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Publication Date

2014-03-19

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March 2014

The work conducted by the U.S. Department of Energy Joint Genome Institute is supported by the Office of Science of the U.S. Department of Energy under Contract No. DE-AC02-05CH11231

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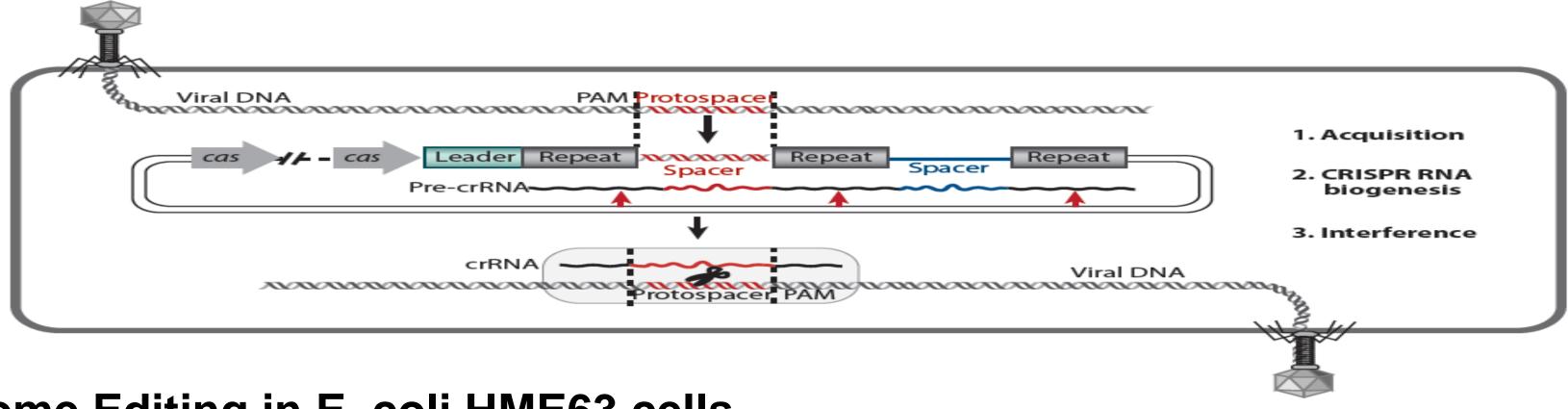


Genome Editing in Escherichia coli with Cas9 and synthetic CRISPRs

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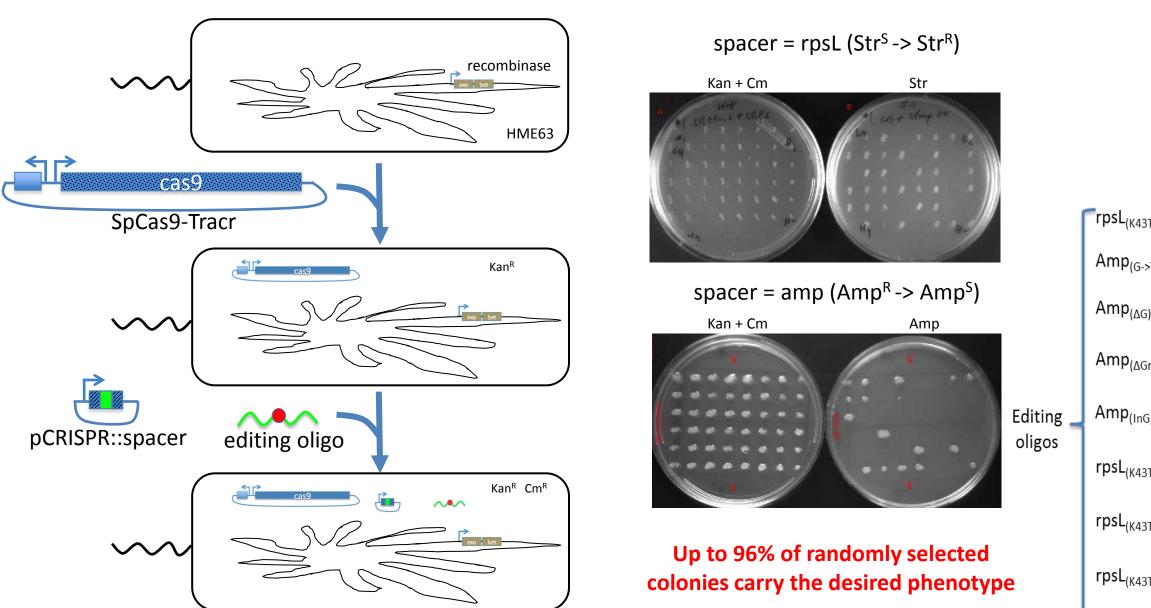
CRISPR systems are prokaryotic adaptive immune systems which integrate short fragments of foreign DNA into the host chromosome at one end of repetitive element known as a CRISPR (clustered regularly interspaced short palindromic repeat). The CRISPR serves as memory, which associated proteins (e.g. Cas9) then read in order to recognize and destroy invasive DNA.

Recently, the Cas9-CRISPR system has proven to be a useful tool for genome editing in eukaryotes, which repair the double stranded breaks made by Cas9 with non-homologous end joining or homologous recombination. Escherichia coli lacks nonhomologous end joining and has a very low homologous recombination rate, effectively rendering targeted Cas9 activity lethal. We have developed a heat curable, serializable, plasmid based system for selectionless Cas9 editing in arbitrary E. coli strains that uses synthetic CRISPRs for targeting and λ -red to effect repairs of double stranded breaks. We have demonstrated insertions, substitutions, and multi-target deletions with our system, which we have tested in several strains.



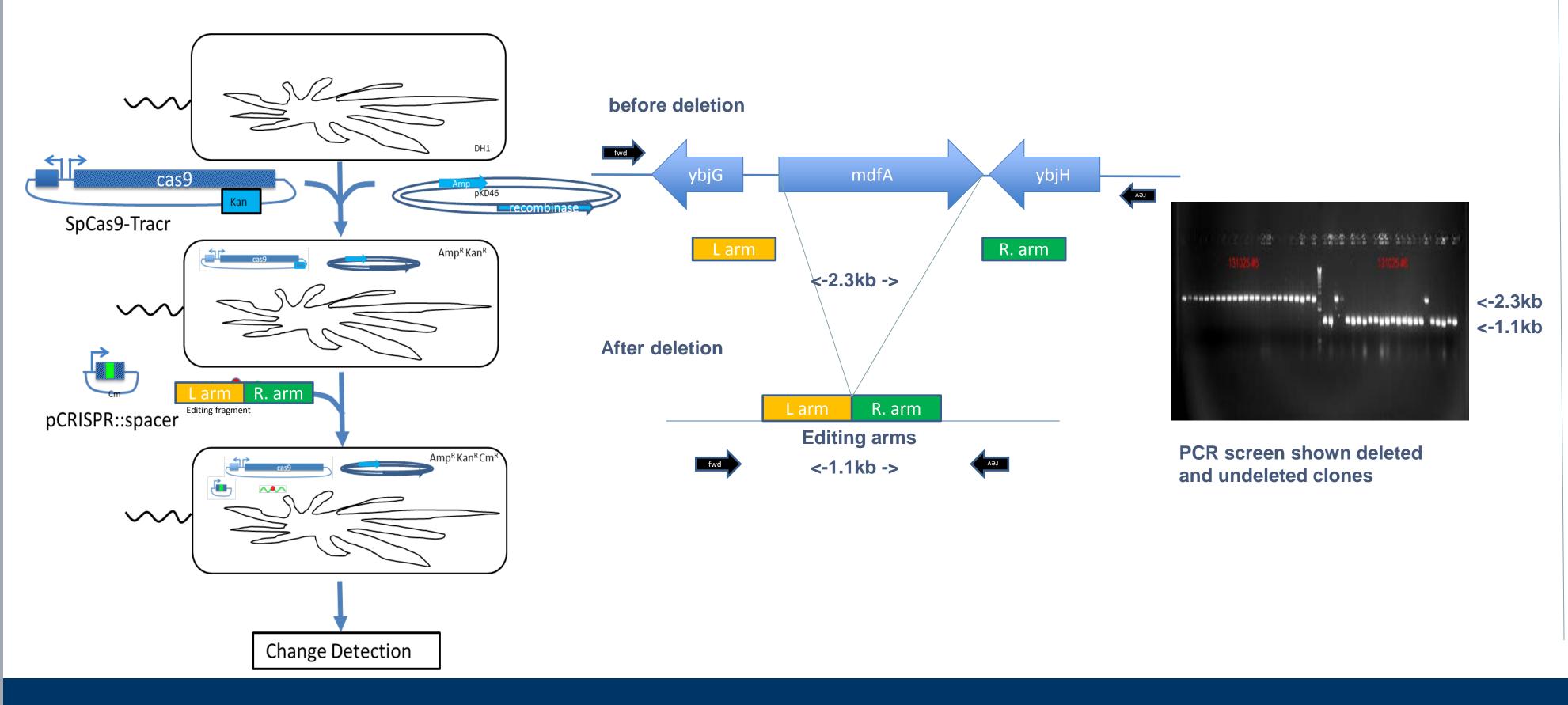
Genome Editing in E. coli HME63 cells (one & two targets)

We have tested several editing conditions of rpsL and Amp in HME63 host cells which have genome integrated λ -red. We have found that: rpsL is easier to edit than amp; oligos causing deletions have the highest success rate; and the first spacer in CRISPR has a higher editing rate than the second.



mdfA gene deletion in DH1 cells

We made mdfA gene deletions in DH1 cells transformed with vector pKD46(λ-red) and vector pBHK-Cas9. The basic procedure, gene and arms structures before and after deletion and results are shown below:



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	pCRISPR								
rpsL		amp rp		rpsL-amp	psL-amp			amp-rpsL	
	Str ^R	Amp ^s	Str ^R	Amp ^s	Str ^R Amp ^S	Amp ^s	Str ^R		
rpsL _(K43T)	96% (23/24)								
Amp _(G->T)		25% (6/24)						
$Amp_{(\Delta G)}$		67% (16/24	4)						
Amp _(ΔGrc)		67% (16/24	4)						
Amp _(InG)		71% (17/24	1)						
rpsL _(K43T) + Amp _{(c}	G->T)		87% (7/8)	25% (2/8)	25% (2/8)	13% (3/24)	13% (3/24)		
rpsL _(K43T) + Amp _{(/}	∆G)		100% (14/14)	21% (3/14)	21% (3/14)	67% (16/24)	67% (16/24)		
rpsL _(K43T) + Amp _{(/}	∆Grc)		94% (16/17)	6% (1/17)	6% (1/17)	29% (7/24)	33% (8/24)		
_rpsL _(K43T) + Amp _{(I}	nG)		63% (15/24)	38% (9/24)	38% (9/24)	54% (13/24)	54% (13/24)		

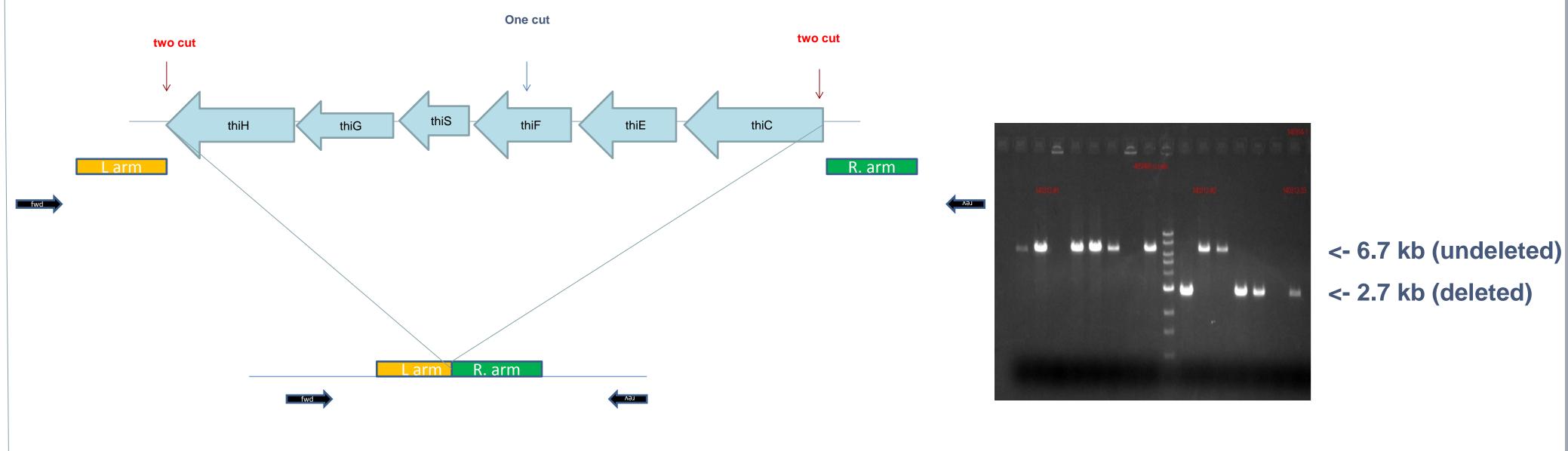
Ten cell membrane transport related genes have been deleted in *E. coli* DH1 cells

sensitivity of the original plasmid.

#	gene
1	mdfA
2	basB
3	exbB
4	glpT
5	mdlB
6	tehA
7	ycjF
8	yhjD
9	yhjG
10	yhjX

A long gene cluster has been deleted in *E. coli* DH1 cells

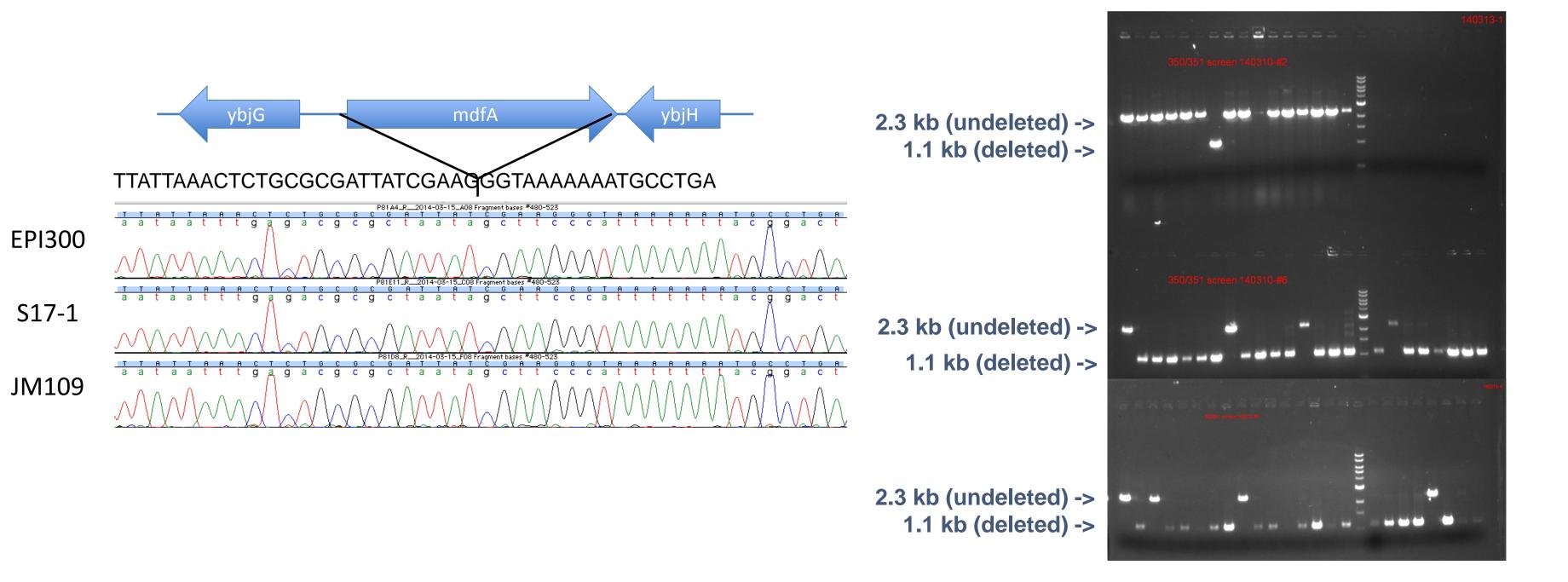
We knocked out the 4kb thiamine synthesis gene cluster in DH1 cells, with single and double spacer CRISPRs.

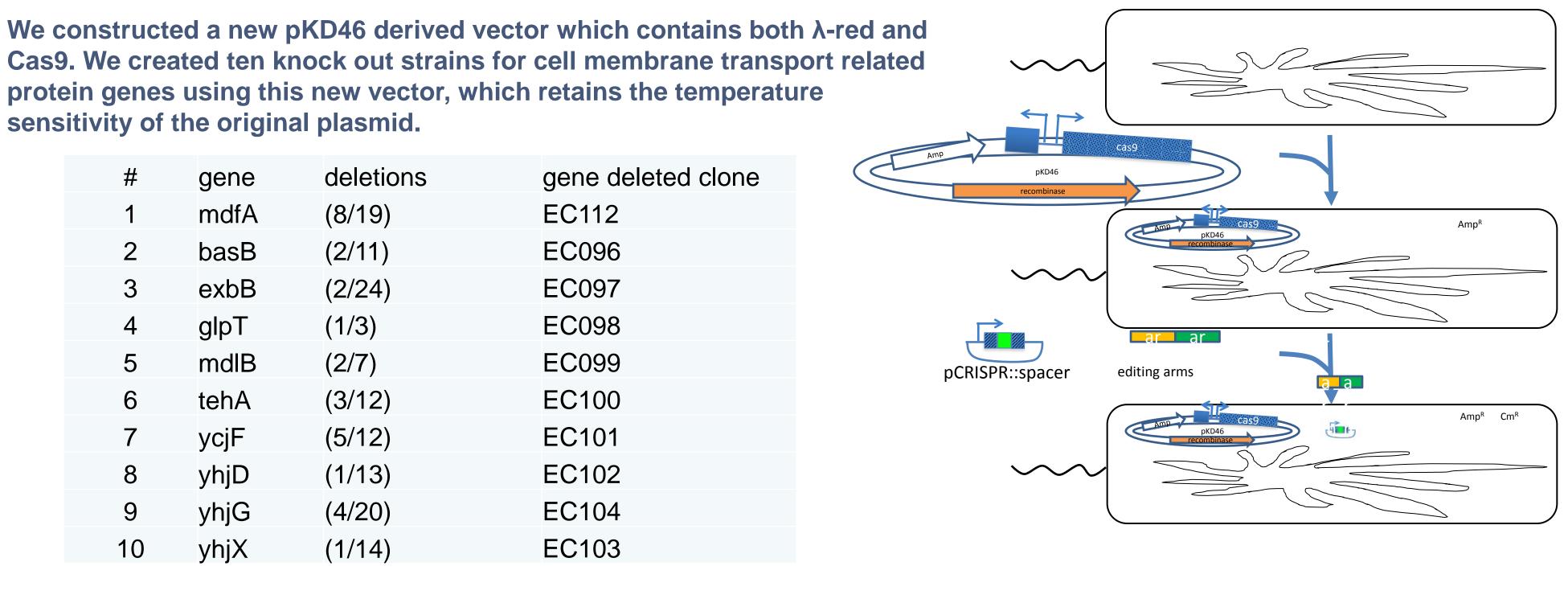


Cas9 Editing Also Works in Other *E. coli* strains

(bottom).

Given our success with *E. coli*, we hope to move into other useful prokaryotic model systems.





Besides HME63 and DH1, we have attempted CRISPR-based editing with the strains EPI300 (top), S17-1 (middle) and JM109

