055	mmyCVR	GATC--recognizing Type II restriction modification system (MmyCV) endonuclease subunit	20
			MMSYN1_0056	mmyC5VM	GATC--recognizing Type II restriction modification system (MmyCV) adenine DNA methyltransferase subunit	5
			MMSYN1_0098	mmyCVIM1	CCATC--recognizing Type II restriction modification system (MmyCVI) adenine DNA methyltransferase subunit 1	8
			MMSYN1_0099	mmyCVIM2	CCATC--recognizing Type II restriction modification system (MmyCVI) adenine DNA methyltransferase subunit 2	0
			MMSYN1_0100	mmyCVIR	CCATC--recognizing Type II restriction modification system (MmyCVI) endonuclease subunit	11
			MMSYN1_0926	NULL	hypothetical protein	6
			MMSYN1_0927	NULL	hypothetical protein	0
			MMSYN1_0590	NULL	type III restriction enzyme, res subunit	9
			MMSYN1_0741	mmyCIIR	NULL	11

		MMSYN1_0742	mmyCIIM	CCTTC-recognizing Type II restriction modification system (MmyCII) adenine/cytosine DNA methyltransferase subunit	24
		MMSYN1_0754	mmyCIIM1	NULL	5
		MMSYN1_0755	mmyCIIM2	GCATC--recognizing Type II restriction modification system (MmyCIII) adenine DNA methyltransferase subunit 2	5
		MMSYN1_0756	mmyCIIR	GCATC--recognizing Type II restriction modification system (MmyCIII) endonuclease subunit	7
		MMSYN1_0767	NULL	ribonucleoside-diphosphate reductase subunit alpha (Ribonucleotide reductase)	3
		MMSYN1_0768	mmyCIVR	GANTC--recognizing Type II restriction modification system (MmyCIV) endonuclease subunit	1

Supplemental Table S2. Transposon insertion data. Only transposons that were inserted between the ninth nucleotide and the 80% point along the length were considered to be disruptive and counted for each gene. Genes are listed in the order of appearance in the genome.

Systematic gene name	Conventional gene name	Type	Product	Functional category	Coordinate start	Coordinate end	Strand	Number of Tn insertions
MMSYN1_0001	dnaA_1	ORF	chromosomal replication initiator protein DnaA	DNA metabolism	1	1353	1	4
MMSYN1_0002	dnaN	ORF	DNA polymerase III, beta subunit	DNA metabolism	1511	2638	1	1
MMSYN1_0003	rnmV	ORF	ribonuclease M5	Transcription	2675	3217	1	2
MMSYN1_0004	ksgA	ORF	dimethyladenosine transferase	Protein synthesis	3207	4007	1	3
MMSYN1_0005	NULL	ORF	hypothetical purine NTPase	Cellular processes	4064	5155	1	0
MMSYN1_0006	gyrB	ORF	DNA gyrase, B subunit	DNA metabolism	5515	7419	1	7
MMSYN1_0007	gyrA	ORF	DNA gyrase, A subunit	DNA metabolism	7435	9939	1	0
MMSYN1_0008	NULL	ORF	ribose/Galactose ABC transporter, permease component II	Transport and binding proteins	10968	9991	-1	11
MMSYN1_0009	NULL	ORF	ABC transporter, permease protein	Transport and binding proteins	13535	10968	-1	31
MMSYN1_0010	NULL	ORF	ribose/Galactose ABC transporter, ATP-binding component	Transport and binding proteins	15141	13525	-1	17
MMSYN1_0011	NULL	ORF	ribose/galactose ABC transporter, substrate-binding component	Transport and binding proteins	16799	15153	-1	1
MMSYN1_0012	metG	ORF	methionine--tRNA ligase	Protein synthesis	18515	16986	-1	8
MMSYN1_0013	NULL	ORF	mycoides cluster lipoprotein, LppA/P72 family	Cell envelope	18716	20302	1	2
MMSYN1_0014	NULL	ORF	mycoides cluster lipoprotein, LppA/P72 family	Cell envelope	20317	21831	1	2
MMSYN1_0015	NULL	ORF	mycoides cluster lipoprotein, LppA/P72 family	Cell envelope	21864	23393	1	3
MMSYN1_0016	NULL	ORF	mycoides cluster lipoprotein, LppA/P72 family	Cell envelope	23411	25009	1	7
MMSYN1_0916	NULL	antisense RNA	NULL	NULL	25111	25215	1	0
MMSYN1_0914	bla	ORF	beta-lactamase TEM (precursor)	Cellular processes	26286	25426	-1	0
MMSYN1_0917	NULL	ORF	transposase, Mutator family	Mobile and extrachromosomal element functions	27529	26357	-1	4
MMSYN1_0918	his3	ORF	imidazoleglycerol-phosphate dehydratase	Amino acid biosynthesis	28301	27639	-1	0
MMSYN1_0913	tetM	ORF	Tn916, tetracycline resistance protein	Mobile and extrachromosomal element functions	29270	31258	1	0
MMSYN1_0915	lacZ	ORF	beta-galactosidase, chain D	Mobile and extrachromosomal element functions	31535	34618	1	1
MMSYN1_0921	tnpA_1	ORF	IS1296 transposase protein A	Mobile and extrachromosomal element functions	35234	35776	1	7
MMSYN1_0922	tnpB_1	ORF	IS1296 transposase protein B	Mobile and extrachromosomal element functions	35914	36645	1	15
MMSYN1_0019	NULL	ORF	mannitol-1-phosphate 5-dehydrogenase	Energy metabolism	37673	36687	-1	26
MMSYN1_0020	NULL	ORF	transcriptional regulator, RpiR family	Regulatory functions	38471	37674	-1	18
MMSYN1_0021	NULL	ORF	PTS system, mannitol-permease iia component	Transport and binding proteins	38921	38505	-1	6
MMSYN1_0022	NULL	ORF	sorbitol-6-phosphate 2-dehydrogenase (Glucitol-6-phosphate dehydrogenase) (Ketosephosphate reductase)	Energy metabolism	39679	38921	-1	4
MMSYN1_0023	NULL	ORF	PTS system, mannitol-permease iibc component	Transport and binding proteins	41238	39679	-1	12
MMSYN1_0024	NULL	ORF	NULL	Unknown function	42891	41509	-1	9
MMSYN1_0025	rpsR	ORF	ribosomal protein S18	Protein synthesis	43511	43284	-1	0
MMSYN1_0026	NULL	ORF	single-strand binding protein	DNA metabolism	43971	43531	-1	0
MMSYN1_0027	NULL	ORF	30S ribosomal protein S6	Protein synthesis	44396	43983	1	0
MMSYN1_0028	NULL	ORF	cold-shock DNA-binding domain, putative	Cellular processes	44810	44601	-1	1
MMSYN1_0029	NULL	ORF	fmn-dependent NADH-azoreductase (fmn-dependent nadh-azocompound oxidoreductase) (azo-dye reductase)	Energy metabolism	44998	45597	-1	0
MMSYN1_0030	NULL	ORF	abc transporter, ATP-binding protein	Transport and binding proteins	46668	45634	-1	0
MMSYN1_0031	hsIO	ORF	chaperonin HsIO	Protein fate	47582	46716	-1	23

MMSYN1_0032	NULL	ORF	GnsA/GnsB family	Regulatory functions	50835	47674	1	0
MMSYN1_0033	NULL	ORF	hypothetical protein	NULL	54116	50958	1	0
MMSYN1_0034	NULL	ORF	efflux ABC transporter, permease protein	Transport and binding proteins	54281	59650	1	22
MMSYN1_0035	NULL	ORF	conserved hypothetical protein	Hypothetical proteins	59775	60968	1	5
MMSYN1_0036	NULL	ORF	D-lactate dehydrogenase	Energy metabolism	61277	62263	1	3
MMSYN1_0037	NULL	ORF	malate permease	Transport and binding proteins	62282	63406	1	6
MMSYN1_0038	NULL	ORF	conserved hypothetical protein	Hypothetical proteins	63762	65045	1	2
MMSYN1_0039	NULL	ORF	peptidase, M41 family	Protein fate	67033	65087	-1	7
MMSYN1_0041	NULL	ORF	conserved hypothetical protein	Hypothetical proteins	67265	68110	1	8
MMSYN1_0040	NULL	ORF	tRNA(Ile)-lysidine synthase (tRNA(Ile)-lysidinesynthetase) (tRNA(Ile)-2-lysyl-cytidine synthase)	Biosynthesis of cofactors, prosthetic groups, and carriers	69299	68094	-1	4
MMSYN1_0042	NULL	ORF	transcriptional regulator, RpiR family protein	Regulatory functions	70129	69302	-1	2
MMSYN1_0043	NULL	ORF	methyltransferase	Central intermediary metabolism	70903	70181	-1	4
MMSYN1_0044	NULL	ORF	DNA polymerase III delta subunit	DNA metabolism	71643	70903	-1	4
MMSYN1_0045	tmk	ORF	dTMP kinase	Purines, pyrimidines, nucleosides, and nucleotides	72262	71621	-1	3
MMSYN1_0046	NULL	ORF	DNA repair protein RecM	DNA metabolism	72855	72265	-1	1
MMSYN1_0047	dnaX	ORF	DNA polymerase III, gamma/tau subunit	DNA metabolism	74863	72857	-1	12
MMSYN1_0048	NULL	ORF	cytosine deaminase	Purines, pyrimidines, nucleosides, and nucleotides	75412	74945	-1	6
MMSYN1_0049	srpB	ncRNA	NULL	NULL	75491	75393	-1	0
MMSYN1_0050	guaC	ORF	GMP reductase	Purines, pyrimidines, nucleosides, and nucleotides	76491	75529	-1	10
MMSYN1_0051	NULL	ORF	conserved hypothetical protein	Hypothetical proteins	77202	76906	-1	0
MMSYN1_0052	NULL	ORF	hypothetical protein	NULL	77647	77327	-1	0
MMSYN1_0053	NULL	ORF	NULL	Cell envelope	79851	77755	-1	17
MMSYN1_0054	NULL	ORF	AhpC/TSA family protein	Unknown function	80449	80000	-1	6
MMSYN1_0055	mmyCVR	ORF	GATC--recognizing Type II restriction modification system (MmyCV) endonuclease subunit	DNA metabolism	81977	80688	-1	20
MMSYN1_0056	mmyC5VM	ORF	GATC--recognizing Type II restriction modification system (MmyCV) adenine DNA methyltransferase subunit	DNA metabolism	82818	81979	-1	5
MMSYN1_0057	NULL	ORF	conserved hypothetical protein	Hypothetical proteins	83287	83577	1	0
MMSYN1_0058	NULL	ORF	conserved hypothetical protein	Hypothetical proteins	83596	84177	1	5
MMSYN1_0059	ald	ORF	alanine dehydrogenase	Energy metabolism	84292	85410	1	26
MMSYN1_0060	NULL	ORF	putative membrane protein	Cell envelope	85704	86528	1	3
MMSYN1_0061	serS	ORF	serine--tRNA ligase	Protein synthesis	86611	87879	1	4
MMSYN1_0062	NULL	ORF	conserved hypothetical protein	Hypothetical proteins	87981	88295	1	4
MMSYN1_0063	NULL	ORF	tRNA-dihydrouridine synthase B	Protein synthesis	88297	89271	1	3
MMSYN1_0064	lysS	ORF	lysine--tRNA ligase	Protein synthesis	89274	90776	1	0
MMSYN1_0065	trxA	ORF	thioredoxin	Energy metabolism	91174	90866	-1	0
MMSYN1_0066	NULL	ORF	putative hydrolase of the HAD family	Unknown function	92027	91185	-1	11
MMSYN1_0067	rrf	rRNA	NULL	NULL	92256	92148	-1	2
MMSYN1_0068	rrl	rRNA	NULL	NULL	95225	92331	-1	2
MMSYN1_0069	rrs	rRNA	NULL	NULL	96980	95457	-1	0
MMSYN1_0070	NULL	tRNA	NULL	NULL	97346	97263	-1	0
MMSYN1_0071	NULL	tRNA	NULL	NULL	97424	97349	-1	0
MMSYN1_0072	NULL	ORF	putative membrane protein	Cell envelope	97603	99669	1	18
MMSYN1_0073	NULL	ORF	phosphonate ABC transporter, permease protein PhnE, putative	Transport and binding proteins	102434	99702	-1	12
MMSYN1_0074	phnC	ORF	phosphonate ABC transporter, ATP-binding protein	Transport and binding proteins	103190	102438	-1	1
MMSYN1_0075	NULL	ORF	phosphonate ABC transporter, phosphonate-binding protein, putative	Transport and binding proteins	104574	103204	-1	16
MMSYN1_0076	asnS	ORF	asparagine--tRNA ligase	Protein synthesis	106230	104866	-1	8
MMSYN1_0077	NULL	ORF	putative hydrolase of the HAD family	Unknown function	107078	106239	-1	12
MMSYN1_0078	NULL	ORF	putative hydrolase from alpha/beta family	Central intermediary metabolism	108219	107089	-1	2
MMSYN1_0079	NULL	ORF	probable O-sialoglycoprotein endopeptidase (Glycoprotease)	Protein fate	109199	108243	-1	2

MMSYN1_0080	NULL	ORF	conserved hypothetical protein	Hypothetical proteins	109515	109294	-1	0
MMSYN1_0081	trmE	ORF	tRNA modification GTPase TrmE	Protein synthesis	109715	111073	1	12
MMSYN1_0082	rpsT	ORF	ribosomal protein S20	Protein synthesis	111369	111124	-1	2
MMSYN1_0083	NULL	ORF	conserved hypothetical protein	Hypothetical proteins	112138	111503	-1	2
MMSYN1_0084	NULL	ORF	putative lipoprotein	Cell envelope	113967	112555	-1	11
MMSYN1_0085	NULL	ORF	putative lipoprotein	Cell envelope	116367	114118	-1	10
MMSYN1_0086	NULL	ORF	putative lipoprotein	Cell envelope	117539	116412	-1	7
MMSYN1_0087	NULL	ORF	cell wall anchoring protein	Energy metabolism	118508	118095	-1	5
MMSYN1_0088	NULL	ORF	conserved hypothetical protein	Hypothetical proteins	120617	118767	-1	7
MMSYN1_0089	NULL	ORF	putative lipoprotein	Cell envelope	122567	120876	-1	1
MMSYN1_0923	NULL	ORF	lipofamily protein	Cell envelope	123332	122730	-1	0
MMSYN1_0092	NULL	ORF	putative lipoprotein	Cell envelope	126049	123560	-1	8
MMSYN1_0093	NULL	ORF	putative lipoprotein	Cell envelope	126990	126220	-1	3
MMSYN1_0094	NULL	ORF	putative membrane protein	Cell envelope	127690	126974	-1	2
MMSYN1_0095	secA	ORF	preprotein translocase, SecA subunit	Protein fate	130639	127805	-1	12
MMSYN1_0096	NULL	ORF	Xaa-Pro dipeptidase	Protein fate	130730	131305	1	8
MMSYN1_0097	NULL	ORF	dna polymerase I, 5'-3' exonuclease	DNA metabolism	131380	132291	1	5
MMSYN1_0098	mmyCVIM1	ORF	CCATC--recognizing Type II restriction modification system (MmyCVI) adenine DNA methyltransferase subunit 1	DNA metabolism	132495	133511	1	8
MMSYN1_0099	mmyCVIM2	ORF	CCATC--recognizing Type II restriction modification system (MmyCVI) adenine DNA methyltransferase subunit 2	DNA metabolism	133501	134418	1	0
MMSYN1_0100	mmyCVIR	ORF	CCATC--recognizing Type II restriction modification system (MmyCVI) endonuclease subunit	DNA metabolism	134396	135979	1	11
MMSYN1_0101	NULL	ORF	ATPase	Unknown function	136419	137714	1	8
MMSYN1_0102	NULL	ORF	conserved hypothetical protein	Hypothetical proteins	138374	138649	1	0
MMSYN1_0103	coaE	ORF	dephospho-CoA kinase	Biosynthesis of cofactors, prosthetic groups, and carriers	138651	139208	1	1
MMSYN1_0104	rrmJ	ORF	ribosomal RNA large subunit methyltransferase J	Protein synthesis	140016	139210	-1	2
MMSYN1_0105	NULL	ORF	conserved domain protein	Hypothetical proteins	140231	140016	-1	0
MMSYN1_0106	xseA	ORF	exodeoxyribonuclease VII, large subunit	DNA metabolism	141630	140221	-1	9
MMSYN1_0107	nusB	ORF	transcription antitermination factor NusB	Transcription	142030	141632	-1	1
MMSYN1_0108	NULL	ORF	putative lipoprotein	Cell envelope	143154	142042	-1	4
MMSYN1_0109	NULL	ORF	apurinic endonuclease Apn1	DNA metabolism	144049	143180	-1	4
MMSYN1_0110	NULL	ORF	riboflavin kinase	Biosynthesis of cofactors, prosthetic groups, and carriers	144794	144042	-1	1
MMSYN1_0111	NULL	tRNA	NULL	NULL	144944	144869	-1	0
MMSYN1_0112	NULL	ORF	peptidase, S41 family	Protein fate	147287	145008	-1	16
MMSYN1_0113	NULL	ORF	glycosyltransferase	Cell envelope	147625	148869	1	0
MMSYN1_0114	NULL	ORF	glycosyltransferase	Cell envelope	149863	148943	-1	5
MMSYN1_0115	NULL	ORF	utp--glucose-1-phosphate uridylyltransferase (udp-glucosepyrophosphorylase) (udpgp) (alpha-d-glucosyl-1-phosphateuridylyltransferase) (uridine diphosphoglucose pyrophosphorylase)(general stress protein 33) (Gsp33)	Cell envelope	151183	150311	-1	4
MMSYN1_0116	NULL	ORF	conserved hypothetical protein	Hypothetical proteins	151808	151368	-1	0
MMSYN1_0117	plsY	ORF	acyl-phosphate glycerol 3-phosphate acyltransferase	Fatty acid and phospholipid metabolism	151878	152639	1	1
MMSYN1_0118	NULL	ORF	ABC transporter, ATP-binding protein	Transport and binding proteins	152703	154241	1	8
MMSYN1_0119	NULL	ORF	hydrolase, TatD family	Unknown function	155068	154271	-1	5
MMSYN1_0120	ilvA	ORF	threonine ammonia-lyase	Amino acid biosynthesis	155264	156490	1	11
MMSYN1_0121	NULL	ORF	putative membrane protein	Cell envelope	156705	158285	1	7
MMSYN1_0122	NULL	ORF	conserved hypothetical protein	Hypothetical proteins	158297	159157	1	0
MMSYN1_0123	vlcD	ORF	lipoprotein, putative (VlcD)	Cell envelope	159440	160150	1	5
MMSYN1_0124	NULL	ORF	hexosephosphate transport protein	Transport and binding proteins	160552	161883	1	0
MMSYN1_0125	NULL	ORF	PTS system, N-acetylglucosamine-specific iibc component	Transport and binding proteins	162231	163934	1	3

MMSYN1_0126	gltX	ORF	glutamate--tRNA ligase	Protein synthesis	164067	165518	1	1
MMSYN1_0127	NULL	ORF	HD domain protein	Unknown function	165521	166735	1	11
MMSYN1_0128	NULL	ORF	conserved hypothetical protein	Hypothetical proteins	166761	167189	1	0
MMSYN1_0129	pyrG	ORF	CTP synthase	Purines, pyrimidines, nucleosides, and nucleotides	167281	168879	1	2
MMSYN1_0130	NULL	ORF	conserved hypothetical protein	Hypothetical proteins	169010	169984	1	0
MMSYN1_0131	fba	ORF	fructose-1,6-bisphosphate aldolase, class II	Energy metabolism	170143	171036	1	1
MMSYN1_0132	NULL	ORF	AAA family ATPase	Unknown function	171185	172246	1	3
MMSYN1_0133	NULL	ORF	conserved hypothetical protein	Hypothetical proteins	172239	174512	1	4
MMSYN1_0134	NULL	ORF	putative membrane protein	Cell envelope	176106	174619	-1	15
MMSYN1_0135	NULL	ORF	hypothetical protein	NULL	176562	176449	-1	0
MMSYN1_0136	NULL	ORF	glycerophosphodiester phosphodiesterase	Fatty acid and phospholipid metabolism	176702	177406	1	1
MMSYN1_0137	rpmE	ORF	ribosomal protein L31	Protein synthesis	177566	177844	1	2
MMSYN1_0138	NULL	ORF	conserved hypothetical protein	Hypothetical proteins	177917	179815	1	9
MMSYN1_0139	NULL	ORF	DHH family protein	Unknown function	179825	180775	1	8
MMSYN1_0140	tdk	ORF	thymidine kinase	Purines, pyrimidines, nucleosides, and nucleotides	180777	181406	1	0
MMSYN1_0141	prfA	ORF	peptide chain release factor 1	Protein synthesis	181409	182503	1	4
MMSYN1_0142	prmC	ORF	protein-(glutamine-N5) methyltransferase, release factor-specific	Protein fate	182496	183344	1	5
MMSYN1_0143	NULL	ORF	putative membrane protein	Cell envelope	183353	184825	1	8
MMSYN1_0144	NULL	ORF	conserved hypothetical protein	Hypothetical proteins	184834	185334	1	0
MMSYN1_0145	NULL	ORF	conserved hypothetical protein	Hypothetical proteins	185449	186363	1	0
MMSYN1_0146	NULL	ORF	conserved hypothetical protein	Hypothetical proteins	186592	187299	1	2
MMSYN1_0147	NULL	ORF	cardiolipin synthetase	Fatty acid and phospholipid metabolism	187299	188828	1	1
MMSYN1_0148	rpsL	ORF	ribosomal protein S12	Protein synthesis	188952	189371	1	0
MMSYN1_0149	rpsG	ORF	ribosomal protein S7	Protein synthesis	189458	189925	1	1
MMSYN1_0150	fusA	ORF	translation elongation factor G	Protein synthesis	189950	192019	1	1
MMSYN1_0151	tuf	ORF	translation elongation factor Tu	Protein synthesis	192151	193338	1	2
MMSYN1_0152	NULL	ORF	PTS system glucose-specific eiic ba component	Transport and binding proteins	193471	195336	1	5
MMSYN1_0153	NULL	ORF	glycosyl hydrolase, family 31	Energy metabolism	195320	197590	1	20
MMSYN1_0154	lap	ORF	leucyl aminopeptidase	Protein fate	197743	199098	1	1
MMSYN1_0155	NULL	ORF	NULL	Hypothetical proteins	200904	201506	1	4
MMSYN1_0156	trmB	ORF	tRNA (guanine-N(7)-)-methyltransferase	Protein synthesis	202329	201664	-1	11
MMSYN1_0157	mgtE	ORF	magnesium transporter	Transport and binding proteins	203734	202331	-1	11
MMSYN1_0158	ssrA	tmRNA	NULL	NULL	203879	204289	1	0
MMSYN1_0159	NULL	ORF	putative lipoprotein	Cell envelope	204414	206543	1	2
MMSYN1_0160	AbiGIA	ORF	abortive infection protein AbiGII	Cellular processes	207315	206563	-1	11
MMSYN1_0161	AbiGIB	ORF	abortive infection protein AbiGI	Cellular processes	207998	207402	-1	4
MMSYN1_0162	NULL	ORF	NULL	Cell envelope	209415	208209	-1	3
MMSYN1_0163	alaS	ORF	alanine--tRNA ligase	Protein synthesis	212219	209529	-1	11
MMSYN1_0164	NULL	ORF	conserved hypothetical protein	Hypothetical proteins	212787	212293	-1	5
MMSYN1_0165	NULL	ORF	oligopeptide ABC transporter, permease component	Transport and binding proteins	213005	214249	1	3
MMSYN1_0166	NULL	ORF	oligopeptide ABC transporter, permease component I	Transport and binding proteins	214265	215275	1	0
MMSYN1_0167	NULL	ORF	oligopeptide ABC transporter, ATP-binding component	Transport and binding proteins	215289	216989	1	6
MMSYN1_0168	NULL	ORF	ABC transporter, ATP-binding protein, putative	Transport and binding proteins	216991	218859	1	1
MMSYN1_0169	NULL	ORF	putative lipoprotein	Cell envelope	218876	221977	1	1
MMSYN1_0170	NULL	ORF	ATPase	Unknown function	223690	222395	-1	16
MMSYN1_0171	NULL	ORF	ATPase	Unknown function	225089	223785	-1	9
MMSYN1_0172	NULL	ORF	conserved hypothetical protein	Unknown function	225321	226202	1	5
MMSYN1_0173	NULL	ORF	mycoides cluster lipoprotein, LppA/P72 family	Cell envelope	227933	226236	-1	8
MMSYN1_0174	NULL	ORF	conserved hypothetical protein	Hypothetical proteins	228150	228296	1	1
MMSYN1_0175	NULL	ORF	mycoides cluster lipoprotein, LppA/P72 family	Cell envelope	230015	228333	-1	16
MMSYN1_0176	pgmB	ORF	beta-phosphoglucomutase	Energy metabolism	230754	230125	-1	7
MMSYN1_0177	NULL	ORF	neopullulanase	Energy metabolism	232553	230754	-1	4
MMSYN1_0178	NULL	ORF	neopullulanase	Energy metabolism	234468	232672	-1	14
MMSYN1_0179	NULL	ORF	putative lipoprotein	Cell envelope	234726	236525	1	1

MMSYN1_0180	NULL	ORF	putative lipoprotein	Cell envelope	236820	238610	1	12
MMSYN1_0181	NULL	ORF	hypothetical protein	NULL	238692	239183	1	11
MMSYN1_0182	NULL	ORF	NULL	Transport and binding proteins	239198	241615	1	6
MMSYN1_0183	NULL	ORF	maltose ABC transporter permease protein	Transport and binding proteins	241630	244170	1	15
MMSYN1_0184	NULL	ORF	multiple sugar-binding transport ATP-binding protein MsmK	Transport and binding proteins	244172	245257	1	13
MMSYN1_0185	NULL	ORF	glycosyl hydrolase, family 65	Central intermediary metabolism	245365	247662	1	18
MMSYN1_0186	NULL	ORF	trehalose-6-phosphate hydrolase (Alpha,alpha-phosphotrehalase)	Energy metabolism	247664	249268	1	6
MMSYN1_0187	NULL	ORF	transcriptional regulator, GntR family	Regulatory functions	249291	250010	1	3
MMSYN1_0188	pepF	ORF	oligoendopeptidase F	Protein fate	251832	250039	-1	3
MMSYN1_0189	NULL	ORF	conserved hypothetical protein	Hypothetical proteins	252515	251832	-1	5
MMSYN1_0190	NULL	ORF	leucyl aminopeptidase	Protein fate	253886	252531	-1	7
MMSYN1_0191	NULL	ORF	ATPase	Unknown function	254180	253998	-1	0
MMSYN1_0192	NULL	ORF	chromate ion transporter	Transport and binding proteins	254459	255079	1	6
MMSYN1_0193	NULL	ORF	chromate ion transporter	Transport and binding proteins	255079	255756	1	12
MMSYN1_0194	NULL	ORF	NULL	Hypothetical proteins	255890	256849	1	6
MMSYN1_0195	NULL	ORF	ABC transporter, permease protein	Transport and binding proteins	260323	257213	-1	21
MMSYN1_0196	NULL	ORF	spermidine/putrescine ABC transporter, permease protein	Transport and binding proteins	261300	260308	-1	0
MMSYN1_0197	NULL	ORF	spermidine/putrescine import ATP-binding protein PotA	Transport and binding proteins	262355	261300	-1	3
MMSYN1_0198	rplT	ORF	ribosomal protein L20	Protein synthesis	263088	262729	-1	1
MMSYN1_0199	rplM	ORF	ribosomal protein L35	Protein synthesis	263298	263107	-1	0
MMSYN1_0200	infC	ORF	translation initiation factor IF-3	Protein synthesis	263869	263324	-1	0
MMSYN1_0201	def	ORF	peptide deformylase	Protein fate	264660	264058	-1	0
MMSYN1_0202	NULL	ORF	methyltransferase	DNA metabolism	264734	265291	1	0
MMSYN1_0203	gmk	ORF	guanylate kinase (GMP kinase)	Purines, pyrimidines, nucleosides, and nucleotides	265294	266187	1	1
MMSYN1_0204	sun	ORF	ribosomal RNA small subunit methyltransferase B	Protein synthesis	266177	267436	1	3
MMSYN1_0205	typA	ORF	GTP-binding protein TypA/BipA	Regulatory functions	269269	267440	-1	5
MMSYN1_0206	NULL	ORF	NULL	Cell envelope	269514	270271	1	3
MMSYN1_0207	NULL	ORF	putative lipoprotein	Cell envelope	270334	271125	1	5
MMSYN1_0208	NULL	ORF	putative lipoprotein	Cell envelope	271254	272045	1	5
MMSYN1_0209	murQ	ORF	N-acetylmuramic acid 6-phosphate etherase	Cell envelope	273016	272099	-1	9
MMSYN1_0210	NULL	ORF	PTS system N-acetylmuramic acid-specific eiibc component (eiibc-murnac)	Signal transduction	274706	273009	-1	23
MMSYN1_0211	NULL	ORF	transcription regulator GntR	Regulatory functions	275661	274828	-1	3
MMSYN1_0212	NULL	ORF	conserved hypothetical protein	Hypothetical proteins	275868	275665	-1	2
MMSYN1_0213	eno	ORF	phosphopyruvate hydratase	Energy metabolism	276076	277431	1	0
MMSYN1_0214	NULL	ORF	PAP2 superfamily domain membrane protein	Unknown function	277498	278319	1	3
MMSYN1_0215	NULL	ORF	conserved hypothetical protein	Hypothetical proteins	278321	278752	1	0
MMSYN1_0216	hpt_1	ORF	hypoxanthine phosphoribosyltransferase	Purines, pyrimidines, nucleosides, and nucleotides	278758	279330	1	0
MMSYN1_0217	NULL	ORF	glycerol uptake facilitator protein	Transport and binding proteins	280163	279390	-1	2
MMSYN1_0218	glpK	ORF	glycerol kinase	Energy metabolism	281721	280204	-1	6
MMSYN1_0219	glpO	ORF	glycerol oxydase	Fatty acid and phospholipid metabolism	282901	281738	-1	11
MMSYN1_0220	pfkA	ORF	6-phosphofructokinase	Energy metabolism	283236	284216	1	0
MMSYN1_0221	pyk	ORF	pyruvate kinase	Energy metabolism	284287	285723	1	0
MMSYN1_0222	thrS	ORF	threonine--tRNA ligase	Protein synthesis	285988	287907	1	2
MMSYN1_0223	NULL	ORF	NADH oxidase (noxase)	Energy metabolism	288390	289754	1	1
MMSYN1_0224	NULL	ORF	probable lipoate-protein ligase A (Lipoate--proteinligase)	Cell envelope	289757	290761	1	7
MMSYN1_0225	pdhA	ORF	pyruvate dehydrogenase (acetyl-transferring) E1 component, alpha subunit	Energy metabolism	290805	291917	1	0
MMSYN1_0226	pdhB	ORF	pyruvate dehydrogenase E1 component subunit beta (Scomplex, 36 kDa subunit)	Energy metabolism	291917	292906	1	2

MMSYN1_0227	pdhC	ORF	dihydrolipoamide acetyltransferase component of pyruvate dehydrogenase complex	Energy metabolism	292935	294260	1	0
MMSYN1_0228	lpdA	ORF	dihydrolipoyl dehydrogenase	Energy metabolism	294279	296168	1	1
MMSYN1_0229	pta	ORF	phosphate acetyltransferase	Energy metabolism	296190	297158	1	0
MMSYN1_0230	ackA	ORF	acetate kinase	Energy metabolism	297171	298352	1	5
MMSYN1_0231	NULL	ORF	putative lipoprotein	Cell envelope	298421	300376	1	8
MMSYN1_0232	coaD	ORF	pantetheine-phosphate adenylyltransferase	Biosynthesis of cofactors, prosthetic groups, and carriers	300386	300808	1	8
MMSYN1_0233	ptsP	ORF	phosphoenolpyruvate-protein phosphotransferase	Transport and binding proteins	300902	302623	1	6
MMSYN1_0234	NULL	ORF	PTS system glucose-specific eiicba component (eiicba-glc) (eii-glc/eiii-glc)	Transport and binding proteins	302705	303169	1	0
MMSYN1_0235	NULL	ORF	conserved hypothetical protein	Hypothetical proteins	303170	303460	1	0
MMSYN1_0236	dhaL	ORF	dihydroxyacetone kinase, L subunit	Regulatory functions	303533	304159	1	3
MMSYN1_0237	NULL	ORF	dihydroxyacetone kinase, phosphotransfer subunit	Fatty acid and phospholipid metabolism	304167	304562	1	0
MMSYN1_0238	rpsD	ORF	ribosomal protein S4	Protein synthesis	305233	304607	-1	1
MMSYN1_0239	NULL	ORF	conserved hypothetical protein	Hypothetical proteins	305488	307275	1	14
MMSYN1_0240	thiI	ORF	thiamine biosynthesis/tRNA modification protein ThiI	Biosynthesis of cofactors, prosthetic groups, and carriers	307283	308470	1	1
MMSYN1_0241	ctpA	ORF	NULL	Protein fate	308601	311333	1	13
MMSYN1_0242	NULL	ORF	conserved hypothetical protein	Hypothetical proteins	311451	313136	1	8
MMSYN1_0243	NULL	ORF	putative lipoprotein	Cell envelope	313147	315438	1	7
MMSYN1_0244	NULL	ORF	putative lipoprotein	Cell envelope	315501	317768	1	9
MMSYN1_0245	NULL	ORF	putative membrane protein	Cell envelope	318242	320383	1	10
MMSYN1_0246	NULL	ORF	E1-E2 ATPase subfamily, putative	Transport and binding proteins	323316	320410	-1	16
MMSYN1_0247	ysxC	ORF	ribosome biogenesis GTP-binding protein YsxC	Protein synthesis	323915	323325	-1	1
MMSYN1_0248	NULL	ORF	conserved hypothetical protein	Hypothetical proteins	324469	323909	-1	5
MMSYN1_0249	NULL	ORF	conserved hypothetical protein	Hypothetical proteins	325049	324471	-1	9
MMSYN1_0250	NULL	ORF	conserved hypothetical protein	Hypothetical proteins	325741	325052	-1	4
MMSYN1_0251	NULL	ORF	conserved hypothetical protein	Hypothetical proteins	325823	326515	1	5
MMSYN1_0252	NULL	ORF	oxidoreductase	Central intermediary metabolism	327238	326516	-1	1
MMSYN1_0253	NULL	ORF	transcription elongation factor GreA	Regulatory functions	327756	327283	-1	4
MMSYN1_0254	uvrC	ORF	excinuclease ABC subunit C	DNA metabolism	329633	327879	-1	9
MMSYN1_0255	NULL	ORF	conserved hypothetical protein	Hypothetical proteins	330704	329643	-1	11
MMSYN1_0256	NULL	ORF	Amino acid permease superfamily protein	Transport and binding proteins	332392	330770	-1	13
MMSYN1_0257	NULL	ORF	hydrolase	Central intermediary metabolism	334249	332498	-1	18
MMSYN1_0258	NULL	ORF	oxidoreductase	Central intermediary metabolism	335094	334375	-1	3
MMSYN1_0259	NULL	ORF	NAD(+)/nadh kinase, putative	Biosynthesis of cofactors, prosthetic groups, and carriers	335903	335106	-1	3
MMSYN1_0260	valS	ORF	valine--tRNA ligase	Protein synthesis	338632	336014	-1	11
MMSYN1_0261	thiN	ORF	NULL	Biosynthesis of cofactors, prosthetic groups, and carriers	339345	338719	-1	7
MMSYN1_0262	rpe	ORF	NULL	Energy metabolism	340097	339420	-1	2
MMSYN1_0263	rsgA	ORF	ribosome small subunit-dependent GTPase A	Protein synthesis	341001	340099	-1	8
MMSYN1_0264	NULL	ORF	serine/threonine protein kinase	Unknown function	342126	341011	-1	9
MMSYN1_0268	NULL	ORF	NULL	Cellular processes	342883	342126	-1	13
MMSYN1_0269	NULL	ORF	conserved hypothetical protein	Hypothetical proteins	344321	342912	-1	18
MMSYN1_0270	NULL	ORF	ATPase, YjeE family	Unknown function	344441	344857	1	1
MMSYN1_0271	NULL	ORF	glycoprotease family protein	Protein fate	344859	345422	1	5
MMSYN1_0272	NULL	ORF	efflux ABC transporter, permease protein	Transport and binding proteins	350779	345458	-1	36
MMSYN1_0273	NULL	ORF	hypothetical protein	NULL	350992	354132	1	8
MMSYN1_0274	NULL	ORF	putative lipoprotein	Cell envelope	354147	354761	1	1
MMSYN1_0275	NULL	ORF	putative lipoprotein	Cell envelope	354901	355422	1	0
MMSYN1_0276	NULL	ORF	NULL	Cell envelope	355682	356302	1	0
MMSYN1_0277	NULL	ORF	putative lipoprotein	Cell envelope	356463	356975	1	0
MMSYN1_0278	NULL	ORF	PTS system fructose-specific enzyme iiaabc component	Transport and binding proteins	359429	357015	-1	5
MMSYN1_0279	NULL	ORF	conserved hypothetical protein	Hypothetical proteins	359688	359975	1	0
MMSYN1_0280	NULL	tRNA	NULL	NULL	360219	360308	1	2

MMSYN1_0281	NULL	ORF	conserved hypothetical protein	Hypothetical proteins	360428	361108	1	1
MMSYN1_0282	proS	ORF	proline--tRNA ligase	Protein synthesis	361089	362513	1	0
MMSYN1_0283	rnhA	ORF	ribonuclease HI	Transcription	362526	363143	1	2
MMSYN1_0284	NULL	ORF	conserved hypothetical protein	Hypothetical proteins	363145	364032	1	3
MMSYN1_0285	lepA	ORF	GTP-binding protein LepA	Unknown function	364056	365858	1	1
MMSYN1_0286	NULL	ORF	NULL	Hypothetical proteins	365884	366690	1	0
MMSYN1_0287	aspS	ORF	aspartate--tRNA ligase	Protein synthesis	368431	366707	-1	13
MMSYN1_0288	hisS	ORF	histidine--tRNA ligase	Protein synthesis	369684	368440	-1	8
MMSYN1_0289	rbfA	ORF	ribosome-binding factor A	Transcription	369869	370222	1	1
MMSYN1_0290	truB	ORF	tRNA pseudouridine synthase B	Protein synthesis	370272	371150	1	0
MMSYN1_0291	NULL	ORF	riboflavin kinase (Flavokinase)	Biosynthesis of cofactors, prosthetic groups, and carriers	371137	371691	1	0
MMSYN1_0292	NULL	ORF	peptidase, S41 family	Protein fate	373759	371714	-1	22
MMSYN1_0293	NULL	ORF	putative lipoprotein	Cell envelope	375754	373784	-1	0
MMSYN1_0294	rpsO	ORF	ribosomal protein S15	Protein synthesis	375967	376233	1	0
MMSYN1_0295	NULL	tRNA	NULL	NULL	376293	376366	1	0
MMSYN1_0296	NULL	ORF	conserved hypothetical protein	Hypothetical proteins	376464	377108	1	5
MMSYN1_0297	infB	ORF	translation initiation factor IF-2	Protein synthesis	378989	377127	-1	1
MMSYN1_0298	NULL	ORF	ribosomal protein L7A family	Protein synthesis	379310	379011	-1	0
MMSYN1_0299	NULL	ORF	conserved hypothetical protein	Hypothetical proteins	379578	379297	-1	0
MMSYN1_0300	nusA	ORF	transcription elongation factor NusA	Transcription	381313	379559	-1	0
MMSYN1_0301	NULL	ORF	conserved hypothetical protein	Hypothetical proteins	381816	381322	-1	1
MMSYN1_0302	NULL	ORF	nitroreductase family protein	Unknown function	382579	381929	-1	2
MMSYN1_0303	polC	ORF	DNA polymerase III, alpha subunit, Gram-positive type	DNA metabolism	387040	382592	-1	9
MMSYN1_0304	cdsA	ORF	phosphatidate cytidyltransferase	Fatty acid and phospholipid metabolism	388077	387049	-1	5
MMSYN1_0305	NULL	ORF	peptidase, M24 family	Protein fate	389352	388276	-1	3
MMSYN1_0306	NULL	ORF	hypothetical protein	NULL	390282	389506	-1	0
MMSYN1_0307	NULL	ORF	integrase core domain protein	Unknown function	390558	390911	1	0
MMSYN1_0308	trpS	ORF	tryptophan--tRNA ligase	Protein synthesis	391003	392013	1	1
MMSYN1_0309	NULL	ORF	conserved hypothetical protein	Hypothetical proteins	392911	392042	-1	7
MMSYN1_0310	NULL	ORF	conserved hypothetical protein	Hypothetical proteins	393024	393824	1	14
MMSYN1_0311	NULL	ORF	RmuC domain protein	Unknown function	394955	393879	-1	12
MMSYN1_0312	NULL	ORF	conserved hypothetical protein	Hypothetical proteins	395171	397891	1	7
MMSYN1_0313	trmFO2	ORF	methylenetetrahydrofolate--tRNA-(uracil-5)- methyltransferase trmFO 2	Protein synthesis	398248	399522	1	2
MMSYN1_0314	NULL	ORF	putative membrane protein	Cell envelope	399627	400361	1	0
MMSYN1_0315	NULL	ORF	conserved hypothetical protein	Hypothetical proteins	400483	400635	1	0
MMSYN1_0316	tkt	ORF	transketolase	Energy metabolism	400694	402664	1	1
MMSYN1_0317	NULL	ORF	conserved hypothetical protein	Hypothetical proteins	402680	402925	1	4
MMSYN1_0318	NULL	ORF	conserved hypothetical protein	Hypothetical proteins	402993	404537	1	10
MMSYN1_0319	NULL	ORF	putative lipoprotein	Cell envelope	404627	407524	1	5
MMSYN1_0320	NULL	ORF	triacylglycerol lipase	Fatty acid and phospholipid metabolism	407532	408329	1	2
MMSYN1_0321	NULL	ORF	NULL	Cell envelope	408482	408910	1	0
MMSYN1_0322	NULL	ORF	divergent AAA domain family	Unknown function	409235	410692	1	6
MMSYN1_0323	NULL	ORF	putative lipoprotein	Cell envelope	412203	410710	-1	13
MMSYN1_0324	NULL	ORF	conserved hypothetical protein	Hypothetical proteins	412896	412372	-1	18
MMSYN1_0325	NULL	ORF	putative membrane protein	Cell envelope	414261	415751	1	3
MMSYN1_0326	NULL	ORF	conserved hypothetical protein	Hypothetical proteins	415769	416530	1	0
MMSYN1_0327	scpA	ORF	ScpA protein	DNA metabolism	416540	417376	1	4
MMSYN1_0328	scpB	ORF	segregation and condensation protein B	DNA metabolism	417360	417989	1	0
MMSYN1_0329	NULL	ORF	ribosomal large subunit pseudouridine synthase B (rRNA-uridine isomerase B) (rRNA pseudouridylylate synthase B)	Protein synthesis	418057	418815	1	0
MMSYN1_0330	NULL	ORF	deoxyguanosine kinase	Purines, pyrimidines, nucleosides, and nucleotides	418825	419442	1	2
MMSYN1_0331	NULL	ORF	conserved hypothetical protein	DNA metabolism	419454	420167	1	3
MMSYN1_0332	NULL	ORF	conserved hypothetical protein	Hypothetical proteins	420267	421094	1	0
MMSYN1_0333	vlcA	ORF	lipoprotein, putative (VlcA)	Cell envelope	421586	422005	1	0
MMSYN1_0334	vlcB	ORF	lipoprotein, putative (VlcB)	Cell envelope	422445	422924	1	1
MMSYN1_0335	vlcC	ORF	lipoprotein, putative (VlcC)	Cell envelope	423315	423773	1	0
MMSYN1_0336	NULL	ORF	PTS system, IIA component	Transport and binding proteins	423939	424388	1	0
MMSYN1_0337	NULL	ORF	PTS system ascorbate-specific enzyme IIC/IIB	Transport and binding proteins	424400	426208	1	5

MMSYN1_0338	NULL	ORF	putative lipoprotein	Cell envelope	426379	427098	1	0
MMSYN1_0339	NULL	ORF	Na+ ABC transporter, ATP-binding component	Transport and binding proteins	427501	429321	1	7
MMSYN1_0340	NULL	ORF	ABC transporter, permease protein , putative	Transport and binding proteins	429337	431127	1	2
MMSYN1_0341	NULL	ORF	viral A-type inclusion protein, putative	Unknown function	431156	432556	1	2
MMSYN1_0342	NULL	ORF	NULL	Cell envelope	432682	434868	1	4
MMSYN1_0343	NULL	ORF	conserved hypothetical protein	Hypothetical proteins	435005	435700	1	1
MMSYN1_0344	ppa	ORF	inorganic diphosphatase	Central intermediary metabolism	436316	435756	-1	1
MMSYN1_0345	NULL	ORF	conserved hypothetical protein	Hypothetical proteins	436455	437345	1	4
MMSYN1_0346	NULL	ORF	conserved hypothetical protein	Hypothetical proteins	437411	438106	1	1
MMSYN1_0347	cmk	ORF	cytidylate kinase	Purines, pyrimidines, nucleosides, and nucleotides	438115	438777	1	0
MMSYN1_0348	engA	ORF	ribosome-associated GTPase EngA	Protein synthesis	438784	440091	1	4
MMSYN1_0349	gpsA	ORF	glycerol-3-phosphate dehydrogenase [NAD(P)+] (NAD(P)H-dependent glycerol-3-phosphate dehydrogenase)	Fatty acid and phospholipid metabolism	440093	441082	1	1
MMSYN1_0350	hup	ORF	DNA-binding protein HU	DNA metabolism	441114	441386	1	0
MMSYN1_0352	NULL	ORF	conserved hypothetical protein	Hypothetical proteins	441441	441989	1	1
MMSYN1_0351	recU	ORF	recombination protein U	DNA metabolism	442461	441952	-1	1
MMSYN1_0353	NULL	ORF	NULL	Unknown function	442525	442902	1	2
MMSYN1_0354	NULL	ORF	NULL	Cell envelope	443061	444476	1	6
MMSYN1_0355	NULL	ORF	putative lipoprotein	Cell envelope	444649	445872	1	1
MMSYN1_0356	rnpB	ribozyme	NULL	NULL	445958	446302	1	1
MMSYN1_0357	NULL	ORF	putative competence-damage inducible protein	Cellular processes	446339	446809	1	4
MMSYN1_0358	recA	ORF	protein RecA	DNA metabolism	446852	447889	1	2
MMSYN1_0359	NULL	ORF	conserved hypothetical protein	Hypothetical proteins	448025	449554	1	2
MMSYN1_0360	ffh	ORF	signal recognition particle protein	Protein fate	449588	450931	1	2
MMSYN1_0361	NULL	ORF	conserved hypothetical protein	Unknown function	450935	451402	1	4
MMSYN1_0362	rpsP	ORF	ribosomal protein S16	Protein synthesis	451493	451771	1	0
MMSYN1_0363	rimM	ORF	16S rRNA processing protein RimM	Transcription	451803	452297	1	0
MMSYN1_0364	trmD	ORF	tRNA (guanine-N1)-methyltransferase	Protein synthesis	452299	453021	1	0
MMSYN1_0365	rpIS	ORF	ribosomal protein L19	Protein synthesis	453023	453406	1	3
MMSYN1_0366	ylqF	ORF	ribosome biogenesis GTP-binding protein YlqF	Protein synthesis	453505	454455	1	4
MMSYN1_0367	rnhB	ORF	ribonuclease HII	Transcription	454449	455072	1	5
MMSYN1_0368	NULL	ORF	conserved hypothetical protein	Hypothetical proteins	456890	455094	-1	8
MMSYN1_0369	NULL	ORF	YeeE/YedE family protein, putative	Unknown function	458131	456893	-1	3
MMSYN1_0370	NULL	ORF	single-strand binding family protein	DNA metabolism	458292	458597	1	0
MMSYN1_0371	NULL	ORF	ABC transporter, permease and ATP-binding componen	Transport and binding proteins	458816	460687	1	6
MMSYN1_0372	NULL	ORF	ABC transporter, permease and ATP-binding componen	Transport and binding proteins	460703	462556	1	13
MMSYN1_0373	NULL	ORF	conserved hypothetical protein	Hypothetical proteins	462590	464197	1	1
MMSYN1_0374	NULL	tRNA	NULL	NULL	464253	464329	1	2
MMSYN1_0375	NULL	ORF	conserved hypothetical protein	Hypothetical proteins	464383	465123	1	5
MMSYN1_0376	NULL	ORF	conserved hypothetical protein	Hypothetical proteins	465125	465439	1	0
MMSYN1_0377	cgtA	ORF	Obg family GTPase CgtA	Protein synthesis	465510	466811	1	3
MMSYN1_0378	nadE	ORF	NAD+ synthetase	Biosynthesis of cofactors, prosthetic groups, and carriers	466813	467550	1	2
MMSYN1_0379	NULL	ORF	conserved hypothetical protein	Hypothetical proteins	467567	467845	1	0
MMSYN1_0380	NULL	ORF	putative nicotinate-nucleotide adenyllyltransferase	Biosynthesis of cofactors, prosthetic groups, and carriers	467863	468960	1	8
MMSYN1_0381	mtnN	ORF	MTA/SAH nucleosidase	Purines, pyrimidines, nucleosides, and nucleotides	468965	469624	1	0
MMSYN1_0382	NULL	ORF	deoxynucleoside kinase	Purines, pyrimidines, nucleosides, and nucleotides	469634	470272	1	0
MMSYN1_0383	NULL	ORF	putative lipoprotein	Cell envelope	470394	471113	1	3
MMSYN1_0384	NULL	ORF	putative lipoprotein	Cell envelope	471190	471927	1	0
MMSYN1_0385	NULL	ORF	NULL	Cell envelope	471937	472617	1	1
MMSYN1_0386	NULL	ORF	putative lipoprotein	Cell envelope	472656	473501	1	3
MMSYN1_0387	trmU	ORF	tRNA (5-methylaminomethyl-2-thiouridylate)-methyltransferase	Protein synthesis	473609	474736	1	4

MMSYN1_0388	NULL	ORF	conserved hypothetical protein	Hypothetical proteins	474783	475400	1	4
MMSYN1_0389	NULL	ORF	conserved hypothetical protein	Hypothetical proteins	475476	477620	1	2
MMSYN1_0390	fmt	ORF	methionyl-tRNA formyltransferase	Protein synthesis	477610	478563	1	2
MMSYN1_0391	efp	ORF	translation elongation factor P	Protein synthesis	478650	479204	1	4
MMSYN1_0392	NULL	ORF	conserved hypothetical protein	Hypothetical proteins	479222	479524	1	0
MMSYN1_0393	tig	ORF	trigger factor	Protein fate	479541	480827	1	6
MMSYN1_0394	lon	ORF	ATP-dependent protease La	Protein fate	480950	483310	1	2
MMSYN1_0395	rarA	ORF	recombination factor protein RarA	DNA metabolism	483409	484644	1	2
MMSYN1_0396	NULL	ORF	putative lipoprotein	Cell envelope	486898	484673	-1	14
MMSYN1_0397	NULL	ORF	putative lipoprotein	Cell envelope	489240	486949	-1	1
MMSYN1_0398	NULL	ORF	putative lipoprotein	Cell envelope	491742	489280	-1	12
MMSYN1_0399	NULL	ORF	NULL	Transport and binding proteins	491892	497153	1	12
MMSYN1_0400	NULL	ORF	ThiJ/Pfpl family protein	Unknown function	497201	497752	1	0
MMSYN1_0401	NULL	ORF	NULL	Protein fate	497850	499634	1	9
MMSYN1_0402	NULL	ORF	putative metalloprotease	Protein fate	499639	500133	1	6
MMSYN1_0403	era	ORF	GTP-binding protein Era	Protein synthesis	500137	501042	1	8
MMSYN1_0404	recO	ORF	DNA repair protein RecO	DNA metabolism	501042	501791	1	0
MMSYN1_0405	glyS	ORF	glycine--tRNA ligase	Protein synthesis	501855	503225	1	4
MMSYN1_0406	dnaG	ORF	DNA primase	DNA metabolism	503260	505098	1	1
MMSYN1_0407	rpoD	ORF	RNA polymerase sigma-A factor	Transcription	505101	506621	1	0
MMSYN1_0408	NULL	ORF	conserved hypothetical protein	Hypothetical proteins	506621	507298	1	1
MMSYN1_0409	NULL	ORF	NIF3 family protein	Transcription	507285	508061	1	3
MMSYN1_0410	NULL	ORF	superfamily II DNA and RNA helicase	DNA metabolism	508070	509431	1	2
MMSYN1_0411	NULL	ORF	putative membrane protein	Cell envelope	509471	510985	1	3
MMSYN1_0412	NULL	ORF	putative membrane protein	Cell envelope	511101	515255	1	5
MMSYN1_0413	apt	ORF	adenine phosphoribosyltransferase	Purines, pyrimidines, nucleosides, and nucleotides	515267	515779	1	0
MMSYN1_0414	NULL	ORF	RelA/SpoT family protein	Cellular processes	515862	518126	1	14
MMSYN1_0415	smc	ORF	chromosome segregation protein SMC	DNA metabolism	521129	518163	-1	2
MMSYN1_0416	NULL	ORF	conserved hypothetical protein	Hypothetical proteins	521824	521435	-1	1
MMSYN1_0417	NULL	ORF	cdse	Unknown function	522282	521827	-1	2
MMSYN1_0418	rnc	ORF	ribonuclease III	Transcription	523113	522415	-1	5
MMSYN1_0419	plsX	ORF	fatty acid/phospholipid synthesis protein PlsX	Fatty acid and phospholipid metabolism	524107	523103	-1	2
MMSYN1_0420	NULL	ORF	dihydroxyacetone kinase 2 domain protein	Unknown function	525783	524140	-1	5
MMSYN1_0421	NULL	ORF	conserved hypothetical protein	Hypothetical proteins	526119	525808	-1	0
MMSYN1_0422	rpmB	ORF	ribosomal protein L28	Protein synthesis	526288	526485	1	0
MMSYN1_0423	NULL	tRNA	NULL	NULL	526549	526633	1	0
MMSYN1_0424	NULL	ORF	conserved hypothetical protein	Hypothetical proteins	526716	527159	1	2
MMSYN1_0425	NULL	ORF	phosphate ABC transporter, substrate-binding component	Transport and binding proteins	527248	528378	1	1
MMSYN1_0426	NULL	ORF	phosphate ABC transport system, permease component	Transport and binding proteins	528430	530520	1	2
MMSYN1_0427	pstB	ORF	phosphate ABC transporter, ATP-binding protein	Transport and binding proteins	530513	531322	1	0
MMSYN1_0428	phoU	ORF	phosphate transport system regulatory protein PhoU	Regulatory functions	531331	532005	1	0
MMSYN1_0429	NULL	ORF	peptidase, M41 family	Cellular processes	532072	533301	1	5
MMSYN1_0430	NULL	ORF	putative transcriptional regulator	Regulatory functions	533291	533626	1	0
MMSYN1_0431	NULL	ORF	conserved hypothetical protein	Hypothetical proteins	533614	534387	1	0
MMSYN1_0432	metK	ORF	methionine adenosyltransferase	Central intermediary metabolism	534597	535760	1	0
MMSYN1_0433	NULL	ORF	copper homeostasis protein	Transport and binding proteins	535751	536434	1	0
MMSYN1_0434	trmFO	ORF	tRNA:M(5)U-54 methyltransferase	Protein synthesis	536427	537743	1	0
MMSYN1_0435	NULL	ORF	phosphomannose isomerase type I	Energy metabolism	537769	538698	1	6
MMSYN1_0436	ung	ORF	uracil-DNA glycosylase (UDG)	DNA metabolism	538691	539344	1	1
MMSYN1_0437	NULL	ORF	cmp-binding-factor	Transport and binding proteins	539417	540397	1	0
MMSYN1_0438	NULL	ORF	protein hit	Unknown function	540826	540428	-1	0
MMSYN1_0439	NULL	ORF	putative lipoprotein	Cell envelope	542985	540829	-1	9
MMSYN1_0440	NULL	ORF	putative lipoprotein	Cell envelope	545921	542985	-1	3
MMSYN1_0441	NULL	ORF	probable cysteine desulfurase	Central intermediary metabolism	546124	547362	1	5
MMSYN1_0442	NULL	ORF	nitrogen fixation protein nifu	Central intermediary metabolism	547365	547802	1	1
MMSYN1_0443	mthfs	ORF	5-formyltetrahydrofolate cyclo-ligase	Central intermediary metabolism	547795	548358	1	3

MMSYN1_0444	NULL	ORF	endopeptidase O	Protein fate	548379	550274	1	17
MMSYN1_0445	pgi	ORF	glucose-6-phosphate isomerase	Energy metabolism	550494	551777	1	6
MMSYN1_0446	NULL	ORF	conserved hypothetical protein	Hypothetical proteins	551789	552253	1	5
MMSYN1_0447	NULL	ORF	dUTPase superfamily	Purines, pyrimidines, nucleosides, and nucleotides	552275	552778	1	6
MMSYN1_0448	NULL	ORF	rRNA methylase	Protein synthesis	552795	553562	1	0
MMSYN1_0449	tnpA_2	ORF	IS1296 transposase protein A	Mobile and extrachromosomal element functions	553645	554187	1	0
MMSYN1_0450	tnpB_2	ORF	IS1296 transposase protein B	Mobile and extrachromosomal element functions	554325	555056	1	0
MMSYN1_0451	NULL	ORF	NADP-dependent glyceraldehyde-3-phosphate dehydrogenase (non-phosphorylating glyceraldehyde 3-phosphate dehydrogenase)(glyceraldehyde-3-phosphate dehydrogenase [nadp+]) (triosephosphatedehydrogenase)	Energy metabolism	555218	556633	1	0
MMSYN1_0452	parE	ORF	DNA topoisomerase IV, B subunit	DNA metabolism	556820	558751	1	1
MMSYN1_0453	parC	ORF	DNA topoisomerase IV, A subunit	DNA metabolism	558753	561449	1	3
MMSYN1_0454	NULL	ORF	hypothetical protein	NULL	561557	563740	1	5
MMSYN1_0455	NULL	ORF	NULL	Cell envelope	565299	563782	-1	0
MMSYN1_0924	NULL	ORF	conserved domain protein	Hypothetical proteins	565789	566184	1	0
MMSYN1_0460	NULL	ORF	bacterial surface protein 26-residue repeat protein (3 repeats)	Unclassified	566641	570003	1	10
MMSYN1_0461	tnpB_3	ORF	IS1296 transposase protein B	Mobile and extrachromosomal element functions	570785	570054	-1	7
MMSYN1_0462	tnpA_3	ORF	IS1296 transposase protein A	Mobile and extrachromosomal element functions	571465	570923	-1	0
MMSYN1_0463	NULL	ORF	NADH dependent flavin oxidoreductase	Energy metabolism	572708	571530	-1	11
MMSYN1_0464	NULL	ORF	lipoate--protein ligase	Protein fate	573745	572708	-1	1
MMSYN1_0465	NULL	ORF	conserved hypothetical protein	Hypothetical proteins	574580	573723	-1	0
MMSYN1_0466	NULL	ORF	glycine cleavage system H protein	Energy metabolism	574926	574582	-1	1
MMSYN1_0467	NULL	ORF	triacylglycerol lipase	Fatty acid and phospholipid metabolism	575113	575907	1	6
MMSYN1_0468	NULL	ORF	lipase-esterase	Fatty acid and phospholipid metabolism	575909	576703	1	7
MMSYN1_0469	NULL	ORF	lipase-esterase	Fatty acid and phospholipid metabolism	576697	577506	1	0
MMSYN1_0470	NULL	ORF	conserved hypothetical protein	Hypothetical proteins	578658	577525	-1	5
MMSYN1_0471	NULL	ORF	hypothetical protein	NULL	578920	578789	-1	0
MMSYN1_0472	NULL	ORF	putative lipoprotein	Cell envelope	578922	580322	1	5
MMSYN1_0473	NULL	ORF	ABC transporter, ATP binding protein	Transport and binding proteins	580469	581188	1	2
MMSYN1_0474	NULL	ORF	integral membrane protein	Cell envelope	581188	581943	1	1
MMSYN1_0475	ldh	ORF	L-lactate dehydrogenase	Energy metabolism	583028	582072	-1	0
MMSYN1_0476	nagA	ORF	N-acetylglucosamine-6-phosphate deacetylase	Central intermediary metabolism	584237	583080	-1	5
MMSYN1_0477	NULL	ORF	conserved hypothetical protein	Hypothetical proteins	584406	585140	1	3
MMSYN1_0478	NULL	ORF	conserved hypothetical protein	Hypothetical proteins	585736	585152	-1	6
MMSYN1_0479	NULL	ORF	NULL	Hypothetical proteins	587387	585741	-1	13
MMSYN1_0480	NULL	ORF	conserved hypothetical protein	Hypothetical proteins	587539	589539	1	0
MMSYN1_0481	vlcE	ORF	lipoprotein, putative (VlcE)	Cell envelope	590048	589611	-1	2
MMSYN1_0482	rpsU	ORF	ribosomal protein S21	Protein synthesis	590364	590528	1	1
MMSYN1_0483	ruvA	ORF	holliday junction DNA helicase RuvA	DNA metabolism	590637	591197	1	3
MMSYN1_0484	ruvB	ORF	holliday junction ATP-dependent DNA helicase RuvB	DNA metabolism	591214	592137	1	17
MMSYN1_0485	NULL	ORF	dihydrolipoamide dehydrogenase	Energy metabolism	592215	593573	1	16
MMSYN1_0486	NULL	ORF	conserved hypothetical protein	Hypothetical proteins	594398	593589	-1	1
MMSYN1_0487	NULL	ORF	conserved hypothetical protein	Hypothetical proteins	594474	595394	1	8
MMSYN1_0488	yqeH	ORF	ribosome biogenesis GTPase YqeH	Protein synthesis	595403	596506	1	3
MMSYN1_0489	dinB	ORF	DNA polymerase IV	DNA metabolism	597738	596515	-1	3
MMSYN1_0490	NULL	ORF	papain family cysteine protease, putative	Protein fate	597882	600620	1	17

MMSYN1_0491	udk	ORF	uridine kinase	Purines, pyrimidines, nucleosides, and nucleotides	601321	600698	-1	9
MMSYN1_0492	NULL	ORF	conserved hypothetical protein	Hypothetical proteins	601785	601345	-1	3
MMSYN1_0493	NULL	ORF	Xaa-His dipeptidase	Protein fate	603207	601858	-1	10
MMSYN1_0494	NULL	ORF	putative N-acetylmannosamine-6-phosphate 2-epimerase (ManNAc-6-P epimerase)	Central intermediary metabolism	604043	603363	-1	1
MMSYN1_0495	NULL	ORF	ROK family protein	Unknown function	604977	604102	-1	4
MMSYN1_0496	NULL	ORF	NULL	Energy metabolism	605419	604970	-1	2
MMSYN1_0497	NULL	ORF	sodium:solute symporter family	Transport and binding proteins	607131	605428	-1	25
MMSYN1_0498	nanA	ORF	N-acetylneuraminate lyase (N-acetylneuraminic acidaldolase) (N-acetylneuraminate pyruvate-lyase) (Sialic acid lyase)(Sialate lyase) (Sialic acid aldolase)	Central intermediary metabolism	608020	607133	-1	0
MMSYN1_0499	rpmA	ORF	ribosomal protein L27	Protein synthesis	608466	608185	-1	2
MMSYN1_0500	NULL	ORF	conserved hypothetical protein	Hypothetical proteins	608731	608468	-1	1
MMSYN1_0501	rplU	ORF	ribosomal protein L21	Protein synthesis	609087	608785	-1	0
MMSYN1_0503	NULL	ORF	conserved hypothetical protein	Hypothetical proteins	609634	609233	-1	1
MMSYN1_0504	NULL	ORF	conserved hypothetical protein	Hypothetical proteins	610544	609657	-1	9
MMSYN1_0505	NULL	ORF	putative lipoprotein	Cell envelope	610920	611993	1	0
MMSYN1_0506	NULL	tRNA	NULL	NULL	612174	612086	-1	0
MMSYN1_0507	NULL	tRNA	NULL	NULL	612260	612185	-1	0
MMSYN1_0508	NULL	tRNA	NULL	NULL	612339	612265	-1	0
MMSYN1_0509	NULL	tRNA	NULL	NULL	612429	612346	-1	1
MMSYN1_0510	NULL	tRNA	NULL	NULL	612511	612436	-1	0
MMSYN1_0511	NULL	ORF	conserved hypothetical protein	Hypothetical proteins	613261	612638	-1	0
MMSYN1_0512	plsC	ORF	1-acyl-sn-glycerol-3-phosphate acyltransferase	Fatty acid and phospholipid metabolism	614248	613310	-1	1
MMSYN1_0513	acpS	ORF	holo-[acyl-carrier-protein] synthase	Fatty acid and phospholipid metabolism	614746	614414	-1	3
MMSYN1_0514	NULL	ORF	conserved hypothetical protein	Hypothetical proteins	615842	614766	-1	13
MMSYN1_0515	NULL	ORF	deoxycytidylate deaminase (dCMP deaminase)	Purines, pyrimidines, nucleosides, and nucleotides	616365	615883	-1	3
MMSYN1_0516	NULL	ORF	putative membrane protein	Cell envelope	617669	616368	-1	6
MMSYN1_0517	NULL	ORF	ribosomal large subunit pseudouridine synthase D	Protein synthesis	618594	617662	-1	5
MMSYN1_0518	lspA	ORF	signal peptidase II	Protein fate	619183	618575	-1	0
MMSYN1_0519	ileS	ORF	isoleucine--tRNA ligase	Protein synthesis	621921	619174	-1	6
MMSYN1_0520	NULL	ORF	conserved hypothetical protein	Hypothetical proteins	623603	622614	-1	7
MMSYN1_0521	NULL	ORF	conserved hypothetical protein	Hypothetical proteins	624032	623616	-1	0
MMSYN1_0522	ftsZ	ORF	cell division protein FtsZ	Cellular processes	625201	624044	-1	13
MMSYN1_0523	NULL	ORF	conserved hypothetical protein	Hypothetical proteins	626476	625316	-1	14
MMSYN1_0524	mraW	ORF	S-adenosyl-methyltransferase MraW	Cell envelope	627411	626485	-1	7
MMSYN1_0525	mraZ	ORF	protein MraZ	Unknown function	627821	627420	-1	8
MMSYN1_0526	rpmF	ORF	ribosomal protein L32	Protein synthesis	628107	627928	-1	0
MMSYN1_0527	NULL	ORF	conserved hypothetical protein	Hypothetical proteins	628640	628122	-1	0
MMSYN1_0528	pheT	ORF	phenylalanyl-tRNA synthetase, beta subunit	Protein synthesis	631024	628640	-1	7
MMSYN1_0529	pheS	ORF	phenylalanyl-tRNA synthetase, alpha subunit	Protein synthesis	632085	631033	-1	1
MMSYN1_0530	NULL	ORF	conserved hypothetical protein	Hypothetical proteins	632723	632115	-1	3
MMSYN1_0531	NULL	ORF	efflux ABC transporter, permease protein	Transport and binding proteins	637180	632732	-1	7
MMSYN1_0532	rrf	rRNA	NULL	NULL	637404	637296	-1	0
MMSYN1_0533	rri	rRNA	NULL	NULL	640373	637479	-1	0
MMSYN1_0534	rrs	rRNA	NULL	NULL	642127	640604	-1	0
MMSYN1_0535	argS	ORF	arginine--tRNA ligase	Protein synthesis	644003	642339	-1	9
MMSYN1_0536	frr	ORF	ribosome recycling factor	Protein synthesis	644553	644005	-1	4
MMSYN1_0537	pyrH	ORF	UMP kinase	Purines, pyrimidines, nucleosides, and nucleotides	645277	644564	-1	1
MMSYN1_0538	NULL	ORF	conserved hypothetical protein	Hypothetical proteins	646016	645411	-1	1
MMSYN1_0539	tsf	ORF	translation elongation factor Ts	Protein synthesis	646903	646016	-1	0
MMSYN1_0540	rpsB	ORF	ribosomal protein S2	Protein synthesis	647793	646915	-1	2
MMSYN1_0541	dnaJ	ORF	chaperone protein DnaJ	Protein fate	649119	648001	-1	1
MMSYN1_0542	dnaK	ORF	chaperone protein DnaK	Protein fate	650958	649183	-1	3
MMSYN1_0543	grpE	ORF	co-chaperone GrpE	Protein fate	651619	651017	-1	5

MMSYN1_0544	hrcA	ORF	heat-inducible transcription repressor HrcA	Regulatory functions	652643	651621	-1	1
MMSYN1_0545	NULL	ORF	ATPase family associated with various cellular activities (AAA) protein	Unknown function	654789	652648	-1	6
MMSYN1_0546	NULL	ORF	NULL	Unknown function	655188	654952	-1	0
MMSYN1_0547	NULL	ORF	NULL	Unknown function	655817	655176	-1	8
MMSYN1_0548	NULL	ORF	rRNA Methylase	Protein synthesis	656362	655817	-1	2
MMSYN1_0549	NULL	ORF	Ham1 family	Unknown function	656977	656375	-1	0
MMSYN1_0550	NULL	ORF	NULL	Cell envelope	657179	659694	1	11
MMSYN1_0551	NULL	ORF	putative lipoprotein	Cell envelope	659874	662378	1	18
MMSYN1_0552	NULL	ORF	conserved hypothetical integrative conjugal element protein	Mobile and extrachromosomal element functions	662695	663483	1	0
MMSYN1_0553	NULL	ORF	conserved hypothetical integrative conjugal element protein	Mobile and extrachromosomal element functions	663752	664993	1	3
MMSYN1_0554	NULL	ORF	C-5 cytosine-specific DNA methylase	Mobile and extrachromosomal element functions	665166	665999	1	0
MMSYN1_0555	NULL	ORF	membrane protein, putative (TraD/TraG family)	Mobile and extrachromosomal element functions	666028	668043	1	16
MMSYN1_0556	NULL	ORF	conserved hypothetical integrative conjugal element protein	Mobile and extrachromosomal element functions	668059	669015	1	11
MMSYN1_0557	NULL	ORF	conserved hypothetical integrative conjugal element protein	Mobile and extrachromosomal element functions	668999	669916	1	0
MMSYN1_0558	NULL	ORF	single-strand binding family protein	Mobile and extrachromosomal element functions	669931	670347	1	2
MMSYN1_0559	NULL	ORF	conserved hypothetical integrative conjugal element protein	Mobile and extrachromosomal element functions	670612	671802	1	2
MMSYN1_0560	NULL	ORF	putative lipoprotein	Mobile and extrachromosomal element functions	672040	673572	1	2
MMSYN1_0561	NULL	ORF	conserved hypothetical integrative conjugal element protein	Mobile and extrachromosomal element functions	673574	673765	1	0
MMSYN1_0562	NULL	ORF	conserved hypothetical integrative conjugal element protein	Mobile and extrachromosomal element functions	673862	674092	1	0
MMSYN1_0563	NULL	ORF	putative membrane protein	Mobile and extrachromosomal element functions	674120	676843	1	5
MMSYN1_0564	NULL	ORF	conserved hypothetical integrative conjugal element protein	Mobile and extrachromosomal element functions	676950	677135	1	0
MMSYN1_0565	NULL	ORF	conserved hypothetical integrative conjugal element protein	Mobile and extrachromosomal element functions	677225	677602	1	4
MMSYN1_0566	NULL	ORF	NULL	Mobile and extrachromosomal element functions	677609	679531	1	5
MMSYN1_0567	NULL	ORF	putative membrane protein	Mobile and extrachromosomal element functions	679556	682399	1	7
MMSYN1_0568	NULL	ORF	conserved hypothetical integrative conjugal element protein	Mobile and extrachromosomal element functions	682412	683077	1	6
MMSYN1_0569	NULL	ORF	putative membrane protein	Mobile and extrachromosomal element functions	683124	688091	1	7
MMSYN1_0570	NULL	ORF	conserved hypothetical integrative conjugal element protein	Mobile and extrachromosomal element functions	688547	689293	1	0
MMSYN1_0571	NULL	ORF	conserved hypothetical integrative conjugal element protein	Mobile and extrachromosomal element functions	689489	689854	1	0
MMSYN1_0572	NULL	ORF	CobQ/CobB/MinD/ParA nucleotide binding domain, putative	Mobile and extrachromosomal element functions	690078	690992	1	4

MMSYN1_0573	NULL	ORF	conserved hypothetical integrative conjugal element protein	Mobile and extrachromosomal element functions	691042	692274	1	0
MMSYN1_0574	NULL	ORF	putative lipoprotein	Cell envelope	692861	695401	1	12
MMSYN1_0575	atpD_1	ORF	ATP synthase F1, beta subunit	Energy metabolism	696836	695457	-1	11
MMSYN1_0576	atpA_1	ORF	FOF1 ATP synthase, alpha subunit	Energy metabolism	698383	696836	-1	9
MMSYN1_0577	NULL	ORF	conserved hypothetical protein	Hypothetical proteins	700691	698388	-1	4
MMSYN1_0578	NULL	ORF	conserved hypothetical protein	Hypothetical proteins	701136	700693	-1	0
MMSYN1_0579	NULL	ORF	conserved hypothetical protein	Hypothetical proteins	702047	701136	-1	6
MMSYN1_0580	NULL	ORF	conserved hypothetical protein	Hypothetical proteins	702543	702049	-1	6
MMSYN1_0581	NULL	ORF	putative membrane protein	Cell envelope	703981	702518	-1	8
MMSYN1_0582	NULL	ORF	putative lipoprotein	Cell envelope	706598	704013	-1	23
MMSYN1_0583	NULL	ORF	mycoplasma virulence signal region (Myco_arth_vir_N) family	Unknown function	708873	706621	-1	21
MMSYN1_0584	NULL	ORF	putative lipoprotein	Cell envelope	711715	709145	-1	2
MMSYN1_0585	NULL	ORF	mycoplasma virulence signal region (Myco_arth_vir_N) family	Unknown function	713984	711735	-1	9
MMSYN1_0586	NULL	ORF	putative lipoprotein	Cell envelope	716732	714177	-1	11
MMSYN1_0587	NULL	ORF	mycoplasma virulence signal region (Myco_arth_vir_N) family	Unknown function	718999	716747	-1	13
MMSYN1_0588	NULL	ORF	putative lipoprotein	Cell envelope	721780	719219	-1	12
MMSYN1_0589	NULL	ORF	mycoplasma virulence signal region (Myco_arth_vir_N) family	Unknown function	724058	721800	-1	18
MMSYN1_0925	NULL	ORF	conserved domain protein	Hypothetical proteins	725553	724657	-1	1
MMSYN1_0926	NULL	ORF	hypothetical protein	NULL	726226	725660	-1	6
MMSYN1_0927	NULL	ORF	hypothetical protein	NULL	726177	726560	1	0
MMSYN1_0590	NULL	ORF	type III restriction enzyme, res subunit	DNA metabolism	727071	726553	-1	9
MMSYN1_0591	mmyCImod	ORF	NULL	DNA metabolism	728260	727058	-1	18
MMSYN1_0592	NULL	ORF	cdsf	Unknown function	730587	729115	-1	1
MMSYN1_0593	NULL	ORF	hypothetical protein	NULL	731089	730811	-1	0
MMSYN1_0594	NULL	ORF	putative membrane protein	Cell envelope	732998	731220	-1	12
MMSYN1_0595	NULL	ORF	NULL	Hypothetical proteins	733270	734646	1	3
MMSYN1_0596	NULL	ORF	hypothetical protein	NULL	735282	737948	1	13
MMSYN1_0597	NULL	ORF	NULL	Unknown function	738368	738793	1	8
MMSYN1_0598	NULL	ORF	conserved hypothetical protein	Hypothetical proteins	739136	740662	1	0
MMSYN1_0599	NULL	ORF	conserved hypothetical protein	Hypothetical proteins	740941	740801	-1	2
MMSYN1_0600	NULL	ORF	RNA-metabolising metallo-beta-lactamase family	Transcription	741755	743587	1	6
MMSYN1_0601	NULL	ORF	putative membrane protein	Cell envelope	743662	744606	1	3
MMSYN1_0602	NULL	ORF	NULL	Hypothetical proteins	744738	746000	1	1
MMSYN1_0604	NULL	ORF	LemA family	Unknown function	746503	747171	1	5
MMSYN1_0603	NULL	snoRNA	NULL	NULL	746854	746941	1	0
MMSYN1_0605	NULL	ORF	hypothetical protein	NULL	747354	747662	1	0
MMSYN1_0606	pgk	ORF	phosphoglycerate kinase	Energy metabolism	749143	747929	-1	0
MMSYN1_0607	gap	ORF	glyceraldehyde-3-phosphate dehydrogenase, type I	Energy metabolism	750271	749255	-1	2
MMSYN1_0608	NULL	ORF	primosomal protein	DNA metabolism	751310	750372	-1	6
MMSYN1_0609	NULL	ORF	chromosome replication initiation/membrane attachment protein	DNA metabolism	752504	751320	-1	3
MMSYN1_0610	mutM	ORF	DNA-formamidopyrimidine glycosylase	DNA metabolism	753485	752661	-1	0
MMSYN1_0611	polA	ORF	DNA polymerase I superfamily	DNA metabolism	756231	753496	-1	8
MMSYN1_0612	NULL	ORF	DNA polymerase III, alpha subunit subfamily, putative	DNA metabolism	759203	756240	-1	11
MMSYN1_0613	tyrS	ORF	tyrosine--tRNA ligase	Protein synthesis	760642	759398	-1	8
MMSYN1_0614	NULL	ORF	nicotinate phosphoribosyltransferase	Biosynthesis of cofactors, prosthetic groups, and carriers	761712	760651	-1	9
MMSYN1_0615	NULL	ORF	phenylalanine-tRNA ligase	Energy metabolism	762298	761690	-1	0
MMSYN1_0616	NULL	ORF	EDD domain protein, DegV family, putative	Unknown function	762373	763212	1	0
MMSYN1_0617	NULL	ORF	DegV family protein	Unknown function	763223	764074	1	0
MMSYN1_0618	NULL	tRNA	NULL	NULL	764184	764110	-1	3
MMSYN1_0619	NULL	tRNA	NULL	NULL	764297	764222	-1	0
MMSYN1_0620	NULL	ORF	ferric uptake regulator	Regulatory functions	764837	764373	-1	4
MMSYN1_0621	NULL	ORF	conserved domain protein	Hypothetical proteins	765059	764838	-1	0
MMSYN1_0622	NULL	ORF	putative lipoprotein	Cell envelope	765445	765083	-1	1
MMSYN1_0623	NULL	ORF	conserved hypothetical protein	Hypothetical proteins	766502	765432	-1	8
MMSYN1_0624	NULL	tRNA	NULL	NULL	766678	766603	-1	2
MMSYN1_0625	arcC_1	ORF	carbamate kinase 1	Energy metabolism	767731	766799	-1	2
MMSYN1_0626	aguA	ORF	agmatine deiminase	Central intermediary metabolism	768942	767848	-1	5

MMSYN1_0627	NULL	ORF	NULL	Energy metabolism	770367	768949	-1	11
MMSYN1_0628	argF	ORF	ornithine carbamoyltransferase	Amino acid biosynthesis	771491	770394	-1	13
MMSYN1_0629	NULL	ORF	hypothetical protein	NULL	772163	771786	-1	1
MMSYN1_0630	NULL	ORF	ABC transporter, ATP-binding component	Transport and binding proteins	772384	773271	1	2
MMSYN1_0631	NULL	ORF	NULL	Transport and binding proteins	773273	774037	1	3
MMSYN1_0632	NULL	ORF	conserved hypothetical protein	Hypothetical proteins	774547	774071	-1	4
MMSYN1_0633	NULL	ORF	putative membrane protein	Cell envelope	776197	774638	-1	2
MMSYN1_0634	leuS	ORF	leucine--tRNA ligase	Protein synthesis	778678	776264	-1	7
MMSYN1_0635	NULL	tRNA	NULL	NULL	778892	778816	-1	0
MMSYN1_0636	NULL	ORF	putative lipoprotein	Cell envelope	781754	778965	-1	9
MMSYN1_0637	rpsI	ORF	ribosomal protein S9	Protein synthesis	782311	781913	-1	2
MMSYN1_0638	rplM	ORF	ribosomal protein L13	Protein synthesis	782766	782311	-1	3
MMSYN1_0639	NULL	ORF	efflux ABC transporter, permease protein	Transport and binding proteins	787041	782896	-1	7
MMSYN1_0640	NULL	ORF	tRNA pseudouridine synthase A (tRNA-uridine isomerase) (tRNA pseudouridylate synthase I)	Protein synthesis	787891	787136	-1	0
MMSYN1_0641	NULL	ORF	ABC transporter, permease component	Transport and binding proteins	788904	787894	-1	0
MMSYN1_0642	NULL	ORF	cobalt import ATP-binding protein CbiO 1	Transport and binding proteins	789829	788918	-1	0
MMSYN1_0643	NULL	ORF	cobalt import ATP-binding protein CbiO 2	Transport and binding proteins	791043	789817	-1	2
MMSYN1_0644	rplQ	ORF	ribosomal protein L17	Protein synthesis	791510	791151	-1	0
MMSYN1_0645	rpoA	ORF	DNA-directed RNA polymerase, alpha subunit	Transcription	792483	791530	-1	0
MMSYN1_0646	rpsK	ORF	30S ribosomal protein S11	Protein synthesis	792876	792487	-1	0
MMSYN1_0647	rpsM	ORF	30S ribosomal protein S13	Protein synthesis	793267	792902	-1	0
MMSYN1_0648	rpmJ	ORF	ribosomal protein L36	Protein synthesis	793417	793304	-1	0
MMSYN1_0649	infA	ORF	translation initiation factor IF-1	Protein synthesis	793710	793486	-1	0
MMSYN1_0650	map	ORF	methionine aminopeptidase, type I	Protein fate	794477	793722	-1	4
MMSYN1_0651	adk	ORF	adenylate kinase	Purines, pyrimidines, nucleosides, and nucleotides	795118	794477	-1	6
MMSYN1_0652	secY	ORF	preprotein translocase, SecY subunit	Protein fate	796694	795246	-1	0
MMSYN1_0653	rplO	ORF	ribosomal protein L15	Protein synthesis	797131	796694	-1	0
MMSYN1_0654	rpsE	ORF	30S ribosomal protein S5	Protein synthesis	797914	797150	-1	0
MMSYN1_0655	rplR	ORF	ribosomal protein L18	Protein synthesis	798283	797933	-1	0
MMSYN1_0656	rplF	ORF	ribosomal protein L6	Protein synthesis	798851	798309	-1	0
MMSYN1_0657	rpsH	ORF	ribosomal protein S8	Protein synthesis	799254	798865	-1	0
MMSYN1_0658	rpsN	ORF	ribosomal protein S14p/S29e	Protein synthesis	799459	799274	-1	0
MMSYN1_0659	rplE	ORF	50S ribosomal protein L5 (BL6)	Protein synthesis	800020	799478	-1	0
MMSYN1_0660	rplX	ORF	ribosomal protein L24	Protein synthesis	800365	800039	-1	0
MMSYN1_0661	rplN	ORF	ribosomal protein L14	Protein synthesis	800747	800379	-1	0
MMSYN1_0662	rpsQ	ORF	30S ribosomal protein S17	Protein synthesis	801020	800763	-1	0
MMSYN1_0663	rpmC	ORF	50S ribosomal protein L29	Protein synthesis	801436	801020	-1	0
MMSYN1_0664	rplP	ORF	ribosomal protein L16	Protein synthesis	801849	801436	-1	0
MMSYN1_0665	rpsC	ORF	ribosomal protein S3	Protein synthesis	802553	801852	-1	0
MMSYN1_0666	rplV	ORF	ribosomal protein L22	Protein synthesis	802906	802571	-1	0
MMSYN1_0667	rpsS	ORF	ribosomal protein S19	Protein synthesis	803196	802930	-1	0
MMSYN1_0668	rplB	ORF	ribosomal protein L2	Protein synthesis	804066	803218	-1	0
MMSYN1_0669	rplW	ORF	ribosomal protein L23	Protein synthesis	804405	804121	-1	0
MMSYN1_0670	rplD	ORF	ribosomal protein L4/L1 family	Protein synthesis	805031	804405	-1	0
MMSYN1_0671	rplC	ORF	50S ribosomal protein L3	Protein synthesis	805715	805044	-1	5
MMSYN1_0672	rpsJ	ORF	ribosomal protein S10	Protein synthesis	806099	805791	-1	0
MMSYN1_0673	dhaK	ORF	dihydroxyacetone kinase, DhaK subunit	Regulatory functions	807349	806351	-1	3
MMSYN1_0674	NULL	ORF	trehalose-6-phosphate hydrolase (Alpha, alpha-phosphotrehalase)	Energy metabolism	809085	807457	-1	35
MMSYN1_0675	NULL	ORF	PTS system, trehalose-specific iibc component	Transport and binding proteins	810640	809093	-1	14
MMSYN1_0676	NULL	ORF	transcription regulator, LacI family	Regulatory functions	811692	810706	-1	7
MMSYN1_0677	NULL	ORF	putative membrane protein	Cell envelope	812217	813128	1	1
MMSYN1_0678	NULL	tRNA	NULL	NULL	813445	813370	-1	0
MMSYN1_0679	NULL	tRNA	NULL	NULL	813533	813458	-1	0
MMSYN1_0680	NULL	tRNA	NULL	NULL	813616	813541	-1	0
MMSYN1_0681	NULL	tRNA	NULL	NULL	813699	813624	-1	0
MMSYN1_0682	NULL	ORF	putative lipoprotein	Cell envelope	814964	813801	-1	7
MMSYN1_0683	NULL	ORF	conserved hypothetical protein	Hypothetical proteins	815832	815077	-1	8

MMSYN1_0684	folD	ORF	bifunctional protein FolD	Biosynthesis of cofactors, prosthetic groups, and carriers	816688	815822	-1	0
MMSYN1_0685	NULL	ORF	sodium transport protein	Transport and binding proteins	818298	816697	-1	10
MMSYN1_0686	NULL	ORF	K+, Na+ uptake protein integral membrane subunit	Cell envelope	818377	819105	1	4
MMSYN1_0687	gatB	ORF	glutamyl-tRNA(Gln) amidotransferase, B subunit	Protein synthesis	820571	819132	-1	7
MMSYN1_0688	gatA	ORF	glutamyl-tRNA(Gln) amidotransferase subunit A (Glu-ADTsubunit A)	Protein synthesis	822030	820573	-1	6
MMSYN1_0689	gatC	ORF	glutamyl-tRNA(Gln) amidotransferase, C subunit	Protein synthesis	822326	822030	-1	6
MMSYN1_0690	ligA	ORF	DNA ligase, NAD-dependent	DNA metabolism	824334	822328	-1	17
MMSYN1_0691	NULL	ORF	putative membrane protein	Cell envelope	826359	824338	-1	10
MMSYN1_0692	NULL	ORF	23S rRNA pseudouridine synthase	Protein synthesis	827270	826362	-1	10
MMSYN1_0693	NULL	ORF	conserved , caax amino protease family	Transport and binding proteins	828241	827273	-1	5
MMSYN1_0694	NULL	ORF	phosphocarrier, HPr family	Regulatory functions	828566	828297	-1	1
MMSYN1_0695	NULL	ORF	UvrD/REP helicase domain protein	DNA metabolism	830799	828631	-1	3
MMSYN1_0696	NULL	ORF	RDD family protein	Transport and binding proteins	831571	830816	-1	3
MMSYN1_0697	NULL	ORF	glycosyltransferase	Cell envelope	832527	831571	-1	0
MMSYN1_0698	NULL	ORF	lipoprotein. putative	Cell envelope	833904	832678	-1	7
MMSYN1_0699	msrA/B	ORF	peptide methionine sulfoxide reductase MsrA/msrB	Protein fate	834922	833993	-1	8
MMSYN1_0700	NULL	ORF	putative lipoprotein	Cell envelope	837222	835036	-1	25
MMSYN1_0701	NULL	ORF	putative lipoprotein	Cell envelope	839818	837470	-1	29
MMSYN1_0702	NULL	ORF	transmembrane protein	Cell envelope	840729	839827	-1	16
MMSYN1_0703	NULL	ORF	conserved hypothetical protein	Unknown function	842691	840856	-1	25
MMSYN1_0704	NULL	ORF	conserved hypothetical protein	Hypothetical proteins	843260	842694	-1	0
MMSYN1_0705	NULL	ORF	C-5 cytosine-specific DNA methylase	DNA metabolism	844099	843263	-1	20
MMSYN1_0706	NULL	ORF	alkylphosphonate ABC transporter, permease component	Transport and binding proteins	846117	844369	-1	4
MMSYN1_0707	NULL	ORF	alkylphosphonate ABC transporter, ATP-binding component	Transport and binding proteins	846830	846081	-1	0
MMSYN1_0708	NULL	ORF	alkylphosphonate ABC transporter, substrate-bindin	Transport and binding proteins	848307	846844	-1	3
MMSYN1_0710	NULL	ORF	hydrolase of the HAD family	Unknown function	849393	848530	-1	10
MMSYN1_0711	NULL	ORF	aminotransferase	Central intermediary metabolism	849525	850715	1	2
MMSYN1_0712	NULL	ORF	endoribonuclease L-PSP, putative	Transcription	850725	851126	1	5
MMSYN1_0713	NULL	ORF	conserved hypothetical protein	Hypothetical proteins	852493	851162	-1	13
MMSYN1_0714	NULL	ORF	conserved hypothetical protein	Hypothetical proteins	853779	852523	-1	6
MMSYN1_0715	NULL	ORF	conserved hypothetical protein	Hypothetical proteins	855234	853966	-1	5
MMSYN1_0716	NULL	ORF	conserved hypothetical protein	Hypothetical proteins	855376	856518	1	2
MMSYN1_0717	NULL	tRNA	NULL	NULL	856724	856800	1	0
MMSYN1_0718	NULL	tRNA	NULL	NULL	856848	856924	1	0
MMSYN1_0719	NULL	tRNA	NULL	NULL	856935	857010	1	0
MMSYN1_0720	NULL	tRNA	NULL	NULL	857015	857091	1	0
MMSYN1_0721	NULL	tRNA	NULL	NULL	857103	857179	1	0
MMSYN1_0722	NULL	tRNA	NULL	NULL	857222	857314	1	0
MMSYN1_0723	NULL	tRNA	NULL	NULL	857337	857412	1	0
MMSYN1_0724	NULL	tRNA	NULL	NULL	857415	857491	1	1
MMSYN1_0725	NULL	tRNA	NULL	NULL	857500	857575	1	0
MMSYN1_0726	nagB	ORF	glucosamine-6-phosphate deaminase	Central intermediary metabolism	857683	858417	1	0
MMSYN1_0727	tpiA	ORF	triose-phosphate isomerase	Energy metabolism	858515	859261	1	3
MMSYN1_0728	NULL	ORF	HAD-superfamily hydrolase subfamily IIB, protein	Unknown function	859254	860090	1	2
MMSYN1_0729	gpml	ORF	2,3-bisphosphoglycerate-independent phosphoglycerate mutase	Energy metabolism	860093	861688	1	1
MMSYN1_0730	NULL	ORF	conserved hypothetical protein	Hypothetical proteins	861788	862387	1	2
MMSYN1_0731	NULL	ORF	conserved hypothetical protein	Hypothetical proteins	862389	863402	1	4
MMSYN1_0732	deoC	ORF	deoxyribose-phosphate aldolase	Purines, pyrimidines, nucleosides, and nucleotides	864122	863454	-1	0
MMSYN1_0733	NULL	ORF	phosphoglucomutase or phosphomannomutase	Energy metabolism	865810	864134	-1	17
MMSYN1_0734	pdp	ORF	pyrimidine-nucleoside phosphorylase	Purines, pyrimidines, nucleosides, and nucleotides	865972	867285	1	6

MMSYN1_0735	tnpB_4	ORF	IS1296 transposase protein B	Mobile and extrachromosomal element functions	868071	867340	-1	9
MMSYN1_0736	tnpA_4	ORF	IS1296 transposase protein A	Mobile and extrachromosomal element functions	868751	868209	-1	7
MMSYN1_0737	NULL	ORF	NULL	Transport and binding proteins	869103	868816	-1	2
MMSYN1_0738	NULL	ORF	hypothetical protein	NULL	869264	869142	-1	0
MMSYN1_0739	NULL	ORF	NULL	Transport and binding proteins	869403	869269	-1	0
MMSYN1_0740	NULL	ORF	hypothetical protein	NULL	869608	869453	-1	2
MMSYN1_0741	mmyCIIR	ORF	NULL	DNA metabolism	870719	869727	-1	11
MMSYN1_0742	mmyCIIM	ORF	CCTTC-recognizing Type II restriction modification system (MmyCII) adenine/cytosine DNA methyltransferase subunit	DNA metabolism	873225	870721	-1	24
MMSYN1_0743	fruA	ORF	PTS system, Fructose specific IIB subunit family	Energy metabolism	875396	873360	-1	21
MMSYN1_0744	pfkB	ORF	1-phosphofructokinase	Energy metabolism	876334	875399	-1	14
MMSYN1_0745	NULL	ORF	transcriptional regulator of the fructose operon, DeoR family	Regulatory functions	877032	876334	-1	8
MMSYN1_0746	NULL	ORF	conserved hypothetical protein	Hypothetical proteins	877185	878165	1	10
MMSYN1_0747	NULL	ORF	purine nucleoside phosphorylase	Purines, pyrimidines, nucleosides, and nucleotides	878368	879021	1	2
MMSYN1_0748	NULL	ORF	IS1296 transposase EH	Mobile and extrachromosomal element functions	879533	879069	-1	3
MMSYN1_0749	NULL	ORF	lysophospholipase	Fatty acid and phospholipid metabolism	880493	879588	-1	7
MMSYN1_0750	NULL	ORF	viral A-type inclusion protein, putative	Unknown function	883649	880596	-1	3
MMSYN1_0751	NULL	ORF	viral A-type inclusion protein, putative	Unknown function	886715	883674	-1	13
MMSYN1_0752	NULL	ORF	cell filamentation protein (fic)	Unknown function	887085	887657	1	4
MMSYN1_0753	NULL	ORF	DNA-damage-inducible protein J	DNA metabolism	887865	888137	1	0
MMSYN1_0754	mmyCIIM1	ORF	NULL	DNA metabolism	889081	888176	-1	5
MMSYN1_0755	mmyCIIM2	ORF	GCATC--recognizing Type II restriction modification system (MmyCIII) adenine DNA methyltransferase subunit 2	DNA metabolism	890162	889074	-1	5
MMSYN1_0756	mmyCIIR	ORF	GCATC--recognizing Type II restriction modification system (MmyCIII) endonuclease subunit	DNA metabolism	890279	892318	1	7
MMSYN1_0757	NULL	ORF	conserved hypothetical protein	Hypothetical proteins	893441	892356	-1	17
MMSYN1_0758	NULL	ORF	beta-glucosidase	Energy metabolism	894831	893443	-1	14
MMSYN1_0759	NULL	ORF	sugar kinase, ROK family	Regulatory functions	895702	894824	-1	4
MMSYN1_0760	NULL	ORF	PTS system, fructose-specific IIA component	Transport and binding proteins	896162	895704	-1	1
MMSYN1_0761	NULL	ORF	glycosyl hydrolase, family 38	DNA metabolism	898842	896176	-1	30
MMSYN1_0762	NULL	ORF	PTS system, fructose-specific iibc component	Transport and binding proteins	900695	898854	-1	18
MMSYN1_0763	NULL	ORF	putative lipoprotein	Cell envelope	901486	900710	-1	8
MMSYN1_0764	hpt_2	ORF	hypoxanthine phosphoribosyltransferase	Purines, pyrimidines, nucleosides, and nucleotides	902203	901652	-1	4
MMSYN1_0765	purB	ORF	adenylosuccinate lyase	Purines, pyrimidines, nucleosides, and nucleotides	903537	902239	-1	4
MMSYN1_0766	purA	ORF	adenylosuccinate synthase	Purines, pyrimidines, nucleosides, and nucleotides	904828	903530	-1	5
MMSYN1_0767	NULL	ORF	ribonucleoside-diphosphate reductase subunit alpha (Ribonucleotide reductase)	Purines, pyrimidines, nucleosides, and nucleotides	905201	905049	-1	3
MMSYN1_0768	mmyCIVR	ORF	GANTC--recognizing Type II restriction modification system (MmyCIV) endonuclease subunit	DNA metabolism	905697	905182	-1	1
MMSYN1_0769	mmyCIVM	ORF	GANTC--recognizing Type II restriction modification system (MmyCIV) adenine DNA methylase subunit	DNA metabolism	906578	905859	-1	2
MMSYN1_0770	NULL	ORF	conserved hypothetical protein	Hypothetical proteins	907484	906639	-1	4

MMSYN1_0771	nrdE	ORF	ribonucleoside-diphosphate reductase, alpha subunit	Purines, pyrimidines, nucleosides, and nucleotides	909752	907590	-1	8
MMSYN1_0772	nrdI	ORF	NrdI protein	Purines, pyrimidines, nucleosides, and nucleotides	910212	909739	-1	1
MMSYN1_0773	nrdF	ORF	ribonucleoside-diphosphate reductase, beta subunit	Purines, pyrimidines, nucleosides, and nucleotides	911240	910221	-1	4
MMSYN1_0774	secG	ORF	preprotein translocase, SecG subunit	Protein fate	911539	911823	1	0
MMSYN1_0775	NULL	ORF	3'-5' exoribonuclease, VacB/RNase II family	Transcription	911859	913973	1	10
MMSYN1_0776	smpB	ORF	SsrA-binding protein	Protein synthesis	913983	914429	1	7
MMSYN1_0777	NULL	ORF	conserved hypothetical protein	Hypothetical proteins	914429	914914	1	4
MMSYN1_0778	NULL	ORF	conserved hypothetical protein	Hypothetical proteins	915034	915285	1	0
MMSYN1_0779	NULL	ORF	PTS system, eic domain protein	Transport and binding proteins	915336	917573	1	0
MMSYN1_0780	tnpA_5	ORF	IS1296 transposase protein A	Mobile and extrachromosomal element functions	917651	918193	1	0
MMSYN1_0781	tnpB_5	ORF	IS1296 transposase protein B	Mobile and extrachromosomal element functions	918331	919062	1	2
MMSYN1_0782	NULL	ORF	NULL	Cellular processes	919157	920284	1	2
MMSYN1_0783	NULL	ORF	glucokinase	Energy metabolism	920380	921345	1	7
MMSYN1_0784	arcC_2	ORF	carbamate kinase 1	Energy metabolism	922345	921413	-1	0
MMSYN1_0785	NULL	ORF	arginine/ornithine antiporter	Transport and binding proteins	923821	922358	-1	1
MMSYN1_0786	arcB	ORF	ornithine carbamoyltransferase (ArcB)	Amino acid biosynthesis	924895	923900	-1	6
MMSYN1_0787	mgtA	ORF	magnesium-importing ATPase	Transport and binding proteins	927984	925156	-1	14
MMSYN1_0788	NULL	ORF	conserved hypothetical protein	Hypothetical proteins	928331	929518	1	3
MMSYN1_0789	atpC	ORF	ATP synthase, delta subunit	Energy metabolism	929889	929590	-1	4
MMSYN1_0790	atpD_2	ORF	ATP synthase F1, beta subunit	Energy metabolism	931316	929889	-1	8
MMSYN1_0791	atpG	ORF	ATP synthase F1, gamma subunit	Energy metabolism	932167	931325	-1	2
MMSYN1_0792	atpA	ORF	ATP synthase F1, alpha subunit	Energy metabolism	933746	932169	-1	4
MMSYN1_0793	atpH	ORF	ATP synthase F1, delta subunit	Energy metabolism	934303	933758	-1	6
MMSYN1_0794	atpF	ORF	ATP synthase F0, B subunit	Energy metabolism	934850	934305	-1	8
MMSYN1_0795	atpE	ORF	ATP synthase c chain	Energy metabolism	935184	934879	-1	5
MMSYN1_0796	atpB	ORF	ATP synthase FO, A subunit	Energy metabolism	936077	935214	-1	10
MMSYN1_0797	NULL	ORF	conserved hypothetical protein	Hypothetical proteins	936313	936077	-1	2
MMSYN1_0798	upp	ORF	uracil phosphoribosyltransferase	Purines, pyrimidines, nucleosides, and nucleotides	937238	936615	-1	0
MMSYN1_0799	glyA	ORF	glycine hydroxymethyltransferase	Amino acid biosynthesis	938579	937338	-1	5
MMSYN1_0800	rpiB	ORF	ribose 5-phosphate isomerase B	Energy metabolism	939006	938563	-1	1
MMSYN1_0801	NULL	ORF	conserved hypothetical protein	Hypothetical proteins	939085	939381	1	3
MMSYN1_0802	NULL	ORF	putative lipoprotein	Cell envelope	941581	939386	-1	17
MMSYN1_0803	rpoC	ORF	DNA-directed RNA polymerase, beta' subunit	Transcription	945438	941671	-1	3
MMSYN1_0804	rpoB	ORF	DNA-directed RNA polymerase, beta subunit	Transcription	949325	945450	-1	9
MMSYN1_0805	NULL	ORF	conserved hypothetical protein	Hypothetical proteins	950490	949315	-1	2
MMSYN1_0806	rplL	ORF	ribosomal protein L7/L12	Protein synthesis	951029	950661	-1	2
MMSYN1_0807	rplJ	ORF	50S ribosomal protein L10	Protein synthesis	951595	951098	-1	1
MMSYN1_0809	rplA	ORF	ribosomal protein L1	Protein synthesis	952502	951822	-1	7
MMSYN1_0810	rplK	ORF	ribosomal protein L11	Protein synthesis	952930	952502	-1	6
MMSYN1_0811	galU	ORF	UTP-glucose-1-phosphate uridylyltransferase	Cell envelope	954020	953142	-1	7
MMSYN1_0812	NULL	ORF	glycosyltransferase	Cell envelope	955926	954550	-1	5
MMSYN1_0813	galE	ORF	UDP-glucose 4-epimerase	Energy metabolism	956226	957224	1	3
MMSYN1_0814	glf	ORF	UDP-galactopyranose mutase	Cell envelope	957238	958425	1	0
MMSYN1_0815	NULL	ORF	conserved hypothetical protein	Hypothetical proteins	958511	958648	1	0
MMSYN1_0928	NULL	ORF	hypothetical protein	NULL	959442	958936	-1	0
MMSYN1_0929	NULL	ORF	conserved domain protein	Hypothetical proteins	959417	959686	1	0
MMSYN1_0816	NULL	ORF	integrase core domain protein	Unknown function	959695	960048	1	0
MMSYN1_0817	NULL	ORF	conserved hypothetical protein	Hypothetical proteins	961114	960185	-1	4
MMSYN1_0818	NULL	ORF	prolipoprotein diacylglycerol transferase	Protein fate	962557	961127	-1	2
MMSYN1_0819	trxB	ORF	thioredoxin-disulfide reductase	Energy metabolism	963498	962566	-1	3
MMSYN1_0820	NULL	ORF	prolipoprotein diacylglycerol transferase	Protein fate	965062	963482	-1	7

MMSYN1_0821	hprK	ORF	HPr kinase/phosphorylase (HPrK/P) (HPr(Ser)kinase/phosphorylase)	Regulatory functions	966014	965073	-1	6
MMSYN1_0822	NULL	ORF	putative membrane protein	Cell envelope	966772	966098	-1	3
MMSYN1_0823	folC	ORF	folate synthetase-polyglutamyl folate synthetase	Biosynthesis of cofactors, prosthetic groups, and carriers	967904	966789	-1	5
MMSYN1_0824	uvrA	ORF	excinuclease ABC subunit A	DNA metabolism	970737	967897	-1	26
MMSYN1_0825	uvrB	ORF	excinuclease ABC subunit B	DNA metabolism	972743	970746	-1	13
MMSYN1_0826	holA	ORF	DNA polymerase III, delta subunit	DNA metabolism	973028	973978	1	3
MMSYN1_0827	NULL	ORF	conserved hypothetical protein	Hypothetical proteins	973981	975447	1	4
MMSYN1_0828	NULL	tRNA	NULL	NULL	975613	975687	1	0
MMSYN1_0829	NULL	ORF	deoxyribonuclease, TatD family	DNA metabolism	975825	976622	1	0
MMSYN1_0830	NULL	ORF	conserved hypothetical protein	Hypothetical proteins	976624	976884	1	0
MMSYN1_0831	prs	ORF	ribose-Phosphate pyrophosphokinase (rppk) (phosphoribosylpyrophosphate synthetase) (p-rib-pp synthetase) (prpp synthetase)	Purines, pyrimidines, nucleosides, and nucleotides	977064	978098	1	10
MMSYN1_0832	pth	ORF	aminoacyl-tRNA hydrolase	Protein synthesis	978524	979084	1	0
MMSYN1_0833	rplI	ORF	ribosomal protein L9	Protein synthesis	979205	979648	1	0
MMSYN1_0834	dnaB	ORF	replicative DNA helicase	DNA metabolism	979651	980967	1	6
MMSYN1_0835	NULL	ORF	putative lipoprotein	Cell envelope	981034	982341	1	0
MMSYN1_0836	NULL	ORF	conserved hypothetical protein	Hypothetical proteins	982483	983409	1	2
MMSYN1_0837	cysS	ORF	cysteine--tRNA ligase	Protein synthesis	983418	984743	1	12
MMSYN1_0838	NULL	ORF	RNA methyltransferase, TrmH family, group 3	Protein synthesis	984745	985479	1	2
MMSYN1_0839	secE	ORF	preprotein translocase, SecE subunit	Protein fate	985701	986024	1	1
MMSYN1_0840	nusG	ORF	transcription antitermination protein nusG	Transcription	986041	986682	1	7
MMSYN1_0841	NULL	ORF	hypothetical protein	NULL	987122	993043	1	55
MMSYN1_0842	NULL	ORF	oligopeptide ABC transporter, solute-binding protein	Transport and binding proteins	993053	996010	1	27
MMSYN1_0843	NULL	ORF	oligopeptide ABC transporter, permease component	Transport and binding proteins	996010	997083	1	8
MMSYN1_0844	NULL	ORF	oligopeptide ABC transporter, permease component	Transport and binding proteins	997085	998095	1	8
MMSYN1_0845	NULL	ORF	oligopeptide ABC transporter, ATP-binding component	Transport and binding proteins	998103	999548	1	18
MMSYN1_0846	NULL	ORF	oligopeptide ABC transporter, ATP-binding component	Transport and binding proteins	999541	1000863	1	8
MMSYN1_0267	tnpB_6	ORF	IS1296 transposase protein B	Mobile and extrachromosomal element functions	1001631	1000900	-1	0
MMSYN1_0265	tnpA_6	ORF	IS1296 transposase protein A	Mobile and extrachromosomal element functions	1002311	1001769	-1	5
MMSYN1_0849	NULL	ORF	lipoprotein	Cell envelope	1002898	1002392	-1	4
MMSYN1_0850	NULL	ORF	conserved hypothetical protein	Hypothetical proteins	1003970	1003095	-1	2
MMSYN1_0851	NULL	ORF	putative lipoprotein	Cell envelope	1004219	1004037	-1	0
MMSYN1_0852	NULL	ORF	conserved hypothetical protein	Hypothetical proteins	1004615	1004385	-1	5
MMSYN1_0853	NULL	ORF	conserved hypothetical protein	Hypothetical proteins	1005324	1004605	-1	19
MMSYN1_0854	NULL	ORF	conserved hypothetical protein	Hypothetical proteins	1005833	1005324	-1	2
MMSYN1_0855	NULL	ORF	PTS system, iibc component, putative	Transport and binding proteins	1007533	1005833	-1	6
MMSYN1_0856	NULL	ORF	PTS system, iibc component, putative	Transport and binding proteins	1009322	1007610	-1	17
MMSYN1_0858	NULL	ORF	putative transcriptional regulator	Regulatory functions	1009630	1011018	1	4
MMSYN1_0857	NULL	ORF	SIS domain protein	Unknown function	1011820	1011005	-1	2
MMSYN1_0859	NULL	ORF	DNA topoisomerase domain protein	DNA metabolism	1012008	1013969	1	7
MMSYN1_0860	NULL	ORF	putative lipoprotein	Cell envelope	1014841	1014116	-1	10
MMSYN1_0861	NULL	ORF	conserved hypothetical protein	Hypothetical proteins	1016126	1015242	-1	9
MMSYN1_0862	NULL	ORF	conserved hypothetical protein	Hypothetical proteins	1016943	1016113	-1	1
MMSYN1_0863	NULL	ORF	putative lipoprotein	Cell envelope	1018279	1016930	-1	12
MMSYN1_0864	NULL	ORF	ABC transporter, ATP-binding protein	Transport and binding proteins	1018961	1018257	-1	9
MMSYN1_0865	NULL	ORF	ABC transporter, permease protein	Transport and binding proteins	1020834	1018963	-1	32
MMSYN1_0866	NULL	ORF	putative lipoprotein	Cell envelope	1021860	1020973	-1	2
MMSYN1_0867	NULL	ORF	conserved hypothetical protein	Hypothetical proteins	1022692	1021862	-1	3
MMSYN1_0868	NULL	ORF	lipoprotein. putative	Cell envelope	1023872	1022679	-1	17
MMSYN1_0869	NULL	ORF	ABC transporter, permease component	Transport and binding proteins	1025786	1023891	-1	8

MMSYN1_0870	NULL	ORF	C4-dicarboxylate anaerobic carrier superfamily	Transport and binding proteins	1027662	1025896	-1	14
MMSYN1_0871	NULL	ORF	zinc metalloprotease	Protein fate	1028438	1027731	-1	7
MMSYN1_0872	ychF	ORF	GTP-binding protein YchF	Unknown function	1029504	1028410	-1	14
MMSYN1_0873	NULL	ORF	conserved hypothetical protein	Hypothetical proteins	1029740	1029540	-1	5
MMSYN1_0874	gidB	ORF	16S rRNA methyltransferase GidB	Protein synthesis	1030437	1029742	-1	13
MMSYN1_0875	pgsA	ORF	CDP-diacylglycerol--glycerol-3-phosphate 3-phosphatidyltransferase	Fatty acid and phospholipid metabolism	1031033	1030437	-1	19
MMSYN1_0876	NULL	ORF	amino acid permease	Transport and binding proteins	1032715	1031135	-1	8
MMSYN1_0877	NULL	ORF	putative membrane protein	Cell envelope	1033542	1032862	-1	2
MMSYN1_0878	NULL	ORF	amino acid permease	Transport and binding proteins	1035007	1033514	-1	4
MMSYN1_0879	NULL	ORF	E1-E2 ATPase subfamily, putative	Transport and binding proteins	1037767	1035110	-1	27
MMSYN1_0880	hup	ORF	NULL	DNA metabolism	1038822	1037851	-1	11
MMSYN1_0881	NULL	ORF	hexose phosphate transport protein	Transport and binding proteins	1040565	1039138	-1	7
MMSYN1_0882	NULL	ORF	conserved hypothetical protein	Hypothetical proteins	1041414	1040770	-1	3
MMSYN1_0883	asnA	ORF	aspartate--ammonia ligase	Amino acid biosynthesis	1042451	1041471	-1	11
MMSYN1_0884	NULL	ORF	conserved hypothetical protein	Hypothetical proteins	1042655	1043413	1	2
MMSYN1_0885	gidA	ORF	tRNA uridine 5-carboxymethylaminomethyl modification enzyme GidA	Protein synthesis	1045562	1043673	-1	6
MMSYN1_0886	NULL	ORF	proton/glutamate symporter	Transport and binding proteins	1047287	1045710	-1	9
MMSYN1_0887	NULL	ORF	NULL	Cellular processes	1048650	1047307	-1	26
MMSYN1_0888	NULL	ORF	pyrazinamidase/nicotinamidase	Biosynthesis of cofactors, prosthetic groups, and carriers	1048868	1049368	1	3
MMSYN1_0889	NULL	ORF	NULL	Hypothetical proteins	1050091	1049414	-1	5
MMSYN1_0890	NULL	ORF	conserved hypothetical protein	Hypothetical proteins	1050847	1050248	-1	9
MMSYN1_0891	lppQ	ORF	lipoprotein Q, putative (LppQ)	Cell envelope	1051424	1052758	1	6
MMSYN1_0892	NULL	ORF	putative membrane protein	Cell envelope	1053008	1054231	1	16
MMSYN1_0893	NULL	ORF	putative membrane protein	Cell envelope	1054362	1055567	1	12
MMSYN1_0894	NULL	ORF	viral A-type inclusion protein repeat protein	Unknown function	1057914	1055650	-1	15
MMSYN1_0895	NULL	ORF	conserved hypothetical protein	Hypothetical proteins	1060185	1057924	-1	40
MMSYN1_0896	NULL	ORF	conserved hypothetical protein	Hypothetical proteins	1062757	1060502	-1	8
MMSYN1_0897	NULL	ORF	conserved hypothetical protein	Hypothetical proteins	1065028	1062767	-1	9
MMSYN1_0898	NULL	ORF	conserved hypothetical protein	Hypothetical proteins	1067475	1065223	-1	10
MMSYN1_0899	NULL	ORF	conserved hypothetical protein	Hypothetical proteins	1069739	1067499	-1	7
MMSYN1_0900	vlcF	ORF	lipoprotein, putative (VlcF)	Cell envelope	1070055	1070690	1	1
MMSYN1_0901	vlcG	ORF	lipoprotein, putative (VlcG)	Cell envelope	1070923	1071534	1	5
MMSYN1_0902	vlcH	ORF	lipoprotein, putative (VlcH)	Cell envelope	1071824	1072303	1	4
MMSYN1_0903	vlcI	ORF	lipoprotein (VlcI)	Cell envelope	1072804	1073379	1	9
MMSYN1_0904	vlcJ	ORF	prolipoprotein, putative (VlcJ)	Hypothetical proteins	1073640	1074323	1	3
MMSYN1_0905	NULL	ORF	NULL	Unknown function	1074750	1074592	-1	0
MMSYN1_0906	NULL	ORF	choline/ethanolamine kinase, putative	Unknown function	1075967	1075251	-1	4
MMSYN1_0907	NULL	ORF	conserved hypothetical protein	Hypothetical proteins	1076761	1075967	-1	1
MMSYN1_0908	oxaA	ORF	membrane protein OxaA	Cell envelope	1078028	1076838	-1	6
MMSYN1_0909	rnpA	ORF	ribonuclease P protein component	Transcription	1078375	1078046	-1	0
MMSYN1_0910	rpmH	ORF	ribosomal protein L34	Protein synthesis	1078516	1078382	-1	0

Supplemental Table S3. The numbers of deleted genes in each functional category in the eight-deletion mycoplasma strain. Percentages of the total gene count for the category are shown in brackets. Functional categories are based on published work (Gibson et al., 2010). NULL includes all 41 RNA genes and 19 hypothetical protein genes. Less biased numbers excluding genes within the restriction systems (RE), the integrative conjugal element (ICE), and the cluster of variable lipoprotein of large colony (vlc) genes are also shown.

Functional category	Deleted in the eight-deletion strain	Deleted in the eight-deletion strain (excluding RE, ICE, vlc)	Total
Amino acid biosynthesis	0 (0%)	0 (0%)	6
Biosynthesis of cofactors, prosthetic groups, and carriers	0 (0%)	0 (0%)	14
Cell envelope	18 (15%)	14 (12%)	118
Cellular processes	0 (0%)	0 (0%)	12
Central intermediary metabolism	1 (6%)	1 (6%)	17
DNA metabolism	10 (16%)	0 (0%)	63
Energy metabolism	3 (5%)	3 (5%)	61
Fatty acid and phospholipid metabolism	0 (0%)	0 (0%)	16
Hypothetical proteins	9 (6%)	9 (6%)	147
Mobile and extrachromosomal element functions	9 (24%)	2 (5%)	38
NULL	3 (5%)	2 (3%)	59
Protein fate	2 (6%)	2 (6%)	36
Protein synthesis	0 (0%)	0 (0%)	113
Purines, pyrimidines, nucleosides, and nucleotides	0 (0%)	0 (0%)	29
Regulatory functions	1 (5%)	1 (5%)	19
Signal transduction	0 (0%)	0 (0%)	1
Transcription	1 (6%)	1 (6%)	18
Transport and binding proteins	10 (11%)	10 (11%)	87
Unclassified	0 (0%)	0 (0%)	1
Unknown function	2 (4%)	2 (4%)	56

Supplemental Table S4. Genotyping of genomes generated using the Green Monster process.

(A) Data from crosses where genotyping was performed on all deletions at once.

Cross	Number of strains with the indicated number of deletions in the genome					Average number of deletions per strain	Standard Deviation	Sample Size	Expected number for unsorted cells	p-value (vs. unsorted)
	0	1	2	3	4					
ΔA × ΔB Expt 1	0	9	3	-	-	1.3	0.5	12	1	-
ΔA × ΔB Expt 2	1	15	8	-	-	1.3	0.6	24	1	0.06
ΔA × ΔB Expt 2 unsorted	3	17	4	-	-	1.0	0.6	24	1	-
ΔA × ΔB Expt 3	1	6	14	-	-	1.6	0.6	21	1	0.0001
ΔA × ΔB Expt 3 unsorted	3	15	2	-	-	1.0	0.5	20	1	-
ΔC × ΔD Expt 1	0	21	3	-	-	1.1	0.3	24	1	-
ΔC × ΔD Expt 2	1	18	3	-	-	1.1	0.4	22	1	0.2
ΔC × ΔD Expt 2 unsorted	1	22	1	-	-	1.0	0.3	24	1	-
ΔE × ΔI Expt 1	1	8	3	-	-	1.2	0.6	12	1	-
ΔE × ΔI Expt 2	1	13	5	-	-	1.2	0.5	19	1	0.2
ΔE × ΔI Expt 2 unsorted	1	20	3	-	-	1.1	0.4	24	1	-
ΔL × ΔN Expt 1	3	32	13	-	-	1.2	0.5	48	1	0.03
ΔL × ΔN Expt 1 unsorted	3	19	2	-	-	1.0	0.5	24	1	-
ΔA ΔB × ΔC ΔD	Quadruple mutants were selected after sequential genotyping of deletions					-	-	-	-	-
ΔE ΔI × ΔL ΔN Expt 1	0	1	1	2	1	2.6	1.1	5	2	-
ΔE ΔI × ΔL ΔN Expt 2	0	0	4	0	1	2.4	0.9	5	2	-
ΔE ΔI × ΔL ΔN Expt 3	0	0	4	0	2	2.7	1.0	6	2	-
ΔE ΔI × ΔL ΔN Expt 4	0	1	2	1	2	2.7	1.2	6	2	-
ΔE ΔI × ΔL ΔN Expt 5	0	0	4	0	2	2.7	1.0	6	2	-
ΔE ΔI × ΔL ΔN Expt 6	0	1	2	0	1	2.3	1.3	4	2	-
ΔA ΔB ΔC ΔD × ΔE ΔI ΔL ΔN	Octuple mutants were selected after sequential genotyping of deletions					-	-	-	-	-
ΔE ΔI × ΔN Expt 1	0	1	2	0	-	1.7	0.6	3	1.5	-
ΔE ΔI × ΔN Expt 2	0	0	3	3	-	2.5	0.5	6	1.5	-
ΔE ΔI × ΔN Expt 3	0	0	3	3	-	2.5	0.5	6	1.5	-
ΔE ΔI × ΔN Expt 4	0	0	5	5	-	2.5	0.5	10	1.5	-
ΔA ΔB ΔC ΔD × ΔE ΔI ΔN	Septuple mutants were selected after sequential genotyping of deletions					-	-	-	-	-

(B) Data from the crosses of ΔA ΔB and ΔC ΔD where sequential genotyping was performed on deletions to identify strains carrying a desired genome.
*: Based on the data for unsorted samples, the deletions do not appear to be segregated independently.

Cross	Number of strains containing those two deletions that are immediately upstream and downstream of the desired region of recombination	Sample size	p-value* (vs. unsorted)	Number of strains carrying all the introduced deletions	Sample size
ΔA ΔB × ΔC ΔD Expt 1	0	12	0.9	-	-
ΔA ΔB × ΔC ΔD Expt 1 unsorted	1	12	-	0	1
ΔA ΔB × ΔC ΔD Expt 2	2	12	0.3	0	2
ΔA ΔB × ΔC ΔD Expt 2 unsorted	1	12	-	0	1
ΔA ΔB × ΔC ΔD Expt 3	4	12	0.02	2	4
ΔA ΔB × ΔC ΔD Expt 3 unsorted	0	12	-	-	-
ΔA ΔB × ΔC ΔD Expt 4	2	12	0.08	1	2
ΔA ΔB × ΔC ΔD Expt 4 unsorted	0	12	-	-	-
ΔA ΔB × ΔC ΔD Expt 5	4	12	0.08	1	4
ΔA ΔB × ΔC ΔD Expt 5 unsorted	1	12	-	1	1
ΔA ΔB × ΔC ΔD Expt 6	4	12	0.08	1	4
ΔA ΔB × ΔC ΔD Expt 6 unsorted	1	12	-	0	1

(C) Data from the crosses for generating octuple and septuple genomes where sequential genotyping was used to identify strains carrying a desired genome.

Cross	Number of strains containing those two deletions that are immediately upstream and downstream of the desired region of recombination	Number of strains carrying these deletions in a single genome	Sample size	Number of strains carrying all the introduced deletions	Sample size
ΔA ΔB ΔC ΔD × ΔE ΔI ΔL ΔN Expt 1	5	5	24	2	5
ΔA ΔB ΔC ΔD × ΔE ΔI ΔL ΔN Expt 2	5	3	24	3	3
ΔA ΔB ΔC ΔD × ΔE ΔI ΔN Expt 1	9	7	37	2	7
ΔA ΔB ΔC ΔD × ΔE ΔI ΔN Expt 2	15	12	66	5	12

Supplemental Table S5. Doubling time values for mycoplasma deletion strains. Mutants displaying noticeably reduced growth rates are indicated in bold.

Strain	Doubling time (min)					
	Replicate 1	Replicate 2	Replicate 3	Replicate 4	Average	Standard deviation
JCVI-syn1.0	64	67	59	-	63	4
JCVI-syn1.0 $\Delta 1-6$ (restriction-defective strain)	57	61	59	60	59	2
JCVI-syn1.0 ΔA	75	73	-	-	74	2
JCVI-syn1.0 ΔB	74	72	-	-	73	1
JCVI-syn1.0 ΔC	67.9	68.6	-	-	68.3	0.5
JCVI-syn1.0 ΔD	75	77	-	-	76	2
JCVI-syn1.0 ΔE	69	71	-	-	70	1
JCVI-syn1.0 ΔI	72	69	-	-	70	3
JCVI-syn1.0 ΔN	70	72	-	-	71	2
JCVI-syn1.0 ΔL	139	139	136	-	138	2
JCVI-syn1.0 $\Delta 1-6 \Delta A$ $\Delta B \Delta C \Delta D \Delta E \Delta I \Delta N$ (seven-deletion strain)	65	61	62	62	63	2
JCVI-syn1.0 $\Delta 1-6 \Delta A$ $\Delta B \Delta C \Delta D \Delta E \Delta I \Delta L \Delta N$ (eight-deletion strain)	112	108	117	-	113	5

Supplemental Table S6. List of redundant gene pairs in the JCVI-syn1.0 genome.

Refer to Methods for criteria used for selecting these genes. The coordinates of the genes are indicated in brackets.

The gene shown in red (MMSYN1_0560) is the only gene deleted in the multi-deletion genomes described in this study.

Query	Hit	E-value	Percent length	Percent identity
MMSYN1_0921 tnpA 1 CDS [35233:35776]	MMSYN1_0265 tnpA 6 CDS [1001768:1002311]	0.0E+00	1	1
MMSYN1_0921 tnpA 1 CDS [35233:35776]	MMSYN1_0780 tnpA 5 CDS [917650:918193]	0.0E+00	1	1
MMSYN1_0921 tnpA 1 CDS [35233:35776]	MMSYN1_0449 tnpA 2 CDS [553644:554187]	0.0E+00	1	1
MMSYN1_0921 tnpA 1 CDS [35233:35776]	MMSYN1_0736 tnpA 4 CDS [868208:868751]	0.0E+00	1	0.969
MMSYN1_0921 tnpA 1 CDS [35233:35776]	MMSYN1_0462 tnpA 3 CDS [570922:571465]	0.0E+00	1	0.967
MMSYN1_0922 tnpB 1 CDS [35913:36645]	MMSYN1_0267 tnpB 6 CDS [1000899:1001631]	0.0E+00	1	1
MMSYN1_0922 tnpB 1 CDS [35913:36645]	MMSYN1_0781 tnpB 5 CDS [918330:919062]	0.0E+00	1	1
MMSYN1_0922 tnpB 1 CDS [35913:36645]	MMSYN1_0461 tnpB 3 CDS [570053:570785]	0.0E+00	1	1
MMSYN1_0922 tnpB 1 CDS [35913:36645]	MMSYN1_0450 tnpB 2 CDS [554324:555056]	0.0E+00	1	1
MMSYN1_0922 tnpB 1 CDS [35913:36645]	MMSYN1_0735 tnpB 4 CDS [867339:868071]	0.0E+00	1	0.973
MMSYN1_0067 rrf rRNA [92147:92256]	MMSYN1_0532 rrf rRNA [637295:637404]	4.6E-52	1	0.991
MMSYN1_0068 rrl rRNA [92330:95225]	MMSYN1_0533 rrl rRNA [637478:640373]	0.0E+00	1	1
MMSYN1_0069 rrs rRNA [95456:96980]	MMSYN1_0534 rrs rRNA [640603:642127]	0.0E+00	1	0.998
MMSYN1_0071 tRNA-Lys tRNA [97348:97424]	MMSYN1_0507 tRNA-Lys tRNA [612184:612260]	1.4E-35	1	1
MMSYN1_0113 glycosyltransferase CDS [147624:148869]	MMSYN1_0812 glycosyltransferase CDS [954549:955926]	0.0E+00	0.904	0.867
MMSYN1_0154 lap CDS [197742:199098]	MMSYN1_0190 leucyl aminopeptidase CDS [252530:253886]	0.0E+00	1	0.869
MMSYN1_0307 integrase core domain protein CDS [390557:390911]	MMSYN1_0816 integrase core domain protein CDS [959694:960048]	0.0E+00	1	1
MMSYN1_0323 putative lipoprotein CDS [410709:412203]	MMSYN1_0560 putative lipoprotein CDS [672039:673572]	0.0E+00	0.975	0.941
MMSYN1_0449 tnpA 2 CDS [553644:554187]	MMSYN1_0265 tnpA 6 CDS [1001768:1002311]	0.0E+00	1	1
MMSYN1_0449 tnpA 2 CDS [553644:554187]	MMSYN1_0780 tnpA 5 CDS [917650:918193]	0.0E+00	1	1
MMSYN1_0449 tnpA 2 CDS [553644:554187]	MMSYN1_0736 tnpA 4 CDS [868208:868751]	0.0E+00	1	0.969
MMSYN1_0449 tnpA 2 CDS [553644:554187]	MMSYN1_0462 tnpA 3 CDS [570922:571465]	0.0E+00	1	0.967
MMSYN1_0450 tnpB 2 CDS [554324:555056]	MMSYN1_0267 tnpB 6 CDS [1000899:1001631]	0.0E+00	1	1
MMSYN1_0450 tnpB 2 CDS [554324:555056]	MMSYN1_0781 tnpB 5 CDS [918330:919062]	0.0E+00	1	1
MMSYN1_0450 tnpB 2 CDS [554324:555056]	MMSYN1_0461 tnpB 3 CDS [570053:570785]	0.0E+00	1	1
MMSYN1_0450 tnpB 2 CDS [554324:555056]	MMSYN1_0735 tnpB 4 CDS [867339:868071]	0.0E+00	1	0.973
MMSYN1_0461 tnpB 3 CDS [570053:570785]	MMSYN1_0267 tnpB 6 CDS [1000899:1001631]	0.0E+00	1	1
MMSYN1_0461 tnpB 3 CDS [570053:570785]	MMSYN1_0781 tnpB 5 CDS [918330:919062]	0.0E+00	1	1
MMSYN1_0461 tnpB 3 CDS [570053:570785]	MMSYN1_0735 tnpB 4 CDS [867339:868071]	0.0E+00	1	0.973
MMSYN1_0462 tnpA 3 CDS [570922:571465]	MMSYN1_0265 tnpA 6 CDS [1001768:1002311]	0.0E+00	1	0.967
MMSYN1_0462 tnpA 3 CDS [570922:571465]	MMSYN1_0780 tnpA 5 CDS [917650:918193]	0.0E+00	1	0.967
MMSYN1_0462 tnpA 3 CDS [570922:571465]	MMSYN1_0736 tnpA 4 CDS [868208:868751]	0.0E+00	1	0.96
MMSYN1_0625 arcC 1 CDS [766798:767731]	MMSYN1_0784 arcC 2 CDS [921412:922345]	0.0E+00	1	0.987
MMSYN1_0735 tnpB 4 CDS [867339:868071]	MMSYN1_0267 tnpB 6 CDS [1000899:1001631]	0.0E+00	1	0.973
MMSYN1_0735 tnpB 4 CDS [867339:868071]	MMSYN1_0781 tnpB 5 CDS [918330:919062]	0.0E+00	1	0.973
MMSYN1_0736 tnpA 4 CDS [868208:868751]	MMSYN1_0265 tnpA 6 CDS [1001768:1002311]	0.0E+00	1	0.969
MMSYN1_0736 tnpA 4 CDS [868208:868751]	MMSYN1_0780 tnpA 5 CDS [917650:918193]	0.0E+00	1	0.969
MMSYN1_0780 tnpA 5 CDS [917650:918193]	MMSYN1_0265 tnpA 6 CDS [1001768:1002311]	0.0E+00	1	1
MMSYN1_0781 tnpB 5 CDS [918330:919062]	MMSYN1_0267 tnpB 6 CDS [1000899:1001631]	0.0E+00	1	1
MMSYN1_0855 PTS system, iibc component, putative CDS [1005832:1007533]	MMSYN1_0856 PTS system, iibc component, putative CDS [1007609:1009322]	0.0E+00	0.993	0.887

Inverse PCR for identifying sites of transposon insertion

Construction of the MET15-marked version of JCVI-syn1.0

Preparation of template DNA for generating linearization fragments

Construction of linearization fragments

Confirmation of the correct integration of linearization fragments

Construction of deletion cassettes

- *Deletion A*

- *Deletion B*

- *Deletion C*

- Deletion D

- Deletion E

- Deletion F

- *Deletion G*

MMSYN1_0585CR_F0	TCTATTCAAGGAGTAAAATAgcggccgcTGAGAATGGTAT
MMSYN1_0585CR_F	TTTAATAGATATAAACATATGAAATTCTATTCAAGGAGTAAAATA
MMSYN1_0585CR_R	ACTAATAATTTATTACACGTTTCATAAAATATTACTTCCTTTTAaggttacgcTAGGGATAACAG

<i>- Deletion H</i>	
MMSYN1_0687CR_F0	ATTTAAAAGAAAGTATTAACTgcggccgcTGAGAATGGTAT
MMSYN1_0687CR_F	AACAACCATTTAGGTTGTTTTCTTTATTTAAAAGAAAGTATTAACT
MMSYN1_0687CR_R	TTTAACTGAAGAACAATAAAAAATGGGCAGTGCCCATTTTTTTTAagttacgcTAGGGATAACAG
<i>- Deletion I</i>	
MMSYN1_0698CF_F0	TATTTTAGGAAATGAAGCAAgcggccgcTGAGAATGGTAT
MMSYN1_0698CF_F	ATAAAAAATTGTATTTTTAAAATAAATATTTTAGGAAATGAAGCAA
MMSYN1_0698CF_R	TAAAAAAATAGAAAATTATGAGTTTATAAAAAAGGAAAAATAATTagttacgcTAGGGATAACAG
<i>- Deletion J</i>	
MMSYN1_0741CR_F0	TTATTTTATTAAGTTTTAAAgcggccgcTGAGAATGGTAT
MMSYN1_0741CR_F	ATAATGAAAGCAAATAAGCTTTAATTATTTTATTAAGTTTTAAA
MMSYN1_0741CR_R	ATTAGCGTATTAATTTTAGCTAATAAACAAATATATTGAAAATCTagttacgcTAGGGATAACAG
<i>- Deletion K</i>	
MMSYN1_0754CF_F0	GAACTTTTTTAATACAAATAgcggccgcTGAGAATGGTAT
MMSYN1_0754CF_F	TAAATAAAAAGTTCTTGGTACCCAAGAACTTTTTTAATACAAATA
MMSYN1_0754CF_R	ATGCTAATATTTATGGAGCTTATCTTTTATATAAAAAGGATTTATagttacgcTAGGGATAACAG
<i>- Deletion L</i>	
MMSYN1_0840CF_F0	TTAGTTAGGAGAAACAAATTgcggccgcTGAGAATGGTAT
MMSYN1_0840CF_F	ACTTATTTAGATTAATCAAAGCAATTTAGTTAGGAGAAACAAATT
MMSYN1_0840CF_R	AAATTTTAGTCCGTGTTTATGGTAGCGGGGGGAACTAGCATTTTTagttacgcTAGGGATAACAG
<i>- Deletion M</i>	
MMSYN1_0868CR_F0	AAAAGAAAGGAAGGGAAATAgcggccgcTGAGAATGGTAT
MMSYN1_0868CR_F	ACTTGAACCTATAAGTGTATATATAAAAAGAAAGGAAGGGAAATA
MMSYN1_0868CR_R	AAAGGTAAGATAGCAAAAGCGATTGATATATTAATAAGAGTTTTTtagttacgcTAGGGATAACAG
<i>- Deletion N</i>	
MMSYN1_0889CF_F0	TAAAAATAGCATTTAAGATTgcggccgcTGAGAATGGTAT
MMSYN1_0889CF_F	AAATATATTAATATATCATTAATAAATAAATAAGCATTTAAGATT
MMSYN1_0900CF_R	AAAAATCTCTAAATCTTTTAATAAGAATTAGAGACTAATGAATTAagttacgcTAGGGATAACAG

<i>Confirmation of correct integration of deletion cassettes</i>	
TEFterm_seq	ATATGGTATTGATAATCCTG
TEFpr_seq	ATGCAAATGATTATACATGG
URA3_seq_2	GCATTGGGTCAACAGTATAG
GFP_GT_R	CCTGAGAAAGCAACCTGACC

The first primer (upstream primer) for each deletion was paired with TEFterm_seq (KanMX4 cassette) or URA3_seq_2 (GFP cassette). The second primer (downstream primer) was paired with TEFpr-seq (KanMX4 cassette) or GFP_GT_R (GFP cassette). The third and fourth primers (GTIF and GTIR primers) were used to analyze the loss of wild-type sequences.

<i>- Deletion A</i>	
MMSYN1_0021_GTOF	TCCTTTAAAAAGAGTTGTAGTTTTGA
MMSYN1_0921_GTOF	GGCGCTTTCTCATAGCTCAC
MMSYN1_0019_GTIF	TTTTGTTGATGTTTTAGTTGATAGGA
MMSYN1_0019_GTIR	AGAACAATGCAAAGCATTTAACA
<i>- Deletion B</i>	
MMSYN1_0084_GTOR	CGCCGATAAGTGCGATTAAA
MMSYN1_0088_GTOF	GCAAGATATGCGATATGTACTAAGC
MMSYN1_0086_GTIF	TGATGGATTCAACCACCAAT
MMSYN1_0086_GTIR	TTCAGCTTGCATTTCTTTGC
<i>- Deletion C</i>	
MMSYN1_0180_GTOF	TCCCTTATTTACTTGGCGAAA
MMSYN1_0186_GTOR	CACTTGGTAAAGGAGTTTTTAAATCA
MMSYN1_0182_GTIF	TGAATTCCAGGAGTAGGTCCA
MMSYN1_0182_GTIR	TGAATCCATTCCAGTTGAAAA
<i>- Deletion D</i>	
MMSYN1_0241_GTOF	AAAATGGAGAATTTGCACAAGAA
MMSYN1_0246_GTOF	CGCAAAAATTTAAAGGGGTTT
MMSYN1_0244_GTIF	AAAGCTCAAATCGCTCAAAA
MMSYN1_0244_GTIR	TCAACTTCTTTTGTTTTTCATCTT
<i>- Deletion E</i>	
MMSYN1_0573_GTOR	GGGGGCAACTTTTCCTTATC
MMSYN1_0550_GTOF	TGTTTTTCGCAAATTATACACTTTTT
MMSYN1_0562_GTIF	TTGTAATTTGTTTTGCAATTATCA
MMSYN1_0562_GTIR	GCAATTATTGTTATTAATAGTGTTGTT
<i>- Deletion F</i>	
MMSYN1_0579_GTOR	AAATTCATTCATTTTCTTCATCAGC
MMSYN1_0583_GTOF	GCGCCTTATTCTCAAAAGGA
MMSYN1_0581_GTIF	AAGGTGGAGAACTTATGAAATGC
MMSYN1_0581_GTIR	TTTACAAATACTTCATGAGTTGATGG

- Deletion G

MMSYN1_0589_GTOF
MMSYN1_0585_GTOR
MMSYN1_0587_GTIF
MMSYN1_0587_GTIR

GGATGTCGGGTTGTGTCAAT
GGGGCTTGTTTTGTTGAAGT
GGGTGAGGACCTCCTGATG
TTGTGATTCCATCACCTTTT

- Deletion H

MMSYN1_0693_GTOF
MMSYN1_0687_GTOR
MMSYN1_0690_GTIF
MMSYN1_0690_GTIR

GAAGAACAAGCAATCAAAGCAA
ATGATTGATGAAGAACTGATCC
TTTCCAGCTGAAATCAAACAAA
TCTGGAATAACATCTCCAGCTTT

- Deletion I

MMSYN1_0698_GTOR
MMSYN1_0703_GTOF
MMSYN1_0701_GTIF
MMSYN1_0701_GTIR

AGCATTTTGACACCAACTTTCT
CAAGATTTCAAATTTAAAGGCAAAA
CCAGCTGAAGCAGGAATAACT
AAAATAATTTAGCGTTTCTAAAATCA

- Deletion J

MMSYN1_0746_GTOR
MMSYN1_0741_GTOR
MMSYN1_0744_GTIF
MMSYN1_0744_GTIR

TTCTTTTTGGATCTCCTGCAA
CAATCCAATGTTTAAACCTGCT
ACGGTGTTGGGTGTGATCTT
TGCAAATAATTCATAATGTTTGG

- Deletion K

MMSYN1_0754_GTOR
MMSYN1_0758_GTOF
MMSYN1_0756_GTIF
MMSYN1_0756_GTIR

GCTGATAAAAACGCAAAACG
TGGTGGAGCTATTAGTCAAAATCA
AAAAAGGCATTTTGTTATGGTAAT
AAGCCAGTAGATTCAAACAAACG

- Deletion L

MMSYN1_0840_GTOF
MMSYN1_0846_GTOR
MMSYN1_0843_GTIF
MMSYN1_0843_GTIR

TGAACTGGATCAGGAAGTTTAGG
GGATTGTCTCCTGTACAATTCAGA
AATGACTTTGTTTGGGTAAGATTT
TGGTATTCCAGCTGATCGAC

- Deletion M

MMSYN1_0876_GTOF
MMSYN1_0868_GTOR
MMSYN1_0872_GTIF
MMSYN1_0872_GTIR

CCAAGACCATTTGGTCCAATAC
AATTATCATAAACATCAAATCCAGGAG
AATGCTAGCAGATCAAACAACAG
TTGAGAATTTGATTTTCAGCAA

- Deletion N

MMSYN1_0889_GTOR
MMSYN1_0904_GTOR
MMSYN1_0897_GTIF
MMSYN1_0897_GTIR
MMSYN1_0902_GTIF
MMSYN1_0902_GTIR

GGTTATGATGTTGATGTTGATTTAGAA
AACGACACCGCCATTAAAAA
AAAGATAAAACAAACAGAAAATCAAGAA
TTGACTATTTTGATCAATTCTTAAAGC
GCTGCAGTAATTGCTTGTTGG
CGCCTTTTAAATATTTGCTTGTTG

Multiplex PCR for confirming the integrity of the genomes

syn1_1F
syn1_1R
syn1_2F
syn1_2R
syn1_3F
syn1_3R
syn1_4F
syn1_4R
700F
701R
900F-2
901R-2

TCTACCATTCCAACATCCACA
GCAGATATTGGTTTGAGAAACG
TGGACCTAGTAATGCCAGTGAA
GCTTTAGCATTATTTCCAGCA
ATATCCAGGAGGAGCACCAA
TGAACATGAAATTGCAAAAGTTG
CCAAAAGGAGGATTACCGATG
AAAAATTCACTGACAAAGAAGTTGAA
GAAGTTAGTGACGGATATGCAAG
ATTATATCCAGTTGGAACCTCTG
GAAGTATGATTTCCAGAACAAAAC
AACTAGCTCCGTGTTGCTTTG

Construction of tdTomato expression constructs

- tdTomato insert

JS_tdTomato_tetO2_F
JS_tdTomato_tetO2_R

TAAATTACCGGATCAATTCGAAAAAATGGTTAGCAAGGGCGAGGA
CAGGCCTGTTTAAACGGATCTTACTTGTACAGCTCGTCCA

- pCM251 backbone

tdTomato/mCherry_pCM251
tdTomato/mCherry_pCM251

CATTTTTTTTCGAATTGATCCGGTAATTTAGTGTGTG
GATCCGTTTAAACAGGCCTGTTAACATC

- ADH1 promoter

ADH1pr_F
ADH1pr_R

TTGACCACACCTCTACCGGCAGATCAAGAAATGATGGTAAATGAAATAGG
GACCTCCTCGCCCTTGCTAACCATgtatatgagatAGTTGATTGTATGC

- pCM251-mCherry backbone without tetO₂ pr

ADH1pr_Ins_F
ADH1pr_Ins_R

GATCTGCCGGTAGAGGTG
ATGGTTAGCAAGGGCGAGGA

Construction of a hygromycin B resistance marker

- TDH3 promoter

TDH3pr_F	GCTCGGTACCCGGGGATCCTCTAGATTCGAGTTTATCATTATCAATACTG
TDH3pr_R	TTTGTGTTGTTATGTGTGTTTATTCGAACTAAGTTCTTGGTGTTTTA

- hph open reading frame

hph_F	ATAAACACACATAAACAAACAAAATGGGTAAAAAGCCTGAACTCACCG
hph_R	TATGAATGAATATTCCACTTTCTTTTATTCCCTTGCCCTCGGACGAGTG

- GAL7 terminator

GAL7term_F	CACTCGTCCGAGGGCAAAGGAATAAAAAGAAAGTGGAATATTCATTCATA
GAL7term_R	CTATGACCATGATTACGCCAAGCTTAATATTCCAGATTTTACTTACAAGC

- pUC19 vector backbone

pUC19_F	AAGCTTGGCGTAATCATGGTCATAG
pUC19_R	TCTAGAGGATCCCCGGGTACCGAGC

Construction of a plasmid containing a tdTomato reporter gene and a hygromycin B resistance marker

Gibson_RFP_into_HpH_F	TAGGCGTATCACGAGGCCCTTTCAGCCAGGCGGGGCCATTTACC
Gibson_RFP_into_HpH_R	CCGTCATCACCGAAACGCGCGAGACGGCCGCAAATTAAAGCCTTCGAG
HpH_Backbone_FWD	GTCTCGCGCGTTTCGG
HpH_Backbone_REV	GAAAGGGCCTCGTGATACG

Construction of a genome linearization fragmemt containing tdTomato and hph

Telo_RFP_Hph_Prox	GCACGGCCCCTAGGGCCTCTTTAAAAGCTTGACCGAGAGCAATCCAGCCAGGCGGGGCCATTTACC
Telo_RFP_Hph_Dist	ccccaacccaacccaacccaacccaaccccaaAGCTGATACCGCTCGCCG

Optimization of the translation initiation sequence in the GFP reporter gene

Fix_Kozak_pYOGM057F	GATCCAAAAAATGTCCAAAGGAGAGAACTTTTCACTGGAGTTGTCC
Fix_Kozak_pYOGM057R	CTTCTCCTTTGGACATTTTTTTGGATCCCCCGAATTGATCCGGTAATTTAG

Construction of a plasmid used for recircularizing the genome

Cir_b_(syn1)_1F	actgcGAGCTC AGATCTACCAACGCTCTGGAAAG
Cir_b_(syn1)_1R	acgta GTCGAC AGATCT CTACCTTTTATCTTGCTC