Table S1. Primers used for probe preparation by PCR

Target	Primer name	Sequence (5'→3')	Position		Accession number
			Start	End	
rrlH (23S rRNA)	23S-1F	CGATGGGAAACGGGTTAATA	292794	292813	AE006468
	23S-1R	CTTGCGCTGACCCCATCAAT	293293	293274	AE006468
rrlH (23S rRNA)	23S-2F	TGTCGGGTAAGTTCCGACCT	293364	293383	AE006468
	23S-2R	GGAGTACCTTTTATCCGTTG	293863	293844	AE006468
bla $_{\text{CMY-2}}$	blc1F	TTTATCCAATCCGCGCTCGA	57894	57918	AB571791
	bla$_{\text{CMY-2}}$R	TTCCCGCCGTTGAGGTAAAC	58363	58344	AB571791
floR	1-93194F	TGCCGAAAATTCAGATGCTC	93194	93213	AB571791
	floRR	GTATTGTCTTCACGGTGTCC	93593	93574	AB571791
aphA7	2-431F	TGCGCCGGTTGCATTCGATT	431	450	AB571792
	2-866R	TATCAGAAAAACTCATCGAG	866	847	AB571792
bla $_{\text{TEM-1}}$	bla$_{\text{TEM-1}}$F1	AGCATCTTACGGATGGCATG	518	537	AB571794
	bla$_{\text{TEM-1}}$R1	AGTGAGGCACCTATCTCAGC	1037	1018	AB571794
tetA	tetAF1	GGCACAGGCTACATCCTGCT	2022	2041	AB571795
	tetAR1	TCAAATCATCGGCGTCCTGC	2491	2472	AB571795
spvB	spvBF	AGCAGTTTTTATCGCCTGGA	29546	29527	AE006471
	spvBR	GGTGGAACATCAGGACTTGG	29021	29040	AE006471
STM0558	STM0558F	GATTACGTTCTGGCATCTGT	616841	616860	AE006468
	STM0558R	GGTCTTCAATGAAGAAGCCA	617340	617321	AE006468
STM1330	STM1330F	CTGCCCGTAGTATTATTAAG	1408561	1408580	AE006468
	STM1330R	ACCCGGTTTTCCAGTGCAGC	1409030	1409011	AE006468
L-3553_1.021c	1.021cF	TGGAACTCAAGGCCATTACC	17333	17352	AB571791
	1.021cR	TTTCGGCTTTCTAGCTCTGG	17785	17766	AB571791

Table S2. Primers used for amplification of antimicrobial resistance regions located on pST3553

Region	Primer name	Sequence (5'→3')	Position		Accession number
			Start	End	
L-3553_2	2-1F	TGAACAATAAAACTGTCTGC	1	20	AB571792
	2-866R	TATCAGAAAAACTCATCGAG	866	847	AB571792
L-3553_3	3-1F	ACCCTGGTAAATGCTTCAAT	1	20	AB571793
	3-1040R	ACGCTCAGTGGAACGAAAAC	1040	1021	AB571793
L-3553_4	4-1F	GGCCTCGTGATACGCCTATT	1	20	AB571794
	4-1330R	AGTGTCAGCAGGTTCTGATA	1567	1548	AB571794
L-3553_5	5-1F	ATAGCCGGTTCTCGCAAGGA	1	20	AB571795
	5-2941R	TAGCCCGATACGATTGATGG	2941	2922	AB571795

Table S3. Primers used for PCR scannning of the GI-VII-6

Segment	Primer name	Sequence (5'→3')	Position[a]	
			Start	End
1	S1-F	TAAGCGGCAGGCTACTATCG	1	20
	S1-R	CAGGATCAAACTGCACTATG	2457	2438
2	S2-F	AACGTAGATCGGTGAGAGATCGGAAGCGAG	1511	1540
	S2-R	CTCAATGAAGATGAACAAGGCGAAGCCAAC	12173	12144
3	S3-F	AACTGCGGGTCAAGGATCTGGATTTCGATC	6172	6201
	S3-R	CAAGCTCTGGAGCGTACTGACGGTAAAACA	16611	16582
4	S4-F	GCTGGTTTCAGCGTAGAACCAACCGGCATA	16222	16251
	S4-R	CATTCAGTCAGCAATTGACTGCTCTCTGGA	26691	26662
5	S5-F	CCTTGCCATCAGCTTCCATGAACCAACCGA	26302	26331
	S5-R	TGAGGTGCTGGTAAACGCAGAGACACAGAC	36771	36742
6	S6-F	GCGAAACGCTGTTGCAGGTAAACCAACATC	36382	36411
	S6-R	AAGAGCGTTCTGGTGGCGTTGATGTTCTCT	46851	46822
7	S7-F	CATTCCTTCCGGGATGCCACGGAACACAAT	46462	46491
	S7-R	TACCCGCACAGGGATAGAGGCCTTGCTTAA	56931	56902
8	S8-F	TACGGGAGGGAGTGCATAAACATGGGCTGT	56542	56571
	S8-R	TGGTGGCAAAAGATGTACTCAATCTGCGGG	67055	67026
9	S9-F	CCAACCTGCTCTGGATCAACCTTGTCGATG	66551	66580
	S9-R	TTTGATAGCTTCGAGTGGCGCTCAGGTCAT	77125	77096
10	S10-F	GTCTCAGGAAAGGAAAAGCCCCTGGCAAGA	76746	76775
	S10-R	GTTTGCTCATTCAAGTAGCCGGTACTTGGC	87205	87176
11	S11-F	TAAAAGGCCTGCTGGATACAGAGGGTACTC	86816	86845
	S11-R	GCCAAGGCACTTGGTATCAG	93189	93170
12	S12-F	AAATTCCCGTTGCACATAGC	92716	92735
	S12-R	GTACCGAAGCCCAGAGTCAA	96051	96032
13	S13-F	CCCTCCTCTTTCCCACTAGC	95571	95590
	S13-R	CACCAGGAGCAGAAGCACGT	98905	98886
14	S14-F	ACTTATCCGATGCGAGCGGC	98826	98845
	S14-R	GCTTCTGCAGTTCGCCAACC	100105	100086
15	S15-F	AGGATTTCGGTAGTGCTCTG	99846	99865
	S15-R	GGCTATGGCC GCTTTCTTTT	101125	101106
16	S16-F	CCGCACCCTATACATTTAGC	101016	101035
	S16-R	TTGAACAGGAGCCGGAAACCATCGTGGTGA	107365	107336
17	S17-F	CAGCGAGCTGCACACCTTCATCAAAGGGAA	106976	107005
	S17-R	CTGACCACGTTGACGAAAAGATGCAAACGC	117290	117261
18	S18-F	TGGCTTGCTGGTTGATCAATTGGCTTTGAG	116952	116981
	S18-R	GCTACAGAGATCTTCACATCAACCCAGACT	124943	124914
19	S19-F	CTCGATACCAGCTTTGGCCG	124792	124811
	S19-R	TTGGATGCTGTATGCAATAC	127710	127691

[a] Nucleotide no. described in AB571791

Table S4. Primers used for PCR mapping of each resistance gene

PCR	Primer name	Sequence (5'→3')	Position		Accession number
			Start	End	
1	1-2251F	AAGGTCTCCGCGAATGTCCG	2251	2270	AB571791
	sul1R	TTCAAAAGCTGAAGTCGGCG	2792	2773	AB571791
2	qacEΔ1F	ATTATGACAACGGCGGAAGG	3601	3620	AB571791
	1-3932R	TGGAAGAATTTATTCGCTTT	3932	3913	AB571791
3	1-4581F	CCAGCAACGTTGATTCCAGA	4581	4600	AB571791
	dfrA12R	TTCTTCCCAATGCTCAACGA	5180	5161	AB571791
4	dfrA12F	TTGCCGATAGACTCAAAGGT	5401	5420	AB571791
	intI1R	ACAGAAATGCCTCGACTTCG	5913	5894	AB571791
5	intI1F	TATGACCAGACCTTTCAGCG	6474	6493	AB571791
	1-6940R	CACATGGTGTCGTTTTCAGA	6940	6921	AB571791
6	1-56894F	CAGAATGATTAAGCAAGGCC	56894	56913	AB571791
	sugE1R	AGAGAGCATGGCGATACTGA	57363	57344	AB571791
7	blc1F	TTTATCCAATCCGCGCTCGA	57894	57913	AB571791
	bla$_{\text{CMY-2}}$R	TTCCCGCCGTTGAGGTAAAC	58363	58344	AB571791
8	bla$_{\text{CMY-2}}$F	AACGTCTTACTAACCGATCC	59044	59063	AB571791
	ISEcp1R	GCTCTGTGGATAACTTGCAG	59603	59584	AB571791
9	1-87554F	TCCAGATGTATGCTATTCTG	87554	87573	AB571791
	sul2R	TGAGATAGGCCACACCACGC	87993	87974	AB571791
10	sul2F	ATTGCGGCTGCGCTTCGATT	88274	88293	AB571791
	strAR	CTCGACCTTTGAGCCAAATG	88743	88724	AB571791
11	strAF	AACTCTTCAATGCACGGGTC	89144	89163	AB571791
	strBR	TCGGCAACGATGTGAGAGAG	89643	89624	AB571791
12	strBF	GAGACGACCTTTGTCTCGAT	89994	90013	AB571791
	tetRR2	ATGGATTGGCGAAAAGGAGG	90843	90824	AB571791
13	tetAF2	TTGTCCAGGCAGGTGGATGA	92504	92523	AB571791
	1-92993R	TGGCTGGCAATGTCTAGCAA	92993	92974	AB571791
14	1-93194F	TGCCGAAAATTCAGATGCTC	93194	93213	AB571791
	floRR	GTATTGTCTTCACGGTGTCC	93593	93574	AB571791
15	floRF	AGAATTGGCCGTCGCCCGAT	94304	94323	AB571791
	1-94773R	GAACGCTGAGTGCGCCCATG	94773	94754	AB571791
16	2-1F	TGAACAATAAAACTGTCTGC	1	20	AB571792
	2-866R	TATCAGAAAAACTCATCGAG	866	847	AB571792
17	3-1F	ACCCTGGTAAATGCTTCAAT	1	20	AB571793
	bla$_{\text{TEM-1}}$R2	AGTACTCAACCAAGTCATTC	350	331	AB571793
18	bla$_{\text{TEM-1}}$F2	GATAAATCTGGAGCCGGTGA	731	750	AB571793
	3-1040R	ACGCTCAGTGGAACGAAAAC	1040	1021	AB571793
19	4-1F	GGCCTCGTGATACGCCTATT	1	20	AB571794
	bla$_{\text{TEM-1}}$R2	AGTACTCAACCAAGTCATTC	502	483	AB571794
20	bla$_{\text{TEM-1}}$F2	GATAAATCTGGAGCCGGTGA	883	902	AB571794
	4-1330R	AGCGCCTTACCGAGCAGAAA	1330	1311	AB571794
21	tetAF2	TTGTCCAGGCAGGTGGATGA	2130	2149	AB571795
	5-2630R	GAGCGGGTTTAACCTACTTC	2630	2611	AB571795

Table S5. Characteristics of ORFs in genomic island GI-VII-6

ORF	Gene	Location[a] (start-stop)	Length (amino acid)	Product	Accession no. and sequence similarity	% Identity
L-3553_1.001		52-672	206	Regulatory protein	AE006468; STM0869, Regulatory protein, *Salmonella* Typhimurium strain LT2	100
L-3553_1.002	*insB1*	736-1452	238	IS*26* transposase	FJ621588; InsB, plasmid pAR060302 (*Escherichia*	100
L-3553_1.003c		1881-1594	95	Hypothetical protein	FJ621588; hypothetical protein, plasmid pAR060302 (*E. coli*)	100
L-3553_1.004c		2405-1905	166	Hypothetical protein	FJ621588; hypothetical protein, plasmid pAR060302 (*E. coli*) HQ332785; hypothetical protein, plasmid pCK41 (*Edwardsiella tarda*)	100 100
L-3553_1.005c	*sul1*	3372-2533	279	Dihydropteroate synthase	FJ621588; Sul 1, plasmid pAR060302 (*E. coli*) HQ332785; dihydropteroate synthase, plasmid pCK41 (*E. tarda*)	100 100
L-3553_1.006c	*qacEΔ1*	3713-3366	115	Quaternary ammonium compound-resistance protein	Fj621588; QacEdelta1, plasmid pAR060302 (*E. coli*)	100
L-3553_1.007c	*aadA2*	4668-3877	263	Aminoglycoside adenyltransferase	HQ332785; aminoglycoside resistance protein, plasmid pCK41 (*E. tarda*)	100
L-3553_1.008c	*dfrA12*	5573-5076	165	Dihydrofolate reductase	HQ332785; dihydrofolate reductase, plasmid pCK41 (*E. tarda*)	100
L-3553_1.009	*intI1*	5718-6731	337	Class 1 integrase	HQ332785; integrase, plasmid pCK41 (*E. tarda*) FJ621588; IntI1, plasmid pAR060302 (*E. coli*)	99 99
L-3553_1.010		7037-7594	185	Resolvase	FJ621588; resolvase family recombinase family protein, plasmid pAR060302 (*E. coli*)	100
L-3553_1.011	*tnpA*	7597-10569	990	Transposase	FJ621588; TnpA, plasmid pAR060302 (*E. coli*)	99
L-3553_1.012	*tnpA*	10648-11652	334	IS*4321* transposase	FJ621588; InsD2, plasmid pAR060302 (*E. coli*)	100
L-3553_1.013c		12067-11834	77	Hypothetical protein	FJ621588; hypothetical protein, plasmid pAR060302 (*E. coli*)	100
L-3553_1.014c		12406-12128	92	Hypothetical protein	FJ621588; hypothetical protein, plasmid pAR060302 (*E. coli*)	100
L-3553_1.015c		14120-12393	575	Primase-helicase family protein	FJ621588; primase-helicase family protein, plasmid pAR060302 (*E. coli*)	100
L-3553_1.016c		14684-14298	128	Hypothetical protein	FJ621588; hypothetical protein, plasmid pAR060302 (*E. coli*)	100
L-3553_1.017c		16027-15143	294	Hypothetical protein	FJ621588; hypothetical protein, plasmid pAR060302 (*E. coli*)	100
L-3553_1.018c		16626-16069	185	Hypothetical protein	FJ621588; hypothetical protein, plasmid pAR060302 (*E. coli*)	100
L-3553_1.019c		16951-16700	83	Hypothetical protein	FJ621588; hypothetical protein, plasmid pAR060302 (*E. coli*)	100
L-3553_1.020c		17201-16932	89	Hypothetical protein	FJ621588; hypothetical protein, plasmid pAR060302 (*E. coli*)	100
L-3553_1.021c		17799-17194	201	HD phosphohydrolase family protein	FJ621588; HD phosphohydrolase family protein, plasmid pAR060302 (*E. coli*)	100
L-3553_1.022c		18074-17871	67	Hypothetical protein	FJ621588; hypothetical protein, plasmid pAR060302 (*E. coli*)	100
L-3553_1.023c		20729-18276	817	Phosphoadenosine phosphosulfate reductase family protein	FJ621588; phosphoadenosine phosphosulfate reductase family protein, plasmid pAR060302 (*E. coli*)	100
L-3553_1.024c		21203-20817	128	Hypothetical protein	FJ621588; hypothetical protein, plasmid pAR060302 (*E. coli*)	100
L-3553_1.025c		21990-21436	184	Hypothetical protein	FJ621588; hypothetical protein, plasmid pAR060302 (*E. coli*)	100
L-3553_1.026c		22495-22064	143	Hypothetical protein	FJ621588; hypothetical protein, plasmid pAR060302 (*E. coli*)	100
L-3553_1.027c		24181-22556	541	C-5 cytosine-specific DNA methylase	FJ621588; Dcm, plasmid pAR060302 (*E. coli*)	100
L-3553_1.028c		24642-24259	127	Hypothetical protein	FJ621588; hypothetical protein, plasmid pAR060302 (*E. coli*)	99
L-3553_1.029c		24983-24639	114	Hypothetical protein	FJ621588; hypothetical protein, plasmid pAR060302 (*E. coli*)	100
L-3553_1.030c		25528-25175	117	Hypothetical protein	FJ621588; hypothetical protein, plasmid pAR060302 (*E. coli*)	100
L-3553_1.031c		25788-25597	63	Hypothetical protein	FJ621588; hypothetical protein, plasmid pAR060302 (*E. coli*)	100
L-3553_1.032c		26121-25846	91	Hypothetical protein	FJ621588; hypothetical protein, plasmid pAR060302 (*E. coli*)	100
L-3553_1.033c		26578-26126	150	Hypothetical protein	FJ621588; hypothetical protein, plasmid pAR060302 (*E. coli*)	100
L-3553_1.034c		26957-26568	129	Hypothetical protein	FJ621588; hypothetical protein, plasmid pAR060302 (*E. coli*)	100

L-3553_1.035c		27243-27019	74	Ferredoxin family member protein	FJ621588ferredoxin family member protein, plasmid pAR060302 (*E. coli*)	100
L-3553_1.036c		28193-27309	294	Hypothetical protein	FJ621588; hypothetical protein, plasmid pAR060302 (*E. coli*)	100
L-3553_1.037c		28767-28267	166	Hypothetical protein	FJ621588; hypothetical protein, plasmid pAR060302 (*E. coli*)	100
L-3553_1.038c		29397-28858	179	Hypothetical protein	FJ621588; hypothetical protein, plasmid pAR060302 (*E. coli*)	100
L-3553_1.039c		29997-29662	111	Hypothetical protein	FJ621588; hypothetical protein, plasmid pAR060302 (*E. coli*)	100
L-3553_1.0340c		31855-30059	598	Hypothetical protein	FJ621588; hypothetical protein, plasmid pAR060302 (*E. coli*)	100
L-3553_1.041c		33217-31940	425	Hypothetical protein	FJ621588; hypothetical protein, plasmid pAR060302 (*E. coli*)	100
L-3553_1.042c		34427-33417	336	Hypothetical protein	FJ621588; hypothetical protein, plasmid pAR060302 (*E. coli*)	100
L-3553_1.043c		35479-34490	329	Phage recombination protein	FJ621588; Bet, plasmid pAR060302 (*E. coli*)	100
L-3553_1.044c		36104-35574	176	Single-stranded DNA-binding protein	FJ621588; Ssb, plasmid pAR060302 (*E. coli*)	100
L-3553_1.045c		37073-36165	302	Hypothetical protein	FJ621588; hypothetical protein, plasmid pAR060302 (*E. coli*)	100
L-3553_1.046c	*bet*	38052-37084	322	ATPase associated with various cellular activities (AAA) family protein	FJ621588; ATPase associated with various cellular activities (AAA) family protein, plasmid pAR060302 (*E. coli*)	100
L-3553_1.047c	*ssb*	38523-38272	83	Hypothetical protein	FJ621588; hypothetical protein, plasmid pAR060302 (*E. coli*)	100
L-3553_1.048c		39162-38761	133	Hypothetical protein	FJ621588; hypothetical protein, plasmid pAR060302 (*E. coli*)	100
L-3553_1.049		39376-40017	213	Hypothetical protein	FJ621588; hypothetical protein, plasmid pAR060302 (*E. coli*)	100
L-3553_1.050		40140-41000	286	Hypothetical protein	FJ621588; hypothetical protein, plasmid pAR060302 (*E. coli*)	100
L-3553_1.051c	*traN*	43846-41039	935	Type IV conjugative transfer system protein	FJ621588; TraN, plasmid pAR060302 (*E. coli*)	100
L-3553_1.052c	*traU*	44957-43950	335	Type IV conjugative transfer system protein	FJ621588; TraU, plasmid pAR060302 (*E. coli*)	100
L-3553_1.053c		45625-44954	223	Hypothetical protein	FJ621588; hypothetical protein, plasmid pAR060302 (*E. coli*)	100
L-3553_1.054c	*traW*	46887-45622	421	Type IV conjugative transfer system protein	FJ621588; TraW, plasmid pAR060302 (*E. coli*)	100
L-3553_1.055c	*trhF*	47380-46850	176	Type IV conjugative transfer system signal peptidase	FJ621588; TrhF, plasmid pAR060302 (*E. coli*)	100
L-3553_1.056c		47694-47377	105	Hypothetical protein	FJ621588; hypothetical protein, plasmid pAR060302 (*E. coli*)	100
L-3553_1.057c	*traC*	50156-47709	815	Type IV conjugative transfer system protein	FJ621588; TraC, plasmid pAR060302 (E. coli)	100
L-3553_1.058c		50860-50153	235	Hypothetical protein	FJ621588; hypothetical protein, plasmid pAR060302 (*E. coli*)	100
L-3553_1.059c		56495-51009	1828	Hypothetical protein	FJ621588; hypothetical protein, plasmid pAR060302 (*E. coli*)	100
L-3553_1.060c		56966-56541	141	Hypothetical protein	FJ621588; hypothetical protein, plasmid pAR060302 (*E. coli*)	100
L-3553_1.061	*sugE1*	57100-57540	146	Quaternary ammonium compound-resistance protein	FJ621588; SugE1, plasmid pAR060302 (*E. coli*)	99
L-3553_1.062c	*blc1*	58070-57537	177	Outer membrane lipoprotein	FJ621588; Blc1, plasmid pAR060302 (*E. coli*)	100
L-3553_1.063c	*bla*$_{\text{CMY-2}}$	59309-58164	381	AmpC beta-lactamase	FJ621588; AmpC, plasmid pAR060302 (*E. coli*)	100
L-3553_1.064c	*tnpA*	60895-59633	420	Transposase	FJ621588; transposase InsC3 for insertion sequence IS*Ec9* , plasmid pAR060302 (*E. coli*)	100
L-3553_1.065c	*traA*	61572-61180	130	Type IV conjugative transfer system protein	FJ621588; TraA, plasmid pAR060302 (*E. coli*)	100
L-3553_1.066c	*traV*	62154-61576	192	Type IV conjugative transfer system protein	FJ621588; TraV, plasmid pAR060302 (*E. coli*)	100
L-3553_1.067c	*traB*	63467-62151	438	Type IV conjugative transfer system protein	FJ621588; TraB, plasmid pAR060302 (*E. coli*)	100
L-3553_1.068c		64381-63464	305	TraK family protein	FJ621588; TraK family protein, plasmid pAR060302 (*E. coli*)	100
L-3553_1.069c	*traE*	64991-64365	208	Type IV conjugative transfer system protein	FJ621588; TraE, plasmid pAR060302 (*E. coli*)	99
L-3553_1.070c	*traL*	65269-64988	93	Type IV conjugative transfer system protein	FJ621588; TraL, plasmid pAR060302 (*E. coli*)	100
L-3553_1.071c		65791-65414	125	Hypothetical protein	FJ621588; hypothetical protein, plasmid pAR060302 (*E. coli*)	100

L-3553_1.072c	pseudo gene	66739-66115	-	Hypothetical protein	FJ621588; hypothetical protein, plasmid pAR060302 (*E. coli*)	
L-3553_1.073c		67188-66811	125	Hypothetical protein	FJ621588; hypothetical protein, plasmid pAR060302 (*E. coli*)	100
L-3553_1.074c		67644-67198	148	Hypothetical protein	FJ621588; hypothetical protein, plasmid pAR060302 (*E. coli*)	100
L-3553_1.075c		68283-67654	209	Hypothetical protein	FJ621588; hypothetical protein, plasmid pAR060302 (*E. coli*)	100
L-3553_1.076c		68824-68240	194	Hypothetical protein	FJ621588; hypothetical protein, plasmid pAR060302 (*E. coli*)	100
L-3553_1.077c	*traD*	70700-68835	621	Type IV conjugative transfer system protein	FJ621588; TraD, plasmid pAR060302 (*E. coli*)	100
L-3553_1.078c	*traI*	73669-70697	990	Type IV conjugative transfer system protein	FJ621588; TraI, plasmid pAR060302 (*E. coli*)	100
L-3553_1.079		73822-74454	210	Hypothetical protein	FJ621588; hypothetical protein, plasmid pAR060302 (*E. coli*)	100
L-3553_1.080		74436-74669	77	Hypothetical protein	FJ621588; hypothetical protein, plasmid pAR060302 (*E. coli*)	100
L-3553_1.081	*topB*	74669-76861	730	DNA topoisomerase III	FJ621588; TopB, plasmid pAR060302 (*E. coli*)	100
L-3553_1.082		76876-77364	162	Hypothetical protein	FJ621588; hypothetical protein, plasmid pAR060302 (*E. coli*)	100
L-3553_1.083c		77733-77455	92	Hypothetical protein	FJ621588; hypothetical protein, plasmid pAR060302 (*E. coli*)	100
L-3553_1.084c		78583-77966	205	Hypothetical protein	FJ621588; hypothetical protein, plasmid pAR060302 (*E. coli*)	100
L-3553_1.085c		79295-78639	218	Hypothetical protein	FJ621588; hypothetical protein, plasmid pAR060302 (*E. coli*)	100
L-3553_1.086c		80722-79295	475	Hypothetical protein	FJ621588; hypothetical protein, plasmid pAR060302 (*E. coli*)	100
L-3553_1.087c		81226-80726	166	Hypothetical protein	FJ621588; hypothetical protein, plasmid pAR060302 (*E. coli*)	100
L-3553_1.088c		81567-81235	110	Hypothetical protein	FJ621588; hypothetical protein, plasmid pAR060302 (*E. coli*)	100
L-3553_1.089c		82058-81552	168	Hypothetical protein	FJ621588; hypothetical protein, plasmid pAR060302 (*E. coli*)	100
L-3553_1.090c		82725-82051	224	Hypothetical protein	FJ621588; hypothetical protein, plasmid pAR060302 (*E. coli*)	100
L-3553_1.091c		82981-82700	93	Hypothetical protein	FJ621588; hypothetical protein, plasmid pAR060302 (*E. coli*)	100
L-3553_1.092c		83360-82974	128	Hypothetical protein	FJ621588; hypothetical protein, plasmid pAR060302 (*E. coli*)	99
L-3553_1.093		83913-84548	211	Hypothetical protein	FJ621588; hypothetical protein, plasmid pAR060302 (*E. coli*)	100
L-3553_1.094c		84873-84601	90	Hypothetical protein	FJ621588; hypothetical protein, plasmid pAR060302 (*E. coli*)	100
L-3553_1.095c		86103-84922	393	Hypothetical protein	FJ621588; hypothetical protein, plasmid pAR060302 (*E. coli*)	100
L-3553_1.096c		86892-86107	261	Hypothetical protein	FJ621588; hypothetical protein, plasmid pAR060302 (*E. coli*)	100
L-3553_1.097c		87377-87066	103	Hypothetical protein	FJ621588; hypothetical protein, plasmid pAR060302 (*E. coli*)	100
L-3553_1.098	*sul2*	87684-88499	271	Dihydropteroate synthase	FJ621588; Sul2, plasmid pAR060302 (*E. coli*)	100
L-3553_1.099	*strA*	88560-89363	267	Streptomycin resistance protein	FJ621588; StrA, plasmid pAR060302 (*E. coli*)	99
L-3553_1.100	*strB*	89369-90199	276	Streptomycin resistance protein	FJ621588; StrB, plasmid pAR060302 (*E. coli*)	100
L-3553_1.101		90505-90747	80	Hypothetical protein	FJ621588; hypothetical protein, plasmid pAR060302 (*E. coli*)	99
L-3553_1.102c	*tetR*	91456-90779	225	Tetracycline repressor protein	FJ621588; TetR, plasmid pAR060302 (*E. coli*)	100
L-3553_1.103	*tetA*	91460-92734	424	Tetracycline resistance protein	FJ621588; TetA, plasmid pAR060302 (*E. coli*)	100
L-3553_1.104c		92889-92665	74	Hypothetical protein	FJ621588; hypothetical protein, plasmid pAR060302 (*E. coli*)	100
L-3553_1.105c		93306-93001	101	Hypothetical protein	FJ621588; hypothetical protein, plasmid pAR060302 (*E. coli*)	100
L-3553_1.106c	*floR*	94548-93334	404	Chloramphenicol/florfenicol resistance protein	FJ621588; FloR, plasmid pAR060302 (*E. coli*)	99
L-3553_1.107c		95649-94765	294	Hypothetical protein	FJ621588; hypothetical protein, plasmid pAR060302 (*E. coli*)	100
L-3553_1.108c	*insA*	97173-95680	497	Transposase	FJ621588; InsA, plasmid pAR060302 (*E. coli*)	100
L-3553_1.109c		97608-97384	74	Hypothetical protein	FJ621588; hypothetical protein, plasmid pAR060302 (*E. coli*)	100
L-3553_1.110c	*parA*	98342-97605	245	Plasmid stabilization protein, resolvase	FJ621588; ParA, plasmid pAR060302 (*E. coli*)	100

L-3553_1.111		98449-98940	163	Hypothetical protein	FJ621588; hypothetical protein, plasmid pAR060302 (*E. coli*)	100
L-3553_1.112c	*insB2*	99690-98974	238	IS*26* transposase	FJ621588; InsB, plasmid pAR060302 (*E. coli*)	100
L-3553_1.113	*insB3*	100211-100933	240	IS*26* transposase	FJ621588; InsB, plasmid pAR060302 (*E. coli*)	99
L-3553_1.114c		101645-101148	165	Hypothetical protein	FJ621588; hypothetical protein, plasmid pAR060302 (*E. coli*)	100
L-3553_1.115c		102109-101648	153	Hypothetical protein	FJ621588; hypothetical protein, plasmid pAR060302 (*E. coli*)	100
L-3553_1.116		102233-102568	111	Hypothetical protein	FJ621588; hypothetical protein, plasmid pAR060302 (*E. coli*)	100
L-3553_1.117c		103053-102583	156	Hypothetical protein	FJ621588; hypothetical protein, plasmid pAR060302 (*E. coli*)	100
L-3553_1.118c		103417-103046	123	Hypothetical protein	FJ621588; hypothetical protein, plasmid pAR060302 (*E. coli*)	100
L-3553_1.119		103281-103841	186	Hypothetical protein	FJ621588; hypothetical protein, plasmid pAR060302 (*E. coli*)	100
L-3553_1.120c		104511-103963	182	Hypothetical protein	FJ621588; hypothetical protein, plasmid pAR060302 (*E. coli*)	100
L-3553_1.121		104674-105024	116	Hypothetical protein	FJ621588; hypothetical protein, plasmid pAR060302 (*E. coli*)	100
L-3553_1.122		105029-105331	100	Hypothetical protein	FJ621588; hypothetical protein, plasmid pAR060302 (*E. coli*)	99
L-3553_1.123c		105651-105358	97	Hypothetical protein	FJ621588; hypothetical protein, plasmid pAR060302 (*E. coli*)	100
L-3553_1.124c		106011-105739	90	Hypothetical protein	FJ621588; hypothetical protein, plasmid pAR060302 (*E. coli*)	100
L-3553_1.125c		106596-106069	175	Hypothetical protein	FJ621588; hypothetical protein, plasmid pAR060302 (*E. coli*)	100
L-3553_1.126c		107684-106827	285	Hypothetical protein	FJ621588; hypothetical protein, plasmid pAR060302 (*E. coli*)	100
L-3553_1.127c		107898-107671	75	Hypothetical protein	FJ621588; hypothetical protein, plasmid pAR060302 (*E. coli*)	100
L-3553_1.128c		108419-107901	172	Hypothetical protein	FJ621588; hypothetical protein, plasmid pAR060302 (*E. coli*)	100
L-3553_1.129c		108862-108416	148	Hypothetical protein	FJ621588; hypothetical protein, plasmid pAR060302 (*E. coli*)	100
L-3553_1.130c		109221-108862	119	Hypothetical protein	FJ621588; hypothetical protein, plasmid pAR060302 (*E. coli*)	100
L-3553_1.131c		109706-109278	142	Hypothetical protein	FJ621588; hypothetical protein, plasmid pAR060302 (*E. coli*)	100
L-3553_1.132c		110600-109740	286	Hypothetical protein	FJ621588; hypothetical protein, plasmid pAR060302 (*E. coli*)	100
L-3553_1.133c		111524-110616	302	Peptidase S49 family protein	FJ621588; hypothetical protein, plasmid pAR060302 (*E. coli*)	100
L-3553_1.134c		113393-112194	399	Transposase	FJ621588; hypothetical protein, plasmid pAR060302 (*E. coli*)	100
L-3553_1.135		114660-115022	120	Hypothetical protein	FJ621588; hypothetical protein, plasmid pAR060302 (*E. coli*)	100
L-3553_1.136c	*traG*	118674-115060	1204	Type IV conjugative transfer system protein	FJ621588; TraG, plasmid pAR060302 (*E. coli*)	100
L-3553_1.137c	*traH*	120120-118687	477	Type IV conjugative transfer system protein	FJ621588; TraH, plasmid pAR060302 (*E. coli*)	100
L-3553_1.138c	*traF*	121150-120122	342	Type IV conjugative transfer system protein	FJ621588; TraF, plasmid pAR060302 (*E. coli*)	99
L-3553_1.139c		122784-121273	503	UvrD/REP helicase family protein	FJ621588; UvrD/REP helicase family protein, plasmid pAR060302 (*E. coli*)	100
L-3553_1.140c		124111-123071	346	Hypothetical protein	FJ621588; hypothetical protein, plasmid pAR060302 (*E. coli*)	100
L-3553_1.141	*insB4*	125038-125754	238	IS*26* transposase	FJ621588; InsB, plasmid pAR060302 (*E. coli*)	100
L-3553_1.142c		127604-125919	561	Putative transport protein	AE006468; STM0870, Putative transport protein, *Salmonella* Typhimurium strain LT2	99

[a] Nucleotide no. described in AB571791

Table S6. Core genome SNVs among serovar Typhimurium strains

Nucleotide position on LT2	*S*. Typhimurium strains							Information of *S*. Typhimurium LT2 chromosomal DNA		
	LT2	T000240	DT104	14028S	L-3553	SL1344	D23580	Gene-ID	Gene	Function of products
140	A	C	A	A	A	A	A			
831	T	T	C	C	C	C	C	STM0002	*thrA*	bifunctional aspartokinase I/homeserine dehydrogenase I
5129	T	T	T	T	T	T	C	STM0005	*yaaA*	hypothetical protein
9724	A	A	G	A	A	A	A	STM0009	*yaaH*	hypothetical protein
12366	C	C	C	C	C	T	C	STM0012	*dnaK*	molecular chaperone DnaK
13723	C	C	C	C	C	C	T	STM0013	*dnaJ*	chaperone protein DnaJ
15716	A	A	A	A	A	A	G	STM0014	-	putative transcriptional regulator
15775	T	T	G	G	G	G	G	STM0014	-	putative transcriptional regulator
15949	C	C	C	C	C	C	T	STM0014	-	putative transcriptional regulator
17435	C	C	C	T	C	C	C	STM0017	-	hypothetical protein
20011	C	C	C	T	T	T	T			
23058	C	C	C	C	C	A	C			
23156	A	A	G	G	G	G	G			
25548	T	T	T	T	T	A	T	STM0022	*bcfB*	fimbrial chaparone
25722	C	C	T	C	C	C	C	STM0022	*bcfB*	fimbrial chaparone
27184	C	C	T	C	C	C	C	STM0023	*bcfC*	fimbrial usher
29155	A	A	G	A	A	A	A	STM0024	*bcfD*	fimbrial subunit
30693	C	C	T	C	C	C	C	STM0027	*bcfG*	fimbrial chaparone
31305	T	T	T	T	T	T	A	STM0028	*bcfH*	putative thiol-disulfide isomerase
34090	G	G	T	G	G	G	G	STM0030	-	putative transcriptional regulator
34091	A	A	G	G	G	G	G	STM0030	-	putative transcriptional regulator
34754	C	G	G	G	G	G	G	STM0031	-	putative transcriptional regulator
35844	A	A	G	A	A	A	A	STM0032	-	putative arylsulfatase
35965	A	A	G	G	G	G	G	STM0032	-	putative arylsulfatase
36413	G	G	G	G	G	G	A	STM0032	-	putative arylsulfatase
37175	C	C	C	C	C	T	C	STM0033	-	putative 5'-nucleotidase
37797	T	T	T	T	C	T	T	STM0033	-	putative 5'-nucleotidase
39957	G	G	A	G	G	G	G			
43331	A	A	A	A	A	T	A	STM0037	-	putative cytoplasmic protein
43577	G	G	A	G	G	G	G	STM0037	-	putative cytoplasmic protein
45126	G	G	G	G	G	G	A	STM0038	-	putative arylsulfatase
47955	C	C	C	T	C	C	C	STM0040	*nhaR*	transcriptional activator NhaR
51973	C	C	C	C	T	C	C			
54863	G	G	G	G	G	A	G	STM0046	*ileS*	isoleucyl-tRNA synthetase
57550	C	C	T	C	C	C	C	STM0048	*slpA*	FKBP-type peptidyl-prolyl cis-trans isomerase
63253	G	G	G	A	A	A	A	STM0053	-	putative transcriptional regulator
68394	A	A	T	A	A	A	A			
70089	G	G	G	A	A	A	A	STM0060	*citE2*	putative citrate lyase beta chain
71394	C	C	C	C	C	C	T	STM0061	*citF2*	putative citrate lyase alpha chain/citrate-ACP transferase
74584	G	G	G	G	T	G	G	STM0064	*dapB*	dihydrodipicolinate reductase
75382	G	G	G	G	G	G	T			
75491	C	C	C	C	C	C	T			
75586	A	A	G	A	A	A	A			
75854	T	T	T	T	T	T	C			
75868	C	C	C	C	C	T	C			
77150	A	A	A	A	G	A	A	STM0067	*carB*	carbamoyl phosphate synthase large subunit
77382	C	C	C	C	C	T	C	STM0067	*carB*	carbamoyl phosphate synthase large subunit
80521	A	A	A	A	A	G	A			
84502	C	C	C	C	C	T	C	STM0072	*caiB*	crotonobetainyl-CoA:carnitine CoA-transferase
87074	T	T	T	C	C	C	C	STM0074	*caiT*	L-carnitine/gamma-butyrobetaine antiporter
88361	C	C	C	C	C	T	C			
88843	G	G	A	G	G	G	G	STM0075	*fixA*	putative electron transfer flavoprotein FixA
89080	C	C	C	C	T	C	C	STM0075	*fixA*	putative electron transfer flavoprotein FixA
91041	T	T	C	C	C	C	C	STM0077	*fixC*	putative oxidoreductase FixC
91336	G	G	G	G	G	A	G	STM0077	*fixC*	putative oxidoreductase FixC
94927	C	T	C	C	C	C	C	STM0082	-	putative secreted protein
98144	G	G	A	G	G	G	G			
99551	T	T	T	T	T	G	T	STM0086	*kefC*	glutathione-regulated potassium-efflux system protein KefC
101101	C	C	C	C	C	T	C	STM0087	*folA*	dihydrofolate reductase
103018	T	T	G	G	G	G	G	STM0090	*ksgA*	dimethyladenosine transferase
104421	C	C	A	A	A	A	A	STM0091	*pdxA*	4-hydroxythreonine-4-phosphate dehydrogenase
105132	C	C	C	C	C	C	T	STM0092	*surA*	peptidyl-prolyl cis-trans isomerase SurA
107231	A	A	A	T	T	T	T	STM0093	*imp*	organic solvent tolerance protein
109555	C	C	G	C	C	C	C	STM0095	*rluA*	23S rRNA/tRNA pseudouridine synthase A
114441	G	G	G	G	G	G	A	STM0097	*polB*	DNA polymerase II
114465	C	C	C	C	C	C	T	STM0097	*polB*	DNA polymerase II
117658	G	G	A	G	G	G	G	STM0101	*araD*	L-ribulose-5-phosphate 4-epimerase
120742	C	C	T	C	C	C	C	STM0103	*araB*	ribulokinase
120876	C	C	T	C	C	C	C	STM0103	*araB*	ribulokinase
123364	G	G	G	A	A	A	A	STM0105	*yabI*	hypothetical protein
127292	G	G	G	G	G	A	G	STM0109	*yabN*	transcriptional regulator SgrR
127747	T	T	C	C	C	C	C	STM0109	*yabN*	transcriptional regulator SgrR
127898	G	G	A	G	G	G	G	STM0109	*yabN*	transcriptional regulator SgrR
134492	A	A	A	A	A	C	A			
135868	T	T	C	C	C	C	C			
136572	G	G	G	A	G	G	G	STM0116	*ilvI*	acetolactate synthase 3 catalytic subunit
141192	A	A	A	A	A	A	G	STM0120	*mraW*	S-adenosyl-methyltransferase MraW

141965	T	T	T	C	T	T	T	STM0122	*ftsI*	division specific transpeptidase
142471	A	A	G	A	A	A	A	STM0122	*ftsI*	division specific transpeptidase
144008	C	C	C	T	C	C	C	STM0123	*murE*	UDP-N-acetylmuramoylalanyl-D-glutamate--2,6-diaminopimelate
144474	C	C	C	C	C	C	T	STM0123	*murE*	UDP-N-acetylmuramoylalanyl-D-glutamate--2,6-diaminopimelate
153434	C	C	C	C	G	C	C	STM0130	*ddl*	D-alanine--D-alanine ligase
153820	C	C	C	C	C	T	C	STM0131	*ftsQ*	cell division protein FtsQ
154974	C	C	A	C	C	C	C	STM0132	*ftsA*	cell division protein FtsA
161385	C	C	T	C	C	C	C	STM0136	*secA*	preprotein translocase subunit SecA
162621	T	T	T	T	T	C	T	STM0139	*yacF*	hypothetical protein
166348	A	G	G	G	G	G	G	STM0143	*hofB*	hypothetical protein
168062	G	G	A	G	G	G	G	STM0144	*ppdD*	putative major pilin subunit
169825	A	A	G	G	G	G	G	STM0146	*ampD*	N-acetyl-anhydromuranmyl-L-alanine amidase
171840	G	G	G	G	G	G	A	STM0149	-	Na+/galactoside symporter
172583	C	C	C	T	C	C	C	STM0149	-	Na+/galactoside symporter
174483	C	C	C	C	C	C	T	STM0150	*aroP*	aromatic amino acid transporter
177553	A	A	G	G	G	G	G	STM0152	*aceE*	pyruvate dehydrogenase subunit E1
180034	C	G	G	G	G	G	G	STM0153	*aceF*	dihydrolipoamide acetyltransferase
180035	G	C	C	C	C	C	C	STM0153	*aceF*	dihydrolipoamide acetyltransferase
182695	G	G	G	G	T	G	G			
184305	C	G	G	G	G	G	G	STM0157	*yacH*	putative outer membrane protein
184306	G	C	C	C	C	C	C	STM0157	*yacH*	putative outer membrane protein
185256	A	A	G	G	G	G	G	STM0157	*yacH*	putative outer membrane protein
185381	G	G	G	A	G	G	G	STM0157	*yacH*	putative outer membrane protein
186678	C	A	C	C	C	C	C	STM0158	*acnB*	bifunctional aconitate hydratase 2/2-methylisocitrate dehydratase
188939	A	A	A	A	C	A	A	STM0159	-	putative restriction endonuclease
192226	A	T	T	T	T	T	T	STM0162	-	putative inner membrane protein
193186	A	A	A	A	A	A	G	STM0163	*pdxA*	4-hydroxythreonine-4-phosphate dehydrogenase 2
193606	C	C	T	C	C	C	C	STM0164	-	putative transcriptional regulator
194733	T	T	T	T	T	T	C	STM0165	*speD*	S-adenosylmethionine decarboxylase
198181	C	C	C	C	C	C	T			
198539	G	G	G	A	G	G	G	STM0169	*gcd*	glucose dehydrogenase
203177	T	T	T	G	G	G	G	STM0173	*yadH*	putative transport protein
206940	T	T	T	T	T	T	C	STM0175	*stiC*	putativie fimbrial usher
208395	C	C	C	C	C	C	T	STM0177	*stiA*	putative fimbrial subunit
208858	A	A	A	A	T	A	A	STM0177	*stiA*	putative fimbrial subunit
211778	C	C	C	C	C	C	T	STM0181	*panC*	pantoate--beta-alanine ligase
212139	C	T	C	C	C	C	C	STM0181	*panC*	pantoate--beta-alanine ligase
212766	G	G	G	G	G	G	A	STM0182	*panB*	3-methyl-2-oxobutanoate hydroxymethyltransferase
215515	C	C	C	C	C	T	C	STM0185	*yadB*	glutamyl-Q tRNA(Asp) synthetase
217153	G	G	A	G	G	G	G	STM0187	*sfsA*	sugar fermentation stimulation protein A
218047	C	C	C	C	C	C	A	STM0188	*ligT*	2'-5' RNA ligase
218107	C	C	C	C	C	A	C	STM0188	*ligT*	2'-5' RNA ligase
218109	C	C	T	C	C	C	C	STM0188	*ligT*	2'-5' RNA ligase
224363	C	C	T	C	C	C	C	STM0191	*fhuA*	ferrichrome outer membrane transporter
226287	A	A	A	A	A	A	G	STM0192	*fhuC*	iron-hydroxamate transporter ATP-binding subunit
228054	C	C	C	T	T	T	T	STM0194	*fhuB*	iron-hydroxamate transporter permease subunit
229972	C	C	A	A	A	A	A			
230364	G	G	T	G	G	G	G			
230402	G	G	G	G	G	G	A			
233282	C	C	C	C	C	C	A	STM0196	*stfC*	putative fimbrial outer membrane usher
233671	G	G	G	G	G	G	T	STM0196	*stfC*	putative fimbrial outer membrane usher
240045	A	A	C	C	C	C	C	STM0203	*yadQ*	chloride channel protein
241385	C	C	T	C	C	C	C	STM0206	*btuF*	vitamin B12-transporter protein BtuF
247979	G	G	G	G	G	T	G	STM0212	-	putative inner membrane protein
250053	C	C	C	G	C	C	C	STM0213	*dapD*	2,3,4,5-tetrahydropyridine-2,6-carboxylate N-succinyltransferase
252714	G	G	G	G	T	G	G	STM0214	*glnD*	PII uridylyl-transferase
253595	G	G	G	G	G	G	A	STM0215	*map*	methionine aminopeptidase
255291	T	T	T	A	A	A	A	STM0217	*tsf*	elongation factor Ts
255727	G	G	G	G	G	G	A	STM0217	*tsf*	elongation factor Ts
257179	T	T	C	T	T	T	T	STM0219	*frr*	ribosome recycling factor
260965	G	G	G	G	G	G	A	STM0222	*cdsA*	CDP-diglyceride synthase
264106	G	G	G	A	A	A	A	STM0224	*yaeT*	outer membrane protein assembly factor YaeT
271617	G	G	G	G	G	G	A	STM0231	*dnaE*	DNA polymerase III subunit alpha
272969	G	G	G	G	G	A	G	STM0231	*dnaE*	DNA polymerase III subunit alpha
274981	C	C	C	C	C	C	T	STM0233	-	putative endochitinase
277017	C	C	C	T	C	C	C	STM0234	*ldcC*	lysine decarboxylase 2
277971	G	G	A	G	G	G	G	STM0234	*ldcC*	lysine decarboxylase 2
282230	A	A	G	A	A	A	A			
284164	G	G	G	G	G	G	C	STM0242	*proS*	prolyl-tRNA synthetase
285510	A	A	G	A	A	A	A			
286024	G	G	G	G	A	G	G	STM0245	*metQ*	DL-methionine transporter substrate-binding subunit
286834	A	A	A	G	A	A	A	STM0246	*yaeE*	DL-methionine transporter permease subunit
288835	C	T	T	T	T	T	T			
288843	C	A	A	A	A	A	A			
288853	C	T	T	T	T	T	T			
290875	C	C	T	C	C	C	C			
294788	T	C	T	T	T	T	T			
295760	G	G	A	A	A	A	A	STM0255	*dkgB*	2,5-diketo-D-gluconate reductase B
296614	C	C	C	C	C	C	T	STM0256	*yafC*	putative transcriptional regulator
297120	T	C	T	T	T	T	T	STM0257	-	putative drug efflux protein
299197	C	C	C	C	C	T	C	STM0259	*yafE*	putative methyltransferase

302642	C	C	C	C	C	C	T	STM0262	*yafS*	putative SAM-dependent methyltransferase
307524	C	A	C	C	C	C	C	STM0268	-	putative cytoplasmic protein
307628	A	A	A	G	G	G	G	STM0268	-	putative cytoplasmic protein
309248	G	G	G	G	T	G	G	STM0270	-	putative cytoplasmic protein
309918	A	A	A	A	A	A	G	STM0270	-	putative cytoplasmic protein
311694	C	T	C	C	C	C	C	STM0272	-	putative chaperone ATPase
312123	C	C	C	C	C	T	C	STM0272	-	putative chaperone ATPase
321819	C	C	C	C	C	C	T	STM0282	-	hypothetical protein
323629	C	C	C	C	C	C	T	STM0284	-	putative Shiga-like toxin A subunit
325108	C	C	C	A	C	C	C	STM0285	-	putative inner membrane protein
327384	T	T	C	C	C	C	C	STM0285	-	putative inner membrane protein
328323	A	A	G	A	A	A	A	STM0286	-	putative cytoplasmic protein
331388	T	T	T	A	A	A	A	STM0289	-	putative cytoplasmic protein
332322	A	A	T	A	A	A	A	STM0290	-	putative cytoplasmic protein
338965	A	A	C	A	A	A	A	STM0294	-	putative cytoplasmic protein
338966	A	A	C	A	A	A	A	STM0294	-	putative cytoplasmic protein
341734	C	C	C	T	T	T	T			
341796	T	T	C	C	C	C	C			
343179	A	A	A	A	C	A	A	STM0300	*safB*	putative fimbrial assembly chaparone
347857	T	T	T	T	T	T	G			
348452	C	C	T	C	C	C	C			
348964	G	G	A	G	G	G	G	STM0304	*sinR*	transcriptional regulator
357736	G	G	G	G	G	G	T			
359602	A	A	G	G	G	G	G			
359640	C	C	C	C	C	C	T			
360185	C	C	C	C	C	T	C			
361434	G	G	G	G	G	G	A	STM0316	*pepD*	aminoacyl-histidine dipeptidase
366668	C	C	C	C	C	C	A	STM0321	*proB*	gamma-glutamyl kinase
368985	A	A	A	A	G	A	A			
373986	G	G	G	G	G	A	G	STM0329	-	isopropylmalate isomerase large subunit
374185	A	A	A	A	A	C	A	STM0329	-	isopropylmalate isomerase large subunit
375965	C	C	T	C	C	C	C	STM0332	-	putative hydrolase/acyltransferase
377350	C	C	T	C	C	C	C	STM0333	-	putative transcriptional regulator
378430	T	T	T	T	T	T	C			
378729	T	T	G	T	T	T	T	STM0335	-	putative outer membrane protein
379060	C	C	T	T	T	T	T	STM0336	*stbE*	putative fimbrial chaparone
382202	C	C	C	C	T	C	C	STM0338	*stbC*	putative fimbrial usher
383521	C	C	C	T	T	T	T	STM0338	*stbC*	putative fimbrial usher
389638	C	C	C	C	T	C	C	STM0345	-	putative inner membrane protein
389715	T	T	C	C	C	C	C	STM0345	-	putative inner membrane protein
390850	G	G	G	A	A	A	A	STM0346	-	putative outer membrane protein
391264	T	T	T	T	G	T	T	STM0347	-	putative response regulator
406693	T	T	C	C	C	C	C	STM0358.S	*res*	DNA restriction enzyme
409770	G	G	G	G	G	G	A	STM0360	-	cytochrome BD2 subunit I
410832	C	C	C	T	C	C	C	STM0361	-	cytochrome BD2 subunit II
413408	C	C	T	T	T	T	T	STM0364	*foxA*	ferrioxamine receptor
415588	T	T	C	C	C	C	C			
417611	C	C	T	C	C	C	C	STM0367	*prpR*	prp operon regulator
417746	G	G	G	G	A	G	G			
418594	A	A	G	G	G	G	G	STM0368	*prpB*	2-methylisocitrate lyase
423502	C	C	C	G	C	C	C	STM0371	*prpE*	propionyl-CoA synthetase
425938	G	G	A	G	G	G	G	STM0373	*yaiU*	flagellar protein
428839	C	C	A	C	C	C	C			
430479	G	G	G	G	G	G	A	STM0376	*sbmA*	transport protein
433146	G	G	G	G	G	A	G			
434816	C	C	C	C	C	T	C	STM0381	-	putative inner membrane protein
436647	C	C	C	C	T	C	C	STM0382	-	putative permease
439885	C	C	C	T	C	C	C	STM0386	*proC*	pyrroline-5-carboxylate reductase
441538	T	T	T	C	T	T	T	STM0389	*yaiA*	hypothetical protein
442992	G	G	G	G	G	G	A	STM0392	*rdgC*	recombination associated protein
444469	G	G	G	G	G	T	G	STM0393	*yajF*	fructokinase
445700	C	C	C	C	C	C	A	STM0394	*araJ*	MFS transport protein AraJ
446646	C	C	C	T	C	C	C	STM0395	*sbcC*	exonuclease subunit SbcC
447744	G	G	T	G	G	G	G	STM0395	*sbcC*	exonuclease subunit SbcC
450071	C	C	C	T	T	T	T	STM0396	*sbcD*	exonuclease subunit SbcD
453047	C	C	C	T	T	T	T			
459592	C	C	C	T	C	C	C	STM0404	*queA*	S-adenosylmethionine:tRNA ribosyltransferase-isomerase
462747	A	A	G	G	G	G	G	STM0407	*secD*	preprotein translocase subunit SecD
462946	A	A	T	A	A	A	A	STM0407	*secD*	preprotein translocase subunit SecD
463791	A	A	G	G	G	G	G	STM0407	*secD*	preprotein translocase subunit SecD
464454	G	A	G	G	G	G	G	STM0408	*secF*	preprotein translocase subunit SecF
470791	A	A	A	A	A	A	G	STM0416	*ribD*	bifunctional diaminohydroxyphosphoribosylaminopyrimidine deaminase/5-amino-6-(5-phosphoribosylamino)uracil reductase
475569	G	G	G	G	G	G	T	STM0422	*dxs*	1-deoxy-D-xylulose-5-phosphate synthase
477023	C	C	C	C	C	C	A	STM0423	*ispA*	geranyltranstransferase
479087	A	A	A	A	A	G	A	STM0425	*thiI*	thiamine biosynthesis protein ThiI
482756	C	C	C	C	C	A	C	STM0429	*phnS*	2-aminoethylphosphonate transporter
484902	G	G	G	G	A	G	G	STM0431	*phnW*	2-aminoethylphosphonate--pyruvate transaminase
486041	G	T	G	G	G	G	G	STM0432	*phnX*	phosphonoacetaldehyde hydrolase
489592	T	T	T	T	T	T	A	STM0436.S	*yajR*	putative transport protein
490461	A	A	A	A	A	A	G	STM0437	-	putative periplasmic protein

490849	T	T	G	T	T	T	T	STM0437	-	putative periplasmic protein
491810	T	T	T	T	C	T	T			
493059	G	G	G	G	G	G	A	STM0438	-	TPR repeat-containing protein
496806	C	C	C	C	C	C	T	STM0442	*cyoB*	cytochrome o ubiquinol oxidase subunit I
507278	C	C	C	C	C	C	A	STM0450	*lon*	DNA-binding ATP-dependent protease La
508382	G	G	G	T	T	T	T			
508400	G	G	A	G	G	G	G			
510179	G	G	A	A	A	A	A	STM0452	*cypD*	peptidyl-prolyl cis-trans isomerase (rotamase D)
512997	C	C	C	C	T	C	C	STM0456	*ybaE*	putative ABC transporter periplasmic binding protein
516664	A	A	A	A	A	G	A	STM0459	*ybaO*	putative transcriptional regulator
516923	C	C	T	C	C	C	C	STM0460	*mdlA*	putative multidrug transporter membraneツ·ATP-binding
518770	T	T	T	T	T	G	T	STM0461	*mdlB*	putative multidrug transporter membraneツ·ATP-binding
518889	C	C	C	T	T	C	C	STM0461	*mdlB*	putative multidrug transporter membraneツ·ATP-binding
519202	G	A	G	G	G	G	G	STM0461	*mdlB*	putative multidrug transporter membraneツ·ATP-binding
523579	G	G	G	G	G	G	T	STM0465	*ybaY*	hypothetical protein
523977	G	G	G	G	G	A	G	STM0466	*ybaZ*	putative methyltransferase
524450	C	C	C	C	C	T	T	STM0467	*ffs*	4.5S ribosomal RNA
525085	C	C	C	C	C	T	C	STM0468	*ylaB*	hypothetical protein
530899	C	T	C	C	C	C	C	STM0475	*acrB*	acridine efflux pump
534852	G	G	G	G	G	G	A	STM0478	*aefA*	potassium efflux protein KefA
537672	T	T	T	T	T	T	C	STM0478	*aefA*	potassium efflux protein KefA
538479	C	C	C	C	A	C	C	STM0479	-	putative transposase
538936	T	T	G	T	T	T	T	STM0480	*ybaM*	hypothetical protein
546889	C	C	A	C	C	C	C			
548807	A	A	A	A	A	A	T	STM0490	*aes*	acetyl esterase
549075	C	C	C	T	C	C	C	STM0491	*gsk*	inosine-guanosine kinase
550434	C	C	C	C	C	T	C	STM0492	*ybaL*	putative cation:proton antiport protein
550509	A	G	A	A	A	A	A	STM0492	*ybaL*	putative cation:proton antiport protein
553916	C	C	T	C	C	C	C	STM0494	*ushA*	bifunctional UDP-sugar hydrolase/5'-nucleotidase periplasmic precursor
554049	A	A	C	C	C	C	C	STM0494	*ushA*	bifunctional UDP-sugar hydrolase/5'-nucleotidase periplasmic precursor
554639	A	A	T	A	A	A	A	STM0494	*ushA*	bifunctional UDP-sugar hydrolase/5'-nucleotidase periplasmic precursor
554796	T	T	T	G	G	G	G	STM0494	*ushA*	bifunctional UDP-sugar hydrolase/5'-nucleotidase periplasmic precursor
560258	C	C	T	C	C	C	C	STM0498	*copA*	copper exporting ATPase
561284	G	G	G	G	A	G	G	STM0500	*ybbJ*	hypothetical protein
564215	C	C	T	C	C	C	C	STM0504	*ybbN*	putative thioredoxin protein
564234	A	A	A	A	A	G	A	STM0504	*ybbN*	putative thioredoxin protein
569820	T	T	T	T	T	T	G	STM0509	-	putative outer membrane protein
571460	T	T	T	T	A	T	T	STM0510	*sfbA*	putative ABC-type transport system ATPase component
571519	C	C	C	C	C	T	C	STM0510	*sfbA*	putative ABC-type transport system ATPase component
577029	G	G	G	G	A	G	G	STM0516	*allR*	DNA-binding transcriptional repressor AllR
594945	G	G	T	G	G	G	G	STM0531	*ylbF*	putative cytoplasmic protein
597223	G	G	G	G	G	G	C	STM0534	*purE*	phosphoribosylaminoimidazole carboxylase catalytic subunit
597736	C	C	C	C	A	C	C			
603166	C	C	C	C	C	T	C	STM0542	*folD*	bifunctional 5,10-methylene-tetrahydrofolate dehydrogenase/ 5,10-methylene-tetrahydrofolate cyclohydrolase
604119	A	A	A	A	A	A	G			
608439	C	C	T	C	C	C	C	STM0546	*fimD*	outer membrane usher protein precursor
609408	T	T	C	T	T	T	T	STM0547	*fimH*	minor fimbrial subunit
614585	C	C	C	C	C	T	C			
616004	A	A	A	A	A	G	A	STM0557	-	putative inner membrane protein
618504	G	G	G	G	G	G	A			
621429	G	G	A	G	G	G	G	STM0564	-	pyridine nucleotide-disulfide oxidoreductase
621718	C	C	C	C	C	T	C			
622448	G	G	G	G	G	G	A	STM0566	-	putative inner membrane protein
622477	T	T	T	T	T	T	C	STM0566	-	putative inner membrane protein
627098	T	T	C	C	C	C	C			
627712	C	C	C	A	C	C	C	STM0570	*apeE*	outer membrane esterase
630704	G	G	G	G	G	A	G	STM0571	-	putative inner membrane protein
632172	C	C	C	C	C	T	C			
632409	G	G	G	G	G	A	G	STM0572	-	putative phosphosugar isomerase
632782	T	T	G	T	T	T	T	STM0572	-	putative phosphosugar isomerase
635011	C	C	C	C	C	C	A	STM0574	-	putative PTS system mannose-specific enzyme IID
635607	C	A	C	C	C	C	C	STM0575	-	putative inner membrane protein
636118	A	A	A	A	A	T	A	STM0576	-	putative PTS system mannose-specific enzyme IIAB
637394	C	C	C	C	C	T	C	STM0578	*nfnB*	dihydropteridine reductase
643271	A	A	A	A	A	A	G	STM0585	*fepA*	outer membrane receptor FepA
643363	G	G	G	G	G	G	A	STM0585	*fepA*	outer membrane receptor FepA
643756	T	T	C	C	C	C	C	STM0585	*fepA*	outer membrane receptor FepA
644850	C	C	T	C	C	C	C	STM0586	*fes*	enterobactin/ferric enterobactin esterase
647793	C	C	C	C	C	T	C	STM0588	*entF*	enterobactin synthase subunit F
649578	G	G	G	T	T	T	T			
650671	G	G	G	A	A	A	A	STM0589	*fepE*	ferric enterobactin transport protein FepE
651525	T	T	T	T	T	T	C	STM0590	*fepC*	iron-enterobactin transporter ATP-binding protein
652835	G	G	T	G	G	G	G	STM0592	*fepD*	iron-enterobactin transporter membrane protein
653711	T	T	C	T	T	T	T	STM0593	*ybdA*	enterobactin exporter EntS
656075	C	C	C	C	C	A	C			
657656	G	G	G	G	A	G	G	STM0596	*entE*	enterobactin synthase subunit E
657751	G	G	G	G	G	G	A	STM0596	*entE*	enterobactin synthase subunit E

658249	A	A	A	A	A	A	G	STM0596	*entE*	enterobactin synthase subunit E
659315	C	C	C	C	C	C	T	STM0597	*entB*	2,3-dihydro-2,3-dihydroxybenzoate synthetase
660265	T	T	G	G	G	G	G	STM0598	*entA*	2,3-dihydroxybenzoate-2,3-dehydrogenase
660389	T	T	C	C	C	C	C	STM0598	*entA*	2,3-dihydroxybenzoate-2,3-dehydrogenase
662642	A	A	A	A	A	C	A	STM0600	*cstA*	carbon starvation protein
663064	T	T	C	C	C	C	C	STM0600	*cstA*	carbon starvation protein
668815	G	G	G	G	G	G	A	STM0606	*ybdO*	putative transcriptional regulator
669418	C	C	T	C	C	C	C	STM0607	*dsbG*	disulfide isomerase/thiol-disulfide oxidase
669477	C	C	C	C	C	T	C	STM0607	*dsbG*	disulfide isomerase/thiol-disulfide oxidase
672108	C	C	C	A	A	A	A	STM0609	*ahpF*	alkyl hydroperoxide reductase F52a subunit
672516	T	T	T	C	C	C	C	STM0609	*ahpF*	alkyl hydroperoxide reductase F52a subunit
675623	G	G	G	G	G	G	A	STM0611	-	putative oxidoreductase protein
683010	G	G	G	T	G	G	G	STM0619	*citG*	triphosphoribosyl-dephospho-CoA synthase
685310	T	T	T	T	T	G	T	STM0621	*citF*	citrate lyase alpha chain/citrate-ACP transferase
686421	A	A	A	T	A	A	A	STM0623	*citD*	citrate lyase subunit gamma
691291	C	C	T	C	C	C	C	STM0627	*dcuC*	C4-dicarboxylate transporter DcuC
693928	G	G	A	G	G	G	G	STM0631	*ybeM*	putative hydrolase
695456	G	G	A	G	G	G	G	STM0633	*lipA*	lipoyl synthase
700109	C	C	C	C	C	A	C	STM0638	*rlpA*	rare lipoprotein A
702031	C	C	C	C	T	C	C	STM0640	*mrdA*	penicillin-binding protein 2
703633	C	C	T	C	C	C	C	STM0640	*mrdA*	penicillin-binding protein 2
706762	C	C	C	C	T	C	C	STM0644	*cobD*	threonine-phosphate decarboxylase
708149	G	G	G	T	T	T	T	STM0646	*holA*	DNA polymerase III subunit delta
708828	T	T	C	T	T	T	T	STM0647	*rlpB*	LPS-assembly lipoprotein RlpB
709871	C	C	T	C	C	C	C	STM0648	*leuS*	leucyl-tRNA synthetase
716263	T	T	T	T	T	T	G	STM0652	-	putative sigma-54 dependent transcriptional regulator
717867	C	C	T	C	C	C	C	STM0654	*ybeQ*	TPR repeat-containing protein
719621	A	A	C	C	C	C	C	STM0656	*ybeS*	putative molecular chaperone
721438	C	C	A	C	C	C	C	STM0658	*ybeV*	putative molecular chaperone
723890	T	C	T	T	T	T	T	STM0659	*hscC*	putative heatshock protein
723896	G	A	G	G	G	G	G	STM0659	*hscC*	putative heatshock protein
725796	C	C	C	C	T	C	C	STM0661	*rihA*	ribonucleoside hydrolase 1
727059	A	A	C	A	A	A	A	STM0662	*gltL*	glutamate/aspartate transporter
729093	T	T	T	G	G	G	G	STM0665	*gltI*	glutamate and aspartate transporter subunit
731355	G	G	G	G	G	G	T	STM0666	*lnt*	apolipoprotein N-acyltransferase
733520	A	A	G	A	A	A	A	STM0669	*phoL*	putative phosphate starvation-inducible protein
734482	C	C	C	T	T	T	T			
740118	C	C	T	C	C	C	C	STM0680	*asnB*	asparagine synthetase B
745011	C	C	C	C	C	C	T			
748711	A	A	A	A	A	G	A	STM0686	*glnS*	glutaminyl-tRNA synthetase
754091	G	G	T	G	G	G	G	STM0691	-	tricarballylate dehydrogenase
755687	C	C	C	C	C	T	C	STM0692	-	putative transcriptional regulator
757823	G	G	G	A	A	A	A	STM0695	*ybfE*	LexA regulated protein
764175	C	C	C	T	C	C	C	STM0701	*speF*	ornithine decarboxylase
765034	G	G	G	G	A	G	G	STM0701	*speF*	ornithine decarboxylase
766222	G	G	A	A	A	A	A			
767823	C	C	C	C	C	T	C	STM0703	*kdpD*	sensor protein KdpD
768637	T	T	T	T	C	T	T	STM0703	*kdpD*	sensor protein KdpD
771212	A	A	A	A	A	G	A	STM0705	*kdpB*	potassium-transporting ATPase subunit B
772524	G	G	G	G	A	G	G	STM0706	*kdpA*	potassium-transporting ATPase subunit A
773204	A	A	G	G	G	G	G	STM0706	*kdpA*	potassium-transporting ATPase subunit A
776378	C	C	C	C	T	C	C	STM0710	*ybgH*	POT family transport protein
776965	G	G	G	G	G	T	G	STM0710	*ybgH*	POT family transport protein
778611	T	T	T	T	T	T	C	STM0711	*ybgI*	putative hydrolase-oxidase
779768	A	A	A	T	T	T	T	STM0713	*ybgK*	putative carboxylase
784495	G	G	G	G	G	A	G	STM0719	-	putative UDP-galactopyranose mutase
791144	A	A	A	G	A	A	A	STM0725	-	putative glycosyltransferase
795023	T	T	C	T	T	T	T	STM0729	*abrB*	putative transport protein
797195	T	T	C	C	C	C	C	STM0730	*gltA*	type II citrate synthase
799240	G	G	G	G	G	G	T	STM0734	*sdhA*	succinate dehydrogenase flavoprotein subunit
801427	A	A	A	A	G	A	A			
803994	G	G	A	G	G	G	G	STM0736	*sucA*	2-oxoglutarate dehydrogenase E1 component
806380	C	C	C	C	C	T	C	STM0738	*sucC*	succinyl-CoA synthetase subunit beta
808797	A	A	A	A	A	A	G			
809077	A	A	C	C	C	C	C			
809549	G	G	A	G	G	G	G	STM0740	*cydA*	cytochrome d terminal oxidase polypeptide subunit I
822373	C	C	C	C	T	C	C	STM0758	*ybgR*	zinc transporter ZitB
823015	T	T	C	C	C	C	C			
824986	C	C	C	G	C	C	C	STM0761	-	fumarate hydratase
827228	C	C	C	T	T	T	T	STM0763.s	-	transcriptional regulator
829687	A	A	C	C	C	C	C	STM0765	-	putative cation transporter
830161	C	C	C	C	C	T	C			
830395	T	T	T	T	T	C	C			
830431	C	C	C	C	C	T	T			
833835	A	A	A	A	A	A	G	STM0769	-	putative cytoplasmic protein
840291	C	C	C	C	T	C	C	STM0775	*galT*	galactose-1-phosphate uridylyltransferase
842595	T	T	C	C	C	C	C	STM0777	-	putative inner membrane protein
844732	C	C	C	C	C	C	T	STM0779	*modE*	DNA-binding transcriptional regulator ModE
844882	C	A	C	C	C	C	C	STM0779	*modE*	DNA-binding transcriptional regulator ModE
845874	C	C	C	T	T	T	T	STM0781	*modA*	molybdate transporter periplasmic protein
845877	G	G	A	G	G	G	G	STM0781	*modA*	molybdate transporter periplasmic protein

846022	C	C	C	C	C	C	T	STM0781	*modA*	molybdate transporter periplasmic protein
849044	C	C	T	T	T	T	T			
849340	G	G	G	G	G	A	G	STM0785	*ybhE*	6-phosphogluconolactonase
854699	C	C	C	C	T	C	C	STM0789	*hutC*	histidine utilization repressor
855344	G	G	G	G	G	G	T			
857768	T	T	C	C	C	C	C	STM0791	*hutH*	histidine ammonia-lyase
860887	G	G	G	G	G	G	A	STM0794	*bioB*	biotin synthetase
861294	G	G	G	G	G	A	G	STM0795	*bioF*	8-amino-7-oxononanoate synthase
865056	C	C	T	C	C	C	C	STM0798	*uvrB*	excinuclease ABC subunit B
867857	G	G	G	A	G	G	G	STM0800	*slrP*	leucine-rich repeat-containing protein
869448	G	G	G	G	A	G	G	STM0801	*ybhK*	putative cytoplasmic protein
877191	G	G	G	G	G	T	G	STM0812	*ybhO*	cardiolipin synthase 2
878380	A	A	A	A	A	A	G	STM0813	*ybhP*	putative cytoplasmic protein
880432	C	C	C	T	C	C	C	STM0815	*ybhR*	putative transport protein
884840	G	G	G	G	G	C	G	STM0819	*ybiH*	putative DNA-binding transcriptional regulator
885912	A	A	T	A	A	A	A	STM0820	*rhlE*	ATP-dependent RNA helicase RhlE
890367	G	G	A	G	G	G	G			
890922	G	G	G	G	G	G	A			
891553	A	A	G	A	A	A	A	STM0826	*ybiN*	putative SAM-dependent methyltransferase
892158	C	C	C	C	T	C	C	STM0826	*ybiN*	putative SAM-dependent methyltransferase
896855	A	A	A	A	A	A	T	STM0830	*glnH*	glutamine ABC transporter periplasmic protein
897153	C	C	C	C	C	C	T			
898135	G	T	G	G	G	G	G			
898152	G	G	G	G	T	G	G			
903224	C	C	T	C	C	C	C	STM0836	*ybiR*	putative transporter
903231	C	C	C	C	C	C	A	STM0836	*ybiR*	putative transporter
903600	C	C	C	C	C	A	C	STM0836	*ybiR*	putative transporter
905034	C	C	C	T	T	T	T			
906561	C	C	C	C	C	T	C	STM0838	*ybiT*	putative ABC transporter ATPase component
908111	G	G	G	T	G	G	G	STM0840	*ybiV(2)*	putative hydrolase
910763	C	C	C	C	C	C	T	STM0842	*ybiV(1)*	putative hydrolase
911995	C	C	T	C	C	C	C	STM0843	*pflF*	putative pyruvate formate lyase
918814	C	C	T	C	C	C	C	STM0848	*yliA*	glutathione transporter ATP-binding protein
923926	C	C	C	G	C	C	C	STM0852	*yliG*	putative FeS oxidoreductase
927331	G	G	G	G	G	G	A	STM0855	-	putative electron transfer protein beta subunit
931369	C	C	C	T	C	C	C	STM0858	-	putative dehydrogenase
935197	C	C	C	C	C	C	A	STM0862	*yliJ*	putative glutathione S-transferase
939071	A	A	C	C	C	C	C	STM0866	*mdfA*	multidrug translocase
939278	G	G	G	G	G	A	G	STM0866	*mdfA*	multidrug translocase
939536	A	A	A	A	A	A	G	STM0866	*mdfA*	multidrug translocase
940825	G	G	G	G	G	A	G	STM0868	-	putative transport protein/regulator
945783	G	G	A	G	G	G	G	STM0873	*ybjC*	hypothetical protein
951136	C	C	C	C	C	T	C	STM0879	*potH*	putrescine transporter subunit: membrane component of ABC superfamily
951655	C	C	C	C	A	C	C	STM0879	*potH*	putrescine transporter subunit: membrane component of ABC superfamily
953338	C	C	C	T	T	T	T	STM0882	*rumB*	23S rRNA methyluridine methyltransferase
953979	T	T	T	T	T	C	T	STM0882	*rumB*	23S rRNA methyluridine methyltransferase
955747	G	G	G	A	A	A	A	STM0884	*ulaA*	ascorbate-specific PTS system enzyme IIC
960593	G	G	G	G	G	A	G	STM0890	*artI*	arginine transport system
962579	G	A	A	A	A	A	A			
1006260	A	A	G	G	G	G	G	STM0931	*ybjR*	putative aminidase
1008447	T	T	C	T	T	T	T	STM0933	*ybjT*	putative nucleoside-diphosphate-sugar epimerase
1008800	T	T	G	T	T	T	T	STM0933	*ybjT*	putative nucleoside-diphosphate-sugar epimerase
1010626	C	C	C	T	T	T	T	STM0935	*poxB*	pyruvate dehydrogenase
1010876	C	C	C	C	C	C	T	STM0935	*poxB*	pyruvate dehydrogenase
1011134	A	A	A	A	A	A	G	STM0935	*poxB*	pyruvate dehydrogenase
1012978	T	T	T	T	T	C	T	STM0937	*hcp*	hydroxylamine reductase
1016587	C	G	G	G	G	G	G	STM0939	*ybjD*	hypothetical protein
1016588	G	C	C	C	C	C	C	STM0939	*ybjD*	hypothetical protein
1019131	C	C	C	C	C	C	T	STM0941	*ybjY*	macrolide transporter subunit MacA
1021955	G	G	G	G	G	G	A	STM0943	*cspD*	stress response protein
1033710	G	G	G	A	A	G	G	STM0957	*cydD*	cysteine/glutathione ABC transporter membrane/ATP-binding
1039304	G	G	G	G	A	G	G	STM0960	*ftsK*	DNA translocase FtsK
1042477	G	G	G	G	T	G	G	STM0962	*ycaJ*	recombination factor protein RarA
1043107	C	C	C	A	A	A	A	STM0962	*ycaJ*	recombination factor protein RarA
1047990	A	A	G	A	A	A	A	STM0965	*dmsB*	anaerobic dimethyl sulfoxide reductase subunit B
1048639	C	C	T	C	C	C	C	STM0966	*dmsC*	anaerobic dimethyl sulfoxide reductase subunit C
1050732	G	G	G	G	G	A	G	STM0968	*ycaD*	putative MFS family transporter protein
1054707	G	G	G	G	G	G	T	STM0972	-	SopD-like protein
1056907	A	A	G	G	G	G	G	STM0973	*pflB*	pyruvate formate lyase I
1068646	C	C	C	C	C	T	C	STM0983	*ycaI*	hypothetical protein
1070394	G	G	T	G	G	G	G	STM0983	*ycaI*	hypothetical protein
1072252	C	C	C	C	C	T	C	STM0985	*lpxK*	tetraacyldisaccharide 4'-kinase
1074020	C	C	C	C	C	C	T	STM0986	*ycaQ*	putative cytoplasmic protein
1074484	T	T	T	T	T	A	T			
1077001	G	G	G	A	A	A	A	STM0990	*ycbC*	hypothetical protein
1082214	C	C	C	C	C	C	T	STM0994	*mukB*	cell division protein MukB
1083182	C	C	T	C	C	C	C	STM0994	*mukB*	cell division protein MukB
1084462	G	G	G	G	G	G	T	STM0994	*mukB*	cell division protein MukB
1086344	C	C	C	C	C	C	T	STM0995	*ycbB*	hypothetical protein

1086996	C	C	C	C	C	T	C			
1091084	A	A	A	G	A	A	A			
1091092	G	G	G	G	G	A	G			
1091225	T	T	T	T	T	T	C			
1091258	T	T	C	T	T	T	C			
1091323	A	A	A	G	G	G	G			
1091384	G	G	T	G	G	G	G			
1094630	T	T	T	T	C	T	T	STM1002	-	diaminopropionate ammonia-lyase
1095018	T	T	C	C	C	C	C	STM1002	-	diaminopropionate ammonia-lyase
1144044	G	G	G	G	G	A	G			
1147052	G	G	A	G	G	G	G	STM1058	*pyrD*	dihydroorotate dehydrogenase 2
1151058	C	C	C	C	C	C	A	STM1061	*rlmL*	23S rRNA m(2)G2445 methyltransferase
1152488	T	T	C	C	C	C	C	STM1062	*uup*	ABC transporter ATPase component
1154448	T	T	C	T	T	T	T	STM1063	*pqiA*	paraquat-inducible protein A
1154497	G	G	G	G	G	A	G	STM1063	*pqiA*	paraquat-inducible protein A
1154898	C	C	T	C	C	C	C	STM1063	*pqiA*	paraquat-inducible protein A
1157394	T	T	T	T	T	G	T			
1157968	G	G	A	A	A	A	A	STM1067	*fabA*	3-hydroxydecanoyl-(acyl carrier protein) dehydratase
1159447	A	A	A	G	G	G	G	STM1068	*lonH*	putative protease
1162991	G	G	G	G	G	G	A			
1167139	C	C	C	C	T	C	C	STM1075	*helD*	DNA helicase IV
1167750	T	T	T	T	C	T	T	STM1075	*helD*	DNA helicase IV
1181938	G	G	G	G	A	G	G	STM1094	*pipD*	pathogenicity island-encoded protein D
1185063	G	G	A	G	G	G	G			
1186029	C	C	C	T	C	C	C	STM1099	*hpaB*	4-hydroxyphenylacetate catabolism
1186244	A	A	A	A	A	G	A	STM1099	*hpaB*	4-hydroxyphenylacetate catabolism
1188121	A	A	A	G	G	G	G			
1189483	A	A	A	G	A	A	A	STM1101	*hpaG*	4-hydroxyphenylacetate catabolism
1191508	C	C	G	C	C	C	C	STM1103	*hpaD*	4-hydroxyphenylacetate catabolism
1191831	T	T	T	T	T	T	G			
1195022	T	T	T	T	T	C	T	STM1107	*hpaX*	4-hydroxyphenylacetate catabolism
1195147	C	C	C	C	C	A	C	STM1107	*hpaX*	4-hydroxyphenylacetate catabolism
1197770	A	A	G	G	G	G	G	STM1110	-	hypothetical protein
1197788	C	C	T	C	C	C	C	STM1110	-	hypothetical protein
1207649	C	C	C	C	C	C	A			
1212882	G	G	G	A	A	A	A	STM1125	*putP*	major sodium/proline symporter
1213760	C	C	C	C	T	C	C			
1217151	C	C	C	C	C	C	A	STM1128	-	putative sodium/glucose cotransporter
1217428	G	G	G	A	G	G	G	STM1128	-	putative sodium/glucose cotransporter
1219017	A	A	G	A	A	A	A			
1219398	G	G	G	G	G	G	A			
1219943	C	C	C	C	C	C	T	STM1130	-	putative inner membrane protein
1227565	G	G	T	T	T	T	T	STM1138	*ycdZ*	putative inner membrane protein
1229616	A	A	A	C	A	A	A	STM1141	*csgE*	curli assembly protein CsgE
1230558	C	C	C	C	T	C	C			
1230605	G	G	G	G	G	G	T			
1230714	C	C	C	C	C	C	T			
1237939	C	C	C	A	A	A	A	STM1150	*mdoG*	glucan biosynthesis protein G
1241488	G	G	G	G	G	G	A	STM1154	*yceE*	drug efflux system protein MdtG
1243549	T	T	T	C	T	T	T			
1245301	G	G	G	G	G	A	G	STM1157	*yceI*	hypothetical protein
1249049	C	C	C	C	T	C	C	STM1163	*pyrC*	dihydroorotase
1250251	G	G	G	A	A	A	A			
1251870	T	T	C	C	C	C	C	STM1166	*yceL*	multidrug resistance protein MdtH
1252452	A	A	G	G	G	G	G			
1253962	A	A	G	G	G	G	G	STM1169	*mviM*	putative virulence protein
1264878	C	C	G	C	C	C	C	STM1182	*flgJ*	flagellar rod assembly protein/muramidase FlgJ
1266547	G	G	G	G	G	A	G	STM1183	*flgK*	flagellar hook-associated protein FlgK
1271648	C	C	C	C	C	C	T			
1272124	G	G	G	T	G	G	G			
1275061	G	G	G	G	G	G	A	STM1189	*maf*	Maf-like protein
1285864	G	G	G	G	G	G	A	STM1202	*ycfH*	putative metallodependent hydrolase
1286971	C	C	C	C	C	C	A	STM1203	*ptsG*	glucose-specific PTS system IIBC components
1289038	C	C	C	T	C	C	C	STM1204	*fhuE*	ferric-rhodotorulic acid outer membrane transporter
1289726	G	G	G	T	G	G	G	STM1204	*fhuE*	ferric-rhodotorulic acid outer membrane transporter
1293721	T	G	T	T	T	T	T	STM1210	*ycfP*	hypothetical protein
1295008	G	G	A	G	G	G	G	STM1211	*ndh*	respiratory NADH dehydrogenase 2
1295195	A	A	A	A	A	A	G	STM1211	*ndh*	respiratory NADH dehydrogenase 2
1295482	A	A	T	T	T	T	T	STM1211	*ndh*	respiratory NADH dehydrogenase 2
1297535	C	C	A	C	C	C	C	STM1214	*ycfR*	putative outer membrane protein
1297827	C	C	C	C	C	T	C	STM1215	*ycfS*	putative periplasmic protein
1300412	G	G	G	G	G	A	G	STM1216	*mfd*	transcription-repair coupling factor
1325786	A	A	C	A	A	A	A			
1328310	T	T	T	G	G	G	G	STM1240	*envF*	putative envelope lipoprotein
1330273	A	A	G	A	A	A	A	STM1242	*envE*	putative envelope protein
1332863	G	G	G	G	G	G	T			
1333741	A	A	A	A	A	A	T			
1339533	C	C	C	C	C	T	C	STM1255	-	putative ABC transporter periplasmic binding protein
1340207	A	A	A	A	A	A	G	STM1255	-	putative ABC transporter periplasmic binding protein
1340820	A	A	A	A	C	A	A	STM1256	-	putative ABC transporter protein
1345335	G	G	G	G	G	C	G	STM1261	-	putative cytoplasmic protein

1349404	T	T	T	C	C	C	C	STM1267	-	putative cytoplasmic protein
1351518	A	A	G	G	G	G	G	STM1271	*yeaR*	putative cytoplasmic protein
1355815	C	C	C	C	C	C	A	STM1278	*yeaN*	putative amino acid/amine transport protein
1366249	G	G	G	G	T	G	G	STM1287	-	arylsulfatase regulator
1368428	C	C	C	C	C	C	T			
1369868	G	G	G	G	G	G	A			
1373336	C	C	C	C	A	C	C	STM1295	*sppA*	protease 4
1376514	A	A	A	A	A	T	A	STM1297	*selD*	selenophosphate synthetase
1376541	G	G	A	G	G	G	G	STM1297	*selD*	selenophosphate synthetase
1379089	G	G	G	G	G	G	A	STM1299	*gdhA*	glutamate dehydrogenase
1384413	G	G	G	G	A	G	G	STM1304	*astA*	arginine succinyltransferase
1385909	G	G	A	G	G	G	G	STM1305	*astD*	succinylglutamic semialdehyde dehydrogenase
1386863	T	T	C	C	C	C	C	STM1306	*astB*	succinylarginine dihydrolase
1389962	C	C	A	C	C	C	C	STM1309	-	nucleotide excision repair endonuclease
1391065	G	G	A	G	G	G	G			
1392139	T	T	C	T	T	T	T			
1392521	G	G	G	G	G	G	A	STM1313	*celB*	N,N'-diacetylchitobiose-specific PTS system transporter subunit IIC
1395638	C	C	C	C	C	C	A	STM1316	*celF*	phospho-beta-glucosidase/cellobiose-6-phosphate hydrolase
1397550	T	T	C	T	T	T	T	STM1318	*katE*	hydroperoxidase II
1399017	T	T	T	T	T	T	C	STM1318	*katE*	hydroperoxidase II
1399878	A	A	G	G	G	G	G	STM1319	*cedA*	cell division modulator
1402748	G	G	A	G	G	G	G	STM1322	*yniC*	2-deoxyglucose-6-phosphatase
1407904	G	G	A	G	G	G	G	STM1328	-	putative outer membrane protein
1407960	G	G	G	G	A	G	G	STM1328	-	putative outer membrane protein
1411141	T	T	T	T	T	C	T	STM1332	*rfc*	O-antigen polymerase
1418133	G	G	G	G	G	A	G	STM1338	*pheT*	phenylalanyl-tRNA synthetase subunit beta
1419373	A	A	C	A	A	A	A			
1421248	C	C	C	C	C	T	C	STM1342	*btuD*	vitamin B12-transporter ATPase
1423128	G	G	G	G	G	A	G	STM1344	*ydiV*	hypothetical protein
1424483	C	C	C	C	C	T	C	STM1345	*ydiU*	hypothetical protein
1426855	C	C	C	C	A	C	C	STM1348	*ydiA*	hypothetical protein
1427125	C	C	T	C	C	C	C	STM1348	*ydiA*	hypothetical protein
1430871	G	G	A	G	G	G	G	STM1350	*ydiD*	short chain acyl-CoA synthetase
1432074	C	C	C	C	C	C	T	STM1351	*ydiT*	putative ferredoxin
1433078	C	C	C	G	C	C	C	STM1352	*ydiS*	hypothetical protein
1433404	A	A	A	A	T	A	A	STM1352	*ydiS*	hypothetical protein
1434449	G	G	G	G	G	G	T	STM1353	*ydiR*	electron transfer flavoprotein subunit YdiR
1434552	G	G	G	A	A	A	A	STM1354	*ydiQ*	putative electron transfer flavoprotein YdiQ
1434804	C	C	C	A	A	A	A	STM1354	*ydiQ*	putative electron transfer flavoprotein YdiQ
1435143	G	G	G	G	G	A	G	STM1354	*ydiQ*	putative electron transfer flavoprotein YdiQ
1436405	A	A	A	A	A	C	A	STM1355	*ydiP*	putative transcriptional regulator
1438217	C	C	C	T	T	T	T	STM1357.S	*ydiF*	putative acetyl-CoA/acetoacetyl-CoA transferase beta subunit
1441370	C	C	C	C	C	A	C	STM1360	*ydiN*	putative transport protein
1442885	C	C	C	C	T	C	C			
1443088	G	G	G	G	G	A	G	STM1361	*ydiM*	putative transport protein
1444106	C	C	C	C	C	C	T	STM1361	*ydiM*	putative transport protein
1447539	C	C	T	C	C	C	C	STM1365	*ydiJ*	putative oxidase
1449287	G	G	T	G	G	G	G	STM1365	*ydiJ*	putative oxidase
1450438	G	G	G	G	A	G	G			
1453535	T	T	T	T	T	T	C	STM1370	*sufB*	cysteine desulfurase activator complex subunit SufB
1454734	C	C	T	C	C	C	C	STM1371	*sufC*	cysteine desulfurase ATPase component
1458632	C	C	T	C	C	C	C	STM1375	*ynhG*	hypothetical protein
1461717	A	A	A	A	G	A	A			
1464205	T	T	A	T	T	T	T	STM1381	*orf245*	putative cytoplasmic protein
1464653	A	A	T	A	A	A	A	STM1381	*orf245*	putative cytoplasmic protein
1467642	G	G	G	G	G	G	A	STM1383	*ttrA*	tetrathionate reductase complex subunit A
1468517	A	A	A	A	A	A	G	STM1383	*ttrA*	tetrathionate reductase complex subunit A
1469873	C	C	C	T	T	T	T	STM1384	*ttrC*	tetrathionate reductase complex subunit C
1469905	C	C	C	T	T	T	T	STM1384	*ttrC*	tetrathionate reductase complex subunit C
1472575	C	C	T	C	C	C	C	STM1386	*ttrS*	sensory histidine kinase
1472610	T	T	T	T	T	T	G	STM1386	*ttrS*	sensory histidine kinase
1475448	T	T	C	C	C	C	C	STM1390	*orf242*	putative regulatory protein
1475757	C	C	C	C	T	C	C	STM1390	*orf242*	putative regulatory protein
1475791	T	T	T	G	G	G	G	STM1390	*orf242*	putative regulatory protein
1478843	C	C	C	C	C	C	T	STM1392	*ssrA*	sensor kinase
1479444	T	T	T	T	T	T	C	STM1392	*ssrA*	sensor kinase
1479744	A	G	A	A	A	A	A			
1482737	C	C	C	C	T	C	C	STM1395	*ssaD*	virulence protein
1484647	A	A	A	A	A	A	G	STM1399	*sscA*	secretion system chaparone
1486104	C	C	C	C	C	C	T	STM1400	*sseC*	translocation machinery component
1490997	G	T	G	G	G	G	G	STM1409	*ssaJ*	needle complex inner membrane lipoprotein
1491462	C	G	C	C	C	C	C	STM1410	-	putative cytoplasmic protein
1491909	T	T	T	T	T	T	C	STM1411	*ssaK*	type III secretion system apparatus protein
1492648	T	T	T	T	T	T	C	STM1412	*ssaL*	type III secretion system apparatus protein
1493940	A	A	A	A	G	A	A	STM1414	*ssaV*	secretion system apparatus protein SsaV
1496024	C	C	A	C	C	C	C	STM1415	*ssaN*	type III secretion system ATPase
1500750	T	T	T	T	G	T	T	STM1422	*ssaU*	secretion system apparatus protein SsaU
1501100	C	C	C	C	C	C	T	STM1422	*ssaU*	secretion system apparatus protein SsaU
1503292	C	G	G	G	G	G	G	STM1425	*ydhE*	multidrug efflux protein
1503293	G	C	C	C	C	C	C	STM1425	*ydhE*	multidrug efflux protein
1507887	G	G	G	G	G	G	A	STM1429	*ydhB*	putative DNA-binding transcriptional regulator

1509948	G	G	G	A	A	A	A	STM1431	*sodB*	superoxide dismutase
1511393	G	G	A	G	G	G	G	STM1433	*ydhD*	hypothetical protein
1514452	G	G	G	C	G	G	G	STM1437	*ydhM*	putative transcriptional repressor
1514714	A	A	A	A	A	A	G			
1517198	C	C	A	C	C	C	C	STM1441	-	putative inner membrane protein
1519038	C	C	T	C	C	C	C	STM1442	*ydhJ*	putative multidrug resistance efflux pump
1520176	C	G	G	G	G	G	G	STM1444	*slyA*	transcriptional regulator SlyA
1520177	G	C	C	C	C	C	C	STM1444	*slyA*	transcriptional regulator SlyA
1522102	G	G	A	G	G	G	G	STM1446	*anmK*	anhydro-N-acetylmuramic acid kinase
1522658	G	A	G	G	G	G	G			
1523590	C	C	C	C	C	C	T	STM1449	*tyrS*	tyrosyl-tRNA synthetase
1528100	C	C	C	C	T	C	C			
1528912	C	C	C	C	C	T	C	STM1453	*nth*	endonuclease III
1535782	A	A	A	A	A	A	G			
1536627	C	G	G	G	G	G	G	STM1462.S	*ydgJ*	putative oxidoreductase
1536628	G	C	C	C	C	C	C	STM1462.S	*ydgJ*	putative oxidoreductase
1540174	T	T	T	C	T	T	T	STM1466	*ydgA*	putative periplasmic protein
1545530	T	T	T	T	T	T	C	STM1470	*tus*	DNA replication terminus site-binding protein
1549620	T	C	T	T	T	T	T			
1552081	C	C	C	A	A	A	A			
1552325	C	T	T	T	T	T	T	STM1476	*ydgC*	putative inner membrane protein
1552332	C	C	C	C	C	T	C	STM1476	*ydgC*	putative inner membrane protein
1553421	G	G	G	G	T	G	G	STM1477	*ydgI*	putative amino acid transporter
1556840	G	G	C	G	G	G	G	STM1479	*pntA*	NAD(P) transhydrogenase subunit alpha
1556842	C	C	T	C	C	C	C	STM1479	*pntA*	NAD(P) transhydrogenase subunit alpha
1559600	A	G	A	A	A	A	A	STM1481	*tqsA*	putative transport protein
1560093	C	C	C	C	C	C	A			
1561243	T	T	T	T	T	T	C	STM1484	-	putative protease
1562642	A	A	G	G	G	G	G			
1566127	C	C	C	C	C	T	C	STM1488	*mlc*	pts operon transcriptional repressor
1566995	A	A	A	A	G	A	A	STM1489	*bioD*	putative dithiobiotin synthetase
1569157	T	T	T	T	T	T	G	STM1491	-	proline/glycine betaine transport systems
1572232	T	T	C	C	C	C	C			
1572279	G	G	A	G	G	G	G	STM1495	*ynfI*	twin-argninine leader-binding protein DmsD
1575217	C	C	C	C	C	C	T	STM1498	-	putative dimethyl sulphoxide reductase
1578624	C	C	C	C	C	T	C	STM1499	-	putative dimethyl sulphoxide reductase chain A1
1597961	G	G	G	G	G	G	A			
1601132	G	G	G	G	T	G	G			
1604077	G	G	G	G	G	G	A			
1605312	G	G	G	G	G	G	C	STM1528	-	putative outer membrane protein
1606313	T	T	T	T	T	T	C			
1609324	C	C	T	C	C	C	C	STM1533	-	putative hydrogenase
1609983	T	C	T	T	T	T	T	STM1534	-	putative hydrogenase
1613237	C	C	C	C	C	T	C	STM1538	-	putative hydrogenase-1 large subunit
1616050	C	C	C	C	C	T	C	STM1540	-	putative hydrolase
1623223	T	T	T	T	T	T	A	STM1546	-	hypothetical protein
1629704	T	T	C	T	T	T	T			
1629710	G	G	G	G	A	G	G			
1634667	G	G	G	G	G	A	G	STM1556	-	putative Na+/H+ antiporter
1634850	G	G	A	G	G	G	G	STM1557	-	putative aminotransferase
1635911	G	G	G	G	G	G	A	STM1557	-	putative aminotransferase
1636881	A	A	A	A	A	G	A	STM1558	-	putative glycosyl hydrolase
1638874	T	C	T	T	T	T	T	STM1559	-	putative glycosyl hydrolase
1641020	C	C	C	C	C	C	T	STM1560	-	putative alpha amylase
1641846	A	A	T	A	A	A	A	STM1560	-	putative alpha amylase
1646053	G	G	G	G	G	G	A	STM1566	*sfcA*	malate dehydrogenase
1647708	G	G	A	G	G	G	G			
1648363	C	C	C	T	T	T	T	STM1567	*adhP*	alcohol dehydrogenase
1648485	C	C	T	C	C	C	C	STM1567	*adhP*	alcohol dehydrogenase
1654528	C	C	T	C	C	C	C	STM1571	*yddG*	hypothetical protein
1663133	G	G	G	G	G	G	A	STM1577	*narZ*	nitrate reductase 2 alpha subunit
1665367	G	T	G	G	G	G	G	STM1578	*narY*	nitrate reductase 2 beta subunit
1666715	A	A	G	A	A	A	A	STM1580	*narV*	nitrate reductase 2 gamma subunit
1667356	G	G	G	G	G	G	T			
1670711	C	C	C	C	T	C	C	STM1584	*ansP*	L-asparagine transport protein
1679999	G	G	G	G	G	G	A	STM1593	*srfA*	putative virulence protein
1681257	A	A	A	G	A	A	A	STM1594	*srfB*	putative virulence protein
1685999	A	A	A	A	A	A	T	STM1595	*srfC*	putative virulence protein
1686788	G	G	G	G	G	A	G			
1688685	G	G	G	G	G	G	A	STM1598	*ydcR*	putative regulatory protein
1689580	T	T	T	T	G	T	T	STM1598	*ydcR*	putative regulatory protein
1693045	G	G	G	G	G	A	G	STM1602	*sifB*	secreted effector protein
1693583	G	G	A	G	G	G	G	STM1603	*yncJ*	putative periplasmic protein
1696282	C	C	C	C	C	T	C			
1696377	T	T	T	T	T	C	T	STM1606	-	putative benzoate membrane transport protein
1698750	C	C	T	C	C	C	C	STM1608	*tehB*	tellurite resistance protein TehB
1707488	C	C	C	T	C	C	C	STM1619	-	cryptic aminoglycoside resistance gene
1709528	G	G	G	G	G	G	A	STM1621	-	putative periplasmic protein
1711289	G	G	G	G	G	G	A	STM1622	*mdoD*	glucan biosynthesis protein D
1712022	C	C	C	C	C	C	T	STM1623	-	putative carboxylesterase
1713519	C	C	C	T	C	C	C	STM1624	-	putative cytoplasmic protein

1715973	C	G	G	G	G	G	G	STM1626	*trg*	methyl-accepting chemotaxis protein III
1715974	G	C	C	C	C	C	C	STM1626	*trg*	methyl-accepting chemotaxis protein III
1719464	A	A	A	A	A	A	G			
1719593	A	A	A	G	G	G	G			
1719600	A	A	A	A	A	A	T			
1720793	G	G	G	G	G	A	G	STM1630	-	putative inner membrane protein
1721077	T	T	T	T	T	T	G			
1721078	A	A	A	A	A	A	T			
1726885	C	C	C	C	C	C	T	STM1637	-	putative inner membrane protein
1727217	G	G	G	G	G	G	A	STM1637	-	putative inner membrane protein
1728535	T	T	T	T	T	T	G			
1728633	C	C	T	C	C	C	C			
1729842	A	A	A	A	A	A	C	STM1639	*cybB*	cytochrome b561
1734882	G	G	G	T	T	T	T	STM1641	*hrpA*	ATP-dependent RNA helicase HrpA
1737576	A	G	A	A	A	A	A	STM1646	*ydbH*	hypothetical protein
1744629	T	T	T	T	C	T	T	STM1651	*nifJ*	putative pyruvate-flavodoxin oxidoreductase
1747291	T	T	T	T	C	T	T			
1747315	G	G	G	A	G	G	G	STM1654	*ydaO*	C32 tRNA thiolase
1750432	G	G	A	G	G	G	G	STM1656	*zntB*	zinc transporter
1752424	C	C	C	A	A	A	A	STM1657	-	putative methyl-accepting chemotaxis protein
1753235	A	A	C	C	C	C	C	STM1658	*ydaL*	hypothetical protein
1755042	G	G	A	G	G	G	G	STM1660.S	*fnr*	fumarate/nitrate reduction transcriptional regulator
1760231	A	A	G	G	G	G	G	STM1667	-	putative thiol peroxidase
1760464	G	G	G	G	G	G	A	STM1668	-	hypothetical protein
1762533	G	G	G	G	G	A	G	STM1669	-	invasin-like protein
1764140	G	G	G	G	G	G	A			
1766075	A	A	C	C	C	C	C			
1766388	C	T	C	C	C	C	C			
1767821	G	G	G	G	G	G	A	STM1674	-	putative regulatory protein
1767910	G	G	G	G	G	G	A	STM1674	-	putative regulatory protein
1769578	C	T	C	C	C	C	C	STM1676	-	putative aldo/keto reductase
1770492	G	G	G	G	T	G	G	STM1677	-	putative transcriptional regulator
1772479	G	G	G	G	A	G	G	STM1679	*mppA*	periplasmic murein tripeptide transport protein
1774909	G	G	G	G	G	G	A	STM1681	*ycjG*	putative chloromuconate cycloisomerase
1787886	G	G	T	G	G	G	G	STM1695	*sapD*	peptide transport protein
1788469	C	C	C	C	T	C	C	STM1696	*sapF*	peptide transport protein
1790318	T	T	T	T	T	T	C	STM1698	-	putative inner membrane protein
1791603	C	C	T	T	T	T	T	STM1698A	-	hypothetical protein
1791757	G	G	G	G	A	G	G	STM1699	*ycjE*	putative cytoplasmic protein
1791955	G	G	G	G	G	A	G	STM1699	*ycjE*	putative cytoplasmic protein
1794104	A	A	G	G	G	G	G	STM1701	*yciW*	putative cytoplasmic protein
1795072	A	A	A	A	C	A	A	STM1702	*rnb*	exoribonuclease II
1798548	G	G	G	A	G	G	G			
1802625	A	A	A	A	A	G	A	STM1708	*yciM*	tetratricopeptide repeat protein
1804153	G	G	G	G	T	G	G	STM1711	*ribA*	GTP cyclohydrolase II
1807705	T	C	T	T	T	T	T			
1811292	T	T	T	T	T	T	C	STM1714	*topA*	DNA topoisomerase I
1818364	C	C	C	T	C	C	C			
1819011	G	G	A	G	G	G	G	STM1723	*trpE*	anthranilate synthase component I
1819111	A	A	A	C	C	C	C	STM1723	*trpE*	anthranilate synthase component I
1821180	C	C	T	T	T	T	T	STM1724	*trpD*	bifunctional glutamine amidotransferase/anthranilate phosphoribosyltransferase
1824055	C	C	C	C	C	T	C	STM1726	*trpB*	tryptophan synthase subunit beta
1826859	A	A	A	A	G	A	A	STM1730	*yciE*	putative cytoplasmic protein
1832849	T	T	C	C	C	C	C			
1833733	T	A	T	T	T	T	T	STM1739	*cls*	cardiolipin synthetase
1834692	G	G	G	G	T	G	G			
1835453	G	G	A	G	G	G	G	STM1741	-	putative voltage-gated potassium channel
1838555	G	G	G	G	A	G	G			
1841633	T	T	C	T	T	T	T			
1851523	G	A	G	G	G	G	G			
1852945	G	G	A	G	G	G	G			
1852948	T	T	C	T	T	T	T			
1855104	T	T	T	T	T	T	A	STM1760	-	TPR repeat-containing protein
1858306	T	T	T	T	T	T	C	STM1763	*narH*	nitrate reductase 1 beta subunit
1864253	G	G	G	G	G	T	G			
1868812	C	C	C	T	C	C	C	STM1770	*chaB*	cation transport regulator
1871120	G	G	A	G	G	G	G	STM1772	*kdsA*	2-dehydro-3-deoxyphosphooctonate aldolase
1874952	C	C	T	C	C	C	C	STM1777	*hemA*	glutamyl-tRNA reductase
1882182	C	C	C	T	T	T	T	STM1784	*ychF*	GTP-dependent nucleic acid-binding protein EngD
1885235	T	T	C	C	C	C	C	STM1786	-	hydrogenase-1 small subunit
1891427	C	C	C	G	G	G	G	STM1792	-	putative cytochrome oxidase subunit I
1893429	T	T	T	T	T	T	C			
1895034	C	C	C	C	C	C	T			
1895814	A	A	G	A	A	A	A	STM1796	*treA*	trehalase
1896582	A	A	T	T	T	T	T	STM1796	*treA*	trehalase
1899779	G	G	G	A	G	G	G			
1903952	G	G	G	G	G	A	G	STM1803	*dadA*	D-amino acid dehydrogenase small subunit
1905645	A	A	G	A	A	A	A	STM1804.S	*ycgB*	SpoVR family protein
1910115	C	C	C	C	A	C	C			
1919931	G	G	A	G	G	G	G	STM1821	*yoaA*	putative DNA helicase

1924613	G	G	G	A	A	A	A	STM1826	*sdaA*	L-serine deaminase I/L-threonine deaminase I
1924975	G	G	G	A	A	A	A	STM1827.S	-	putative diguanylate cyclase/phosphodiesterase
1931188	C	T	C	C	C	C	C	STM1832	*manZ*	mannose-specific PTS system protein IID
1931734	T	T	G	G	G	G	G	STM1833	-	hypothetical protein
1932974	C	C	C	C	A	C	C	STM1835	*rrmA*	23S rRNA methyltransferase A
1933420	C	C	T	C	C	C	C	STM1835	*rrmA*	23S rRNA methyltransferase A
1937261	G	G	G	G	G	G	A	STM1841	-	hypothetical protein
1938616	C	C	T	T	T	T	C			
1939956	T	T	C	C	C	C	C	STM1843	-	putative transport protein
1953539	C	C	T	C	C	C	C	STM1856	-	putative cytoplasmic protein
1955831	G	G	G	G	G	A	G	STM1858	-	putative cytoplasmic protein
1966250	A	A	A	A	A	A	G	STM1869A	-	hypothetical protein
1968415	T	T	T	T	T	T	C	STM1873	-	hypothetical protein
1973546	A	G	A	A	A	A	A	STM1879	*ptrB*	protease 2
1975552	C	C	C	C	C	G	C			
1976770	G	G	G	G	T	G	G	STM1883	*purT*	phosphoribosylglycinamide formyltransferase 2
1977615	G	G	G	G	G	C	G			
1990238	C	C	T	C	C	C	C	STM1895	*ruvA*	Holliday junction DNA helicase RuvA
1991586	T	T	T	T	T	C	T	STM1896	-	putative cytoplasmic protein
1992301	C	C	T	C	C	C	C			
1996646	C	T	C	C	C	C	C	STM1901	*aspS*	aspartyl-tRNA synthetase
1999662	C	C	T	C	C	C	C	STM1905	*yecO*	putative SAM-dependent methyltransferase
2000243	C	C	C	C	C	T	C	STM1906	*yecP*	putative enzyme
2001565	G	G	G	G	G	G	T	STM1907	*cutC*	copper homeostasis protein CutC
2006248	A	A	C	A	A	A	A	STM1910	-	putative penicillin-binding protein
2009795	C	C	C	C	C	C	T	STM1913	*flhA*	flagellar biosynthesis protein FlhA
2011217	T	T	T	T	T	A	T	STM1914	*flhB*	flagellar biosynthesis protein FlhB
2018120	G	G	G	G	G	G	A	STM1921	*cheA*	chemotaxis protein CheA
2018225	A	A	A	G	A	A	A	STM1921	*cheA*	chemotaxis protein CheA
2022500	C	C	C	C	C	T	C			
2023495	C	C	A	C	C	C	C	STM1928	*otsA*	trehalose-6-phosphate synthase
2025018	G	G	G	G	G	A	G	STM1929	*otsB*	trehalose-6-phosphate phosphatase
2025944	G	G	G	A	G	G	G			
2026496	T	T	C	T	T	T	T	STM1931	*araH*	putative intracellular protease/amidase
2026918	T	T	T	T	T	C	T			
2027036	G	G	G	A	G	G	G			
2027304	A	A	A	A	A	G	A	STM1932	*ftnB*	ferritin-like protein
2029703	G	G	G	A	G	G	G	STM1935	*ftn*	ferritin
2030723	A	A	C	C	C	C	C	STM1937	*tyrP*	tyrosine-specific transport protein
2032535	C	C	A	C	C	C	C			
2034141	C	C	C	C	C	C	A	STM1940	-	putative cell wall-associated hydrolase
2035537	T	T	T	C	T	T	T			
2035593	G	G	G	A	A	G	G	STM1944	*glyW*	Gly tRNA
2037109	C	C	G	G	G	G	G	STM1946	*uvrC*	excinuclease ABC subunit C
2040642	G	G	G	G	G	G	A	STM1951	*yecC*	putative amino-acid ABC transporter ATP-binding protein YecC
2047552	C	C	C	C	C	C	T	STM1958	*fliB*	lysine-N-methylase
2048380	C	C	T	C	C	C	C	STM1959	*fliC*	flagellin
2051354	G	G	G	G	C	G	G	STM1962	*fliT*	flagellar biosynthesis protein FliT
2052884	G	G	A	G	G	G	G	STM1963	*amyA*	cytoplasmic alpha-amylase
2053069	A	A	A	A	T	A	A	STM1963	*amyA*	cytoplasmic alpha-amylase
2053660	C	C	C	C	T	C	C			
2054606	G	G	G	G	A	G	G	STM1965	*yedE*	putative inner membrane protein
2055379	C	C	T	T	T	T	T			
2062982	G	G	G	G	G	G	A			
2065664	C	C	C	C	C	C	T	STM1979	*fliP*	flagellar biosynthesis protein FliP
2067721	A	A	A	A	A	C	A	STM1982	*rcsA*	colanic acid capsular biosynthesis activation protein A
2069338	G	G	G	G	G	A	G	STM1986	*yedP*	mannosyl-3-phosphoglycerate phosphatase
2070890	G	G	G	G	G	G	C	STM1987	-	putative inner membrane protein
2077341	A	A	C	C	C	C	C			
2078230	G	G	G	G	C	G	G	STM1995	*ompS*	putative porin
2083488	A	A	C	C	C	C	C			
2084385	G	G	T	G	G	G	G			
2089975	G	G	T	G	G	G	G	STM2008	-	putative periplasmic protein
2090521	A	A	A	G	A	A	A			
2094081	C	C	T	T	T	T	T	STM2011.1n	-	hypothetical protein
2094970	C	C	T	C	C	C	C	STM2013	*yeeO*	hypothetical protein
2096138	G	G	G	A	A	A	A			
2096642	G	G	G	A	G	G	G	STM2015	*erfK*	hypothetical protein
2097684	G	G	A	G	G	G	G	STM2016	*cobT*	nicotinate-nucleotide--dimethylbenzimidazole phosphoribosyltransferase
2099474	T	T	G	T	T	T	T	STM2018	*cobU*	adenosylcobinamide kinase/adenosylcobinamide-phosphate guanylyltransferase
2101442	T	T	G	G	G	G	G	STM2020	*cbiO*	cobalt transporter ATP-binding subunit
2102871	T	T	T	T	T	T	C	STM2022	*cbiN*	cobalt transport protein CbiN
2108781	G	A	G	G	G	G	G	STM2030	*cbiT*	cobalt-precorrin-6Y C(15)-methyltransferase
2110038	A	A	A	A	A	A	C	STM2032	*cbiD*	cobalt-precorrin-6A synthase
2110162	C	C	C	C	C	G	C	STM2032	*cbiD*	cobalt-precorrin-6A synthase
2113543	C	C	T	C	C	C	C	STM2035	*cbiA*	cobyrinic acid a,c-diamide synthase
2116472	A	A	A	A	A	T	A			
2120298	G	G	G	G	A	G	G	STM2041	*pduD*	propanediol dehydratase medium subunit
2123545	T	T	C	C	C	C	C	STM2046	*pduK*	polyhedral body protein

2123666	T	T	T	T	T	C	T	STM2046	*pduK*	polyhedral body protein
2124041	G	G	G	G	G	A	G	STM2047	*pduL*	propanediol utilization protein
2130352	G	G	G	A	G	G	G	STM2054	*pduT*	polyhedral body protein
2130370	A	A	G	A	A	A	A	STM2054	*pduT*	polyhedral body protein
2135887	T	T	T	T	C	T	T			
2135902	G	G	G	G	G	G	T			
2137757	A	A	A	C	C	C	C	STM2063	*phsC*	thiosulfate reductase cytochrome B subunit
2140960	C	C	C	C	A	C	C			
2142134	A	A	A	A	A	A	G	STM2066	*sopA*	secreted effector protein
2147801	A	A	G	G	G	A	G	STM2069	*yeeY*	putative transcriptional regulator
2148762	G	G	G	G	G	G	T	STM2070	*yeeZ*	putative dehydratase
2149820	T	T	T	T	T	C	T	STM2071	*hisG*	ATP phosphoribosyltransferase
2156113	G	G	G	G	A	G	G	STM2077	*hisF*	imidazole glycerol phosphate synthase subunit HisF
2167502	A	A	G	A	A	A	A			
2167964	T	T	C	T	T	T	T	STM2087	*rfbV*	abequosyltransferase
2168225	G	G	A	G	G	G	G	STM2087	*rfbV*	abequosyltransferase
2169801	C	C	T	T	T	T	T	STM2088	*rfbX*	putative O-antigen transferase
2177518	G	A	G	G	G	G	G	STM2097	*rfbB*	dTDP-glucose 4,6 dehydratase
2184325	A	A	A	A	A	G	A	STM2102	*wzxC*	colanic acid exporter
2187677	C	C	C	C	T	C	C	STM2104	*cpsG*	phosphomannomutase
2188242	G	G	G	A	G	G	G	STM2104	*cpsG*	phosphomannomutase
2189080	C	C	C	C	T	C	C	STM2105.S	*manC*	mannose-1-phosphate guanylyltransferase
2190240	A	A	A	A	A	G	A	STM2106	*wcaI*	putative glycosyl transferase
2191362	T	T	T	T	T	T	C	STM2107	*wcaH*	GDP-mannose mannosyl hydrolase
2191404	G	G	A	G	G	G	G	STM2107	*wcaH*	GDP-mannose mannosyl hydrolase
2191550	C	C	C	C	C	C	T	STM2107	*wcaH*	GDP-mannose mannosyl hydrolase
2194910	C	C	T	T	T	T	T	STM2111	*wcaE*	putative glycosyl transferase
2204926	T	T	C	C	C	C	C			
2208952	A	A	G	G	G	G	G	STM2123	*yegE*	putative diguanylate cyclase/phosphodiesterase
2210753	G	G	G	A	G	G	G	STM2123	*yegE*	putative diguanylate cyclase/phosphodiesterase
2212755	G	G	G	G	G	G	A	STM2125	*yegD*	putative chaperone
2214143	C	A	C	C	C	C	C			
2219136	G	G	A	G	G	G	G	STM2128	*yegO*	multidrug efflux system subunit MdtC
2219610	G	G	G	A	A	A	A	STM2128	*yegO*	multidrug efflux system subunit MdtC
2223484	A	A	G	G	G	G	G	STM2130	*baeS*	signal transduction histidine-protein kinase BaeS
2224295	T	T	T	T	T	T	C	STM2130	*baeS*	signal transduction histidine-protein kinase BaeS
2227675	G	G	G	G	G	G	A	STM2135	-	putative inner membrane protein
2228198	G	G	G	G	G	T	G	STM2135	-	putative inner membrane protein
2233063	T	T	C	C	C	C	C			
2233222	G	A	G	G	G	G	G	STM2139	-	putative inner membrane protein
2233224	C	C	C	T	C	C	C	STM2139	-	putative inner membrane protein
2245590	C	C	C	C	C	C	T	STM2150	*stcC*	putative outer membrane protein
2246408	T	T	T	T	C	T	T	STM2151	*stcB*	putative periplasmic chaperone protein
2250050	C	C	C	C	C	A	C	STM2155	*metG*	methionyl-tRNA synthetase
2252448	G	G	G	G	G	G	A	STM2156	*yehR*	putative lipoprotein
2253935	G	G	A	G	G	G	G	STM2158	*yehT*	putative two-component response-regulatory protein YehT
2255075	G	G	T	G	G	G	G	STM2159	*yehU*	putative sensor kinase
2256194	G	G	G	A	A	A	A			
2258915	G	G	G	G	A	G	G	STM2164	*yehY*	putative ABC-type proline/glycine betaine transport system permease component
2259118	A	A	G	A	A	A	A	STM2164	*yehY*	putative ABC-type proline/glycine betaine transport system permease component
2260019	A	A	A	A	A	G	A	STM2164	*yehY*	putative ABC-type proline/glycine betaine transport system permease component
2261851	G	G	A	G	G	G	G	STM2166	*bglX*	periplasmic beta-D-glucoside glucohydrolase
2261930	C	T	C	C	C	C	C	STM2166	*bglX*	periplasmic beta-D-glucoside glucohydrolase
2263075	C	C	C	C	T	C	C	STM2166	*bglX*	periplasmic beta-D-glucoside glucohydrolase
2269176	C	C	C	C	C	C	T	STM2172	*yohG*	multidrug resistance outer membrane protein MdtQ
2276875	A	A	T	A	A	A	A			
2279715	T	T	T	T	C	T	T	STM2183	*cdd*	cytidine deaminase
2280219	T	T	T	T	C	T	T			
2285729	C	C	C	C	C	A	C	STM2189	*mglA*	galactose/methyl galaxtoside transporter ATP-binding protein
2286684	G	G	G	A	G	G	G	STM2190	*mglB*	galactose transport protein
2288684	C	C	C	C	T	C	C	STM2191	*galS*	DNA-binding transcriptional regulator GalS
2289745	G	G	G	G	T	G	G	STM2192	*yeiB*	hypothetical protein
2292650	A	A	G	G	G	G	G	STM2195	-	putative transcriptional regulator
2292679	T	T	T	G	T	T	T			
2294960	G	G	A	G	G	G	G	STM2197	-	putative phosphoserine phosphatase
2300302	G	G	G	G	G	T	G	STM2200	*lysP*	lysine transporter
2301558	T	T	C	C	C	C	C	STM2202	*yeiH*	putative inner membrane protein
2310555	C	C	T	C	C	C	C			
2310867	C	C	C	A	C	C	C	STM2211.S	*yeiP*	elongation factor P
2311464	G	A	G	G	G	G	G			
2317914	C	C	T	T	T	T	T	STM2216	*yejA*	putative ABC transporter periplasmic binding protein
2320062	C	C	C	C	C	C	A	STM2218	*yejE*	putative ABC-type dipeptide/oligopeptide/nickel transport system permease component
2327212	A	G	A	A	A	A	A	STM2225	-	putative inner membrane protein
2330464	C	C	C	C	C	T	C	STM2228	*yejM*	putative hydrolase
2331390	C	C	C	G	G	G	G	STM2230.1c	-	DNA polymerase V subunit
2333632	C	C	C	C	C	C	T	STM2232	*oafA*	O-antigen acetylase
2334940	G	G	G	G	A	G	G	STM2234	-	putative phage tail fiber assembly protein
2335806	G	G	G	G	A	G	G	STM2235	-	hypothetical protein

2338686	G	T	G	G	G	G	G	STM2238	-	hypothetical protein
2339590	G	G	G	G	G	G	A	STM2240	-	putative cytoplasmic protein
2340946	A	A	A	A	T	A	A	STM2241	*sspH2*	leucine-rich repeat-containing protein
2341776	A	A	A	A	A	A	G	STM2241	*sspH2*	leucine-rich repeat-containing protein
2342912	C	C	C	C	C	C	A	STM2241	*sspH2*	leucine-rich repeat-containing protein
2354256	C	C	C	C	A	C	C	STM2255	*napC*	cytochrome c-type protein NapC
2355055	T	T	T	T	T	T	G	STM2257	*napH*	quinol dehydrogenase membrane component
2356160	T	T	C	C	C	C	C	STM2258	*napG*	quinol dehydrogenase periplasmic component
2357045	C	C	C	G	G	C	C	STM2259	*napA*	nitrate reductase catalytic subunit
2359039	C	C	C	C	C	C	T	STM2260	*napD*	assembly protein for periplasmic nitrate reductase
2359409	G	G	A	G	G	G	G	STM2261	*napF*	ferredoxin-type protein
2359975	A	A	A	A	A	A	G			
2368441	C	C	C	C	C	A	C	STM2269	*yojN*	phosphotransfer intermediate protein in two-component regulatory system with RcsBC
2370614	T	T	C	C	C	C	C	STM2270	*rcsB*	transcriptional regulator RcsB
2376089	C	T	C	C	C	C	C	STM2272	*gyrA*	DNA gyrase subunit A
2376100	G	A	G	G	G	G	G	STM2272	*gyrA*	DNA gyrase subunit A
2376488	T	T	C	C	C	C	C			
2380402	T	G	T	T	T	T	T	STM2276	*ubiG*	3-demethylubiquinone-9 3-methyltransferase
2383166	G	G	G	G	T	G	G	STM2277	*nrdA*	ribonucleotide-diphosphate reductase subunit alpha
2385484	C	C	C	C	C	C	G	STM2280	-	putative permease
2390185	C	C	C	A	A	A	A			
2390879	G	G	G	G	G	A	G	STM2284	*glpA*	sn-glycerol-3-phosphate dehydrogenase subunit A
2392178	G	G	T	G	G	G	G	STM2285	*glpB*	anaerobic glycerol-3-phosphate dehydrogenase subunit B
2394751	A	A	A	A	G	A	A			
2399139	T	T	T	G	T	T	T	STM2291	*yfaW*	putative galactonate dehydratase
2402527	C	A	C	C	C	C	C			
2406621	C	C	C	T	C	C	C	STM2299	*yfbG*	bifunctional UDP-glucuronic acid decarboxylase/UDP-4-amino-4-deoxy-L-arabinose formyltransferase
2408881	T	T	T	T	T	T	G	STM2300	-	putative cytoplasmic protein
2413094	G	G	G	G	G	G	A	STM2306	*menC*	O-succinylbenzoate synthase
2413556	C	C	C	C	C	T	C	STM2306	*menC*	O-succinylbenzoate synthase
2417681	G	G	T	G	G	G	G	STM2310	*menF*	menaquinone-specific isochorismate synthase
2419201	G	G	A	G	G	G	G	STM2312	*elaA*	hypothetical protein
2419206	C	C	C	C	C	C	T	STM2312	*elaA*	hypothetical protein
2420280	G	G	G	G	G	A	G	STM2313	*elaC*	ribonuclease Z
2423708	G	G	G	G	G	A	G			
2425105	G	G	G	A	A	A	A	STM2316.S	*nuoN*	NADH dehydrogenase subunit N
2427979	C	G	G	G	G	G	G	STM2318	*nuoL*	NADH dehydrogenase subunit L
2428886	G	G	G	A	G	G	G	STM2318	*nuoL*	NADH dehydrogenase subunit L
2429197	A	A	G	G	G	G	G	STM2318	*nuoL*	NADH dehydrogenase subunit L
2431244	T	T	C	C	C	C	C	STM2322	*nuoH*	NADH dehydrogenase subunit H
2435407	G	G	G	A	G	G	G	STM2324	*nuoF*	NADH dehydrogenase I subunit F
2440328	C	C	T	C	C	C	C	STM2330	*lrhA*	NADH dehydrogenase transcriptional repressor
2441275	T	T	G	G	G	G	G			
2441640	C	C	C	C	C	C	T			
2444770	G	G	T	G	G	G	G	STM2333	*yfbS*	putative response regulator
2446575	T	T	A	T	T	T	T	STM2335	*yfbU*	hypothetical protein
2454136	G	G	G	A	G	G	G	STM2341	-	putative transketolase
2461433	G	G	A	G	G	G	G	STM2350	*yfcH*	putative sugar nucleotide epimerase
2463340	C	C	C	C	C	C	T	STM2352	*hisM*	histidine/lysine/arginine/ornithine transport protein
2465452	T	T	T	G	G	G	G			
2466224	G	G	G	G	G	G	T	STM2355	*argT*	lysine/arginine/ornithine transport protein
2467952	A	A	G	G	G	G	G	STM2357	-	putative amino acid transporter
2468486	C	C	C	C	G	C	C	STM2357	-	putative amino acid transporter
2473030	C	C	C	C	C	T	C	STM2361	-	putative regulatory protein
2473561	G	G	G	G	G	G	A	STM2361	-	putative regulatory protein
2475937	A	A	A	C	A	A	A	STM2363	*cvpA*	colicin V production protein
2478628	A	A	C	C	C	C	C			
2479059	C	C	C	C	C	C	T	STM2366	*accD*	acetyl-CoA carboxylase subunit beta
2483421	G	G	G	T	G	G	G	STM2370	*pdxB*	erythronate-4-phosphate dehydrogenase
2484469	T	T	G	T	T	T	T	STM2371	*flk*	flagella biosynthesis regulator
2485260	A	A	A	A	A	T	A	STM2372	-	hypothetical protein
2500654	C	G	G	G	G	G	G	STM2389	*fadI*	3-ketoacyl-CoA thiolase
2500655	G	C	C	C	C	C	C	STM2389	*fadI*	3-ketoacyl-CoA thiolase
2502198	C	C	A	C	C	C	C			
2503219	A	A	G	G	G	G	G	STM2391	*fadL*	long-chain fatty acid outer membrane transporter
2505071	A	A	G	G	G	G	G	STM2393	*yfdC*	hypothetical protein
2506832	G	G	G	G	G	A	G	STM2395	*pgtE*	outer membrane protease
2507049	G	G	G	G	G	G	A			
2509974	G	G	G	G	G	T	G	STM2397	*pgtB*	phosphoglycerate transport system sensor protein
2511317	C	C	C	C	C	C	T	STM2398	*pgtC*	phosphoglycerate transport regulatory protein precursor
2513257	A	A	G	G	G	G	G	STM2399	*pgtP*	transporter
2513575	C	T	C	C	C	C	C			
2518417	A	A	A	A	A	A	C	STM2403	*glk*	glucokinase
2518834	C	C	T	C	C	C	C	STM2403	*glk*	glucokinase
2520189	T	T	T	T	T	G	T	STM2404	-	hypothetical protein
2520622	G	G	G	G	G	A	G	STM2405	-	indolepyruvate decarboxylase
2521161	C	C	C	C	C	T	C	STM2405	-	indolepyruvate decarboxylase
2525573	T	T	T	T	T	T	C	STM2409	*nupC*	nucleoside transport
2528800	C	C	C	C	T	C	C			

2529829	T	T	T	T	T	T	C	STM2414	*yfeD*	putative negative regulator
2533021	C	C	C	C	C	C	T	STM2420	*xapR*	DNA-binding transcriptional activator XapR
2533918	C	C	T	C	C	C	C	STM2421	*xapB*	xanthosine permease
2535401	C	C	C	C	C	T	C			
2535477	T	T	C	C	C	C	C			
2537941	C	G	G	G	G	G	G	STM2425	*yfeH*	putative Na+-dependent transporter
2537942	G	C	C	C	C	C	C	STM2425	*yfeH*	putative Na+-dependent transporter
2540863	G	G	G	G	A	G	G	STM2427	*ligA*	NAD-dependent DNA ligase LigA
2541905	A	A	A	T	T	T	T	STM2428	*zipA*	cell division protein ZipA
2543500	G	G	A	G	G	G	G	STM2430	*cysK*	cysteine synthase A
2547739	C	C	T	C	C	C	C	STM2435	*pdxK*	pyridoxal kinase
2547787	C	C	C	C	C	C	T	STM2435	*pdxK*	pyridoxal kinase
2550665	C	G	G	G	G	G	G	STM2438	*yfeK*	hypothetical protein
2550666	G	C	C	C	C	C	C	STM2438	*yfeK*	hypothetical protein
2552605	A	A	G	G	G	G	G			
2558758	C	C	C	C	C	C	T	STM2447	-	hypothetical protein
2560309	C	C	C	C	A	C	C			
2561061	C	C	C	C	A	C	C	STM2450	*amiA*	N-acetylmuramoyl-l-alanine amidase I
2563057	G	G	G	G	G	A	G	STM2453	-	putative cytoplasmic protein
2564038	C	C	T	C	C	C	C			
2565407	G	G	C	G	G	G	G	STM2455	*eutK*	putative carboxysome structural protein
2565589	A	A	G	G	G	G	G	STM2455	*eutK*	putative carboxysome structural protein
2576512	T	T	T	T	T	T	G	STM2466	*eutD*	phosphotransacetylase
2580125	C	C	C	C	C	C	A	STM2472	*maeB*	malic enzyme
2583315	G	G	G	G	A	G	G	STM2473	*talA*	transaldolase A
2584636	A	A	G	G	G	G	G	STM2474	*tktB*	transketolase
2584720	C	C	C	T	C	C	C	STM2474	*tktB*	transketolase
2584998	T	T	T	C	C	C	C	STM2474	*tktB*	transketolase
2585220	G	G	A	G	G	G	G	STM2474	*tktB*	transketolase
2585231	C	C	C	C	C	C	A	STM2474	*tktB*	transketolase
2585551	G	G	A	G	G	G	G			
2586108	A	A	G	G	G	G	G	STM2476	*ypfG*	putative periplasmic protein
2590671	A	A	G	G	G	G	G	STM2479	*aegA*	putative oxidoreductase Fe-S binding subunit
2590854	C	C	A	C	C	C	C	STM2479	*aegA*	putative oxidoreductase Fe-S binding subunit
2591077	C	C	C	C	C	C	T	STM2479	*aegA*	putative oxidoreductase Fe-S binding subunit
2594861	A	A	G	G	G	G	G	STM2481	*acrD*	aminoglycoside/multidrug efflux system
2595441	A	A	A	C	A	A	A	STM2481	*acrD*	aminoglycoside/multidrug efflux system
2601697	T	T	T	T	C	T	T	STM2486	-	putative inner membrane protein
2614589	C	C	T	C	C	C	C	STM2500	*purN*	phosphoribosylglycinamide formyltransferase
2618816	G	G	A	A	A	A	A	STM2503	-	putative diguanylate cyclase
2620930	G	G	G	G	T	G	G			
2624168	A	G	G	G	G	G	G	STM2510	*guaA*	GMP synthase
2627901	A	A	G	G	G	G	G	STM2513	*shdA*	AIDA autotransporter-like protein
2629307	G	G	G	G	G	A	G	STM2513	*shdA*	AIDA autotransporter-like protein
2632379	A	A	A	A	A	T	A	STM2513	*shdA*	AIDA autotransporter-like protein
2633672	G	G	G	A	G	G	G	STM2513	*shdA*	AIDA autotransporter-like protein
2633865	A	A	G	A	A	A	A			
2637463	G	G	G	G	G	C	G	STM2514	*ratB*	putative outer membrane protein
2638509	C	C	C	C	C	C	A	STM2514	*ratB*	putative outer membrane protein
2639741	G	G	G	G	G	G	A	STM2514	*ratB*	putative outer membrane protein
2641514	G	G	G	G	G	G	A	STM2514	*ratB*	putative outer membrane protein
2641554	G	G	G	G	G	A	G	STM2514	*ratB*	putative outer membrane protein
2642351	G	G	G	A	A	A	A	STM2515	*ratA*	putative outer membrane protein
2643093	T	T	A	T	T	T	T	STM2515	*ratA*	putative outer membrane protein
2643606	C	C	C	C	C	C	A	STM2515	*ratA*	putative outer membrane protein
2657220	T	T	T	T	T	C	T	STM2523	*ispG*	4-hydroxy-3-methylbut-2-en-1-yl diphosphate synthase
2659303	T	T	A	A	A	A	A	STM2525	*yfgB*	hypothetical protein
2661659	G	C	C	C	C	C	C	STM2528	-	putative dimethylsulfoxide reductase
2662168	C	C	C	C	C	C	T	STM2528	-	putative dimethylsulfoxide reductase
2664465	A	A	A	A	A	A	T	STM2530	-	putative anaerobic dimethylsulfoxide reductase
2667864	G	G	G	G	G	G	A	STM2532	-	putative inner membrane lipoprotein
2668958	G	G	G	A	A	A	A	STM2532	-	putative inner membrane lipoprotein
2673130	T	T	T	T	T	C	T	STM2533	*sseA*	3-mercaptopyruvate sulfurtransferase
2674612	G	G	G	G	G	G	A	STM2534	-	putative cytoplasmic protein
2681894	T	T	T	T	T	T	C	STM2543	*nifS*	cysteine desulfurase
2681944	G	G	G	G	G	G	A	STM2543	*nifS*	cysteine desulfurase
2682184	T	T	T	T	T	C	T	STM2543	*nifS*	cysteine desulfurase
2687938	A	A	A	A	A	A	G	STM2549	*asrB*	anaerobic sulfite reductase subunit B
2690688	G	G	G	G	A	G	G	STM2552	-	hypothetical protein
2695925	C	C	C	C	C	C	T	STM2556	*hmpA*	nitric oxide dioxygenase
2695983	G	T	T	T	T	T	T	STM2556	*hmpA*	nitric oxide dioxygenase
2696246	T	T	G	G	G	G	G	STM2556	*hmpA*	nitric oxide dioxygenase
2698171	A	A	A	A	A	A	C	STM2557	*cadC*	DNA-binding transcriptional activator CadC
2698301	G	G	G	G	G	G	A			
2698341	A	A	C	C	C	C	C			
2701974	C	C	C	C	C	C	T	STM2559	*cadA*	lysine decarboxylase 1
2704353	G	G	G	G	G	G	A	STM2562	*yfhA*	putative transcriptional regulator
2705384	G	G	G	G	A	G	G	STM2562	*yfhA*	putative transcriptional regulator
2708004	C	C	C	C	A	C	C			
2711140	G	G	G	G	G	G	A	STM2565	*purG*	phosphoribosylformylglycinamidine synthase
2712424	T	T	T	C	T	T	T	STM2567	*yfhD*	putative transglycosylase

2715610	G	G	G	G	G	G	T	STM2570	-	putative phosphotransferase system IIB component
2715924	C	C	T	C	C	C	C	STM2570	-	putative phosphotransferase system IIB component
2716762	G	G	G	G	G	G	T	STM2571	*murQ*	N-acetylmuramic acid-6-phosphate etherase
2720067	A	A	A	G	G	G	G	STM2574	-	putative permease
2721952	C	T	C	C	C	C	C			
2724018	C	C	T	C	C	C	C	STM2580	*era*	GTP-binding protein Era
2726129	A	A	G	G	G	G	G	STM2582	*lepB*	signal peptidase I
2780666	G	G	A	G	G	G	G	STM2641	*nadB*	L-aspartate oxidase
2783835	G	G	G	G	G	G	T	STM2643	*srmB*	ATP-dependent RNA helicase SrmB
2788821	G	G	G	A	A	A	A	STM2649	*trxC*	thioredoxin 2
2789927	G	G	A	G	G	G	G	STM2651	*yfiQ*	putative acetyl-CoA synthetase
2795747	T	C	T	T	T	T	T			
2796138	A	A	A	A	A	A	C	STM2655	-	putative cytoplasmic protein
2803030	C	C	C	C	C	C	T	STM2660	*clpB*	protein disaggregation chaperone
2803964	C	T	C	C	C	C	C	STM2660	*clpB*	protein disaggregation chaperone
2806099	C	A	C	C	C	C	C	STM2662	*rluD*	23S rRNA pseudouridine synthase D
2810793	A	A	A	A	A	A	T	STM2669	*tyrA*	bifunctional chorismate mutase/prephenate dehydrogenase
2811966	G	G	G	G	G	G	A	STM2670	*aroF*	phospho-2-dehydro-3-deoxyheptonate aldolase
2812647	T	T	C	T	T	T	T			
2817453	T	T	T	T	T	T	C	STM2677	*ffh*	signal recognition particle protein
2821355	G	G	A	G	G	G	G	STM2680	-	putative cytoplasmic protein
2823440	G	A	G	G	G	G	G	STM2684	*recN*	recombination and repair protein
2823633	C	C	C	C	C	T	C	STM2684	*recN*	recombination and repair protein
2825863	C	C	C	C	C	C	A	STM2686	*yfjF*	hypothetical protein
2826432	G	G	G	G	T	G	G			
2827785	A	A	A	A	C	A	A			
2828278	C	C	C	C	T	C	C			
2828753	G	G	G	A	A	A	A			
2829374	A	A	A	A	A	A	C			
2830108	A	A	G	G	G	G	G			
2830916	A	A	G	A	A	A	A			
2832489	C	C	C	C	T	C	C			
2836699	G	G	G	C	C	C	C			
2839424	G	G	G	G	G	C	G	STM2690	-	putative outer membrane efflux protein
2840931	G	G	G	G	G	G	T	STM2691	-	putative ABC transporter transmembrane region
2842909	G	G	G	A	G	G	G	STM2692	-	HlyD family secretion protein
2843257	G	G	G	G	G	G	A	STM2692	-	HlyD family secretion protein
2843936	T	T	C	C	C	C	C			
2879694	G	G	A	G	G	G	G	STM2741	-	putative periplasmic protein
2885696	C	C	T	C	C	C	C			
2888245	G	G	G	G	G	G	A			
2888294	C	C	T	C	C	C	C			
2891738	G	G	T	G	G	G	G	STM2753	-	putative dehydrogenase
2892779	G	G	G	T	G	G	G	STM2754	-	putative hexulose 6 phosphate synthase
2894454	A	A	G	G	G	G	G	STM2756	-	putative sugar phosphate aminotransferase
2896952	G	G	G	A	A	G	G	STM2758	-	putative phosphotransferase system IIC component
2897121	C	C	C	A	C	C	C	STM2758	-	putative phosphotransferase system IIC component
2899518	A	A	G	G	G	G	G			
2899632	T	T	T	T	A	T	T			
2899633	T	T	T	T	A	T	T			
2901350	A	A	A	A	A	A	G			
2901787	C	C	C	C	C	C	T	STM2761	-	putative inner membrane protein
2903088	G	G	G	G	C	G	G	STM2761	-	putative inner membrane protein
2905934	G	G	G	A	A	A	A			
2906853	G	G	G	G	G	G	A			
2907246	C	C	T	C	C	C	C	STM2765	-	putative transposase
2910964	C	C	A	C	C	C	C	STM2768	-	putative transposase
2912403	C	C	C	C	C	T	C			
2913677	A	A	G	G	G	G	G	STM2771	*fljB*	flagellin
2915715	T	T	T	T	T	T	A			
2917432	G	G	G	G	A	G	G	STM2773	*iroB*	putative glycosyl transferase
2921028	C	C	C	C	C	T	C	STM2774	*iroC*	putative ABC transporter protein
2921136	G	G	G	T	G	G	G	STM2774	*iroC*	putative ABC transporter protein
2921235	G	G	G	G	G	G	T			
2923430	C	C	T	C	C	C	C	STM2776	*iroE*	putative hydrolase
2925309	A	A	G	G	G	G	G	STM2777	*iroN*	outer membrane receptor FepA
2926210	C	C	C	C	C	C	T			
2926293	C	C	C	C	C	C	T			
2928483	T	T	C	C	C	C	C	STM2781	*virK*	virulence protein
2931759	C	C	T	C	C	C	C	STM2783	*nixA*	putative nickel transporter
2937751	G	G	G	A	G	G	G			
2938278	C	C	A	C	C	C	C	STM2789	-	hypothetical protein
2939015	C	C	C	C	C	T	C	STM2790	*ygaF*	hydroxyglutarate oxidase
2940892	A	A	G	G	G	G	G	STM2791	*gabD*	succinate-semialdehyde dehydrogenase I
2945099	T	T	T	T	G	T	T	STM2794	*ygaE*	DNA-binding transcriptional regulator CsiR
2946009	A	G	A	A	A	A	A			
2948018	A	A	G	G	G	G	G			
2950876	T	T	T	T	A	T	T	STM2803	-	putative regulatory protein
2952081	A	A	A	A	A	C	A	STM2805	*nrdH*	glutaredoxin-like protein
2952421	G	G	G	A	G	G	G	STM2806	*nrdI*	ribonucleotide reductase stimulatory protein
2952690	G	G	G	G	G	G	A	STM2807	*nrdE*	ribonucleotide-diphosphate reductase subunit alpha

2954098	G	G	G	G	G	T	G	STM2807	*nrdE*	ribonucleotide-diphosphate reductase subunit alpha
2957219	G	G	G	G	G	A	G	STM2810	*proW*	glycine betaine transporter membrane protein
2960108	C	C	C	C	C	C	T	STM2812	-	putative inner membrane protein
2961288	G	G	G	G	G	A	G	STM2813	*emrR*	transcriptional repressor MprA
2964207	C	C	C	C	C	C	A	STM2815	*emrB*	putative multidrug transport protein
2967926	C	T	C	C	C	C	C	STM2818	*gshA*	glutamate--cysteine ligase
2976451	G	G	G	G	G	G	A	STM2830	*ygaD*	competence damage-inducible protein A
2976538	C	C	C	C	C	C	T			
2979237	C	C	C	C	C	C	G	STM2833	*srlE*	glucitol/sorbitol-specific enzyme IIB component
2983237	C	C	C	A	A	A	A	STM2838.S	*gutQ*	D-arabinose 5-phosphate isomerase
2983684	G	G	G	G	G	G	A	STM2839	*ygaA*	anaerobic nitric oxide reductase transcription regulator
2985196	A	A	A	A	A	A	G	STM2840	-	anaerobic nitric oxide reductase flavorubredoxin
2985328	C	C	C	C	C	T	C	STM2840	-	anaerobic nitric oxide reductase flavorubredoxin
2985352	G	G	G	T	T	T	T	STM2840	-	anaerobic nitric oxide reductase flavorubredoxin
2991947	C	C	C	C	C	A	C	STM2845	*hycI*	hydrogenase 3 maturation protease
2992399	G	G	G	G	G	G	A	STM2846	*hycH*	hydrogenase 3 large subunit processing protein
2996778	C	G	G	G	G	G	G	STM2851	*hycC*	formate hydrogenlyase subunit 3
2996779	G	C	C	C	C	C	C	STM2851	*hycC*	formate hydrogenlyase subunit 3
3000993	G	G	A	G	G	G	G	STM2855	*hypB*	hydrogenase nickel incorporation protein HypB
3001171	A	A	T	A	A	A	A	STM2856	*hypC*	hydrogenase assembly chaperone
3005617	A	A	C	C	C	C	C	STM2859	*fhlA*	formate hydrogen-lyase transcriptional activator
3006427	G	G	G	G	G	G	T	STM2861	*sitA*	putative periplasmic binding protein
3010824	T	T	C	C	C	C	C			
3012559	C	T	C	C	C	C	C	STM2867	*hilC*	invasion regulatory protein
3013468	C	C	T	C	C	C	C	STM2868	*orgC*	putative cytoplasmic protein
3015966	C	C	C	C	C	C	T	STM2872	*prgJ*	needle complex minor subunit
3019004	G	G	G	T	T	T	T			
3025770	G	G	G	A	G	G	G	STM2882	*sipA*	secreted effector protein
3029704	C	C	C	C	C	C	T	STM2885	*sipB*	translocation machinery component
3037770	T	A	T	T	T	T	T	STM2894	*invC*	ATP synthase SpaL
3039255	G	G	G	G	G	T	G	STM2896	*invA*	needle complex export protein
3040504	C	C	C	C	C	C	T	STM2897	*invE*	invasion protein
3052754	C	C	A	C	C	C	C	STM2909	*mutS*	DNA mismatch repair protein MutS
3055765	A	A	G	G	G	G	G	STM2913	-	putative permease
3055950	A	A	G	G	G	G	G	STM2913	-	putative permease
3056329	A	A	G	G	G	G	G	STM2913	-	putative permease
3056347	T	T	A	A	A	A	A	STM2913	-	putative permease
3059163	C	C	C	T	T	T	T	STM2916	*ygbL*	putative aldolase
3059472	G	G	G	G	G	A	G	STM2917	*ygbK*	putative tRNA synthase
3059660	C	C	C	T	T	C	C	STM2917	*ygbK*	putative tRNA synthase
3061697	G	G	G	A	G	G	G			
3063978	T	T	T	T	T	T	C	STM2922	-	putative 3-polyprenyl-4-hydroxybenzoate decarboxylase
3064925	T	T	G	T	T	T	T	STM2922	-	putative 3-polyprenyl-4-hydroxybenzoate decarboxylase
3066486	A	T	T	T	T	T	T	STM2924	*rpoS*	RNA polymerase sigma factor RpoS
3079061	A	A	A	C	C	C	C	STM2938	-	putative cytoplasmic protein
3079665	G	G	A	G	G	G	G	STM2939	*ygcH*	putative cytoplasmic protein
3079837	G	G	A	G	G	G	G	STM2939	*ygcH*	putative cytoplasmic protein
3086563	G	G	G	G	G	G	A	STM2944	*ygcB*	putative helicase
3086589	C	C	C	C	A	C	C	STM2944	*ygcB*	putative helicase
3090184	C	C	C	C	C	T	C	STM2947	*cysI*	sulfite reductase subunit beta
3093568	C	C	A	A	A	A	A	STM2950	-	putative metal-dependent hydrolase
3095499	G	G	G	G	G	G	T			
3096598	T	T	G	G	G	G	G	STM2951	*ygcF*	hypothetical protein
3097053	G	G	A	G	G	G	G	STM2951	*ygcF*	hypothetical protein
3097670	G	G	G	G	T	G	G	STM2952	*eno*	phosphopyruvate hydratase
3110314	C	C	C	C	C	C	T	STM2959	-	putative glycerate kinase 2
3110627	C	C	C	C	A	C	C	STM2960	*gudD*	d-glucarate dehydratase
3112160	G	G	G	G	G	G	T	STM2961	*ygcY*	putative D-glucarate dehydratase
3116518	C	C	T	T	T	T	T	STM2965	*yqcC*	putative cytoplasmic protein
3119237	G	G	G	A	A	A	A	STM2969	*ygdH*	putative nucleotide binding
3120407	T	T	T	T	T	C	C			
3122772	C	C	C	C	C	C	A	STM2971	*sdaB*	L-serine dehydratase/L-threonine deaminase 2
3122883	C	C	C	C	C	C	T	STM2971	*sdaB*	L-serine dehydratase/L-threonine deaminase 2
3127204	G	G	G	T	T	T	T			
3130701	G	G	G	G	G	G	A	STM2977	*fucK*	L-fuculokinase
3133164	C	C	C	C	C	C	T	STM2980	*ygdE*	putative RNA 2'-O-ribose methyltransferase
3134944	T	T	T	T	T	T	C	STM2982	*gcvA*	DNA-binding transcriptional activator GcvA
3139107	C	C	C	C	G	C	C	STM2987	*ygdL*	putative enzyme
3140874	G	G	G	G	A	G	G			
3141410	C	C	C	C	T	C	C	STM2991	*amiC*	N-acetylmuramoyl-L-alanine amidase
3142791	C	C	T	C	C	C	C			
3144590	A	A	C	A	A	A	A	STM2993	*recD*	exonuclease V subunit alpha
3149721	C	C	T	C	C	C	C	STM2995	*ptr*	protease III
3154019	C	G	G	G	G	G	G	STM2996	*recC*	exonuclease V subunit gamma
3154020	G	C	C	C	C	C	C	STM2996	*recC*	exonuclease V subunit gamma
3160341	C	A	C	C	C	C	C	STM3003	*ptsP*	fused phosphoenolpyruvate-protein phosphotransferase PtsP/GAF domain
3160598	G	G	G	A	A	A	A	STM3003	*ptsP*	fused phosphoenolpyruvate-protein phosphotransferase PtsP/GAF domain
3167119	G	G	G	G	G	A	G	STM3009	*ygeD*	lysophospholipid transporter LplT
3167375	C	C	C	C	T	C	C	STM3009	*ygeD*	lysophospholipid transporter LplT

3170412	A	A	A	A	A	A	C			
3178899	C	C	C	C	C	C	T	STM3018	*kduI*	5-keto-4-deoxyuronate isomerase
3178958	C	C	C	T	C	C	C	STM3018	*kduI*	5-keto-4-deoxyuronate isomerase
3179295	G	G	A	G	G	G	G			
3179596	C	C	C	C	C	C	T			
3181796	T	T	C	C	C	C	C	STM3020	-	putative transcriptional regulator
3182918	C	C	C	C	C	C	A	STM3022	-	putative transport protein
3185984	A	A	G	G	G	G	G	STM3025	-	putative cytoplasmic protein
3186110	C	C	C	C	A	C	C	STM3025.1N	-	hypothetical protein
3187521	C	C	C	C	C	A	C	STM3026	-	putative outer membrane protein
3188690	A	A	C	C	C	C	C	STM3028	*stdB*	putative outer membrane usher protein
3188898	G	G	G	G	A	G	G	STM3028	*stdB*	putative outer membrane usher protein
3189347	C	C	C	C	C	C	T	STM3028	*stdB*	putative outer membrane usher protein
3192155	T	T	C	T	T	T	T			
3193640	T	T	T	T	T	T	C			
3193667	G	G	G	A	A	A	A			
3196738	A	A	G	A	A	A	A	STM3036	-	putative inner membrane protein
3197389	C	C	C	C	C	T	C			
3199172	G	G	G	G	A	G	G			
3199810	G	G	G	A	G	G	G	STM3040	*lysS*	lysyl-tRNA synthetase
3211852	C	C	T	C	C	C	C			
3214949	G	G	A	G	G	G	G	STM3053	*gcvP*	glycine dehydrogenase
3214963	T	T	T	T	T	T	C	STM3053	*gcvP*	glycine dehydrogenase
3219132	C	G	G	G	G	G	G	STM3057	*ubiH*	2-octaprenyl-6-methoxyphenyl hydroxylase
3219133	G	C	C	C	C	C	C	STM3057	*ubiH*	2-octaprenyl-6-methoxyphenyl hydroxylase
3227308	T	T	T	T	G	T	T	STM3065	*yggE*	hypothetical protein
3228202	C	C	C	C	C	C	T	STM3066	*yggA*	arginine exporter protein
3228883	C	C	C	C	C	C	A	STM3067	*yggB*	mechanosensitive channel MscS
3230295	T	T	T	T	T	T	C	STM3068	*fba*	fructose-bisphosphate aldolase
3232996	C	C	C	T	C	C	C			
3234909	T	T	T	G	T	T	T	STM3073	-	putative ABC-type cobalt transport system permease component
3242909	C	T	T	T	T	T	T	STM3081	-	putative malate/L-lactate dehydrogenase
3245034	C	C	T	C	C	C	C	STM3083	-	putative mannitol dehydrogenase
3245559	G	G	A	G	G	G	G	STM3083	-	putative mannitol dehydrogenase
3245958	T	T	T	T	T	C	T			
3248790	A	A	A	C	C	C	C			
3249039	G	G	G	A	A	A	A	STM3086	*speA*	arginine decarboxylase
3253161	A	A	G	A	A	A	A			
3257005	G	G	T	G	G	G	G	STM3095	*gshB*	glutathione synthetase
3258645	G	G	G	G	G	G	A	STM3096	*yqgE*	hypothetical protein
3259904	C	C	A	C	C	C	C			
3263061	C	C	C	C	C	C	A	STM3103	*yggV*	putative deoxyribonucleotide triphosphate pyrophosphatase
3264056	C	C	C	T	T	T	T	STM3104	*yggW*	coproporphyrinogen III oxidase
3270606	C	C	C	C	A	C	C	STM3112	*mltC*	murein transglycosylase C
3271644	A	A	A	C	A	A	A	STM3113	*nupG*	nucleoside transport
3273896	C	C	C	C	C	C	T	STM3114	*speC*	ornithine decarboxylase
3274223	G	G	G	G	G	A	G	STM3114	*speC*	ornithine decarboxylase
3274853	T	T	C	T	T	T	T	STM3114	*speC*	ornithine decarboxylase
3277442	T	T	C	T	T	T	T	STM3118	-	putative acetyl-CoA hydrolase
3278781	G	G	G	G	G	T	G	STM3120	-	putative transcriptional regulator
3279516	A	A	G	A	A	A	A	STM3120	-	putative transcriptional regulator
3280350	G	G	G	G	G	G	A	STM3121	-	putative transcriptional regulator
3281777	C	C	A	C	C	C	C	STM3122	-	putative arylsulfatase
3286324	A	A	C	C	C	C	C	STM3126	-	putative amino acid transporter
3286531	G	G	G	T	T	T	T	STM3126	-	putative amino acid transporter
3291903	G	G	G	G	T	G	G			
3294569	C	C	C	C	C	T	C	STM3134	-	putative permease
3295358	G	G	G	G	G	G	A	STM3134	-	putative permease
3298019	C	C	C	T	C	C	C	STM3136	-	putative D-mannonate oxidoreductase
3299179	T	T	C	T	T	T	T	STM3137	-	glucuronate isomerase
3300344	T	T	T	T	T	T	C			
3301720	T	T	T	T	T	C	T			
3301744	C	C	C	C	C	C	A			
3301971	G	G	G	G	G	G	A			
3303628	G	G	G	T	G	G	G	STM3139	*gsp*	bifunctional glutathionylspermidine amidase/glutathionylspermidine synthetase
3306122	G	G	G	G	A	G	G	STM3142	-	putative periplasmic ferrichrome-binding protein
3308232	T	T	G	T	T	T	T	STM3145	*hybE*	hydrogenase 2-specific chaperone
3312458	A	A	A	A	A	A	G	STM3149	*hybA*	hydrogenase 2 protein HybA
3318138	A	A	G	G	G	G	G	STM3156	-	putative cytoplasmic protein
3322921	G	G	G	G	G	G	A	STM3162	*yghB*	hypothetical protein
3323324	G	G	G	G	G	A	G	STM3163	*yqhC*	putative transcriptional regulator
3325007	G	G	G	G	A	G	G	STM3164	*yqhD*	putative alcohol dehydrogenase
3327035	A	A	A	A	A	A	G	STM3166.S	-	putative cation transporter
3327172	G	G	G	G	G	C	G	STM3166.S	-	putative cation transporter
3327910	G	G	G	G	G	A	G			
3331488	A	A	A	A	A	A	G			
3332793	T	T	T	C	C	C	C	STM3170	-	putative inner membrane protein
3333171	A	A	G	G	G	G	G	STM3171	*ygiK*	putative transporter
3333205	G	G	G	G	T	G	G	STM3171	*ygiK*	putative transporter
3334784	C	C	T	C	C	C	C	STM3172	*sufI*	repressor protein for FtsI

3338968	T	G	T	T	T	T	T	STM3174	*parC*	DNA topoisomerase IV subunit A
3340037	G	G	G	G	G	G	A	STM3175	-	putative regulatory protein
3342548	T	T	T	T	T	C	T	STM3178	*ygiY*	sensor protein QseC
3343870	G	G	A	G	G	G	G			
3344609	G	A	G	G	G	G	G	STM3181	*parE*	DNA topoisomerase IV subunit B
3346013	A	A	C	C	C	C	C	STM3182	*yqiA*	esterase YqiA
3348801	C	C	A	C	C	C	C	STM3186	*tolC*	outer membrane channel protein
3350888	A	A	G	A	A	A	A	STM3187	*ygiB*	hypothetical protein
3352258	G	G	G	G	C	G	G	STM3189	*ygiD*	hypothetical protein
3352680	G	G	T	G	G	G	G	STM3189	*ygiD*	hypothetical protein
3353879	G	G	G	G	G	T	G			
3367568	G	G	G	A	A	G	G	STM3202	*ygiF*	putative cytoplasmic protein
3367727	C	C	C	C	C	T	C	STM3202	*ygiF*	putative cytoplasmic protein
3381955	C	C	C	C	C	A	C	STM3216	-	putative methyl-accepting chemotaxis protein
3385038	G	G	G	G	G	A	G	STM3218	*oat*	putrescine--2-oxoglutarate aminotransferase
3388419	C	C	C	C	C	C	T	STM3220	*ygjO*	putative methyltransferase
3391158	G	G	G	A	A	A	A	STM3223	*ygjR*	putative dehydrogenase
3397114	C	C	C	G	C	C	C	STM3230	*yqjE*	putative inner membrane protein
3397974	G	G	A	G	G	G	G	STM3232	*yqjF*	hypothetical protein
3397976	C	C	C	A	C	C	C	STM3232	*yqjF*	hypothetical protein
3400747	G	G	G	G	G	G	T	STM3235	*yhaJ*	putative transcriptional regulator
3400867	C	C	C	C	C	C	A	STM3235	*yhaJ*	putative transcriptional regulator
3402615	G	G	G	G	G	A	G	STM3238	*yhaN*	putative inner membrane protein
3404997	T	T	C	C	C	C	C			
3405055	G	A	G	G	G	G	G	STM3240	*tdcG*	L-serine deaminase
3405571	A	A	A	C	A	A	A	STM3240	*tdcG*	L-serine deaminase
3405877	G	G	G	A	G	G	G	STM3240	*tdcG*	L-serine deaminase
3406291	A	A	G	A	A	A	A	STM3240	*tdcG*	L-serine deaminase
3408946	A	A	A	A	G	A	A	STM3242	*tdcD*	propionate/acetate kinase
3409912	G	C	G	G	G	G	G	STM3242	*tdcD*	propionate/acetate kinase
3413523	T	T	T	T	T	T	C			
3418690	C	C	T	C	C	C	C	STM3250	*garD*	galactarate dehydrogenase
3421919	A	A	A	A	G	A	A	STM3252	*agaR*	AGA operon transcriptional repressor
3430154	C	C	C	A	C	C	C	STM3260	-	PTS family galactitol-specific enzyme IIC
3434415	C	C	C	C	C	T	C	STM3264	*yraM*	putative transglycosylase
3438052	T	T	T	T	T	T	G	STM3269	*yhbO*	putative intracellular proteinase
3442687	T	T	C	C	C	C	C	STM3276	*yhbW*	hypothetical protein
3443998	G	G	G	G	G	G	A	STM3277	-	putative inner membrane protein
3445144	A	A	G	A	A	A	A	STM3279	*mtr*	tryptophan permease
3446095	A	A	G	A	A	A	A			
3447713	G	G	G	G	G	A	G	STM3280.S	*deaD*	ATP-dependent RNA helicase DeaD
3450847	A	A	A	A	A	A	G	STM3282	*pnp*	polynucleotide phosphorylase/polyadenylase
3452119	T	T	T	T	T	C	T	STM3284	*truB*	tRNA pseudouridine synthase B
3456658	G	G	G	G	G	A	G	STM3287	*nusA*	transcription elongation factor NusA
3456822	G	G	G	A	A	A	A	STM3287	*nusA*	transcription elongation factor NusA
3457042	C	C	C	C	C	C	T	STM3287	*nusA*	transcription elongation factor NusA
3460273	G	G	G	G	G	A	G			
3462272	G	G	G	G	G	G	A			
3464151	G	G	G	G	G	A	G	STM3295	*folP*	dihydropteroate synthase
3467076	C	C	T	C	C	C	C	STM3297	*rrmJ*	23S rRNA methyltransferase J
3469318	T	T	T	T	T	C	T	STM3300	*dacB*	D-alanyl-D-alanine carboxypeptidase/endopeptidase
3469459	C	C	C	C	G	C	C	STM3300	*dacB*	D-alanyl-D-alanine carboxypeptidase/endopeptidase
3474609	A	A	A	A	A	G	A	STM3306	*nlp*	DNA-binding transcriptional regulator Nlp
3481318	T	T	A	T	T	T	T	STM3315	*yrbH*	D-arabinose 5-phosphate isomerase
3481993	G	G	G	G	G	C	G	STM3316	*yrbI*	3-deoxy-D-manno-octulosonate 8-phosphate phosphatase
3487935	T	T	T	C	C	C	C			
3488112	C	C	C	C	C	A	C			
3489454	G	G	G	A	G	G	G	STM3326	*mtgA*	monofunctional biosynthetic peptidoglycan transglycosylase
3490577	A	A	G	G	G	G	G	STM3328	*arcB*	aerobic respiration control sensor protein ArcB
3501032	G	G	G	G	G	G	T	STM3332	*yhcG*	putative cytoplasmic protein
3508984	G	G	G	G	G	A	G	STM3339	*nanA*	N-acetylneuraminate lyase
3510309	G	G	G	G	G	G	A	STM3341	*sspB*	ClpXP protease specificity-enhancing factor
3512047	G	G	G	G	G	G	C	STM3343	-	putative cytoplasmic protein
3515572	T	T	G	T	T	T	T	STM3348	*degQ*	serine endoprotease
3523562	G	G	G	G	G	G	A	STM3355	-	tartrate dehydratase subunit alpha
3525112	G	G	A	A	A	A	A			
3528669	A	A	A	A	A	G	A			
3528768	G	G	G	A	G	G	G			
3534782	A	A	G	G	G	G	G	STM3368	*tldD*	protease TldD
3535393	G	G	G	G	C	G	G	STM3368	*tldD*	protease TldD
3536641	A	A	A	G	G	A	A	STM3369	*yhdP*	hypothetical protein
3540267	G	G	G	A	A	A	A	STM3370	*cafA*	ribonuclease G
3542848	C	C	C	C	C	T	C	STM3373	*mreC*	rod shape-determining protein MreC
3545552	G	G	G	G	T	G	G	STM3375	*yhdA*	regulatory protein CsrD
3547736	G	G	G	A	G	G	G	STM3376	*yhdH*	putative oxidoreductase
3549630	G	G	G	G	G	G	A	STM3378	-	putative sulfite oxidase subunit YedZ
3551483	T	T	T	T	C	T	T	STM3380	*accC*	acetyl-CoA carboxylase biotin carboxylase subunit
3552732	T	T	C	T	T	T	T	STM3382	*panF*	sodium/panthothenate symporter
3555368	G	G	A	G	G	G	G	STM3384	*yhdG*	tRNA-dihydrouridine synthase B
3560053	T	T	T	T	T	T	C	STM3389	*envR*	DNA-binding transcriptional regulator EnvR
3560217	A	A	A	A	A	A	T	STM3389	*envR*	DNA-binding transcriptional regulator EnvR

3562519	G	G	G	A	G	G	G	STM3391	*acrF*	multidrug transport protein
3562532	G	G	G	G	G	G	A	STM3391	*acrF*	multidrug transport protein
3578972	T	T	T	T	T	T	C	STM3408	*sun*	16S rRNA methyltransferase B
3581969	C	C	C	C	C	T	C	STM3412	*zntR*	zinc-responsive transcriptional regulator
3583787	G	G	G	G	G	G	A	STM3415	*rpoA*	DNA-directed RNA polymerase subunit alpha
3587589	G	A	G	G	G	G	G	STM3421	*rplO*	50S ribosomal protein L15
3588212	A	A	A	G	A	A	A	STM3423	*rpsE*	30S ribosomal protein S5
3595755	C	C	A	A	A	A	A	STM3440	*rplC*	50S ribosomal protein L3
3596704	C	C	C	C	C	T	C			
3599978	C	C	C	C	T	C	C	STM3446	*fusA*	elongation factor G
3602425	G	G	G	G	G	G	A	STM3448	*rpsL*	30S ribosomal protein S12
3602827	T	T	T	T	T	T	G			
3603833	T	T	T	T	C	T	T	STM3451	*yheN*	sulfur transfer complex subunit TusD
3606259	G	G	G	A	G	G	G			
3607523	C	C	C	C	C	C	A	STM3457	*kefB*	glutathione-regulated potassium-efflux system protein KefB
3607712	G	G	A	G	G	G	G	STM3457	*kefB*	glutathione-regulated potassium-efflux system protein KefB
3609825	G	G	G	T	T	T	T			
3612722	G	G	G	A	A	A	A	STM3462	*yheT*	putative hydrolase
3617896	C	C	A	A	A	A	A	STM3467	*yhfK*	putative inner membrane protein
3618179	G	G	G	T	G	G	G	STM3467	*yhfK*	putative inner membrane protein
3618254	G	G	G	G	G	G	A	STM3467	*yhfK*	putative inner membrane protein
3619157	A	A	A	G	A	A	A	STM3468	*argD*	bifunctional N-succinyldiaminopimelate-aminotransferase/acetylornithine transaminase protein
3619299	C	C	T	C	C	C	C	STM3468	*argD*	bifunctional N-succinyldiaminopimelate-aminotransferase/acetylornithine transaminase protein
3619657	G	G	G	G	G	A	G	STM3468	*argD*	bifunctional N-succinyldiaminopimelate-aminotransferase/acetylornithine transaminase protein
3622576	T	T	T	T	G	T	T	STM3473	*yhfC*	hypothetical protein
3623270	C	C	C	A	A	A	A			
3626874	T	T	T	T	C	T	T	STM3476	*nirC*	nitrite transporter NirC
3628928	T	T	T	T	T	C	T			
3629354	A	A	A	A	A	A	G	STM3478	*bigA*	putative surface-exposed virulence protein
3630285	T	T	T	T	T	T	A	STM3478	*bigA*	putative surface-exposed virulence protein
3630588	C	C	C	C	C	C	G	STM3478	*bigA*	putative surface-exposed virulence protein
3631668	C	C	T	C	C	C	C	STM3478	*bigA*	putative surface-exposed virulence protein
3632631	C	C	C	C	C	A	C	STM3478	*bigA*	putative surface-exposed virulence protein
3633454	A	A	A	A	A	C	A	STM3478	*bigA*	putative surface-exposed virulence protein
3634258	G	G	G	A	A	A	A	STM3478	*bigA*	putative surface-exposed virulence protein
3634394	G	G	G	A	G	G	G	STM3478	*bigA*	putative surface-exposed virulence protein
3635961	G	G	G	G	G	A	G	STM3480	*yhfL*	putative outer membrane lipoprotein
3636277	G	G	A	G	G	G	G	STM3481	*trpS*	tryptophanyl-tRNA synthetase
3639470	A	A	A	A	A	G	A	STM3484	*dam*	DNA adenine methylase
3646646	A	A	A	A	A	G	A	STM3493	*mrcA*	peptidoglycan synthetase
3653837	A	A	G	A	A	A	A	STM3498	*hslO*	Hsp33-like chaperonin
3654053	G	G	G	G	G	A	G	STM3498	*hslO*	Hsp33-like chaperonin
3665587	G	G	A	G	G	G	G	STM3506	*feoB*	ferrous iron transport protein B
3666566	G	G	T	G	G	G	G	STM3507	*yhgG*	putative cytoplasmic protein
3670795	C	C	T	T	T	T	T	STM3512	*gntT*	high-affinity gluconate permease
3674777	C	C	C	C	C	C	T	STM3514	*malP*	maltodextrin phosphorylase
3676592	A	A	G	G	G	G	G			
3681781	C	C	A	A	A	A	A	STM3519	*rtcB*	putative cytoplasmic protein
3682652	C	C	A	A	A	A	A			
3686777	G	G	G	G	A	G	G	STM3523	*glpR*	DNA-binding transcriptional repressor GlpR
3692182	C	C	A	C	C	C	C	STM3528	-	putative periplasmic phosphate-binding protein
3693898	A	A	C	C	C	C	C			
3695761	G	G	A	A	A	A	A	STM3531	-	putative dihydroxyacid dehydratase
3695893	C	T	C	C	C	C	C	STM3531	-	putative dihydroxyacid dehydratase
3705667	C	C	C	C	C	C	A	STM3537	*glgX*	glycogen debranching enzyme
3710649	G	G	G	G	G	A	G	STM3541	*gntU*	low affinity gluconate transporter
3710782	C	C	C	C	C	C	T	STM3541	*gntU*	low affinity gluconate transporter
3715491	A	A	A	A	A	G	A			
3715500	C	C	C	C	C	A	C			
3715662	G	G	G	G	G	A	G	STM3546	*yhhY*	putative acetyltransferase YhhY
3717410	T	C	C	C	C	C	C	STM3547.Sc	-	putative transcriptional regulator
3718976	G	G	G	A	A	A	A	STM3549	-	putative inner membrane protein
3718992	C	C	A	C	C	C	C	STM3549	-	putative inner membrane protein
3722230	T	T	T	T	T	T	G			
3723167	T	T	C	C	C	C	C	STM3553	*ugpQ*	cytoplasmic glycerophosphodiester phosphodiesterase
3723279	T	T	T	T	T	T	A	STM3553	*ugpQ*	cytoplasmic glycerophosphodiester phosphodiesterase
3730150	T	T	C	T	T	T	T	STM3562	*livM*	leucine/isoleucine/valine transporter permease subunit
3732617	T	T	T	T	T	C	T	STM3564	*livK*	high-affinity branched-chain amino acid transporter
3732993	T	T	T	T	C	T	T	STM3564	*livK*	high-affinity branched-chain amino acid transporter
3734482	G	G	G	G	G	A	G			
3742757	A	A	G	A	A	A	A	STM3576	*zntA*	zinc/cadmium/mercury/lead-transporting ATPase
3749077	C	C	T	C	C	C	C	STM3581.S	*yhhS*	major facilitator superfamily transporter
3755103	A	A	A	G	A	A	A	STM3586.S	*yhiH*	putative ABC-type multidrug transport system ATPase component
3755210	A	A	G	G	G	G	G	STM3586.S	*yhiH*	putative ABC-type multidrug transport system ATPase component
3757093	C	C	C	C	C	C	T	STM3588	*yhiN*	putative periplasmic protein
3762673	T	T	T	T	T	T	C	STM3592	*yhiP*	inner membrane transporter YhiP
3765625	C	C	C	C	C	C	T	STM3594	*prlC*	oligopeptidase A
3767032	G	G	A	G	G	G	G	STM3595	-	putative phosphatase
3768626	G	A	G	G	G	G	G	STM3597	*gor*	glutathione reductase

3771752	A	A	A	A	A	A	G	STM3599	-	anaerobic C4-dicarboxylate transporter
3774462	C	C	T	C	C	C	C			
3777169	C	C	C	T	T	T	T	STM3603	*treF*	trehalase
3778750	C	C	C	C	T	C	C	STM3604	-	putative inner membrane protein
3779214	G	G	A	G	G	G	G	STM3605	-	putative phage endolysin
3781216	G	G	G	G	A	G	G	STM3607	*yhjC*	putative transcriptional regulator
3783305	G	G	G	G	A	G	G	STM3609	*yhjE*	putative transport protein
3789085	A	A	G	A	A	A	A	STM3613	*yhjJ*	putative Zn-dependent peptidase
3789768	C	C	C	C	T	C	C	STM3613	*yhjJ*	putative Zn-dependent peptidase
3795976	C	C	C	A	C	C	C	STM3616	*yhjL*	cellulose synthase subunit BcsC
3795998	C	C	C	C	C	A	C	STM3616	*yhjL*	cellulose synthase subunit BcsC
3798330	C	C	C	C	C	A	C	STM3617	-	endo-1,4-D-glucanase
3804923	C	C	A	A	A	A	A	STM3622	*yhjS*	putative cytoplasmic protein
3807159	G	G	G	G	G	G	A	STM3624	*yhjU*	putative inner membrane protein
3809409	T	T	T	T	T	T	C	STM3625	*yhjV*	putative transport protein
3811894	C	C	C	C	G	C	C	STM3627	*dppD*	dipeptide transporter ATP-binding subunit
3826329	G	G	G	A	A	A	A	STM3638	*lpfC*	long polar fimbrial outer membrane usher protein
3828318	T	T	C	C	C	C	C			
3830783	G	G	T	G	G	G	G	STM3644	*bisC*	biotin sulfoxide reductase
3835448	G	G	G	G	G	A	G			
3841447	C	C	C	T	T	T	T	STM3655	*glyS*	glycyl-tRNA synthetase subunit beta
3842990	C	C	C	C	C	T	C	STM3657	-	putative outer membrane lipoprotein
3844540	G	G	G	G	G	G	A	STM3659	*yiaB*	putative inner membrane protein
3845185	C	A	C	C	C	C	C	STM3660	*xylB*	xylulokinase
3846435	C	T	C	C	C	C	C			
3848519	C	C	C	T	T	T	T	STM3662	*xylR*	xylose operon regulatory protein
3848536	A	A	G	G	G	G	G	STM3662	*xylR*	xylose operon regulatory protein
3848774	C	C	C	C	C	A	C	STM3662	*xylR*	xylose operon regulatory protein
3851361	A	G	G	G	G	G	G	STM3664	*malS*	periplasmic alpha-amylase precursor
3858615	G	G	A	G	G	G	G	STM3671	*yiaM*	2,3-diketo-L-gulonate TRAP transporter small permease protein
3862449	A	A	A	A	A	G	A	STM3674	*lyxK*	L-xylulose kinase
3864221	G	G	G	G	A	G	G	STM3677	*sgbE*	L-ribulose-5-phosphate 4-epimerase
3865189	C	C	C	C	C	C	A	STM3678	-	putative regulatory protein
3872569	G	G	G	G	G	G	A	STM3682	*selB*	selenocysteinyl-tRNA-specific translation factor
3873955	G	G	G	G	G	A	G	STM3683	*selA*	selenocysteine synthase
3874213	A	A	G	G	G	G	G	STM3684	*yibF*	putative glutathione S-transferase
3874933	G	G	G	A	G	G	G			
3875000	C	C	C	C	A	C	C			
3877158	A	A	G	A	A	A	A	STM3685	*mtlA*	mannitol-specific enzyme IIABC component
3878678	C	C	C	A	A	A	A	STM3687	*mtlR*	mannitol repressor protein
3879147	C	C	C	T	C	C	C			
3880454	C	C	C	C	C	C	T			
3880787	A	A	C	A	A	A	A	STM3690	-	putative inner membrane lipoprotein
3885235	C	T	C	C	C	C	C	STM3691	-	putative inner membrane protein
3885946	G	A	G	G	G	G	G	STM3692	*lldP*	L-lactate permease
3886469	G	G	A	G	G	G	G	STM3692	*lldP*	L-lactate permease
3888646	A	C	A	A	A	A	A	STM3694	*lldD*	L-lactate dehydrogenase
3891759	G	G	G	G	C	G	G	STM3697	-	putative mandelate racemase
3893050	T	T	T	T	T	T	C	STM3698	-	putative permease
3894569	C	C	C	C	T	C	C	STM3699	*cysE*	serine acetyltransferase
3898235	G	G	G	G	G	G	A	STM3704	*pmgI*	phosphoglyceromutase
3901594	C	C	T	C	C	C	C	STM3707	*yibD*	putative glycosyl transferase
3901838	A	A	A	A	A	A	G	STM3707	*yibD*	putative glycosyl transferase
3906689	G	A	A	A	A	A	A	STM3711	*rfaF*	ADP-heptose:LPS heptosyltransferase II
3906733	A	A	G	G	G	G	G	STM3711	*rfaF*	ADP-heptose:LPS heptosyltransferase II
3907096	T	T	G	G	G	G	G	STM3711	*rfaF*	ADP-heptose:LPS heptosyltransferase II
3907114	C	C	C	C	C	T	C	STM3711	*rfaF*	ADP-heptose:LPS heptosyltransferase II
3909034	C	C	C	T	C	C	C	STM3713	*rfaL*	O-antigen ligase
3910608	T	C	T	T	T	T	T	STM3714	*rfaK*	putative hexose transferase
3915074	G	G	G	T	T	T	T	STM3719	*rfaB*	UDP-D-galactose:(glucosyl)lipopolysaccharide-1,6-D-galactosyltransferase
3916407	G	G	G	G	A	G	G	STM3721	*rfaP*	lipopolysaccharide core biosynthetic protein
3923165	C	C	C	C	C	C	A	STM3729	*radC*	DNA repair protein RadC
3926163	C	C	C	C	C	A	C	STM3733	*pyrE*	orotate phosphoribosyltransferase
3927727	A	A	A	A	A	A	G	STM3735	*yicC*	hypothetical protein
3929662	C	C	G	C	C	C	C	STM3737	-	putative Zn-dependent hydrolase
3932528	A	A	G	G	G	G	G	STM3739	*ligB*	NAD-dependent DNA ligase LigB
3938950	T	T	T	T	C	T	T	STM3744	*recG*	ATP-dependent DNA helicase RecG
3939204	G	G	G	G	G	G	A	STM3745	-	putative cytoplasmic protein
3942451	G	G	G	G	G	G	A	STM3747	*yicE*	putative purine/xanthine transport protein
3942797	C	C	C	T	T	C	C	STM3748	*yicH*	putative inner membrane protein
3948001	C	C	C	T	T	T	T	STM3750	*yicJ*	putative transporter
3952050	T	T	T	T	T	C	T	STM3755	*rhuM*	putative cytoplasmic protein
3953645	A	A	A	G	G	A	A			
3956981	T	T	A	T	T	T	T	STM3757	*misL*	putative autotransporter
3959696	T	T	T	T	T	T	C			
3963918	A	A	G	G	G	G	G	STM3763	*mgtB*	Mg2+ transporter
3964087	A	A	A	A	A	A	G	STM3763	*mgtB*	Mg2+ transporter
3970719	G	G	G	G	G	G	T	STM3770	-	putative phosphotransferase system enzyme IIC
3971057	G	G	A	G	G	G	G	STM3770	-	putative phosphotransferase system enzyme IIC
3971590	C	C	C	T	C	C	C	STM3771	-	putative phosphotransferase system enzyme IIB

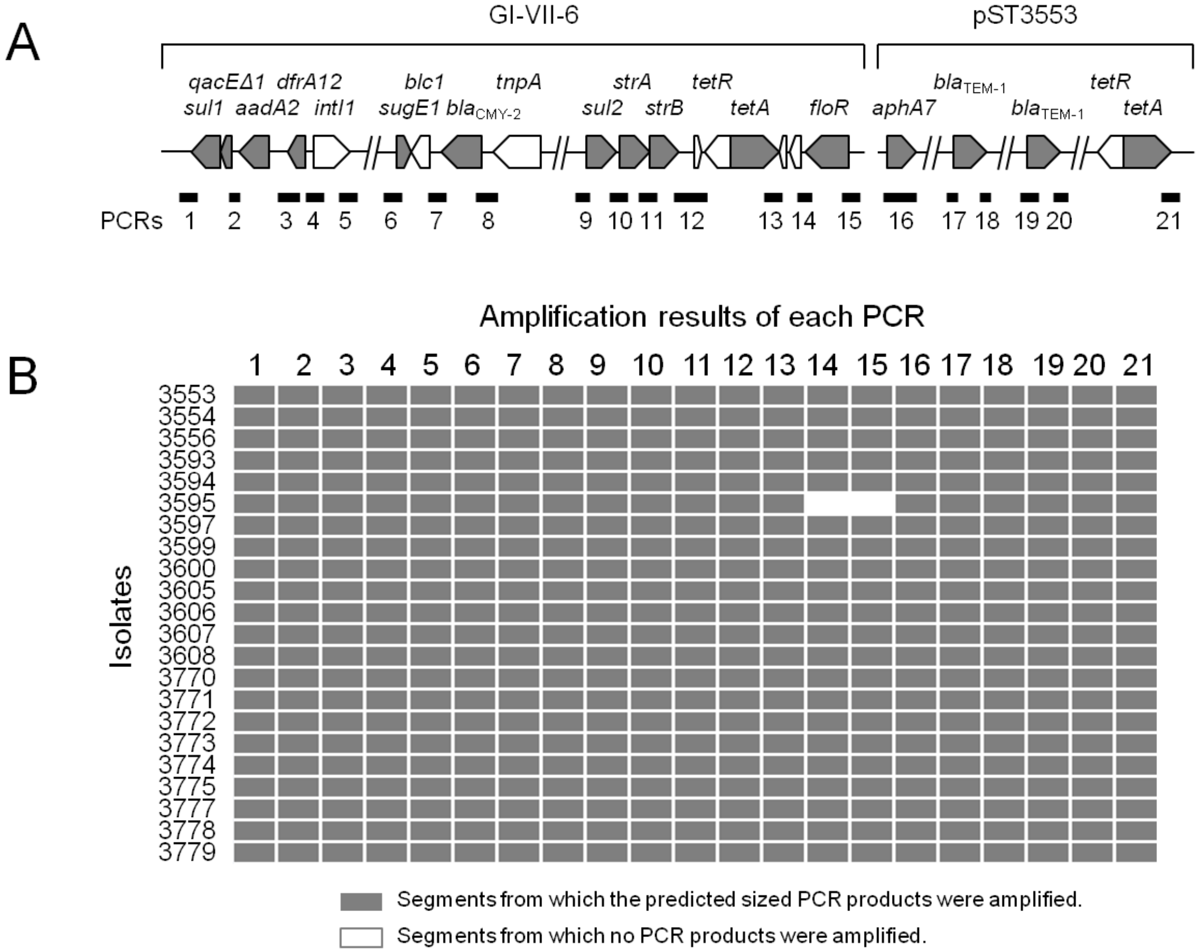
3974491	C	C	C	T	T	T	T	STM3773	-	putative transcriptional regulator
3975123	T	T	T	T	T	T	C	STM3773	-	putative transcriptional regulator
3981285	T	T	T	T	C	T	T	STM3781	-	putative sugar kinase
3982349	A	A	A	A	A	A	G	STM3782	-	putative PTS system galactitol-specific enzyme IIC component
3982395	C	C	C	C	C	C	A	STM3782	-	putative PTS system galactitol-specific enzyme IIC component
3982602	G	G	A	G	G	G	G	STM3782	-	putative PTS system galactitol-specific enzyme IIC component
3983464	G	G	G	G	G	G	A	STM3782	-	putative PTS system galactitol-specific enzyme IIC component
3984416	C	T	C	C	C	C	C	STM3784	-	phosphotransferase system mannitol/fructose-specific IIA
3987005	A	A	A	A	A	A	G	STM3787	*uhpT*	sugar phosphate antiporter
3988307	C	C	C	C	C	T	C	STM3788	*uhpC*	regulatory protein UhpC
3988449	G	G	G	G	G	G	T	STM3788	*uhpC*	regulatory protein UhpC
3994628	G	G	A	G	G	G	G			
3997414	C	C	C	C	T	C	C	STM3796	*ilvB*	acetolactate synthase catalytic subunit
4004538	G	G	G	G	G	G	A	STM3802	*dsdA*	D-serine dehydratase
4005232	G	G	T	G	G	G	G	STM3802	*dsdA*	D-serine dehydratase
4006079	G	G	A	A	A	A	A	STM3803	*yidF*	putative cytoplasmic protein
4007917	C	C	C	C	C	A	C	STM3807	*yidE*	hypothetical protein
4011434	T	T	T	T	T	T	C	STM3811	*yidR*	putative cytoplasmic protein
4012079	T	T	T	T	T	T	C	STM3811	*yidR*	putative cytoplasmic protein
4030718	T	T	A	T	T	T	T	STM3828	*dgoA*	galactonate dehydratase
4034116	G	G	A	G	G	G	G			
4039068	C	C	C	T	C	C	C	STM3835	*gyrB*	DNA gyrase subunit B
4042015	C	C	T	C	C	C	C	STM3836	*recF*	recombination protein F
4043906	G	G	G	G	G	G	A	STM3838	*dnaA*	chromosomal replication initiation protein
4044185	A	A	A	A	A	A	G	STM3838	*dnaA*	chromosomal replication initiation protein
4050025	C	C	C	A	A	A	A			
4050785	T	T	T	A	A	A	A			
4052471	T	T	T	T	T	C	T	STM3846.s	-	putative reverse transcriptase
4052651	C	C	C	C	C	C	T	STM3846.s	-	putative reverse transcriptase
4053588	C	C	A	C	C	C	C			
4054220	G	G	A	G	G	G	G	STM3847	*yidY*	multidrug efflux system protein MdtL
4059719	G	G	G	G	T	G	G	STM3852	*yieH*	6-phosphogluconate phosphatase
4062113	G	G	G	G	G	G	A	STM3855	*pstA*	phosphate transporter permease subunit PtsA
4076962	G	G	G	G	G	G	A	STM3867	*atpA*	F0F1 ATP synthase subunit alpha
4078626	C	C	C	C	C	T	C	STM3869	*atpF*	F0F1 ATP synthase subunit B
4082772	G	G	G	G	A	G	G	STM3874	*gidA*	tRNA uridine 5-carboxymethylaminomethyl modification enzyme
4084017	G	G	G	G	T	G	G			
4084165	C	C	C	T	T	T	T			
4085256	G	G	G	G	A	G	G			
4089567	T	T	T	T	T	T	G			
4094382	G	G	A	G	G	G	G	STM3883	*rbsC*	ribose ABC transporter permease protein
4097899	G	G	G	G	G	T	G	STM3887	*yieO*	putative tranport protein
4107104	C	C	C	C	C	T	C	STM3899	*yifB*	putative ATP-dependent protease
4110058	G	G	A	G	G	G	G	STM3901	*ilvG*	acetolactate synthase 2 catalytic subunit
4111926	G	G	A	G	G	G	G			
4112694	T	T	T	T	T	C	T	STM3904	*ilvD*	dihydroxy-acid dehydratase
4121121	G	G	G	G	G	G	A	STM3912	*rep*	ATP-dependent DNA helicase Rep
4133983	T	T	T	T	C	T	T	STM3925	*wecE*	TDP-4-oxo-6-deoxy-D-glucose transaminase
4136031	C	C	C	C	T	C	C	STM3926	*wzxE*	O-antigen translocase
4136277	G	G	G	G	G	G	T	STM3927	-	4-alpha-L-fucosyltransferase
4136675	A	A	A	A	A	G	A	STM3927	-	4-alpha-L-fucosyltransferase
4137573	A	A	A	A	A	G	A	STM3928	*wecF*	putative common antigen polymerase
4140028	G	G	G	C	C	C	C	STM3930	*yifK*	putative transport protein YifK
4150724	C	C	C	G	C	C	C	STM3943	*cyaY*	frataxin-like protein
4153239	C	C	C	C	C	C	T	STM3948	*yigA*	hypothetical protein
4158327	G	G	G	G	G	A	G	STM3952	*corA*	magnesium/nickel/cobalt transporter CorA
4158778	C	C	C	C	C	C	T	STM3952	*corA*	magnesium/nickel/cobalt transporter CorA
4159293	T	T	T	T	T	T	C	STM3953	*yigF*	putative inner membrane protein
4166265	C	C	C	C	C	T	C	STM3961	*pldB*	lysophospholipase L2
4168743	G	G	G	T	G	G	G	STM3964	*metR*	metE/metH regulator
4169785	C	C	C	T	T	T	T	STM3965	*metE*	5-methyltetrahydropteroyltriglutamate--homocysteine S-methyltransferase
4170512	C	C	C	T	T	T	T	STM3965	*metE*	5-methyltetrahydropteroyltriglutamate--homocysteine S-methyltransferase
4173785	C	C	A	C	C	C	C			
4174788	A	A	G	A	A	A	A			
4181172	G	G	A	G	G	G	G	STM3974	*tatB*	sec-independent translocase
4182484	C	C	C	C	T	C	C	STM3976.S	*yigW*	DNase TatD
4184690	C	C	C	C	C	C	T	STM3978	*yigC*	3-octaprenyl-4-hydroxybenzoate decarboxylase
4186236	G	T	G	G	G	G	G	STM3980	-	putative outer membrane protein
4186828	T	T	C	C	C	C	C	STM3980	-	putative outer membrane protein
4189514	C	C	C	C	C	C	T	STM3983	*fadB*	multifunctional fatty acid oxidation complex subunit alpha
4193570	C	C	C	C	C	C	T	STM3985	*yigZ*	hypothetical protein
4195049	C	C	T	C	C	C	C	STM3986	*trkH*	potassium transporter
4212874	C	C	C	C	C	T	C	STM4005	*glnG*	nitrogen regulation protein NR(I)
4212998	A	A	A	A	A	A	G	STM4005	*glnG*	nitrogen regulation protein NR(I)
4224046	A	A	A	A	A	G	A	STM4015	-	putative cytoplasmic protein
4228130	C	C	C	C	C	C	A	STM4018	*yihP*	GPH family transport protein
4234300	T	T	C	C	C	C	C	STM4023	*yihU*	putative oxidoreductase
4234719	G	G	G	G	G	G	A			
4235079	C	C	T	C	C	C	C	STM4024.S	*yihV*	putative sugar kinase

4244367	C	C	T	C	C	C	C	STM4036	*fdoH*	formate dehydrogenase-O beta subunit
4246576	G	G	G	G	G	G	A	STM4037	*fdoG*	formate dehydrogenase alpha subunit
4249877	C	C	A	C	C	C	C	STM4039	-	putative inner membrane lipoprotein
4255655	A	C	A	A	A	A	A	STM4045	*rhaD*	rhamnulose-1-phosphate aldolase
4256890	C	C	C	T	T	T	T	STM4046	*rhaA*	L-rhamnose isomerase
4259767	A	A	T	A	A	A	A	STM4048	*rhaS*	transcriptional activator RhaS
4260000	G	G	A	G	G	G	G			
4260510	G	G	G	G	G	A	G	STM4049	*rhaR*	transcriptional activator RhaR
4262199	A	A	A	A	A	G	A			
4262511	G	G	A	G	G	G	G			
4267942	G	G	A	G	G	G	G	STM4057	-	putative inner membrane protein
4269000	T	T	C	C	C	C	C	STM4058	*cpxA*	two-component sensor protein
4271394	C	C	C	T	C	C	C	STM4061	*fieF*	ferrous iron efflux protein F
4271667	C	C	C	C	C	C	G	STM4061	*fieF*	ferrous iron efflux protein F
4273163	A	A	A	G	A	A	A	STM4062	*pfkA*	6-phosphofructokinase
4274567	G	G	G	G	G	G	A			
4278245	G	G	G	G	G	G	A	STM4067	-	putative ADP-ribosylglycohydrolase
4281820	A	A	G	G	G	G	G	STM4072	*ydeV*	autoinducer-2 (AI-2) kinase
4282003	C	C	C	C	C	T	C	STM4072	*ydeV*	autoinducer-2 (AI-2) kinase
4282691	C	C	C	C	C	C	T	STM4073	*ydeW*	putative transcriptional repressor
4287709	G	G	A	G	G	G	G	STM4077	*yneA*	putative sugar transport protein
4292455	T	T	T	T	T	A	T	STM4084	*fpr*	ferredoxin-NADP reductase
4294969	G	G	A	G	G	G	G	STM4086	*glpK*	glycerol kinase
4294985	A	A	G	G	G	G	G	STM4086	*glpK*	glycerol kinase
4295488	C	C	C	C	C	C	T	STM4086	*glpK*	glycerol kinase
4297171	C	C	C	C	A	C	C	STM4088	*yiiU*	putative cytoplasmic protein
4299004	G	G	G	G	T	G	G	STM4090	*menA*	1,4-dihydroxy-2-naphthoate octaprenyltransferase
4299090	C	C	C	C	C	C	T			
4302716	A	A	A	T	A	A	A	STM4094	*cytR*	DNA-binding transcriptional regulator CytR
4304963	C	C	C	C	C	T	C	STM4095	*priA*	primosome assembly protein PriA
4307064	C	C	C	C	T	C	C	STM4098	-	putative arylsulfate sulfotransferase
4313563	C	C	C	C	C	T	C	STM4102	-	putative inner membrane protein
4313609	A	A	G	G	G	G	G	STM4102	-	putative inner membrane protein
4317766	T	T	G	G	G	G	G	STM4104	-	putative 5'-nucleotidase/2',3'-cyclic phosphodiesterase
4319888	C	C	T	T	T	T	T	STM4106	*katG*	hydroperoxidase
4324758	G	G	C	G	G	G	G	STM4110	*ptsA*	PEP-protein phosphotransferase
4329614	G	G	G	G	G	A	G	STM4114	*pflD*	putative formate acetyltransferase 2
4333591	A	A	A	A	A	G	A	STM4118	*yijP*	hypothetical protein
4338081	C	C	C	C	T	C	C			
4364880	G	A	G	G	G	G	G	STM4151	*rplJ*	50S ribosomal protein L10
4366519	A	A	G	G	G	G	G	STM4153	*rpoB*	DNA-directed RNA polymerase subunit beta
4369438	C	C	T	T	T	T	T	STM4153	*rpoB*	DNA-directed RNA polymerase subunit beta
4369753	C	C	C	C	C	C	T	STM4153	*rpoB*	DNA-directed RNA polymerase subunit beta
4375214	T	T	T	C	C	C	C			
4375769	T	T	T	T	T	T	C	STM4157	-	putative cytoplasmic protein
4376461	G	G	G	A	G	G	G			
4376730	C	C	T	C	C	C	C	STM4158	-	putative cytoplasmic protein
4377220	A	A	A	A	A	C	A	STM4159	*thiH*	thiamine biosynthesis protein ThiH
4381369	A	A	A	T	A	A	A	STM4164	*thiC*	thiamine biosynthesis protein ThiC
4384227	G	A	A	A	A	A	A	STM4167	*hemE*	uroporphyrinogen decarboxylase
4384994	C	C	C	C	C	C	T	STM4167	*hemE*	uroporphyrinogen decarboxylase
4386273	A	A	A	A	A	G	A	STM4169	*yjaG*	putative cytoplasmic protein
4389262	C	C	C	C	T	C	C	STM4173	*hydH*	sensor protein ZraS
4392288	C	C	C	C	C	T	C	STM4175	*purD*	phosphoribosylamine--glycine ligase
4399629	A	A	A	A	A	A	G			
4399635	A	A	C	A	A	A	C			
4400415	C	C	C	A	A	A	A	STM4181	*yjaB*	hypothetical protein
4408461	C	C	C	C	T	C	C	STM4188.S	*metH*	B12-dependent methionine synthase
4414011	C	C	C	C	C	A	C	STM4190	*pepE*	peptidase E
4416952	G	G	G	T	G	G	G	STM4195	-	putative Na+-dependent transporter
4419314	G	G	G	A	A	A	A			
4419826	G	G	G	G	A	G	G	STM4198	-	putative cytoplasmic protein
4425190	C	C	C	C	C	C	T	STM4204	-	putative inner membrane protein
4431253	C	C	C	T	T	T	T	STM4211	-	putative phage tail protein
4432145	C	C	C	C	A	C	C	STM4211	-	putative phage tail protein
4436536	C	C	T	T	T	T	T	STM4217	-	putative soluble lytic murein transglycosylase
4436710	C	C	C	T	C	C	C	STM4217	-	putative soluble lytic murein transglycosylase
4437535	C	C	C	C	C	C	T			
4438492	C	C	C	T	C	C	C	STM4220	*lysC*	aspartate kinase III
4439926	T	T	T	T	A	T	T			
4442750	G	G	G	A	A	A	A	STM4223	*yjbF*	putative outer membrane lipoprotein
4445007	G	G	T	G	G	G	G	STM4225	*yjbH*	putative outer membrane lipoprotein
4450313	C	C	C	C	T	C	C	STM4229	*malE*	maltose ABC transporter periplasmic protein
4456522	G	G	G	C	C	C	C	STM4235	*plsB*	glycerol-3-phosphate acyltransferase
4462372	G	G	A	A	A	A	A			
4462523	T	T	T	C	C	C	C			
4465206	G	G	G	T	T	T	T	STM4244	*pspG*	phage shock protein G
4469863	G	G	G	G	G	G	A	STM4248	*tyrB*	aromatic amino acid aminotransferase
4472680	C	C	C	C	C	C	G	STM4253	-	putative outer membrane lipoprotein
4473459	G	G	A	G	G	G	G	STM4254	*uvrA*	excinuclease ABC subunit A
4479124	C	C	C	C	C	C	T	STM4258	-	putative methyl-accepting chemotaxis protein

4482340	C	C	C	C	T	C	C	STM4260	-	cation efflux pump
4485170	A	A	G	A	A	A	A	STM4261	-	putative inner membrane protein
4485899	C	A	C	C	C	C	C	STM4261	-	putative inner membrane protein
4486898	C	C	C	C	T	C	C	STM4261	-	putative inner membrane protein
4492562	T	T	C	C	C	C	C	STM4261	-	putative inner membrane protein
4493493	A	A	A	T	A	A	A	STM4261	-	putative inner membrane protein
4494357	C	C	C	C	C	C	T	STM4261	-	putative inner membrane protein
4494860	A	A	A	A	A	A	G	STM4261	-	putative inner membrane protein
4500085	T	T	T	T	C	T	T	STM4262	-	putative ABC-type bacteriocin/lantibiotic exporter
4514655	C	C	C	C	T	C	C	STM4275	*acs*	acetyl-CoA synthetase
4515571	G	G	G	G	G	A	G	STM4275	*acs*	acetyl-CoA synthetase
4516874	C	C	C	C	C	C	A	STM4277	*nrfA*	cytochrome c552
4521798	A	A	T	A	A	A	A	STM4281	*nrfE*	formate-dependent nitrite reductase
4526698	A	A	A	G	A	A	A	STM4285	*fdhF*	formate dehydrogenase
4526717	T	T	C	C	C	C	C	STM4285	*fdhF*	formate dehydrogenase
4528169	C	C	C	C	C	C	A	STM4286	*lpxO*	putative dioxygenase
4528350	A	A	C	A	A	A	A	STM4286	*lpxO*	putative dioxygenase
4535276	A	G	A	A	A	A	A	STM4293	*yjdB*	putative cell division protein
4535645	A	A	A	A	A	A	G	STM4293	*yjdB*	putative cell division protein
4536161	T	T	C	T	T	T	T	STM4294	*yjdE*	arginine:agmatin antiporter
4537685	T	T	T	T	G	T	T	STM4295	*adiY*	transcriptional activator
4537713	A	G	A	A	A	A	A	STM4295	*adiY*	transcriptional activator
4548480	T	T	T	T	T	T	C			
4551274	G	G	G	G	A	G	G	STM4304	*dcuS*	sensory histidine kinase DcuS
4551677	G	G	A	G	G	G	G			
4555195	C	C	C	C	C	C	T	STM4307	-	putative anaerobic dimethylsulfoxide reductase subunit C
4559142	C	C	T	T	T	T	T			
4561036	G	A	A	A	A	A	A	STM4315	-	putative DNA-binding protein
4561212	T	T	T	C	T	T	T	STM4315	-	putative DNA-binding protein
4561979	A	A	A	G	A	A	A			
4564666	G	G	G	G	G	G	A			
4568781	A	A	G	A	A	A	A	STM4323	*dipZ*	thiol:disulfide interchange protein precursor
4574373	A	A	A	A	A	A	C	STM4328	*yjeH*	inner membrane protein YjeH
4578525	G	G	T	G	G	G	G			
4582025	C	C	C	T	T	T	T	STM4339	*blc*	outer membrane lipoprotein Blc
4582487	T	T	T	A	A	A	A	STM4340	*frdD*	fumarate reductase subunit D
4587142	T	T	C	T	T	T	T			
4587173	A	A	A	A	A	G	A			
4590084	G	G	G	A	A	A	A	STM4347	*yjeP*	hypothetical protein
4591806	C	C	C	C	C	C	T	STM4347	*yjeP*	hypothetical protein
4594426	C	C	C	C	C	T	C	STM4349	*yjeQ*	ribosome-associated GTPase
4595988	C	C	A	C	C	C	C	STM4351	-	putative arginine-binding periplasmic protein
4597156	C	C	C	T	T	T	T			
4599152	T	T	C	C	C	C	C	STM4356	*yjeF*	hypothetical protein
4599227	A	A	A	T	A	A	A	STM4356	*yjeF*	hypothetical protein
4602744	A	C	C	C	C	C	C	STM4359	*mutL*	DNA mismatch repair protein
4603961	T	T	T	A	A	A	A	STM4360	*miaA*	tRNA delta(2)-isopentenylpyrophosphate transferase
4605299	T	T	G	G	G	G	G	STM4362	*hflX*	putative GTPase HflX
4607491	C	C	C	C	C	C	T	STM4363	*hflK*	FtsH protease regulator HflK
4609669	A	A	A	A	A	A	T	STM4366	*purA*	adenylosuccinate synthetase
4611636	G	G	A	G	G	G	G	STM4368	*vacB*	exoribonuclease R
4615412	C	C	C	C	C	T	C	STM4371	*yjfJ*	putative phage shock protein A
4615424	C	C	C	C	C	T	C	STM4371	*yjfJ*	putative phage shock protein A
4615757	C	C	T	C	C	C	C	STM4372	-	putative potassium channels
4622084	C	C	A	C	C	C	C			
4622105	T	T	C	C	C	C	C			
4625349	C	C	C	C	C	T	C	STM4383.S	*ulaA*	ascorbate-specific PTS system enzyme IIC
4625967	T	T	T	T	T	T	C	STM4383.S	*ulaA*	ascorbate-specific PTS system enzyme IIC
4628048	G	G	G	A	A	G	G	STM4386	*ulaD*	3-keto-L-gulonate-6-phosphate decarboxylase
4631400	C	G	G	G	G	G	G	STM4393	*rpsR*	30S ribosomal protein S18
4631401	G	C	C	C	C	C	C	STM4393	*rpsR*	30S ribosomal protein S18
4632428	A	A	A	A	A	A	C	STM4395	*yifZ*	putative permease
4633564	G	G	G	G	A	G	G	STM4396	*ytfB*	putative cell envelope opacity-associated protein A
4634616	G	G	A	G	G	G	G			
4634965	G	G	C	G	G	G	G	STM4398	*cycA*	D-alanine/D-serine/glycine permease
4636893	C	C	T	C	C	C	C	STM4399	*ytfE*	iron-sulfur cluster repair di-iron protein
4639675	G	G	G	G	G	G	C	STM4403	*cpdB*	bifunctional 2',3'-cyclic nucleotide 2'-phosphodiesterase/3'-nucleotidase periplasmic precursor protein
4641522	A	A	A	G	A	A	A			
4648481	G	G	G	G	A	G	G	STM4410	*ytfN*	putative periplasmic protein
4651658	A	A	A	G	A	A	A	STM4411	*ytfP*	putative cytoplasmic protein
4653583	C	C	C	T	T	T	T	STM4413	-	putative metallo-dependent hydrolase
4657427	A	A	A	A	G	A	A	STM4416	*mpl*	UDP-N-acetylmuramate/L-alanyl-gamma-D-glutamyl-meso-diaminopimelate ligase
4658213	T	T	T	T	C	T	T			
4659182	A	A	A	A	A	A	G	STM4417	-	putative transcriptional regulator
4659705	C	C	C	C	C	C	T	STM4418	-	sugar transporter
4660101	C	C	T	C	C	C	C	STM4418	-	sugar transporter
4660685	G	G	G	G	G	G	A	STM4418	-	sugar transporter
4661013	C	C	C	C	T	C	C			
4661027	A	A	A	A	A	A	G			

4661047	A	A	A	A	A	A	T			
4661135	C	C	C	C	A	C	C			
4661252	G	G	A	G	G	G	G			
4663927	T	T	T	C	C	C	C			
4664869	T	T	C	C	C	C	C	STM4421	-	putative NAD-dependent aldehyde dehydrogenase
4665624	G	G	G	T	G	G	G			
4668287	C	T	C	C	C	C	C	STM4425	-	putative dehydrogenase
4669309	C	C	C	C	C	C	A	STM4426	*srfJ*	lysosomal glucosyl ceramidase-like protein
4672081	C	T	C	C	C	C	C	STM4428	-	major facilitator superfamily transporter
4672647	C	C	C	C	C	T	C			
4674037	C	C	C	C	C	A	C			
4674537	G	G	G	G	A	G	G			
4674556	C	C	C	C	C	T	C			
4674563	G	G	G	G	G	G	T			
4674658	A	A	A	G	G	G	G			
4676929	G	G	A	G	G	G	G	STM4433	-	myo-inositol 2-dehydrogenase
4677361	C	C	C	C	C	C	T	STM4433	-	myo-inositol 2-dehydrogenase
4680574	C	C	C	C	T	C	C	STM4436	-	putative endonuclease
4688204	A	A	A	G	G	G	G	STM4446	-	putative selenocysteine synthase
4688218	G	G	A	G	G	G	G	STM4446	-	putative selenocysteine synthase
4692783	T	T	T	T	T	T	C	STM4452	*nrdD*	anaerobic ribonucleoside triphosphate reductase
4695056	C	C	C	T	C	C	C	STM4452.1N	-	hypothetical protein
4696102	A	A	G	G	G	G	G	STM4453	*treC*	trehalose-6-phosphate hydrolase
4696794	A	A	A	G	G	G	G			
4704522	C	T	C	C	C	C	C	STM4460	*pyrB*	aspartate carbamoyltransferase catalytic subunit
4710799	A	A	G	A	A	A	A			
4714926	T	T	C	T	T	T	T			
4721265	C	C	C	C	C	T	C	STM4477	*pepA*	leucyl aminopeptidase
4723337	T	T	T	T	T	T	C	STM4479	*yjgP*	putative permease
4726062	G	G	A	A	A	A	A	STM4482	*idnT*	L-idonate transport protein
4726414	G	A	G	G	G	G	G	STM4482	*idnT*	L-idonate transport protein
4728225	C	C	C	C	C	C	T	STM4484	*idnD*	L-idonate 5-dehydrogenase
4728664	G	G	G	G	G	G	T	STM4484	*idnD*	L-idonate 5-dehydrogenase
4731205	A	A	A	T	T	T	T			
4738039	T	T	T	T	C	T	T	STM4491	-	putative ATP-dependent Lon protease
4739510	C	C	C	C	C	T	C	STM4492	-	putative cytoplasmic protein
4743011	G	G	A	G	G	G	G	STM4494	-	putative ABC-type sugar/spermidine/putrescine transport system ATPase component
4743454	G	A	A	A	A	A	A	STM4495	-	putative type II restriction enzyme methylase subunit
4744946	G	G	G	G	G	A	G	STM4495	-	putative type II restriction enzyme methylase subunit
4744948	T	T	T	T	T	T	C	STM4495	-	putative type II restriction enzyme methylase subunit
4745869	G	G	A	G	G	G	G	STM4495	-	putative type II restriction enzyme methylase subunit
4759191	A	A	A	A	T	A	A	STM4504	-	putative cytoplasmic protein
4759294	A	A	A	A	A	A	G	STM4504	-	putative cytoplasmic protein
4769942	C	C	C	T	C	C	C	STM4515	*yjiJ*	putative sugar transporter
4773172	C	T	C	C	C	C	C	STM4517	*yjiO*	putative transport protein
4774303	G	G	G	G	G	G	A			
4774507	A	A	A	A	C	A	A	STM4519	-	putative NAD-dependent aldehyde dehydrogenase
4775386	C	C	A	C	C	C	C	STM4519	-	putative NAD-dependent aldehyde dehydrogenase
4776414	G	G	A	G	G	G	G	STM4522	-	putative inner membrane protein
4776612	T	T	C	C	C	C	C	STM4522	-	putative inner membrane protein
4779280	T	T	T	C	C	C	C	STM4525	*hsdM*	DNA methylase M
4781357	G	G	T	T	T	T	T	STM4526	*hsdR*	type I restriction enzyme EcoKI subunit R
4782055	C	C	C	C	A	C	C	STM4526	*hsdR*	type I restriction enzyme EcoKI subunit R
4784402	T	T	T	C	T	T	T			
4789826	C	C	C	T	C	C	C			
4792592	A	A	A	A	A	A	G	STM4534	-	putative transcriptional regulator
4797427	G	G	G	G	G	G	A	STM4538	-	putative PTS permease
4797660	A	A	A	G	A	A	A	STM4539	-	putative glucosamine-fructose-6-phosphate aminotransferase
4798048	G	G	C	G	G	G	G	STM4539	-	putative glucosamine-fructose-6-phosphate aminotransferase
4799038	G	G	G	A	A	A	A	STM4540.S	-	putative glucosamine-fructose-6-phosphate aminotransferase
4802775	C	C	C	C	C	T	C			
4808578	G	G	T	G	G	G	G	STM4550	*fhuF*	ferric iron reductase involved in ferric hydroximate transport
4809421	C	C	C	C	C	C	T	STM4551	-	hypothetical protein
4809660	T	T	C	C	C	C	C	STM4551	-	hypothetical protein
4809879	A	G	A	A	A	A	A	STM4551	-	hypothetical protein
4810102	G	G	T	T	T	T	T	STM4551	-	hypothetical protein
4814121	G	G	A	G	G	G	G	STM4560	*prfC*	peptide chain release factor 3
4815318	C	C	C	C	C	T	C	STM4560	*prfC*	peptide chain release factor 3
4815575	T	T	T	C	T	T	T			
4818418	C	C	T	C	C	C	C	STM4564	*yjjV*	putative deoxyribonuclease YjjV
4818528	C	C	C	T	C	C	C	STM4564	*yjjV*	putative deoxyribonuclease YjjV
4821799	A	A	A	A	G	A	A	STM4567	*deoC*	deoxyribose-phosphate aldolase
4825467	T	T	T	T	T	T	G	STM4570	*deoD*	purine nucleoside phosphorylase
4829063	A	A	G	A	A	A	A	STM4573	*stjC*	putative periplasmic chaperone protein
4832867	C	G	G	G	G	G	G	STM4577	*smp*	hypothetical protein
4832868	G	C	C	C	C	C	C	STM4577	*smp*	hypothetical protein
4834494	A	A	A	A	A	A	G	STM4579	*radA*	DNA repair protein RadA
4838783	A	A	A	A	A	A	G	STM4581	*yjjK*	putative ABC transporter ATP-binding protein
4841924	A	A	A	A	A	A	G	STM4584	*yjjX*	NTPase
4845204	A	A	G	G	G	G	G	STM4589	*creC*	sensory histidine kinase CreC

4847906	T	G	T	T	T	T	T	STM4591	*sthE*	putative major fimbrial subunit
4848918	C	C	T	C	C	C	C			
4850062	A	A	C	C	C	C	C	STM4593	*sthB*	putative fimbrial usher protein
4851987	A	A	G	A	A	A	A	STM4593	*sthB*	putative fimbrial usher protein
4854108	G	G	G	T	G	G	G	STM4596	-	putative inner membrane protein
4856993	A	A	C	C	C	C	C	STM4600	*lasT*	putative RNA methyltransferase



Isolates	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19	20	21
3553	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■
3554	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■
3556	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■
3593	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■
3594	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■
3595	■	■	■	■	■	■	■	■	■	■	■	■	■	□	□	■	■	■	■	■	■
3597	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■
3599	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■
3600	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■
3605	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■
3606	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■
3607	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■
3608	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■
3770	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■
3771	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■
3772	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■
3773	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■
3774	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■
3775	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■
3777	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■
3778	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■
3779	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■

■ Segments from which the predicted sized PCR products were amplified.

□ Segments from which no PCR products were amplified.

FIG. S1. Summary for PCR mapping of resistance regions among 22 clonally related *S.* Typhimurium isolates. (A) Schematic representation of the structure of antimicrobial resistance regions in GI-VII-6 and pST3553 by PCR amplification of 21 fragments containing the 5' and/or 3' end of each resistance gene. (B) Gray and white rectangles indicate segments from which the predicted size of PCR products were amplified or not amplified, respectively.

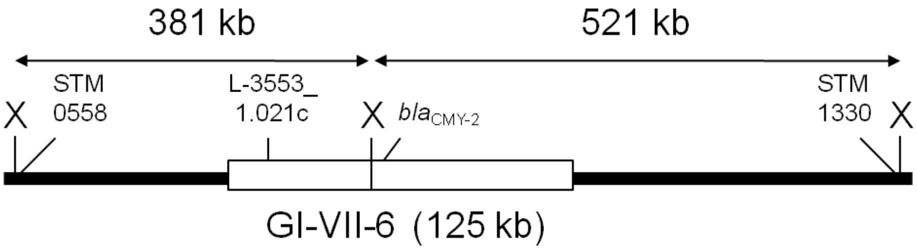


FIG. S2. Schematic view of predicted XbaI-digested fragments containing GI-VII-6 based on the sequence data of *S*. Typhimurium strain LT2 (GenBank accession no. AE006468). The open rectangle indicates GI-VII-6 integrated in the chromosome of *S*. Typhimurium. “X,” refers to XbaI restriction sites. To detect fragments of the predicted sizes of 381 kb and 521 kb, Southern blot analysis was performed using probes hybridized with genes STM0558 and L-3553_1.021c for the 381-kb fragment, and *bla*$_{\text{CMY-2}}$ and STM1330 for the 521-kb fragment.