

## Supplementary material

Fig. S1 Cell size of NC-7 in different osmolality media. The area of cells was measured in Image J, and histograms of measured areas are shown. Cell sizes are similar in MLB from 340-0 mM NaCl. In LB 170 mM NaCl cell size is somewhat larger, and at 68 and 34 mM NaCl they show a spread to much larger size.

Fig S2 Growth of L forms in each medium assayed by Coomassie dye, as detailed in Methods. (a) NC-7 cells growing in the indicated media. Cells in each medium were diluted 100 or 50-fold in the same medium. The 100-fold dilutions were for cells cultured in MLB (340 mM NaCl), MLB (136 mM NaCl), LB (170 mM NaCl) and LB (68 mM NaCl). The 50-fold dilutions were for cells cultured in MLB (0 mM NaCl) and LB (34 mM NaCl). (b) *B. subtilis* LR-2L. 100-fold dilutions were for cells cultured in 2xPAB+SMM (0.5 M sucrose) and 2xPAB+SMM (0.2 M sucrose). 50-fold dilutions were for cells cultured in 2xPAB+SMM (0 M sucrose) and LB (170 mM NaCl) + 10mM MgCl<sub>2</sub>. The vertical axis is the amount of Coomassie dye that bound to cells and was resolubilized by destainer.

Fig. S3 The change of the ratio of long/short axis length after treatment by Chir-090 and EDTA. Because NC-7 has amorphous shapes, we defined the short axis to be the diameter of the largest circle that could be inscribed inside the cell, and the long axis to be a diameter of the smallest circle that could circumscribe the cell. The ratio of the long/short axis is 1 for a spherical shape and increases for elongated shapes. (a) Distribution of the ratio for NC-7 in MLB (340 mM NaCl). (b) This NC-7 was treated with Chir-090 as shown in Fig. 2d. (c) NC-7 was treated with 10 mM EDTA as shown in Fig. 3a.

Fig. S4 Localization of fully functional FtsZ-YFP expressed in NC-7. (a) shows the YFP signal and (b) the corresponding DIC image. Asterisks shows potential Z rings rarely formed at constriction sites. Bar is 10 μm.

Fig. S5 Localization of FtsZ-YFP-mts expressed in NC-7. FtsZ rings and spirals were seen in some cells. Bar is 10 μm.

Fig. S6 Diameter of LR-2L in different osmolality media. About 100 LR-2L cells were measured in each indicated medium. The box includes the 25-75%, the whiskers minimum-maximum and the dots show the few outlier cells.

Table S1 Genotypes and sources of bacterial strains or genomic sequences.

Table S2 Genomic sequencing results for NC-7. The reference sequence is W3110 genome (NC\_007779.1). Blue color shows the different mutations compared to NC-7/34

Table S3 Genomic sequencing results for NC-7/34. The reference sequence is W3110 genome (NC\_007779.1). Red color shows the different mutations compared to NC-7.

Movie S1 and S2. NC-7 in low osmolality (34 mM NaCl) LB medium lysed and divided following removal of divalent cations by EDTA. In Movie S2 membrane tubule (outer membrane) release was also observed. The rate of these movies is 12 s/s.

Movie S3. Division of NC-7 in osmoprotective medium, MLB. The rate of the movie is 120 s/s.

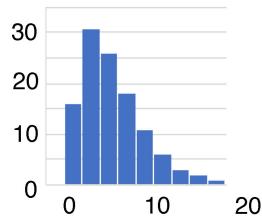
Movie S4. Division of NC-7 by budding in MLB. The rate of the movie is 120 s/s.

Movie S5. NC-7 was cultured in MLB and 10 mM EDTA was added to remove divalent cations. The division shown in this movie occurred ~5 min after addition of EDTA. The rate of movie is 12 s/s.

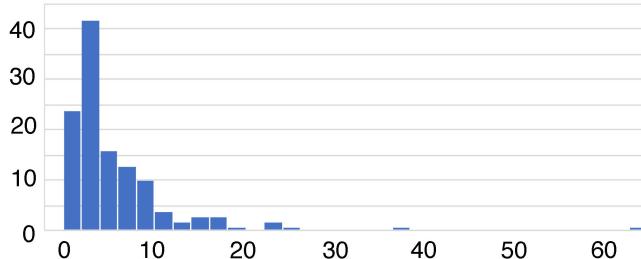
Movie S6. NC-7 in EDTA extruding a membrane tubule in low osmolality (51 mM NaCl) LB medium. The tubule extrudes from a protrusion, which relaxes to spherical as the extrusion grows. The rate of movie is 12 s/s.

number of cells

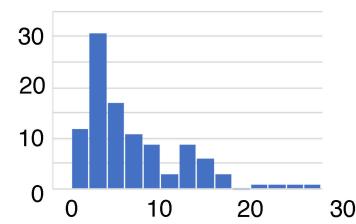
MLB (340 mM NaCl)



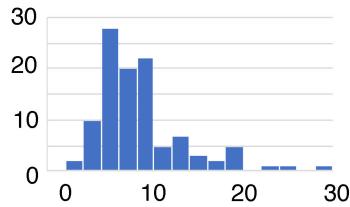
MLB (136 mM NaCl)



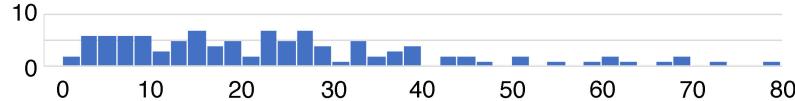
MLB (0 mM NaCl)



LB (170 mM NaCl)



LB (68 mM NaCl)



LB (34 mM NaCl)

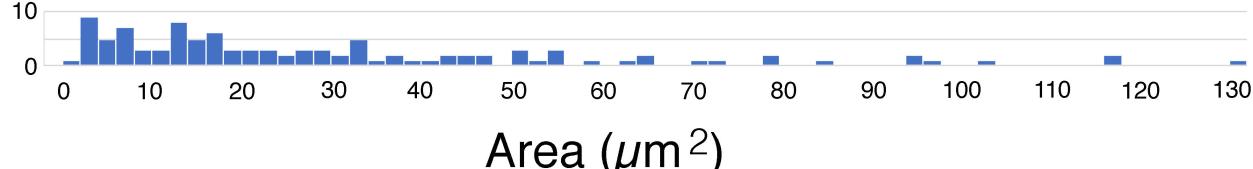


Fig. S1

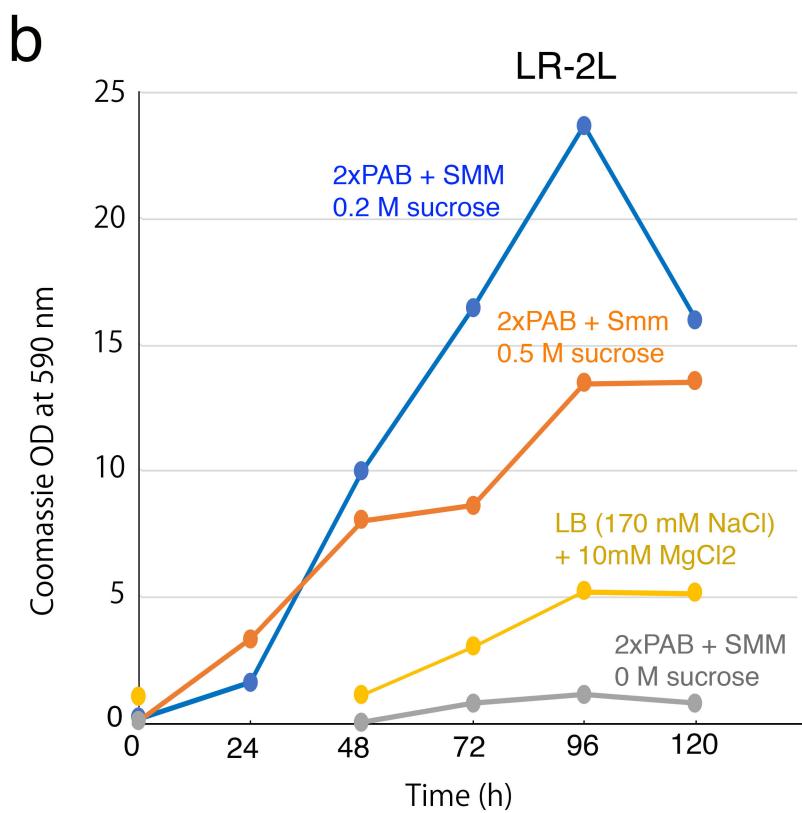
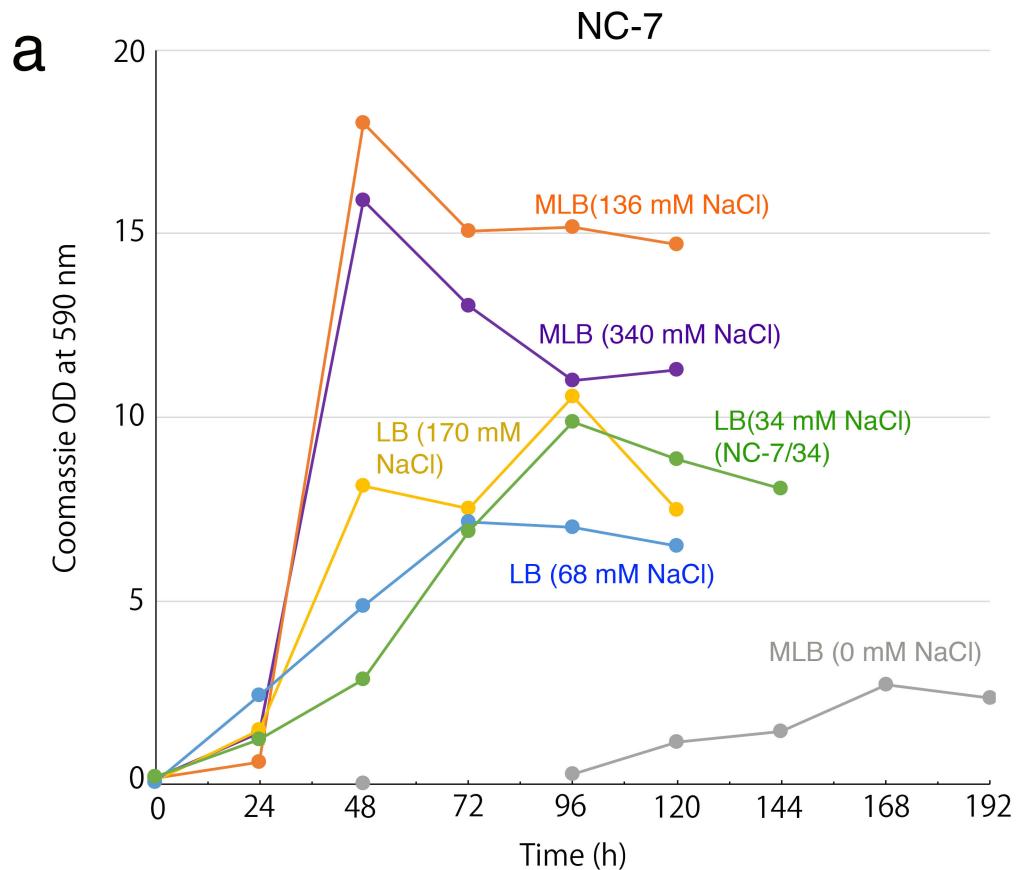
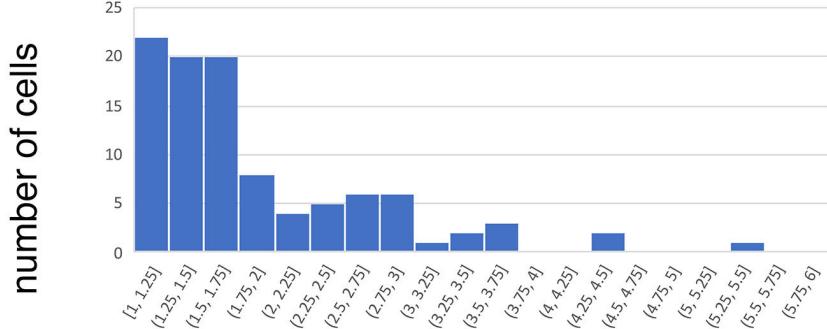


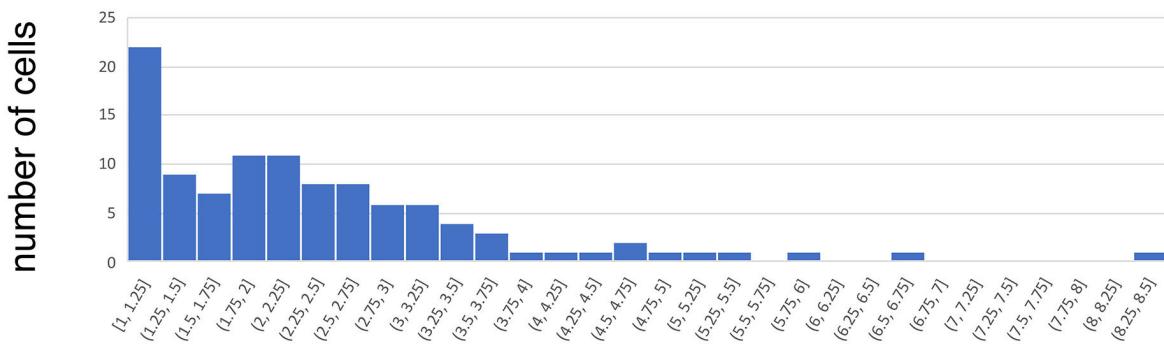
Fig. S2

**a** MLB (340 mM NaCl)

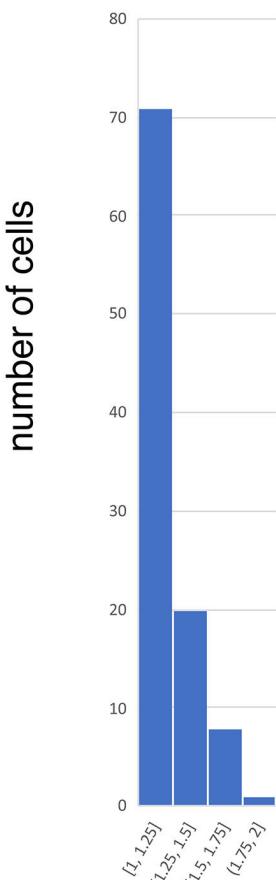
Ratio of long/short axis of cells



**b** LB (34 mM NaCl)



**c** + CHIR-090



**d** + 10 mM EDTA

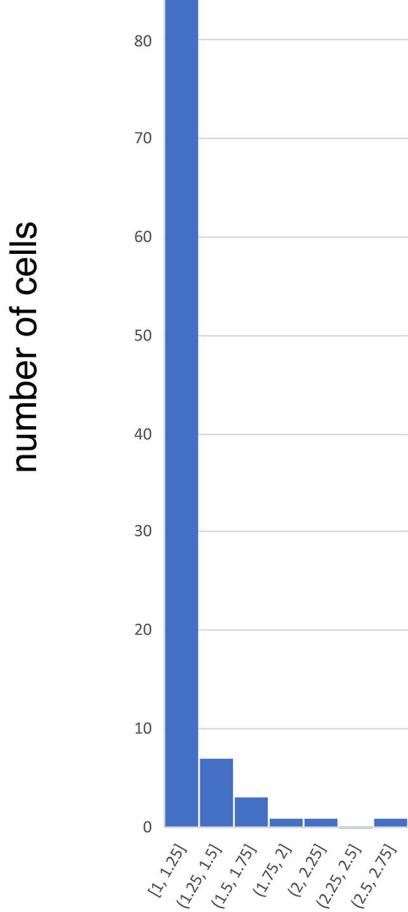
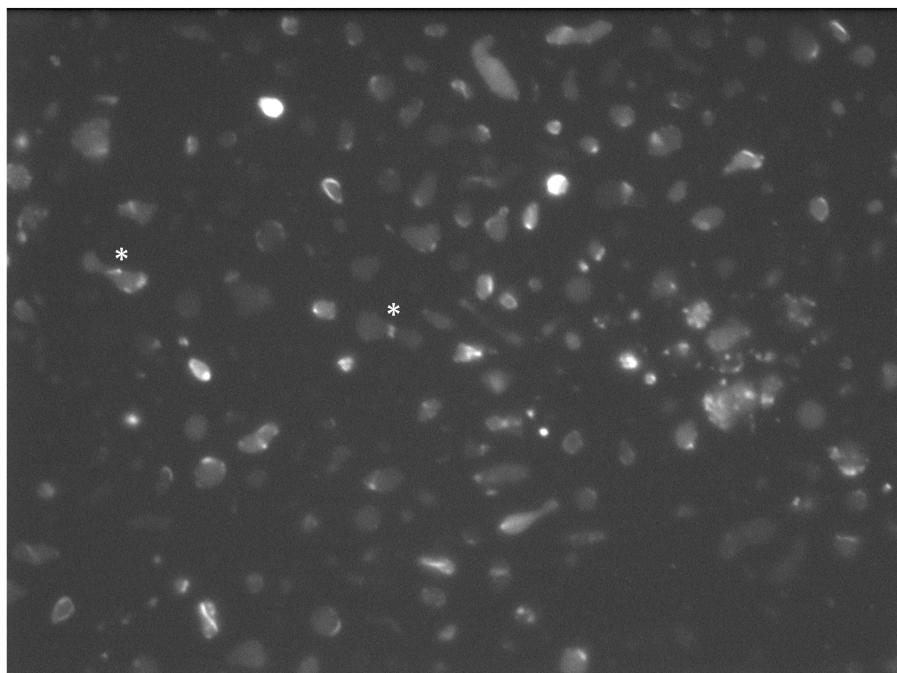


Fig. S3

a



b

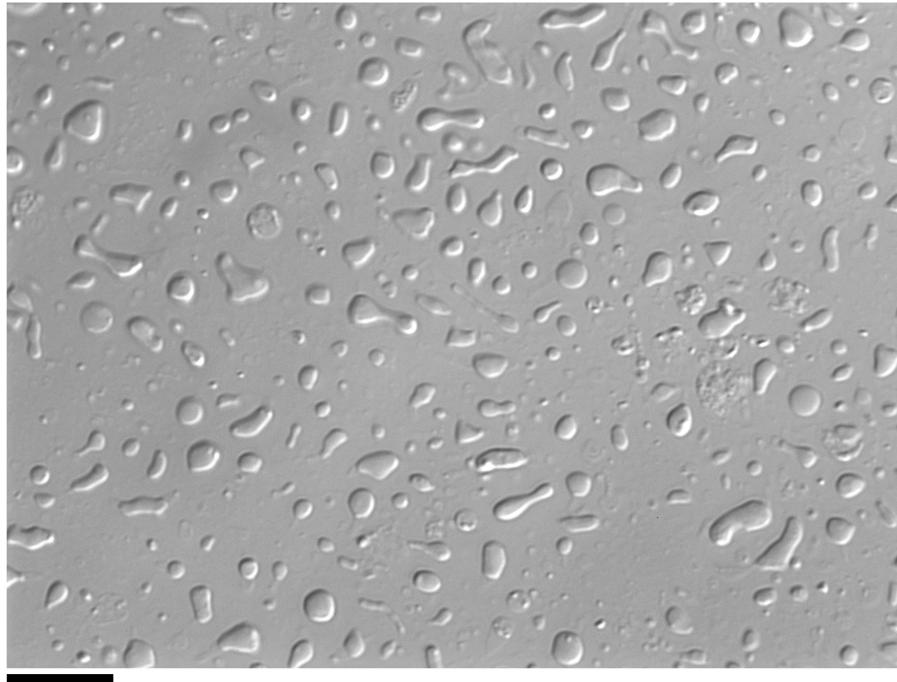
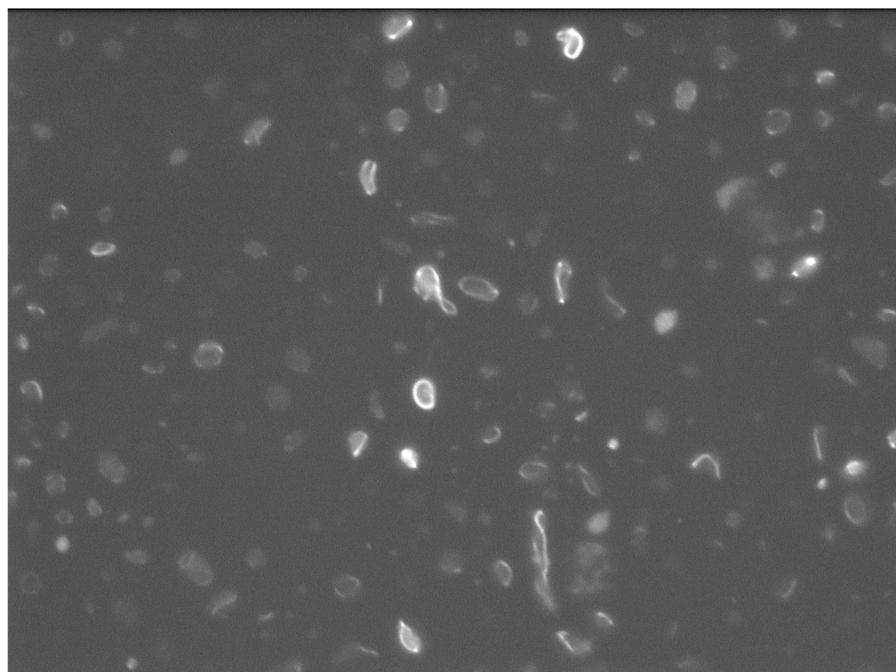


Fig. S4

a



b

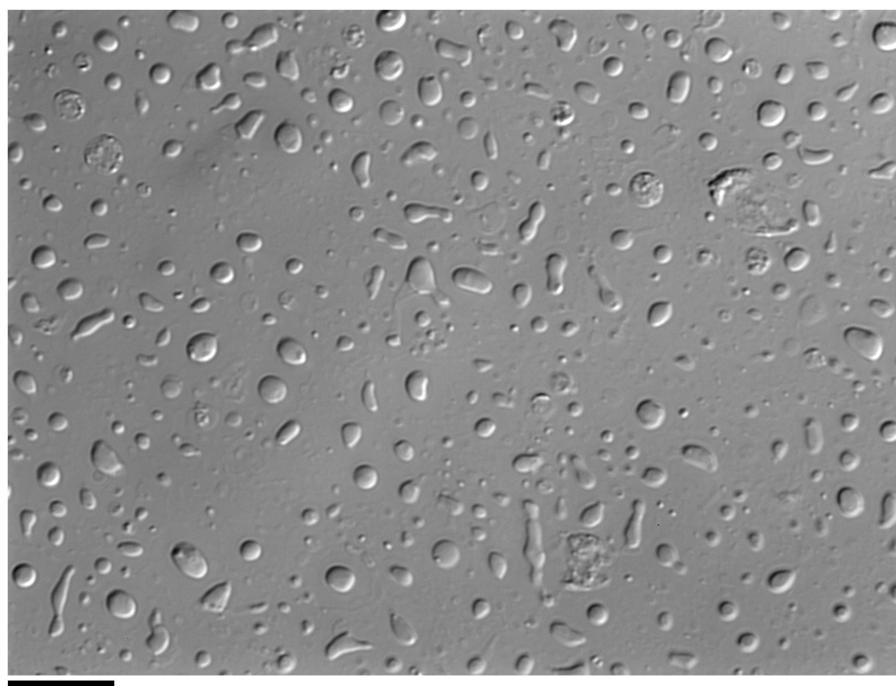


Fig.S5

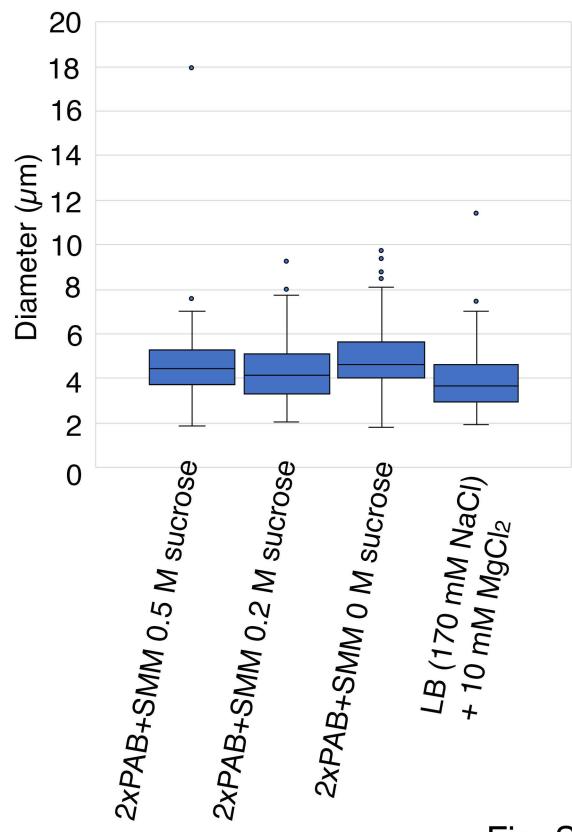


Fig. S6

Table S1 Genotypes and sources of bacterial strains or genomic sequences.

Strains	Genotype	Source
3301	K-12 wild type <a href="http://www.nbrc.nite.go.jp/NBRC2/NBRCatalogueDetailServlet?ID=NBRC&amp;CAT=00003301">http://www.nbrc.nite.go.jp/NBRC2/NBRCatalogueDetailServlet?ID=NBRC&amp;CAT=00003301</a>	(1)
W3110	(derivative from K-12) F <sup>-</sup> lambda <sup>-</sup> IN(rrnD-rrnE)1 rph-1	NCBI Ref Seq: NC_007779.1
JM109	(derivative from K-12) F' traD36 proA <sup>+</sup> B <sup>+</sup> lacI <sup>q</sup> Δ(lacZ)M15/ Δ(lac-proAB) glnV44 e14gyrA96 recA1 relA1 endA1 thi hsdR17	(2)
NC-7	Stable L form derived from 3301 mutated with a mutagen MNG	(1)
NC-7/51	NC-7 adapted to LB with 51 mM NaCl	this work
NC-7/34	NC-7 adapted to LB with 34 mM NaCl	this work
LR-2	Bs115 xseB* (Frameshift 22T>-)	(3)

## References

1. Onoda T, Oshima A, Nakano S, Matsuno A. Morphology, growth and reversion in a stable L-form of *Escherichia coli*. JGenMicrobiol. 1987;133:527-34.
2. Yanisch-Perron C, Vieira J, Messing J. Improved M13 phage cloning vectors and host strains: nucleotide sequences of the M13mp18 and pUC19 vectors. Gene. 1985;33(1):103-19.
3. Mercier R, Kawai Y, Errington J. Excess membrane synthesis drives a primitive mode of cell proliferation. Cell. 2013;152(5):997-1007.

## SNPs in NC-7

Reference: W3110 genome (NC\_007779.1)

Blue color: mutations that NC-7/34 does not have

Table S2

reference position	ref_base<->sample_base	gene	aa_mutation	mutate_type	gene_pos_start	gene_pos_end	Total Depth	Mutation gene name
15136	C<->T	+	C<->C	Synonymous	14168	15298	200	200 dnaj - Chaperone protein DnaJ
31866	G<->A	+	P<->P	Synonymous	30817	34038	249	249 carB - Carbamoyl-phosphate synthase large chain
61618	G<->A	-	W<->*	Premature_stop	60358	63264	191	190 rapA - RNA polymerase-associated protein RapA
78795	T<->C	+	V<->A	Nonsynonymous	77621	78799	206	206 setA - Sugar efflux transporter A
97378	C<->T	+	L<->L	Synonymous	97087	98403	183	183 murD - UDP-N-acetylmuramoylalanine--D-glutamate ligase
105062	C<->T	+	P<->S	Nonsynonymous	103982	105244	218	217 ftsA - Cell division protein FtsA
111392	C<->T	+	P<->S	Nonsynonymous	111044	111433	236	236 mutT - 8-oxo-dGTP diphosphatase
132188	C<->T	+	P<->S	Nonsynonymous	131615	134212	239	239 acnB - Aconitate hydratase B
132526	C<->T	+	G<->G	Synonymous	131615	134212	191	191 acnB - Aconitate hydratase B
134941	T<->C	-	H<->H	Synonymous	134788	135582	200	200 speD - S-adenosylmethionine decarboxylase proenzyme
150554	G<->A	-	V<->I	Nonsynonymous	149715	150953	211	211 yadC - Putative fimbrial-like adhesin protein
198729	C<->T	+	L<->F	Nonsynonymous	197928	200360	230	230 bama - Outer membrane protein assembly factor BamA
199515	G<->A	+	G<->S	Nonsynonymous	197928	200360	188	187 bamA - Outer membrane protein assembly factor BamA
203991	C<->T	+	T<->M	Nonsynonymous	203348	204496	210	210 ipxB - Lipid-A-disaccharide synthase
212759	C<->T	+	V<->V	Synonymous	212331	213629	240	239 tils - tRNA(Ile)-lysidine synthase
234048	G<->A	-	R<->R	Synonymous	234027	234782	187	187 gloB - Hydroxyacylglutathione hydrolase GloB
235748	G<->A	-	W<->*	Premature_stop	235535	236002	205	205 rmhA - Ribonuclease H
246249	G<->A	-	G<->E	Nonsynonymous	246242	246502	182	182 dinJ - Antitoxin DinJ
256834	C<->T	+	T<->I	Nonsynonymous	256527	257771	195	195 frsA - Esterase FrsA
258484	G<->T	-	R<->C	Nonsynonymous	258269	259324	184	183 phoE - Outer membrane pore protein E precursor
271981	G<->A	-	G<->E	Nonsynonymous	271692	272117	248	248 hypothetical protein
273150	C<->T	+	N<->N	Synonymous	272071	273216	136	136 hypothetical protein
283759	T<->G	+	A<->M	Synonymous	282425	284392	229	228 yafF - D-xylonate dehydratase YafF
286919	C<->T	+	P<->S	Nonsynonymous	286013	287623	230	228 yagH - Putative beta-xylosidase
288812	G<->A	-	A<->T	Nonsynonymous	288525	289529	184	183 argF - Ornithine carbamoyltransferase subunit F
306063	G<->A	-	V<->M	Nonsynonymous	306031	308556	203	202 ecpC - Probable outer membrane usher protein EcpC precursor
321132	G<->A	+	A<->T	Nonsynonymous	320832	321551	221	221 ykgE - Uncharacterized protein YkgE
337962	G<->A	+	A<->A	Synonymous	337549	338967	203	203 yahG - Uncharacterized protein YahG
340335	C<->T	+	T<->M	Nonsynonymous	339389	340339	181	181 yahl - Carbamate kinase-like protein Yahl
346855	G<->A	-	Q<->Q	Synonymous	346081	347667	204	203 prpR - Propionate catabolism operon regulatory protein
364950	G<->A	-	D<->N	Nonsynonymous	362455	365529	173	173 lacZ - Beta-galactosidase
398307	G<->A	-	G<->D	Nonsynonymous	398249	398557	204	203 yaiY - Inner membrane protein YaiY
403872	C<->T	+	L<->L	Synonymous	402927	404042	204	204 dgcC - Probable diquinate cyclase DgcC
433738	C<->T	+	R<->C	Nonsynonymous	432679	433782	218	217 ribD - Riboflavin biosynthesis protein RibD
449023	C<->T	-	A<->A	Synonymous	447874	449865	199	199 cyoB - Cytochrome o ubiquinol oxidase subunit I
450121	G<->A	-	A<->A	Synonymous	449887	450834	233	232 HMPREF1608_04559 - Ubiquinol oxidase subunit 2
454754	C<->T	+	T<->I	Nonsynonymous	454357	455655	201	201 tig - Trigger factor
460180	C<->T	+	S<->F	Nonsynonymous	458112	460466	219	219 lon - Lon protease
524387	C<->T	+	I<->L	Synonymous	522485	526765	205	201 rhdS - Protein RhsD
534446	C<->T	+	P<->L	Nonsynonymous	533140	534921	221	221 gcl - Glyoxylate carboligase
541956	T<->C	+	V<->A	Nonsynonymous	541112	542257	237	234 glkK - Glycerate 3-kinase
542970	T<->C	-	F<->L	Nonsynonymous	542485	543270	183	183 allE - (S)-ureidoglycine aminohydrolase
547694	A<->G	+	E<->E	Synonymous	547581	547841	246	245 hypothetical protein
588685	C<->T	-	A<->V	Nonsynonymous	587205	590177	235	234 bacteriophage N4 adsorption protein A
720326	T<->C	-	V<->A	Nonsynonymous	716684	720882	202	199 speF - Inducible ornithine decarboxylase
845812	G<->A	-	D<->N	Nonsynonymous	843677	845902	197	197 MscC - Mechanosensitive ion channel
861269	G<->A	-	G<->D	Nonsynonymous	860596	863028	180	179 ybiW - Putative formate acetyltransferase 3
932433	T<->C	-	S<->P	Nonsynonymous	931507	932472	188	188 trxB - Thioredoxin reductase
963494	A<->C	+	T<->P	Nonsynonymous	962417	964090	190	189 rpsA - 30S ribosomal protein S1
973612	C<->A	-	P<->Q	Nonsynonymous	973044	973823	205	205 elyC - Envelope biogenesis factor ElyC
996238	C<->T	-	A<->V	Nonsynonymous	995265	996410	193	192 ssuD - Alkanesulfonate monooxygenase
1008500	A<->G	+	I<->V	Nonsynonymous	1008266	1010374	169	169 rlmL - Ribosomal RNA large subunit methyltransferase K/L
1093686	T<->C	+	V<->A	Nonsynonymous	1093298	1094656	151	148 GGDEF domain-containing protein
1109401	C<->A	-	P<->Q	Nonsynonymous	1109361	1110518	197	197 mdcC - Glucans biosynthesis protein C
1153518	G<->A	+	V<->V	Start_s	1153516	1154757	158	158 fabF - 3-oxoacyl-[acyl-carrier-protein] synthase 2
1171413	T<->C	-	I<->P	Nonsynonymous	1170989	1171951	166	165 LysM peptidoglycan-binding domain-containing protein
1191557	T<->C	-	T<->T	Synonymous	1191353	1192024	179	178 phoP - Transcriptional regulatory protein PhoP
1195272	C<->T	-	Q<->*	Premature_stop	1194244	1195350	185	185 mmnA - tRNA-specific 2-thiouridylase MmnA
1244877	C<->T	+	P<->S	Nonsynonymous	1244757	1245368	156	156 emtA - Endo-type membrane-bound lytic murein transglycosylase A
1283734	A<->G	+	K<->R	Nonsynonymous	1281441	1285184	189	189 narZ - Nitrate reductase, alpha subunit
1303706	A<->T	+	N<->Y	Nonsynonymous	1302896	1304527	173	173 oppA - Oligopeptide ABC transporter substrate-binding protein
1308450	T<->G	+	S<->A	Nonsynonymous	1307478	1308482	140	139 oppF - Oligopeptide transport ATP-binding protein OppF
1342851	G<->A	+	D<->N	Nonsynonymous	1342272	1343441	154	154 ycmI - Lipopolysaccharide assembly protein B
1352278	T<->C	-	M<->T	Nonsynonymous	1351965	1352753	206	204 fabI - Enoyl-[acyl-carrier-protein] reductase [NADH] FabI
1360573	A<->G	-	Y<->C	Nonsynonymous	1359516	1360901	190	190 puuP - Putrescine importer PuuP
1395099	C<->T	+	A<->A	Synonymous	1394941	1396554	180	179 mppA - Periplasmic murein peptide-binding protein precursor
1401237	A<->C	-	I<->L	Nonsynonymous	1400488	1401240	187	187 fnr - Fumarate and nitrate reduction regulatory protein
1419558	A<->G	-	E<->E	Synonymous	1419552	1419722	208	206 ydaE - Uncharacterized protein YdaE
1460853	A<->G	+	H<->R	Nonsynonymous	1460768	1462195	210	210 paaH - 3-hydroxybutyryl-CoA dehydrogenase PaaH
1727618	A<->G	-	E<->G	Nonsynonymous	1727395	1727634	195	195 ydhL - Uncharacterized protein YdhL
1842973	G<->A	-	G<->S	Nonsynonymous	1842497	1843117	245	243 ynjF - Predicted phosphatidyl transferase, inner membrane protein
1853155	C<->T	+	P<->P	Synonymous	1852574	1853590	196	196 ansA - Cyttoplasmic asparagine I
1862439	T<->C	-	V<->A	Nonsynonymous	1861970	1863046	233	232 ydjL - Uncharacterized zinc-type alcohol dehydrogenase-like protein
1881449	G<->A	-	G<->R	Nonsynonymous	1881303	1881662	212	211 yearA - Uncharacterized protein YearA
1935684	C<->T	-	A<->V	Nonsynonymous	1934507	1936318	205	205 edd - Phosphogluconate dehydratase
2034560	T<->C	-	V<->V	Synonymous	2034521	2035216	220	220 yedJ - Uncharacterized protein YedJ
2042570	C<->A	+	A<->D	Nonsynonymous	2041615	2042619	220	220 mononuclear molybdenum enzyme YedY
2075625	G<->A	+	S<->S	Synonymous	2073676	2076795	236	234 antigen 43
2079713	C<->T	+	T<->I	Nonsynonymous	2079706	2080080	179	179 G943_02322 - Toxin YeeV
2105304	G<->A	-	E<->K	Nonsynonymous	2105077	2105256	188	188 wblB - Lipopolysaccharide biosynthesis protein /pseudo
2117087	T<->C	-	M<->T	Nonsynonymous	2116639	2118033	173	173 wcaM - Colanic acid biosynthesis protein WcaM precursor
2143227	C<->T	-	Q<->*	Premature_stop	2141896	2143749	186	186 gmd - GDP-mannose 4,6-dehydratase
2159947	A<->G	+	T<->A	Nonsynonymous	2157400	2160522	191	189 mdtB - Multidrug resistance protein MdtB
2164514	C<->A	+	P<->Q	Nonsynonymous	2163601	2165016	214	214 mdtD - Putative multidrug resistance protein MdtD
2204520	T<->C	+	I<->T	Nonsynonymous	2203613	2207245	232	229 yehI - Uncharacterized protein YehI
2204648	G<->A	+	A<->T	Nonsynonymous	2203613	2207245	205	202 yehI - Uncharacterized protein YehI
2224957	A<->G	-	S<->G	Nonsynonymous	2223026	2225323	211	210 bglX - Beta-D-glucoside glucohydrolase, periplasmic
2236680	G<->A	+	A<->T	Nonsynonymous	2236212	2236931	205	205 sanA - Uncharacterized protein
2251784	G<->A	-	G<->D	Nonsynonymous	2250397	2251866	217	217 lypS - Lysine-specific permease
2252272	G<->A	-	A<->A	Synonymous	2252071	2252952	210	210 Uncharacterized HTH-type transcriptional regulator YeiE
2312900	C<->T	-	R<->R	Synonymous	2312675	2313739	237	237 ada - 6-O-methylguanine DNA methyltransferase
2386003	G<->A	-	D<->N	Nonsynonymous	2385752	2386213	195	195 elaA - Protein ElaA
2400347	C<->T	-	I<->F	Nonsynonymous	2400012	2400566	172	172 nuoJ - NADH:ubiquinone oxidoreductase, membrane subunit J
2433637	A<->G	-	M<->V	Nonsynonymous	2433503	2434072	200	200 ubiX - Flavin prenyltransferase UbiX
2435840	A<->G	-	T<->A	Nonsynonymous	2435721	2436209	196	194 cvpA - Colicin V production protein

2445091	G<->A	-	G<->D	Nonsynonymous	2444388	2445566	179	179 <i>yfcJ</i> - Uncharacterized MFS-type transporter YfcJ
2509335	C<->T	-	R<->R	Synonymous	2507436	2509931	205	204 <i>fryA</i> - Multiphosphoryl transfer protein 1
2513255	C<->T	-	T<->I	Nonsynonymous	2512093	2513340	207	207 <i>yfcJ</i> - Uncharacterized MFS-type transporter YfcJ
2513309	T<->C	-	V<->A	Nonsynonymous	2512093	2513340	200	200 <i>yfcJ</i> - Uncharacterized MFS-type transporter YfcJ
2573345	G<->A	-	E<->E	Synonymous	2572958	2573659	196	196 <i>eutQ</i> - Ethanolamine utilization protein EutQ
2607052	G<->A	+	V<->I	Nonsynonymous	2605573	2607153	174	173 <i>hyfF</i> - Hydrogenase-4 component F
2630956	G<->A	-	G<->D	Nonsynonymous	2629614	2631191	214	214 <i>guaA</i> - GMP synthase [glutamine-hydrolyzing]
2645124	A<->G	-	E<->E	Synonymous	2643669	2645981	193	193 <i>pbpC</i> - Penicillin-binding protein 1C
2677153	G<->A	-	V<->I	Nonsynonymous	2677040	2678023	199	199 <i>yphF</i> - ABC transporter periplasmic-binding protein yphF
2686208	G<->A	-	A<->T	Nonsynonymous	2686125	2687459	205	205 <i>glrR</i> - Transcriptional regulatory protein GlrR
2712527	C<->T	+	P<->S	Nonsynonymous	2711552	2712886	201	201 <i>srmB</i> - ATP-dependent RNA helicase SrmB
2720188	C<->T	+	P<->L	Nonsynonymous	2718609	2721269	208	207 <i>pka</i> - Protein lysine acetyltransferase Pka
2734071	G<->A	-	M<->I	Nonsynonymous	2733687	2734667	177	177 <i>rldD</i> - Ribosomal large subunit pseudouridine synthase D
2749579	C<->T	+	C<->C	Synonymous	2749487	2750365	201	201 <i>yfjB</i> - NAD kinase
2777205	G<->A	-	G<->D	Nonsynonymous	2776802	2781382	201	201 <i>ypjA</i> - Uncharacterized outer membrane protein YpjA precursor
2820080	C<->G	-	G<->G	Synonymous	2818037	2820667	170	170 <i>alaS</i> - Alanine--tRNA ligase
2825442	G<->A	+	R<->H	Nonsynonymous	2825048	2826007	206	205 <i>sreE</i> - PTS system glucitol/sorbitol-specific EIIB component
2830412	G<->A	-	P<->P	Synonymous	2829431	2830945	198	198 <i>Anaerobic nitric oxide reductase transcription regulator NorR</i>
2852385	G<->A	+	W<->*	Premature_stop	2851910	2852920	203	203 <i>hypE</i> - Carbamoyl dehydratase HypE
2860426	C<->T	+	A<->V	Nonsynonymous	2860086	2860994	221	221 <i>ltdD</i> - L-threonate dehydrogenase
2866111	T<->C	-	*<->Q	Nonsynonymous	2865215	2866207	272	272 <i>RNA polymerase sigma factor RpoS Qualifiers:Pseudo</i>
2878492	G<->A	-	G<->G	Synonymous	2878444	2879043	236	236 <i>casE</i> - CRISPR system Cascade subunit CasE
2885753	G<->A	-	W<->*	Premature_stop	2883209	2885875	226	226 <i>ygcB</i> - CRISPR-associated endonuclease/helicase Cas3
2894674	G<->A	-	V<->M	Nonsynonymous	2894432	2895211	263	263 <i>ygcR</i> - Putative electron transfer flavoprotein subunit YgcR
2952371	G<->A	-	Q<->Q	Synonymous	2951117	2954659	219	219 <i>recB</i> - RecBCD enzyme subunit RecB
2955570	G<->A	-	Q<->Q	Synonymous	2954652	2957540	243	243 <i>ptrA</i> - Protease 3 precursor
2960104	C<->T	-	V<->V	Synonymous	2957716	2961084	234	234 <i>recC</i> - RecBCD enzyme subunit RecC
2964118	G<->A	-	V<->V	Synonymous	2963818	2964693	201	201 <i>lgt</i> - Protoprotein diacylglycerol transferase
2969176	C<->T	+	S<->F	Nonsynonymous	2969076	2969789	238	238 <i>ygdQ</i> - UDP-0053 inner membrane protein YgdQ
2972309	G<->A	-	G<->G	Synonymous	2971325	2972518	231	231 <i>lptI</i> - Lysophospholipid transporter LptI
3005140	C<->T	+	R<->C	Nonsynonymous	3004918	3006108	237	237 <i>ygeW</i> - Putative carbamoyltransferase YgeW
3007720	A<->G	+	M<->V	Nonsynonymous	3007420	3008631	215	215 <i>ygeY</i> - Uncharacterized protein YgeY
3013111	C<->T	-	N<->N	Synonymous	3012943	3013713	220	220 <i>yqeC</i> - Uncharacterized protein YqeC
3021172	C<->T	+	R<->C	Nonsynonymous	3019972	3022842	214	212 <i>A1WS_03602</i> - Selenate reductase subunit YgfN
3034334	G<->A	-	V<->M	Nonsynonymous	3033840	3034838	250	250 peptide chain release factor 2
3055384	T<->C	+	V<->A	Nonsynonymous	3054843	3055445	188	187 <i>1, 5-formyltetrahydrofolate cyclo-ligase</i>
3056063	A<->G	-	H<->R	Nonsynonymous	3055834	3057066	226	226 <i>serA</i> - Phosphoglycerate dehydrogenase
3056725	G<->A	-	E<->E	Synonymous	3055834	3057066	225	225 <i>serA</i> - Phosphoglycerate dehydrogenase
3065829	A<->G	-	M<->V	Start_nonsyn	3064933	3065829	197	196 <i>ygfI</i> - Uncharacterized HTH-type transcriptional regulator YgfI
3075082	G<->A	-	G<->D	Nonsynonymous	3074835	3076112	239	239 <i>yggP</i> - Uncharacterized protein YggP
3083267	G<->A	-	G<->D	Nonsynonymous	3082591	3084567	224	223 <i>speA</i> - Biosynthetic arginine decarboxylase
3095359	C<->T	+	T<->I	Nonsynonymous	3095337	3095930	210	209 <i>rdgB</i> - dITP/XTP pyrophosphatase
3116446	G<->A	-	T<->T	Synonymous	3113206	3117768	198	197 <i>yghJ</i> - Putative lipoprotein AcfD homolog precursor
3123063	T<->C	-	H<->H	Synonymous	3122892	3124115	231	231 <i>glcF</i> - Glycolate oxidase iron-sulfur subunit
3124976	G<->A	-	G<->E	Nonsynonymous	3124126	3125178	244	244 <i>glcE</i> - Glycolate oxidase subunit GlcE
3133017	G<->A	+	L<->L	Synonymous	3132787	3133479	200	200 <i>yghT</i> - Uncharacterized ATP-binding protein YghT
3146218	G<->A	-	V<->I	Nonsynonymous	3145512	3146275	198	198 dienelactone hydrolase Qualifiers: Pseudo
3155719	C<->T	+	R<->R	Synonymous	3155279	3156106	255	255 <i>dkgA</i> - 2,5-diketo-D-gluconic acid reductase A
3180093	C<->T	+	H<->H	Synonymous	3179077	3180237	230	230 <i>ygiC</i> - Putative acid--amine ligase YgiC
3182749	G<->A	-	G<->D	Nonsynonymous	3182469	3183122	236	234 <i>ribB</i> - 3,4-dihydroxy-2-butaneone 4-phosphate synthase
3202707	C<->A	-	S<->R	Nonsynonymous	3201966	3202787	211	210 <i>uppP</i> - Undecaprenyl-diphosphatase
3213880	G<->A	-	E<->K	Nonsynonymous	3213623	3214129	243	243 <i>mug</i> - G/U mismatch-specific DNA glycosylase
3214544	G<->A	-	A<->T	Nonsynonymous	3214383	3215147	206	204 <i>yqjH</i> - NADPH-dependent ferric-chelate reductase
3223777	C<->T	+	A<->V	Nonsynonymous	3221289	3224381	208	208 <i>ebgA</i> - Evolved beta-galactosidase subunit alpha
3297658	G<->A	-	T<->T	Synonymous	3296953	3297993	183	183 <i>yraQ</i> - UFP0718 protein YraQ
3300142	G<->A	-	V<->I	Nonsynonymous	3300110	3300613	218	218 Uncharacterized N-acetyltransferase YhbS
3301440	C<->T	+	A<->V	Nonsynonymous	3301340	3302335	211	211 <i>yhbU</i> - Uncharacterized protease YhbU precursor
3308518	G<->A	-	A<->T	Nonsynonymous	3307895	3308779	186	186 <i>nlpI</i> - Lipoprotein NlpI precursor
3327081	G<->A	-	A<->T	Nonsynonymous	3326890	3327519	194	193 <i>rlmE</i> - Ribosomal RNA large subunit methyltransferase E
3327329	G<->A	-	G<->D	Nonsynonymous	3326890	3327519	277	275 <i>rlmE</i> - Ribosomal RNA large subunit methyltransferase E
3331262	G<->A	-	L<->L	Synonymous	3330437	3331609	195	195 <i>obj</i> - GTPase Obj
3339263	G<->A	-	D<->N	Nonsynonymous	3339111	3339920	201	200 Intermembrane phospholipid transport system ATP-binding protein MlaF
3340526	C<->T	+	L<->F	Nonsynonymous	3340130	3341107	261	261 <i>yrbG</i> - Inner membrane protein YrbG
3369470	G<->A	-	A<->T	Nonsynonymous	3369330	3370205	201	201 <i>nanK</i> - N-acetylmannosamine kinase
3387896	A<->C	-	T<->P	Nonsynonymous	3386076	3388043	216	215 p-hydroxybenzoic acid efflux pump subunit AaeB
3408433	C<->T	+	F<->F	Synonymous	3407462	3408913	189	189 <i>panF</i> - Sodium/pantothenate symporter
3411949	C<->T	+	I<->L	Synonymous	3411508	3412392	196	196 <i>yhdI</i> - DNA adenine methyltransferase YhdJ
3435534	C<->T	-	S<->S	Synonymous	3435420	3436115	232	232 <i>yjaH</i> - Uncharacterized protein YjaH
3545428	G<->A	+	E<->K	Nonsynonymous	3544315	3545766	226	225 <i>frvB</i> - Fructose-like PTS system EIIBC component
3549903	C<->T	-	I<->L	Synonymous	3549832	3550665	223	223 <i>fdhD</i> - Sulfur carrier protein FdhD
3556206	G<->A	+	A<->T	Nonsynonymous	3555453	3556382	207	206 <i>fdhE</i> - Protein FdhE
3563967	C<->T	+	V<->V	Synonymous	3563110	3564006	230	228 <i>yihU</i> - 3-Sulfolactaldehyde reductase
3638274	C<->T	-	A<->V	Nonsynonymous	3636536	3638698	512	511 <i>uvrD</i> - DNA helicase
3665074	C<->T	-	I<->I	Synonymous	3664159	3665421	525	524 <i>wecC</i> - UDP-N-acetyl-D-mannosamine dehydrogenase
3665373	C<->T	-	P<->S	Nonsynonymous	3664159	3665421	593	592 <i>wecD</i> - UDP-N-acetyl-D-mannosamine dehydrogenase
3669068	C<->T	-	I<->L	Synonymous	3669005	3670264	488	488 <i>rho</i> - Transcription termination factor Rho
3677879	C<->T	-	S<->F	Nonsynonymous	3677236	3678711	548	548 <i>ilvC</i> - Ketol-acid reductoisomerase (NADP+)
3697901	G<->T	-	G<->V	Nonsynonymous	3679462	3698454	212	212 <i>rbsR</i> - Ribose operon repressor
3708128	G<->A	+	A<->T	Nonsynonymous	3707078	3708529	209	209 <i>viaA</i> - Protein ViaA
3708738	T<->C	-	H<->H	Synonymous	3708534	3709526	233	233 <i>asnA</i> - Aspartate--ammonia ligase
3709275	C<->T	-	H<->H	Synonymous	3708534	3709526	208	208 <i>asnA</i> - Aspartate--ammonia ligase
3737455	G<->A	+	W<->*	Premature_stop	3737288	3738010	263	263 Uncharacterized protein VieK
3739732	C<->T	-	S<->F	Nonsynonymous	3739242	3739907	210	210 <i>yieH</i> - 6-phosphogluconate phosphatase
3765362	G<->A	+	E<->E	Synonymous	3765255	3765944	240	239 <i>dgrO</i> - Galactonate operon transcriptional repressor
3768002	C<->T	+	L<->L	Synonymous	3767417	3768565	218	218 <i>dgoB</i> - D-galactonate dehydratase
3769336	G<->A	+	D<->N	Nonsynonymous	3768685	3769777	234	233 <i>dgoT</i> - D-galactonate transporter
3810387	C<->T	-	L<->L	Synonymous	3810079	3811470	223	223 <i>xanP</i> - Xanthine permease XanP
3819632	G<->A	+	V<->I	Nonsynonymous	3819245	3820927	254	254 <i>ligB</i> - DNA ligase B
3846193	C<->T	-	S<->F	Nonsynonymous	3845496	3846428	222	221 <i>hldD</i> - ADP-L-glycero-D-manno-heptose-6-epimerase
3857348	G<->A	+	A<->T	Nonsynonymous	3856754	3857773	260	260 <i>gpsA</i> - Glycerol-3-phosphate dehydrogenase [NAD(P)+]
3863639	C<->T	-	L<->L	Synonymous	3863388	3863750	255	253 <i>ybl</i> - Uncharacterized protein Ybl
3879961	G<->A	+	D<->N	Nonsynonymous	3879166	3880557	234	234 <i>selA</i> - L-seryl-tRNA(Sec) selenium transferase
3911121	G<->A	+	A<->A	Synonymous	3911044	3912498	254	253 <i>lyx</i> - L-xylose-3-keto-L-gulonate kinase
3921623	G<->A	+	D<->N	Nonsynonymous	3921371	3922081	292	292 <i>yafA</i> - Uncharacterized protein YafF
3944732	G<->A	+	R<->R	Synonymous	3944466	3945182	245	245 cellulose biosynthesis protein BcsQ
3946134	T<->C	+	F<->S	Nonsynonymous	3945179	3947797	257	256 Cellulose synthase catalytic subunit [UDP-forming] bcsA
3947486	G<->A	+	V<->I	Nonsynonymous	3945179	3947797	215	214 Cellulose synthase catalytic subunit [UDP-forming] bcsA
3956311	G<->A	+	A<->A	Synonymous	3954797	3956785	246	245 <i>yhjk</i> - Cyclic-di-GMP phosphodiesterase
3980100	C<->T	-	R<->C	Nonsynonymous	3980026	3981183	224	224 <i>mdtE</i> - Multidrug resistance protein mdtE

4044826 C<->T	+	S<->F	Nonsynonymous	4044012	4044938	212	212 High-affinity branched-chain amino acid transport system permease protein LivH
4096319 G<->A	+	V<->M	Nonsynonymous	4095572	4096342	248	248 bioH - Pimeloyl-[acyl-carrier protein] methyl ester esterase
4106900 C<->A	-	C<->*	Premature_stop	4105976	4107598	228	228 pckA - Phosphoenolpyruvate carboxykinase (ATP)
4127720 G<->A	+	A<->T	Nonsynonymous	4126778	4127782	237	237 trpS - Tryptophan-tRNA ligase
4134023 A<->C	+	D<->A	Nonsynonymous	4133080	4134384	232	232 yhfI - Uncharacterized protein YhfI
4153852 C<->T	-	L<->L	Synonymous	4153664	4154296	221	221 cAMP-activated global transcriptional regulator CRP
4154211 A<->C	-	K<->T	Nonsynonymous	4153664	4154296	217	217 cAMP-activated global transcriptional regulator CRP
4174425 A<->G	-	H<->R	Nonsynonymous	4174196	4174873	182	182 Type 4 prepilin-like proteins leader peptide-processing enzyme gspO
4175529 C<->T	-	P<->S	Nonsynonymous	4174873	4175334	186	185 gspM - Putative type II secretion system protein M
4185186 C<->T	+	Q<->*	Premature_stop	4185018	4186487	186	186 gspA - Export protein A for general secretion pathway
4187209 A<->G	+	T<->A	Nonsynonymous	4187146	4187457	227	226 rpsJ - 30S ribosomal protein S10
4218060 A<->T	+	Q<->L	Nonsynonymous	4217870	4218799	219	219 metAS - Homoserine O-succinyltransferase
4220395 G<->A	+	G<->D	Nonsynonymous	4219068	4220669	188	186 aceB - Malate synthase
4228142 C<->T	+	T<->I	Nonsynonymous	4227418	4231101	221	220 meth - Methionine synthase
4253829 C<->T	+	A<->V	Nonsynonymous	4253144	4254064	215	215 malM - Maltose operon periplasmic protein precursor
4323774 T<->C	-	Y<->H	Nonsynonymous	4323439	4324284	227	227 Alpha-D-ribose 1-methylphosphonate 5-phosphate C-P lyase phnI
4328795 G<->A	-	G<->E	Nonsynonymous	4328014	4329030	258	257 phnD - Phosphonates-binding periplasmic protein precursor
4330404 T<->C	-	Y<->H	Nonsynonymous	4329976	4330419	246	246 crfC - Clamp-binding protein CrfC
4393271 G<->A	-	A<->A	Synonymous	4390727	4394050	222	222 Miniconductance mechanosensitive channel MscM
4411451 C<->T	+	L<->L	Synonymous	4411334	4413775	256	254 rnr - Ribonuclease R
4412798 C<->T	+	P<->S	Nonsynonymous	4411334	4413775	205	204 rnr - Ribonuclease R
4415449 C<->T	+	I<->L	Synonymous	4415233	4415931	224	222 yjfJ - Uncharacterized protein YjfJ precursor
4426690 C<->T	+	I<->I	Synonymous	4426388	4426852	215	213 ptxA - Ascorbate-specific PTS system, EIa component
4431520 G<->A	-	A<->T	Nonsynonymous	4431308	4432102	194	193 yjfZ - Uncharacterized protein YjfZ
4431658 G<->A	-	G<->S	Nonsynonymous	4431308	4432102	187	185 yjfZ - Uncharacterized protein YjfZ
4505698 G<->A	-	V<->M	Start_nonsyn	4505468	4505698	222	221 Lipopolysaccharide export system permease protein LptF
4510917 C<->T	+	F<->F	Synonymous	4509967	4511085	232	232 yjhC - 1,5-anhydro-D-fructose reductase
4558942 C<->T	+	A<->C	Synonymous	4557581	4559041	281	280 uxuB - D-mannonate oxidoreductase
4583277 G<->A	-	P<->P	Synonymous	4582638	4584017	224	224 5-methylcytosine-specific restriction enzyme McrBC, subunit McrB
4622443 C<->T	+	D<->D	Synonymous	4622003	4622782	230	230 deoC - Deoxyribose-phosphate aldolase
4624423 T<->C	+	R<->R	Synonymous	4624283	4625506	204	204 deoB - Phosphopentomutase
4627768 C<->T	+	R<->R	Synonymous	4626449	4627780	250	249 yjjJ - Toxin YjjJ
4632715 T<->C	+	S<->P	Nonsynonymous	4631995	4633227	215	212 nadR - Trifunctional NAD biosynthesis/regulator protein NadR

## SNPs (intergenic)

reference position	ref_base<->sample_base	mutate_type	Total Depth	Mutation Depth
197926 C<->T	intergenic		203	203
296550 C<->T	intergenic		237	237
582068 C<->T	intergenic		223	223
880916 C<->T	intergenic		196	196
1006361 A<->G	intergenic		183	181
1092779 T<->C	intergenic		171	171
1401247 G<->A	intergenic		176	173
2092069 T<->C	intergenic		156	156
2141860 G<->A	intergenic		216	215
2708958 C<->T	intergenic		195	195
2816944 C<->T	intergenic		118	118
2816953 A<->T	intergenic		135	134
2816959 T<->A	intergenic		144	142
2816980 G<->A	intergenic		184	184
2855617 C<->T	intergenic		194	194
2941871 C<->T	intergenic		210	210
2943644 A<->G	intergenic		200	200
2985962 C<->T	intergenic		189	189
3006110 C<->T	intergenic		223	223
3275045 C<->T	intergenic		217	217
3464900 T<->C	intergenic		285	284
3566228 G<->A	intergenic		199	199
3689634 G<->A	intergenic		497	495
3929803 A<->G	intergenic		203	202
3932435 C<->T	intergenic		258	258
3932468 C<->T	intergenic		262	262
3975735 G<->A	intergenic		229	229
4161616 G<->A	intergenic		206	206
4189879 G<->A	intergenic		201	200
4227228 T<->C	intergenic		228	228
4297744 A<->G	intergenic		214	213
4342921 C<->T	intergenic		241	239
4514918 T<->C	intergenic		204	204

## insertion/deletion mutations

reference position start	reference position end	mutation type	Depth	gene name
4399749	4399750	G Deletion	188	
4428525	4428526	C Deletion	200	nrrE - Bifunctional NAD(P)H-hydrate repair enzyme
2175523	2175523	CGGAT Insertion	155	ulaF - L-ribulose-5-phosphate 4-epimerase UlaF
723943	723944	T Deletion	156	gatC - PTS system galactitol-specific EIIC component
				kdpD - Sensor protein KdpD

## insertion/deletion mutations (intergenic)

379293 380066 G Deletion 230

## SNPs in NC-7/34

Reference: W3110 genome (NC\_007779.1)

Red color: mutations that NC-7 does not have

Table S3

reference position	ref_base<->sample_base	gene direction	aa_mutation	mutate_type	gene_pos_start	gene_pos_end	Total Depth	Mutation Depth	gene name
2927	A<->G	+	T<->A	Nonsynonymous	2801	3733	269	269	thrB - Homoserine kinase
15136	C<->T	+	C<->C	Synonymous	14169	15298	259	258	dnaJ - Chaperone protein DnaJ
21550	A<->G	+	I<->L	Nonsynonymous	21407	22348	268	268	rfb - Bifunctional riboflavin kinase/FMN adenyltransferase
31866	G<->A	+	I<->P	Nonsynonymous	30817	34038	268	268	carB - Carbamoyl-phosphate synthase large chain
33956	G<->A	+	G<->D	Nonsynonymous	30817	34038	301	299	carB - Carbamoyl-phosphate synthase large chain
61618	G<->A	-	W<->*	Premature_stop	60358	63264	263	262	rpaA - RNA polymerase-associated protein RpaP
78795	T<->C	+	V<->A	Nonsynonymous	77621	78799	240	240	setA - Sugar efflux transporter A
97378	C<->T	+	I<->L	Nonsynonymous	97087	98403	285	284	mrdN - UDP-N-acetylglucosamine--D-glutamate ligase
100541	G<->C	+	A<->Y	Nonsynonymous	99644	100711	233	233	mung - UDP-N-acetylglucosamine-N-acetylglucosaminide pyrophosphoryl-undecaprenol N-acetylglucosamine transferase
105062	C<->T	+	C<->S	Nonsynonymous	103982	105244	266	266	ftsA - Cell division protein FtsA
111392	C<->T	+	F<->S	Nonsynonymous	111044	111433	275	273	mutT - 8-oxo-dGTP diphosphatase
132188	C<->T	+	F<->S	Nonsynonymous	131615	134212	306	304	acnB - Aconitase hydratase B
132526	C<->T	+	G<->G	Synonymous	131615	134212	279	276	acnB - Aconitase hydratase B
134941	T<->C	-	H<->K	Nonsynonymous	134788	135582	249	249	speD - S-adenosylmethionine decarboxylase proenzyme
137392	G<->A	+	G<->R	Nonsynonymous	137083	138633	289	288	cueO - Multicopper oxidase (Laccase)
150554	G<->A	-	V<->I	Nonsynonymous	149715	150953	242	241	yadC - Putative fimbrial-like adhesin protein
168300	G<->C	+	E<->K	Nonsynonymous	167484	169727	255	255	fhuA - Ferrichrome-iron receptor FhuA
181508	T<->C	+	S<->P	Nonsynonymous	180884	182308	294	294	degP - Periplasmic serine endopeptidase DegP precursor
184465	A<->G	-	E<->E	Synonymous	184257	185069	260	260	yael - Phosphodiesterase Yael
190123	G<->A	+	A<->T	Nonsynonymous	198974	190599	265	265	psbS - 30S ribosomal protein S2
192429	T<->C	+	V<->A	Nonsynonymous	191855	192580	308	308	pyrH - Uridylate kinase
198729	C<->T	+	I<->P	Nonsynonymous	197928	200360	261	261	bamA - Outer membrane protein assembly factor BamA
199515	G<->C	+	G<->S	Nonsynonymous	197928	200360	271	270	bamA - Outer membrane protein assembly factor BamA
199536	T<->C	+	S<->P	Nonsynonymous	197928	200360	267	266	bamA - Outer membrane protein assembly factor BamA
203991	C<->T	+	T<->M	Nonsynonymous	203348	204496	294	292	lpbX - Lipid A-disaccharide synthase
212759	C<->T	+	V<->V	Synonymous	212331	213629	286	286	tisS - tRNA(Ile)-lysine synthase
234048	G<->C	-	F<->K	Synonymous	234027	234782	280	279	globB - Hydroxycyclutathione hydrolase GlobB
235748	G<->A	-	W<->*	Premature_stop	235535	236002	263	263	rnhA - Ribonuclease H
241768	A<->G	-	G<->G	Synonymous	240859	243303	279	277	fadE - Acyl-CoA dehydrogenase
246249	G<->A	-	G<->E	Nonsynonymous	246242	246502	267	267	dirD - Antitoxin DinJ
252983	T<->C	+	V<->A	Nonsynonymous	252709	253161	298	298	yafP - Uncharacterized N-acetyltransferase YafP
253836	G<->A	+	R<->K	Synonymous	253666	254202	276	276	peptide chain release factor H
256834	C<->T	+	T<->I	Nonsynonymous	256527	257771	241	241	frsA - FtsR-like protein
271981	G<->A	-	G<->E	Nonsynonymous	271692	272117	292	291	hypothetical protein
273150	C<->T	+	M<->N	Synonymous	272071	273216	178	178	hypothetical protein
287359	T<->G	+	A<->A	Nonsynonymous	284245	284392	268	268	yagF - D-yxylate dehydratase YagF
287900	A<->G	-	T<->A	Nonsynonymous	287628	288386	293	293	yagI - Uncharacterized HTH-type transcriptional regulator YagI
337962	G<->A	+	A<->A	Synonymous	337549	338967	284	283	yahG - Uncharacterized protein YahG
338492	G<->A	+	G<->D	Nonsynonymous	337549	338967	292	288	yahG - Uncharacterized protein YahG
340335	C<->T	+	T<->M	Nonsynonymous	339389	340239	340	340	yahI - Carbamate kinase-like protein YahI
346855	G<->A	-	Q<->Y	Synonymous	346081	347667	238	238	prkP - Propionate catabolism operon regulatory protein
351061	T<->C	+	I<->P	Nonsynonymous	350439	351890	292	291	prpD - 2-methylcitrate dehydratase
364450	G<->C	-	D<->N	Nonsynonymous	362455	365529	254	254	lacZ - Beta-galactosidase
372497	A<->G	+	E<->G	Nonsynonymous	372145	373095	294	294	mhfp - Acetaldehyde dehydrogenase
398307	G<->C	-	G<->D	Nonsynonymous	398249	398557	236	235	yaiV - Inner membrane protein YaiV
403872	C<->T	+	I<->L	Synonymous	402927	404042	249	247	ggcC - Probable diguanylate cyclase DgcC
438249	T<->C	-	Y<->H	Nonsynonymous	437559	439401	250	250	obsX - 1-deoxy-D-xylulose-5-phosphate synthase
438644	C<->T	-	E<->G	Nonsynonymous	437559	439401	272	271	obsX - 1-deoxy-D-xylulose-5-phosphate synthase
449023	C<->T	-	A<->K	Synonymous	447874	449865	241	241	cyoB - Cytochrome C ubiquinol oxidase subunit I
450121	G<->C	-	A<->A	Synonymous	449887	450834	297	297	HMPEF1608_04599 - Ubiquinol oxidase subunit 2
451523	T<->C	-	I<->T	Nonsynonymous	451294	452769	266	266	ampG - Protein AmpG
457454	C<->T	+	T<->I	Nonsynonymous	454357	456555	258	258	tigF - Trigger factor
460180	C<->T	+	S<->P	Nonsynonymous	458112	460466	217	217	lon - Lon protease
473993	T<->C	-	P<->F	Synonymous	473525	474385	253	253	tesB - Acyl-CoA thioesterase II
493792	G<->A	+	G<->D	Nonsynonymous	493629	494234	276	275	recF - Recombination protein RecF
534446	C<->T	+	P<->L	Nonsynonymous	533140	534921	225	225	gcl - Glycylate carboligase
542970	T<->C	-	F<->I	Nonsynonymous	542485	543270	241	240	alleE - (S)-ureidoglycine amidohydrolase
547694	A<->G	+	E<->E	Synonymous	547581	547841	290	290	hypothetical protein
575425	C<->T	-	I<->I	Synonymous	574981	576048	235	233	poinP - OmpC
586865	C<->T	-	A<->Y	Nonsynonymous	587205	590177	291	290	bacteriophage N4 adsorption protein A
723991	C<->T	-	H<->H	Synonymous	721252	724836	256	255	HMPEF1620_04415 - Histidine kinase KdpD
832354	A<->G	+	K<->R	Nonsynonymous	831294	832658	261	261	rhiE - ATP-dependent RNA helicase RhiE
845812	G<->A	-	D<->R	Nonsynonymous	843677	845902	246	245	MscS Mechanosensitive ion channel
882901	G<->C	-	A<->Y	Nonsynonymous	882398	883156	243	243	deobR - Deoxyribose operon repressor
932433	T<->C	-	S<->Y	Nonsynonymous	931507	932472	281	281	trxB - Thioredoxin reductase
946646	G<->A	+	N<->A	Synonymous	946293	947441	267	266	ycaB - Uncharacterized MFS-type transporter YcaB
963494	A<->C	-	T<->C	Nonsynonymous	962417	964090	270	269	pspA - 30S ribosomal protein S1
963678	A<->G	-	Q<->R	Nonsynonymous	962417	964090	288	288	pspA - 30S ribosomal protein S1
973612	C<->A	-	P<->Q	Nonsynonymous	973044	973823	265	264	elyC - Envelope biogenesis factor ElyC
977944	T<->C	-	I<->L	Synonymous	976748	981208	265	265	mkbB - Chromosome partition protein MkbB
993869	G<->A	-	N<->D	Nonsynonymous	993699	994466	228	228	slubB - Aliphatic sulfonates import ATP-binding protein SsluB
1008500	A<->G	+	V<->Y	Nonsynonymous	1008266	1010374	225	225	rmlB - Ribosomal RNA large subunit methyltransferase RmlB
1067792	T<->C	-	I<->L	Synonymous	1067534	1068130	269	268	EC5598_1114 - NAD(P)H dehydrogenase (quinone)
1093686	T<->C	+	V<->A	Nonsynonymous	1093298	1094656	238	238	GGEDEF domain-containing protein
1109401	C<->A	-	M<->Q	Nonsynonymous	1109361	1110518	256	256	mglc - Glucans biosynthesis protein C
1112445	T<->C	+	*<->Stop_nonsyn	Premature_stop	1110912	1112447	245	244	mdgG - Glucans biosynthesis protein G precursor
1112445	T<->C	+	M<->R	Synonymous	1112440	1114983	245	244	mdgH - Glucans biosynthesis glucosyltransferase H
1171413	T<->C	-	I<->P	Nonsynonymous	1170899	1171951	227	227	lysM - Peptidoglycan-binding domain-containing protein LysM
1191557	T<->C	-	T<->P	Nonsynonymous	1191353	1192024	240	239	phoP - Transcriptional regulatory protein PhoP
1195272	C<->T	-	Q<->*	Premature_stop	1194244	1195350	252	251	mmmA - tRNA-specific 2-thiouridylase MmM
1234562	C<->T	-	I<->G	Synonymous	1234077	1234607	237	236	bbdB - Disulfide bond formation protein BbdB
1283734	A<->G	+	K<->R	Nonsynonymous	1281441	1285184	234	233	narZ - Nitrate reductase, alpha subunit
1303706	A<->C	+	M<->Y	Nonsynonymous	1302896	1304527	229	229	oppA - Oligopeptide ABC transporter substrate-binding protein OppA
1308450	T<->G	+	S<->C	Nonsynonymous	1307487	1308482	203	203	oppP - Oligopeptide transport ATP-binding protein OppP
1327427	A<->G	+	Q<->R	Nonsynonymous	1326460	1328355	210	210	YcfQ - Uncharacterized protein YcfQ
1342851	G<->A	+	D<->K	Nonsynonymous	1342272	1343441	196	195	ycIM - Lipopolysaccharide assembly protein YcIM
1352278	T<->C	-	M<->T	Nonsynonymous	1351965	1352753	285	285	fabI - Enoyl-[acyl-carrier-protein] reductase [NADH] FabI
1360097	C<->T	-	R<->C	Nonsynonymous	1359516	1360901	216	216	puuP - Putrescine Importer PuuP
1360573	A<->G	-	Y<->C	Nonsynonymous	1359516	1360901	226	226	puuP - Putrescine Importer PuuP
1381065	T<->C	+	Y<->K	Nonsynonymous	1379598	1381865	253	252	ycfT - Uncharacterized glycosyl hydrolase YcfT
1394948	A<->C	+	H<->R	Nonsynonymous	1394941	1396554	263	263	mppA - Periplasmic murein peptide-binding protein precursor
1395099	P<->C	+	A<->A	Synonymous	1394941	1396554	263	263	mppA - Periplasmic murein peptide-binding protein precursor
1401237	A<->C	-	X<->L	Nonsynonymous	1400488	1401240	263	262	fnr - Fumarate and nitrate reduction regulatory protein
1671278	A<->G	-	Y<->C	Nonsynonymous	1670424	1671306	269	268	YnfL - Uncharacterized HTH-type transcriptional regulator YnfL
1727618	A<->G	-	E<->G	Nonsynonymous	1727395	1727634	246	246	YdhL - Uncharacterized protein YdhL
1746084	A<->G	+	Q<->Y	Nonsynonymous	1745711	1746544	247	247	mdtK - Multidrug resistance protein MdtK
1795437	T<->C	-	R<->G	Synonymous	1795272	1795823	247	247	btuE - Thioredoxin/glutathione peroxidase BtuE
1799022	T<->C	-	C<->R	Nonsynonymous	1797271	1799658	270	267	phfT - Phenylalanine -tRNA ligase beta subunit
1842973	G<->A	-	G<->S	Nonsynonymous	1842497	1843117	308	306	wifL - Predicted phosphatidyl transferase, inner membrane protein
1921492	C<->T	+	S<->P	Nonsynonymous	1920427	1924683	230	230	pphA - Serine/threonine-protein phosphatase 1
2035304	G<->C	-	E<->K	Nonsynonymous	2035077	2035256	242	242	edd - Phosphogluconate dehydratase
2117087	T<->C	-	M<->P	Nonsynonymous	2116639	2118033	270	270	wcmA - Colanic acid biosynthesis protein WcmA precursor
2129694	C<-								

2389995	A<->G	-	Y<->C	NonSynonymous	2388665	2390392	271	271	yfbK - Uncharacterized protein YfbK
2396554	A<->G	-	A<->A	NonSynonymous	2396182	2397711	294	294	nuoM - NADH-quinone oxidoreductase subunit M
2400347	C<->T	-	I<->F	NonSynonymous	2400012	2400566	270	270	nuoL - NADHubiquinone oxidoreductase, membrane subunit J
2406205	T<->C	-	T<->T	NonSynonymous	2404888	2406225	253	253	nuoE - NADH-quinone oxidoreductase subunit F
2407444	T<->C	-	W<->R	NonSynonymous	2406725	2408515	260	260	nuoC - NADH-quinone oxidoreductase subunit C/D
2432695	A<->G	-	I<->L	NonSynonymous	2432455	2433237	273	273	argT - Lysine-arginine-ornithine-binding periplasmic protein
2433637	A<->G	-	M<->V	NonSynonymous	2433503	2434072	219	219	ubx - Flavin prenyltransferase UbX
2435840	A<->G	-	T<->A	NonSynonymous	2435721	2436209	244	244	cypA - Colicin V production protein
2441303	T<->C	-	P<->L	NonSynonymous	2441082	2442095	289	289	usg - USG-1 protein
2443392	G<->A	+	G<->G	NonSynonymous	2443396	2444391	277	277	fliK - Flagellar regulator fliK
2513309	T<->C	-	V<->A	NonSynonymous	2512093	2513340	259	259	yfd - Uncharacterized MFS-type transporter Yfd
2546998	T<->C	-	V<->A	NonSynonymous	2546250	2547125	267	267	Sulfate transport system permease protein CysW
2573245	G<->A	-	E<->E	NonSynonymous	2572958	2573659	281	281	eutQ - Ethanolamine utilization protein EutQ
2603511	C<->T	+	G<->G	NonSynonymous	2603467	2604906	269	269	hydF - Hydrogenase-4 component D
2607052	G<->C	+	V<->I	NonSynonymous	2605573	2607153	266	266	hydF - Hydrogenase-4 component F
2630956	G<->C	-	G<->G	NonSynonymous	2629614	2631191	242	242	guA - GMP synthase [glutamine-hydrolyzing]
2645124	A<->G	-	E<->E	NonSynonymous	2643669	2645981	246	246	ppcB - Penicillin-binding protein 1C
2649982	T<->C	+	V<->A	NonSynonymous	2645982	2650943	236	236	yfhl - Uncharacterized lipoprotein Yfhl precursor
2655895	C<->T	-	A<->V	NonSynonymous	2655741	2657591	305	305	hsca - Chaperone protein HscA
2671153	G<->C	-	V<->I	NonSynonymous	2677040	2678023	241	241	yphF - ABC transporter periplasmic-binding protein YphF
2683546	C<->T	-	G<->G	NonSynonymous	2682910	2684163	258	256	glyA - Serine hydroxymethyltransferase
2686208	G<->C	-	A<->G	NonSynonymous	2686125	2687459	269	268	grfR - Transcriptional regulatory protein GrfR
2688453	C<->T	-	S<->S	NonSynonymous	2688327	2689754	251	249	grkR - Sensor histidine kinase GrkR
2712527	C<->T	+	P<->S	NonSynonymous	2711552	2712886	272	273	srmB - ATP-dependent RNA helicase SrmB
2715811	T<->C	+	H<->H	NonSynonymous	2715140	2716099	271	271	ung - Uracil-DNA glycosylase
2716872	G<->A	-	A<->T	NonSynonymous	2716147	2717184	271	270	yifF - Hypothetical RNA/RNA methyltransferase yifF
2720188	C<->T	+	P<->I	NonSynonymous	2718069	2721269	287	286	pka - Protein lysine acetyltransferase Pka
2734071	G<->A	-	M<->I	NonSynonymous	2733687	2734667	265	264	rflD - Ribosomal large subunit pseudouridine synthase D
2749579	C<->T	+	C<->C	NonSynonymous	2749487	2750365	247	247	yfbJ - NAD kinase
2757391	A<->G	+	N<->S	NonSynonymous	2757300	2757512	290	290	alpA - DNA-binding transcriptional activator AlpA
2777205	G<->C	-	G<->D	NonSynonymous	2776802	2781382	237	236	ypjA - Uncharacterized outer membrane protein YpjA precursor
2811738	T<->C	+	X<->N	NonSynonymous	2811272	2812810	263	262	embB - Multidrug export protein EmbB
2820080	C<->G	-	G<->G	NonSynonymous	2818037	2820667	234	234	al5 - Alanine--RNA ligase
2830412	G<->A	-	P<->P	NonSynonymous	2829431	2830945	323	323	Anaerobic nitric oxide reductase transcription regulator NorR
2852385	G<->C	+	W<->*	Premature_stop	2851910	2852920	274	274	hypE - Carbamoyl dehydratase HypE
2860426	C<->T	+	A<->V	NonSynonymous	2860086	2860994	312	312	ltnD - L-threonate dehydrogenase
2866111	T<->C	-	*<->Q	NonSynonymous	2865215	2866207	302	302	RNA polymerase sigma factor RpoS Qualifiers:Pseudo
2866662	A<->G	-	S<->G	NonSynonymous	2866270	2867409	297	297	nlpD - Outer membrane lipoprotein
2869181	A<->G	-	P<->P	NonSynonymous	2868911	2869690	272	272	trdU - RNA pseudouridine synthase D
2878492	G<->A	-	G<->G	NonSynonymous	2878444	2879043	273	273	casE - CRISPR system Cascade subunit CasE
2885753	G<->C	-	W<->*	Premature_stop	2883209	2885875	258	258	ygbC - CRISPR-associated endonuclease/helicase Cas3
2894674	G<->C	-	V<->M	NonSynonymous	2894432	2895211	346	345	ygrC - Putative electron transfer flavoprotein subunit YgrC
2952371	G<->T	-	Q<->Q	NonSynonymous	2951117	2954659	266	266	recB - RecBCD enzyme subunit RecB
2955708	G<->C	-	Q<->Q	NonSynonymous	2954652	2957540	283	282	ptrA - Protease 3 precursor
2964118	G<->C	-	V<->V	NonSynonymous	2963818	2964693	253	253	lgt - Prolipoprotein diacylglycerol transferase
2966847	G<->A	-	J<->A	NonSynonymous	2964844	2967090	298	297	Phosphoenolpyruvate-protein phosphotransferase ptsP
2969176	C<->T	+	S<->F	NonSynonymous	2969076	2969789	267	267	yqdQ - UPP0053 inner membrane protein YqdQ
2972309	G<->C	-	G<->H	NonSynonymous	2971325	2972518	276	276	lptB - Lysophospholipid transporter LptB
3021172	C<->T	+	P<->C	NonSynonymous	3019972	3022842	294	294	A1W5_03602 - Selenate reductase subunit YgfN
3034334	G<->C	-	V<->M	NonSynonymous	3033840	3034838	302	301	pepC - Peptide chain release factor 2
3050670	A<->G	-	S<->G	NonSynonymous	3049771	3050973	320	320	3'-Octaprenylophenol hydroxylase ubil
3056063	A<->G	-	H<->R	NonSynonymous	3055834	3057066	289	288	serA - Phosphoglycerate dehydrogenase
3056725	G<->C	-	E<->E	NonSynonymous	3055834	3057066	238	238	serB - Phosphoglycerate dehydrogenase
3075082	G<->A	-	G<->D	NonSynonymous	3074835	3076112	286	286	yggP - Uncharacterized protein YggP
3082627	G<->C	-	G<->D	NonSynonymous	3082591	3084567	286	286	spqA - Biosynthetic arginine decarboxylase
3095359	C<->T	+	T<->I	NonSynonymous	3095337	3095930	286	286	rdgB - dITP/dTTP pyrophosphatase
3116446	G<->C	-	Z<->P	NonSynonymous	3113206	3117668	284	284	yghI - Putative lipoprotein Afcd homolog precursor
3123063	T<->C	-	H<->E	NonSynonymous	3122892	3124115	300	300	glcF - Glycolate oxidase iron-sulfur subunit
3124976	G<->C	-	E<->E	NonSynonymous	3124126	3125178	293	293	glcE - Glycolate oxidase subunit GlcE
3140476	T<->C	-	G<->G	NonSynonymous	3131924	3141645	313	313	hybC - Probable large subunit, hydrogenase-2
3142618	G<->C	-	V<->Y	NonSynonymous	3145512	3146275	294	294	dielactone hydrolase Qualifiers: Pseudo
3155719	C<->T	+	H<->R	NonSynonymous	3152579	3156106	338	338	dkgA - 2,5-diketo-D-gluconic acid reductase A
3180093	C<->T	+	H<->H	NonSynonymous	3179077	3180237	286	286	yglC - Putative acid-amino ligase YglC
3182749	G<->C	-	G<->D	NonSynonymous	3182469	3183122	247	246	nfbB - 3,4-dihydroxy-2-butane 4-phosphate synthase
3181800	T<->C	+	V<->A	NonSynonymous	3186056	3186851	276	276	yqlG - Putative outer membrane usher protein YqlG precursor
3202707	C<->T	-	S<->R	NonSynonymous	3201966	3202787	290	289	uppB - Undecaprenyl-diphosphatase
3213880	G<->C	-	E<->K	NonSynonymous	3213623	3214219	292	290	mug - G/U mismatch-specific DNA glycosylase
3214544	G<->C	-	A<->T	NonSynonymous	3214216	3215147	291	291	yjhI - NADPH-dependent ferric-chelate reductase
3223777	C<->T	+	A<->V	NonSynonymous	3221289	3224381	279	279	ebgA - Evolved beta-galactosidase subunit alpha
3297658	G<->C	-	T<->T	NonSynonymous	3296953	3297993	273	273	yraQ - UPF0718 protein YraQ
3301042	G<->C	-	V<->I	NonSynonymous	3300110	3300613	306	306	Uncharacterized N-acetyltransferase Yhbs
3301440	C<->T	+	A<->V	NonSynonymous	3301340	3302335	250	250	yhbl - Uncharacterized protease Yhbl precursor
3308518	G<->C	-	A<->P	NonSynonymous	3307895	3308779	258	257	nlpI - Lipoprotein NlpI precursor
3315263	G<->A	-	A<->T	NonSynonymous	3313197	3315869	291	291	infB - Translation initiation factor IF-2
3316033	C<->T	-	A<->V	NonSynonymous	3315894	3317381	270	269	nusA - Transcription termination/antitermination protein NusA
3327081	G<->C	-	A<->V	NonSynonymous	3326890	3327519	289	288	rmlE - Ribosomal RNA large subunit methyltransferase E
3327329	G<->C	-	G<->D	NonSynonymous	3326890	3327519	312	311	rmlE - Ribosomal RNA large subunit methyltransferase
3331262	G<->A	-	I<->L	NonSynonymous	3330437	3331609	254	253	obgB - GTPase Obg
3334249	A<->G	+	D<->K	NonSynonymous	3333565	3334536	241	241	ispB - Octaprenyl diphosphate synthase
3339263	G<->C	-	D<->K	NonSynonymous	3339111	3339290	266	265	Intermembrane phospholipid transport system ATP-binding protein MiaF
3340526	C<->T	+	I<->F	NonSynonymous	3340130	3341107	323	323	yrbG - Inner membrane protein YrbG
3343985	G<->A	+	D<->N	NonSynonymous	3343799	3344524	282	281	abcR - ABC transporter ATP-binding protein
3367484	T<->C	+	V<->A	NonSynonymous	3367678	3367697	248	248	yhfC - Uncharacterized protein YhfC precursor
3369470	G<->C	-	A<->T	NonSynonymous	3369330	3370205	288	288	hank - N-acetylmannosamine kinase
3387896	A<->C	-	T<->>	NonSynonymous	3386076	3388043	266	266	p-hydroxybenzoic acid efflux pump subunit AaeB
3408433	C<->T	+	F<->F	NonSynonymous	3407462	3408913	236	235	panF - Sodium/pantothenate symporter
3411949	C<->T	+	I<->K	NonSynonymous	3411508	3412392	271	271	yhdI - DNA adenine methylation transferase YhdI
3420551	C<->T	+	A<->Y	NonSynonymous	3419989	3421170	261	261	Putative amino-acid ABC transporter permease protein Yhdx
3435534	T<->C	-	S<->K	NonSynonymous	3435420	3436115	285	285	yjhI - Uncharacterized protein YjhI
3454994	A<->G	-	Q<->R	NonSynonymous	3454520	3455436	293	291	rhoB - DNA-directed RNA polymerase subunit beta
3493366	A<->G	-	E<->E	NonSynonymous	3493072	3494151	274	274	frwC - Fructose-like permease IIC component 2
3523688	T<->C	+	S<->S	NonSynonymous	3523415	3523714	290	289	yisA - UPF0381 protein YisA
3536348	T<->C	+	Y<->R	NonSynonymous	3536156	3537190	269	269	ratB - Ratmannose-proton symporter
3545428	G<->C	+	E<->K	NonSynonymous	3545435	3545766	281	281	fryB - Fructose-like PTS system EIIBC component
3549903	C<->T	-	I<->L	NonSynonymous	3549832	3550665	272	272	fdhD - Sulfur carrier protein FdhD
3552981	A<->C	+	N<->D	NonSynonymous	3551945	3553909	302	302	AI17_013680 - Formate dehydrogenase-N subunit alpha - UniProt
3556206	G<->A	-	A<->P	NonSynonymous	3555453	3556382	266	264	fhdE - Protein FhdE
3561840	A<->G	-	H<->K	NonSynonymous	3561227	3562012	277	277	Escherichia coli D-DeoR family transcriptional regulator
3624880	T<->C	-	V<->V	NonSynonymous	3624706	3625605	248	247	bipB - Biotin transporter
3630274	C<->T	-	A<->V	NonSynonymous	3636536	3636989	278	277	wvdD - DNA helicase
3665074	C<->T	-	I<->I	NonSynonymous	3664159	3665421	238	237	wecc - UDP-N-acetyl-D-mannosamine dehydrogenase
3669068	C<->T	-	I<->L	NonSynonymous	3669005	3670264	237	237</	

3946134 T<->C	+	F<->S	Nonsynonymous	3945179	3947797	296	296 Cellulose synthase catalytic subunit [UDP-forming] bcsA
3947486 GC->A	+	V<->I	Nonsynonymous	3945179	3947797	289	289 Cellulose synthase catalytic subunit [UDP-forming] bcsA
3956311 GC->A	+	A<->A	Synonymous	3954797	3956785	291	291 yjjk - Cyclic-di-GMP phosphodiesterase
<b>3959538 C&lt;-&gt;T</b>	<b>+</b>	<b>A&lt;-&gt;V</b>	<b>Nonsynonymous</b>	<b>3958475</b>	<b>3959971</b>	<b>340</b>	<b>340 ECVG_03971 - Protein Yjjl</b>
3980100 C<->T	-	R<->C	Nonsynonymous	3980026	3981183	289	288 mdte - Multidrug resistance protein mdte
<b>3997881 C&lt;-&gt;T</b>	<b>+</b>	<b>K&lt;-&gt;V</b>	<b>Nonsynonymous</b>	<b>3997283</b>	<b>3998035</b>	<b>295</b>	<b>294 rsmi - Ribosomal RNA small subunit methyltransferase J</b>
<b>4008613 T&lt;-&gt;C</b>	<b>+</b>	<b>S&lt;-&gt;V</b>	<b>Synonymous</b>	<b>4007825</b>	<b>4009447</b>	<b>267</b>	<b>267 yjjl - Uncharacterized protein Yjjl</b>
4044826 C<->T	+	S<->P	Nonsynonymous	4044012	4044938	274	274 High-affinity branched-chain amino acid transport system permease protein LivH
4096319 GC->A	+	V<->M	Nonsynonymous	4095572	4096342	247	247 bioH - Pimelyl-[acyl-carrier protein] methyl ester esterase
4106900 C<->T	-	C<->A	Premature_stop	4105976	4107598	285	284 pckA - Phosphoenolpyruvate carboxykinase (ATP)
4127720 GC->A	+	A<->R	Nonsynonymous	4126778	4127782	312	312 trpD - Tryptophan tRNA ligase
4134023 A<->C	+	D<->A	Nonsynonymous	4133080	4134384	265	265 yjff - Uncharacterized protein Yjff
<b>4142794 T&lt;-&gt;C</b>	<b>-</b>	<b>I&lt;-&gt;P</b>	<b>Nonsynonymous</b>	<b>4142607</b>	<b>4143413</b>	<b>299</b>	<b>297 nric - Nitrate transporter Nric</b>
4152052 C<->T	-	I<->L	Synonymous	4153664	4154296	267	267 cAMP-activated global transcriptional regulator CRP
4154211 A<->C	-	K<->T	Nonsynonymous	4153664	4154296	269	269 cAMP-activated global transcriptional regulator CRP
4174425 A<->G	-	H<->R	Nonsynonymous	4174196	4174673	237	237 Type 4 prepilin-like proteins leader peptide-processing enzyme gspO
4175229 C<->T	-	P<->S	Nonsynonymous	4174873	4175334	291	291 gspM - Putative type II secretion system protein M
4185166 C<->T	+	Q<->E	Premature_stop	4185018	4186487	240	238 gspA - Export protein A for general secretion pathway
4187209 A<->G	+	T<->A	Nonsynonymous	4187146	4187457	324	324 gspJ - 30S ribosomal protein S10
<b>4203298 A&lt;-&gt;C</b>	<b>-</b>	<b>T&lt;-&gt;P</b>	<b>Nonsynonymous</b>	<b>4202522</b>	<b>4203898</b>	<b>266</b>	<b>285 trkA - Trk system potassium uptake protein TrkA</b>
4218060 A<->T	+	Q<->K	Nonsynonymous	4217870	4218799	284	284 metAS - Homoserine O-succinyltransferase
4228142 C<->T	+	I<->L	Nonsynonymous	4227418	4231101	253	253 metH - Methionine synthase
<b>4228511 T&lt;-&gt;C</b>	<b>+</b>	<b>V&lt;-&gt;A</b>	<b>Nonsynonymous</b>	<b>4227418</b>	<b>4231101</b>	<b>280</b>	<b>280 metH - Methionine synthase</b>
4253829 C<->T	+	A<->Y	Nonsynonymous	4253144	4254064	254	253 malM - Maltoose operon periplasmic protein precursor
4323774 T<->C	-	Y<->B	Nonsynonymous	4323439	4324284	297	297 Alpha-D-bose operon periplasmic protein 5-phosphate C-P lyase phnJ
4328795 GC->A	-	G<->E	Nonsynonymous	4328014	4329030	334	334 phnD - Phosphates-binding periplasmic protein precursor
<b>4333081 G&lt;-&gt;A</b>	<b>+</b>	<b>A&lt;-&gt;E</b>	<b>Synonymous</b>	<b>4331813</b>	<b>4334041</b>	<b>324</b>	<b>324 crfC - Clamp-binding protein CrfC</b>
4393271 GC->A	-	A<->S	Synonymous	4390727	4394050	328	328 Miniconductance mechanosensitive channel MscM
<b>4411432 A&lt;-&gt;G</b>	<b>+</b>	<b>K&lt;-&gt;K</b>	<b>Synonymous</b>	<b>4411334</b>	<b>4413775</b>	<b>294</b>	<b>294 mr - Ribonuclease R</b>
4411451 C<->T	+	I<->L	Synonymous	4411334	4413775	304	304 mr - Ribonuclease R
4412798 C<->T	+	P<->S	Nonsynonymous	4411334	4413775	279	278 mr - Ribonuclease R
4415149 GC->T	+	I<->L	Synonymous	4415233	4415931	328	328 yjff - Uncharacterized protein Yjff precursor
4426690 C<->T	+	X<->I	Synonymous	4426388	4426852	277	277 ptxA - Ascorbate-specific PTS system, EIa component
<b>4491780 C&lt;-&gt;T</b>	<b>+</b>	<b>R&lt;-&gt;P</b>	<b>Nonsynonymous</b>	<b>4490998</b>	<b>4491998</b>	<b>297</b>	<b>297 Lipopolysaccharide export system permease protein LptF</b>
4505698 GC->A	-	V<->M	Start_nonsyn	4505468	4505698	283	282 Lipopolysaccharide export system permease protein LptF
4510917 C<->T	+	F<->P	Synonymous	4509967	4511085	240	239 yjfc - 1,5-anhydro-D-fructose reductase
<b>4563196 C&lt;-&gt;T</b>	<b>-</b>	<b>A&lt;-&gt;A</b>	<b>Synonymous</b>	<b>4563034</b>	<b>4564206</b>	<b>328</b>	<b>328 luda - Isopasanyl dipeptidase</b>
<b>4565975 A&lt;-&gt;C</b>	<b>+</b>	<b>A&lt;-&gt;A</b>	<b>Synonymous</b>	<b>4565610</b>	<b>4566164</b>	<b>309</b>	<b>309 kptA - RNA 2'-phosphotransferase</b>
4583277 G<->A	-	P<->P	Synonymous	4582638	4584017	289	289 5-methylcytosine-specific restriction enzyme McrBC, subunit McrB
4622443 C<->T	+	D<->D	Synonymous	4622003	4622782	263	263 deoC - Deoxyribose-phosphate aldolase
4627768 C<->T	+	R<->R	Synonymous	4626449	4627780	319	318 yjjj - Toxin Yjjj

## SNPs (intergenic)

reference position	ref_base<>sample_base	mutate_type	Total Depth	Mutation Depth	
197926 C<->T	intergenic		226	226	
296550 C<->T	intergenic		276	275	
<b>489161 T&lt;-&gt;C</b>	<b>intergenic</b>	<b>234</b>	<b>234</b>		
582068 C<->T	intergenic		249	247	
664388 T<->C	intergenic		237	236	
880916 C<->T	intergenic		249	249	
911515 C<->T	intergenic		263	263	
<b>1228629 A&lt;-&gt;G</b>	<b>intergenic</b>	<b>223</b>	<b>223</b>		
<b>1401247 G&lt;-&gt;A</b>	<b>intergenic</b>	<b>270</b>	<b>270</b>		
2092069 T<->C	intergenic		231	231	
2141860 G<->A	intergenic		227	227	
2708958 C<->T	intergenic		291	291	
2816944 C<->T	intergenic		109	109	
2816953 A<->C	intergenic		121	121	
2816959 T<->A	intergenic		134	133	
2816980 G<->C	intergenic		173	173	
2855617 C<->T	intergenic		243	243	
2941871 C<->T	intergenic		294	294	
2985962 C<->T	intergenic		252	251	
3006110 C<->T	intergenic		277	277	
3275045 C<->T	intergenic		266	266	
<b>3374562 A&lt;-&gt;G</b>	<b>intergenic</b>	<b>246</b>	<b>245</b>		
<b>3461024 T&lt;-&gt;C</b>	<b>intergenic</b>	<b>246</b>	<b>246</b>		
3464900 T<->C	intergenic		264	264	
<b>3512196 A&lt;-&gt;T</b>	<b>intergenic</b>	<b>290</b>	<b>290</b>		
3566228 G<->A	intergenic		239	237	
<b>3689634 G&lt;-&gt;A</b>	<b>intergenic</b>	<b>275</b>	<b>274</b>		
3932435 C<->T	intergenic		291	291	
3932468 G<->T	intergenic		285	285	
3975735 G<->A	intergenic		266	266	
4161616 G<->A	intergenic		276	276	
4189879 T<->C	intergenic		257	257	
4227228 T<->C	intergenic		288	288	
4342921 C<->T	intergenic		284	284	
<b>4378916 T&lt;-&gt;C</b>	<b>intergenic</b>	<b>280</b>	<b>279</b>		
4514918 T<->G	intergenic		263	263	

## insertion/deletion mutations

reference position start	reference position end	mutation	mutate_type	Depth	gene name
4399749	4399750	G	Deletion	249	nrrE - Bifunctional NAD(P)H-hydrate repair enzyme
3031519	3031519	C	Insertion	244	yqfQ - Uncharacterized protein YqfQ precursor
3444350	3444351	C	Deletion	249	thiG - Thiazole synthase
3220087	3220088	G	Deletion	227	hypothetical protein
4428525	4428526	C	Deletion	243	ulaF - L-ribulose-5-phosphate 4-epimerase UlaF
2175523	2175523	CGGAT	Insertion	230	gatC - PTS system galactitol-specific EIIC component
92585	92585	G	Insertion	261	Peptidoglycan D,D-transpeptidase FtsI
3421692	3421693	G	Deletion	196	amino acid ABC transporter permease
1089485	1089486	T	Deletion	191	Poly-beta-1,6-N-acetyl-D-glucosamine N-deacetylase PgaB
996702	996702	T	Insertion	219	ssuA - Putative aliphatic sulfonates-binding protein precursor
2857105	2857105	CCGGAG	Insertion	232	mutS - DNA mismatch repair protein MutS
551479	551480	T	Deletion	227	purK - NS-carboxyaminoimidazole ribonucleotide synthase
34112	34113	T	Deletion	192	hypothetical protein
547832	547832	G	Insertion	258	hypothetical protein
118899	118899	TG	Insertion	225	ampD - N-acetyl-anhydromuramyl-L-alanine amidase
1711533	1711533	CTGG	Insertion	237	rSD - Ion-translocating oxidoreductase complex subunit D
1004576	1004576	G	Insertion	204	ycbf - Uncharacterized fimbrial chaperone YcbF precursor
93307	93308	G	Deletion	225	murE - UDP-N-acetylmuramoy-L-alanyl-D-glutamate-2,6
1237850	1237851	G	Deletion	184	ycgB - Uncharacterized protein YcgB
228970	228971	G	Deletion	149	inosine/guanosine kinase
4610767	4610767	G	Insertion	121	tRNA-Leu

## insertion/deletion mutations (intergenic)

379293 380066 G Deletion 230