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Supplementary Information for

High throughput functional variant screens *via* in-vivo production of single-stranded DNA

Max G. Schubert, Daniel B. Goodman, Timothy M. Wannier, Divjot Kaur[f], Fahim Farzadfard, Timothy K. Lu, Seth L.Shipman, and George M. Church

Max Schubert
Email: mgschubert@gmail.com

This PDF file includes:

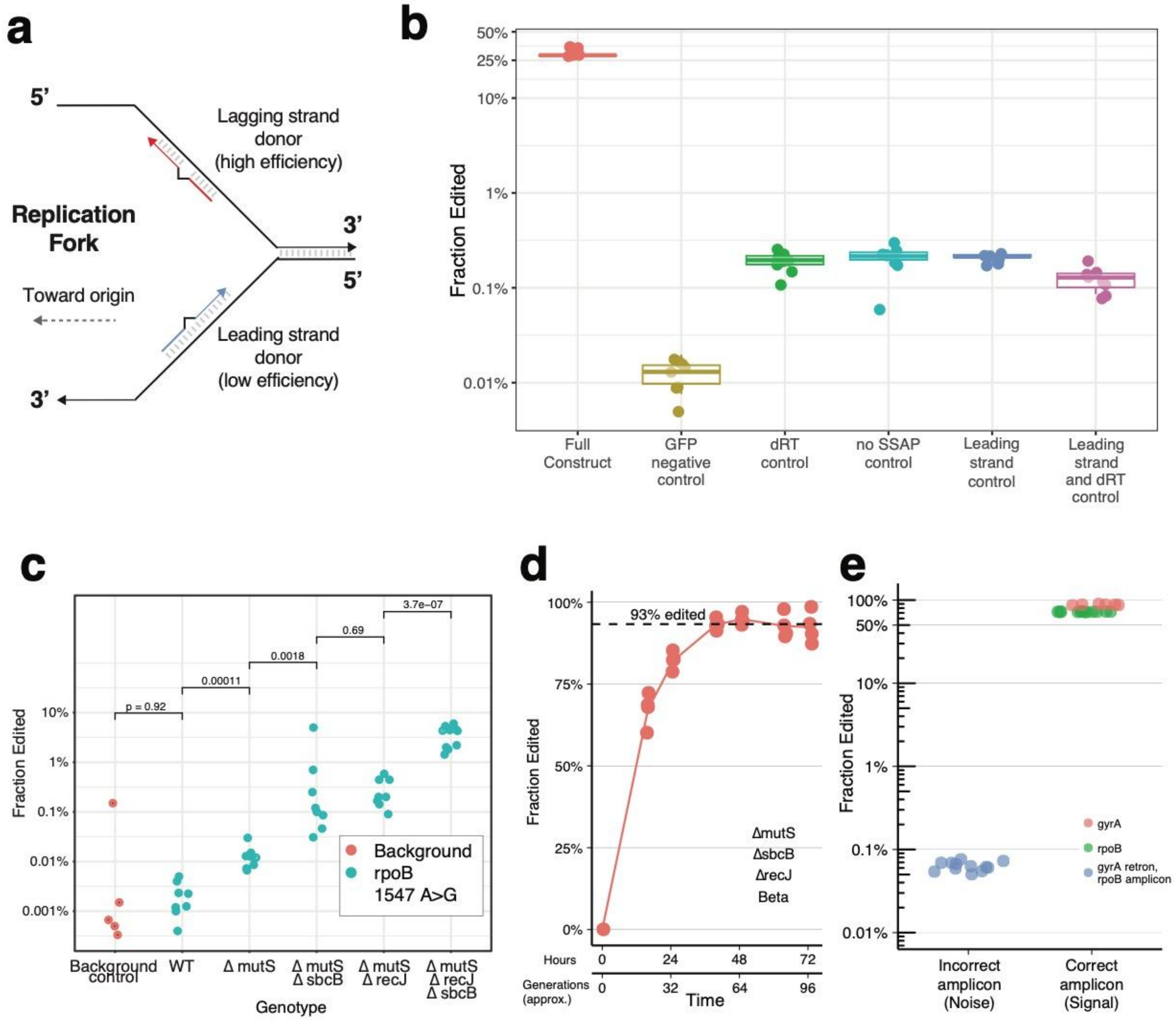
Figures S1 to S6
Tables S1-S4

Other supplementary materials for this manuscript include the following:

All data and scripts necessary to reproduce figures and analysis can be found at https://github.com/churchlab/rlr including additional formats of the supplemental files contained here.

Supplemental_Dataset_S1 (supplemental sequence maps): generalized genbank plasmid maps for Retron Recombineering plasmids used in this study, and a sf.GFP-expressing control plasmid, supplied in Genbank format in a single text file. Please note that some sequence analysis software may require separation into separate files and changing extension to '.gb'.

Supplemental_Dataset_S2: Filtered mutations observed in whole genome sequencing (summarized in figure S4).



Supplemental Figure 1:

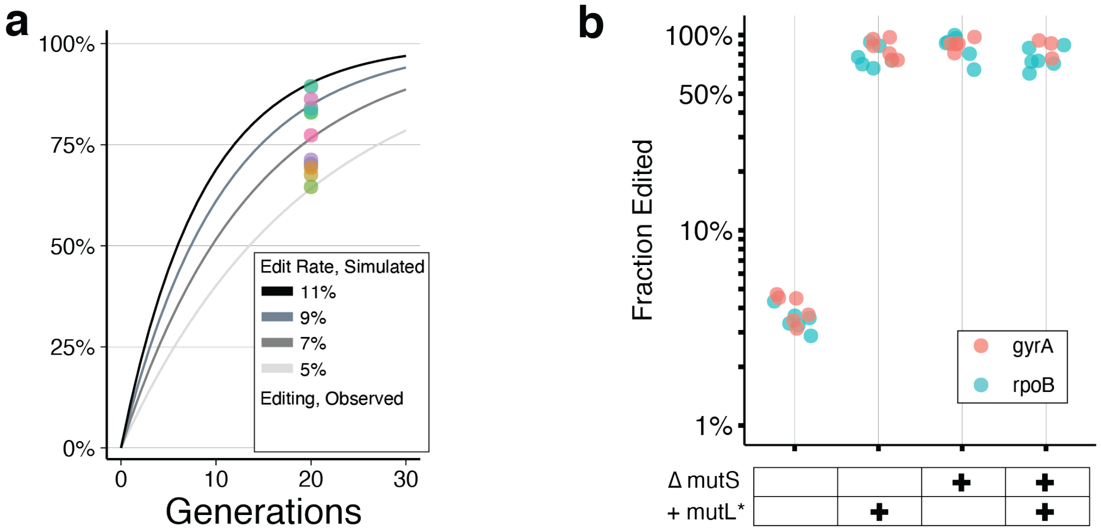
(a) A diagram of the replication fork, depicting recombineering donors annealing to either the leading strand of replication, or the lagging strand of replication.

(b) A confirmation of the mechanism of editing. Editing was compared between the full RLR system expressing the gyrA 248 C>T donor using Beta as a Single-stranded annealing protein (SSAP), and control constructs expressing only GFP, having an inactivated retron reverse-transcriptase active site (dRT) and/or reverse-complemented donor DNA annealing to the leading strand, or which do not express an SSAP protein. Editing was performed in the ΔmutS ΔrecJ ΔsbcB background, with Beta as an SSAP. Individual measurements are represented with dots, and the data is summarized by box plots in the style of Tukey.

(c) The edited fraction of cells, measured phenotypically by resistance to rifampicin at 25ug/mL. These results confirm those shown in Figure 2B, but are measured by plating for CFU, rather than by amplicon sequencing at the edited locus.

(d) The continuous nature of Retron editing. Δ*mutS* Δ*recJ* Δ*sbcB* cells expressing the gyrA retron with Beta as an SSAP were sampled during continuous growth and induction in a turbidostat. The edited fraction of the *gyrA* locus was determined by amplicon deep sequencing over time. This data also depicted in figure 2C, but with inferred generations of growth on the X axis rather than time.

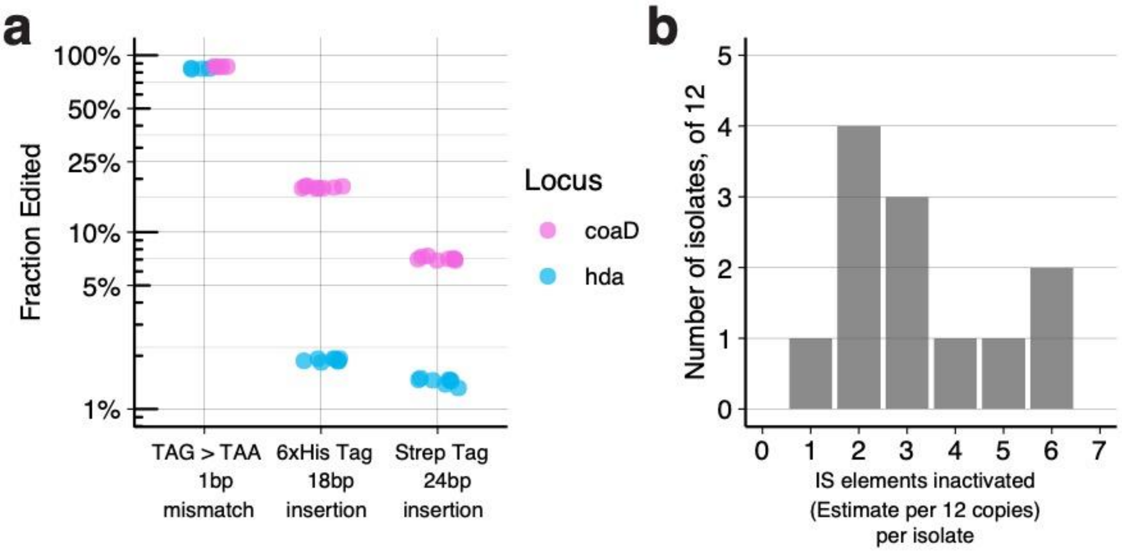
e) Control experiment characterizing error and noise. A culture editing *gyrA* was subjected to amplicon-NGS of the non-edited *rpoB* locus, to determine a background level of editing in the assay, alongside positive controls treated normally. Background editing is most likely due to sequencing error and mis-assigned indices. The mean of this background signal is depicted by a green dotted line in figure 2B, below which



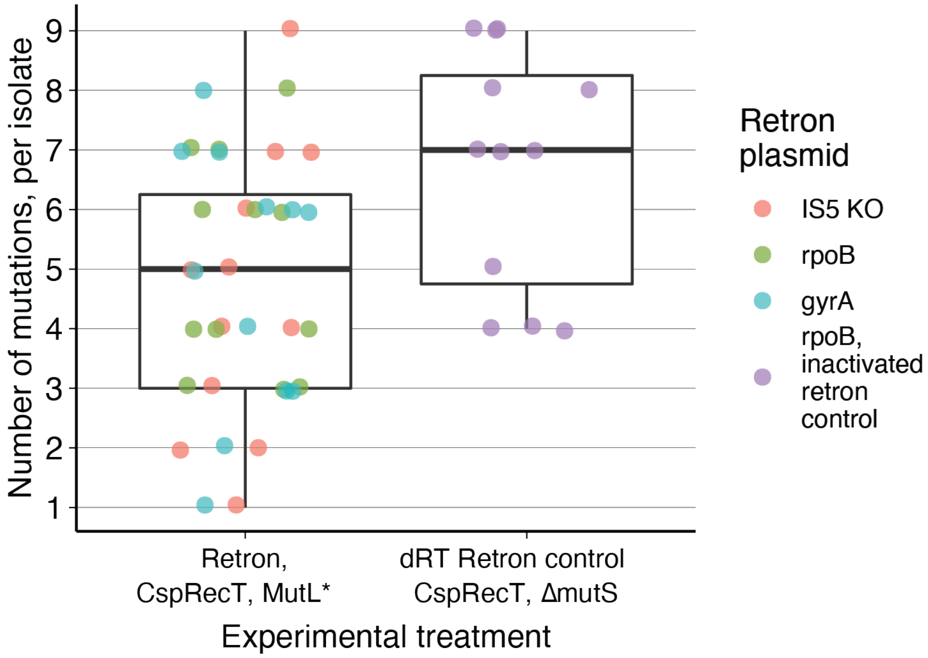
Supplemental Figure 2:

a) Mean edited fraction of the loci in figure 2d are shown alongside a simulated editing trajectory of alleles with neutral fitness effect, as per the model introduced in figure S5. This estimate is suggestive of editing rate of 5-11% per generation for these allele.

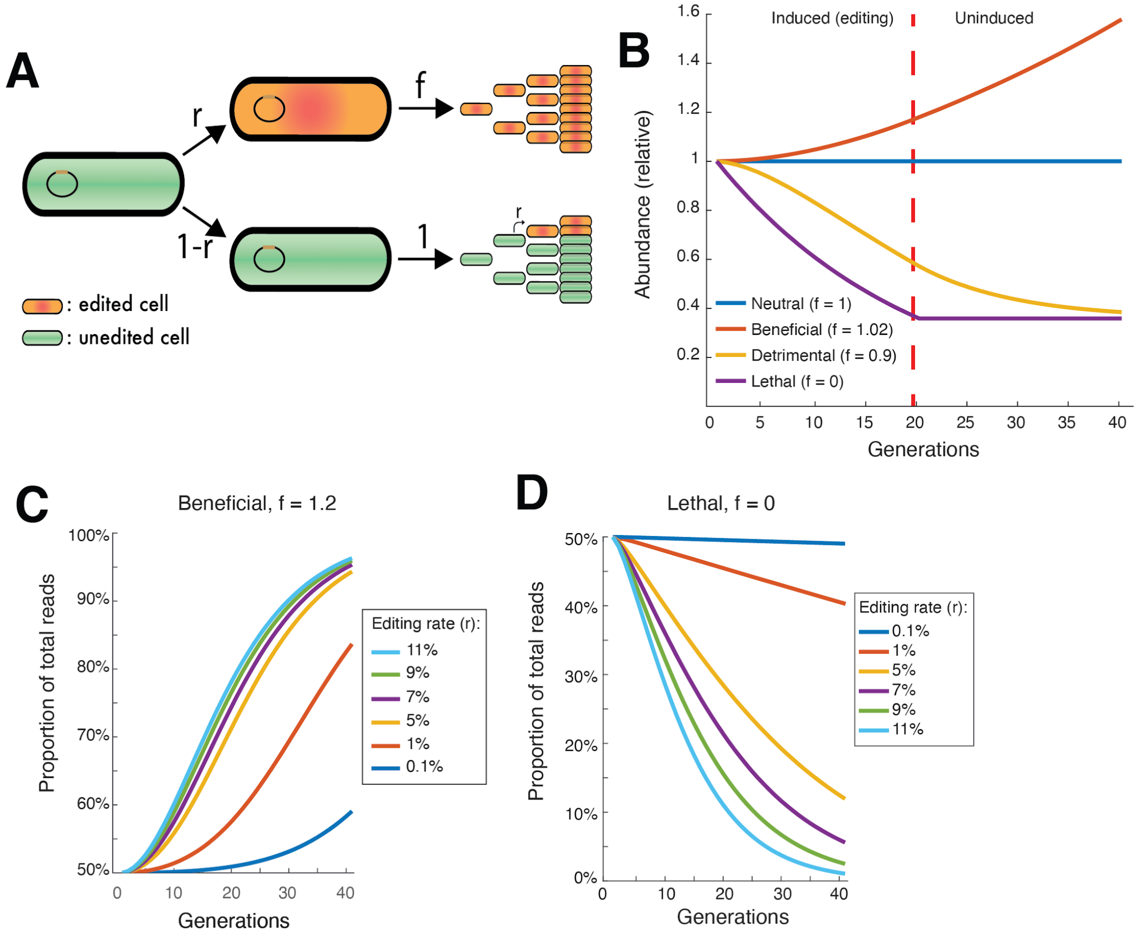
b) Retron plasmids with and without a dominant-negative MutL-E32K variant (mutL*) were expressed in batch growth, in strains with and without inactivation of mutS (ΔmutS). Retron plasmids targeted gyrA and rpoB loci as per figure 2b and used CspRecT as an SSAP. Four replicate experiments per locus and condition are indicated with dots.



Supplemental Figure 3:
a) For two essential genes, hda and coaD, retrons were used to incorporate C-terminal tags, to determine the efficiency of incorporating longer insertions. Fraction edited was determined by amplicon-NGS as previously. Results of 8 replicate experiments are depicted with dots, alongside experiments shown in Figure 2D for the same loci, for comparison. Unlike the 1bp mismatch experiment, edited amplicons for insertions are approximately 10% longer than the non-edited amplicons, possibly introducing PCR bias toward un-edited sequences. This makes the edited fractions reported here likely an under-estimate.
b) A retron targeting the 12 copies of the IS5 transposase with a small inactivating insertion was expressed, and whole-genome sequencing was performed on isolates. The number of IS elements inactivated was estimated from the allelic fraction of the inactivation allele observed within reads.



Supplemental Figure 4:
Before and after induction and editing, whole genome sequencing was performed on isolates to measure overall mutagenesis, and search for off-target editing. 12 isolates for each of three retron donors expressing mutL*, and an inactivated retron control in a ΔmutS strain were sequenced, alongside their parent strains, and the number of mutations per isolate are depicted with individual dots, and summarized by box plots per plasmid type.



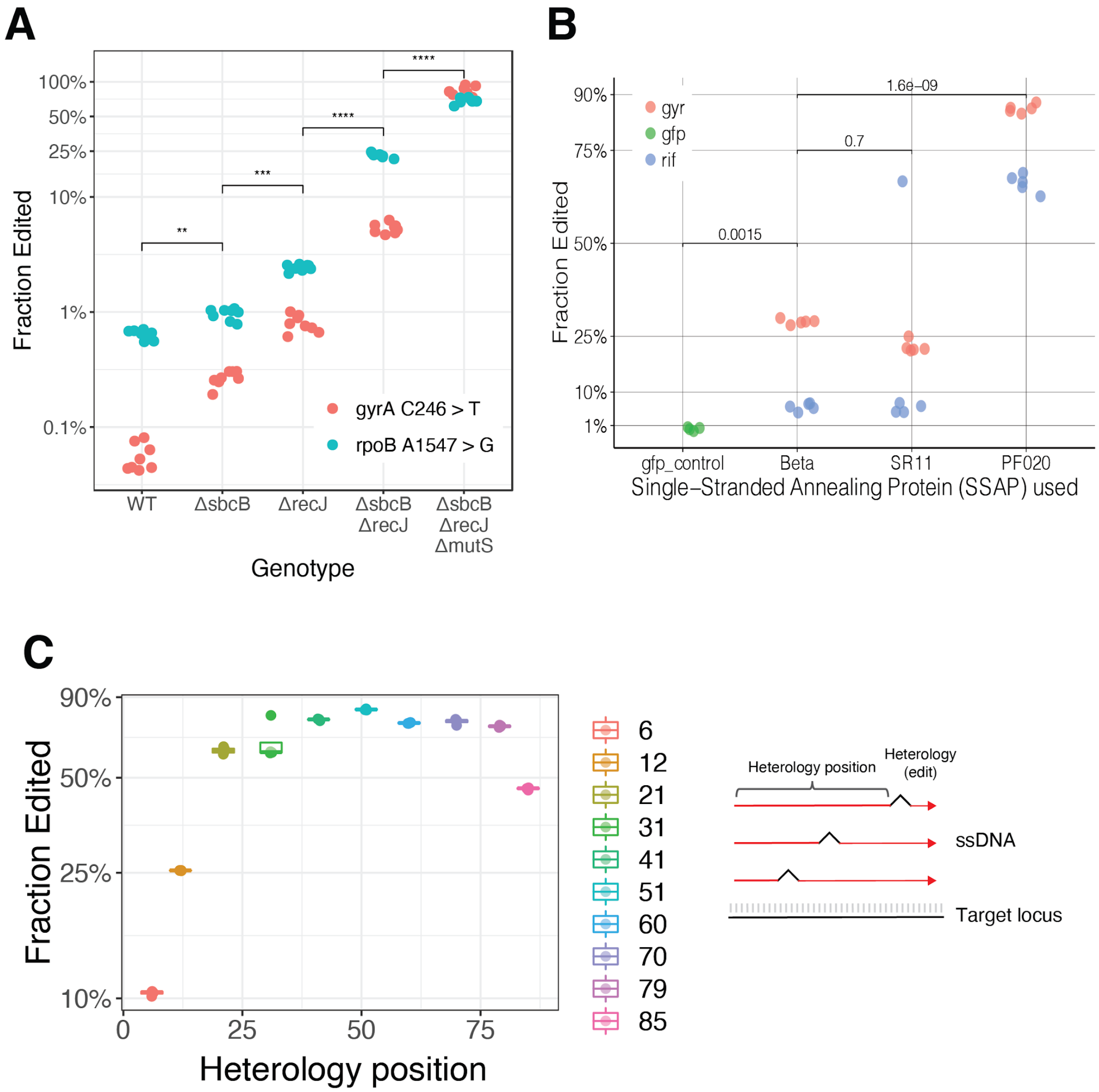
Supplemental figure 5:

(A) A population genetics model describing the Retron Library Recombineering (RLR) process. Each generation, a cell has probability "r" of being successfully edited by the retron construct it bears, and if so edited, propagates at rate "f" determined by the fitness of this mutation in future generations. If not edited in a given generation, which occurs at a rate 1-r, editing may occur in future generations.

(B) The population genetics model predicts that for beneficial alleles, the editing process can be halted (red vertical line), and the lineage of cells marked with the beneficial retron will continue to become more abundant. In contrast, for deleterious or lethal mutations, continued decrease in abundance of a barcoded population is dependent on continued induction and editing.

(C) The growth of populations bearing a retron conferring mutations with growth rate 120% that of the parent (f = 1.2) are simulated, for different rates of editing (r). Population size compared to a simulated neutral parent control, and thus proportion of barcode reads observed, is depicted on the Y axis. The signal observed for beneficial alleles is large, and does not vary substantially if editing frequency varies among alleles. This is compatible with quantitative measurement of beneficial allele fitness, even if editing rate varies somewhat. Additionally, beneficial alleles can be detected even with inefficient editing.

(D) Simulated growth of populations as in Figure S2C, except with a Lethal mutation ($f = 0$). In contrast with Figure S2C, the signal for deleterious or lethal alleles is comparatively small, and scales with editing rate to a greater degree. This indicates that quantification of deleterious phenotypes will be clouded by differences in editing rate among alleles to a greater degree, and that deleterious phenotypes require more efficient editing and/or editing over more generations for robust detection.

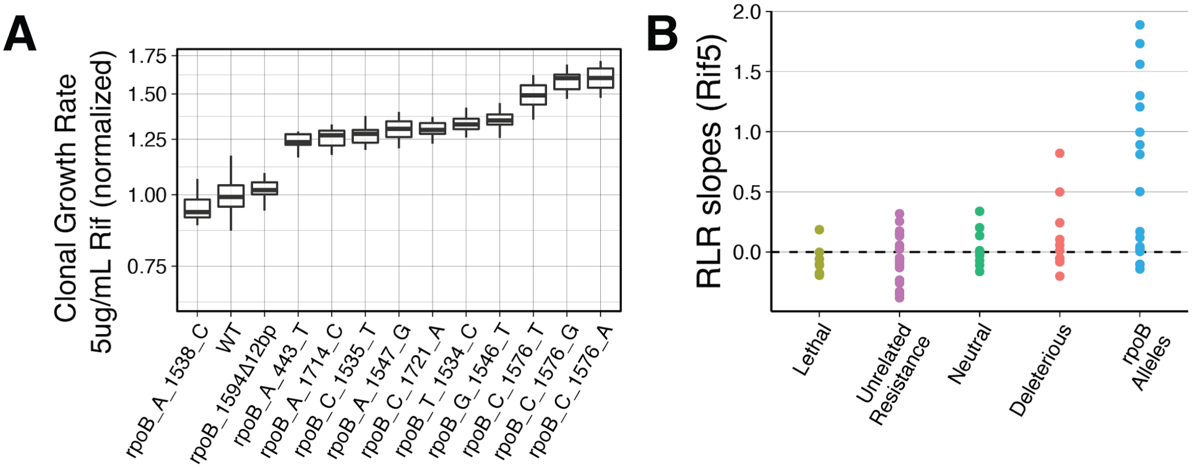


Supplemental figure 6:

(A) The effect of genotype on editing efficiency when the CspRecT is used rather than Beta as an SSAP. Individual measurements of the edited fraction of cells by amplicon sequencing are depicted by dots, for two loci. **** signifies $p < 0.0001$, *** signifies $p < 0.001$, and ** signifies $p < 0.01$, for two-tailed unpaired t-tests performed for comparisons indicated in brackets.

(B) The effect of SSAP protein on editing efficiency. Edited fraction of cells after batch growth was measured by amplicon sequencing for two loci. Retron constructs used Beta, “SR11”, or CspRecT as their SSAP, or expressed only GFP as a negative control. Independent measurements are represented with dots, and p-values of two-tailed, unpaired t-tests are given for the comparisons shown.

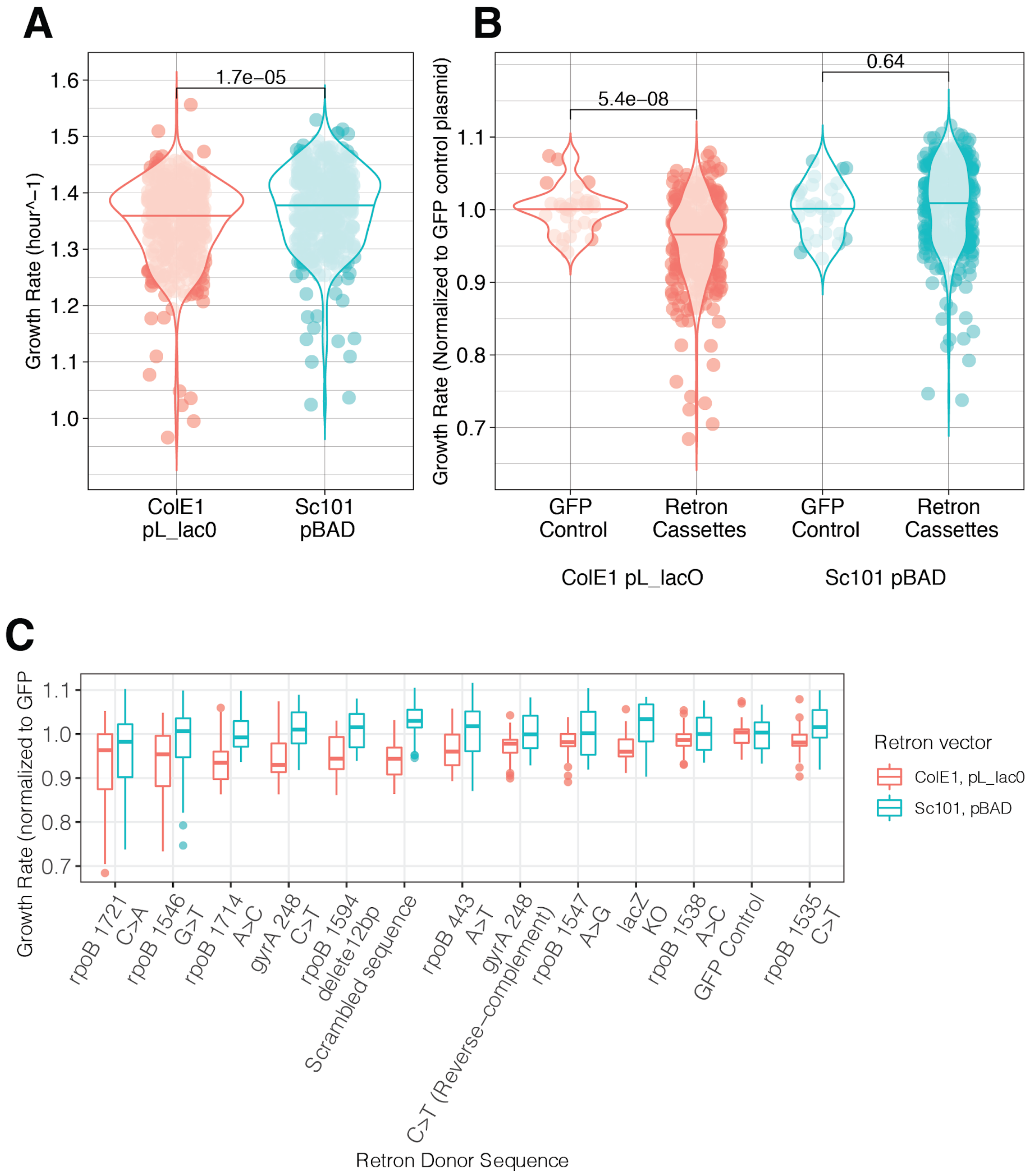
(C) The effect of heterology position within a 90-mer donor DNA was determined for the gyrA 246 C>T mutation, using CspRecT as an SSAP. Donors conferring this mutation were constructed with the heterologous mutation present in different locations within the donor, as indicated in the diagram. Individual cultures were grown and induced for approximately 20 generations. Box plots in the style of Tukey are shown, and the 4 replicate measurements are additionally represented with dots.



Supplemental Figure 7:

(A) *rpoB* mutants conferring rifampicin resistance were constructed in the Δ*mutS* Δ*recJ* Δ*sbcB* background via oligonucleotide recombineering[3], and growth rates were measured in batch growth with sub-inhibitory rifampicin (5ug/ml). Data is shown normalized to the parental (WT, Δ*mutS* Δ*recJ* Δ*sbcB*) growth rate.

(B) Summary of RLR enrichment observed in a pooled, quantitative experiment over time. RLR enrichment rate (slope) for all alleles across 3 replicate experiments is indicated by a dot, and different classes of mutants are separated by color.

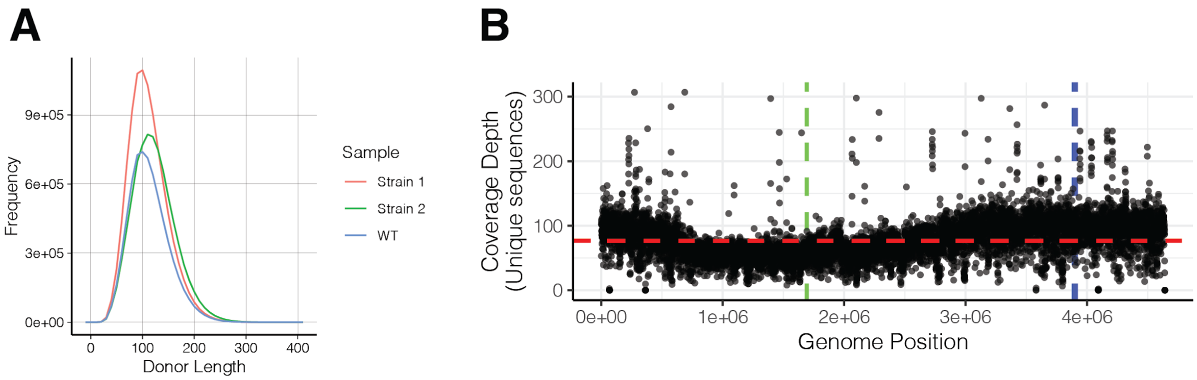


Supplemental Figure 8:

(A) Where previous studies used a medium-copy ColE1 vector and pL_lacO promoter for expression of the retron components, expression from a low-copy (sc101) vector is less detrimental to growth. Absolute growth rates are pooled here for 12 expressed retron constructs, and violin plot outlines depict the distribution of the data, with the width of outlines indicating the proportion of the data with a given value. Horizontal lines depict the mean growth rate for each vector type. P value for a t-test comparing data for both vector types is given.

(B) Retrons are expressed from the ColE1 vector, they are significantly depressed in growth rate compared to sfGFP expressed in the same manner, whereas 12 retrons expressed from the SC101 vector cannot be distinguished, as a population. Growth rate is shown normalized to the GFP control construct for each vector type, and horizontal lines depict the mean growth rate for each condition. P values for t-tests are given for the comparisons indicated with brackets.

(C) Growth rates for 12 induced retron constructs, normalized to the GFP-expressing control plasmid for each vector type. Constructs are ordered by mean growth rate, and box-and-whisker plots are depicted in the style of Tukey, with outlier observations represented by dots.



Supplemental Figure 9

(A) Retron donor size distribution for three representative genomic DNA libraries. Strains 1 and 2 were evolved, Trimethoprim-resistant *E. coli*, and "WT" is *E. coli* MG1655.

(B) Depth of coverage of a representative genomic retron library is depicted. Dots indicate the mean coverage of unique retron donor sequences across 500bp windows of the genome. The mean coverage across all windows is 78, and is indicated with a dashed red line. Dashed gray lines mark the genomic positions of the origin and terminus of the genome, helping to clarify increased coverage as DNA content increases with proximity to the origin.

Supplemental_Table_S1 (Supplemental sequences): annotated list of selected oligonucleotides used in the study

oligonucleotide name	oligonucleotide sequence	oligonucleotide description
TetA_KO_tetR_bla_F	CTCGCAGAAAGAAACATATCCATGAAATCCCGCCCCGAATTCATatgaccgatgatgaagaaaagaatttgaaacttagttta	integrate bla at λ:tetR of ECNR1, Fwd
TetA_KO_tetR_bla_R	CATTATTTGCCGACTACCTTGGTGATCTCGCCTTTCACGTAGTGGACAAActgttataaaaaaaggatcaattttgaactctctccc	integrate bla at λ:tetR of ECNR1, Rev
araBAD fwd (kanfrt)	GAGCGTGACCAGGTTGTGTTTTGGCAGCGCCAGGTTGGCTATTCCGGGGATCCGTCGACC	inactivate araBAD, Fwd
arabad rev	CTGACGCTTTTTATCGCAACTCTCTACTGTTTCTCCATACTGTAGGCTGGAGCTGCTTCG	inactivate araBAD, Rev
mutSkan_total_del_fwd	CTAACAATTCCCGATAGTCTTTTGCTATCGGGAATATTAACGACGAATTCAGGAAACCCG	mutS inactivate, Fwd
mutSkan_total_del_rev	GGTTATGTCCGGTTCCCTGATATTAAATGGGGTGTGATGGGAATTCAGGAAAACAGACAG	mutS inactivate, Rev
oMS_0178	g*a*ggcaattcagcgggcaagtctgccgtttcatcgacttcacgTTATCAaagttgtatctgttgtttcacgcgaattatttaccgctggt	recJ inactivation oligo
oMS_0179	g*g*cagacagcagaaataacggatttaacctaatgatgaatgacTAATGAcaacaatctaccttttttgtttcacgattacgaaacctttgg	sbcB inactivation oligo
oMS_733	CCTACACGACGCTCTTCCGATCTNGTTACCCTGACCGTCTACCAG	gyrA fwd genomic PCR1
oMS_734	CCTACACGACGCTCTTCCGATCTNNGTTACCCTGACCGTCTACCAG	
oMS_744	CCTACACGACGCTCTTCCGATCTNNNGTTACCCTGACCGTCTACCAG	
oMS_739	GAGTTCAGACGTGTGCTCTTCCGATCTNNCTGGAACAAAGCCTATAAAAAATCTGCC	gyrA rev genomic PCR1

oMS_740	GAGTTCAGACGTGTGCTCTTCCGATCTNCTGGAACAAAGCCTATAAAAAATCTGCC	
oMS_745	GAGTTCAGACGTGTGCTCTTCCGATCTNNNCTGGAACAAAGCCTATAAAAAATCTGCC	
oMS_729	CCTACACGACGCTCTTCCGATCTNCTGATGCCACAGGATATGATCAACG	rpoB fwd genomic PCR1
oMS_730	CCTACACGACGCTCTTCCGATCTNNCTGATGCCACAGGATATGATCAACG	
oMS_735	GAGTTCAGACGTGTGCTCTTCCGATCTNNGAGTGCGGAGATACGACGTTTG	rpoB rev genomic PCR1
oMS_736	GAGTTCAGACGTGTGCTCTTCCGATCTNGAGTGCGGAGATACGACGTTTG	
retron_donor_fwd_1	cctacacgacgctcttccgatctNNTCTGAGTTACTGTCTGTTTTCCTGAATTC	for amplification of retron donors from plasmid, Fwd
retron_donor_fwd_2	cctacacgacgctcttccgatctNNBTCTGAGTTACTGTCTGTTTTCCTGAATTC	
retron_donor_fwd_3	cctacacgacgctcttccgatctNNNHTCTGAGTTACTGTCTGTTTTCCTGAATTC	
retron_donor_fwd_4	cctacacgacgctcttccgatctNNNNBTCTGAGTTACTGTCTGTTTTCCTGAATTC	
retron_donor_fwd_5	cctacacgacgctcttccgatctTCTGAGTTACTGTCTGTTTTCCTGAATTC	
retron_donor_rev_1	gagttcagacgtgtgctcttccgatctNAAGTGTTCAAATATTCAGCGGATTTCATG	for amplification of retron donors from plasmid, Rev
retron_donor_rev_2	gagttcagacgtgtgctcttccgatctNVAAGTGTTCAAATATTCAGCGGATTTCATG	
retron_donor_rev_3	gagttcagacgtgtgctcttccgatctNNVAAGTGTTCAAATATTCAGCGGATTTCATG	

retron_donor_rev_4	gagttcagacgtgtgctcttccgatctNNNDAAGTGTTCAAATATTCAGCGGATTTCATG	
murF fwd	cctacacgacgctcttccgatctACGATTTTAGTTAAGGGTTCACGTAG	for amplification of TAG>TAA loci from genome
yafF fwd	cctacacgacgctcttccgatctTGCGAAAAGCAGCCATGGAC	
pgpA fwd	cctacacgacgctcttccgatctCGCAGGCATCCTGTATTTATCG	
sucB fwd	cctacacgacgctcttccgatctGCGAATCCGTGGGCTTCCTG	
lolA fwd	cctacacgacgctcttccgatctCTGTGGATGCAGCGAAATTTAC	
lpxK fwd	cctacacgacgctcttccgatctGTAGACGCACAGCTTTCAGG	
fabH fwd	cctacacgacgctcttccgatctTAAGCCGGGGCAGTTGGTTC	
hemA fwd	cctacacgacgctcttccgatctCCAACGAAATCACTTCAACAGG	
fliN fwd	cctacacgacgctcttccgatctGTTGCCGATAAATATGGCGTG	
hda fwd	cctacacgacgctcttccgatctccGGCCTACGAATACTATGGATTAAC	
mreC fwd	cctacacgacgctcttccgatctGGAAAACAATCAGGTTATCCGGC	
coaD fwd	cctacacgacgctcttccgatctCTCTTCATCGTTGGTGAAAGAGG	
murF rev	gagttcagacgtgtgctcttccgatctCGATGGCGCGAAACGTCAG	
yafF rev	gagttcagacgtgtgctcttccgatctAAAGTTTCCGGCATGGCAGG	
pgpA rev	gagttcagacgtgtgctcttccgatctCGAACTGGAAACGCCGTATAAAC	

sucB rev	gagttcagacgtgtgctcttccgatctCTTCAATTGCCGGAGAAGGC	
lolA rev	gagttcagacgtgtgctcttccgatctCTAAATTTTCTGGCCGCATACG	
lpxK rev	gagttcagacgtgtgctcttccgatctATTACGCGCATCAGCAAGG	
fabH rev	gagttcagacgtgtgctcttccgatctGCCAGCATTCCAACGGTTTG	
hemA rev	gagttcagacgtgtgctcttccgatctGCTTCCAGTTTGGCAACGATAG	
fliN rev	gagttcagacgtgtgctcttccgatctGGGCAATAATGGCGATGAGTG	
hda rev	gagttcagacgtgtgctcttccgatctATCAGTTGGATCGTGCGTCG	
mreC rev	gagttcagacgtgtgctcttccgatctTCTCCACAAAGGGCTACGCC	
coaD rev	gagttcagacgtgtgctcttccgatcttGCCAGAAGTAATTCATGCGC	
oMS_890	/5Phos/GAATTCAGGAAAACAGAGAGACCgAACTCCAGTCUACACTCTACACGctGGTCTCGTTTCCTGAATTC*T	Custom Hairpin adapter, ligates to TA-tailed genomic fragments
oMS_888	GACTGGAGTTcGGTCTCTCTGT	5prime fwd primer for amplifying genomic fragments
oMS_889	ACACTCTACACGctGGTCTCG	3prime rev primer for amplifying genomic fragments
oMS_891	ATTCAGGTCTCGGAAACCCGTTTTTCTGACG	genomic Vector Fwd, for genomic insert retron vector
oMS_892	TATAGGTCTCAACAGACAGTAACTCAGATTCAATGC	genomic Vector Rev, for genomic insert retron vector
oMS_957	T*A*AAAAAAATTGTCGCCACTATACGTAAAGCGTAAACCGTCGTCaACTGGTGCGAGGATGATGTTGAGGAAAATTTTATATTCTGCTGGC	MAGE oligo for introduction of [C->t].49764 mutation

		(folA region)
oMS_958	C*A*GGTATGGCGGCCCATAATCACGGGTTTATTTAAGGTGTTGCGTTTAAACCAGGCGAGcTCGGCAGGCAGGTTCCACGGCATGGCGTTT	MAGE oligo for introduction of [T->g].49902 mutation (folA region)
oMS_959	A*A*TTCTATACAAAATTACCGCCGCTCCAGAATCTCAcAGCAATAGCTGTGAGAGTTCTGCGCATCAGCATCGTGGAATTCGCTGAATACC	MAGE oligo for introduction of [T->g].50279 mutation (folA region)
oMS_960	G*T*GCGTAATCTCAGACAGCGGGTTGTTCTGGTCCATAAACTGAGGCAGCTGGCTGGAACCGAAGAACTCTTTCACTGCTGCGGAAATCGG	MAGE oligo for introduction of rpoB_1547A.G mutation
oMS_961	A*G*ATACGACGTTTGTGCGTAATCTCAGACAGCGGGTTGTTCTGGCCCATAAACTGAGACAGCTGGCTGGAACCGAAGAACTCTTTCACTG	MAGE oligo for introduction of rpoB_1534T.C mutation
oMS_962	C*C*GTAGTGAGTCGGGTGTACGTCTCGAACTTCGAAGCCTGCACGATCACGGGTCAGACCGCCTGGGCCGAGTGCGGAGATACGACGTTTG	MAGE oligo for introduction of rpoB_A_1623_T mutation
oMS_963	C*G*GACCTTCAGGGGTTTCGATTGGACATACGCGACCGTAGTGAGCCGGGTGTACGTCTCGAACTTCGAAGCCTGCACGTTCACGGGTCAG	MAGE oligo for introduction of rpoB_A_1657_G mutation
oMS_964	C*G*GACCTTCAGGGGTTTCGATTGGACATACGCGACCGTAGTGAGACGGGTGTACGTCTCGAACTTCGAAGCCTGCACGTTCACGGGTCAG	MAGE oligo for introduction of rpoB_A_1657_T mutation
oMS_965	A*C*GGGTCAGACCGCCTGGGCCGAGTGCGGAGATACGACGTTTGTTCGTAATCTCAGACAGCGGGTTGTTCTGGTCCATAAACTGAGACAG	MAGE oligo for introduction of rpoB_C_1576_A mutation
oMS_966	A*C*GGGTCAGACCGCCTGGGCCGAGTGCGGAGATACGACGTTTGTCCGTAATCTCAGACAGCGGGTTGTTCTGGTCCATAAACTGAGACAG	MAGE oligo for introduction of rpoB_C_1576_G mutation
oMS_967	C*G*GGTCAGACCGCCTGGGCCGAGTGCGGAGATACGACGTTTGTACGTAATCTCAGACAGCGGGTTGTTCTGGTCCATAAACTGAGACAGC	MAGE oligo for introduction of rpoB_C_1576_T

		mutation
oMS_968	C*G*GGTCAGACCGCCTGGGCCGAGTGCGGAGATACGACGTTTGTGAATAATCTCAGACAGCGGGTTGTTCTGGTCCATAAACTGAGACAGC	MAGE oligo for introduction of rpoB_CG_1574_TT mutation
oMS_969	A*T*ACGACGTTTGTGCGTAATCTCAGACAGCGGGTTGTTCTGGTCTATAAACTGAGACAGCTGGCTGGAACCGAAGAACTCTTTCACTGCT	MAGE oligo for introduction of rpoB_G_1545_A mutation
oMS_970	A*T*ACGACGTTTGTGCGTAATCTCAGACAGCGGGTTGTTCTGGTCAATAAACTGAGACAGCTGGCTGGAACCGAAGAACTCTTTCACTGCT	MAGE oligo for introduction of rpoB_G_1545_T mutation
i5_2_1	aatgatacggcgaccaccgagatctacacaagccattacactctttccctacacgacgctcttccgat	Custom Illumina i5 index 2_1
i5_2_2	aatgatacggcgaccaccgagatctacacttcggtaaacactctttccctacacgacgctcttccgat	Custom Illumina i5 index 2_2
i5_2_3	aatgatacggcgaccaccgagatctacacTATAGCCTacactctttccctacacgacgctcttccgat	Custom Illumina i5 index 2_3
i5_2_4	aatgatacggcgaccaccgagatctacacATAGAGGCacactctttccctacacgacgctcttccgat	Custom Illumina i5 index 2_4
i5_2_5	aatgatacggcgaccaccgagatctacacCCTATCCTacactctttccctacacgacgctcttccgat	Custom Illumina i5 index 2_5
i5_2_6	aatgatacggcgaccaccgagatctacacGGCTCTGAacactctttccctacacgacgctcttccgat	Custom Illumina i5 index 2_6
i5_2_7	aatgatacggcgaccaccgagatctacacAGGCGAAGacactctttccctacacgacgctcttccgat	Custom Illumina i5 index 2_7
i5_2_8	aatgatacggcgaccaccgagatctacacTAATCTTAacactctttccctacacgacgctcttccgat	Custom Illumina i5 index 2_8
i5_2_9	aatgatacggcgaccaccgagatctacacCAGGACGTacactctttccctacacgacgctcttccgat	Custom Illumina i5 index 2_9
i5_2_10	aatgatacggcgaccaccgagatctacacGTACTGACacactctttccctacacgacgctcttccgat	Custom Illumina i5 index 2_10
PCR2_r01_8me	CAAGCAGAAGACGGCATACGAGATCCGTGAGA	Custom Illumina i7 index 1 (A1)

r	GTGACTGGAGTTCAGACGTGTGCTCTT	
PCR2_r02_8mer	CAAGCAGAAGACGGCATACGAGATCATCAAGTGTGACTGGAGTTCAGACGTGTGCTCTT	Custom Illumina i7 index 2 (A2)
PCR2_r03_8mer	CAAGCAGAAGACGGCATACGAGATAAGACGGAGTGACTGGAGTTCAGACGTGTGCTCTT	Custom Illumina i7 index 3 (A3)
PCR2_r04_8mer	CAAGCAGAAGACGGCATACGAGATCGAACTTAGTGACTGGAGTTCAGACGTGTGCTCTT	Custom Illumina i7 index 4 (A4)
PCR2_r05_8mer	CAAGCAGAAGACGGCATACGAGATGATAGACAGTGACTGGAGTTCAGACGTGTGCTCTT	Custom Illumina i7 index 5 (A5)
PCR2_r06_8mer	CAAGCAGAAGACGGCATACGAGATGGTGCGAAGTGACTGGAGTTCAGACGTGTGCTCTT	Custom Illumina i7 index 6 (A6)
PCR2_r07_8mer	CAAGCAGAAGACGGCATACGAGATCACCTTACGTGACTGGAGTTCAGACGTGTGCTCTT	Custom Illumina i7 index 7 (A7)
PCR2_r08_8mer	CAAGCAGAAGACGGCATACGAGATCCTAATCCGTGACTGGAGTTCAGACGTGTGCTCTT	Custom Illumina i7 index 8 (A8)
PCR2_r09_8mer	CAAGCAGAAGACGGCATACGAGATAACGTGATGTGACTGGAGTTCAGACGTGTGCTCTT	Custom Illumina i7 index 9 (A9)
PCR2_r10_8mer	CAAGCAGAAGACGGCATACGAGATAGTACAAGGTGACTGGAGTTCAGACGTGTGCTCTT	Custom Illumina i7 index 10 (A10)
PCR2_r11_8mer	CAAGCAGAAGACGGCATACGAGATAACCGAGAGTGACTGGAGTTCAGACGTGTGCTCTT	Custom Illumina i7 index 11 (A11)
PCR2_r12_8mer	CAAGCAGAAGACGGCATACGAGATAACGCTTAGTGACTGGAGTTCAGACGTGTGCTCTT	Custom Illumina i7 index 12 (A12)
PCR2_r13_8me	CAAGCAGAAGACGGCATACGAGATAAGGTACA	Custom Illumina i7 index 13 (B1)

r	GTGACTGGAGTTCAGACGTGTGCTCTT	
PCR2_r14_8mer	CAAGCAGAAGACGGCATACGAGATACAGCAGAGTGACTGGAGTTCAGACGTGTGCTCTT	Custom Illumina i7 index 14 (B2)
PCR2_r15_8mer	CAAGCAGAAGACGGCATACGAGATACCTCCAAGTGACTGGAGTTCAGACGTGTGCTCTT	Custom Illumina i7 index 15 (B3)
PCR2_r16_8mer	CAAGCAGAAGACGGCATACGAGATACGTATCAGTGACTGGAGTTCAGACGTGTGCTCTT	Custom Illumina i7 index 16 (B4)
PCR2_r17_8mer	CAAGCAGAAGACGGCATACGAGATACTATGCAGTGACTGGAGTTCAGACGTGTGCTCTT	Custom Illumina i7 index 17 (B5)
PCR2_r18_8mer	CAAGCAGAAGACGGCATACGAGATAGAGTCAAGTGACTGGAGTTCAGACGTGTGCTCTT	Custom Illumina i7 index 18 (B6)
PCR2_r19_8mer	CAAGCAGAAGACGGCATACGAGATAGCAGGAAGTGACTGGAGTTCAGACGTGTGCTCTT	Custom Illumina i7 index 19 (B7)
PCR2_r20_8mer	CAAGCAGAAGACGGCATACGAGATCAACCACAGTGACTGGAGTTCAGACGTGTGCTCTT	Custom Illumina i7 index 20 (B8)
PCR2_r21_8mer	CAAGCAGAAGACGGCATACGAGATCAAGACTAGTGACTGGAGTTCAGACGTGTGCTCTT	Custom Illumina i7 index 21 (B9)
PCR2_r22_8mer	CAAGCAGAAGACGGCATACGAGATCAATGGAAGTGACTGGAGTTCAGACGTGTGCTCTT	Custom Illumina i7 index 22 (B10)
PCR2_r23_8mer	CAAGCAGAAGACGGCATACGAGATCACTTCGAGTGACTGGAGTTCAGACGTGTGCTCTT	Custom Illumina i7 index 23 (B11)
PCR2_r24_8mer	CAAGCAGAAGACGGCATACGAGATCAGCGTTAGTGACTGGAGTTCAGACGTGTGCTCTT	Custom Illumina i7 index 24 (B12)
PCR2_r25_8me	CAAGCAGAAGACGGCATACGAGATCATACCAA	Custom Illumina i7 index 25 (C1)

r	GTGACTGGAGTTCAGACGTGTGCTCTT	
PCR2_r26_8mer	CAAGCAGAAGACGGCATACGAGATCCAGTTCAGTGACTGGAGTTCAGACGTGTGCTCTT	Custom Illumina i7 index 26 (C2)
PCR2_r27_8mer	CAAGCAGAAGACGGCATACGAGATCCGAAGTAGTGACTGGAGTTCAGACGTGTGCTCTT	Custom Illumina i7 index 27 (C3)
PCR2_r28_8mer	CAAGCAGAAGACGGCATACGAGATCCTCCTGAGTGACTGGAGTTCAGACGTGTGCTCTT	Custom Illumina i7 index 28 (C4)
PCR2_r29_8mer	CAAGCAGAAGACGGCATACGAGATCGCATACAGTGACTGGAGTTCAGACGTGTGCTCTT	Custom Illumina i7 index 29 (C5)
PCR2_r30_8mer	CAAGCAGAAGACGGCATACGAGATCTGAGCCAGTGACTGGAGTTCAGACGTGTGCTCTT	Custom Illumina i7 index 30 (C6)
PCR2_r31_8mer	CAAGCAGAAGACGGCATACGAGATCTGGCATAGTGACTGGAGTTCAGACGTGTGCTCTT	Custom Illumina i7 index 31 (C7)
PCR2_r32_8mer	CAAGCAGAAGACGGCATACGAGATGAATCTGAGTGACTGGAGTTCAGACGTGTGCTCTT	Custom Illumina i7 index 32 (C8)
PCR2_r33_8mer	CAAGCAGAAGACGGCATACGAGATGAGCTGAAGTGACTGGAGTTCAGACGTGTGCTCTT	Custom Illumina i7 index 33 (C9)
PCR2_r34_8mer	CAAGCAGAAGACGGCATACGAGATGCCACATAGTGACTGGAGTTCAGACGTGTGCTCTT	Custom Illumina i7 index 34 (C10)
PCR2_r35_8mer	CAAGCAGAAGACGGCATACGAGATGCGAGTAAGTGACTGGAGTTCAGACGTGTGCTCTT	Custom Illumina i7 index 35 (C11)
PCR2_r36_8mer	CAAGCAGAAGACGGCATACGAGATGCTAACGAGTGACTGGAGTTCAGACGTGTGCTCTT	Custom Illumina i7 index 36 (C12)
PCR2_r37_8me	CAAGCAGAAGACGGCATACGAGATGCTCGGTAG	Custom Illumina i7 index 37 (D1)

r	TGACTGGAGTTCAGACGTGTGCTCTT	
PCR2_r38_8mer	CAAGCAGAAGACGGCATACGAGATGGAGAACAGTGACTGGAGTTCAGACGTGTGCTCTT	Custom Illumina i7 index 38 (D2)
PCR2_r39_8mer	CAAGCAGAAGACGGCATACGAGATGTACGCAAGTGACTGGAGTTCAGACGTGTGCTCTT	Custom Illumina i7 index 39 (D3)
PCR2_r40_8mer	CAAGCAGAAGACGGCATACGAGATGTCGTAGAGTGACTGGAGTTCAGACGTGTGCTCTT	Custom Illumina i7 index 40 (D4)
PCR2_r41_8mer	CAAGCAGAAGACGGCATACGAGATGTCTGTCAGTGACTGGAGTTCAGACGTGTGCTCTT	Custom Illumina i7 index 41 (D5)
PCR2_r42_8mer	CAAGCAGAAGACGGCATACGAGATTAGGATGAGTGACTGGAGTTCAGACGTGTGCTCTT	Custom Illumina i7 index 42 (D6)
PCR2_r43_8mer	CAAGCAGAAGACGGCATACGAGATTATCAGCAGTGACTGGAGTTCAGACGTGTGCTCTT	Custom Illumina i7 index 43 (D7)
PCR2_r44_8mer	CAAGCAGAAGACGGCATACGAGATTCCGTCTAGTGACTGGAGTTCAGACGTGTGCTCTT	Custom Illumina i7 index 44 (D8)
PCR2_r45_8mer	CAAGCAGAAGACGGCATACGAGATTCTTCACAGTGACTGGAGTTCAGACGTGTGCTCTT	Custom Illumina i7 index 45 (D9)
PCR2_r46_8mer	CAAGCAGAAGACGGCATACGAGATTGAAGAGAGTGACTGGAGTTCAGACGTGTGCTCTT	Custom Illumina i7 index 46 (D10)
PCR2_r47_8mer	CAAGCAGAAGACGGCATACGAGATTGGAACAAGTGACTGGAGTTCAGACGTGTGCTCTT	Custom Illumina i7 index 47 (D11)
PCR2_r48_8mer	CAAGCAGAAGACGGCATACGAGATTGGCTTCAGTGACTGGAGTTCAGACGTGTGCTCTT	Custom Illumina i7 index 48 (D12)
PCR2_r49_8me	CAAGCAGAAGACGGCATACGAGATTGGTGGTAG	Custom Illumina i7 index 49 (E1)

r	TGACTGGAGTTCAGACGTGTGCTCTT	
PCR2_r50_8mer	CAAGCAGAAGACGGCATACGAGATTTCACGCAGTGACTGGAGTTCAGACGTGTGCTCTT	Custom Illumina i7 index 50 (E2)
PCR2_r51_8mer	CAAGCAGAAGACGGCATACGAGATAATCCGTCGTGACTGGAGTTCAGACGTGTGCTCTT	Custom Illumina i7 index 51 (E3)
PCR2_r52_8mer	CAAGCAGAAGACGGCATACGAGATAATGTTGCGTGACTGGAGTTCAGACGTGTGCTCTT	Custom Illumina i7 index 52 (E4)
PCR2_r53_8mer	CAAGCAGAAGACGGCATACGAGATACACGACCGTGACTGGAGTTCAGACGTGTGCTCTT	Custom Illumina i7 index 53 (E5)
PCR2_r54_8mer	CAAGCAGAAGACGGCATACGAGATACAGATTCGTGACTGGAGTTCAGACGTGTGCTCTT	Custom Illumina i7 index 54 (E6)
PCR2_r55_8mer	CAAGCAGAAGACGGCATACGAGATAGATGTACGTGACTGGAGTTCAGACGTGTGCTCTT	Custom Illumina i7 index 55 (E7)
PCR2_r56_8mer	CAAGCAGAAGACGGCATACGAGATCAAGGAGCGTGACTGGAGTTCAGACGTGTGCTCTT	Custom Illumina i7 index 56 (E8)
PCR2_r57_8mer	CAAGCAGAAGACGGCATACGAGATCCATCCTCGTGACTGGAGTTCAGACGTGTGCTCTT	Custom Illumina i7 index 57 (E9)
PCR2_r58_8mer	CAAGCAGAAGACGGCATACGAGATCCGACAACGTGACTGGAGTTCAGACGTGTGCTCTT	Custom Illumina i7 index 58 (E10)
PCR2_r59_8mer	CAAGCAGAAGACGGCATACGAGATCCTCTATCGTGACTGGAGTTCAGACGTGTGCTCTT	Custom Illumina i7 index 59 (E11)
PCR2_r60_8mer	CAAGCAGAAGACGGCATACGAGATCGACACACGTGACTGGAGTTCAGACGTGTGCTCTT	Custom Illumina i7 index 60 (E12)
PCR2_r61_8me	CAAGCAGAAGACGGCATACGAGATCGGATTGCG	Custom Illumina i7 index 61 (F1)

r	TGACTGGAGTTCAGACGTGTGCTCTT	
PCR2_r62_8mer	CAAGCAGAAGACGGCATACGAGATGAACAGGCGTGACTGGAGTTCAGACGTGTGCTCTT	Custom Illumina i7 index 62 (F2)
PCR2_r63_8mer	CAAGCAGAAGACGGCATACGAGATGACAGTGCGTGACTGGAGTTCAGACGTGTGCTCTT	Custom Illumina i7 index 63 (F3)
PCR2_r64_8mer	CAAGCAGAAGACGGCATACGAGATGAGTTAGCGTGACTGGAGTTCAGACGTGTGCTCTT	Custom Illumina i7 index 64 (F4)
PCR2_r65_8mer	CAAGCAGAAGACGGCATACGAGATGATGAATCGTGACTGGAGTTCAGACGTGTGCTCTT	Custom Illumina i7 index 65 (F5)
PCR2_r66_8mer	CAAGCAGAAGACGGCATACGAGATGCCAAGACGTGACTGGAGTTCAGACGTGTGCTCTT	Custom Illumina i7 index 66 (F6)
PCR2_r67_8mer	CAAGCAGAAGACGGCATACGAGATACAAGCTAGTGACTGGAGTTCAGACGTGTGCTCTT	Custom Illumina i7 index 67 (F7)
PCR2_r68_8mer	CAAGCAGAAGACGGCATACGAGATAAACATCGGTGACTGGAGTTCAGACGTGTGCTCTT	Custom Illumina i7 index 68 (F8)
PCR2_r69_8mer	CAAGCAGAAGACGGCATACGAGATACATTGGCGTGACTGGAGTTCAGACGTGTGCTCTT	Custom Illumina i7 index 69 (F9)
PCR2_r70_8mer	CAAGCAGAAGACGGCATACGAGATACCACTGTGTGACTGGAGTTCAGACGTGTGCTCTT	Custom Illumina i7 index 70 (F10)
PCR2_r71_8mer	CAAGCAGAAGACGGCATACGAGATCGCTGATCGTGACTGGAGTTCAGACGTGTGCTCTT	Custom Illumina i7 index 71 (F11)
PCR2_r72_8mer	CAAGCAGAAGACGGCATACGAGATCAGATCTGGTGACTGGAGTTCAGACGTGTGCTCTT	Custom Illumina i7 index 72 (F12)
PCR2_r73_8me	CAAGCAGAAGACGGCATACGAGATCTGTAGCCG	Custom Illumina i7 index 73 (G1)

r	TGACTGGAGTTCAGACGTGTGCTCTT	
PCR2_r74_8mer	CAAGCAGAAGACGGCATACGAGATAGTGGTCAGTGACTGGAGTTCAGACGTGTGCTCTT	Custom Illumina i7 index 74 (G2)
PCR2_r75_8mer	CAAGCAGAAGACGGCATACGAGATAACAACCAGTGACTGGAGTTCAGACGTGTGCTCTT	Custom Illumina i7 index 75 (G3)
PCR2_r76_8mer	CAAGCAGAAGACGGCATACGAGATACACAGAAGTGACTGGAGTTCAGACGTGTGCTCTT	Custom Illumina i7 index 76 (G4)
PCR2_r77_8mer	CAAGCAGAAGACGGCATACGAGATACGCTCGAGTGACTGGAGTTCAGACGTGTGCTCTT	Custom Illumina i7 index 77 (G5)
PCR2_r78_8mer	CAAGCAGAAGACGGCATACGAGATAGATCGCAGTGACTGGAGTTCAGACGTGTGCTCTT	Custom Illumina i7 index 78 (G6)
PCR2_r79_8mer	CAAGCAGAAGACGGCATACGAGATAGTCACTAGTGACTGGAGTTCAGACGTGTGCTCTT	Custom Illumina i7 index 79 (G7)
PCR2_r80_8mer	CAAGCAGAAGACGGCATACGAGATCGACTGGAGTGACTGGAGTTCAGACGTGTGCTCTT	Custom Illumina i7 index 80 (G8)
PCR2_r81_8mer	CAAGCAGAAGACGGCATACGAGATCTCAATGAGTGACTGGAGTTCAGACGTGTGCTCTT	Custom Illumina i7 index 81 (G9)
PCR2_r82_8mer	CAAGCAGAAGACGGCATACGAGATGACTAGTAGTGACTGGAGTTCAGACGTGTGCTCTT	Custom Illumina i7 index 82 (G10)
PCR2_r83_8mer	CAAGCAGAAGACGGCATACGAGATGTGTTCTAGTGACTGGAGTTCAGACGTGTGCTCTT	Custom Illumina i7 index 83 (G11)
PCR2_r84_8mer	CAAGCAGAAGACGGCATACGAGATAACTCACCGTGACTGGAGTTCAGACGTGTGCTCTT	Custom Illumina i7 index 84 (G12)
PCR2_r85_8me	CAAGCAGAAGACGGCATACGAGATAAGGACAC	Custom Illumina i7 index 85 (H1)

r	GTGACTGGAGTTCAGACGTGTGCTCTT	
PCR2_r86_8mer	CAAGCAGAAGACGGCATACGAGATAGCACCTCGTGACTGGAGTTCAGACGTGTGCTCTT	Custom Illumina i7 index 86 (H2)
PCR2_r87_8mer	CAAGCAGAAGACGGCATACGAGATAGCCATGCGTGACTGGAGTTCAGACGTGTGCTCTT	Custom Illumina i7 index 87 (H3)
PCR2_r88_8mer	CAAGCAGAAGACGGCATACGAGATAGGCTAACGTGACTGGAGTTCAGACGTGTGCTCTT	Custom Illumina i7 index 88 (H4)
PCR2_r89_8mer	CAAGCAGAAGACGGCATACGAGATATCATTCCGTGACTGGAGTTCAGACGTGTGCTCTT	Custom Illumina i7 index 89 (H5)
PCR2_r90_8mer	CAAGCAGAAGACGGCATACGAGATCTAAGGTCGTGACTGGAGTTCAGACGTGTGCTCTT	Custom Illumina i7 index 90 (H6)
PCR2_r91_8mer	CAAGCAGAAGACGGCATACGAGATATGCCTAAGTGACTGGAGTTCAGACGTGTGCTCTT	Custom Illumina i7 index 91 (H7)
PCR2_r92_8mer	CAAGCAGAAGACGGCATACGAGATATTGAGGAGTGACTGGAGTTCAGACGTGTGCTCTT	Custom Illumina i7 index 92 (H8)
PCR2_r93_8mer	CAAGCAGAAGACGGCATACGAGATAAGAGATCGTGACTGGAGTTCAGACGTGTGCTCTT	Custom Illumina i7 index 93 (H9)
PCR2_r94_8mer	CAAGCAGAAGACGGCATACGAGATATAGCGACGTGACTGGAGTTCAGACGTGTGCTCTT	Custom Illumina i7 index 94 (H10)
PCR2_r95_8mer	CAAGCAGAAGACGGCATACGAGATATTGGCTCGTGACTGGAGTTCAGACGTGTGCTCTT	Custom Illumina i7 index 95 (H11)
PCR2_r96_8mer	CAAGCAGAAGACGGCATACGAGATATCCTGTAGTGACTGGAGTTCAGACGTGTGCTCTT	Custom Illumina i7 index 96 (H12)

Supplemental_table_S2: summarized data and source data for Figure 2B. Edited fraction across genotype and SSAP.

genotype	locus	fraction_edited	ssap	well
WT	rpoB	9.32E-05	Beta	A1
WT	rpoB	0.00016102	Beta	A2
WT	rpoB	0.0001508	Beta	A3
WT	rpoB	0.0001307	Beta	A4
WT	rpoB	0.00017252	Beta	A5
WT	rpoB	7.12E-05	Beta	A6
WT	rpoB	0.00011803	Beta	A7
WT	rpoB	0.00014323	Beta	A8
WT	gyrA	3.75E-05	Beta	E1
WT	gyrA	1.58E-05	Beta	E2
WT	gyrA	5.26E-06	Beta	E3
WT	gyrA	1.06E-05	Beta	E4
WT	gyrA	2.66E-05	Beta	E5
WT	gyrA	5.29E-06	Beta	E6

WT	gyrA	5.48E-06	Beta	E7
WT	gyrA	1.13E-05	Beta	E8
ΔmutS	rpoB	0.00029032	Beta	A9
ΔmutS	rpoB	0.00019444	Beta	A10
ΔmutS	rpoB	0.00031214	Beta	A11
ΔmutS	rpoB	0.00020312	Beta	A12
ΔmutS	rpoB	0.00031395	Beta	B9
ΔmutS	rpoB	0.00027199	Beta	B10
ΔmutS	rpoB	0.00025501	Beta	B11
ΔmutS	rpoB	0.00037342	Beta	B12
ΔmutS	gyrA	0.00167809	Beta	E9
ΔmutS	gyrA	0.00145778	Beta	E10
ΔmutS	gyrA	0.00176807	Beta	E11
ΔmutS	gyrA	0.0017596	Beta	E12
ΔmutS	gyrA	0.00165089	Beta	F9
ΔmutS	gyrA	0.00616607	Beta	F10
ΔmutS	gyrA	0.00164878	Beta	F11
ΔmutS	gyrA	0.00152824	Beta	F12

ΔmutS , ΔrecJ	rpoB	0.00322439	Beta	B1
ΔmutS , ΔrecJ	rpoB	0.00291499	Beta	B2
ΔmutS , ΔrecJ	rpoB	0.00331901	Beta	B3
ΔmutS , ΔrecJ	rpoB	0.00294365	Beta	B4
ΔmutS , ΔrecJ	rpoB	0.00329234	Beta	B5
ΔmutS , ΔrecJ	rpoB	0.0032829	Beta	B6
ΔmutS , ΔrecJ	rpoB	0.00312337	Beta	B7
ΔmutS , ΔrecJ	rpoB	0.00352062	Beta	B8
ΔmutS , ΔrecJ	gyrA	0.03687721	Beta	F1
ΔmutS , ΔrecJ	gyrA	0.03631908	Beta	F2
ΔmutS , ΔrecJ	gyrA	0.04317863	Beta	F3
ΔmutS , ΔrecJ	gyrA	0.0344794	Beta	F4
ΔmutS , ΔrecJ	gyrA	0.03569975	Beta	F5
ΔmutS , ΔrecJ	gyrA	0.03528977	Beta	F6
ΔmutS , ΔrecJ	gyrA	0.03638852	Beta	F7
ΔmutS , ΔrecJ	gyrA	0.03654135	Beta	F8
ΔmutS , ΔrecJ, ΔsbcB	rpoB	0.06061889	Beta	C9
ΔmutS , ΔrecJ, ΔsbcB	rpoB	0.05995104	Beta	C10

ΔmutS , ΔrecJ, ΔsbcB	rpoB	0.01053677	Beta	C11
ΔmutS , ΔrecJ, ΔsbcB	rpoB	0.05843985	Beta	C12
ΔmutS , ΔrecJ, ΔsbcB	rpoB	0.05923514	Beta	D1
ΔmutS , ΔrecJ, ΔsbcB	rpoB	0.06256935	Beta	D2
ΔmutS , ΔrecJ, ΔsbcB	rpoB	0.06053654	Beta	D3
ΔmutS , ΔrecJ, ΔsbcB	rpoB	0.06256011	Beta	D4
ΔmutS , ΔrecJ, ΔsbcB	rpoB	0.05899817	Beta	D5
ΔmutS , ΔrecJ, ΔsbcB	rpoB	0.06520138	Beta	D6
ΔmutS , ΔrecJ, ΔsbcB	gyrA	0.28783597	Beta	G9
ΔmutS , ΔrecJ, ΔsbcB	gyrA	0.28481606	Beta	G10
ΔmutS , ΔrecJ, ΔsbcB	gyrA	0.2888569	Beta	G11
ΔmutS , ΔrecJ, ΔsbcB	gyrA	0.26955921	Beta	G12
ΔmutS , ΔrecJ, ΔsbcB	gyrA	0.29316805	Beta	H1
ΔmutS , ΔrecJ, ΔsbcB	gyrA	0.29879149	Beta	H2
ΔmutS , ΔrecJ, ΔsbcB	gyrA	0.29285045	Beta	H3
ΔmutS , ΔrecJ, ΔsbcB	gyrA	0.29838652	Beta	H4
ΔmutS , ΔrecJ, ΔsbcB	gyrA	0.29406375	Beta	H5
ΔmutS , ΔrecJ, ΔsbcB	gyrA	0.29958465	Beta	H6

ΔmutS , ΔrecJ, ΔsbcB, + CspRecT	gyrA	0.84498444	CspRecT	G1
ΔmutS , ΔrecJ, ΔsbcB, + CspRecT	gyrA	0.8508817	CspRecT	G2
ΔmutS , ΔrecJ, ΔsbcB, + CspRecT	gyrA	0.82264361	CspRecT	G3
ΔmutS , ΔrecJ, ΔsbcB, + CspRecT	gyrA	0.8452907	CspRecT	G4
ΔmutS , ΔrecJ, ΔsbcB, + CspRecT	gyrA	0.81406457	CspRecT	G5
ΔmutS , ΔrecJ, ΔsbcB, + CspRecT	gyrA	0.85009398	CspRecT	G6
ΔmutS , ΔrecJ, ΔsbcB, + CspRecT	gyrA	0.84937543	CspRecT	G7
ΔmutS , ΔrecJ, ΔsbcB, + CspRecT	gyrA	0.84486369	CspRecT	G8
ΔmutS , ΔrecJ, ΔsbcB, + CspRecT	rpoB	0.70608883	CspRecT	H1
ΔmutS , ΔrecJ, ΔsbcB, + CspRecT	rpoB	0.68284453	CspRecT	H2
ΔmutS , ΔrecJ, ΔsbcB, + CspRecT	rpoB	0.70397889	CspRecT	H3
ΔmutS , ΔrecJ, ΔsbcB, + CspRecT	rpoB	0.69858698	CspRecT	H4
ΔmutS , ΔrecJ, ΔsbcB, + CspRecT	rpoB	0.70239808	CspRecT	H5
ΔmutS , ΔrecJ, ΔsbcB, + CspRecT	rpoB	0.70515084	CspRecT	H6
ΔmutS , ΔrecJ, ΔsbcB, + CspRecT	rpoB	0.70141649	CspRecT	H7
ΔmutS , ΔrecJ, ΔsbcB, + CspRecT	rpoB	0.70163794	CspRecT	H8
ΔmutS, ΔsbcB	rpoB	0.06134563	Beta	C1
ΔmutS, ΔsbcB	rpoB	0.00136385	Beta	C2

ΔmutS, ΔsbcB	rpoB	0.00131544	Beta	C3
ΔmutS, ΔsbcB	rpoB	0.00154202	Beta	C4
ΔmutS, ΔsbcB	rpoB	0.00135054	Beta	C5
ΔmutS, ΔsbcB	rpoB	0.00145458	Beta	C6
ΔmutS, ΔsbcB	rpoB	0.00154701	Beta	C7
ΔmutS, ΔsbcB	rpoB	0.00158267	Beta	C8
ΔmutS, ΔsbcB	gyrA	0.0145603	Beta	G1
ΔmutS, ΔsbcB	gyrA	0.01433665	Beta	G2
ΔmutS, ΔsbcB	gyrA	0.01419199	Beta	G3
ΔmutS, ΔsbcB	gyrA	0.01401869	Beta	G4
ΔmutS, ΔsbcB	gyrA	0.01334759	Beta	G5
ΔmutS, ΔsbcB	gyrA	0.01271887	Beta	G6
ΔmutS, ΔsbcB	gyrA	0.01318843	Beta	G7
ΔmutS, ΔsbcB	gyrA	0.01315153	Beta	G8

Supplemental_table_S3: summarized data from Figure 3C, showing the enrichment scores for all alleles

SampleNum	rif	Count	nickname	seq_freq	enrichment.post.rif
S65	12.5	0	wecA_ko	4.53E-07	6.57E-05
S66	12.5	1	wecA_ko	2.58E-07	3.41E-05
S67	12.5	0	wecA_ko	3.38E-07	4.01E-05
S68	25	0	wecA_ko	4.03E-07	5.84E-05
S69	25	0	wecA_ko	4.26E-07	5.63E-05
S70	25	0	wecA_ko	5.30E-07	6.29E-05
S71	50	0	wecA_ko	6.00E-07	8.69E-05
S72	50	0	wecA_ko	6.00E-07	7.93E-05
S73	50	0	wecA_ko	6.99E-07	8.30E-05
S74	100	0	wecA_ko	7.82E-07	0.00011328
S75	100	0	wecA_ko	4.63E-07	6.12E-05
S76	100	0	wecA_ko	7.10E-07	8.43E-05
S65	12.5	0	typA_ko	4.53E-07	5.02E-05
S66	12.5	0	typA_ko	2.58E-07	2.98E-05
S67	12.5	0	typA_ko	3.38E-07	3.73E-05

S68	25	0	typA_ko	4.03E-07	4.46E-05
S69	25	0	typA_ko	4.26E-07	4.93E-05
S70	25	0	typA_ko	5.30E-07	5.85E-05
S71	50	0	typA_ko	6.00E-07	6.64E-05
S72	50	0	typA_ko	6.00E-07	6.95E-05
S73	50	0	typA_ko	6.99E-07	7.71E-05
S74	100	0	typA_ko	7.82E-07	8.66E-05
S75	100	0	typA_ko	4.63E-07	5.36E-05
S76	100	0	typA_ko	7.10E-07	7.84E-05
S65	12.5	1	yciW_ko	4.53E-07	3.12E-05
S66	12.5	0	yciW_ko	2.58E-07	1.79E-05
S67	12.5	3	yciW_ko	1.01E-06	6.99E-05
S68	25	485	yciW_ko	0.00019536	0.01347102
S69	25	0	yciW_ko	4.26E-07	2.96E-05
S70	25	0	yciW_ko	5.30E-07	3.65E-05
S71	50	0	yciW_ko	6.00E-07	4.14E-05
S72	50	1	yciW_ko	6.00E-07	4.18E-05

S73	50	0	yciW_ko	6.99E-07	4.82E-05
S74	100	1	yciW_ko	7.82E-07	5.39E-05
S75	100	0	yciW_ko	4.63E-07	3.22E-05
S76	100	0	yciW_ko	7.10E-07	4.90E-05
S65	12.5	0	ptsP_ko	4.53E-07	4.76E-05
S66	12.5	0	ptsP_ko	2.58E-07	2.57E-05
S67	12.5	0	ptsP_ko	3.38E-07	3.54E-05
S68	25	1	ptsP_ko	4.03E-07	4.23E-05
S69	25	1680	ptsP_ko	0.00071526	0.07139618
S70	25	0	ptsP_ko	5.30E-07	5.55E-05
S71	50	0	ptsP_ko	6.00E-07	6.30E-05
S72	50	0	ptsP_ko	6.00E-07	5.99E-05
S73	50	0	ptsP_ko	6.99E-07	7.32E-05
S74	100	0	ptsP_ko	7.82E-07	8.21E-05
S75	100	0	ptsP_ko	4.63E-07	4.62E-05
S76	100	0	ptsP_ko	7.10E-07	7.43E-05
S65	12.5	0	evgA_ko	4.53E-07	6.68E-05

S66	12.5	0	evgA_ko	2.58E-07	3.52E-05
S67	12.5	1	evgA_ko	3.38E-07	4.31E-05
S68	25	0	evgA_ko	4.03E-07	5.94E-05
S69	25	0	evgA_ko	4.26E-07	5.82E-05
S70	25	0	evgA_ko	5.30E-07	6.76E-05
S71	50	0	evgA_ko	6.00E-07	8.85E-05
S72	50	0	evgA_ko	6.00E-07	8.20E-05
S73	50	0	evgA_ko	6.99E-07	8.92E-05
S74	100	0	evgA_ko	7.82E-07	0.00011525
S75	100	0	evgA_ko	4.63E-07	6.32E-05
S76	100	0	evgA_ko	7.10E-07	9.06E-05
S65	12.5	1	ackA_ko	4.53E-07	3.14E-05
S66	12.5	0	ackA_ko	2.58E-07	1.73E-05
S67	12.5	1	ackA_ko	3.38E-07	2.36E-05
S68	25	0	ackA_ko	4.03E-07	2.79E-05
S69	25	1	ackA_ko	4.26E-07	2.85E-05
S70	25	0	ackA_ko	5.30E-07	3.71E-05

S71	50	0	ackA_ko	6.00E-07	4.15E-05
S72	50	0	ackA_ko	6.00E-07	4.02E-05
S73	50	0	ackA_ko	6.99E-07	4.89E-05
S74	100	0	ackA_ko	7.82E-07	5.41E-05
S75	100	0	ackA_ko	4.63E-07	3.10E-05
S76	100	864	ackA_ko	0.00061344	0.04294498
S65	12.5	0	yobF_ko	4.53E-07	6.82E-05
S66	12.5	0	yobF_ko	2.58E-07	3.66E-05
S67	12.5	1	yobF_ko	3.38E-07	4.56E-05
S68	25	0	yobF_ko	4.03E-07	6.07E-05
S69	25	0	yobF_ko	4.26E-07	6.05E-05
S70	25	0	yobF_ko	5.30E-07	7.15E-05
S71	50	0	yobF_ko	6.00E-07	9.03E-05
S72	50	0	yobF_ko	6.00E-07	8.52E-05
S73	50	0	yobF_ko	6.99E-07	9.44E-05
S74	100	0	yobF_ko	7.82E-07	0.00011771
S75	100	0	yobF_ko	4.63E-07	6.57E-05

S76	100	0	yobF_ko	7.10E-07	9.59E-05
S65	12.5	1	dapA_ko	4.53E-07	4.95E-05
S66	12.5	0	dapA_ko	2.58E-07	2.69E-05
S67	12.5	0	dapA_ko	3.38E-07	3.67E-05
S68	25	0	dapA_ko	4.03E-07	4.40E-05
S69	25	0	dapA_ko	4.26E-07	4.44E-05
S70	25	0	dapA_ko	5.30E-07	5.76E-05
S71	50	1	dapA_ko	6.00E-07	6.55E-05
S72	50	0	dapA_ko	6.00E-07	6.26E-05
S73	50	0	dapA_ko	6.99E-07	7.60E-05
S74	100	0	dapA_ko	7.82E-07	8.54E-05
S75	100	0	dapA_ko	4.63E-07	4.83E-05
S76	100	0	dapA_ko	7.10E-07	7.72E-05
S65	12.5	0	dapD_ko	4.53E-07	9.63E-05
S66	12.5	0	dapD_ko	2.58E-07	5.07E-05
S67	12.5	0	dapD_ko	3.38E-07	7.15E-05
S68	25	0	dapD_ko	4.03E-07	8.56E-05

S69	25	0	dapD_ko	4.26E-07	8.38E-05
S70	25	0	dapD_ko	5.30E-07	0.0001121
S71	50	0	dapD_ko	6.00E-07	0.00012746
S72	50	0	dapD_ko	6.00E-07	0.00011814
S73	50	0	dapD_ko	6.99E-07	0.00014787
S74	100	0	dapD_ko	7.82E-07	0.00016607
S75	100	0	dapD_ko	4.63E-07	9.11E-05
S76	100	0	dapD_ko	7.10E-07	0.00015023
S65	12.5	0	dnaJ_ko	4.53E-07	4.29E-05
S66	12.5	0	dnaJ_ko	2.58E-07	2.47E-05
S67	12.5	0	dnaJ_ko	3.38E-07	3.16E-05
S68	25	0	dnaJ_ko	4.03E-07	3.81E-05
S69	25	0	dnaJ_ko	4.26E-07	4.07E-05
S70	25	0	dnaJ_ko	5.30E-07	4.96E-05
S71	50	0	dnaJ_ko	6.00E-07	5.68E-05
S72	50	2428	dnaJ_ko	0.00145703	0.13943068
S73	50	0	dnaJ_ko	6.99E-07	6.54E-05

S74	100	0	dnaJ_ko	7.82E-07	7.40E-05
S75	100	0	dnaJ_ko	4.63E-07	4.43E-05
S76	100	0	dnaJ_ko	7.10E-07	6.64E-05
S65	12.5	1	endA_ko	4.53E-07	3.76E-05
S66	12.5	2652	endA_ko	0.00068314	0.05636256
S67	12.5	0	endA_ko	3.38E-07	2.74E-05
S68	25	0	endA_ko	4.03E-07	3.34E-05
S69	25	1008	endA_ko	0.00042916	0.03540789
S70	25	0	endA_ko	5.30E-07	4.30E-05
S71	50	0	endA_ko	6.00E-07	4.97E-05
S72	50	259	endA_ko	0.00015542	0.01282343
S73	50	1	endA_ko	6.99E-07	5.68E-05
S74	100	0	endA_ko	7.82E-07	6.48E-05
S75	100	0	endA_ko	4.63E-07	3.82E-05
S76	100	0	endA_ko	7.10E-07	5.77E-05
S65	12.5	0	recJ_ko	4.53E-07	2.54E-05
S66	12.5	1639	recJ_ko	0.00042219	0.023002

S67	12.5	0	recJ_ko	3.38E-07	1.84E-05
S68	25	0	recJ_ko	4.03E-07	2.26E-05
S69	25	0	recJ_ko	4.26E-07	2.32E-05
S70	25	0	recJ_ko	5.30E-07	2.88E-05
S71	50	0	recJ_ko	6.00E-07	3.36E-05
S72	50	0	recJ_ko	6.00E-07	3.27E-05
S73	50	0	recJ_ko	6.99E-07	3.80E-05
S74	100	0	recJ_ko	7.82E-07	4.38E-05
S75	100	3918	recJ_ko	0.00181269	0.09875871
S76	100	2	recJ_ko	1.42E-06	7.73E-05
S65	12.5	0	sbcB_ko	4.53E-07	2.94E-05
S66	12.5	0	sbcB_ko	2.58E-07	1.62E-05
S67	12.5	0	sbcB_ko	3.38E-07	2.18E-05
S68	25	1	sbcB_ko	4.03E-07	2.61E-05
S69	25	0	sbcB_ko	4.26E-07	2.68E-05
S70	25	0	sbcB_ko	5.30E-07	3.42E-05
S71	50	1	sbcB_ko	6.00E-07	3.89E-05

S72	50	0	sbcB_ko	6.00E-07	3.78E-05
S73	50	0	sbcB_ko	6.99E-07	4.51E-05
S74	100	0	sbcB_ko	7.82E-07	5.07E-05
S75	100	2	sbcB_ko	9.25E-07	5.83E-05
S76	100	0	sbcB_ko	7.10E-07	4.58E-05
S65	12.5	0	dnaA_ko	4.53E-07	4.50E-05
S66	12.5	0	dnaA_ko	2.58E-07	2.70E-05
S67	12.5	0	dnaA_ko	3.38E-07	3.65E-05
S68	25	0	dnaA_ko	4.03E-07	4.00E-05
S69	25	0	dnaA_ko	4.26E-07	4.46E-05
S70	25	0	dnaA_ko	5.30E-07	5.72E-05
S71	50	1	dnaA_ko	6.00E-07	5.95E-05
S72	50	0	dnaA_ko	6.00E-07	6.29E-05
S73	50	0	dnaA_ko	6.99E-07	7.55E-05
S74	100	0	dnaA_ko	7.82E-07	7.76E-05
S75	100	0	dnaA_ko	4.63E-07	4.85E-05
S76	100	0	dnaA_ko	7.10E-07	7.67E-05

S65	12.5	0	galE_ko	4.53E-07	7.44E-05
S66	12.5	0	galE_ko	2.58E-07	4.08E-05
S67	12.5	0	galE_ko	3.38E-07	5.41E-05
S68	25	0	galE_ko	4.03E-07	6.62E-05
S69	25	1	galE_ko	4.26E-07	6.74E-05
S70	25	272	galE_ko	0.00014411	0.0230831
S71	50	0	galE_ko	6.00E-07	9.85E-05
S72	50	0	galE_ko	6.00E-07	9.49E-05
S73	50	0	galE_ko	6.99E-07	0.00011195
S74	100	0	galE_ko	7.82E-07	0.00012835
S75	100	0	galE_ko	4.63E-07	7.32E-05
S76	100	0	galE_ko	7.10E-07	0.00011373
S65	12.5	0	mutS_ko	4.53E-07	6.58E-05
S66	12.5	1	mutS_ko	2.58E-07	4.10E-05
S67	12.5	0	mutS_ko	3.38E-07	5.61E-05
S68	25	0	mutS_ko	4.03E-07	5.86E-05
S69	25	0	mutS_ko	4.26E-07	6.78E-05

S70	25	0	mutS_ko	5.30E-07	8.80E-05
S71	50	0	mutS_ko	6.00E-07	8.72E-05
S72	50	0	mutS_ko	6.00E-07	9.55E-05
S73	50	0	mutS_ko	6.99E-07	0.00011609
S74	100	1	mutS_ko	7.82E-07	0.0001136
S75	100	0	mutS_ko	4.63E-07	7.37E-05
S76	100	0	mutS_ko	7.10E-07	0.00011794
S65	12.5	0	mutL_ko	4.53E-07	3.33E-05
S66	12.5	0	mutL_ko	2.58E-07	1.85E-05
S67	12.5	0	mutL_ko	3.38E-07	2.50E-05
S68	25	0	mutL_ko	4.03E-07	2.96E-05
S69	25	0	mutL_ko	4.26E-07	3.06E-05
S70	25	0	mutL_ko	5.30E-07	3.93E-05
S71	50	0	mutL_ko	6.00E-07	4.41E-05
S72	50	0	mutL_ko	6.00E-07	4.31E-05
S73	50	0	mutL_ko	6.99E-07	5.18E-05
S74	100	1	mutL_ko	7.82E-07	5.75E-05

S75	100	1	mutL_ko	4.63E-07	3.32E-05
S76	100	0	mutL_ko	7.10E-07	5.26E-05
S65	12.5	5	mcrA_ko	2.26E-06	0.00040154
S66	12.5	0	mcrA_ko	2.58E-07	4.29E-05
S67	12.5	0	mcrA_ko	3.38E-07	5.43E-05
S68	25	0	mcrA_ko	4.03E-07	7.14E-05
S69	25	0	mcrA_ko	4.26E-07	7.08E-05
S70	25	0	mcrA_ko	5.30E-07	8.52E-05
S71	50	0	mcrA_ko	6.00E-07	0.00010634
S72	50	0	mcrA_ko	6.00E-07	9.98E-05
S73	50	0	mcrA_ko	6.99E-07	0.00011244
S74	100	0	mcrA_ko	7.82E-07	0.00013855
S75	100	0	mcrA_ko	4.63E-07	7.70E-05
S76	100	0	mcrA_ko	7.10E-07	0.00011423
S65	12.5	10	marR_mut_V84E	4.53E-06	0.00018641
S66	12.5	0	marR_mut_V84E	2.58E-07	1.07E-05
S67	12.5	1	marR_mut_V84E	3.38E-07	1.49E-05

S68	25	0	marR_mut_V84E	4.03E-07	1.66E-05
S69	25	0	marR_mut_V84E	4.26E-07	1.78E-05
S70	25	1	marR_mut_V84E	5.30E-07	2.34E-05
S71	50	0	marR_mut_V84E	6.00E-07	2.47E-05
S72	50	0	marR_mut_V84E	6.00E-07	2.50E-05
S73	50	0	marR_mut_V84E	6.99E-07	3.09E-05
S74	100	0	marR_mut_V84E	7.82E-07	3.22E-05
S75	100	1	marR_mut_V84E	4.63E-07	1.93E-05
S76	100	0	marR_mut_V84E	7.10E-07	3.14E-05
S65	12.5	1	gyrA_mut_S83L	4.53E-07	2.28E-05
S66	12.5	0	gyrA_mut_S83L	2.58E-07	1.29E-05
S67	12.5	1	gyrA_mut_S83L	3.38E-07	1.69E-05
S68	25	0	gyrA_mut_S83L	4.03E-07	2.03E-05
S69	25	0	gyrA_mut_S83L	4.26E-07	2.14E-05
S70	25	0	gyrA_mut_S83L	5.30E-07	2.66E-05
S71	50	0	gyrA_mut_S83L	6.00E-07	3.02E-05
S72	50	0	gyrA_mut_S83L	6.00E-07	3.02E-05

S73	50	0	gyrA_mut_S83L	6.99E-07	3.50E-05
S74	100	0	gyrA_mut_S83L	7.82E-07	3.94E-05
S75	100	0	gyrA_mut_S83L	4.63E-07	2.33E-05
S76	100	0	gyrA_mut_S83L	7.10E-07	3.56E-05
S65	12.5	1	gyrA_mut_D87G	4.53E-07	1.86E-05
S66	12.5	1	gyrA_mut_D87G	2.58E-07	1.02E-05
S67	12.5	0	gyrA_mut_D87G	3.38E-07	1.39E-05
S68	25	0	gyrA_mut_D87G	4.03E-07	1.66E-05
S69	25	0	gyrA_mut_D87G	4.26E-07	1.68E-05
S70	25	0	gyrA_mut_D87G	5.30E-07	2.18E-05
S71	50	0	gyrA_mut_D87G	6.00E-07	2.46E-05
S72	50	1	gyrA_mut_D87G	6.00E-07	2.37E-05
S73	50	0	gyrA_mut_D87G	6.99E-07	2.87E-05
S74	100	0	gyrA_mut_D87G	7.82E-07	3.21E-05
S75	100	1	gyrA_mut_D87G	4.63E-07	1.83E-05
S76	100	0	gyrA_mut_D87G	7.10E-07	2.92E-05
S65	12.5	0	envZ_mut_A396T	4.53E-07	1.90E-05

S66	12.5	1	envZ_mut_A396T	2.58E-07	1.09E-05
S67	12.5	1	envZ_mut_A396T	3.38E-07	1.47E-05
S68	25	0	envZ_mut_A396T	4.03E-07	1.69E-05
S69	25	1	envZ_mut_A396T	4.26E-07	1.79E-05
S70	25	0	envZ_mut_A396T	5.30E-07	2.31E-05
S71	50	0	envZ_mut_A396T	6.00E-07	2.51E-05
S72	50	0	envZ_mut_A396T	6.00E-07	2.53E-05
S73	50	0	envZ_mut_A396T	6.99E-07	3.05E-05
S74	100	0	envZ_mut_A396T	7.82E-07	3.27E-05
S75	100	0	envZ_mut_A396T	4.63E-07	1.95E-05
S76	100	0	envZ_mut_A396T	7.10E-07	3.10E-05
S65	12.5	0	trkH_mut_T350K	4.53E-07	2.09E-05
S66	12.5	3	trkH_mut_T350K	7.73E-07	3.47E-05
S67	12.5	1	trkH_mut_T350K	3.38E-07	1.48E-05
S68	25	1	trkH_mut_T350K	4.03E-07	1.85E-05
S69	25	0	trkH_mut_T350K	4.26E-07	1.91E-05
S70	25	0	trkH_mut_T350K	5.30E-07	2.32E-05

S71	50	0	trkH_mut_T350K	6.00E-07	2.76E-05
S72	50	0	trkH_mut_T350K	6.00E-07	2.70E-05
S73	50	0	trkH_mut_T350K	6.99E-07	3.05E-05
S74	100	1	trkH_mut_T350K	7.82E-07	3.60E-05
S75	100	1	trkH_mut_T350K	4.63E-07	2.08E-05
S76	100	1	trkH_mut_T350K	7.10E-07	3.10E-05
S65	12.5	4	soxR_mut_D137E	1.81E-06	7.65E-05
S66	12.5	0	soxR_mut_D137E	2.58E-07	1.10E-05
S67	12.5	0	soxR_mut_D137E	3.38E-07	1.43E-05
S68	25	0	soxR_mut_D137E	4.03E-07	1.70E-05
S69	25	290	soxR_mut_D137E	0.00012347	0.00526505
S70	25	0	soxR_mut_D137E	5.30E-07	2.24E-05
S71	50	0	soxR_mut_D137E	6.00E-07	2.53E-05
S72	50	0	soxR_mut_D137E	6.00E-07	2.56E-05
S73	50	0	soxR_mut_D137E	6.99E-07	2.95E-05
S74	100	0	soxR_mut_D137E	7.82E-07	3.30E-05
S75	100	1	soxR_mut_D137E	4.63E-07	1.97E-05

S76	100	0	soxR_mut_D137E	7.10E-07	3.00E-05
S65	12.5	1	ycbZ_mut_S438R	4.53E-07	2.74E-05
S66	12.5	0	ycbZ_mut_S438R	2.58E-07	1.54E-05
S67	12.5	0	ycbZ_mut_S438R	3.38E-07	1.95E-05
S68	25	49	ycbZ_mut_S438R	1.97E-05	0.00119298
S69	25	0	ycbZ_mut_S438R	4.26E-07	2.54E-05
S70	25	0	ycbZ_mut_S438R	5.30E-07	3.06E-05
S71	50	0	ycbZ_mut_S438R	6.00E-07	3.63E-05
S72	50	0	ycbZ_mut_S438R	6.00E-07	3.58E-05
S73	50	0	ycbZ_mut_S438R	6.99E-07	4.04E-05
S74	100	0	ycbZ_mut_S438R	7.82E-07	4.72E-05
S75	100	1	ycbZ_mut_S438R	4.63E-07	2.76E-05
S76	100	1	ycbZ_mut_S438R	7.10E-07	4.10E-05
S65	12.5	3	folA_mut_P21L	1.36E-06	6.23E-05
S66	12.5	0	folA_mut_P21L	2.58E-07	1.20E-05
S67	12.5	1	folA_mut_P21L	3.38E-07	1.58E-05
S68	25	0	folA_mut_P21L	4.03E-07	1.85E-05

S69	25	0	folA_mut_P21L	4.26E-07	1.98E-05
S70	25	0	folA_mut_P21L	5.30E-07	2.47E-05
S71	50	1	folA_mut_P21L	6.00E-07	2.75E-05
S72	50	0	folA_mut_P21L	6.00E-07	2.79E-05
S73	50	0	folA_mut_P21L	6.99E-07	3.26E-05
S74	100	0	folA_mut_P21L	7.82E-07	3.58E-05
S75	100	0	folA_mut_P21L	4.63E-07	2.15E-05
S76	100	0	folA_mut_P21L	7.10E-07	3.31E-05
S65	12.5	2	folA_mut_W30C	9.06E-07	6.56E-05
S66	12.5	0	folA_mut_W30C	2.58E-07	1.94E-05
S67	12.5	1	folA_mut_W30C	3.38E-07	2.62E-05
S68	25	1	folA_mut_W30C	4.03E-07	2.92E-05
S69	25	2	folA_mut_W30C	8.52E-07	6.41E-05
S70	25	0	folA_mut_W30C	5.30E-07	4.10E-05
S71	50	0	folA_mut_W30C	6.00E-07	4.34E-05
S72	50	0	folA_mut_W30C	6.00E-07	4.52E-05
S73	50	0	folA_mut_W30C	6.99E-07	5.41E-05

S74	100	0	folA_mut_W30C	7.82E-07	5.66E-05
S75	100	1	folA_mut_W30C	4.63E-07	3.48E-05
S76	100	0	folA_mut_W30C	7.10E-07	5.50E-05
S65	12.5	66	folA_mut_W30G	2.99E-05	0.00109125
S66	12.5	2	folA_mut_W30G	5.15E-07	1.89E-05
S67	12.5	0	folA_mut_W30G	3.38E-07	1.22E-05
S68	25	0	folA_mut_W30G	4.03E-07	1.47E-05
S69	25	0	folA_mut_W30G	4.26E-07	1.56E-05
S70	25	0	folA_mut_W30G	5.30E-07	1.91E-05
S71	50	0	folA_mut_W30G	6.00E-07	2.19E-05
S72	50	0	folA_mut_W30G	6.00E-07	2.20E-05
S73	50	0	folA_mut_W30G	6.99E-07	2.52E-05
S74	100	0	folA_mut_W30G	7.82E-07	2.85E-05
S75	100	0	folA_mut_W30G	4.63E-07	1.70E-05
S76	100	0	folA_mut_W30G	7.10E-07	2.56E-05
S65	12.5	0	folA_mut_I94L	4.53E-07	1.69E-05
S66	12.5	1	folA_mut_I94L	2.58E-07	9.78E-06

S67	12.5	3	folA_mut_I94L	1.01E-06	3.96E-05
S68	25	0	folA_mut_I94L	4.03E-07	1.51E-05
S69	25	0	folA_mut_I94L	4.26E-07	1.62E-05
S70	25	0	folA_mut_I94L	5.30E-07	2.07E-05
S71	50	0	folA_mut_I94L	6.00E-07	2.24E-05
S72	50	0	folA_mut_I94L	6.00E-07	2.28E-05
S73	50	0	folA_mut_I94L	6.99E-07	2.73E-05
S74	100	1	folA_mut_I94L	7.82E-07	2.92E-05
S75	100	0	folA_mut_I94L	4.63E-07	1.76E-05
S76	100	0	folA_mut_I94L	7.10E-07	2.77E-05
S65	12.5	2	folA_mut_F153S	9.06E-07	3.35E-05
S66	12.5	0	folA_mut_F153S	2.58E-07	9.72E-06
S67	12.5	0	folA_mut_F153S	3.38E-07	1.28E-05
S68	25	0	folA_mut_F153S	4.03E-07	1.49E-05
S69	25	0	folA_mut_F153S	4.26E-07	1.61E-05
S70	25	223	folA_mut_F153S	0.00011815	0.00448491
S71	50	2	folA_mut_F153S	1.20E-06	4.43E-05

S72	50	1	folA_mut_F153S	6.00E-07	2.26E-05
S73	50	1	folA_mut_F153S	6.99E-07	2.65E-05
S74	100	0	folA_mut_F153S	7.82E-07	2.89E-05
S75	100	0	folA_mut_F153S	4.63E-07	1.74E-05
S76	100	1	folA_mut_F153S	7.10E-07	2.70E-05
S65	12.5	1	folA_mut_D27E	4.53E-07	2.73E-05
S66	12.5	1	folA_mut_D27E	2.58E-07	1.56E-05
S67	12.5	1	folA_mut_D27E	3.38E-07	2.16E-05
S68	25	0	folA_mut_D27E	4.03E-07	2.43E-05
S69	25	1	folA_mut_D27E	4.26E-07	2.58E-05
S70	25	0	folA_mut_D27E	5.30E-07	3.39E-05
S71	50	1	folA_mut_D27E	6.00E-07	3.61E-05
S72	50	1	folA_mut_D27E	6.00E-07	3.64E-05
S73	50	0	folA_mut_D27E	6.99E-07	4.47E-05
S74	100	0	folA_mut_D27E	7.82E-07	4.71E-05
S75	100	0	folA_mut_D27E	4.63E-07	2.81E-05
S76	100	0	folA_mut_D27E	7.10E-07	4.54E-05

S65	12.5	0	folA_mut_M20V	4.53E-07	3.69E-05
S66	12.5	2	folA_mut_M20V	5.15E-07	4.22E-05
S67	12.5	2	folA_mut_M20V	6.76E-07	5.57E-05
S68	25	0	folA_mut_M20V	4.03E-07	3.28E-05
S69	25	0	folA_mut_M20V	4.26E-07	3.49E-05
S70	25	0	folA_mut_M20V	5.30E-07	4.37E-05
S71	50	0	folA_mut_M20V	6.00E-07	4.89E-05
S72	50	2	folA_mut_M20V	1.20E-06	9.83E-05
S73	50	0	folA_mut_M20V	6.99E-07	5.77E-05
S74	100	0	folA_mut_M20V	7.82E-07	6.37E-05
S75	100	0	folA_mut_M20V	4.63E-07	3.79E-05
S76	100	0	folA_mut_M20V	7.10E-07	5.86E-05
S65	12.5	0	trkH_mut_G84D	4.53E-07	3.38E-05
S66	12.5	0	trkH_mut_G84D	2.58E-07	1.91E-05
S67	12.5	0	trkH_mut_G84D	3.38E-07	2.70E-05
S68	25	1	trkH_mut_G84D	4.03E-07	3.00E-05
S69	25	0	trkH_mut_G84D	4.26E-07	3.15E-05

S70	25	0	trkH_mut_G84D	5.30E-07	4.24E-05
S71	50	0	trkH_mut_G84D	6.00E-07	4.47E-05
S72	50	0	trkH_mut_G84D	6.00E-07	4.44E-05
S73	50	0	trkH_mut_G84D	6.99E-07	5.60E-05
S74	100	0	trkH_mut_G84D	7.82E-07	5.83E-05
S75	100	0	trkH_mut_G84D	4.63E-07	3.42E-05
S76	100	0	trkH_mut_G84D	7.10E-07	5.69E-05
S65	12.5	1	trkH_mut_I143S	4.53E-07	2.84E-05
S66	12.5	1	trkH_mut_I143S	2.58E-07	1.64E-05
S67	12.5	0	trkH_mut_I143S	3.38E-07	2.07E-05
S68	25	0	trkH_mut_I143S	4.03E-07	2.52E-05
S69	25	0	trkH_mut_I143S	4.26E-07	2.72E-05
S70	25	3	trkH_mut_I143S	1.59E-06	9.75E-05
S71	50	0	trkH_mut_I143S	6.00E-07	3.75E-05
S72	50	0	trkH_mut_I143S	6.00E-07	3.83E-05
S73	50	0	trkH_mut_I143S	6.99E-07	4.29E-05
S74	100	0	trkH_mut_I143S	7.82E-07	4.89E-05

S75	100	0	trkH_mut_I143S	4.63E-07	2.95E-05
S76	100	0	trkH_mut_I143S	7.10E-07	4.36E-05
S65	12.5	0	trkH_mut_L80Q	4.53E-07	3.00E-05
S66	12.5	0	trkH_mut_L80Q	2.58E-07	1.79E-05
S67	12.5	1	trkH_mut_L80Q	3.38E-07	2.28E-05
S68	25	0	trkH_mut_L80Q	4.03E-07	2.66E-05
S69	25	0	trkH_mut_L80Q	4.26E-07	2.95E-05
S70	25	0	trkH_mut_L80Q	5.30E-07	3.58E-05
S71	50	2	trkH_mut_L80Q	1.20E-06	7.94E-05
S72	50	0	trkH_mut_L80Q	6.00E-07	4.16E-05
S73	50	0	trkH_mut_L80Q	6.99E-07	4.72E-05
S74	100	0	trkH_mut_L80Q	7.82E-07	5.17E-05
S75	100	1	trkH_mut_L80Q	4.63E-07	3.21E-05
S76	100	0	trkH_mut_L80Q	7.10E-07	4.80E-05
S65	12.5	1	trkH_mut_L80R	4.53E-07	3.07E-05
S66	12.5	0	trkH_mut_L80R	2.58E-07	1.72E-05
S67	12.5	4047	trkH_mut_L80R	0.00136693	0.09322508

S68	25	0	trkH_mut_L80R	4.03E-07	2.73E-05
S69	25	0	trkH_mut_L80R	4.26E-07	2.84E-05
S70	25	0	trkH_mut_L80R	5.30E-07	3.61E-05
S71	50	1	trkH_mut_L80R	6.00E-07	4.06E-05
S72	50	0	trkH_mut_L80R	6.00E-07	4.00E-05
S73	50	0	trkH_mut_L80R	6.99E-07	4.77E-05
S74	100	0	trkH_mut_L80R	7.82E-07	5.29E-05
S75	100	0	trkH_mut_L80R	4.63E-07	3.08E-05
S76	100	0	trkH_mut_L80R	7.10E-07	4.84E-05
S65	12.5	0	marR_ko	4.53E-07	2.74E-05
S66	12.5	1	marR_ko	2.58E-07	1.59E-05
S67	12.5	1	marR_ko	3.38E-07	2.04E-05
S68	25	0	marR_ko	4.03E-07	2.44E-05
S69	25	0	marR_ko	4.26E-07	2.62E-05
S70	25	0	marR_ko	5.30E-07	3.20E-05
S71	50	2	marR_ko	1.20E-06	7.26E-05
S72	50	0	marR_ko	6.00E-07	3.69E-05

S73	50	0	marR_ko	6.99E-07	4.22E-05
S74	100	0	marR_ko	7.82E-07	4.73E-05
S75	100	0	marR_ko	4.63E-07	2.85E-05
S76	100	0	marR_ko	7.10E-07	4.29E-05
S65	12.5	0	envZ_ko	4.53E-07	3.05E-05
S66	12.5	0	envZ_ko	2.58E-07	1.75E-05
S67	12.5	0	envZ_ko	3.38E-07	2.32E-05
S68	25	1	envZ_ko	4.03E-07	2.71E-05
S69	25	1	envZ_ko	4.26E-07	2.89E-05
S70	25	0	envZ_ko	5.30E-07	3.63E-05
S71	50	0	envZ_ko	6.00E-07	4.03E-05
S72	50	0	envZ_ko	6.00E-07	4.08E-05
S73	50	0	envZ_ko	6.99E-07	4.79E-05
S74	100	0	envZ_ko	7.82E-07	5.26E-05
S75	100	0	envZ_ko	4.63E-07	3.14E-05
S76	100	2	envZ_ko	1.42E-06	9.74E-05
S65	12.5	1	trkH_ko	4.53E-07	2.57E-05

S66	12.5	0	trkH_ko	2.58E-07	1.42E-05
S67	12.5	3	trkH_ko	1.01E-06	5.42E-05
S68	25	0	trkH_ko	4.03E-07	2.29E-05
S69	25	0	trkH_ko	4.26E-07	2.35E-05
S70	25	0	trkH_ko	5.30E-07	2.83E-05
S71	50	1	trkH_ko	6.00E-07	3.40E-05
S72	50	0	trkH_ko	6.00E-07	3.31E-05
S73	50	0	trkH_ko	6.99E-07	3.74E-05
S74	100	1	trkH_ko	7.82E-07	4.43E-05
S75	100	0	trkH_ko	4.63E-07	2.55E-05
S76	100	0	trkH_ko	7.10E-07	3.80E-05
S65	12.5	1	folA_ko	4.53E-07	2.48E-05
S66	12.5	2	folA_ko	5.15E-07	2.86E-05
S67	12.5	0	folA_ko	3.38E-07	1.91E-05
S68	25	0	folA_ko	4.03E-07	2.21E-05
S69	25	0	folA_ko	4.26E-07	2.36E-05
S70	25	0	folA_ko	5.30E-07	2.99E-05

S71	50	0	folA_ko	6.00E-07	3.29E-05
S72	50	0	folA_ko	6.00E-07	3.33E-05
S73	50	0	folA_ko	6.99E-07	3.95E-05
S74	100	0	folA_ko	7.82E-07	4.28E-05
S75	100	1	folA_ko	4.63E-07	2.57E-05
S76	100	0	folA_ko	7.10E-07	4.01E-05
S65	12.5	0	pgi_ko	4.53E-07	2.87E-05
S66	12.5	0	pgi_ko	2.58E-07	1.59E-05
S67	12.5	0	pgi_ko	3.38E-07	2.00E-05
S68	25	0	pgi_ko	4.03E-07	2.55E-05
S69	25	0	pgi_ko	4.26E-07	2.63E-05
S70	25	1	pgi_ko	5.30E-07	3.14E-05
S71	50	0	pgi_ko	6.00E-07	3.80E-05
S72	50	0	pgi_ko	6.00E-07	3.71E-05
S73	50	0	pgi_ko	6.99E-07	4.15E-05
S74	100	0	pgi_ko	7.82E-07	4.95E-05
S75	100	0	pgi_ko	4.63E-07	2.86E-05

S76	100	1	pgi_ko	7.10E-07	4.21E-05
S65	12.5	0	galK_ko	4.53E-07	2.98E-05
S66	12.5	0	galK_ko	2.58E-07	1.82E-05
S67	12.5	0	galK_ko	3.38E-07	2.30E-05
S68	25	0	galK_ko	4.03E-07	2.65E-05
S69	25	0	galK_ko	4.26E-07	3.02E-05
S70	25	0	galK_ko	5.30E-07	3.60E-05
S71	50	0	galK_ko	6.00E-07	3.94E-05
S72	50	0	galK_ko	6.00E-07	4.25E-05
S73	50	0	galK_ko	6.99E-07	4.75E-05
S74	100	0	galK_ko	7.82E-07	5.14E-05
S75	100	0	galK_ko	4.63E-07	3.28E-05
S76	100	0	galK_ko	7.10E-07	4.83E-05
S65	12.5	3	fabA_KO	1.36E-06	7.26E-05
S66	12.5	0	fabA_KO	2.58E-07	1.39E-05
S67	12.5	0	fabA_KO	3.38E-07	1.78E-05
S68	25	0	fabA_KO	4.03E-07	2.15E-05

S69	25	1	fabA_KO	4.26E-07	2.29E-05
S70	25	0	fabA_KO	5.30E-07	2.79E-05
S71	50	0	fabA_KO	6.00E-07	3.21E-05
S72	50	0	fabA_KO	6.00E-07	3.23E-05
S73	50	0	fabA_KO	6.99E-07	3.68E-05
S74	100	0	fabA_KO	7.82E-07	4.18E-05
S75	100	0	fabA_KO	4.63E-07	2.49E-05
S76	100	0	fabA_KO	7.10E-07	3.73E-05
S65	12.5	0	gyrA_KO	4.53E-07	3.52E-05
S66	12.5	0	gyrA_KO	2.58E-07	2.06E-05
S67	12.5	1	gyrA_KO	3.38E-07	2.75E-05
S68	25	0	gyrA_KO	4.03E-07	3.13E-05
S69	25	0	gyrA_KO	4.26E-07	3.40E-05
S70	25	0	gyrA_KO	5.30E-07	4.32E-05
S71	50	0	gyrA_KO	6.00E-07	4.66E-05
S72	50	0	gyrA_KO	6.00E-07	4.80E-05
S73	50	2	gyrA_KO	1.40E-06	0.0001139

S74	100	0	gyrA_KO	7.82E-07	6.07E-05
S75	100	0	gyrA_KO	4.63E-07	3.70E-05
S76	100	0	gyrA_KO	7.10E-07	5.79E-05
S65	12.5	0	lacZ_KO	4.53E-07	3.78E-05
S66	12.5	0	lacZ_KO	2.58E-07	2.17E-05
S67	12.5	0	lacZ_KO	3.38E-07	2.84E-05
S68	25	0	lacZ_KO	4.03E-07	3.37E-05
S69	25	0	lacZ_KO	4.26E-07	3.58E-05
S70	25	0	lacZ_KO	5.30E-07	4.46E-05
S71	50	0	lacZ_KO	6.00E-07	5.01E-05
S72	50	0	lacZ_KO	6.00E-07	5.05E-05
S73	50	0	lacZ_KO	6.99E-07	5.88E-05
S74	100	0	lacZ_KO	7.82E-07	6.53E-05
S75	100	0	lacZ_KO	4.63E-07	3.90E-05
S76	100	0	lacZ_KO	7.10E-07	5.98E-05
S65	12.5	45	lacZ_KO2	2.04E-05	0.00185809
S66	12.5	0	lacZ_KO2	2.58E-07	2.37E-05

S67	12.5	2	lacZ_KO2	6.76E-07	5.81E-05
S68	25	0	lacZ_KO2	4.03E-07	3.67E-05
S69	25	0	lacZ_KO2	4.26E-07	3.92E-05
S70	25	0	lacZ_KO2	5.30E-07	4.56E-05
S71	50	0	lacZ_KO2	6.00E-07	5.47E-05
S72	50	0	lacZ_KO2	6.00E-07	5.52E-05
S73	50	0	lacZ_KO2	6.99E-07	6.01E-05
S74	100	0	lacZ_KO2	7.82E-07	7.12E-05
S75	100	0	lacZ_KO2	4.63E-07	4.26E-05
S76	100	0	lacZ_KO2	7.10E-07	6.11E-05
S65	12.5	0	recA_KO	4.53E-07	3.09E-05
S66	12.5	0	recA_KO	2.58E-07	1.83E-05
S67	12.5	1	recA_KO	3.38E-07	2.37E-05
S68	25	0	recA_KO	4.03E-07	2.75E-05
S69	25	0	recA_KO	4.26E-07	3.03E-05
S70	25	0	recA_KO	5.30E-07	3.71E-05
S71	50	2196	recA_KO	0.0013172	0.08987631

S72	50	0	recA_KO	6.00E-07	4.27E-05
S73	50	0	recA_KO	6.99E-07	4.90E-05
S74	100	1	recA_KO	7.82E-07	5.33E-05
S75	100	0	recA_KO	4.63E-07	3.30E-05
S76	100	0	recA_KO	7.10E-07	4.98E-05
S65	12.5	46	rpoB_A_1538_C	2.08E-05	0.0013945
S66	12.5	138	rpoB_A_1538_C	3.55E-05	0.00237748
S67	12.5	74	rpoB_A_1538_C	2.50E-05	0.00166847
S68	25	81	rpoB_A_1538_C	3.26E-05	0.00218348
S69	25	55	rpoB_A_1538_C	2.34E-05	0.00156611
S70	25	122	rpoB_A_1538_C	6.46E-05	0.00431463
S71	50	77	rpoB_A_1538_C	4.62E-05	0.00309086
S72	50	72	rpoB_A_1538_C	4.32E-05	0.00288973
S73	50	85	rpoB_A_1538_C	5.94E-05	0.00396541
S74	100	53	rpoB_A_1538_C	4.14E-05	0.00277194
S75	100	52	rpoB_A_1538_C	2.41E-05	0.00160903
S76	100	137	rpoB_A_1538_C	9.73E-05	0.00649304

S65	12.5	72350	rpoB_A_1547_G	0.03277419	1.74348159
S66	12.5	257867	rpoB_A_1547_G	0.06642467	3.73486669
S67	12.5	194295	rpoB_A_1547_G	0.06562601	3.49098096
S68	25	28324	rpoB_A_1547_G	0.0114091	0.60692769
S69	25	30207	rpoB_A_1547_G	0.01286067	0.72311823
S70	25	33034	rpoB_A_1547_G	0.01750141	0.93098892
S71	50	227	rpoB_A_1547_G	0.00013616	0.00724322
S72	50	495	rpoB_A_1547_G	0.00029705	0.01670213
S73	50	2695	rpoB_A_1547_G	0.00188346	0.10019068
S74	100	21	rpoB_A_1547_G	1.64E-05	0.00087306
S75	100	1285	rpoB_A_1547_G	0.00059451	0.03342773
S76	100	4	rpoB_A_1547_G	2.84E-06	0.00015107
S65	12.5	0	rpoB_A_1623_T	4.53E-07	2.82E-05
S66	12.5	0	rpoB_A_1623_T	2.58E-07	1.60E-05
S67	12.5	0	rpoB_A_1623_T	3.38E-07	2.11E-05
S68	25	68	rpoB_A_1623_T	2.74E-05	0.00170487
S69	25	1	rpoB_A_1623_T	4.26E-07	2.64E-05

S70	25	0	rpoB_A_1623_T	5.30E-07	3.30E-05
S71	50	0	rpoB_A_1623_T	6.00E-07	3.73E-05
S72	50	0	rpoB_A_1623_T	6.00E-07	3.72E-05
S73	50	0	rpoB_A_1623_T	6.99E-07	4.36E-05
S74	100	0	rpoB_A_1623_T	7.82E-07	4.86E-05
S75	100	1	rpoB_A_1623_T	4.63E-07	2.87E-05
S76	100	0	rpoB_A_1623_T	7.10E-07	4.43E-05
S65	12.5	1	rpoB_A_1657_G	4.53E-07	3.05E-05
S66	12.5	1	rpoB_A_1657_G	2.58E-07	1.81E-05
S67	12.5	0	rpoB_A_1657_G	3.38E-07	2.38E-05
S68	25	0	rpoB_A_1657_G	4.03E-07	2.72E-05
S69	25	0	rpoB_A_1657_G	4.26E-07	2.99E-05
S70	25	0	rpoB_A_1657_G	5.30E-07	3.74E-05
S71	50	0	rpoB_A_1657_G	6.00E-07	4.04E-05
S72	50	2208	rpoB_A_1657_G	0.00132501	0.09319431
S73	50	0	rpoB_A_1657_G	6.99E-07	4.93E-05
S74	100	0	rpoB_A_1657_G	7.82E-07	5.27E-05

S75	100	0	rpoB_A_1657_G	4.63E-07	3.25E-05
S76	100	0	rpoB_A_1657_G	7.10E-07	5.01E-05
S65	12.5	0	rpoB_A_1657_T	4.53E-07	3.10E-05
S66	12.5	0	rpoB_A_1657_T	2.58E-07	1.68E-05
S67	12.5	1	rpoB_A_1657_T	3.38E-07	2.30E-05
S68	25	0	rpoB_A_1657_T	4.03E-07	2.76E-05
S69	25	0	rpoB_A_1657_T	4.26E-07	2.78E-05
S70	25	0	rpoB_A_1657_T	5.30E-07	3.60E-05
S71	50	0	rpoB_A_1657_T	6.00E-07	4.11E-05
S72	50	1	rpoB_A_1657_T	6.00E-07	3.92E-05
S73	50	0	rpoB_A_1657_T	6.99E-07	4.75E-05
S74	100	1	rpoB_A_1657_T	7.82E-07	5.35E-05
S75	100	0	rpoB_A_1657_T	4.63E-07	3.02E-05
S76	100	0	rpoB_A_1657_T	7.10E-07	4.83E-05
S65	12.5	800	rpoB_A_1714_C	0.0003624	0.01765444
S66	12.5	1222	rpoB_A_1714_C	0.00031478	0.01541766
S67	12.5	1809	rpoB_A_1714_C	0.00061102	0.02906726

S68	25	3	rpoB_A_1714_C	1.21E-06	5.89E-05
S69	25	0	rpoB_A_1714_C	4.26E-07	2.09E-05
S70	25	0	rpoB_A_1714_C	5.30E-07	2.52E-05
S71	50	0	rpoB_A_1714_C	6.00E-07	2.92E-05
S72	50	0	rpoB_A_1714_C	6.00E-07	2.94E-05
S73	50	2	rpoB_A_1714_C	1.40E-06	6.65E-05
S74	100	2	rpoB_A_1714_C	1.56E-06	7.61E-05
S75	100	0	rpoB_A_1714_C	4.63E-07	2.27E-05
S76	100	0	rpoB_A_1714_C	7.10E-07	3.38E-05
S65	12.5	220	rpoB_A_443_T	9.97E-05	0.00769318
S66	12.5	1052	rpoB_A_443_T	0.00027099	0.01971743
S67	12.5	1404	rpoB_A_443_T	0.00047422	0.03413992
S68	25	0	rpoB_A_443_T	4.03E-07	3.11E-05
S69	25	12	rpoB_A_443_T	5.11E-06	0.00037174
S70	25	2	rpoB_A_443_T	1.06E-06	7.63E-05
S71	50	0	rpoB_A_443_T	6.00E-07	4.63E-05
S72	50	2089	rpoB_A_443_T	0.0012536	0.09121379

S73	50	0	rpoB_A_443_T	6.99E-07	5.03E-05
S74	100	0	rpoB_A_443_T	7.82E-07	6.03E-05
S75	100	1	rpoB_A_443_T	4.63E-07	3.37E-05
S76	100	3	rpoB_A_443_T	2.13E-06	0.00015334
S65	12.5	39596	rpoB_C_1535_T	0.01793679	1.19574727
S66	12.5	126592	rpoB_C_1535_T	0.03260918	2.19744792
S67	12.5	69145	rpoB_C_1535_T	0.02335475	1.56192447
S68	25	18550	rpoB_C_1535_T	0.00747207	0.49812178
S69	25	14853	rpoB_C_1535_T	0.00632368	0.42613665
S70	25	21118	rpoB_C_1535_T	0.01118831	0.74825482
S71	50	1825	rpoB_C_1535_T	0.00109467	0.0729756
S72	50	445	rpoB_C_1535_T	0.00026704	0.01799533
S73	50	343	rpoB_C_1535_T	0.00023971	0.01603157
S74	100	87	rpoB_C_1535_T	6.80E-05	0.00453268
S75	100	0	rpoB_C_1535_T	4.63E-07	3.12E-05
S76	100	1	rpoB_C_1535_T	7.10E-07	4.75E-05
S65	12.5	483233	rpoB_C_1576_A	0.21890212	15.6722414

S66	12.5	784842	rpoB_C_1576_A	0.2021696	14.6145837
S67	12.5	638289	rpoB_C_1576_A	0.21559156	15.4743802
S68	25	578819	rpoB_C_1576_A	0.2331523	16.6924792
S69	25	520496	rpoB_C_1576_A	0.22160186	16.0193168
S70	25	357000	rpoB_C_1576_A	0.18913857	13.5756806
S71	50	238142	rpoB_C_1576_A	0.14284206	10.2267409
S72	50	274695	rpoB_C_1576_A	0.16484347	11.9163254
S73	50	258562	rpoB_C_1576_A	0.18070151	12.9700991
S74	100	110423	rpoB_C_1576_A	0.0862979	6.17847632
S75	100	135162	rpoB_C_1576_A	0.06253348	4.52046621
S76	100	130502	rpoB_C_1576_A	0.09265574	6.65049309
S65	12.5	240194	rpoB_C_1576_G	0.10880668	8.08910455
S66	12.5	505311	rpoB_C_1576_G	0.13016444	9.17993732
S67	12.5	326547	rpoB_C_1576_G	0.11029608	7.79220043
S68	25	289143	rpoB_C_1576_G	0.1164688	8.65873631
S69	25	233316	rpoB_C_1576_G	0.09933459	7.00564077
S70	25	227468	rpoB_C_1576_G	0.12051253	8.513972

S71	50	261766	rpoB_C_1576_G	0.15701218	11.6728864
S72	50	231843	rpoB_C_1576_G	0.13912814	9.8121084
S73	50	197965	rpoB_C_1576_G	0.13835202	9.77429682
S74	100	201990	rpoB_C_1576_G	0.15785944	11.7358751
S75	100	387174	rpoB_C_1576_G	0.1791283	12.6331471
S76	100	219810	rpoB_C_1576_G	0.15606396	11.0256103
S65	12.5	766570	rpoB_C_1576_T	0.34725236	29.106547
S66	12.5	1246887	rpoB_C_1576_T	0.32118904	24.9071387
S67	12.5	924816	rpoB_C_1576_T	0.3123703	24.9977827
S68	25	840428	rpoB_C_1576_T	0.33853021	28.3754604
S69	25	885610	rpoB_C_1576_T	0.37704962	29.2389406
S70	25	715070	rpoB_C_1576_T	0.37884403	30.3174175
S71	50	684565	rpoB_C_1576_T	0.41061499	34.4175765
S72	50	776184	rpoB_C_1576_T	0.46578521	36.1200893
S73	50	569662	rpoB_C_1576_T	0.39812032	31.8600239
S74	100	656197	rpoB_C_1576_T	0.51283179	42.9853458
S75	100	1102258	rpoB_C_1576_T	0.50996607	39.5461679

S76	100	680647	rpoB_C_1576_T	0.48325584	38.6730892
S65	12.5	0	rpoB_C_1721_A	4.53E-07	2.90E-05
S66	12.5	2087	rpoB_C_1721_A	0.0005376	0.03514962
S67	12.5	26	rpoB_C_1721_A	8.78E-06	0.00057105
S68	25	1	rpoB_C_1721_A	4.03E-07	2.58E-05
S69	25	15	rpoB_C_1721_A	6.39E-06	0.00041755
S70	25	0	rpoB_C_1721_A	5.30E-07	3.45E-05
S71	50	0	rpoB_C_1721_A	6.00E-07	3.85E-05
S72	50	2	rpoB_C_1721_A	1.20E-06	7.85E-05
S73	50	1	rpoB_C_1721_A	6.99E-07	4.54E-05
S74	100	3	rpoB_C_1721_A	2.34E-06	0.00015032
S75	100	1	rpoB_C_1721_A	4.63E-07	3.02E-05
S76	100	0	rpoB_C_1721_A	7.10E-07	4.62E-05
S65	12.5	1968	rpoB_CACTCGGCCCAG_1595_DELETE	0.00089149	0.08260284
S66	12.5	13372	rpoB_CACTCGGCCCAG_1595_DELETE	0.00344453	0.31176625
S67	12.5	5430	rpoB_CACTCGGCCCAG_1595_DELETE	0.00183406	0.16741736
S68	25	5066	rpoB_CACTCGGCCCAG_1595_DELETE	0.00204062	0.18907695

S69	25	6077	rpoB_CACTCGGCCCAG_1595_DELETE	0.00258729	0.23417706
S70	25	5170	rpoB_CACTCGGCCCAG_1595_DELETE	0.00273907	0.25002803
S71	50	927	rpoB_CACTCGGCCCAG_1595_DELETE	0.00055603	0.05152006
S72	50	1585	rpoB_CACTCGGCCCAG_1595_DELETE	0.00095115	0.08608934
S73	50	1379	rpoB_CACTCGGCCCAG_1595_DELETE	0.00096374	0.08797264
S74	100	150	rpoB_CACTCGGCCCAG_1595_DELETE	0.00011723	0.01086197
S75	100	791	rpoB_CACTCGGCCCAG_1595_DELETE	0.00036596	0.0331233
S76	100	82	rpoB_CACTCGGCCCAG_1595_DELETE	5.82E-05	0.00531441
S65	12.5	4	rpoB_CG_1574_TT	1.81E-06	0.00012073
S66	12.5	1	rpoB_CG_1574_TT	2.58E-07	1.71E-05
S67	12.5	2	rpoB_CG_1574_TT	6.76E-07	4.43E-05
S68	25	0	rpoB_CG_1574_TT	4.03E-07	2.68E-05
S69	25	0	rpoB_CG_1574_TT	4.26E-07	2.83E-05
S70	25	0	rpoB_CG_1574_TT	5.30E-07	3.48E-05
S71	50	1	rpoB_CG_1574_TT	6.00E-07	4.00E-05
S72	50	1	rpoB_CG_1574_TT	6.00E-07	3.99E-05
S73	50	1	rpoB_CG_1574_TT	6.99E-07	4.59E-05

S74	100	0	rpoB_CG_1574_TT	7.82E-07	5.21E-05
S75	100	0	rpoB_CG_1574_TT	4.63E-07	3.08E-05
S76	100	0	rpoB_CG_1574_TT	7.10E-07	4.66E-05
S65	12.5	0	rpoB_G_1545_A	4.53E-07	2.08E-05
S66	12.5	4	rpoB_G_1545_A	1.03E-06	4.73E-05
S67	12.5	0	rpoB_G_1545_A	3.38E-07	1.56E-05
S68	25	0	rpoB_G_1545_A	4.03E-07	1.85E-05
S69	25	1	rpoB_G_1545_A	4.26E-07	1.96E-05
S70	25	0	rpoB_G_1545_A	5.30E-07	2.44E-05
S71	50	0	rpoB_G_1545_A	6.00E-07	2.75E-05
S72	50	2631	rpoB_G_1545_A	0.00157885	0.07253659
S73	50	0	rpoB_G_1545_A	6.99E-07	3.22E-05
S74	100	1	rpoB_G_1545_A	7.82E-07	3.58E-05
S75	100	0	rpoB_G_1545_A	4.63E-07	2.13E-05
S76	100	0	rpoB_G_1545_A	7.10E-07	3.28E-05
S65	12.5	2	rpoB_G_1545_T	9.06E-07	4.51E-05
S66	12.5	5663	rpoB_G_1545_T	0.00145875	0.07367214

S67	12.5	6	rpoB_G_1545_T	2.03E-06	0.00010244
S68	25	0	rpoB_G_1545_T	4.03E-07	2.00E-05
S69	25	0	rpoB_G_1545_T	4.26E-07	2.15E-05
S70	25	0	rpoB_G_1545_T	5.30E-07	2.68E-05
S71	50	0	rpoB_G_1545_T	6.00E-07	2.98E-05
S72	50	0	rpoB_G_1545_T	6.00E-07	3.03E-05
S73	50	0	rpoB_G_1545_T	6.99E-07	3.53E-05
S74	100	1	rpoB_G_1545_T	7.82E-07	3.89E-05
S75	100	0	rpoB_G_1545_T	4.63E-07	2.34E-05
S76	100	1	rpoB_G_1545_T	7.10E-07	3.59E-05
S65	12.5	600970	rpoB_G_1546_T	0.27223639	20.5576473
S66	12.5	932750	rpoB_G_1546_T	0.24026963	17.6607245
S67	12.5	794721	rpoB_G_1546_T	0.26842879	19.0230411
S68	25	721553	rpoB_G_1546_T	0.29064654	21.9478706
S69	25	655159	rpoB_G_1546_T	0.2789348	20.5027609
S70	25	528019	rpoB_G_1546_T	0.27974442	19.824959
S71	50	477431	rpoB_G_1546_T	0.28637212	21.6250918

S72	50	371455	rpoB_G_1546_T	0.2229088	16.3846381
S73	50	400180	rpoB_G_1546_T	0.27967424	19.8199853
S74	100	310620	rpoB_G_1546_T	0.24275608	18.3314724
S75	100	530780	rpoB_G_1546_T	0.24556845	18.0502081
S76	100	376402	rpoB_G_1546_T	0.26724347	18.9390397
S65	12.5	1424	rpoB_KO	0.00064506	0.0359368
S66	12.5	0	rpoB_KO	2.58E-07	1.46E-05
S67	12.5	1	rpoB_KO	3.38E-07	1.87E-05
S68	25	3	rpoB_KO	1.21E-06	6.73E-05
S69	25	1	rpoB_KO	4.26E-07	2.41E-05
S70	25	2	rpoB_KO	1.06E-06	5.87E-05
S71	50	0	rpoB_KO	6.00E-07	3.34E-05
S72	50	0	rpoB_KO	6.00E-07	3.40E-05
S73	50	0	rpoB_KO	6.99E-07	3.87E-05
S74	100	0	rpoB_KO	7.82E-07	4.35E-05
S75	100	0	rpoB_KO	4.63E-07	2.62E-05
S76	100	0	rpoB_KO	7.10E-07	3.94E-05

S65	12.5	0	rpsL_KO	4.53E-07	3.82E-05
S66	12.5	0	rpsL_KO	2.58E-07	2.28E-05
S67	12.5	0	rpsL_KO	3.38E-07	3.14E-05
S68	25	0	rpsL_KO	4.03E-07	3.39E-05
S69	25	0	rpsL_KO	4.26E-07	3.76E-05
S70	25	0	rpsL_KO	5.30E-07	4.93E-05
S71	50	0	rpsL_KO	6.00E-07	5.05E-05
S72	50	0	rpsL_KO	6.00E-07	5.30E-05
S73	50	0	rpsL_KO	6.99E-07	6.50E-05
S74	100	0	rpsL_KO	7.82E-07	6.58E-05
S75	100	0	rpsL_KO	4.63E-07	4.09E-05
S76	100	0	rpsL_KO	7.10E-07	6.60E-05

Supplemental_table_S4: summary of aberrantly low and high genomic coverage obtained in the RLR library, resulting from alignment artifacts.

window	mean_window_count	notes
224500	228.046	ribosomal RNA
228500	235.416	ribosomal RNA
274000	306.606	mobile element IS5A
283500	228.31	adjacent to mobile elements IS1B, IS1C, IS30
381500	250.26	mobile element IS2A
574500	284.334	mobile element IS5B
688000	306.722	mobile element IS5D
1395000	296.984	mobile element IS5F
1466500	244.556	adjacent to mobile elements IS2B, IS30C
1649500	243.912	adjacent to mobile element IS2E
2067500	233.486	adjacent to mobile element IS5H
2100500	297.728	adjacent to mobile element IS5I
2287500	235.154	adjacent to mobile element IS5K
2288000	275.48	adjacent to mobile element IS5K
2725000	225.774	adjacent to ribosomal RNA

2726000	233.762	ribosomal RNA
2726500	245.828	ribosomal RNA
2995000	243.252	adjacent to mobile element IS2H
3129000	297.266	adjacent to mobile element IS5LO
3185000	233.872	adjacent to mobile element IS2I
3364500	281.456	adjacent to mobile element IS5R
3424000	256.484	ribosomal RNA
3426000	226.362	ribosomal RNA
3651000	286.762	adjacent to mobile element IS5T
3943000	246.63	ribosomal RNA
4034500	230.372	ribosomal RNA
4035000	228.734	ribosomal RNA
4165500	240.72	ribosomal RNA
4166000	230.952	ribosomal RNA
4168000	246.918	ribosomal RNA
4169500	235.474	ribosomal RNA
4207000	231.986	ribosomal RNA
4207500	230.008	ribosomal RNA

4209500	246.766	ribosomal RNA

window	mean_window_count	notes
67500	0	DE(araD-araB)567, this region absent in BW25113(ΔlacA) parent strain evolved in Baym et al. 2016
68000	0	
68500	0	
69000	0	
69500	0	
70000	0	
361000	0	lacZ4787(del)(::rrnB-3) mutation and ΔlacA alterations in BW25113(lacA) parent strain. No lacZ,Y,A
364500	0	
365000	0	
365500	0	
3581000	0	ryhB antisense RNA region
4093500	0	DE(rhaD-rhaB)568 mutation in BW25113(ΔlacA) parent strain evolved in Baym et al. 2016
4094000	0	
4094500	0	
4095000	0	

4640500	0	yjjY and yjtD loci, end of reference genome sequence. Decreased coverage likely an artifact of BWA-MEM alignment of reads from a circular genome to a linear reference sequence.
4641000	0	
4641500	0	
4642000	0	