

The no-SCAR (Scarless Cas9 Assisted Recombineering) system for genome editing in *Escherichia coli*.

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**Supplementary Information**

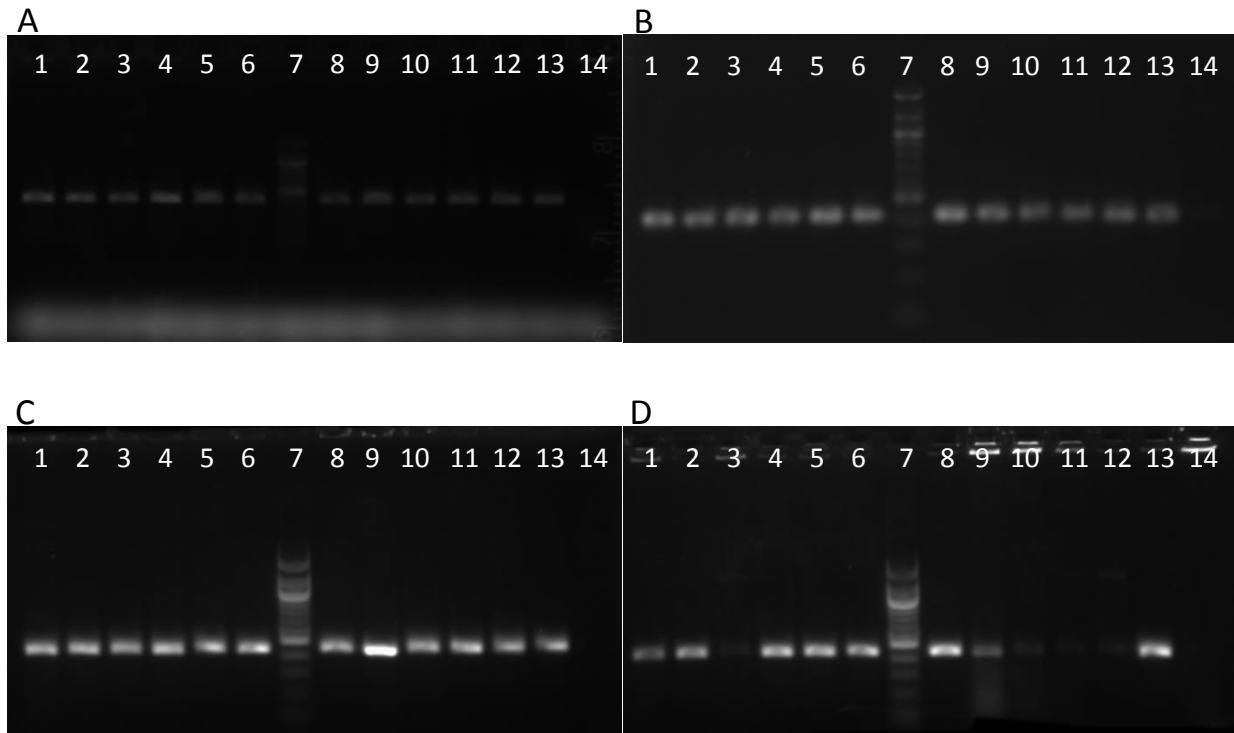


Figure S1. Allele specific genotyping PCR of *ack* point mutations. PCR products were separated on a 1.6% agarose gel. (Top) Colonies from cells that possessed both the pCas9cr4 and pKDsgRNA-*ack* before transforming *ackmut2* oligo. (Bottom) Colonies from cells that possessed only the pKDsgRNA-*ack* plasmid and was then co-transformed with pCas9cr4 and *ackmut2*. The colonies from lanes 3, 10, 11, and 12 were re-screened a second time and 3 of the 4 confirmed to be wild-type. Lane 14 was the wild-type control in which no PCR product was observed. (Lane 7) 100 bp DNA ladder (NEB).

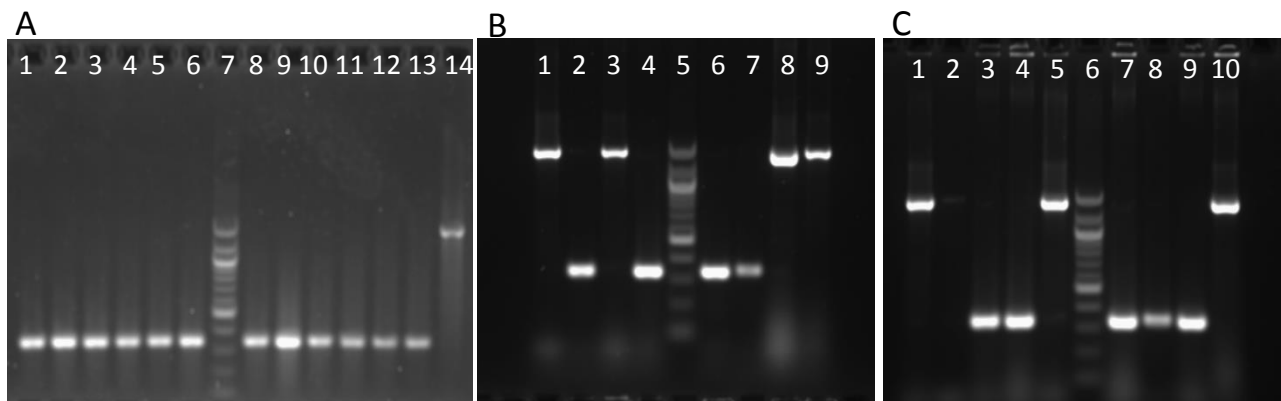


Figure S2. PCR detection of *ack* deletion mutants. PCR products were separated on a 1.6% agarose gel with a 100 bp DNA ladder (NEB). (A) Colonies from cells that possessed both the pCas9cr4 and pKDsgRNA-*ack* before transforming *ackCD* oligonucleotide. Lane 14 possessed a wild-type control. (B + C) Colonies from cells that possessed only the pKDsgRNA-*ack* plasmid and were then co-transformed with pCas9cr4 and *ackCD*.

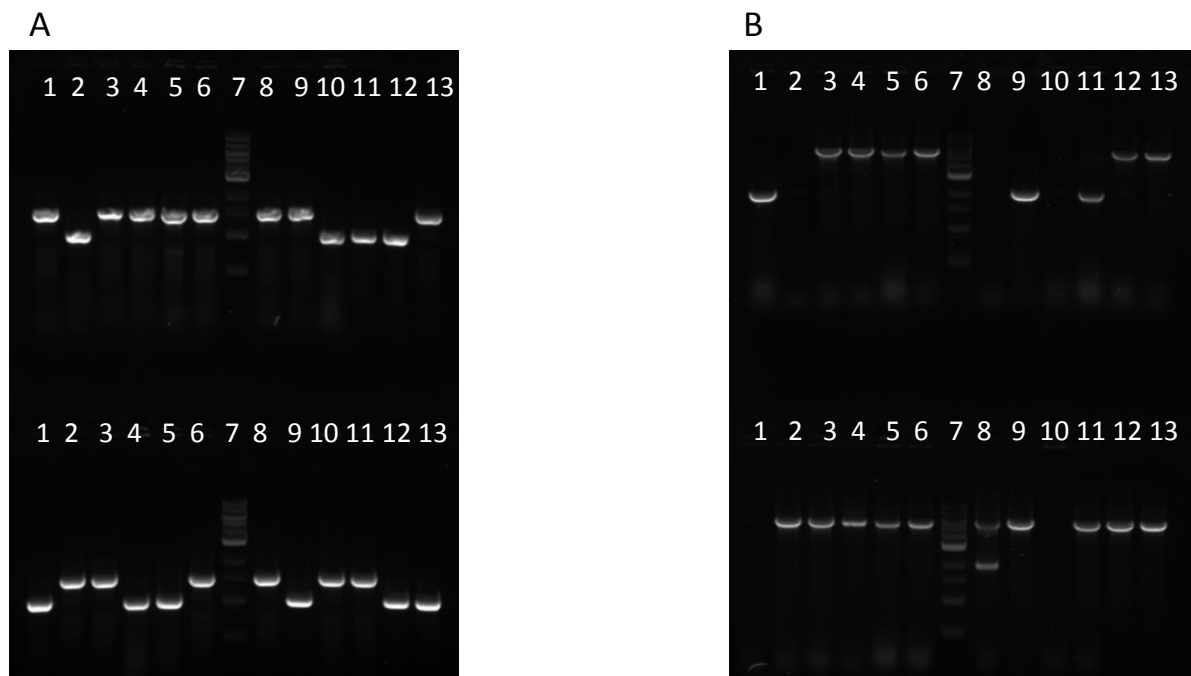


Figure S3. PCR detection of genomic *sspB* and *yqhC-yqhD-dkgA* deletions. PCR products were run on a 0.8% agarose gel. (A) Twenty-four colonies were screened to detect the 477 bp deletion of *sspB*. Ten colonies possessed PCR products of 900 bp, indicating successful deletion of *sspB*, and the remaining 14 colonies had wild-type size of 1400 bp. (B) Twenty-four colonies were screened for the 3200 bp deletion of *yqhC-yqhD-dkgA*. Fifteen colonies possessed wild-type PCR product of 5 kbp, three possessed the 2.2 kbp deletion with a 2 kbp product, one had mix of both products indicating incomplete segregation of the chimeric genotypes, and the PCR reaction failed in 5 of the reactions. A one kb ladder is in lane 7 of each gel.

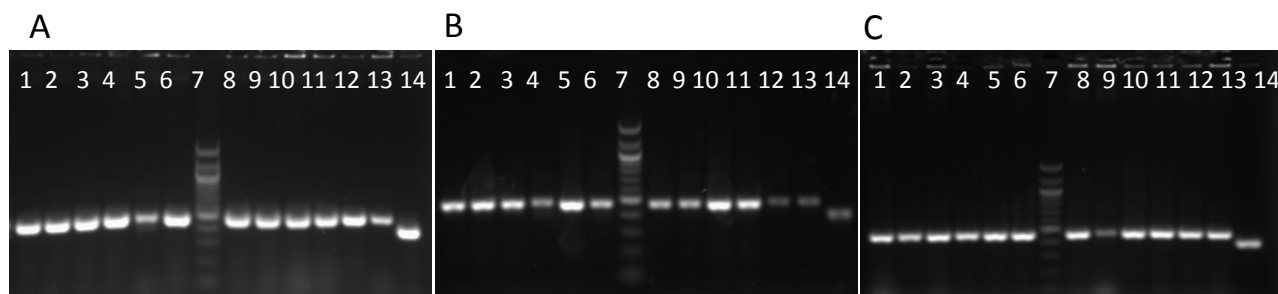


Figure S4. PCR detection of genomic *ssrA* tag insertion at *pfkA*. PCR products were separated on a 1.6% agarose gel with 100 bp ladder in lane 7. (A,B,C) Twelve colonies from three independent experiments were screened by PCR sizing. The wild-type control in lane 14 in each gel shows a size of 391 bp, while all of the experimental colonies have a size increased by 80 bp.

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1 TCGGTTTCAGGGTAAAGGAATCTGCCTTTTTCCGAAATCAT T----- 42
2 TCGGTTTCAGGGTAAAGGAATCTGCCTTTTTCCGAAATCATACGGCCCCA 50
3 TCGGTTTCAGGGTAAAGGAATCTGCCTTTTTCCGAAATCATACGGCCCCA 50
4 TCGGTTTCAGGGTAAAGGAATCTGCCTTTTTCCGAAATCATACGGCCCCA 50
5 TCGGTTTCAGGGTAAAGGAATCTGCCTTTTTCCGAAATCATACGGCCCCA 50
6 TCGGTTTCAGGGTAAAGGAATCTGCCTTTTTCCGAAATCATACGGCCCCA 50

1 ----- 42
2 AGGTCCAAACGGTGAAGGTACCTTAGCTCGCATCCGCATAGTTTTTCGCTA 100
3 AGGTCCAAACGGTGAAGGTACCTTAGCTCGCATCCGCATAGTTTTTCGCTA 100
4 AGGTCCAAACGGTGAAGGTACCTTAGCTCGCATCCGCATAGTTTTTCGCTA 100
5 AGGTCCAAACGGTGAAGGTACCTTAGCTCGCATCCGCATAGTTTTTCGCTA 100
6 AGGTCCAAACGGTGAAGGTACCTTAGCTCGCATCCGCATAGTTTTTCGCTA 100

1 -----AATACAGTTTTTTTCGCGCAGTCCAGCCAGTC 73
2 TAGTTTTTCATCGTTCGCCGCATACAGTTTTTTTCGCGCAGTCCAGCCAGTC 150
3 TAGTTTTTCATCGTTCGCCGCATACAGTTTTTTTCGCGCAGTCCAGCCAGTC 150
4 TAGTTTTTCATCGTTCGCCGCATACAGTTTTTTTCGCGCAGTCCAGCCAGTC 150
5 TAGTTTTTCATCGTTCGCCGCATACAGTTTTTTTCGCGCAGTCCAGCCAGTC 150
6 TAGTTTTTCATCGTTCGCCGCATACAGTTTTTTTCGCGCAGTCCAGCCAGTC 150

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**Figure S5. Sequence alignment of the C-terminus of *pfkA*. Line 1 was the wild-type. Lines 2-6 were putative insertion mutants identified by colony PCR. The sequence confirmed insertion of the *ssrA* tag.**

RBS
PAM

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1 AATTCATTAAAGAGGAGAAAGGATCCATGATTAAGAAAATCGGTGTGTTG
2 AATTCATTAAAGAGGAGAAAGGATCCATGATTAAGAAAATCGGTGTGTTG
3 AATTCATTAAAGAGGAGAAAGGATCCATGATTAAGAAAATCGGTGTGTTG
4 AATTCATTAAAGAGGAGAAAGGATCCATGATTAAGAAAATCGGTGTGTTG
5 AATTCATTAAAGAGGAGAAAGGATCCATGATTAAGAAAATCGGTGTGTTG
6 AATTCATTAAAGAGGAGAAAGGATCCATGATTAAGAAAATCGGTGTGTTG
7 AATTCATTAAAGAGGAGAAAGGATCCATGATTAAGAAAATCGGTGTGTTG
8 AATTCATTAAAGAGGAGAAAGGATCCATGATTAAGAAAATCGGTGTGTTG
9 AATTCATTAAAGAGGAGAAAGGATCCATGATTAAGAAAATCGGTGTGTTG
10 AATTCATTAAAGAGGAGAAAGGATCCATGATTAAGAAAATCGGTGTGTTG
11 AATTCATTAAAGAGGAGAAAGGATCCATGATTAAGAAAATCGGTGTGTTG
12 AATTCATTAAAGAGGAGAAAGGATCCATGATTAAGAAAATCGGTGTGTTG
13 AATTCATTAAAGAGGAGAAAGGATCCATGATTAAGAAAATCGGTGTGTTG
14 AATTCATTAAAGAGGAGAAAGGATCCATGATTAAAGAAATCGGTGTGTTG
15 AATTCATTAAAGAGGAGAAAGGATCCATGATTAAAGAAATCGGTGTGTTG
16 AATTCATTAAAGAGGCAGAAAGGATCCATGATTAAAGAAATCGGTGTGTTG
17 AATTCATTAAAGAGGAGAAAGGATCCATGATTAAAGAAATCGGTGTGTTG
18 AATTCATTAAAGAGTGAGAAAGGATCCATGATTAAAGAAATCGGTGTGTTG
19 AATTCATTAAAGAGTTGAAAGGATCCATGATTAAAGAAATCGGTGTGTTG
20 AATTCATTAAAGAGTCGAAAGGATCCATGATTAAAGAAATCGGTGTGTTG
21 AATTCATTAAAGAGTTGAAAGGATCCATGATTAAAGAAATCGGTGTGTTG
22 AATTCATTAAAGAGGCAGAAAGGATCCATGATTAAAGAAATCGGTGTGTTG
23 AATTCATTAAAGAGGCAGAAAGGATCCATGATTAAAGAAATCGGTGTGTTG
24 AATTCATTAAAGAGTTGAAAGGATCCATGATTAAAGAAATCGGTGTGTTG

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**Figure S6. Sequence alignment of 23 putative *pfkE* RBS mutants. Line 1 is the wild-type sequence. Lines 2-13 were putative mutants that had the wild-type sequence. Lines 14,15, and 17 had the silent mutations but possessed the wild-type RBS sequence. Lines 16, 18-24 possessed the silent mutations and mutations in the RBS.**

Table S1. Plasmids constructed in this study.

Plasmid Name	Origin of Replication	Antibiotic Resistance	Plasmid Description
pKDsg-pfkAEnd	pSC101	Spec/Strep	Protospacer targeting downstream of <i>pfkA</i>
pKDsg-Ack	pSC101	Spec/Strep	Protospacer targeting <i>ack</i>
pKDsg-Apt	pSC101	Spec/Strep	Protospacer targeting <i>apt</i>
pKDsg-rpoB	pSC101	Spec/Strep	Protospacer targeting <i>rpoB</i>
pKDsg-p15A	pSC101	Spec/Strep	Protospacer targeting the p15A origin of replication
pCas9	p15A	Cm	Nuclease positive <i>cas9</i>
pCas9cr1	p15A	Cm	pCas9 with <i>ssrA</i> tag
pCas9cr2	p15A	Cm	pCas9cr1 with constitutive <i>tetR</i>
pCas9cr4	p15A	Cm	pCas9cr2 with 10-fold reduced RBS

Table S2. Primers used for construction of sgRNA plasmids

Primer Name	Oligonucleotide Sequence
Pkdseq1	ccaattgtccatattgcatca
betaR	ttataacctccttagagctcga
P15AF sgRNA	ctatcgtcttgagtccaaccgttttagagctagaaatagcaag
P15A ptet	ggttgactcaagacgataggtgctcagtatctctatcactGA
pfka end F	GTATtaaTGATTTTCGGAAAgttttagagctagaaatagcaag
pfka end Rptet	TTTTCCGAAATCAttaATACgtgctcagtatctctatcactGA
aptR ptet	GCTTActggAAGACCCGAAAgctcagtatctctatcactGA
aptF sgRNA	TTTCGGGTCTTccagTAAGCgttttagagctagaaatagcaagtta
ackF sgRNA	AATAAACAGGAAGCGGCTTTgttttagagctagaaatagcaag
ackR ptet	AAAGCCGCTTCCTGTTTATTgtgctcagtatctctatcactGA

**Table S3. Primers used for genotyping PCR**

<b>Primer Name</b>	<b>Oligonucleotide sequence</b>
aptFmut	gcgatgtcaccagcttagtct
aptR	cgtccaccaccagaactttg
ackFmut	GAAAATGGACGGCAATAAAGACT
ackR	ACATAGAAGTGGCTGGTGCC
ack Up F	CATGCGCTACGCTCTATGG
ack Down R	CGCCTTTGCGTTCCATTGC
pfkA Down F	cgctatcgatctgctgct
pfkA Down R	gcagaattcatgtaggcctg

**Table S4. Oligonucleotides used for chromosomal mutations**

<b>Primer Name</b>	<b>Oligonucleotide sequence (*indicates phosphorothioate bond)</b>
rpoB	C*C*AGCAAGTCGATGCTGAGAGCGTAAGCTTTCGGGTCTTAGACTAAGCTGGTGACATCGCG GAAAAGAATGCCG*G*G
ackmut2	C*C*CGAAGCACGTATCAAATGGAAAATGGACGGCAATAAAGACTAAGCGGCTTTAGGTGCA GGCGCCGCTCACAG*C*G
ackCD	G*T*TAGTACTGGTTCTGAACTGCGGTAGTTCTTCACTGGTTATCCCAACCAACGAAGAACTGG TTATCGC*G*C
pfkaRBS	C*G*CATCACCGCCGCTTGTCAACACACCGATCTTTTTAATCATGGATCCTTTCNNCTCTTTAATG AATTGGCTAAACAA*C*T