

Table S7. Fixed mutations in an *E. coli* evolving population under mild genetic drift effect

Genome position	Mutation	%individuals	Kind	Gene	Description
45,078	C→T	100%	A300V	( <i>CfixC</i> →	predicted oxidoreductase with FAD/NAD(P)-binding domain
83,967	C→T	100%	S61L	( <i>Tcra</i> →	DNA-binding transcriptional repressor-activator for carbon metabolism
103,188	+T	100%	intergenic	( <i>pxC</i> → /	UDP-3-O-acyl N-acetylglucosamine deacetylase/regulator of secA translation
302,914	+C	100%	coding	(1 <i>yagX</i> ←	predicted aromatic compound dioxygenase
305,276	G→A	100%	S88L	( <i>TmatB</i> ←	cryptic Mat fimbriin gene
518,073	+T	100%	intergenic	( <i>ybbP</i> → /	predicted ABC transporter permease/rhsD element protein
539,430	A→G	100%	S243S	( <i>AllC</i> ←	allantoate amidohydrolase
539,932	A→G	100%	V76A	( <i>GallC</i> ←	allantoate amidohydrolase
566,913	T→C	100%	R198R	( <i>ybcM</i> →	DLP12 prophage, predicted DNA-binding transcriptional regulator
704,595	A→G	100%	T466A	( <i>chiP</i> →	chitoporin, uptake of chitosugars
919,281	A→G	100%	E170E	( <i>CmacB</i> →	fused macrolide transporter subunits of ABC superfamily: ATP-binding component/membrane component
980,270	Δ1 bp	100%	coding	(7 <i>ycbB</i> ←	murein L,D-transpeptidase
1,087,350	Δ1 bp	100%	coding	(9 <i>pgaB</i> ←	biofilm adhesin polysaccharide PGA export lipoprotein with a polysaccharide deacetylase activity needed for export
1,124,216	A→G	100%	Y77C	( <i>TrimJ</i> →	ribosomal-protein-S5-alanine N- acetyltransferase
1,172,430	Δ1 bp	100%	intergenic	( <i>mtf</i> ← / +	transcription-repair coupling factor/inner membrane protein
1,214,628	G→A	100%	D46N	( <i>CymgA</i> →	connector protein for RcsB regulation of biofilm
1,297,920	IS5 (+) +Δ	100%	intergenic	( <i>ychE</i> → /	predicted inner membrane protein/oligopeptide transporter subunit
1,377,956	A→G	100%	T195A	( <i>AycJ</i> →	beta-phosphoglucomutase
1,400,464	A→G	100%	R6R	( <i>CGabgB</i> ←	p-aminobenzoyl-glutamate hydrolase, B subunit
1,517,957	A→G	100%	Q157R	( <i>CmcbR</i> →	colanic acid and biofilm gene transcriptional regulator, MqsR-controlled
1,537,360	T→C	100%	S819S	( <i>TnarZ</i> ←	nitrate reductase 2 (NRZ), alpha subunit
1,546,080	A→G	100%	N289S	( <i>AfdnG</i> →	formate dehydrogenase-N, alpha subunit, nitrate- inducible
1,711,543	Δ1 bp	100%	intergenic	( <i>dtpA</i> → /	dipeptide and tripeptide permease A/glutathionine S-transferase
1,854,456	+C	100%	coding	(5 <i>ydjI</i> ←	predicted aldolase
1,933,749	+A	100%	intergenic	( <i>zwf</i> ← / -	glucose-6-phosphate 1-dehydrogenase/predicted DNA-binding transcriptional regulator
2,106,695	A→G	100%	G38G	( <i>GrtbX</i> ←	predicted polysoprenol-linked O-antigen transporter
2,661,742	T→C	100%	G43G	( <i>GyfhR</i> →	S9 peptidase family protein, function unknown
2,734,342	IS1 (+) +Δ	100%	intergenic	( <i>bamD</i> →	lipoprotein required for OM biogenesis, in BamABCDE complex/cold shock protein associated with 30S ribosomal subunit
3,004,979	T→C	100%	I91I	( <i>ATIhyuA</i> →	D-stereospecific phenylhydantoinase
3,316,099	T→C	100%	A65A	( <i>GcyhbX</i> ←	predicted hydrolase, inner membrane
3,349,579	T→C	100%	L59L	( <i>Ti,gttB</i> →	glutamate synthase, large subunit
3,543,623	C→T	100%	A376A	( <i>CmalQ</i> ←	4-alpha-glucanotransferase (amylomaltase)
3,685,449	T→C	100%	D613G	( <i>CbcsB</i> ←	regulator of cellulose synthase, cyclic di-GMP binding
3,793,369	T→C	100%	T208A	( <i>WasU</i> ←	lipopolysaccharide core biosynthesis
4,037,965	A→G	100%	intergenic	( <i>yihG</i> ← /	inner membrane protein, Predicted acyltransferase/fused DNA polymerase I 5'->3' polymerase/3'->5' exonuclease/5'->3' exonuclease
4,094,124	A→G	100%	intergenic	( <i>kdgT</i> → /	2-keto-3-deoxy-D-gluconate transporter/6-N-hydroxylaminopurine resistance protein
4,287,686	+CG	100%	intergenic	( <i>gltP</i> → /	glutamate/aspartate:proton symporter/conserved protein
4,471,270	+T	100%	pseudogene	( <i>yjgN</i> →	inner membrane protein, DUF898 family
4,500,691	G→A	100%	pseudogene	( <i>insO</i> →	pseudogene, IS911 transposase B;IS, phage, Tn; Transposon-related functions; extrachromosomal; transposon related