Correction

GENETICS

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Correction for "CRISPR/Cas9 cleavages in budding yeast reveal templated insertions and strand-specific insertion/deletion profiles," by Brenda R. Lemos, Adam C. Kaplan, Ji Eun Bae, Alexander E. Ferrazzoli, James Kuo, Ranjith P. Anand, David P. Waterman, and James E. Haber, which was first published February 13, 2018; 10.1073/pnas.1716855115 (*Proc Natl Acad Sci USA* 115:E2040–E2047).

The authors note that Fig. 1 and Fig. 2 appeared incorrectly. The corrected figures and their legends appear below.

The authors also note that, in *SI Appendix*, Supplemental Table 2, data for the iPAM sequences in the *CAN1* gene were omitted. The SI has been corrected online. These errors do not affect the conclusions of the article.

Α		qLYS2-1 ^c		[
	5'	GAACCTGTG TTGTGGAGA	5' overhang	Base insert at predicted site	gLYS2-1 ^c	
	5			+A	2	
	5' 3'	GAACCTGTGT TTGTGGAGA	▼ fill-in	+T	74	
	5		L.	+G	24	
	5' 3'	GAACCTGTGTGTTTGTGGAGA	+1 bp insertion	+C	-	
в	5	aLYS2-1 ^w				
_		5				

5' 3'	GAACCTGT GTTG <mark>TGG</mark> AGA CTTGGACAC AACACCTCA	5' overhang	Base insert at predicted site	gLYS2-1 ^w
ς,		Ļ	+A	-
3'	CTTGGACAC CAACACCTCA	fill-in	+T	-
г,		ţ	+G	100
3'	CTTGGACACCAACACCTCA	+1 bp insertion	+C	-

1		
Ľ)	

gLYS2-1 [₩]	5' <u>CCCAGAGAGAACCTGTGTGTGG</u> AGACTCCAACA	3'
gLYS2-1 [¢]	3' GGGTCTCTCTT <u>GGACACCACCTCTGAGGTTGT</u>	5'
gLYS2-2 ^w	5' <u>TGAAAGAGTAACCATTGTTGCGG</u> ACCAATTTACT	3'
gLYS2-2 ^c	3' ACTTTCTCATTGGT <u>AACAACGCCTGGTTAAATGA</u>	5'
gLYS2-3 ^w	5' <u>TGCGGAAGACGCCAAGAAAT</u> TGGTTGAGACGCTA	3'
gLYS2-3 ^c	3' ACGCCTTCTGCGGT <u>TCTTTAACCAACTCTGCGAT</u>	5'
gLYS2-4 ^w	5' <u>CAAAGTGTTTGCCCACGTCAGGG</u> CCAAGGATGAA	3'
gLYS2-4 ^c	3' GTTTCACAAACGGG <u>TGCAGTCCCGGTTCCTACTT</u>	5'
gCAN1-1 ^W	5' <u>TCACAAACACCACCACAGACG</u> TGGGTCAATACCAT	3'
gCAN1-1 ^C	3' AGTGTTTGTGTGGT <u>GGTGGTGGCACCCAGTTATGGTA</u>	5'

D

Base insert at predicted site	gLYS2- 1 ^W	gLYS2- 1 ^c	gLYS2- 2 ^w	gLYS2- 2 ^c	gLYS2- 3 ^w	gLYS2- 3 ^c	gLYS2- 4 ^w	gLYS2- 4 ^c	gCAN1 -1 ^w	gCAN1 -1 ^c
+A	-	2	-	1	-	100	-	11	-	98
+T	-	74	-	76	-	-	1	-	-	2
+G	100	24	100	17	-	-	96	89	100	-
+C	-	-	-	6	-	-	2	-	-	-



Fig. 1. Templated insertions and nonrandom deletions at CRISPR-Cas9 DSBs. (*A*) Templated 1-nt insertions following Cas9-induced DSB, resulting in a 5' 1-nt overhang-mediated gLYS2-1^C. The table shows the percentage of +1 insertions, with shaded values representing expected templated insertions. (*B*) Templated 1-nt insertions following Cas9 induced DSB resulting in a 5' 1-nt overhang mediated gLYS2-1^W. The table shows the percentage of +1 insertions, with shaded values representing expected templated insertions. (*C*) Five pairs of gRNAs targeting either the *LYS2* or *CAN1* locus were designed to cleave five different genomic sites. Paired gRNAs were designed to create a DSB in the same DNA location. (*D*) Percentage of +1 insertions following clasvage from 10 different gRNAs targeting different iPAMs. Shaded values represent the predicted templated insertions for each guide. (*E*) Percent viability from gRNAs targeting the *LYS2* or *CAN1* locus. W and C reflect PAM location on Watson and Crick strands as shown. (*F*) Percentage of Lys2⁻ for each gRNA targeting *LYS2* from viable cells. A statistically significant difference in the percentage of Lys2⁻ cells was found for gRNA pair 2 (*P* = 0.002). NA denotes statistics not applicable because gRNA did not cut well.





C gLYS2-2^c

CCATTGTTGCGG	Indel	Frequency
<u>CCA</u> TTG <mark>T</mark> TTGCGG	+1	35%
<u>CCA</u> TTG-TGCGG	-1	15%
<u>CCA</u> TTGCGG	-3	10%
<u>CCA</u> TTG <mark>G</mark> TTGCGG	+1	8%
<u>CCA</u> TTG <mark>TT</mark> TTGCGG	+2	7%
<u>CCA</u> [- 13]A	-13	5%
<u>CCA</u> TTG <mark>TTT</mark> TTGCGG	+3	5%
<u>CCA</u> TTG <mark>C</mark> TTGCGG	+1	3%
<u>CCA</u> TTG <mark>GG</mark> TTGCGG	+2	2%
<u>CCA</u> TTG <mark>AAA</mark> TTGCGG	+3	1%
<u>CCA</u> TT[- 13]T	-13	1%
<u>CCA</u> TTGA	-6	1%
<u>CCA</u> TGCGG	-4	1%
<u>CCA</u> TTG <mark>CCC</mark> TTGCGG	+3	1%
<u>CCA</u> TTG <mark>GGG</mark> TTGCGG	+3	1%
<u>CCA</u> TTG <mark>ATT</mark> TTGCGG	+3	1%
<u>CCA</u> TTG <mark>GG</mark> TTGCGG	+2	1%
<u>CCA</u> TTG <mark>A</mark> TTGCGG	+1	1%
CCATT-TTGCGG	-1	1%
<u>CCA</u> TTGTTG <mark>a</mark> GG	1bps	1%
<u>CCA</u> TT <mark>a</mark> TTGCGG	1bps	1%
		n=155

gLYS2-2 ^w						
	CCATTGTTG CGG	Indel	Frequency			
	CCATTG <u>CGG</u>	-3	58%			
	CCATT <mark>G</mark> GTTG <u>CGG</u>	+1	10%			
	CCATTG <mark>T</mark> TTG <u>CGG</u>	+1	9%			
	CCATTG <mark>A</mark> TTG <u>CGG</u>	+1	5%			
	CCATTG <mark>TT</mark> TTG <u>CGG</u>	+2	6%			
	CCATTG <mark>TTT</mark> TTG <u>CGG</u>	+3	3%			
	CCATT <mark>GG</mark> GTTG <u>CGG</u>	+2	2%			
	A[-17]C	-17	1%			
	CCATTGTT- <u>CGG</u>	-1	1%			
	CCATTG <mark>TTTT</mark> TTG <u>CGG</u>	+4	1%			
	CCATT <mark>GTG</mark> GTTG <u>CGG</u>	+3	1%			
	CCATTG <mark>ATA</mark> TTG <u>CGG</u>	+3	1%			
	CCATTG <mark>CC</mark> TTG <u>CGG</u>	+2	1%			
	CCATTG <mark>AA</mark> TTG <u>CGG</u>	+2	1%			
	CCATTG <mark>C</mark> TTG <u>CGG</u>	+1	1%			
	CCATTGTgG <u>CGG</u>	1bps	1%			
			n=105			

D gLYS2-2^c pol4∆

gLYS2-2^w pol4∆

<u>CCATTGTTGCGG</u> Indel Fr		requency <u>CCATTGTTG</u>		Indel	Frequency
<u>CCA</u> TTG-TGCGG	-1	64%	CCATTG <u>CGG</u>	-3	94%
<u>CCA</u> -[-13]A	-13	10%	CCATTGΓ-10]A	-10	3%
<u>CCA</u> TTG <mark>T</mark> TTGCGG	+1	7%	CCGTTG CGG	-3	3%
<u>ССА</u> ТТ[-13]-Т	-13	6%		5	n-109
<u>CCA</u> TT[-14]-T	-14	4%			11-105
<u>CCA</u> TTGTTG <mark>a</mark> GG	1bps	1%			
<u>CCA</u> TTGTGG	-3	1%			
		n=70			

Fig. 2. Pol4 is required for templated and nontemplated insertions. (*A*) Insertions during repair of $gLYS2-2^{W}$ and $gLYS2-2^{C}$ DSBs are mostly lost in the absence of *POL4*. (*B*) Effect on NHEJ survival in the absence of *POL4*. (*C*) Indel profile from colonies recovered following DSB from $gLYS2-2^{W}$ and $gLYS2-2^{C}$. (*D*) Indel profile in the absence of *pOl4*. for $gLYS2-2^{W}$ and $gLYS2-2^{W}$ and $gLYS2-2^{C}$.

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