Programmable base editing of A•T to G•C in genomic DNA without DNA cleavage

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Supplementary Table 1. HTS sequencing results and %indel of untreated HEK293T cells and HEK293T cells treated with ABE6.3, ABE7.8, ABE7.9, or ABE7.10 at 17 genomic sites with co-transfection of a corresponding sgRNA expression plasmid. One arbitrarily chosen replicate is shown; the data for all replicates is available from the NCBI sequencing read archive.

Untreated																	1		1					Indel%
Site 1	G ₁	A ₂	A ₃	C ₄	A ₅	C ₆	A ₇	A ₈	A ₉	G ₁₀	C ₁₁	A ₁₂	T ₁₃	A ₁₄	G ₁₅	A ₁₆	C ₁₇	T ₁₈	G ₁₉	C ₂₀	G 0.2	G	G	0.04
c	0.0	0.0	0.0	100.0	0.0	100.0	0.0	0.0	0.0	0.0	100.0	0.0	0.0	0.0	0.0	0.0	100.0	0.0	0.0	99.9	0.0	0.0	0.0	
G	100.0	0.0	0.0	0.0	0.2	0.0	0.0	0.0	0.0	100.0	0.0	0.0	0.0	0.0	100.0	0.0	0.0	0.0	100.0	0.0	99.8	100.0	100.0	
1	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	100.0	0.0	0.0	0.0	0.0	100.0	0.0	0.1	0.0	0.0	0.0	
ABE6.3																								Indel%
Site 1	G ₁	A ₂	A ₃	C ₄	A ₅	C ₆	A ₇	A ₈	A ₉	G ₁₀	C ₁₁	A ₁₂	T ₁₃	A ₁₄	G ₁₅	A ₁₆	C ₁₇	T ₁₈	G ₁₉	C ₂₀	G	G	G	0.15
A C	0.0	99.8	95.1 0.0	0.0 99.9	33.3	0.0 99.8	92.8	94.2	97.2	0.0	0.0	99.9 0.0	0.0 0.0	0.0	0.0	100.0	0.1 99.9	0.0	0.0	0.1	0.0	0.0	0.0	
G	100.0	0.2	4.9	0.0	66.7	0.2	7.2	5.8	2.8	100.0	0.0	0.1	0.0	0.0	100.0	0.0	0.0	0.0	100.0	0.0	100.0	100.0	99.9	
Т	0.0	0.0	0.0	0.1	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	100.0	0.0	0.0	0.0	0.0	100.0	0.0	0.0	0.0	0.0	0.1	
ABE7.8																								Indel%
Site 1	G ₁	A ₂	A ₃	C ₄	A ₅	C ₆	A ₇	A ₈	A ₉	G ₁₀	C ₁₁	A ₁₂	T ₁₃	A ₁₄	G ₁₅	A ₁₆	C ₁₇	T ₁₈	G ₁₉	C ₂₀	G	G	G	0.052
A	0.0	100.0	98.7	0.0	33.2	0.0	98.4	99.1	98.7	0.0	0.0	100.0	0.0	100.0	0.0	100.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	
G	100.0	0.0	1.3	0.0	66.8	0.0	1.6	0.9	1.3	100.0	0.0	0.0	0.0	0.0	100.0	0.0	0.0	0.0	100.0	0.0	100.0) 100.0	100.0	
т	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	100.0	0.0	0.0	0.0	0.0	100.0	0.0	0.0	0.0	0.0	0.0	
ARE7 9																								Indel%
Site 1	G ₁	A ₂	A ₃	C ₄	A ₅	C ₆	A ₇	A ₈	A ₉	G ₁₀	C ₁₁	A ₁₂	T ₁₃	A ₁₄	G ₁₅	A ₁₆	C ₁₇	T ₁₈	G ₁₉	C ₂₀	G	G	G	0.077
Α	0.0	99.9	99.6	0.0	29.6	0.0	98.0	99.4	99.4	0.0	0.0	99.9	0.0	100.0	0.0	100.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	
CG	0.0	0.0	0.0 0.4	100.0	0.0	99.8 0.2	0.0	0.0	0.0 0.6	0.0	100.0	0.0	0.0	0.0	0.0	0.0	100.0	0.0	0.0	99.9	0.0	0.0	0.0	
Т	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	100.0	0.0	0.0	0.0	0.0	100.0	0.0	0.1	0.0	0.0	0.0	
																								Indal0/
Site 1	G,	A	A _a	C.	Ac	Ca	Α,	A	A	G	Car	A ₄₀	Teo	A.,	Ger	A	Cur	Tio	Gro	Coo	G	G	G	0.093
A	0.1	99.9	99.5	0.0	29.4	0.0	78.9	98.7	99.1	0.0	0.0	99.9	0.0	100.0	0.0	100.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.000
С	0.0	0.0	0.0	99.9	0.0	99.9	0.0	0.0	0.0	0.0	100.0	0.0	0.0	0.0	0.0	0.0	100.0	0.0	0.0	99.9	0.0	0.0	0.0	
T	0.1	0.0	0.5	0.0	0.0	0.1	21.1	0.0	0.9	0.0	0.0	0.1	100.0	0.0	0.1	0.0	0.0	100.0	0.0	0.0	0.1	0.1	0.0	
Untreated			6	T		- T			6	0	6	<u>л Гт</u>					Гт	·		_	Δ	6		
Untreated Site 2 A	G ₁ 0.0	A ₂ 100.0	G ₃ 0.0	T ₄ 0.0	A ₅ 99.1	Т ₆ 0.0	G ₇ 0.1	A ₈ 99.8	G ₉ 0.0	G ₁₀ 0.0	C ₁₁	A ₁₂ T 9.9 0	13 A	14 G	6 ₁₅ A	16 C	- ₁₇ T .0 0	- 18 C	G ₁₉ (C ₂₀ 0.0 10	A 00.0	G 0.0	Inc G 0.	<u>del%</u> 046
Untreated Site 2 A C	G ₁ 0.0 0.0	A ₂ 100.0 0.0	G ₃ 0.0 0.0	T ₄ 0.0 0.0	A ₅ 99.1 0.0	T ₆ 0.0 0.0	G ₇ 0.1 0.0	A ₈ 99.8 0.0	G ₉ 0.0 0.0	G ₁₀ 0.0 0.0	C ₁₁ 0.0 9 100.0 0	A ₁₂ T 9.9 0 0.1 0	7 ₁₃ A .0 100 .0 0.	14 G	6 ₁₅ A 0.0 99 0.0 0	16 C 0.9 0 .0 10	.17 T .0 0 0.0 0	- ₁₈ G .0 0	6 ₁₉ (0.0 (0.0 9	C ₂₀ 0.0 1 9.9	A 00.0 0.0	G 0.0 0.0	Inc G 0. 0.0 0.0	<u>del%</u> 046
Untreated Site 2 A C G T	G ₁ 0.0 0.0 99.9 0.1	A ₂ 100.0 0.0 0.0	G ₃ 0.0 0.0 100.0	T ₄ 0.0 0.0 0.0	A₅ 99.1 0.0 0.9	T ₆ 0.0 0.0 0.0	G ₇ 0.1 0.0 99.9	A ₈ 99.8 0.0 0.1	G ₉ 0.0 0.0 99.9 1 0.1	G ₁₀ 0.0 0.0 00.0	C ₁₁ 0.0 9 100.0 0 0.0 0	A ₁₂ T 9.9 0 0.1 0 0.0 0	A 13 A 0 100 .0 0. .0 0. 0 0	14 G 0.0 0 0 0 0 10 0 0	B ₁₅ A 0.0 99 0.0 0 0.0 0	16 C 0.9 0 .0 10 .1 0	17 T .0 0 0.0 0 .0 0	- <u>18</u> C .0 0 .0 0 .0 10	6 ₁₉ (0.0 (0.0 9 00.0 (0.0 (C ₂₀ 0.0 1 9.9 0.1	A 00.0 0.0 0.0 1	G 0.0 0.0 00.0 90.0	Inc G 0. 0.0 0.0 99.9	del% 046
Untreated Site 2 A C G T	G ₁ 0.0 0.0 99.9 0.1	A ₂ 100.0 0.0 0.0 0.0	G ₃ 0.0 0.0 100.0 0.0	T ₄ 0.0 0.0 0.0 100.0	A ₅ 99.1 0.0 0.9 0.0	T ₆ 0.0 0.0 0.0 100.0	G ₇ 0.1 0.0 99.9 0.0	A ₈ 99.8 0.0 0.1 0.1	G ₉ 0.0 0.0 99.9 1 0.1	G ₁₀ 0.0 0.0 00.0 0.0	C ₁₁ 0.0 9 100.0 0 0.0 0 0.0 0	A ₁₂ T 9.9 0 0.1 0 0.0 0 0.0 10	13 A .0 100 .0 0. .0 0. .0 0. .0 0. 0.0 0.	14 G 0.0 0 0 0 0 10 0 0	A 0.0 99 0.0 0 0.0 0 0.0 0 0.0 0	16 C 0.9 0 .0 10 .1 0 .0 0	T .0 0 0.0 0 .0 0 .0 10	18 G .0 0 .0 0 .0 10 0.0 0	6 ₁₉ (0.0 (0.0 9 00.0 (0.0 (C ₂₀ 0.0 11 9.9 0.1 0.0	A 00.0 0.0 0.0 1 0.0	G 0.0 00.0 00.0 9 0.0	Inc G 0. 0.0 0.0 19.9 0.0	<u>del%</u> 046
Untreated Site 2 A C G T ABE6.3	G ₁ 0.0 0.0 99.9 0.1	A ₂ 100.0 0.0 0.0 0.0	G ₃ 0.0 0.0 100.0 0.0	T ₄ 0.0 0.0 0.0 100.0	A ₅ 99.1 0.0 0.9 0.0	T ₆ 0.0 0.0 0.0 100.0	G ₇ 0.1 0.0 99.9 0.0	A ₈ 99.8 0.0 0.1 0.1	G ₉ 0.0 0.0 99.9 1 0.1	G ₁₀ 0.0 0.0 0.0 0.0	C ₁₁ 0.0 9 100.0 0 0.0 0	A ₁₂ T 9.9 0 0.1 0 0.0 0 0.0 10	13 A: .0 100 .0 0. .0 0. .0 0. .0 0.	14 G 0.0 0 0 0 0 10 0 0	6 ₁₅ A 0.0 99 0.0 0 0.0 0 0.0 0	16 C 3.9 0 .0 10 .1 0 .0 0		- ₁₈ G .0 0 .0 10 0.0 10	6 ₁₉ (0.0 (0.0 9 00.0 (0.0 (2 ₂₀ 0.0 11 9.9 0.1	A 00.0 0.0 0.0 1 0.0	G 0.0 00.0 00.0 00.0 0.0	Inc G 0. 0.0 0.0 99.9 0.0 Inc	del% 046 del%
Untreated Site 2 A C G T ABE6.3 Site 2 A	G ₁ 0.0 99.9 0.1 G ₁	A ₂ 100.0 0.0 0.0 0.0 A ₂ 99.4	G ₃ 0.0 100.0 0.0 G ₃	T ₄ 0.0 0.0 100.0 T ₄	A ₅ 99.1 0.0 0.9 0.0 A ₅	T ₆ 0.0 0.0 100.0 T ₆ 0.0	G ₇ 0.1 0.0 99.9 0.0 G ₇	A ₈ 99.8 0.0 0.1 0.1 A ₈	G ₉ 0.0 0.0 99.9 1 0.1 G ₉	G ₁₀ 0.0 0.0 0.0 0.0 0.0 G ₁₀	C ₁₁ 0.0 9 100.0 0 0.0 0 C ₁₁ 0	A_{12} T 9.9 0 0.1 0 0.0 0 0.0 10 A_{12} T 9.9 0	A 13 A 10 00. 0 0. 0.0 0. 13 A 0 99	14 G 0.0 0 0 0 0 10 0 0 14 G 8 0	$\hat{\Theta}_{15}$ A $\hat{1}_{.0}$ 99 $\hat{1}_{.0}$ 0 $\hat{1}_{.0}$ 0 $\hat{1}_{.0}$ 0 $\hat{\Theta}_{15}$ A $\hat{1}_{.0}$ 99	16 C 9.9 0 .0 10 .1 0 .0 0 .16 C 16 C 19 0		18 G .0 0 .0 10 .0 10 .0 0 .0 10 .0 0 .0 0	$\hat{\Theta}_{19}$ (0.0 (0.0 9) 0.0 (0.0 ($\hat{\Theta}_{19}$ (0.0 ($ \begin{array}{c} 2_{20} \\ 2_{0} \\ 9.9 \\ 0.1 \\ 0.0 \\ \hline 2_{20} \\ 0.0 \\ 0.0 \\ $	A 00.0 0.0 0.0 1 0.0 A 19 9	G 0.0 00.0 00.0 0.0 G	G 0. 0.0 0.0 19.9 0.0 G 0.	del% 046 del% 057
Untreated Site 2 A C G T ABE6.3 Site 2 A C	G ₁ 0.0 99.9 0.1 G ₁ 0.0 0.0	A ₂ 100.0 0.0 0.0 0.0 0.0 99.4	G ₃ 0.0 100.0 0.0 G ₃ 0.0 0.0	T ₄ 0.0 0.0 100.0 T ₄ 0.0 0.0	A ₅ 99.1 0.0 0.9 0.0 A ₅ 47.9 0.0	T ₆ 0.0 0.0 100.0 T ₆ 0.0 0.0	G ₇ 0.1 0.0 99.9 0.0 G ₇ 0.1 0.0	A8 99.8 0.0 0.1 0.1 0.1 A8 96.1 0.0 0.0	G9 0.0 0.0 0.0 99.9 1 0.1 0.1 G9 0.0 0.0 0.0	G ₁₀ 0.0 00.0 0.0 0.0 G ₁₀ 0.0 0.0	C11 J 0.0 9 100.0 0 0.0 0 0.0 0 0.0 0 0.0 0 0.0 0 0.0 0 0.0 9 100.0 9 100.0 9	A ₁₂ T 9.9 0 0.1 0 0.0 0 0.0 10 A ₁₂ T 9.9 0 0.1 0	13 A .0 100 .0 0. .0 0. .0 0. .13 A .0 99 .0 0.	14 G 0.0 0 0 10 0 0 14 G 14 G 18 0 1 0		16 C 9.9 0 .0 10 .1 0 .0 0 16 C 0.9 0 .0 10	¹¹⁷ T .0 0 .0 0 .0 10 .0 10 .17 T .0 0 0.0 0	18 G .0 0 .0 10 0.0 0 .0 10 0.0 0 .0 0 .0 0 .0 0 .0 0 .0 0		$ \begin{array}{c} 2_{20} \\ 2_{00} \\ 1_{1} \\ 9.9 \\ 0.1 \\ 0.0 \\ 0.0 \\ $	A 00.0 0.0 0.0 1 0.0 A 09.9 0.0	G 0.0 00.0 0.0 G 0.0 0.0	Inc G 0. 0.0 19.9 0.0 0.0 0.0 0.0 0.0	del% 046 del% 057
Untreated Site 2 A C G T ABE6.3 Site 2 A C G	G ₁ 0.0 99.9 0.1 G ₁ 0.0 0.0 99.9	A ₂ 100.0 0.0 0.0 0.0 99.4 0.0 0.5	G ₃ 0.0 100.0 0.0 G ₃ 0.0 0.0 99.9	T ₄ 0.0 0.0 100.0 T ₄ 0.0 0.0 0.0	A ₅ 99.1 0.0 0.9 0.0 A ₅ 47.9 0.0 52.0	T ₆ 0.0 0.0 100.0 T ₆ 0.0 0.0 0.0	G ₇ 0.1 0.0 99.9 0.0 G ₇ 0.1 0.0 99.8 0.1	A ₈ 99.8 0.0 0.1 0.1 0.1 96.1 0.0 3.8 0.1	G ₉ 0.0 0.0 99.9 1 0.1 0.1 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0	G ₁₀ 0.0 0.0 0.0 0.0 G ₁₀ 0.0 0.0 0.0 99.9	$\begin{array}{c cccc} C_{11} & J \\ 0.0 & 9 \\ 100.0 & 0 \\ 0.0 & 0 \\ \hline \\ C_{11} & J \\ 0.0 & 9 \\ 100.0 & 0 \\ 0.0 & 0 \\ \hline \end{array}$	A_{12} T 9.9 0 0.1 0 0.0 0 0.0 10 A_{12} T 9.9 0 0.1 0 0.0 10	13 A .0 100 .0 0. .0 0. .0 0. .0 0. .13 A .13 A .0 99 .0 0. .0 0.	14 G 0.0 0 0 10 0 0 14 G 1.8 0 1 0 0 0	$\hat{\Theta}_{15}$ A 0.0 99 0.0 0 0.0 0 0.0 0 $\hat{\Theta}_{15}$ A 0.0 99 0.0 0 0.0	16 C 3.9 0 .0 10 .1 0 .0 0 .16 C .16 C .16 C .0 0 .0 0 .0 0	17 T .0 0 .0 0 .0 10 .17 T .0 0 .0 0 .0 0	18 G .0 0 .0 10 .0 10 .0 0 .18 G .0 0 .0 0 .0 0 .0 0 .0 0 .0 0 .0 0	\hat{S}_{19} (0.0 (0.0 (0.0 (0.0 (0.0 (0.0 (0.0 (0.		A 00.0 0.0 0.0 0.0 0.0 A 09.9 0.0 0.0	G 0.0 00.0 0.0 G 0.0 0.0 0.0 0.0 0.0 0.0	Inc G 0. 0.0 19.9 0.0 G 0. 0.0 0.0 0.0 0.0 0.0 0.0	del% 046 del% 057
Untreated Site 2 A C G T ABE6.3 Site 2 A C G T	G ₁ 0.0 99.9 0.1 G ₁ 0.0 0.0 99.9 0.0	A ₂ 100.0 0.0 0.0 99.4 0.0 0.5 0.0	G ₃ 0.0 100.0 0.0 G ₃ 0.0 99.9 0.0	T ₄ 0.0 0.0 100.0 T ₄ 0.0 0.0 0.0 100.0	A ₅ 99.1 0.0 0.9 0.0 A ₅ 47.9 0.0 52.0 0.0	T ₆ 0.0 0.0 100.0 T ₆ 0.0 0.0 0.0 100.0	G7 0.1 0.0 99.9 0.0 G7 0.1 0.0 99.8 0.1	A8 99.8 0.0 0.1 0.1 0.1 96.1 0.0 3.8 0.1	$ \begin{array}{c c} G_9 \\ 0.0 \\ 0.0 \\ 99.9 \\ 1 \\ 0.1 \\ \hline G_9 \\ 0.0 \\ 0.0 \\ 99.9 \\ 0.0 \\ 0.$	G ₁₀ 0.0 0.0 0.0 0.0 G ₁₀ 0.0 0.0 0.0 0.0	C11 J 0.0 \$ 100.0 (100.0) 0.0 \$ 0.0 \$ 100.0 \$ 100.0 \$ 0.0 \$ 0.0 \$ 0.0 \$ 0.0 \$ 0.0 \$ 0.0 \$ 0.0 \$	A ₁₂ T 9.9 0 0.1 0 0.0 10 A ₁₂ T A ₁₂ T 9.9 0 0.1 0 0.0 10 0.1 0 0.0 10	13 A .0 100 .0 0. .0 0. .13 A. .13 O .13 O .13 O .0 0. .0 0. .0 0. .0 0. .0 0. .0 0. .0 0.	14 G 0.0 0 0 10 0 10 1 99 0 0	\hat{S}_{15} A 0.0 99 0.0 0 0.0 0 0.0 0 \hat{S}_{15} A \hat{S}_{15} A 0.0 99 0.0 0 0.0 0	16 C .9 0 .0 10 .1 0 .0 0 .16 C .09 0 .0 0 .0 10 .0 0 .0 0 .0 0	17 T .0 0 .0 0 .0 10 .17 T .0 0 .0 0 .0 0 .0 0 .0 10	18 G .0 0 .0 10 .0 10 .0 0 .0 0 .0 0 .0 0 .0 0 .0 0 .0 0 .0 0 .0 0 .0 0 .0 0	\hat{G}_{19} (0.0 (0.0 (0.0 (0.0 (0.0 (0.0 (0.0 (0.	$ \begin{array}{c ccccccccccccccccccccccccccccccccccc$	A 00.0 0.0 0.0 1 0.0 1 9 9 9 0.0 1 0 1 0.0 1 0 1 1 0 1 1 1 1 1 1 1 1 1 1 1 1 1	G 0.0 0.0 0.0 G 0.0 6 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0	Inc G 0. 0.0 0.0 19.9 0.0 10.0 0.0 10.0 19.9 0.0 19.9 0.0 19.9 0.0	del% 046 del% 057
Untreated Site 2 A C G T ABE6.3 Site 2 A C G T T ABE7.8	G ₁ 0.0 99.9 0.1 G ₁ 0.0 0.0 99.9 0.0	A ₂ 100.0 0.0 0.0 99.4 0.0 0.5 0.0	G ₃ 0.0 100.0 0.0 G ₃ 0.0 99.9 0.0	T ₄ 0.0 0.0 100.0 T ₄ 0.0 0.0 100.0	A ₅ 99.1 0.0 0.9 0.0 47.9 0.0 52.0 0.0	T ₆ 0.0 0.0 100.0 T ₆ 0.0 0.0 0.0 100.0	G ₇ 0.1 99.9 0.0 G ₇ 0.1 0.0 99.8 0.1	A ₈ 99.8 0.0 0.1 0.1 96.1 0.0 3.8 0.1	G9 0.0 0.0 0.0 99.9 1 0.1 0.1 G9 0.0 0.0 0.0 99.9 1 0.0 0.0 90.0 0.0	G ₁₀ 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0	C11 J 0.0 9 100.0 0 0.0 0 0.0 0 0.0 0 0.0 0 0.0 0 0.0 0 0.0 0 0.0 0 0.0 0 0.0 0	A12 T 9.9 0 0.1 0 0.0 10 A12 T 9.9 0 0.1 0 0.0 10 0.1 0 0.1 0 0.0 10	13 A. .0 100 .0 0. .0 0. .0 0. .0 0. .13 A. .0 99 .0 0. .0 0. .0 0.	14 G 0 0 0 0 10 0 14 G 0 18 0 1 1 95 0 0 0 0	B15 A .0 99 .0 0 0.0 0 0.0 0 0.0 0 0.0 0 0.0 99 0.0 0 0.0 0 0.0 0 0.0 0	16 C 9.9 0 .0 10 .1 0 .0 0 .0 0 .0 0 .0 10 .0 0 .0 0	17 T .0 0 .0 10 .17 T .0 0 .0 0 .0 0 .0 0 .0 0 .0 0 .0 0 .0 0 .0 10	18 G .0 0 .0 10 .0 10 .0 0 .18 G .0 0 .0 0 .0 0 .0 0 .0 0 .0 0 .0 9 0.0 0	\hat{s}_{19} (0.0 (0.0 9 0.0 0 0.0 (0.0 (0.0 (0.0 9 9.9 (0.0 ($\begin{array}{c c} C_{20} \\ \hline 0.00 \\ 11 \\ \hline 9.9 \\ 0.1 \\ 0.0 \\ \hline \\ 0.0 \\ \hline \\ 9.9 \\ 0.0 \\ 0 \\ 0.0 \\ \hline \end{array}$	A 00.0 0.0 10.0 A 19.9 0.0 0.0 0.0 10.0	G 0.0 00.0 0.0 G 0.0 0.0 0.0 0.0 0.0 0.0	Inc G 0. 0.0 19.9 0.0 G 0. 0.0 19.9 0.0 100 100 100 100 100 100 100	del% 046 del% 057 del%
Untreated Site 2 A C G T ABE6.3 Site 2 A C G T T ABE7.8 Site 2	$ \begin{array}{c} G_{1} \\ 0.0 \\ 99.9 \\ 0.1 \\ \hline G_{1} \\ 0.0 \\ 99.9 \\ 0.0 \\ \hline G_{1} \\ 0.0 \\ \hline 0.0 \\ 99.9 \\ 0.0 \\ \hline G_{1} \\ 0.0 \\ \hline 0.0 \\ \hline$	A ₂ 100.0 0.0 0.0 0.0 99.4 0.5 0.0 0.5 0.0	G ₃ 0.0 0.0 100.0 0.0 G ₃ 0.0 99.9 0.0 G ₃	T ₄ 0.0 0.0 100.0 T ₄ 0.0 0.0 100.0	A ₅ 99.1 0.0 0.9 0.0 0.0 47.9 0.0 52.0 0.0 52.0 0.0	T ₆ 0.0 0.0 100.0 T ₆ 0.0 0.0 0.0 100.0 T ₆	G ₇ 0.1 0.0 99.9 0.0 G ₇ 0.1 0.1 99.8 0.1	A8 99.8 0.0 0.1 0.1 0.1 99.8 0.0 0.1 0.1 0.0 3.8 0.1 0.1	G_9 0.0 0.0 99.9 1 0.1 G_9 0.0 99.9 1 0.1 G_9 0.0 G_9 0.0 G_9 0.0	G ₁₀ 0.0 0.0 0.0 G ₁₀ 0.0 99.9 0.0 G ₁₀	C11 J 0.0 9 100.0 0 0.0 0 0.0 0 0.0 0 0.0 0 0.0 0 0.0 0 0.0 0 0.0 0 0.0 0 0.0 0 0.0 0 0.0 0	A12 T 9.9 0 0.1 0 0.0 10 A12 T 9.9 0 0.0 10 A12 T 0.0 0 0.0 10 A12 T A12 T	13 A .0 100 .0 0. .0 0. .0 0. .0 0. .13 A .0 99 .0 0. .0 0. .0 0. .0 0. .0 0. .13 A .13 A	14 G 0.0 0 0 10 0 10 14 G 1.8 0 1 99 0 0 1 99 0 0	\hat{s}_{15} A \hat{s}_{10} 99 \hat{s}_{10} 0 \hat{s}_{15} A \hat{s}_{15} A \hat{s}_{15} A \hat{s}_{15} A \hat{s}_{15} A	16 C 3.9 0 .0 10 .1 0 .0 0 .0 0 .0 0 .0 0 .0 0 .0 0 .0 0 .0 0 .0 0 .0 0	17 T 0 0 0.0 0 0.0 0 0.0 10 17 T 0.0 0 0.0 0 0.0 0 0.0 10 10 10 17 T	18 G .0 0 .0 10 .0 10 .0 0 .18 G .0 0 .0 0 .0 0 .0 0 .0 98 0.0 0 .0 0 .0 0 .0 0 .0 0 .0 0 .0 0 .0 0 .0 0 .0 0 .0 0 .0 0	\hat{G}_{19} (0.0 ((0.0 ((0.0 (0.0 (A 00.0 0.0 0.0 1 0.0 99.9 0.0 0.0 0.0 0.0 0.0 0.0	G 0.0 0.0 0.0 0.0 G 0.0 0.0 0.0 0.0 0.0	Inc G 0. 0.0 0.0 0.0 0.0 0.0 0.0 0.0	del% 046 del% 057 del% 050
Untreated Site 2 A C G T ABE6.3 Site 2 A C G T T ABE7.8 Site 2 A C C C G T C C G T C C G T T C C G T T C C G C C C C	$ \begin{array}{c} G_{1} \\ 0.0 \\ 99.9 \\ 0.1 \\ \hline G_{1} \\ 0.0 \\ 99.9 \\ 0.0 \\ \hline G_{1} \\ 0.0 \\ 0.0 \\ \hline G_{1} \\ 0.0 \\ 0.0 \\ \hline \end{array} $	A ₂ 100.0 0.0 0.0 0.0 99.4 0.5 0.5 0.0 A ₂ 99.3 0.0	$\begin{array}{c} G_{3} \\ 0.0 \\ 0.0 \\ 100.0 \\ 0.0 \\ \hline \\ G_{3} \\ 0.0 \\ 99.9 \\ 0.0 \\ \hline \\ G_{3} \\ 0.0 \\ 0.0 \\ \hline \\ 0.0 \\ 0.0 \\ \hline \end{array}$	$\begin{array}{c} T_4 \\ 0.0 \\ 0.0 \\ 100.0 \\ \hline \end{array}$	A ₅ 99.1 0.0 0.9 0.0 47.9 0.0 52.0 0.0 52.0 0.0	T ₆ 0.0 0.0 100.0 T ₆ 0.0 0.0 100.0 T ₆ 0.0 0.0	G7 0.1 0.0 99.9 0.0 G7 0.1 0.0 99.8 0.1 0.0 99.8 0.1 G7 0.1 0.0	A8 99.8 0.0 0.1 0.1 0.1 96.1 0.0 3.8 0.1 0.1 0.0 3.8 0.1 91.7 0.0 0.0 0.1		G ₁₀ 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 G ₁₀ 0.0 G ₁₀ 0.0 0.0	C11 J 0.0 9 100.0 0 0.0 0 0.0 0 0.0 0 0.0 0 0.0 0 0.0 0 0.0 0 0.0 0 0.0 0 0.0 0 0.0 0 0.0 0 0.0 9 0.0 9 0.0 9 0.0 9 0.0 9 0.0 9 0.0 9 0.0 9 0.0 9	A_{12} T 9.9 0 0.1 0 0.0 10 A_{12} T 9.9 0 0.1 0 0.0 10 A_{12} T A_{12} T A_{12} T 9.9 0 0.0 10 A_{12} T 9.9 0 0.0 10	13 A .0 100 .0 0. .0 0. .0 0. .13 A .0 0. .0 0. .0 0. .0 0. .0 0. .13 A .13 A .0 0.0 .0 0.	14 G 0 0 0 0 10 0 14 G 0 1 99 0 0 0 0 14 G 0 14 G 0 14 G 0 0 0 0	\hat{s}_{15} A 0.0 98 0.0 0 0.0 0 0.0 0 \hat{s}_{15} A 0.0 99 0.0 0 \hat{s}_{15} A \hat{s}_{15} A	16 C 9.9 0 .0 10 .1 0 .0 0 .16 C .0 0 .0 0 .0 0 .0 0 .0 0 .0 0 .0 0 .0 0 .0 0 .0 0	17 T .0 0 0.0 0 .0 10 17 T .0 0 .0 10 .17 T .0 0 .0 10 .17 T .17 T .0 0 .0 0 .0 0 .0 0 .0 0	18 C 10 0 .0 10 .0 10 .0 10 .0 0 .0 99 0.0 0 .18 C .18 C .0 0 .0 0 .0 0	\hat{S}_{19} (0.0		A 00.0 0.0 0.0 1 0.0 0.0 0.0 0.0	G 0.0 00.0 G 0.0 G 0.0 G G 0.1 G G 0.0 0.0	Inc G 0. 0.0 0.0 0.0 0.0 0.0 0.0 0.0	del% 046 del% 057 del% 050
Untreated Site 2 A C G T ABE6.3 Site 2 A C G T ABE7.8 Site 2 A C G G T	$\begin{array}{c} G_{1} \\ 0.0 \\ 0.0 \\ 99.9 \\ 0.1 \\ \hline \\ 0.0 \\ 99.9 \\ 0.0 \\ \hline \\ 0.0 \\ \hline \\ G_{1} \\ 0.0 \\ \hline \\ 0.0 \\ 100.0 \\ \end{array}$	A ₂ 100.0 0.0 0.0 99.4 0.0 0.5 0.0 A ₂ 99.3 0.0 0.7	$\begin{array}{c} G_{3} \\ 0.0 \\ 0.0 \\ 100.0 \\ 0.0 \\ \end{array}$	T4 0.0 0.0 100.0 100.0 T4 0.0 0.0 100.0 T4 0.0 0.0 0.0 100.0 T4 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0	A5 99.1 0.0 0.9 0.0 0.0 47.9 0.0 52.0 55.9 0.0 447.9	$\begin{array}{c} T_6 \\ 0.0 \\ 0.0 \\ 0.0 \\ 100.0 \\ \hline \\ T_6 \\ 0.0 \\ 0.0 \\ 100.0 \\ \hline \\ \hline \\ T_6 \\ 0.0 \\ 0.0 \\ 0.0 \\ 0.0 \\ 0.0 \\ 0.0 \\ 0.0 \\ 0.0 \\ 0.0 \\ \hline \end{array}$	G7 0.1 99.9 0.0 G7 0.1 0.0 99.8 0.1 G7 0.1 0.0 99.8 0.1 0.1 0.0 99.8 0.1 0.1 0.1	A8 99.8 0.0 0.1 0.1 0.1 96.1 0.0 3.8 0.1 96.1 0.0 3.8 0.1 91.7 0.0 8.3 0.1	$ \begin{array}{c c} G_9 \\ 0.0 \\ 0.0 \\ 99.9 \\ 0.1 \\ \hline G_9 \\ 0.0 \\ 0.0 \\ 99.9 \\ 0.0 \\ \hline G_9 \\ 0.0 \\ \hline G_9 \\ 0.0 \\ 0.0 \\ 99.9 \\ 9 \end{array} $	G ₁₀ 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 G ₁₀ 0.0 0.0 0.0 0.0 0.0 799.9	C ₁₁ J 0.0 \$ 100.0 \$ 0.0 \$ 0.0 \$ 0.0 \$ 0.0 \$ 0.0 \$ 0.0 \$ 0.0 \$ 0.0 \$ 0.0 \$ 0.0 \$ 0.0 \$ 0.0 \$ 0.0 \$ 0.0 \$ 0.0 \$ 0.0 \$	$\begin{array}{c cccc} A_{12} & T \\ 9.9 & 0 \\ 0.1 & 0 \\ 0.0 & 0 \\ 0.0 & 10 \\ \hline \\ A_{12} & T \\ 9.9 & 0 \\ 0.1 & 0 \\ 0.0 & 10 \\ \hline \\ A_{12} & T \\ 9.9 & 0 \\ 0.1 & 0 \\ 0.1 & 0 \\ 0.1 & 0 \\ 0.1 & 0 \end{array}$	13 A .0 100 .0 0. .0 0. .0 0. .0 0. .0 0. .0 0. .0 0. .13 A. .0 99 .0 0. .0 0. .13 A. .13 A.	I4 G 0.0 0 0 10 0 10 14 G 18 0 1 99 0 0 14 G 100 0 13 99 04 G 05.0 0 00 0	\hat{s}_{15} A 0.0 99 0.0 0 0.0 0 0.0 0 \hat{s}_{15} A \hat{s}_{10} 99 0.0 0 \hat{s}_{15} A \hat{s}_{15} A \hat{s}_{15} A 0.0 99 \hat{s}_{15} A 0.0 99 \hat{s}_{15} A 0.0 99 \hat{s}_{15} A	16 C 9.9 0 .0 10 .1 0 .0 0 .16 C .9 0 .0 0 .0 0 .0 0 .0 0 .0 0 .0 0 .0 0 .0 0 .16 C .0 0 .1 0	17 T .0 0 .0 0 .0 10 17 T .0 0 .0 0 .0 10 .17 T .0 0 .0 10 .17 T .0 10 .0 0 .0 0 .0 0 .0 0 .0 0	18 C 10 0 .0 10 0.0 10 0.0 0 18 C .0 99 0.0 0 18 C .0 0 .0 0 .0 0 .0 0 .0 0 .0 0 .0 10	\hat{S}_{19} (0.0	$\begin{array}{c c} \hline \hline \\ $	A 00.0 0.0 0.0 0.0 1 0.0 1 0.0 1 0.0 1 0.0 1 0.0 1 0.8 0.0 1	G 0.0 0.0 0.0 G 0.0 G G 0.0 G 0.0 G 0.0 0.0	Inc G 0. 0.0 19.9 0.0 G 0. 0.0 19.9 0.0 100 G 0. 0.0 0.0 0.0 0.0	del% del% 057 del% 050
Untreated Site 2 A C G T ABE6.3 Site 2 A C G T ABE7.8 Site 2 A C G T T	$\begin{array}{c} G_1 \\ 0.0 \\ 0.0 \\ 99.9 \\ 0.1 \\ \hline \\ 0.0 \\ 99.9 \\ 0.0 \\ \hline \\ 99.9 \\ 0.0 \\ \hline \\ 0.0 \\ \hline \\ 0.0 \\ 100.0 \\ 0.0 \\ \hline \end{array}$	A ₂ 100.0 0.0 0.0 99.4 0.0 0.5 0.0 A ₂ 99.3 0.0 0.7 0.0	$\begin{array}{c} G_{3} \\ 0.0 \\ 0.0 \\ 100.0 \\ 0.0 \\ \hline \\ 0.0 \\ 99.9 \\ 0.0 \\ \hline \\ G_{3} \\ 0.0 \\ \hline \\ 0.0 \\ 99.9 \\ 0.1 \\ \end{array}$	T ₄ 0.0 0.0 100.0 T ₄ 0.0 100.0 T ₄ 0.0 0.0 0.0 0.0 0.0 100.0 T ₄ 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0	A ₅ 99.1 0.0 0.9 0.0 47.9 0.0 52.0 0.0 85.9 50.0 44.1 0.0	$\begin{array}{c} T_6 \\ 0.0 \\ 0.0 \\ 0.0 \\ 100.0 \\ \hline \\ T_6 \\ 0.0 \\ 0.0 \\ 100.0 \\ \hline \\ T_6 \\ 0.0 \\ 0.0 \\ 0.0 \\ 0.0 \\ 99.9 \\ \end{array}$	G7 0.1 0.0 99.9 0.0 G7 0.1 0.0 99.8 0.1 G7 0.1 99.8 0.1 99.8 0.1 99.9 0.0 99.9 0.0	A8 99.8 0.0 0.1 0.1 0.1 96.1 0.0 3.8 0.1 91.7 0.0 8.3 0.1		G ₁₀ 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0	C ₁₁ J 0.0 \$ 100.0 \$ 0.0 \$ 0.0 \$ 0.0 \$ 0.0 \$ 0.0 \$ 0.0 \$ 0.0 \$ 0.0 \$ 0.0 \$ 0.0 \$ 0.0 \$ 0.0 \$ 0.0 \$ 0.0 \$ 0.0 \$ 0.0 \$	$\begin{array}{c cccc} A_{12} & T \\ 9.9 & 0 \\ 0.1 & 0 \\ 0.0 & 0 \\ 0.0 & 10 \\ \hline \\ A_{12} & T \\ 9.9 & 0 \\ 0.1 & 0 \\ 0.0 & 10 \\ \hline \\ A_{12} & T \\ 9.9 & 0 \\ 0.1 & 0 \\ 0.1 & 0 \\ 0.1 & 0 \\ 0.1 & 0 \\ 0.1 & 0 \\ 0.1 & 0 \\ 0.0 & 10 \\ \hline \end{array}$	13 A. .0 100 .0 0. .0 0. 0.0 0. 0.0 0. 13 A. .0 99 .0 0. .0 0. .0 0. .13 A. .13 A.	I4 G 0.0 0 10 0 10 0 14 G 0 11 90 0 14 G 0 00 0 0 14 0 0 00 0 0 00 0 0 00 0 0 00 0 0	\hat{s}_{15} A 0.0 99 0.0 0 0.0 0 0.0 0 0.0 0 0.0 0 0.0 0 0.0 0 0.0 0 \hat{s}_{15} A \hat{s}_{15} A	16 C .9 0 .0 10 .1 0 .0 0 .0 0 .0 0 .0 10 .0 0 .0 0 .0 0 .0 0 .1 0 .0 0 .0 0 .0 0	17 T .0 0 0.0 0 .0 10 .17 T .0 0 .0 0 .0 0 .0 0 .0 10 .17 T .17 T .0 0 .0 0 .0 0 .0 0 .0 0 .0 0 .0 0 .0 0 .0 0	18 G .0 0 .0 10 .0 0 .0 0 .0 0 .0 0 .0 0 .0 0 .0 0 .0 0 .0 9 0.0 0 .18 G .0 0 .0 0 .0 10 0.0 0	$\hat{\mathbf{s}}_{19}$ (0) $\hat{\mathbf{s}}_{10}$ (0) $\hat{\mathbf{s}}_{10}$ (0) $\hat{\mathbf{s}}_{10}$ (0) $\hat{\mathbf{s}}_{10}$ (0) $\hat{\mathbf{s}}_{19}$ (0) $\mathbf{$	$\begin{array}{c c} \hline \hline \\ $	A 00.0 0.0 0.0 1 0.0 1 0.0 0.0 1 0 1 0 1 0 1 1 0 1 1 1 1 1 1 1 1 1 1 1 1	G 0.0 0.0 0.0 G 0.0 G G 0.0 G 0.0 0.0 G 0.0 0.0	Inc G 0. 0.0 19.9 0.0 G 0. 0.0 19.9 0.0 10.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0	del% del% 057 del% 050
Untreated Site 2 A C G T ABE6.3 Site 2 A C G T ABE7.8 Site 2 A C G T ABE7.8 Site 2 A C G T T ABE7.9	$\begin{array}{c} G_1 \\ 0.0 \\ 0.0 \\ 99.9 \\ 0.1 \\ \hline \\ 0.0 \\ 99.9 \\ 0.0 \\ \hline \\ 99.9 \\ 0.0 \\ \hline \\ 0.0 \\ 0.0 \\ 100.0 \\ 0.0 \\ \hline \end{array}$	A ₂ 100.0 0.0 0.0 0.0 99.4 0.0 0.5 0.0 99.3 0.0 0.7 0.0	$\begin{array}{c} G_{3} \\ 0.0 \\ 0.0 \\ 100.0 \\ 0.0 \\ \end{array}$ $\begin{array}{c} G_{3} \\ 0.0 \\ 99.9 \\ 0.0 \\ \end{array}$ $\begin{array}{c} G_{3} \\ 0.0 \\ 0.0 \\ 99.9 \\ 0.1 \\ \end{array}$	$\begin{array}{c} T_4 \\ 0.0 \\ 0.0 \\ 100.0 \\ \hline \\ 100.0 \\ 0.0 \\ 0.0 \\ 100.0 \\ \hline \\ T_4 \\ 0.0 \\ 0.0 \\ 0.0 \\ 100.0 \\ \hline \end{array}$	A ₅ 99.1 0.0 0.9 0.0 47.9 0.0 52.0 0.0 55.9 0.0 44.1 0.0	$\begin{array}{c} T_6 \\ 0.0 \\ 0.0 \\ 0.0 \\ 100.0 \\ \hline \\ T_6 \\ 0.0 \\ 0.0 \\ 100.0 \\ \hline \\ 100.0 \\ \hline \\ 0.0 \\ 0.1 \\ 0.0 \\ 99.9 \\ \end{array}$	G7 0.1 0.0 99.9 0.0 G7 0.1 0.0 99.8 0.1 G7 0.1 0.0 99.8 0.1 0.0 99.9 0.0 99.9 0.0 99.9 0.0	A ₆ 99.8 99.0 0.0 0.1 0.1 96.1 0.0 3.8 0.1 A ₈ 91.7 0.0 0.3 0.1 0.0	G ₉ [] 0.0 0.0 99.9 1 0.1 0.0 0.0 0.0 99.9 1 0.0 0.0 99.9 1 0.0 0.0 99.9 1 0.0 0.0 99.9 1 0.0 0.0 99.9 1 0.0 0.0	G ₁₀ 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0	$\begin{array}{c ccccc} C_{11} & J \\ 0.0 & \$ \\ 100.0 & 0 \\ 0.0 & 0 \\ 0.0 & 0 \\ \hline \\ C_{11} & J \\ 0.0 & \$ \\ 0.0 & 0 \\ \hline \\ C_{11} & J \\ 0.0 & \$ \\ 0.0 & 0 \\ \hline \\ 0.0 & \$ \\ 0.0 & 0 \\ \hline \end{array}$	A12 T 9.9 0 0.1 0 0.0 10 A12 T 9.9 0 0.0 10 A12 T 9.9 0 0.1 0 0.0 10 A12 T 9.9 0 0.0 10 A12 T 9.9 0 0.1 0 0.1 0 0.1 0 0.1 0 0.1 0	13 A. .0 100. .0 0. .0 0. .13 A. .13 A. .0 0. .0 0. .0 0. .0 0. .0 0. .0 0. .0 0. .0 0. .0 0. .0 0. .0 0. .0 0. .0 0. .0 0. .0 0.	14 G 0.0 0 0 0 0 0 10 0 0 14 G 0 10 0 0 14 G 0 10 0 0 14 G 0 00 0 0 00 0 0 00 0 0	\hat{S}_{15} A \hat{O} 95 \hat{O} 0 \hat{O} 0 \hat{O} 0 \hat{O} 0 \hat{O} 0 \hat{O} 0 \hat{O} 0 \hat{O} 95 \hat{O} 0 \hat{O} 0	16 C .9 0 10 .0 10 10 .0 0 0 .1 0 0 .16 C 0 .16 O 0	i7 T 0.0 0 0.0 0 0.0 0 10 10 17 T 10 0 0.0 0 0.0 0 0.0 0 0.0 0 0.0 0 0.0 0 0.0 0 0.0 0 0.0 0 0.0 0 0.0 0 0.0 0	18 C 0.0 0 0.0 0 0.0 0 18 G 18 G 0.0 0 10 0 18 G 18 G 10 0 10 0 10 0 10 0 0 0 0 0 0 0	\hat{s}_{19} ($\hat{0}, 0$ () ($\hat{0}, 0$ () ($\hat{0}, 0$ () ($\hat{0}, 0$ () () ()	$\begin{array}{c ccccccccccccccccccccccccccccccccccc$	A 00.0 0.0 0.0 0.0 1	G 0.0 0.0 0.0 G 0.0 0.0 0.0 0.0	G 0. 0.0 19.9 0.0 G 0. 0.0 19.9 0.0 19.9 0.0 10.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0	del% del% del% del%
Untreated Site 2 A C G T ABE6.3 Site 2 A C G T ABE7.8 Site 2 A C G T ABE7.8 Site 2 A C G T ABE7.9 Site 2	$\begin{array}{c} G_{1} \\ 0.0 \\ 0.0 \\ 99.9 \\ 0.1 \\ \hline \\ 0.0 \\ 99.9 \\ 0.0 \\ \hline \\ 0.0 \\ \hline \\ 0.0 \\ 100.0 \\ 0.0 \\ \hline 0.0$	A2 100.0 0.0 0.0 0.0 99.4 0.0 0.5 0.0 0.5 0.0 0.7 0.0 0.7 0.0	G3 0.0 0.0 0.0 100.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 99.9 0.0 G3 0.0 99.9 0.0 G3 0.0 99.9 0.1	T ₄ 0.0 0.0 0.0 0.0 100.0 T ₄ 0.0 0.0 0.0 0.0 0.0 0.0 100.0 T ₄ 0.0 0.0 0.0 0.0 0.0 0.0 0.0 100.0 T ₄	A ₅ 99.1 0.9 0.9 0.0 52.0 0.0 55.9 0.0 44.1 0.0	$\begin{array}{c} T_6 \\ 0.0 \\ 0.0 \\ 0.0 \\ 100.0 \\ \hline \\ 100.0 \\ 0.0 \\ 0.0 \\ 0.0 \\ 0.0 \\ 0.0 \\ 0.0 \\ 0.0 \\ \hline \\ 0.0 \\ 99.9 \\ \hline \\ T_6 \\ \hline \\ T_6 \end{array}$	G7 0.1 0.0 99.9 0.0 G7 0.1 0.0 99.8 0.1 G7 0.1 0.0 99.8 0.1 0.0 99.9 0.0 99.9 0.0 99.9 0.0 99.9 0.0	A ₆ 99.8 99.0 0.0 0.1 0.1 A ₆ 0.0 3.8 0.1 A ₆ 91.7 0.0 8.3 0.1 0.4	G ₉ 0.0 0.0 0.0 999.9 1 0.1 0.0 0.0 0.0 999.9 1 0.0 0.0 999.9 1 0.0 0.0 999.9 1 0.0 0.0 999.9 1 0.0 0.0 999.9 1 0.0 0.0 999.9 1 0.0 0.0	G ₁₀ 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0	C11 J 0.0 \$ 100.0 \$ 0.0 \$ 0.0 \$ 0.0 \$ 0.0 \$ 0.0 \$ 0.0 \$ 0.0 \$ 0.0 \$ 0.0 \$ 100.0 \$ 100.0 \$ 0.0 \$ 0.0 \$ 0.0 \$ 0.0 \$ 0.0 \$ 0.0 \$ 0.0 \$ 0.0 \$	A ₁₂ T 0.1 0 0.1 0 0.0 0 10 0 0.0 10 A ₁₂ T 0.1 0 0.0 0 0.0 10 A ₁₂ T 0.1 0 0.1 0 0.1 0 0.0 10	13 A. .0 100. .0 0. .0 0. .13 A.	14 G 0.0 0 0 0 0 0 10 0 0 14 G 0 10 0 0 14 G 0 10 0 0 14 G 0 0 0 0 14 G 0	\hat{S}_{15} A \hat{O}_{10} 95 \hat{O}_{10} 0 \hat{O}_{10} 0 \hat{O}_{15} A \hat{O}_{15} A \hat{O}_{15} A \hat{O}_{15} A \hat{O}_{15} A \hat{O}_{15} A \hat{O}_{15} A	16 C 0.9 0 0.10 10 1.1 0 1.6 C 1.7 0 1.8 C 1.9 0 1.6 C 1.7 0 1.6 C 1.7 0 1.6 C 1.7 0 0 0 1.6 C	i7 T 0.0 0 0.0 0 0.0 0 17 T 17 T 17 T 0.0 0 0.0 0 0.0 0 0.0 0 0.0 0 0.0 0 0.0 0 0.0 0 0.0 0 0.0 0 0.0 0 0.0 0 0.0 0 0.0 0 0.0 0	18 G .0 0 0 .0 10 10 .0 10 0 .0 0 0	3_{19} C 0.0 () 0.0 () 0.0 () 0.0 () 0.0 () 0.0 () 0.0 () 0.0 () 0.0 () 0.0 () 0.0 () 0.0 () 0.0 () 0.0 () 0.0 () 0.0 () 0.0 ()	$\begin{array}{c ccccccccccccccccccccccccccccccccccc$	A 00.0 0.0 0.0 0.0 0.0 19.9 0.0 0.0 19.9 10.8 0.0 0.0 10.8 0.0 0.0 10.8	G 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.	Inc G 0. 0.0 19.9 0.0 19.9 0.0 0.0 10.0 0.0 0.0 0.0 0.0 0.	del% 046 057 057 050 050
Untreated Site 2 A C G T ABE6.3 Site 2 A C G T ABE7.8 Site 2 A C G T ABE7.8 Site 2 A C G T ABE7.9 Site 2 A C G T C G G T C G G T T C G G T T C G G Site 2 A C G G T T C G G Site 2 A C G G Site 2 A C G G Site 2 A C G G T T C G G Site 2 A C G G T T C G G T T C G G Site 2 A C G G Site 2 A C G G Site 2 A C G G Site 2 C Site 2 Site 3 C Site 3 Site 3 C Site 3 C Si Site 3 C Si Site 3 C	$\begin{array}{c} G_1 \\ 0.0 \\ 0.0 \\ 99.9 \\ 0.1 \\ \hline \\ 0.0 \\ 99.9 \\ 0.0 \\ \hline \\ 0.0 \\ 99.9 \\ 0.0 \\ \hline \\ 0.0 \\ 100.0 \\ 0.0 \\ \hline \\ G_1 \\ 0.0 \\ \hline 0.0 $	A ₂ 100.0 0.0 0.0 0.0 99.4 0.0 0.5 0.0 0.5 0.0 0.7 0.0 0.7 0.0 0.7 0.0	G3 0.0 0.0 0.0 100.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 99.9 0.0 63 0.0 99.9 0.1 G3 0.0 0.0 0.0	T ₄ 0.0 0.0 0.0 0.0 100.0 T ₄ 0.0 0.0 0.0 0.0 0.0 0.0 100.0 T ₄ 0.0 0.0 100.0 T ₄ 0.0 0.0 100.0 T ₄ 0.0 0.0	A ₅ 99.1 0.0 0.9 0.0 52.0 0.0 55.9 0.0 44.1 0.0 44.1 0.0	$\begin{array}{c} T_6 \\ 0.0 \\ 0.0 \\ 0.0 \\ 100.0 \\ \hline \\ \hline T_6 \\ 0.0 \\ 0.0 \\ 0.0 \\ 0.0 \\ 0.0 \\ \hline \\ \hline \\ \hline \\ T_6 \\ 0.0 \\ 0.0 \\ \hline \\ $	G7 0.1 99.9 0.0 99.9 0.0 99.8 0.1 G7 0.1 G7 0.1 G7 0.1 G7 0.1 G7 0.1 G7 0.0 99.9 0.0 99.9 0.0	A ₆ 99.8 99.0 0.0 0.1 0.1 0.1 0.1 A ₆ 0.1 A ₈ 0.1 A ₈ 0.1 A ₈ 0.1 A ₈ 0.0 A ₈ 0.0 A ₈ 0.0	G ₉ [] 0.0 0.0 99.9 1 0.1 0.0 G ₉ 0.0 0.0 0.0 99.9 1 0.0 0.0 99.9 1 0.0 0.0 99.9 1 0.0 0.0 99.9 1 0.0 0.0	G ₁₀ [0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.	$\begin{array}{c ccccc} C_{11} & J \\ 0.0 & \$ \\ 100.0 & 0 \\ 0.0 & 0 \\ 0.0 & \$ \\ 0.0 & $ \\ 0.0 & $ \\ 0.0 & $ \\ 0.0 & $ \\ 0.0 & $ \\ 0.0 & $ \\ 0.0 & $ \\ 0.0 & $ \\ 0.0 & $ \\ 0.0 & $ \\ 0.0 & $ \\ 0.0 & $ \\ 0.0 & $ \\ 0.0 & $ \\ 0.0 & $ \\ 0.0 & $ $	A ₁₂ T 0.1 0 0.1 0 0.0 0 0.0 0 10 0 0.0 10 A ₁₂ T 0.1 0 0.0 0 0.0 10 A ₁₂ T 0.1 0 0.1 0 0.1 0 0.0 10	13 A. .0 100. .0 0.0 .0 0.0 .13 A. .13 A. .0 0.0 .13 A. .13 A. .13 A. .13 A. .0 0. .0 0. .13 A. .0 0. .0 0.	14 C 0.0 0 0 0 0 0 0 10 0 14 G 0 15 0 0 14 G 0 10 0 0 14 G 0 0 0 0	\hat{S}_{15} A \hat{O} 95 \hat{O} 0 \hat{O} 0	16 C 9.9 0 10 0 11 0 16 C 17 0 18 C 19 0 10 0 11 0 12 0 16 C 17 0 18 C 19 0 10 0 11 0 10 0 16 C 17 0 18 0 19 0 10 0 10 0 16 C 17 0 18 0 19 0 10 0 10 0 10 0 10 0 10 0	17 T 0.0 0 0.0 0 0.0 0 17 T 17 T 17 T 10 0 0.0 0 0.0 0 0.0 0 0.0 0 0.0 0 0.0 0 0.0 0 0.0 0 0.0 0 0.0 0 0.0 0 0.0 0 0.0 0 0.0 0 0.0 0	18 G 10 0 0 .0 10 10 .0 10 0 .0 10 0 .0 0 0 .0 0 0 .0 0 0 .0 0 0 .0 0 0 .0 0 0 .0 0 0 .0 0 0 .0 0 0 .0 0 0 .0 0 0 .0 0 0 .0 0 0	3_{19} (0.0 ($\begin{array}{c ccccccccccccccccccccccccccccccccccc$	A 00.0 0.0 0.0 1 0.0 100 1 0.0 10000000000	G 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.	Inc G 0. 0.0 19.9 0.0 19.9 0.0 10.0 10.0 10.0 0.0 10.0	del% 046 057 057 050 050
Untreated Site 2 A C G T ABE6.3 Site 2 A C G T ABE7.8 Site 2 A C G T ABE7.8 Site 2 A C G T ABE7.9 Site 2 G G T C G G T C G G T C G G T C G G T C G G Site 2 A C G G Site 2 C Site 2 C Site 2 C G G Site 2 C Site 2 C G G Site 2 C Site 2 Site 2 C Site 2 Site 3 C Site 3 Site 3 C Site 3 C Si Site 3 C Site 3 Site 3 C Si Site 3 Site 3 C Site 3 C	$\begin{array}{c} G_1 \\ 0.0 \\ 0.0 \\ 99.9 \\ 0.1 \\ \hline \\ 0.0 \\ 99.9 \\ 0.0 \\ \hline \\ 99.9 \\ 0.0 \\ \hline \\ 0.0 \\ 100.0 \\ 0.0 \\ \hline \\ 0.0 \\ \hline \\ 0.0 \\ \hline \\ 99.9 \\ 9.9 \end{array}$	A2 100.0 0.0 0.0 0.0 99.4 0.0 0.5 0.0 0.5 0.0 0.7 0.0 0.7 0.0 0.7 0.0 0.7 0.0	G3 0.0 0.0 0.0 100.0 0.0 0.0 0.0 99.9 0.0 G3 0.0 99.9 0.0 G3 0.0 99.9 0.1 G3 0.0 90.0 100.0	T ₄ 0.0 0.0 0.0 0.0 0.0 100.0 T ₄ 0.0 0.0 0.0 0.0 0.0 100.0 T ₄ 0.0 0.0 100.0 T ₄ 0.0 0.0 100.0 T ₄ 0.0 0.0 0.0 0.0	A ₅ 99.1 0.0 0.9 0.0 47.9 0.0 52.0 0.0 55.9 0.0 44.1 0.0 44.1 0.0	$\begin{array}{c} T_6 \\ 0.0 \\ 0.0 \\ 0.0 \\ 100.0 \\ \hline \\ 100.0 \\ 0.0 \\ 0.0 \\ 0.0 \\ 0.0 \\ 0.1 \\ 0.0 \\ 99.9 \\ \hline \\ T_6 \\ 0.0 \\ 0.0 \\ 0.0 \\ 0.0 \\ 0.0 \\ \end{array}$	G7 0.1 0.0 99.9 0.0 99.9 0.0 99.8 0.1 G7 0.1 G7 0.1 G7 0.1 G7 0.1 G7 0.0 99.9 0.0 99.9 0.0	A ₆ 99.8 99.0 0.0 0.1 0.1 0.1 0.0 3.8 0.1 A ₆ 91.7 91.7 0.0 8.3 0.1 A ₆ 90.0 0.0 1.1	G ₉ 0.0 0.0 0.0 999.9 1 0.1 0.0 999.9 1 0.0 0.0 999.9 1 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0	G ₁₀ 0.0 0.0 0.0 00.0 0.0 00.0 0.0 G ₁₀ 0.0	C11 J 0.0 \$ 100.0 \$ 0.0 \$ 0.0 \$ 0.0 \$ 0.0 \$ 0.0 \$ 0.0 \$ 0.0 \$ 0.0 \$ 0.0 \$ 100.0 \$ 0.0 \$ 0.0 \$ 0.0 \$ 0.0 \$ 0.0 \$ 0.0 \$	A ₁₂ T 0.1 0 0.1 0 0.0 0 0.0 0 1 0 0.0 0 1 0 0.0 0 1 0 0.0 0 0.0 0 0.0 0 0.0 0 0.0 10 0.1 0 0.1 0 0.1 0 0.0 10	13 A. .0 100. .0 0. .0 0. .13 A. .0 0. .0 0. .0 0. .0 0. .0 0. .0 0. .0 0. .0 0. .0 0. .0 0. .0 0. .0 0. .0 0. .0 0. .0 0. .0 0. .0 0. .0 0.	14 G 0.0 0 0 0 0 0 0 10 0 0 0 14 G 0 0 14 G 0 0 1 0 0 0 14 G 0 0 15 0 0 0 14 G 0 0 0	\hat{s}_{15} A \hat{s}_{15} A \hat{s}_{10} 95 \hat{s}_{10} 0 \hat{s}_{10} 0 s	16 C 0.9 0 10 1.1 0 0 10 1.6 C 0 0	i7 T 0.0 0	18 G .0 0 0 .0 10 10 .0 10 0 .0 0 0 .0 0 0 .0 0 0 .0 0 0 .0 0 0 .0 0 0 .0 0 0 .0 0 0 .0 0 0 .0 0 0 .0 0 0	3_{10} (0.0 ($\begin{array}{c ccccccccccccccccccccccccccccccccccc$	A 00.0 0.0 A 0.0 0 0.0 0 0.0 0 0 0	G 0.0 0.0 00.0 0.0 00.0 0.0 00.0 0.0 00.0 0.0 00.0 0.0 00.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0	Inc G 0. 0.0 19.9 0.0 19.9 0.0 10.0	del% 046 057 057 050 050
Untreated Site 2 A C G T ABE6.3 Site 2 A C G T ABE7.8 Site 2 A C G T ABE7.8 Site 2 A C G T ABE7.9 Site 2 A C G T T	$\begin{array}{c} G_1 \\ 0.0 \\ 0.0 \\ 99.9 \\ 0.1 \\ \hline \\ 0.0 \\ 99.9 \\ 0.0 \\ \hline \\ 0.0 \\ 99.9 \\ 0.0 \\ \hline \\ G_1 \\ 0.0 \\ 0.0 \\ \hline \\ G_1 \\ 0.0 \\ 0.0 \\ \hline \\ 0.0 \\ \hline \\ 0.0 0.0 \\ \hline \\ 0.0 \\ \hline \\ 0.0 \\ \hline $	A2 100.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.5 0.0 0.5 0.0 0.7 0.0 0.7 0.0 0.7 0.0 0.1 0.0	$\begin{array}{c} G_3 \\ 0.0 \\ 0.0 \\ 100.0 \\ 0.0 \\ 0.0 \\ 99.9 \\ 0.0 \\ 0.0 \\ 99.9 \\ 0.1 \\ \hline G_3 \\ 0.0 \\$	T ₄ 0.0 0.0 0.0 0.0 0.0 100.0 T ₄ 0.0 0.0 0.0 0.0 0.0 100.0 T ₄ 0.0 0.0 100.0 T ₄ 0.0 0.0 100.0	A ₅ 99.1 99.1 0.0 0.9 0.0 7.9 0.0 52.0 0.0 55.9 0.0 44.1 0.0 46.0 0.0 53.9 0.0 6.3 53.9 0.0 0.0	$\begin{array}{c} T_6 \\ 0.0 \\ 0.0 \\ 0.0 \\ 100.0 \\ \hline \\ 100.0 \\ \hline \\ 100.0 \\ \hline \\ \hline \\ T_6 \\ 0.0 \\ 0.1 \\ 0.0 \\ 99.9 \\ \hline \\ \hline \\ T_6 \\ 0.0 \\ 0.0 \\ 0.0 \\ 100.0 \\ \hline \end{array}$	G7 0.1 99.9 0.0 99.9 0.0 99.8 0.1 G7 0.1 G7 0.1 G7 0.1 G7 0.1 99.9 0.0 99.9 0.0 99.9 0.0	A ₆ 99.8 99.0 0.0 0.1 0.1 0.1 0.0 3.8 0.1 A ₆ 91.7 91.7 0.0 8.3 0.1 A ₆ 90.0 0.0 0.0 8.3 0.1	G ₉	G ₁₀ 0.0 0.0 0.0 00.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 G ₁₀ 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0	C11 J 0.0 \$ 100.0 \$ 0.0 \$ 0.0 \$ 0.0 \$ 0.0 \$ 0.0 \$ 0.0 \$ 0.0 \$ 0.0 \$ 0.0 \$ 0.0 \$ 0.0 \$ 0.0 \$ 0.0 \$ 0.0 \$ 0.0 \$ 0.0 \$ 0.0 \$ 0.0 \$ 0.0 \$	A ₁₂ T 0.1 0 0.1 0 0.0 0 0.0 0 1 0 0.0 0 1 0 0.0 0 1 0 0.0 0 0.0 0 0.0 0 0.0 0 0.0 10 0.1 0 0.1 0 0.0 10 0.0 0 0.0 0 0.0 0 0.0 0 0.0 0	13 A. .0 100. .0 0. .0 0. .13 A. .0 0. .13 A. .0 0. .0 0. .0 0. .0 0. .0 0. .0 0. .0 0. .0 0. .0 0. .0 0. .0 0. .0 0. .0 0. .0 0. .0 0. .0 0. .0 0.	14 G 0 0 0 0 0 0 0 0 0 14 G 0 13 0 0 14 G 0 10 0 0 11 98 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	\hat{s}_{15} A \hat{s}_{15} A \hat{s}_{10} 95 \hat{s}_{10} 0 \hat{s}_{10} 0 s	16 C 9.9 0 10 11 0 0 0 16 C 0 0 16 0 0 0 16 0 0 0 16 0 0 0 16 10 10 0 16 0 0 0 16 0 0 0 16 0 0 0 16 0 0 0 16 0 0 0 16 0 0 0 17 0 0 0 16 0 0 0 0 0 0 0 0	i7 T 0.0 0	18 G .0 0 0 .0 10 10 .0 10 0 .0 10 0 .0 0 0 .0 0 0 .0 0 0 .0 0 0 .0 0 0 .0 0 0 .0 0 0 .0 0 0 .0 0 0 .0 0 0 .0 0 0 .0 0 0 .0 0 0	$ \frac{3}{10} $ $ $	$\begin{array}{c ccccccccccccccccccccccccccccccccccc$	A 00.0 0.0 A 0.0 0 0.0 A 0.0 0 0.0 0 0.0 0 0 0	G 0.0 0.0 00.0 0.0 00.0 0.0 00.0 0.0 00.0 0.0 00.0 0.0 00.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0	G 0. 0.0 0.0 0.0 0.0 0.0 0.0 0.0	del% 046 057 057 050 050
Untreated Site 2 A C G T ABE6.3 Site 2 A C G T ABE7.8 Site 2 A C G T ABE7.9 Site 2 A C G T ABE7.9 Site 2 A C G T ABE6.2 T A A C G S T T A A C G S T T A A C S S T T A A A C S S T T A A C S S T T A A C S S T T A A C S S T T A A C S S T T A A C S S T T A A C S S T T A A C S S T T A A C S S T T A A C S S T T A A C S S T T A A C S S T T A A C S S T T A C S S S S S S S S S S S S S S S S S S	$\begin{array}{c} G_1 \\ 0.0 \\ 0.0 \\ 99.9 \\ 0.1 \\ \hline \\ 0.0 \\ 99.9 \\ 0.0 \\ \hline \\ 0.0 \\ 99.9 \\ 0.0 \\ \hline 0.0 \\ $	A2 100.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.5 0.0 0.5 0.0 0.7 0.0 0.7 0.0 0.7 0.0 0.1 0.0	$\begin{array}{c} G_3 \\ 0.0 \\ 0.0 \\ 100.0 \\ 0.0 \\ 0.0 \\ 99.9 \\ 0.0 \\ 0.0 \\ 99.9 \\ 0.1 \\ \hline G_3 \\ 0.0 \\$	T ₄ 0.0 0.0 0.0 0.0 0.0 100.0 T ₄ 0.0 0.0 0.0 0.0 0.0 100.0 T ₄ 0.0 0.0 100.0 T ₄ 0.0 0.0 100.0 T ₄ 0.0 100.0	A ₅ 99.1 99.1 0.0 0.9 0.0 7.9 0.0 52.0 0.0 55.9 0.0 44.1 0.0 46.0 0.0 53.9 0.0 53.9 0.0	$\begin{array}{c} T_6 \\ 0.0 \\ 0.0 \\ 0.0 \\ 100.0 \\ \hline \\ 100.0 \\ \hline \\ 0.0 \\ 0.0 \\ 0.0 \\ 0.0 \\ 0.1 \\ 0.0 \\ 0.1 \\ 0.0 \\ 99.9 \\ \hline \\ \hline \\ T_6 \\ 0.0 \\ 0.0 \\ 0.0 \\ 100.0 \\ \hline \end{array}$	G7 0.1 99.9 0.0 99.9 0.0 99.8 0.1 G7 0.1 G7 0.1 G7 0.1 G7 0.1 99.9 0.0 99.9 0.0 99.9 0.0 99.9 0.0	A ₆ 99.8 99.0 0.0 0.1 0.1 0.1 0.0 3.8 0.1 A ₆ 91.7 91.7 0.0 8.3 0.1 A ₆ 90.0 0.0 0.0 8.3 0.1	$\begin{array}{c c} G_9 & [\\ 0.0 \\ 0.0 \\ 0.0 \\ 999.9 \\ 10.1 \\ \hline \\ G_9 & [\\ 0.0 \\ 0.0 \\ 0.0 \\ 0.0 \\ \hline \\ 0.0 \\ 0.$	G ₁₀ 0.0 0.0 0.0 00.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 G ₁₀ 0.0 G ₁₀ 0.0 G ₁₀ 0.0 G ₁₀ 0.0 0.0 0.0 99.9 0.0 0.0 0.0	C11 J 0.0 \$ 100.0 \$ 0.0 \$ 0.0 \$ 0.0 \$ 0.0 \$ 0.0 \$ 0.0 \$ 0.0 \$ 0.0 \$ 0.0 \$ 100.0 \$ 0.0 \$ 0.0 \$ 0.0 \$ 0.0 \$ 0.0 \$ 0.0 \$ 0.0 \$ 0.0 \$ 0.0 \$ 0.0 \$	A ₁₂ T 0.1 0 0.1 0 0.0 0 0.0 0 1 0 0.0 0 1 0 0.0 0 1 0 0.0 0 0.0 0 0.0 0 0.0 10 0.1 0 0.1 0 0.1 0 0.0 10 0.0 0 0.0 0 0.0 0 0.0 0	13 A. .0 100. .0 0. .0 0. .13 A. .0 0. .0 0. .0 0. .0 0. .0 0. .0 0. .0 0. .0 0. .0 0. .0 0. .0 0. .0 0. .0 0. .0 0. .0 0. .0 0. .0 0. .0 0. .0 0.	I4 G 0 0 0 0 10 0 0 10 0 14 G 0 15 0 0 14 G 0 10 0 0 11 98 0 0 0 0 14 G 0 0 0 0 0 0 0 14 G 0 0 0 0 0 0 0 0 0 0 0 0 0	\hat{s}_{15} A \hat{s}_{15} A \hat{s}_{10} 99 \hat{s}_{10} 0 \hat{s}_{10} 0 s	16 C 9.9 0 10 11 0 0 0 16 C 0 0 16 0 0 0 16 0 0 0 16 0 0 0 16 10 10 0 16 0 0 0 16 0 0 0 16 0 0 0 16 0 0 0 16 0 0 0 16 0 0 0 16 0 0 0 16 0 0 0 16 0 0 0 16 0 0 0	i7 T 0.0 0	18 G .0 0 0 .0 10 10 .0 10 0 .0 0 0 .0 0 0 .0 0 0 .0 0 0 .0 0 0 .0 0 0 .0 0 0 .0 0 0 .0 0 0 .0 0 0 .0 0 0 .0 0 0 .0 0 0 .0 0 0	$ \frac{3}{10} $ $ $	$\begin{array}{c ccccccccccccccccccccccccccccccccccc$	A 00.0 0.0 A 0 0.0 A 0 0 0 0	G 0.0 0.0 00.0 0.0 00.0 1 00.0 1 00.0 1 00.0 1 00.0 1 0.0 0.0 0.0 1 0.0 1 0.0 0.0 0.0 1 0.0 1 0.0 1 0.0 1 0.0 1 0.0 1 0.0 1 0.0 1 0.0 1 0.0 1 0.0 1 0.0 1 0.0 1 0.0 1 0.0 1 0.0 1 0.0 1	G 0. 0.0 0.0 0.0 0.0 0.0 0.0 0.0	del% del% 057 del% 050 del% 042
Untreated Site 2 A C G T ABE6.3 Site 2 A C G T ABE7.8 Site 2 A C G T ABE7.8 Site 2 A C G T ABE7.9 Site 2 A C G T A ABE6.7 Site 2 A C G T T A A A C G T T A A C G T T A A A C G T T A A A C G T T A A A C G T T A A A C G T T A A A C G T T A A A C G T T A A C G T T A A C G T T A A C G G T T A A C G G T T A A C G G T T A A C G G T T A A C G G T T A A C G G T T A A C G G T T A A C G G T T A A C G G T T A A C Site 2 A A C G G T T A A C Site 2 C A C G G T T A C Site 2 C A C G Site 2 C Site 2 Site 2 Site 2 C Site 2 Site 3 Site 2 Site 2 Site 3 Site 2 Site 2 Site 2 Site 3 Site 3 Si Site 3 Site 3 Si Site 3 Site 3 Site 3 Site 3 Si Site	$\begin{array}{c} G_{1} \\ 0.0 \\ 0.0 \\ 99.9 \\ 0.1 \\ \end{array}$ $\begin{array}{c} G_{1} \\ 0.0 \\ 99.9 \\ 0.0 \\ \end{array}$ $\begin{array}{c} 0.0 \\ 0.0 \\ 0.0 \\ 100.0 \\ 0.0 \\ \end{array}$ $\begin{array}{c} G_{1} \\ 0.0 \\ 0.0 \\ 0.0 \\ \end{array}$ $\begin{array}{c} G_{1} \\ 0.0 \\ 0.0 \\ 0.0 \\ \end{array}$	A2 100.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.5 0.0 0.5 0.0 0.7 0.0 0.7 0.0 0.7 0.0 0.1 0.0 0.1 0.0	G3 0.0 0.0 0.0 100.0 0.0 0.0 0.0 99.9 0.0 G3 0.0 99.9 0.0 G3 0.0 99.9 0.1 G3 0.0 0.0 0.0 90.0 0.0 90.0 0.0 G3 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0	T ₄ 0.0 0.0 0.0 0.0 0.0 100.0 T ₄ 0.0 0.0 0.0 0.0 0.0 100.0 T ₄ 0.0 0.0 100.0 T ₄ 0.0 0.0 100.0 100.0 T ₄	A ₅ 99.1 0.0 0.9 0.0 47.9 0.0 52.0 0.0 55.9 0.0 44.1 0.0 44.1 0.0 53.9 0.0 44.1 0.0	$\begin{array}{c} T_6 \\ 0.0 \\ 0.0 \\ 0.0 \\ 100.0 \\ \hline \\ 100.0 \\ \hline \\ 100.0 \\ \hline \\ \hline \\ T_6 \\ 0.0 \\ 0.0 \\ 0.0 \\ 0.0 \\ 0.0 \\ 0.0 \\ 100.0 \\ \hline \\ \hline \\ T_6 \\ \hline \\ \hline \\ T_6 \\ \hline \\ $	G7 0.1 0.0 99.9 0.0 99.9 0.0 99.8 0.1 G7 0.1 G7 0.1 G7 0.1 G7 0.1 99.9 0.0 99.9 0.0 99.9 0.0 99.9 0.0 G7 0.1 0.0 99.9 0.0 G7 0.1 0.0 99.9 0.0	A ₆ 99.8 99.0 0.0 0.1 0.1 0.1 0.0 3.8 0.1 A ₆ 91.7 91.7 0.0 8.3 0.1 A ₆ 90.0 0.0 0.0 A ₆ 10.0 0.0 0.0	G ₉ 0.0 0.0 0.0 999.9 1 0.1 0.0 999.9 1 0.0 0.0 999.9 1 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0	G ₁₀ 0.0 0.0 0.0 00.0 0.0 00.0 0.0 00.0 0.0 00.0 0.0 00.0 0.0 00.0 0.0 00.0 0.0 G10 0.0 G11 0.0	C11 J 0.0 \$ 100.0 \$ 0.0 \$ 0.0 \$ 0.0 \$ 0.0 \$ 0.0 \$ 0.0 \$ 0.0 \$ 0.0 \$ 0.0 \$ 100.0 \$ 0.0 \$ 0.0 \$ 0.0 \$ 0.0 \$ 0.0 \$ 0.0 \$ 0.0 \$ 0.0 \$ 0.0 \$ 0.0 \$ 0.0 \$ 0.0 \$ 0.0 \$	A ₁₂ T 0.1 0 0.1 0 0.0 0 0.0 0 1 0 0.0 0 0.0 0 0.0 0 0.0 0 0.0 0 0.0 0 0.0 0 0.0 10 0.1 0 0.1 0 0.1 0 0.0 10 0.0 0 0.0 0 0.0 0 0.0 10 0.0 10	$\begin{array}{cccccccccccccccccccccccccccccccccccc$	I4 G 0.0 0 0 0 0 0 0 10 0 0 0 14 G 0 0 14 G 0 0 1 0 0 0 14 G 0 0 10 0 0 0 14 G 0 0 14 G 0 0 0 0 0 0 14 G 0 0 14 G 0 0 0 0 0 0 0 0 0 0 0 0 0 0	\hat{s}_{15} A \hat{s}_{15} A \hat{s}	16 C 9.9 0 10 11 0 0 0 16 C 0 0 16 0 0 0 16 0 0 0 16 0 0 0 16 0 0 0 16 0 0 0 16 0 0 0 16 0 0 0 16 0 0 0 16 0 0 0 16 0 0 0 16 0 0 0 16 0 0 0 16 0 0 0	i7 T 0.0 0 0.0 10	18 G .0 0 0 .0 10 10 .0 10 0 .0 0 0 .0 0 0 .0 0 0 .0 0 0 .0 0 0 .0 0 0 .0 0 0 .0 0 0 .0 0 0 .0 0 0 .0 0 0 .0 0 0 .0 0 0 .0 0 0 .0 0 0 .0 0 0 .0 0 0 .0 0 0	$ \frac{3}{10} $ $ $	$ \sum_{20} \sum_{10} \sum_{1$	A 00.0 0.0 0.0 1 0.0 1 0.0 1 0.0 1 0 0 0 0	G 0.0 0.0 00.0 0.0 00.0 1 00.0 1 00.0 1 00.0 1 00.0 1 0.0 1	G 0. 0.0 0.0 0.0 0.0 0.0 0.0 0.0	del% 046 057 057 050 050 042 042
Untreated Site 2 A C G T ABE6.3 Site 2 A C G T ABE7.8 Site 2 A C G T ABE7.9 Site 2 A C G T ABE7.9 Site 2 A C G T A A C G T T A A C C G T T A A C C G T T A A C C G T T A A C C G T T A A C C G T T A A C C G T T A A C C G T T A A C C G T T A A C C G T T A A C C G T T A A C C G T T A A C C G T T A A C C G T T A A C C G T T A A C C G T T A A C C G T T A C C G T T A C C G T T A C C G T T A C C G T T A C C G T T C C Site 2 C A C C C Site 2 C C C C C C C C C C C C C C C C C C C	$\begin{array}{c} G_1 \\ 0.0 \\ 0.0 \\ 99.9 \\ 0.1 \\ \hline \\ 0.0 \\ 99.9 \\ 0.0 \\ \hline \\ 0.0 \\ 99.9 \\ 0.0 \\ \hline 0.0 $	A2 100.0 0.1 0.0 0.1 0.0 0.2 99.9	$\begin{array}{c} G_3 \\ 0.0 \\ 0.0 \\ 100.0 \\ 0.0 \\ 0.0 \\ 99.9 \\ 0.0 \\ 0.0 \\ 99.9 \\ 0.1 \\ 0.0 \\ 0$	$\begin{array}{c} T_4 \\ 0.0 \\ 0.0 \\ 0.0 \\ 100.0 \\ \hline 1$	As 99.1 0.0 0.9 0.0 0.9 0.0 0.0 52.0 0.0 55.9 0.0 46.0 0.0 53.9 0.0 53.9 0.0 53.3 0.0 As 37.1	$\begin{array}{c} T_6 \\ 0.0 \\ 0.0 \\ 0.0 \\ 100.0 \\ \hline \\ 100.0 \\ \hline \\ 100.0 \\ \hline \\ \hline \\ T_6 \\ 0.0 \\ 0.0 \\ 0.1 \\ 0.0 \\ \hline \\ 99.9 \\ \hline \\ \hline \\ T_6 \\ 0.0 \\ \hline \\ 100.0 \\ \hline \\ \hline \\ \hline \\ \hline \\ 0.0 \\ \hline \\ \hline \\ \hline \\ 0.0 \\ \hline \\ $	G7 0.1 0.0 99.9 0.0 99.9 0.0 99.9 0.0 99.8 0.1 G7 0.1 G7 0.1 G7 0.1 99.9 0.0 99.9 0.0 99.9 0.0 99.9 0.0 G7 0.1 0.0 99.9 0.0 G7 0.1	A ₆ 99.8 99.0 0.0 0.1 0.1 0.1 0.0 96.1 0.0 3.8 0.1 A ₆ 91.7 91.7 0.0 A ₆ 90.0 0.0 0.0 A ₆ 90.0 0.0 0.0 A ₆ 97.9	G ₉ [0.0 0.0 99.9 1 0.1 0.0 99.9 1 0.0 0.0 99.9 1 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0	G ₁₀ [] 0.0 0.0 00.0 0.0 00.0 0.0 G ₁₀ 0.0	C11 J 0.0 \$ 100.0 \$ 0.0 \$	A ₁₂ T 9.9 0 9.1 0 0.0 0 0.0 0 0.0 0 0.0 0 0.0 0 0.0 0 0.0 0 0.0 0 0.0 0 0.0 0 0.0 10 A ₁₂ T A ₁₂ T 0.0 10 0.0 10 0.0 10 0.0 10 0.0 10 0.0 10 0.0 10 0.0 10 0.0 10 0.0 10	13 A. .0 100. .0 0. .0 0. .13 A. .0 0. .13 A.	I4 G 0.0 0 0 0 10 0 0 10 0 14 G 0 15 0 0 14 G 0 10 0 0 11 98 0 0 0 0 14 G 0 15 0 0 16 0 0 14 G 0 15 0 0 14 G 0 15 0 0 16 0 0 17 0 0 18 0 0 14 G 0 14 G 0 14 G 0 14 G 0	\hat{s}_{15} A \hat{s}_{15} A \hat{s}	16 C 0.9 0 10 1.1 0 0 0 1.6 C 0 0	i7 T 0.0 0	18 G 10 0 0 .0 10 10 .0 10 0 .0 0 0	$ \frac{3}{10} $ $ $		A 00.0 0.0 0.0 1 0.0 1 0.0 1 0.0 1 0.0 1 0 0 0 0	G 0.0 0.0 00.0 0.0 00.0 1 00.0 1 00.0 1 00.0 1 00.0 1 00.0 1 0.0 1	Inc G 0. 0.0 19.9 0.0 19.9 0.0 19.9 0.0 19.9 0.0 10.0 10.0 10.0 0.0 0.0 0.0	del% 046 057 057 050 042 042 042
Untreated Site 2 A C G T ABE6.3 Site 2 A C G T ABE7.8 Site 2 A C G T ABE7.9 Site 2 A C G T ABE7.9 Site 2 A C G T A ABE6.3 Site 2 A C C G T T A A C G T T A A C G T T A A C G T T A A C G T T A A C G T T A A C G T T A A C G T T A A C G T T A A C G T T A A C G T T A A C G T T A A C G G T T A A C G G T T A A C G G T T A A C G G T T A A C G G T T A A C G G T T A A C G G T T A A C G G T T A C G G T T A C G G T T A C G G T T A C G G T T A C G G T T A C G G T C A C G G T C C G G T C C G G T C C G G T C C G G C G C	$\begin{array}{c} G_{1} \\ 0.0 \\ 0.0 \\ 99.9 \\ 0.1 \\ \hline \\ 0.0 \\ 0.0 \\ 99.9 \\ 0.0 \\ \hline \\ 0.0 0.0 \\ \hline \\ 0.0 \\ \hline 0.0 \\$	A2 100.0 0.1 0.1 0.1	G3 0.0 0.0 0.0 100.0 0.0 0.0 0.0 0.0 0.0 99.9 0.0 0.0 0.0 99.9 0.1 G3 0.0 0.0 0.0 99.9 0.1 G3 0.0 0.0 0.0 0.0 0.0 0.0 0.0	T ₄ 0.0 0.0 0.0 0.0 100.0 T ₄ 0.0 0.0 0.0 0.0 0.0 0.0 100.0 T ₄ 0.0 0.0 0.0 100.0 T ₄ 0.0 0.0 100.0 T ₄ 0.0 100.0 T ₄ 0.0 0.0 0.0 0.0	As 99.1 0.0 0.9 0.0 0.9 0.0 0.0 52.0 0.0 55.9 0.0 As 55.9 0.0 0.0 55.9 0.0 As 55.9 0.0 0.0 As 30.0 As 37.1 0.0 0.0	$\begin{array}{c} T_6 \\ 0.0 \\ 0.0 \\ 0.0 \\ 100.0 \\ \hline \\ 100.0 \\ \hline \\ 100.0 \\ \hline \\ \hline \\ T_6 \\ 0.0 \\ 0.1 \\ 0.0 \\ 0.0 \\ 0.1 \\ 0.0 \\ \hline \\ 99.9 \\ \hline \\ \hline \\ T_6 \\ 0.0 \\ 0.0 \\ \hline \\ 100.0 \\ \hline \\ \hline \\ 0.0 \\ 0.0 \\ 0.0 \\ \hline \\ 0.0 \\ 0.0 \\ 0.0 \\ \hline \\ \hline \end{array}$	G7 0.1 0.0 99.9 0.0 99.9 0.0 99.8 0.1 G7 0.1 99.8 0.0 99.9 0.0 99.9 0.0 99.9 0.0 99.9 0.0 99.9 0.0 99.9 0.0 99.9 0.0 99.9 0.0 99.9 0.0 0.0	Ag 99.8 99.8 0.0 0.1 0.1 0.1 0.1 96.1 0.0 3.8 0.1 Ag 91.7 0.0 0.0 90.7 0.0 0.0 0.0 Ag 90.0 0.0 0.0 Ag 97.9 0.0 2.1	G ₉ 0.0 0.0 0.0 99.9 1 0.1 0.0 99.9 1 0.0 0.0 99.9 1 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0	G10 0.0 0.0 0.0 00.0 0.0 00.0 0.0 G10 0.0	C11 J 0.0 \$ 100.0 \$ 0.0 \$ 0.0 \$ 0.0 \$ 0.0 \$ 0.0 \$ 0.0 \$ 0.0 \$ 0.0 \$ 0.0 \$ 0.0 \$ 100.0 \$ 0.0 \$ 0.0 \$ 0.0 \$ 0.0 \$ 0.0 \$ 0.0 \$ 0.0 \$ 0.0 \$ 0.0 \$ 0.0 \$ 0.0 \$	A ₁₂ T 9.9 0 9.1 0 0.0 0 0.0 0 0.0 0 0.0 0 0.0 0 0.0 0 0.0 0 0.0 0 0.0 0 0.0 0 0.0 10 A ₁₂ T A ₁₂ T 0.0 10 0.0 10 0.0 10 A ₁₂ T 9.9 0 0.0 10 0.0 10 0.0 10 A ₁₂ T 9.9 0 0.0 10	13 A. .0 100 .0 0. .0 0. .13 A. .0 0. .0 0. .0 0. .0 0. .0 0. .0 0. .0 0. .0 0. .0 0. .0 0. .0 0. .0 0. .13 A. .13 A. .13 A. .13 A. .0 0. .0 0.	14 G 0.0 0 0 0 10 0 14 G 0 15 0 0 14 G 0 10 0 0 1 0 0 1 96 0 0 0 0 14 G 0 10 0 0 14 G 0 15 0 0 14 G 0 14 G 0 15 0 0 16 0 0 17 0 0 18 0 0 14 G 0 15 0 0<	\hat{s}_{15} A \hat{s}_{10} 99 \hat{s}_{10} 0 \hat{s}_{15} A \hat{s}_{15} A s	16 C 0.9 0 10 11 0 0 0 16 C 0 0 16 0 0 0 16 0 0 0 16 0 0 0 16 0 0 0 16 0 0 0 16 0 0 0 16 0 0 0 16 0 0 0 16 0 0 0 16 0 0 0 16 0 0 0 16 0 0 0 16 0 0 0 16 0 0 0	i7 T 0.0 0	18 G 10 0 0 .0 10 10 .0 0 0 .0 0 0 .0 0 0 .0 0 0 .0 0 0 .0 0 0 .0 0 0 .0 0 0 .0 0 0 .0 0 0 .0 0 0 .0 0 0 .0 0 0 .0 0 0 .0 0 0 .0 0 0 .0 0 0 .0 0 0	$ \frac{3}{10} $ $ $		A	G 0.0 0.0 0.0 00.0 0.0 00.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0 0.0 0 0.0 0 0.0 0	Inc G 0. 0.0 19.9 0.0 19.9 0.0 19.9 0.0 19.9 0.0 10.0 10.0 10.0 0.0 0.0 0.0	<u>del%</u> 046 057 057 050 <u>del%</u> 042 042

Untreated																								Indel%
Site 3	G ₁	T ₂	C ₃	A ₄	A ₅	G ₆	A ₇	A ₈	A ₉	G ₁₀	C ₁₁	A ₁₂	G ₁₃	A ₁₄	G ₁₅	A ₁₆	C ₁₇	T ₁₈	G ₁₉	C ₂₀	C	G	G	0.11
Α	0.0	0.0	0.0	100.0	100.0	0.0	100.0	0 100.0	100.0	0.0	0.0	100.0	0.0	100.0	0.0	100.0	0.0	0.0	0.0	0.0	0.0	0.1	0.0	
С	0.0	0.0	100.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	100.0	0.0	0.0	0.0	0.0	0.0	100.0	0.0	0.0	100.	0 99.9	0.0	0.0	
G	100.0	0.0	0.0	0.0	0.0	100.0	0.0	0.0	0.0	100.0	0.0	0.0	100.0	0.0	100.0	0.0	0.0	1.7	100.0	0.0	0.0	99.9	99.9	
I	0.0	100.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	98.3	0.0	0.0	0.1	0.0	0.0	
ABE6.3																								Indel%
Site 3	G	T ₂	C ₂	A٩	A۶	Ge	Α-	A。	Ao	Gio	C11	A12	G12	A14	G15	A	C17	T10	G10	Car	С	G	G	0.094
A	0.0	0.0	0.0	97.5	59.8	0.0	95.6	95.6	98.5	0.0	0.0	99.9	0.0	100.0	0.0	100.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.001
С	0.0	0.0	99.9	0.0	0.0	0.0	0.0	0.0	0.1	0.0	100.0	0.0	0.0	0.0	0.0	0.0	100.0	0.0	0.0	100.	0 100.	0.0	0.0	
G	100.0	0.0	0.0	2.4	40.1	99.9	4.4	4.4	1.4	100.0	0.0	0.0	99.9	0.0	99.9	0.0	0.0	0.0	100.0	0.0	0.0	99.9	100.0	
Т	0.0	100.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	100.0	0.0	0.0	0.0	0.0	0.0	
ADE7 0																								ll 10/
ABE7.8		Ŧ	0	•	•								0		0	•	0	-				G	G	Indel%
Site 3	G1	1 ₂	C ₃	A ₄	A ₅	G ₆	87.4	A ₈	A ₉	G ₁₀	C ₁₁	A ₁₂	G ₁₃	A ₁₄	G ₁₅	A ₁₆	C ₁₇	I 18	G ₁₉	C ₂₀		0.0	0.0	0.11
ĉ	0.0	0.0	99.9	0.0	0.0	0.0	0.0	97.5	0.0	0.0	100.0	0.0	0.0	0.0	0.0	0.0	100.0	0.0	0.0	99.0	- 0.0 A 100	0.0	0.0	
Ğ	100.0	0.0	0.0	1.5	29.2	100.0	12.6	2.7	1.8	100.0	0.0	0.1	100.0	0.0	100.0	0.0	0.0	0.0	100.0	0.0	0.0	99.9	99.9	
Т	0.0	100.0	0.1	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	100.0	0.0	0.0	0.0	0.0	0.0	
																			-					
ABE7.9																				-				Indel%
Site 3	G ₁	T ₂	C ₃	A ₄	A ₅	G ₆	A ₇	A ₈	A ₉	G ₁₀	C ₁₁	A ₁₂	G ₁₃	A ₁₄	G ₁₅	A ₁₆	C ₁₇	T ₁₈	G ₁₉	C ₂₀	C	G	G	0.11
A	0.0	0.0	0.0	99.2	66.8	0.0	87.6	98.3	97.0	0.0	0.0	99.9	0.0	100.0	0.0	100.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	
G	100.0	0.0	0.0	0.0	0.0	100.0	12.4	0.0	1.5	100.0		0.0	100.0	0.0	100.0	0.0	0.0	0.0	0.0	99.5	<u> </u>		0.0	
т	0.0	100.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	100.0	0.1	0.0	0.0	0.0	0.3	
•	0.0		0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	100.0	0.1	0.0	0.0	0.0	0.0	
ABE7.10																								Indel%
Site 3	G ₁	T ₂	C ₃	A_4	A ₅	G ₆	A ₇	A ₈	A ₉	G ₁₀	C ₁₁	A ₁₂	G ₁₃	A ₁₄	G ₁₅	A ₁₆	C ₁₇	T ₁₈	G ₁₉	C ₂₀	С	G	G	0.15
A	0.0	0.0	0.1	93.7	44.5	0.0	84.4	98.9	98.6	0.0	0.0	99.9	0.0	100.0	0.0	100.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	
С	0.0	0.0	99.8	0.0	0.0	0.0	0.0	0.0	0.0	0.0	100.0	0.0	0.0	0.0	0.0	0.0	99.9	0.0	0.0	99.8	3 99.9	0.1	0.0	
G	100.0	0.0	0.0	6.3	55.5	99.9	15.6	1.1	1.4	100.0	0.0	0.0	99.9	0.0	99.9	0.0	0.1	0.1	99.8	0.0	0.0	99.8	99.9	
I	0.0	100.0	0.1	0.0	0.1	0.1	0.0	0.0	0.0	0.0	0.0	0.0	0.1	0.0	0.1	0.0	0.0	99.9	0.1	0.2	0.0	0.1	0.1	
Untreated Site 4 A	G ₁ 0.2	A ₂ 100.0	G ₃ 0.0	C ₄ 0.0	A ₅ 99.6	A ₆ 100.0	A ₇ 99.9	G ₈ 0.0	A ₉ 100.0	G ₁₀ 0.0	A ₁₁ 100.0	A ₁₂ 100.0	T ₁₃ 0.0 1	A ₁₄ 00.0	G ₁₅ 0.0 1	A ₁₆ 00.0	C ₁₇ 0.0	T ₁₈ 0.0	G ₁₉ 0.0	T ₂₀ 0.0	A 100.0	G 0.0	G 0.0	Indel% 0.033
Untreated Site 4 A C	G ₁ 0.2 0.0	A ₂ 100.0 0.0	G ₃ 0.0 0.0	C ₄ 0.0 100.0	A ₅ 99.6 0.0	A ₆ 100.0 0.0	A ₇ 99.9 0.0	G ₈ 0.0 0.0	A ₉ 100.0 0.0	G ₁₀ 0.0 0.0	A ₁₁ 100.0 0.0	A ₁₂ 100.0 0.0	T ₁₃ 0.0 1 0.0	A ₁₄ 00.0 0.0	G ₁₅ 0.0 1 0.0	A ₁₆ 00.0 0.0	C ₁₇ 0.0 99.9	T ₁₈ 0.0 0.0	G ₁₉ 0.0 0.0	T ₂₀ 0.0 0.0	A 100.0 0.0	G 0.0 0.1	G 0.0 0.0	Indel% 0.033
Untreated Site 4 A C G	G ₁ 0.2 0.0 99.8	A ₂ 100.0 0.0 0.0	G ₃ 0.0 0.0 100.0	C ₄ 0.0 100.0 0.0	A ₅ 99.6 0.0 0.4	A ₆ 100.0 0.0 0.0	A ₇ 99.9 0.0 0.1	G ₈ 0.0 0.0 100.0	A ₉ 100.0 0.0 0.0	G ₁₀ 0.0 0.0 99.9	A ₁₁ 100.0 0.0 0.0	A ₁₂ 100.0 0.0 0.0	T ₁₃ 0.0 1 0.0 0.0	A ₁₄ 00.0 0.0 0.0 0.0	G ₁₅ 0.0 1 0.0 00.0	A ₁₆ 00.0 0.0 0.0	C ₁₇ 0.0 99.9 0.0	T ₁₈ 0.0 0.0 0.0 0.0	G ₁₉ 0.0 0.0 100.0	T ₂₀ 0.0 0.0 0.0	A 100.0 0.0 0.0	G 0.0 0.1 99.8	G 0.0 0.0 100.0	Indel% 0.033
Untreated Site 4 A C G T	G ₁ 0.2 0.0 99.8 0.0	A ₂ 100.0 0.0 0.0 0.0	G ₃ 0.0 0.0 100.0 0.0	C ₄ 0.0 100.0 0.0 0.0	A ₅ 99.6 0.0 0.4 0.0	A ₆ 100.0 0.0 0.0 0.0	A ₇ 99.9 0.0 0.1 0.0	G ₈ 0.0 0.0 100.0 0.0	A ₉ 100.0 0.0 0.0 0.0	G ₁₀ 0.0 0.0 99.9 0.1	A ₁₁ 100.0 0.0 0.0 0.0	A ₁₂ 100.0 0.0 0.0 0.0	T ₁₃ 0.0 1 0.0 0.0 100.0	A ₁₄ 00.0 0.0 0.0 0.0 1 0.0	G ₁₅ 0.0 1 0.0 00.0 0.0	A ₁₆ 00.0 0.0 0.0 0.0	C ₁₇ 0.0 99.9 0.0 0.0	T ₁₈ 0.0 0.0 0.0 0.0	G ₁₉ 0.0 0.0 100.0 0.0	T ₂₀ 0.0 0.0 0.0 99.9	A 100.0 0.0 0.0 0.0	G 0.0 0.1 99.8 0.0	G 0.0 0.0 100.0 0.0	Indel% 0.033
Untreated Site 4 A C G T ABE6.3	G ₁ 0.2 0.0 99.8 0.0	A ₂ 100.0 0.0 0.0 0.0	G ₃ 0.0 0.0 100.0 0.0	C₄ 0.0 100.0 0.0 0.0	A ₅ 99.6 0.0 0.4 0.0	A ₆ 100.0 0.0 0.0 0.0	A ₇ 99.9 0.0 0.1 0.0	G ₈ 0.0 0.0 100.0 0.0	A ₉ 100.0 0.0 0.0 0.0	G ₁₀ 0.0 0.0 99.9 0.1	A ₁₁ 100.0 0.0 0.0 0.0	A ₁₂ 100.0 0.0 0.0 0.0	T ₁₃ 0.0 1 0.0 0.0 100.0	A ₁₄ 00.0 0.0 0.0 1 0.0	G ₁₅ 0.0 1 0.0 00.0 0.0	A ₁₆ 00.0 0.0 0.0 0.0	C ₁₇ 0.0 99.9 0.0 0.0 0.0	T ₁₈ 0.0 0.0 0.0 0.0 00.0	G ₁₉ 0.0 0.0 100.0 0.0	T ₂₀ 0.0 0.0 0.0 99.9	A 100.0 0.0 0.0 0.0	G 0.0 0.1 99.8 0.0	G 0.0 0.0 100.0 0.0	Indel% 0.033 Indel%
Untreated Site 4 A C G T ABE6.3 Site 4	G ₁ 0.2 0.0 99.8 0.0 G ₁	A ₂ 100.0 0.0 0.0 0.0 A ₂	G ₃ 0.0 0.0 100.0 0.0 G ₃	C ₄ 0.0 100.0 0.0 0.0 C ₄	A ₅ 99.6 0.0 0.4 0.0 A ₅	A ₆ 100.0 0.0 0.0 0.0	A ₇ 99.9 0.0 0.1 0.0 A ₇	G ₈ 0.0 0.0 100.0 0.0	A ₉ 100.0 0.0 0.0 0.0	G ₁₀ 0.0 0.0 99.9 0.1 G ₁₀	A ₁₁ 100.0 0.0 0.0 0.0 A ₁₁	A ₁₂ 100.0 0.0 0.0 0.0	T ₁₃ 0.0 1 0.0 0.0 100.0 T ₁₃	A ₁₄ 00.0 0.0 0.0 1 0.0 A ₁₄	G ₁₅ 0.0 1 0.0 00.0 0.0 G ₁₅	A ₁₆ 00.0 0.0 0.0 0.0 A ₁₆	C ₁₇ 0.0 99.9 0.0 0.0 1 C ₁₇	T ₁₈ 0.0 0.0 0.0 00.0 T ₁₈	G ₁₉ 0.0 0.0 100.0 0.0 G ₁₉	T ₂₀ 0.0 0.0 99.9 T ₂₀	A 100.0 0.0 0.0 0.0	G 0.0 0.1 99.8 0.0	G 0.0 0.0 100.0 0.0 G	Indel% 0.033 Indel% 0.16
Untreated Site 4 C G T ABE6.3 Site 4 A	G ₁ 0.2 0.0 99.8 0.0 G ₁ 0.1	A ₂ 100.0 0.0 0.0 0.0 0.0 9.9	G ₃ 0.0 0.0 100.0 0.0 G ₃ 0.0	C ₄ 0.0 100.0 0.0 0.0 C ₄ 0.0	A ₅ 99.6 0.0 0.4 0.0 A ₅ 53.8	A ₆ 100.0 0.0 0.0 A ₆ 87.8	A ₇ 99.9 0.0 0.1 0.0 A ₇ 95.1	G8 0.0 0.0 100.0 0.0 G8 0.0	A ₉ 100.0 0.0 0.0 0.0 0.0 A ₉ 97.0	G ₁₀ 0.0 99.9 0.1 G ₁₀	A ₁₁ 100.0 0.0 0.0 0.0 0.0 0.0 8 4 ₁₁ 98.5	A ₁₂ 100.0 0.0 0.0 0.0 A ₁₂ 99.7	T ₁₃ 0.0 0.0 100.0 100.0 T ₁₃ 0.0	A ₁₄ 00.0 0.0 0.0 1 0.0 A ₁₄ 99.9	G ₁₅ 0.0 1 0.0 00.0 0.0 G ₁₅ 0.1 1	A ₁₆ 00.0 0.0 0.0 0.0 0.0 A ₁₆ 00.0	C ₁₇ 0.0 99.9 0.0 0.0 0.0 0.1 1 C ₁₇ 0.0	T ₁₈ 0.0 0.0 0.0 00.0 7 18 0.0	G ₁₉ 0.0 0.0 100.0 0.0 G ₁₉ 0.0	T ₂₀ 0.0 0.0 99.9 T ₂₀	A 100.0 0.0 0.0 0.0 A 100.0	G 0.0 0.1 99.8 0.0 G 0.0	G 0.0 0.0 100.0 0.0 G 0.0	Indel% 0.033 Indel% 0.16
Untreated Site 4 A C G T ABE6.3 Site 4 A C	G ₁ 0.2 0.0 99.8 0.0 G ₁ 0.1 0.0	A ₂ 100.0 0.0 0.0 0.0 A ₂ 99.9 0.0	G ₃ 0.0 0.0 100.0 0.0 G ₃ 0.0 0.0	C ₄ 0.0 100.0 0.0 0.0 C ₄ 0.0 99.9	A ₅ 99.6 0.0 0.4 0.0 A ₅ 53.8 0.1	A ₆ 100.0 0.0 0.0 0.0 0.0 87.8	A ₇ 99.9 0.0 0.1 0.0 A ₇ 95.1 0.0	G8 0.0 0.0 100.0 0.0 G8 0.0 0.0	A9 100.0 0.0 0.0 0.0 97.0 0.0	G ₁₀ 0.0 99.9 0.1 G ₁₀ 0.0 0.0	A ₁₁ 100.0 0.0 0.0 0.0 0.0 98.5 0.0	A ₁₂ 100.0 0.0 0.0 0.0 A ₁₂ 99.7 0.0	T ₁₃ 0.0 1 0.0 100.0 100.0 T ₁₃ 0.0 0.0	A ₁₄ 00.0 0.0 1 0.0 A ₁₄ 99.9 0.0	G ₁₅ 0.0 1 0.0 00.0 0.0 G ₁₅ 0.1 1 0.0	A ₁₆ 00.0 0.0 0.0 0.0 0.0 A ₁₆ 00.0 0.0	C ₁₇ 0.0 99.9 0.0 0.0 0.0 0.0 1 C ₁₇ 0.0 0.0 0.0 0.0 0.0	T ₁₈ 0.0 0.0 0.0 0 0.0 0 1 0.0 1 1 0.0 0 0 1	G ₁₉ 0.0 0.0 100.0 0.0 G ₁₉ 0.0 0.0	T ₂₀ 0.0 0.0 99.9 T ₂₀ 0.0 0.0	A 100.0 0.0 0.0 0.0 0.0 A 100.0 0.0	G 0.0 0.1 99.8 0.0 G 0.0 0.0 0.0	G 0.0 0.0 100.0 0.0 G 0.0 0.0 0.0	Indel% 0.033 Indel% 0.16
Untreated Site 4 A G T ABE6.3 Site 4 A C G G T	$ \begin{array}{c} G_1 \\ 0.2 \\ 0.0 \\ 99.8 \\ 0.0 \\ \hline G_1 \\ 0.1 \\ 0.0 \\ 99.9 \\ 0.0 \\ \end{array} $	A ₂ 100.0 0.0 0.0 0.0 99.9 0.0 0.0	G ₃ 0.0 100.0 0.0 G ₃ 0.0 0.0 100.0	$ \begin{array}{c} C_4 \\ 0.0 \\ 100.0 \\ 0.0 \\ \hline C_4 \\ 99.9 \\ 0.0 \\ 0.0 \\ \hline \end{array} $	A ₅ 99.6 0.0 0.4 0.0 A ₅ 53.8 0.1 46.1 0.1	A ₆ 100.0 0.0 0.0 0.0 A ₆ 87.8 0.0 12.2 0.0	A ₇ 99.9 0.0 0.1 0.0 A ₇ 95.1 0.0 4.9	G ₈ 0.0 0.0 0.0 100.0 0.0 G ₈ 0.0 0.0 99.9 0.0 0.0	A9 100.0 0.0 0.0 0.0 97.0 0.0 3.0	G ₁₀ 0.0 99.9 0.1 G ₁₀ 0.0 0.0 100.0	A ₁₁ 100.0 0.0 0.0 0.0 0.0 98.5 0.0 1.5 0.0	A ₁₂ 100.0 0.0 0.0 A ₁₂ 99.7 0.0 0.3 0.0	T ₁₃ 0.0 1 0.0 100.0 T ₁₃ 0.0 0.0 0.0 0.0	A ₁₄ 00.0 0.0 0.0 1 0.0 A ₁₄ 99.9 0.0 0.0 8 0.0 8	G ₁₅ 0.0 1 0.0 00.0 0.0 G ₁₅ 0.1 1 0.0 99.9 0.0	A ₁₆ 00.0 0.0 0.0 0.0 0.0 A ₁₆ 00.0 0.0 1 0.0	$ \begin{array}{c c} C_{17} \\ 0.0 \\ 99.9 \\ 0.0 \\ 0.0 \\ 1 \\ \hline C_{17} \\ 0.0 \\ 00.0 \\ $	T ₁₈ 0.0 0.0 0.0 0.0 0.0 T ₁₈ 0.0 0.0 0.0 0.0 0.0 0.1 2	G ₁₉ 0.0 0.0 100.0 0.0 G ₁₉ 0.0 0.0 0.0 0.0	T ₂₀ 0.0 0.0 99.9 T ₂₀ 0.0 0.0 0.0 0.0	A 100.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0	G 0.0 0.1 99.8 0.0 G 0.0 0.0 100.0	G 0.0 0.0 100.0 0.0 G 0.0 99.9 0.0	Indel% 0.033 Indel% 0.16
Untreated Site 4 A C G T ABE6.3 Site 4 A C G T	$\begin{array}{c} G_1 \\ 0.2 \\ 0.0 \\ 99.8 \\ 0.0 \\ \hline \\ G_1 \\ 0.1 \\ 0.0 \\ 99.9 \\ 0.0 \\ \end{array}$	A ₂ 100.0 0.0 0.0 0.0 99.9 0.0 0.1 0.0	G ₃ 0.0 0.0 100.0 0.0 G ₃ 0.0 0.0 100.0 0.0	C ₄ 0.0 100.0 0.0 0.0 C ₄ 0.0 99.9 0.0 0.0	A5 99.6 0.0 0.4 0.0 53.8 0.1 46.1 0.1	A ₆ 100.0 0.0 0.0 0.0 87.8 0.0 12.2 0.0	A ₇ 99.9 0.0 0.1 0.0 A ₇ 95.1 0.0 4.9 0.0	G ₈ 0.0 0.0 0.0 100.0 0.0 0.0 0.0 99.9 0.0	A ₉ 100.0 0.0 0.0 0.0 97.0 0.0 3.0 0.0	G ₁₀ 0.0 0.0 0.0 99.9 0.1 G ₁₀ 0.0 0.0 0.0 0.0 0.0 0.00 0.0	A ₁₁ 100.0 0.0 0.0 0.0 0.0 0.0 0.0 98.5 0.0 1.5 0.0	A ₁₂ 100.0 0.0 0.0 0.0 99.7 0.0 0.3 0.0	T ₁₃ 0.0 0.0 100.0 T ₁₃ 0.0 0.0 0.0 99.9	A ₁₄ 00.0 0.0 0.0 0.0 A ₁₄ 99.9 0.0 0.0 0.0 \$	G ₁₅ 0.0 1 0.0 00.0 0.0 G ₁₅ 0.1 1 0.0 99.9 0.0	A ₁₆ 00.0 0.0 0.0 0.0 0.0 A ₁₆ 00.0 0.0 0.0 0.0	C ₁₇ 0.0 99.9 0.0 0.0 0.0 0.0 1 C ₁₇ 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0	T18 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.1 39.9	G ₁₉ 0.0 0.0 100.0 0.0 G ₁₉ 0.0 0.0 100.0 0.0	T ₂₀ 0.0 0.0 99.9 T ₂₀ 0.0 0.0 0.0 99.9	A 100.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0	G 0.0 0.1 99.8 0.0 G 0.0 0.0 100.0 0.0	G 0.0 0.0 100.0 0.0 G 0.0 99.9 0.0	Indel% 0.033 Indel% 0.16
Untreated Site 4 A C G T ABE6.3 Site 4 A C G T T ABE7.8	$\begin{array}{c} G_1 \\ 0.2 \\ 0.0 \\ 99.8 \\ 0.0 \\ \hline \\ G_1 \\ 0.1 \\ 0.0 \\ 99.9 \\ 0.0 \\ \end{array}$	A ₂ 100.0 0.0 0.0 0.0 99.9 0.0 0.1 0.0	$\begin{array}{c} G_3 \\ 0.0 \\ 0.0 \\ 100.0 \\ 0.0 \\ \hline \\ 0.0 \\ 0.0 \\ 0.0 \\ \hline \\ 100.0 \\ 0.0 \\ \hline \end{array}$	$\begin{array}{c} C_4 \\ 0.0 \\ 100.0 \\ 0.0 \\ 0.0 \\ \hline \\ 0.0 \\ 99.9 \\ 0.0 \\ 0.0 \\ 0.0 \\ \hline \end{array}$	A5 99.6 0.0 0.4 0.0 53.8 0.1 46.1 0.1	A ₆ 100.0 0.0 0.0 0.0 87.8 0.0 12.2 0.0	A ₇ 99.9 0.0 0.1 0.0 4.7 0.0 4.9 0.0	G8 0.0 0.0 0.0 100.0 0.0 G8 0.0 0.0 0.0 99.9 0.0	A ₉ 100.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 3.0 0.0	G ₁₀ 0.0 99.9 0.1 G ₁₀ 0.0 0.0 100.0 0.0	A ₁₁ 100.0 0.0 0.0 0.0 A ₁₁ 98.5 0.0 1.5 0.0	A ₁₂ 100.0 0.0 0.0 0.0 99.7 0.0 0.3 0.0	T ₁₃ 0.0 1 0.0 100.0 100.0 100.0 T ₁₃ 0.0 0.0 0.0 0.0 99.9 9 9	A ₁₄ 00.0 0.0 0.0 1 0.0 4 ₁₄ 99.9 0.0 0.0 0.0 8 0.0	G ₁₅ 0.0 1 0.0 00.0 0.0 G ₁₅ 0.1 1 0.0 99.9 0.0	A ₁₆ 00.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0	C17 0.0 99.9 0.0 0.0 0.0 0.0 1 C17 0.0 00.0 0.0 0.0 0.0 0.0 0.0 0.0 1	T18 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.1 0.0 0.2 0.1	G ₁₉ 0.0 0.0 100.0 0.0 G ₁₉ 0.0 0.0 0.0 0.0 0.0	T ₂₀ 0.0 0.0 99.9 T ₂₀ 0.0 0.0 0.0 99.9	A 100.0 0.0 0.0 0.0 A 100.0 0.0 0.0 0.0	G 0.0 0.1 99.8 0.0 G 0.0 0.0 100.0 0.0	G 0.0 0.0 100.0 0.0 G 0.0 99.9 0.0	Indel% 0.033 Indel% 0.16
Untreated Site 4 A C G T ABE6.3 Site 4 A C G T ABE7.8 Site 4	G ₁ 0.2 0.0 99.8 0.0 G ₁ 0.1 0.0 99.9 0.0	A ₂ 100.0 0.0 0.0 0.0 99.9 0.0 0.1 0.0	G ₃ 0.0 0.0 100.0 0.0 G ₃ 0.0 0.0 100.0 0.0	C ₄ 0.0 100.0 0.0 0.0 0.0 99.9 0.0 0.0 0.0	A5 99.6 0.0 0.4 0.0 A5 53.8 0.1 46.1 0.1	A ₆ 100.0 0.0 0.0 0.0 0.0 12.2 0.0 12.2 0.0	A ₇ 99.9 0.0 0.1 0.0 95.1 0.0 4.9 0.0	G8 0.0 0.0 0.0 100.0 0.0 G8 0.0 0.0 99.9 0.0 0.0	A9 100.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 3.0 0.0	G ₁₀ 0.0 99.9 0.1 G ₁₀ 0.0 0.0 100.0 0.0	A ₁₁ 100.0 0.0 0.0 0.0 0.0 98.5 0.0 1.5 0.0 1.5 0.0	A ₁₂ 100.0 0.0 0.0 0.0 A ₁₂ 99.7 0.0 0.3 0.0 A ₁₂	T ₁₃ 0.0 1 0.0 100.0 100.0 T ₁₃ 0.0 0.0 99.9	A ₁₄ 00.0 0.0 0.0 1 0.0 A ₁₄ 99.9 0.0 0.0 0.0 8 0.0	G ₁₅ 0.0 1 0.0 00.0 0.0 G ₁₅ 0.1 1 0.0 99.9 0.0 G ₁₅	A ₁₆ 00.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 1 0.0 0.0	C ₁₇ 0.0 99.9 0.0 0.0 1 C ₁₇ 0.0 00.0 0.0 0.0 0.0 0.0 2 C ₁₇	T ₁₈ 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.1 99.9 T ₁₈	G ₁₉ 0.0 0.0 100.0 0.0 G ₁₉ 0.0 0.0 100.0 0.0 100.0 0.0	T ₂₀ 0.0 0.0 99.9 T ₂₀ 0.0 0.0 0.0 99.9	A 100.0 0.0 0.0 0.0 A 100.0 0.0 0.0 0.0 0.0	G 0.0 0.1 99.8 0.0 G 0.0 0.0 100.0 0.0 G G	G 0.0 0.0 100.0 0.0 0.0 99.9 0.0 G G	Indel% 0.033 Indel% 0.16 Indel% 0.12
Untreated Site 4 A C G T ABE6.3 Site 4 A C G G T ABE7.8 Site 4 A	$\begin{array}{c} G_1 \\ 0.2 \\ 0.0 \\ 99.8 \\ 0.0 \\ \hline \\ G_1 \\ 0.1 \\ 0.0 \\ 99.9 \\ 0.0 \\ \hline \\ G_1 \\ 0.1 \\ \hline \\ 0.1 \\ \end{array}$	A ₂ 100.0 0.0 0.0 0.0 99.9 0.0 0.1 0.0 0.1 0.0 99.9	G ₃ 0.0 0.0 100.0 0.0 G ₃ 0.0 0.0 100.0 G ₃ 0.0	$\begin{array}{c} C_4 \\ 0.0 \\ 100.0 \\ 0.0 \\ 0.0 \\ \hline \\ 0.0 \\ 99.9 \\ 0.0 \\ 0.0 \\ \hline \\ C_4 \\ 0.0 \\ \hline \\ \end{array}$	A5 99.6 0.0 0.4 0.0 A5 53.8 0.1 46.1 0.1 A5 77.8	A ₆ 100.0 0.0 0.0 0.0 87.8 0.0 12.2 0.0 12.2 0.0 12.2 0.0 86.5	A ₇ 99.9 0.0 0.1 0.0 95.1 0.0 4.9 0.0 4.9 0.0	G8 0.0 0.0 0.0 100.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 99.9 0.0 G8 0.0 0.0 0.0	A ₉ 100.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 3.0 0.0 3.0 0.0 3.0 98.7	G ₁₀ 0.0 99.9 0.1 G ₁₀ 0.0 0.0 100.0 0.0 G ₁₀ 0.0	A ₁₁ 100.0 0.0 0.0 0.0 0.0 0.0 A ₁₁ 98.5 0.0 1.5 0.0 A ₁₁ 99.7	A ₁₂ 100.0 0.0 0.0 0.0 A ₁₂ 99.7 0.0 0.3 0.0 A ₁₂ 99.7 99.8 99.7 99.8 99.8 99.8 99.8 99.8 99.8 99.8 99.8 99.8 99.8 99.8 99.8 99.8 90	T ₁₃ 0.0 100.0 0.0 0.0 100.0 100.0 100.0 0.0 0.0 0.0 0.0 0.0 99.9 100.0	A ₁₄ 00.0 0.0 0.0 0.0 1 0.0 A ₁₄ 99.9 0.0 0.0 0.0 0.0 0.0 A ₁₄ 00.0 A ₁₄ 00.0	G15 0.0 1 0.0 00.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 99.9 0.0 0.0 0.0 G15 0.0 0.0 0.0	A ₁₆ 00.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0	C ₁₇ 0.0 99.9 0.0 0.0 0.0 0.0 1 C ₁₇ 0.0 0.0 0.0 0.0 0.0 0.0 0.0 1 C ₁₇ 0.0 0.0 0.0 0.0 1 C ₁₇ 0.0 1	T ₁₈ 0.0 0.0 0.0 0.0 0.0 0.0 T ₁₈ 0.0 0.1 99.9 T ₁₈ 0.0	G ₁₉ 0.0 0.0 100.0 0.0 0.0 0.0 100.0 0.0 0.0	$\begin{array}{c} T_{20} \\ 0.0 \\ 0.0 \\ 0.0 \\ 99.9 \end{array}$ $\begin{array}{c} T_{20} \\ 0.0 \\ 0.0 \\ 0.0 \\ 99.9 \end{array}$ $\begin{array}{c} T_{20} \\ 0.0 $	A 100.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0	G 0.0 0.1 99.8 0.0 G 0.0 0.0 100.0 0.0 0.0	G 0.0 0.0 100.0 0.0 0.0 99.9 0.0 G 0.0	Indel% 0.033 Indel% 0.16
Untreated Site 4 A C G T ABE6.3 Site 4 A C G T ABE7.8 Site 4 A C	G ₁ 0.2 0.0 99.8 0.0 G ₁ 0.0 99.9 0.0 G ₁ 0.1	A ₂ 100.0 0.0 0.0 0.0 99.9 0.0 0.1 0.0 0.1 0.0 99.9 0.0	G ₃ 0.0 0.0 100.0 0.0 G ₃ 0.0 0.0 G ₃ 0.0 0.0	C ₄ 0.0 100.0 0.0 0.0 C ₄ 0.0 99.9 0.0 0.0 0.0 C ₄ 0.0 100.0	A5 99.6 0.0 0.4 0.0 53.8 0.1 46.1 0.1 77.8 0.1	A ₆ 100.0 0.0 0.0 0.0 87.8 0.0 12.2 0.0 46 86.5 0.0	A ₇ 99.9 0.0 0.1 0.0 95.1 0.0 4.9 0.0 4.9 0.0	G8 0.0 0.0 0.0 100.0 0.0 0.0 0.0 0.0 0.0 99.9 0.0 G8 0.0 0.0 0.0	A ₉ 100.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 3.0 0.0 3.0 0.0 97.0 0.0 3.0 97.0 0.0 3.0 97.0 0.0	G ₁₀ 0.0 99.9 0.1 G ₁₀ 0.0 0.0 100.0 0.0 G ₁₀ 0.0	A ₁₁ 100.0 0.0 0.0 0.0 A ₁₁ 98.5 0.0 1.5 0.0 A ₁₁ 99.7 0.0	A ₁₂ 100.0 0.0 0.0 0.0 99.7 0.0 0.3 0.0 A ₁₂ 99.7 99.7 9.0 0.0 0.3 0.0 0.3 0.0 99.7 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0	T ₁₃ 0.0 100.0 0.0 0.0 100.0 100.0 100.0 0.0 0.0 0.0 99.9 0.0 7 0.0 0.0 7 0.0 0.0 7 0.0 100.0 7	A ₁₄ 00.0 0.0 0.0 0.0 1 0.0 1 0.0 1 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0	G15 0.0 1 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 99.9 0.0 0.0 0.0 G15 0.0 1 0.0 G15 0.1 1 0.0	A ₁₆ 0.0 0 0.0 0 0.0 0 0.0 0 0.0 1 0.0 0 0.0 1 A ₁₆ 0.0 0 0.0 1 0.0 1 0.0 0 0.0 1	C17 0.0 99.9 0.0 0.0 0.0 0.0 1 C17 0.0 0.0 0.0 0.0 0.0 0.0 0.0 1 C17 0.0 0.0 C17 0.0 0.0 C17 0.0 0.0	T ₁₈ 0.0 0.0 0.0 0.0 0.0 0.0 T ₁₈ 0.0 0.1 99.9 T ₁₈ 0.0 0.1 90.0	G ₁₉ 0.0 0.0 0.0 100.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0	$\begin{array}{c} T_{20} \\ 0.0 \\ 0.0 \\ 0.0 \\ 99.9 \end{array}$ $\begin{array}{c} T_{20} \\ 0.0 \\ 0.0 \\ 0.0 \\ 99.9 \end{array}$ $\begin{array}{c} T_{20} \\ 0.0 \\ 0.0 \\ 0.0 \\ 0.0 \\ 0.0 \\ 0.0 \end{array}$	A 100.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0	G 0.0 0.1 99.8 0.0 0.0 100.0 0.0 0.0 0.0 0.0	G 0.0 0.0 100.0 0.0 99.9 0.0 G 0.0 0.0 0.0	Indel% 0.033 Indel% 0.16 Indel% 0.12
Untreated Site 4 A C G T ABE6.3 Site 4 A C G T ABE7.8 Site 4 A C G C G	G ₁ 0.2 0.0 99.8 0.0 G ₁ 0.1 0.0 99.9 0.0	A ₂ 100.0 0.0 0.0 0.0 0.0 0.1 0.1	G ₃ 0.0 0.0 100.0 0.0 G ₃ 0.0 0.0 100.0 G ₃ 0.0 0.0 100.0	C ₄ 0.0 100.0 0.0 0.0 0.0 99.9 0.0 0.0 0.0	A5 99.6 0.0 0.4 0.0 0.4 0.1 3.8 0.1 46.1 0.1 77.8 0.1 22.1	A ₆ 100.0 0.0 0.0 0.0 0.0 100.0 0.0 12.2 0.0 46 86.5 0.0 13.5	A7 99.9 0.0 0.1 0.0 95.9 0.0 4.9 0.0 4.7 95.9 0.0 4.1	G8 0.0 0.0 0.0 100.0 0.0 G8 0.0 99.9 0.0 G8 0.0 0.0 0.0 99.9 0.0 G8 0.0 0.0 0.0 100.0 100.0	A ₉ 100.0 0.0 0.0 0.0 0.0 3.0 0.0 3.0 0.0 3.0 0.0 3.0 0.0 3.0 0.0 1.3	G10 0.0 0.0 99.9 0.1 G10 0.0	A11 100.0 0.0 0.0 0.0 0.0 0.0 0.0 A11 98.5 0.0 1.5 0.0 0.0 A11 99.7 0.0 0.3	A ₁₂ 100.0 0.0 0.0 0.0 99.7 0.0 0.3 0.0 0.3 0.0 A ₁₂ 99.8 0.0 0.2	T ₁₃ 1 0.0 1 0.0 1 0.0 1 0.0 1 0.0 1 0.0 1 0.0 1 0.0 1 0.0 1 0.0 1 0.0 1 0.0 1 0.0 1 0.0 1 0.0 1	A ₁₄ 00.0 0.0 0.0 0.0 1 99.9 0.0 0.0 0.0 A ₁₄ 99.9 0.0 0.0 A ₁₄ 0.0 0.0 0.0 A ₁₄ 0.0 0.0 0.0	G15 1 0.0 1 0.0 0.0 0.0 0.0 0.0 0.0 G15 0.1 0.1 1 0.0 0.0 G15 0.1 0.1 1 0.0 0.0 99.9 0.0	A ₁₆ 0.0 0.0 0.0 0.0 0.0 0.0 0.0 1 0.0 0.0 1 0.0 0.0	C17 0.0 99.9 0.0 0.0 0.0 0.0 1 C17 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0	T18 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.1 99.9 T18 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0	G19 0.0 0.0 0.0 100.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 100.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 100.0 0.0	T ₂₀ 0.0 0.0 99.9 T ₂₀ 0.0 0.0 0.0 99.9 T ₂₀ 0.0 0.0 0.0 0.0 0.0 0.0	A 100.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0	G 0.0 0.1 99.8 0.0 0.0 100.0 0.0 100.0 0.0 0.0 100.0	G 0.0 0.0 100.0 0.0 0.0 99.9 0.0 G 0.0 0.0 0.0 100.0	Indel% 0.033 0.033 0.16 0.16
Untreated Site 4 A C G T ABE6.3 Site 4 A C G T ABE7.8 Site 4 A C G T T	$\begin{array}{c} G_1 \\ 0.2 \\ 0.0 \\ 99.8 \\ 0.0 \\ \hline \\ 0.1 \\ 0.0 \\ 99.9 \\ 0.0 \\ \hline \\ G_1 \\ 0.1 \\ 0.0 \\ 99.9 \\ 0.0 \\ \hline \end{array}$	A ₂ 100.0 0.0 0.0 0.0 99.9 0.0 0.1 0.0 0.1 0.0	G3 0.0	C ₄ 0.0 100.0 0.0 0.0 99.9 0.0 0.0 0.0 0.0 0.0 100.0 0.0 0.0	A5 99.6 0.0 0.4 0.0 A5 53.8 0.1 46.1 0.1 A5 77.8 0.1 22.1 0.0	A6 100.0 0.0 0.0 0.0 0.0 87.8 0.0 12.2 0.0 86.5 0.0 13.5 0.0	A ₇ 99.9 0.0 0.1 0.0 95.1 0.0 4.9 0.0 4.9 0.0 4.1 0.0	G8 0.0 0.0 0.0 100.0 0.0 0.0 0.0 0.0 0.0 99.9 0.0 G8 0.0 0.0 0.0 90.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0	A ₉ 100.0 0.0 0.0 0.0 0.0 0.0 0.0 3.0 0.0 3.0 0.0 98.7 0.0 1.3 0.0	G10 0.0 0.0 0.0 0.0 0.0 0.1 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0	A11 100.0 0.0 0.0 0.0 0.0 0.0 1.5 0.0 1.5 0.0 1.5 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.3 0.0	A ₁₂ 100.0 0.0 0.0 0.0 A ₁₂ 99.7 0.0 0.3 0.0 A ₁₂ 99.8 0.0 0.2 0.0	T ₁₃ 0.0 1 0.0 100.0 100.0 100.0 T ₁₃ 0.0 0.0 99.9 T ₁₃ 0.0 100.0 100.0 0.0 0.0 0.0 100.0 0.0 0.0 0.0 100.0 100.0 100.0 100.0 100.0	A ₁₄ 00.0 0.0 0.0 0.0 1 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0	G15 0.0 1 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 G15 0.1 1 0.0 99.9 0.0 0.1 1 0.1 1 1 0.0 99.9 0.0 0.0 99.9 0.0 99.9 0.0 0.0	A ₁₆ 0.0 0.0 0.0 0.0 0.0 0.0 0.0 1 0.0 0.0 A ₁₆ 0.0 0.0 1 0.0 1 0.0 1 0.0 1 0.0 1 0.0 1 0.0	C ₁₇ 0.0 99.9 0.0 0.0 0.0 0.0 1 C ₁₇ 0.0 0.0 0.0 0.0 0.0 0.0 0.0 C ₁₇ 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0	T ₁₈ 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.1 29.9 T ₁₈ 0.0 0.1 29.9 T ₁₈ 0.0 0.2 29.8	G ₁₉ 0.0 0.0 0.0 100.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0	$\begin{array}{c} T_{20} \\ 0.0 \\ 0.0 \\ 0.0 \\ 99.9 \end{array}$ $\begin{array}{c} T_{20} \\ 0.0 \\ 0.0 \\ 0.0 \\ 0.0 \\ 99.9 \end{array}$ $\begin{array}{c} T_{20} \\ 0.0 \\ 0.0 \\ 0.0 \\ 0.0 \\ 0.0 \\ 99.9 \end{array}$	A 100.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0	G 0.0 0.1 99.8 0.0 0.0 100.0 0.0 G 0.0 0.0 100.0 0.0 100.0 0.0	G 0.0 0.0 100.0 0.0 G 0.0 99.9 0.0 G 0.0 0.0 100.0 0.0	Indel% 0.033 0.16 0.16 0.12
Untreated Site 4 A C G T ABE6.3 Site 4 A C G T ABE7.8 Site 4 A C G T T	$\begin{array}{c} G_1 \\ 0.2 \\ 0.0 \\ 99.8 \\ 0.0 \\ \hline \\ 0.1 \\ 0.0 \\ 99.9 \\ 0.0 \\ \hline \\ G_1 \\ 0.1 \\ 0.0 \\ 99.9 \\ 0.0 \\ \hline \end{array}$	A ₂ 100.0 0.0 0.0 0.0 0.0 0.0 0.1 0.0 4 ₂ 99.9 0.0 0.1 0.0 0.1 0.0	$\begin{array}{c} G_3 \\ 0.0 \\ 0.0 \\ 100.0 \\ 0.0 \\ 0.0 \\ 0.0 \\ 100.0 \\ 0.0 \\ \hline G_3 \\ 0.0 \\ 0.0 \\ \hline G_3 \\ 0.0 \\ 0.0 \\ 0.0 \\ 0.0 \\ 0.0 \\ 0.0 \\ \hline \end{array}$	C4 0.0 100.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0	A5 99.6 0.0 0.4 0.0 0.4 53.8 0.1 46.1 0.1 77.8 0.1 22.1 0.0	A ₆ 100.0 0.0 0.0 0.0 10.0 0.0 12.2 0.0 A ₆ 88.5 0.0 13.5 0.0	A7 99.9 0.0 0.1 0.0 4.9 0.0 4.9 0.0 4.9 0.0 4.9 0.0 4.1 0.0	G ₈ 0.0 0.0 0.0 100.0 0.0 G ₈ 0.0 99.9 0.0 G ₈ 0.0 0.0 0.0 90.0 0.0 100.0 0.0 0.0 0.0	Ag 100.0 0.0 0.0 0.0 0.0 3.0 0.0 3.0 0.0 3.0 0.0 3.0 0.0 1.3 0.0	G ₁₀ 0.0 0.0 99.9 0.1 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0	A ₁₁ 100.0 0.0 0.0 0.0 0.0 11 98.5 0.0 1.5 0.0 1.5 0.0 0.0 0.0 0.0 0.0 0.3 0.0	A ₁₂ 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.	T ₁₃ 0.0 7 0.0 100.0 100.0 100.0 T ₁₃ 0.0 0.0 0.0 99.9 T ₁₃ 0.0 100.0 T ₁₃ 0.0 0.0 0.0 0.0 0.0 0.0 100.0	A14 00.0 0.0 0.0 0.0 1 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0	G15 0.0 1 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 99.9 0.0	A ₁₆ 00.0 0.0 0.0 0.0 0.0 0.0 0.0 0	C17 0.0 99.9 0.0 0.0 0.0 0.0 1 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0	T ₁₈ 0.0 0.0 0.0 0.0 0.0 0.0 0.0 T18 0.0 0.0 0.1 T18 0.0 0.0 0.0 T18 0.0 0.0 0.0 0.2 2 99.8 8	G ₁₉ 0.0 100.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0	T ₂₀ 0.0 0.0 99.9 T ₂₀ 0.0 0.0 99.9 T ₂₀ 0.0 0.0 0.0 0.0 0.0 99.9	A 100.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0	G 0.0 0.1 99.8 0.0 0.0 0.0 100.0 0.0 0.0 0.0 100.0 0.0	G 0.0 0.0 0.0 0.0 0.0 99.9 0.0 G 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0	Indel% 0.033 Indel% 0.16 Indel%
Untreated Site 4 A C G T ABE6.3 Site 4 A C G G T ABE7.8 Site 4 A C G G T ABE7.9 Site 4	$ \begin{array}{c} G_{1} \\ 0.2 \\ 0.0 \\ 99.8 \\ 0.0 \\ \hline G_{1} \\ 0.1 \\ 0.0 \\ 99.9 \\ 0.0 \\ \hline G_{1} \\ 0.1 \\ 0.0 \\ 99.9 \\ 0.0 \\ \hline G_{1} \\ 0.1 \\ 0.0 \\ \hline G_{2} \\ 0.0 \\ \hline G_{3} \\ 0.0 \\ \hline G_{4} \\ 0.0 \\ \hline G_{5} \\$	A ₂ 100.0 0.0 0.0 0.0 99.9 0.0 0.1 0.0 0.1 0.0 0.1 0.0	G3 0.0 0.0 0.0 100.0 0.0 0.0 0.0 0.0 0.0 100.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0	C ₄ 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.	A ₅ 99.6 0.0 0.4 0.0 0.4 53.8 0.1 46.1 0.1 46.1 0.1 22.1 0.0	A6 100.0 0.0 0.0 0.0 0.0 7.8 0.0 12.2 0.0 A6 86.5 0.0 13.5 0.0 0.0	A ₇ 99.9 0.0 0.1 0.0 4.9 0.0 4.9 0.0 4.7 95.9 0.0 A ₇ 95.9 0.0 A ₇ 0.0 A ₇ 0.0	G8 0.0 0.0 0.0 100.0 0.0 0.0 0.0 0.0 99.9 0.0 0.0 G8 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0	A ₉ 100.0 0.0 0.0 0.0 0.0 0.0 0.0 3.0 0.0 3.0 0.0 3.0 0.0 3.0 0.0 3.0 0.0 3.0 0.0 3.0 0.0 1.3 0.0	G ₁₀ 0.0 99.9 0.1 G ₁₀ 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0	A11 100.0 0.0 0.0 0.0 0.0 0.0 0.0 98.5 0.0 1.5 0.0 A11 99.7 0.0 0.3 0.0	A ₁₂ 100.0 0.0 0.0 0.0 0.0 0.0 0.0 0	T ₁₃ 0.0 0.0 0.0 100.0 100.0 T ₁₃ 0.0 0.0 0.0 99.9 100.0 T ₁₃ 0.0 0.0 0.0 0.0 100.0 100.0 100.0	A ₁₄ 00.0 0.0 0.0 0.0 1 0.0 0.0 A ₁₄ 0.0 0.0 0.0 0.0 0.0 A ₁₄ 0.0 0.0 0.0 A ₁₄ 0.0 0.0 0.0 0.0 0.0 A ₁₄ 0.0 A ₁₄ 0.0 A ₁₄ 0.0	G ₁₅ 0.0 1 0.0 00.0 00.0 00.0 0.1 1 0.0 0.0 G ₁₅ 0.0 0.0 0.0 0.0	A ₁₆ 00.0 0.0 0.0 0.0 0.0 0.0 0.0 A ₁₆ 0.0 0.0 0.0 A ₁₆ 0.0 0.0 0.0 A ₁₆ 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0	C ₁₇ 0.0 99.9 0.0 1 C ₁₇ 0.0 0.0 0.0 C ₁₇ 0.0 0.0 0.0 C ₁₇ 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.	T18 0.0 0.0 0.0 0.0 0.0 718 0.0 0.0 0.0 718 0.0 0.0 0.0 0.1 1 99.9 1 99.8 1	G ₁₉ 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.	T ₂₀ 0.0 0.0 99.9 T ₂₀ 0.0 0.0 0.0 99.9 T ₂₀ 0.0 0.0 0.0 99.9	A 100.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0	G 0.0 0.1 99.8 0.0 0.0 100.0 0.0 100.0 0.0 100.0 0.0 100.0 0.0	G 0.0 0.0 100.0 0.0 0.0 99.9 0.0 99.9 0.0 G 0.0 0.0 0.0 100.0 0.0	Indel% 0.033 Indel% 0.16 Indel% 0.12
Untreated Site 4 A C G T ABE6.3 Site 4 A C G T ABE7.8 Site 4 A C G T T ABE7.9 Site 4 A A BE7.9 Site 4 A	$\begin{array}{c} G_1 \\ 0.2 \\ 0.0 \\ 99.8 \\ 0.0 \\ \hline \\ 0.1 \\ 0.0 \\ 99.9 \\ 0.0 \\ \hline \\ G_1 \\ 0.1 \\ 0.0 \\ 99.9 \\ 0.0 \\ \hline \\ G_1 \\ 0.$	A ₂ 100.0 0.0 0.0 0.0 0.0 0.0 0.1 0.0 0.1 0.0 0.1 0.0 0.1 0.0 0.1 0.0 0.1 0.0 0.0	G3 O.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0	C4 0.0 100.0 0.0	A5 99.6 0.0 0.4 0.0 0.4 0.0 0.4 0.1 3.8 0.1 0.1 A6 77.8 0.1 22.1 0.0 0.1 A6 77.8	A ₆ 100.0 0.0 0.0 0.0 87.8 0.0 12.2 0.0 12.2 0.0 13.5 0.0 13.5 0.0	A7 99.9 0.0 0.1 0.0 0.1 0.0 0.0 4.1 0.0 4.1 0.0 4.1 0.0 4.2 0.0 4.3 0.0	G8 0.0 0.0 0.0 100.0 0.0 G8 0.0 0.0 0.0 99.9 0.0 G8 0.0 0.0 0.0 90.0 0.0 G8 0.0 0.0 0.0 G8 0.0 0.0 0.0 0.0 0.0	Ag 100.0 0.0 0.0 0.0 0.0 0.0 0.0 Ag 97.0 0.0 0.0 Ag 99.7 0.0 1.3 0.0 1.3 0.0 98.7	G ₁₀ 0.0 99.9 0.1 G ₁₀ 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0	A ₁₁ 100.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 1.5 0.0 1.5 0.0 0.0 0.3 0.0 0.3 0.0 A ₁₁ 99.8	A ₁₂ 100.0 0.0 0.0 0.0 0.0 0.0 0.0 0	T ₁₃ 0.0 0.0 0.0 0.0 0.0 100.0 0.0 T ₁₃ 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 100.0 T ₁₃ 0.0 100.0 100.0	A ₁₄ 00.0 0.0 0.0 0.0 1	G ₁₅ 0.0 1 0.0 0.0 0.0 G ₁₅ 0.1 1 0.0 99.9 0.0 G ₁₅ 0.1 1 0.0 99.9 0.0 G ₁₅ 0.1 1 0.0 99.9	A ₁₆ 00.0 0.0 0.0 0.0 0.0 0.0 0.0 A ₁₆ 0.0 A ₁₆ 0.0 A ₁₆ 0.0 A ₁₆ 0.0	C ₁₇ 0.0 99.9 0.0 0.0 0.0 0.1 1 C ₁₇ 0.0 0.0 0.0 C ₁₇ 0.0 0.0 0.0 0.0 0.0 C ₁₇ 0.0 0.0 0.0 C ₁₇ 0.0 C ₁₇ 0.0 O ₀ 0.0	T18 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.1 0 0.0 0.0 0.1 0 0.0 0.0 0.1 0 0.0 0.0 0.1 0 0.2 1 199.8 1 T18 0	G ₁₉ 0.0 0.0 100.0 0.0 0.0 100.0 0.0 0.0 0.0	$\begin{array}{c} T_{20} \\ 0.0 \\ 0.0 \\ 0.0 \\ 99.9 \\ \hline T_{20} \\ 0.0 \\ 0.0 \\ 99.9 \\ \hline T_{20} \\ 0.0 \\ 0.0 \\ 99.9 \\ \hline T_{20} \\ 0.0 \\ 0.$	A 100.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0	G 0.0 0.1 99.8 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0	G 0.0 0.0 100.0 0.0 99.9 0.0 99.9 0.0 G 0.0 0.0 100.0 0.0 100.0 0.0	Indel% 0.033 0.033 0.16 0.16 0.12 Indel% 0.10
Untreated Site 4 A C G T ABE6.3 Site 4 A C G T ABE7.8 Site 4 A C G T ABE7.9 Site 4 A C G T Site 4 A C G T Site 4 A C G C G T Site 4 A C C G T C C G T C C C C C C C C C C C C	$\begin{array}{c} G_1 \\ 0.2 \\ 0.0 \\ 99.8 \\ 0.0 \\ \hline \\ 0.1 \\ 0.0 \\ 99.9 \\ 0.0 \\ \hline \\ G_1 \\ 0.1 \\ 0.0 \\ \hline \\ 99.9 \\ 0.0 \\ \hline \\ G_1 \\ 0.1 \\ 0.0 \\ \hline \\ G_1 \\ 0.0 \\ \hline \end{array}$	A ₂ 100.0 0.0 0.0 0.0 0.0 0.0 0.0 0.1 0.0 0.1 0.0 0.1 0.0 0.1 0.0 0.0	G3 O.0 0.0 0.0 100.0 0.0 0.0 0.0 0.0 0.0 100.0 0.0 0.0 0.0 0.0 0.0 G3 0.0 0.0 0.0 G3 0.0 0.0 0.0	C4 0.0 100.0 0.0	A5 99.6 0.0 0.4 0.0 A6 53.8 0.1 46.1 0.1 A6 77.8 0.1 22.1 0.0 A6 73.6 0.0	A6 100.0 0.0 0.0 0.0 0.0 87.8 0.0 12.2 0.0 A6 86.5 0.0 13.5 0.0 0.0	A7 99.9 0.0 0.1 0.0 0.1 0.0 0.0 A7 95.9 0.0 4.1 0.0 0.0	G ₈ 0.0 0.0 0.0 100.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 G ₈ 0.0 0.0 0.0	Ag 100.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 Ag 97.0 0.0 0.0 1.3 0.0 Ag 98.7 0.0 0.0	G ₁₀ 0.0 99.9 0.1 G ₁₀ 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0	A ₁₁ 100.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 1.5 0.0 98.5 0.0 1.5 0.0 0.3 0.0 99.8 0.0	A12 100.0 0.0	T ₁₃ 0.0 10.0 0.0 0.0 100.0 100.0 T ₁₃ 0.0 0.0 0.0 99.9 T ₁₃ 0.0 100.0 T ₁₃ 0.0 100.0 100.0 T ₁₃ 0.0 100.0 100.0 T ₁₃ 0.0 100.0 100.0	A ₁₄ 00.0 0.0 0.0 0.0 1 0.0 1 0.0 1 0.0 1 0.0 0.0 0.0 1 0.0 1 0.0 0.0 0.0 0.0 0.0 1 0.0 0.0 0.0 1 0.0 1 0.0 1 0.0 0.0	G ₁₅ 0.0 1 0.0 0.0 0.0 0.0 0.1 1 0.0 99.9 0.0 G ₁₅ 1 0.0 99.9 0.0 G ₁₅ 0.1 1 0.0 99.9 0.0 0.0 G ₁₅ 0.0 0.0	A ₁₆ 00.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 A ₁₆ 0.0 0.0 0.0	C17 0.0 99.9 0.0 0.0 1 C17 0.0 0.0 0 0.0 0 0.0 0.0 0.0 1 C17 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 C17 0.0 0.0 0.0	T18 0.0 0.0 0.0 0.0 0.0 T18 0.0 0.0 0.0 T18 0.0 0.0 0.0 T18 0.0 0.0 0.0 T18 0.0 0.0 0.2 799.8 T18 T18 0.0	G ₁₉ 0.0 100.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0	T ₂₀ 0.0 0.0 99.9 T ₂₀ 0.0 0.0 99.9 T ₂₀ 0.0 0.0 99.9 T ₂₀ 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0	A 100.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0	G 0.0 0.1 99.8 0.0 0.0 G 0.0 100.0 0.0 0.0 0.0 G 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0	G 0.0 0.0 100.0 0.0 99.9 0.0 99.9 0.0 G 0.0 0.0 100.0 0.0 0.0 0.0 0.0	Indel% 0.033 0.033 0.16 0.16 0.12 Indel% 0.10
Untreated Site 4 A C G T ABE6.3 Site 4 A C G T ABE7.8 Site 4 A C G T ABE7.9 Site 4 A C G G T	$\begin{array}{c} G_1 \\ 0.2 \\ 0.0 \\ 99.8 \\ 0.0 \\ \hline \\ 0.1 \\ 0.1 \\ 0.1 \\ 0.0 \\ 99.9 \\ 0.0 \\ \hline \\ G_1 \\ 0.0 \\ 99.9 \\ 0.0 \\ \hline \\ G_1 \\ 0.1 \\ 0.0 \\ 99.9 \\ 0.0 \\ \hline \end{array}$	A2 100.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0	G3 0.0 0.0 0.0 100.0 0.0 G3 0.0	C4 0.0 100.0 0.0	A ₅ 99.6 0.0 0.4 0.0 0.4 0.0 0.4 0.0 0.4 0.1 36.3 0.1 46.1 0.1 0.1 22.1 0.0 A ₆ 0.0 A ₆ 0.0 26.3 26.3	A ₆ 100.0 0.0 0.0 0.0 0.0 0.0 0.0 A ₆ 87.8 0.0 12.2 0.0 0.0 A ₆ 0.0 13.5 0.0 A ₆ 0.0 20.1 20.1	A7 99.9 0.0 0.1 0.0 0.0 A7 95.1 0.0 4.9 0.0 0.0 A7 95.9 0.0 4.1 0.0 4.1 0.0 0.0 A7 0.0	G ₈ 0.0 0.0 0.0 100.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 99.9 0.0 0.0 0.0 0.0 0.0 0.0 0.0 100.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0	Ag 100.0 0.0 0.0 0.0 0.0 0.0 0.0 Ag 97.0 0.0 0.0 3.0 0.0 Ag 98.7 0.0 1.3 0.0 1.3	G ₁₀ 0.0 99.9 0.1 G ₁₀ 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0	A ₁₁ 100.0 0.0 0.0 0.0 0.0 0.0 11 98.5 0.0 1.5 0.0 99.7 0.0 0.3 0.0 99.8 0.0 0.2	A12 100.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.1	T ₁₃ 0.0 1 0.0 100.0 100.0 100.0 T ₁₃ 0.0 0.0 99.9 T ₁₃ 0.0 100.0 100.0 0.0 0.0 0.0 100.0	A ₁₄ 00.0 0.0 0.0 0.0 0.0 0.0 0.0 A ₁₄ 00.0 0.0 0.0 A ₁₄ 00.0 0.0 0.0 A ₁₄ 00.0 A ₁₄ 0.0 0.0 0.0 A ₁₄ 0.0 0.0 0.0	G15 0.0 1 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 G15 1 0.0 0.0 0.0 G15 0.0 0.0 0.0 0.0	A ₁₆ 00.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 A ₁₆ 0.0 0.0 0.0 A ₁₆ 0.0 0.0 0.0	C17 0.0 99.9 0.0 0.0 0.0 0.0 1 C17 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0	T18 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.1 2 299.9 0.0 0.2 2 7 18 0.0 0.0 0.2 2	G ₁₉ 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.	$\begin{array}{c} T_{20} \\ 0.0 \\ 0.0 \\ 0.0 \\ 0.0 \\ 99.9 \\ \hline T_{20} \\ 0.0 \\ 0.0 \\ 0.0 \\ 99.9 \\ \hline T_{20} \\ 0.0 \\ 0.0 \\ 0.0 \\ 99.9 \\ \hline T_{20} \\ 0.0 \\ 0.$	A 100.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0	G 0.0 0.1 99.8 0.0 0.0 100.0 0.0 100.0 0.0 100.0 0.0 100.0 0.0	G 0.0 0.0 100.0 0.0 0.0 99.9 0.0 99.9 0.0 G 0.0 0.0 100.0 G 0.0 0.0 100.0	Indel% 0.033 0.16 0.16 0.12 Indel% 0.10
Untreated Site 4 A C G T ABE6.3 Site 4 A C G T ABE7.8 Site 4 A C G T ABE7.9 Site 4 A C G T Site 4 A C G T T	$\begin{array}{c} G_1 \\ 0.2 \\ 0.0 \\ 99.8 \\ 0.0 \\ \hline \\ 0.1 \\ 0.1 \\ 0.0 \\ \hline \\ 99.9 \\ 0.0 \\ \hline \\ G_1 \\ 0.1 \\ 0.0 \\ 99.9 \\ 0.0 \\ \hline \\ G_1 \\ 0.1 \\ 0.0 \\ \hline \\ 99.9 \\ 0.0 \\ \hline \end{array}$	A2 100.0 0.0 0.0 0.0 0.0 99.9 0.0 0.1 0.0 99.9 0.0 90.9 0.0 9.0 0.1 0.0 99.9 0.0 0.1 0.0	G ₃ 0.0 0.0	C4 0.0 100.0 0.0	A ₅ 99.6 0.0 0.4 0.0 0.4 0.0 0.4 0.0 0.4 0.0 0.4 0.1 0.1 A ₅ 0.1 46.1 0.1 22.1 0.0 A ₆ 0.0 26.3 0.0	A ₆ 100.0 0.0 0.0 0.0 0.0 0.0 0.0 A ₆ 12.2 0.0 12.2 0.0 12.2 0.0 13.5 0.0	A7 99.9 0.0 0.1 0.0 0.0 A7 95.1 0.0 4.9 0.0 4.9 0.0 4.1 0.0 4.1 0.0 6.0	G8 0.0 0.0 0.0 100.0 0.0 0.0 0.0 99.9 0.0 G8 0.0 0.0 0.0 99.9 0.0 G8 0.0 0.0 0.0 G8 0.0 100.0 0.0 100.0 0.0	Ag 100.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 Ag 98.7 0.0 0.0 Ag 98.7 1.3 0.0	G ₁₀ 0.0 99.9 0.1 G ₁₀ 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0	A ₁₁ 100.0 0.0 0.0 0.0 0.0 0.0 11 98.5 0.0 1.5 0.0 1.5 0.0 0.3 0.0 0.3 0.0 99.8 0.0 0.2 0.0	A12 100.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.1 0.0	T ₁₃ 0.0 1 0.0 100.0 100.0 100.0 T ₁₃ 0.0 0.0 99.9 T ₁₃ 0.0 100.0 100.0	A ₁₄ 00.0 0.0 1 0.0 1 0.0 1 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 1 0.0 1 0.0 1	G15 0.0 1 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 G15 0.0 1 0.0 0.0 G15 0.0 0.0 0.0 0.0 G15 0.0 1 0.0 0.0 G15 0.0 1 0.0 0.0 0.0 0.0 0.0	A ₁₆ 00.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 A ₁₆ 0.0 0.0 0.0 0.0 0.0 0.0 0.0	C17 0.0 99.9 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0	T18 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.1 2 718 0.0 0.0 0.2 718 0.0 0.0 0.2 99.8 3	G ₁₉ 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.	T ₂₀ 0.0 0.0 0.0 0.0 99.9 T ₂₀ 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 99.9	A 100.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0	G 0.0 0.1 99.8 0.0 99.8 0.0 0.0 0.0 0.0 0.0 100.0 0.0 0.0 G 0.0 0.0 G 0.0 0.0 G 0.0 0.0 100.0 0.0 0.0 0.0 0.0 0.0	G 0.0 0.0 0.0 100.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 100.0 0.0 100.0 0.0	Indel% 0.033 Indel% 0.16 Indel% 0.12 Indel% 0.10
Untreated Site 4 A C G T ABE6.3 Site 4 A C G T ABE7.8 Site 4 A C G T ABE7.9 Site 4 A C G T	$\begin{array}{c} G_1 \\ 0.2 \\ 0.0 \\ 99.8 \\ 0.0 \\ \hline \\ 0.1 \\ 0.0 \\ 99.9 \\ 0.0 \\ \hline \\ G_1 \\ 0.1 \\ 0.0 \\ 99.9 \\ 0.0 \\ \hline \\ G_1 \\ 0.1 \\ 0.0 \\ \hline \\ 99.9 \\ 0.0 \\ \hline \end{array}$	A ₂ 100.0 0.0 0.0 99.9 0.0 0.1 0.1 0.0 0.1 0.0 0.1 0.0 0.1 0.0 0.1 0.0	G3 0.0	C4 0.0 100.0 0.0	A5 99.6 0.0 0.4 0.0 53.8 0.1 53.8 0.1 46.1 0.1 77.8 0.1 22.1 0.0 26.3 0.0	A ₆ 100.0 0.0 0.0 0.0 87.8 0.0 12.2 0.0 13.5 0.0 13.5 0.0 20.1 0.0	A7 99.9 0.0 0.1 0.0 0.0 A7 95.1 0.0 0.0 A7 95.9 0.0 0.0 A7 95.9 0.0 0.0 A7 93.4 0.0 6.6 0.0 0.0	G8 0.0 0.0 0.0 100.0 0.0 0.0 99.9 0.0 99.9 0.0 0.0 100.0 0.0 68 0.0 0.0 0.0 100.0 0.0 68 0.0 0.0 100.0 0.0 100.0 0.0 100.0 0.0 0.0	Ag 100.0 0.0 0.0 0.0 0.0 97.0 0.0 97.0 0.0 1.3 0.0 4.3 98.7 0.0 1.3 0.0 1.3 0.0	G ₁₀ 0.0 99.9 0.1 G ₁₀ 0.0 0.0 0.0 0.0 0.0 0.0 G ₁₀ 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0	A ₁₁ 100.0 0.0 0.0 0.0 0.0 98.5 0.0 1.5 0.0 1.5 0.0 0.3 0.0 0.3 0.0 99.8 0.0 0.2 0.0	A ₁₂ 100.0 0.0 0.0 0.0 99.7 0.0 0.3 0.0 99.8 0.0 0.2 0.0 0.2 0.0 0.1 0.0	T ₁₃ 0.0 0.0 0.0 0.0 0.0 100.0 0.0 0.0 0.0 0.0 0.0 99.9 0.0 7.13 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 100.0 0.0 100.0 100.0	A ₁₄ 00.0 0.0 0.0 0.0 1 0.0 1 0.0 1 0.0 1 0.0 1	G ₁₅ 0.0 1 0.0 0.0 0.0 0.0 0.1 1 0.0 0.0 0.1 1 0.0 0.0 0.1 1 0.0 0.0 0.1 1 0.0 0.0 0.1 1 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0	A ₁₆ 0 00.0 0 0.0 0 0.0 0 0.0 0 0.0 0 0.0 0 0.0 1 0.0 0 0.0 1 0.0 0 0.0 1 0.0 0 0.0 0 0.0 0 0.0 0 0.0 0 0.0 0	C ₁₇ 0.0 99.9 0.0 0.0 0.0 0.1 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0	T18 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.2 2 718 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.2 2 39.8 3	G ₁₉ 0.0 0.0 100.0 0.0 0.0 0.0 0.0 0.0 0.0 0	$\begin{array}{c} T_{20} \\ 0.0 \\ 0.0 \\ 0.0 \\ 99.9 \\ \hline \\ T_{20} \\ 0.0 \\ 0.0 \\ 0.0 \\ 99.9 \\ \hline \\ T_{20} \\ 0.0 \\ 0.0 \\ 0.0 \\ 0.0 \\ 99.9 \\ \hline \\ \hline \\ T_{20} \\ 0.0 \\ 0.0 \\ 99.9 \\ \hline \end{array}$	A 100.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0	G 0.0 0.1 99.8 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0	G 0.0 0.0 0.0 0.0 0.0 0.0 0.0 99.9 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 100.0 0.0	Indel% 0.033 Indel% 0.16 Indel% 0.12 Indel%
Untreated Site 4 A C G T ABE6.3 Site 4 A C G G T ABE7.8 Site 4 A C G G T ABE7.9 Site 4 A C G G T ABE7.9 Site 4 A C G G T A BE6.3 Site 4 A C G G T A A BE6.3 Site 4 A C G G T A A BE6.3 Site 4 A C G G T A A BE6.3 Site 4 A C G G T A A BE6.3 Site 4 A C G G T A A BE6.3 Site 4 A C G G T A A BE6.3 Site 4 A C G G T A C G G T A C G G T A C G G T A C G G T A C G G T A C G G T A C G G T A C G G G T A C G G G T A C G G G T A C G G G T A C G G G T A A C G G G T A A C Site 4 A C G G T A A BE7.8 Site 4 C G G G C G G G G G G G G G G G G G G	$\begin{array}{c} G_1 \\ 0.2 \\ 0.0 \\ 99.8 \\ 0.0 \\ \hline \\ 0.1 \\ 0.0 \\ 99.9 \\ 0.0 \\ \hline \\ G_1 \\ 0.1 \\ 0.0 \\ 99.9 \\ 0.0 \\ \hline \\ G_1 \\ 0.1 \\ 0.0 \\ 99.9 \\ 0.0 \\ \hline \end{array}$	A ₂ 100.0 0.0 0.0 99.9 0.0 0.1 0.0 0.1 0.0 0.1 0.0 0.1 0.0 0.1 0.0 0.1 0.0	G3 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0	C4 0.0 100.0 0.0	A5 99.6 0.0 0.4 0.0 53.8 0.1 46.1 0.1 22.1 0.0 77.8 0.1 22.1 0.0 26.3 0.0 26.3 0.0	A ₆ 100.0 0.0 0.0 0.0 87.8 0.0 12.2 0.0 13.5 0.0 20.1 0.0	A7 99.9 0.0 0.1 0.0 0.0 4.9 0.0 4.9 0.0 4.1 0.0 4.1 0.0 4.1 0.0 4.1 0.0 4.1 0.0 4.1 0.0	G8 0.0 0.0 0.0 100.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0	Ag 100.0 0.0 0.0 0.0 0.0 97.0 0.0 97.0 0.0 1.3 0.0 1.3 0.0 1.3 0.0 1.3 0.0	G ₁₀ 0.0 99.9 0.1 G ₁₀ 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0	A ₁₁ 100.0 0.0 0.0 0.0 0.0 0.0 98.5 0.0 1.5 0.0 1.5 0.0 0.15 0.0 0.3 0.0 0.2 0.0	A ₁₂ 100.0 0.0 0.0 0.0 0.0 0.0 0.0 0	T ₁₃ 0.0 0.0 0.0 0.0 0.0 100.0 0.0 7.13 0.0 0.0 0.0 99.9 0.0 100.0 100.0 100.0 100.0 0.0 0.0 100.0 100.0	A ₁₄ 00.0 0.0 0.0 0.0 1 0.0 1 0.0 1 0.0 1 0.0 1 0.0 1	G15 0.0 1 0.0 0.0 0.0 0.0 0.1 1 0.0 0.0 G15 0.1 1 0.0 G15 0.0 0.0 0.0 G15 0.0 1 0.0 G15 0.0 1 0.0 G15 0.0 1 0.0 G0.0 1 0.0 0.0 O.0 0.0 0.0 0.0	A ₁₆ 00.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0	C ₁₇ 0.0 99.9 0.0 0.0 1 C ₁₇ 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0	T18 0.0 0.0 0.0 0.0 0.0 0.0 0.0 T18 0.0 0.0 0.0 T18 0.0 0.0 0.0 T18 0.0 0.0 0.0 0.2 2 99.8 0.0 T18 0.0 T18 0.0 0.0 0.0 0.2 2 99.8 3	G ₁₉ 0.0 100.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0	$\begin{array}{c} T_{20} \\ 0.0 \\ 0.0 \\ 0.0 \\ 99.9 \\ \hline T_{20} \\ 0.0 \\ 0.0 \\ 0.0 \\ 99.9 \\ \hline T_{20} \\ 0.0 \\ 0.0 \\ 0.0 \\ 0.0 \\ 99.9 \\ \hline T_{20} \\ 0.0 \\ 0.$	A 100.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0	G 0.0 0.1 99.8 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0	G 0.0 0.0 100.0 0.0 99.9 0.0 99.9 0.0 6 0.0 0.0 100.0 0.0 100.0 0.0 100.0 0.0	Indel% 0.033 Indel% 0.16 Indel% 0.10 Indel%
Untreated Site 4 A C G T ABE6.3 Site 4 A C G T ABE7.8 Site 4 A C G T ABE7.9 Site 4 A C G T T ABE7.10 Site 4 A C G T	$\begin{array}{c} G_1 \\ 0.2 \\ 0.0 \\ 0.0 \\ 0.0 \\ \hline \\ 0.1 \\ 0.0 \\ 99.9 \\ 0.0 \\ \hline \\ G_1 \\ 0.1 \\ 0.0 \\ 99.9 \\ 0.0 \\ \hline \\ G_1 \\ 0.1 \\ 0.0 \\ 99.9 \\ 0.0 \\ \hline \\ G_1 \\ 0.1 \\ 0.0 \\ \hline \\ 0.0 \\ \hline \\ G_1 \\ 0.0 \\ \hline \\ 0.0 \\ \hline \end{array}$	A ₂ 100.0 0.0 0.0 0.0 0.0 0.0 0.0 0.1 0.0 0.1 0.0 0.1 0.0 0.1 0.0 0.1 0.0 0.1 0.0 0.1 0.0 0.0	G3 O.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0	C4 0.0 100.0 0.0	A5 99.6 0.0 0.4 0.0 7.8 0.1 46.1 0.1 46.1 0.1 22.1 0.0 22.1 0.0 26.3 0.0 26.3 0.0 26.3 0.0 26.3 0.0	A ₆ 100.0 0.0 0.0 0.0 0.0 87.8 0.0 12.2 0.0 A ₆ 86.5 0.0 13.5 0.0 20.1 0.0 20.1 0.0 20.1	A7 99.9 0.0 0.1 0.0 0.0 4.9 0.0 4.9 0.0 4.9 0.0 4.7 95.9 0.0 4.1 0.0 4.1 0.0 4.1 0.0 6.6 0.0 6.6 0.0 6.6 0.0 6.6 0.0 6.6	G8 0.0 0.0 0.0 100.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0	Ag 100.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 Ag 97.0 0.0 0.0 Ag 99.7 0.0 1.3 0.0 1.3 0.0 1.3 0.0 1.3 0.0 1.3 0.0 1.3 0.0 1.3 0.0 1.3 0.0 98.7 0.0 1.3 0.0 1.3	G ₁₀ 0.0 99.9 0.1 G ₁₀ 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0	A ₁₁ 100.0 0.0 0.0 0.0 0.0 0.0 11 98.5 0.0 1.5 0.0 1.5 0.0 0.0 0.3 0.0 0.3 0.0 0.2 0.0 0.2 0.0 A ₁₁	A12 100.0 0.0 0.0 0.0 0.0 0.0 0.0 A12 99.7 0.0 0.3 0.0 0.0 A12 99.8 0.0 0.2 0.0 0.1 0.1 0.0 A12 99.9 A12 0.0 A12 0.0 A12 0.0 0.0 0.0	T ₁₃ 0.0 0.0 0.0 0.0 0.0 100.0 0.0 T ₁₃ 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 100.0 T ₁₃ 0.0 100.0 100.0 T ₁₃ 0.0 100.0 100.0 T ₁₃ 0.0 0.0 100.0	A ₁₄ 00.0 0.0 0.0 0.0 1 0.0 1 0.0 1 0.0 1 0.0 1 0.0 1 0.0 1 0.0 1 0.0 0.0 0.0 1 0.0 0.0 0.0 1 0.0 1 0.0 1 0.0 1 0.0 1 0.0 1	G15 0.0 1 0.0 0.0 0.0 0.0 0.1 1 0.0 0.0 G15 0.1 1 0.0 99.9 0.0 0.0 1 0.0 G15 0.0 1 0.0 1 0.0 G15 0.0 1 0.0 1 0.0 0.0 1 0.0 1 0.0 1 0.0 0.0 1 0.0 1 0.0 0.0 1 0.0<	A ₁₆ 00.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 A ₁₆ 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0	C ₁₇ 0.0 99.9 0.0 0.0 0.0 0.1 1 C ₁₇ 0.0 0.0 0.0 0.0 1 C ₁₇ 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 1 C ₁₇ 0 C ₁₇ 0	T18 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.1 1 0.0 0.0 0.1 1 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.2 2 999.8 1 T18 0	G ₁₉ 0.0 100.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0	$\begin{array}{c} T_{20} \\ 0.0 \\ 0.0 \\ 0.0 \\ 0.0 \\ 99.9 \end{array}$	A 100.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0	G 0.0 0.1 99.8 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0	G 0.0 0.0 0.0 100.0 0.0 0.0 0.0 99.9 0.0 G 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0	Indel% 0.033 Indel% 0.16 Indel% 0.12 Indel% 0.10
Untreated Site 4 A C G T ABE6.3 Site 4 A C G T ABE7.8 Site 4 A C G T T ABE7.9 Site 4 A C G T T ABE7.10 Site 4 A C G T T ABE7.10 Site 4 C G T T	$\begin{array}{c} G_1 \\ 0.2 \\ 0.0 \\ 99.8 \\ 0.0 \\ \hline \\ 0.1 \\ 0.1 \\ 0.0 \\ 99.9 \\ 0.0 \\ \hline \\ G_1 \\ 0.1 \\ 0.0 \\ 99.9 \\ 0.0 \\ \hline \\ G_1 \\ 0.0 \\ 99.9 \\ 0.0 \\ \hline \\ G_1 \\ 0.0 \\ 99.9 \\ 0.0 \\ \hline \\ G_1 \\ 0.0 \\ 0.0 \\ \hline \\ G_1 \\ 0.0 \\ 0.0 \\ \hline \\ \end{array}$	A ₂ 100.0 0.0 0.0 0.0 0.0 0.0 0.1 0.0 0.1 0.0 0.1 0.0 0.1 0.0 0.1 0.0 0.1 0.0 0.1 0.0 0.0	G3 O.0 0.0 0.0 100.0 0.0 0.0 0.0 0.0 0.0 100.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 G3 0.0 0.0 0.0	C4 0.0 100.0 0.0 0.0 0.0 0.0 0.0 99.9 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0	A5 99.6 0.0 0.1 53.8 0.1 46.1 0.1 A6 77.8 0.1 22.1 0.0 26.3 0.0 26.3 0.0 26.3 0.0 26.3 0.0	A ₆ 100.0 0.0 0.0 0.0 0.0 87.8 0.0 12.2 0.0 A ₆ 86.5 0.0 13.5 0.0 0.0 A ₆ 0.0 20.1 0.0 A ₆ 0.0 A ₆ 0.0	A7 99.9 0.0 0.1 0.0 0.0 A7 0.0	G ₈ 0.0 0.0 0.0 100.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 G ₈ 0.0 0.0 0.0	Ag 100.0 0.0 0.0 0.0 0.0 0.0 0.0 3.0 0.0 Ag 99.7 0.0 1.3 0.0 1.3 0.0 1.3 0.0 1.3 0.0 1.3 0.0 1.3 0.0 1.3 0.0 0.0	G ₁₀ 0.0 99.9 0.1 G ₁₀ 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0	A ₁₁ 100.0 0.0 0.0 0.0 0.0 0.0 0.0 11 98.5 0.0 1.5 0.0 99.7 0.0 0.3 0.0 0.3 0.0 0.2 0.0 0.2 0.0 99.9 0.0	A12 100.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.1 0.0 0.1 0.0 0.1 0.0 0.1 0.0 0.1 0.0	T ₁₃ 0.0 10.0 0.0 0.0 100.0 100.0 T ₁₃ 0.0 0.0 0.0 99.9 0.0 100.0 100.0 T ₁₃ 0.0 0.0 0.0 0.0 0.0 0.0 100.0	A ₁₄ 00.0 0.0 0.0 0.0 1 0.0 1 0.0 1 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 A ₁₄ 0.0 0.0 0.0 A ₁₄ 0.0 0.0 0.0 A ₁₄ 0.0 A ₁₄ 0.0 A ₁₄ 0.0	G ₁₅ 0.0 1 0.0 0.0 0.0 0.0 0.0 0.0 G ₁₅ 0.0 0.0	A ₁₆ 0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 A ₁₆ 0.0 0.0	C ₁₇ 0.0 99.9 0.0 0.0 0.0 0.0 1 C ₁₇ 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0	T18 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.1 2 718 0.0 0.0 0.0 0.1 2 99.8 3 718 0.0 0.0 0.0 0.2 2 99.8 3 718 0.0 0.0 0.0 0.2 2 99.8 3 718 0.0 0.0 0.0 0.0 0.0	G ₁₉ 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.	$\begin{array}{c} T_{20} \\ 0.0 \\ 0.0 \\ 0.0 \\ 0.0 \\ 99.9 \\ \hline T_{20} \\ 0.0 \\ 0.0 \\ 0.0 \\ 99.9 \\ \hline T_{20} \\ 0.0 \\ 0.0 \\ 0.0 \\ 0.0 \\ 99.9 \\ \hline T_{20} \\ 0.0 \\ 0.$	A 100.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0	G 0.0 0.1 99.8 0.0 0.0 G 0.0 100.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0	G 0.0 0.0 0.0 100.0 0.0 G 0.0 0.0 0.0 99.9 0.0 G 0.0 0.0 0.0 0.0 0.0 0.0 0.0 100.0 0.0 G 0.0 0.0 0.0 G 0.0 0.0 0.0 0.0 0.0 G 0.0 0.0 0.0	Indel% 0.033 0.033 0.16 0.16 0.12 Indel% 0.10 Indel% 0.27
Untreated Site 4 A C G T ABE6.3 Site 4 A C G T ABE7.8 Site 4 A C G T ABE7.9 Site 4 A C G T ABE7.10 Site 4 A C G G T	$\begin{array}{c} G_1 \\ 0.2 \\ 0.0 \\ 99.8 \\ 0.0 \\ \hline \\ 0.1 \\ 0.1 \\ 0.0 \\ 99.9 \\ 0.0 \\ \hline \\ G_1 \\ 0.1 \\ 0.0 \\ 99.9 \\ 0.0 \\ \hline \\ G_1 \\ 0.0 \\ 99.9 \\ 0.0 \\ \hline \\ G_1 \\ 0.0 \\ 0.0 \\ \hline \\ 0.0 \\ \hline \\ 0.0 \\ 100.0 \\ \hline \end{array}$	A2 100.0 0.0 0.0 0.0 0.0 0.0 99.9 0.0 0.1 0.0 90.9 0.0 0.1 0.0 99.9 0.0 0.0 0.1 0.0 0.1 0.0 0.1 0.0 0.1 0.0 0.1 0.0 0.1 0.0 0.0	G3 O.0 0.0 0.0 100.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0	C4 0.0 100.0 0.0	A ₅ 99.6 0.0 0.4 0.0 0.4 0.0 0.1 46.1 0.1 77.8 0.1 22.1 0.0 A ₆ 6 73.6 0.0 26.3 0.0 A ₆ 5 0.0 26.3 0.0 26.3 0.1 53.6	A6 100.0 0.0 0.0 0.0 0.0 0.0 0.0 7.0 7.0 7.0 7.0 7.0 7.0 7.0 7.0 7.16 0.0 0.0 0.0 20.1 0.0 0.0 20.1 0.0 20.2 7.16 0.0 28.3 3.0	A7 99.9 0.0 0.0 0.1 0.0 0.0 0.0 4.9 0.0 4.9 0.0 4.1 0.0 4.1 0.0 6.6 0.0 A7 93.4 0.0 6.6 0.0 9.4 9.0 9.4 0.0 0.0	G8 0.0 0.0 0.0 100.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 100.0 0.0 0.0 0.0 100.0 0.0 0.0 0.0 100.0 0.0 0.0 0.0	Ag 100.0 0.0 0.0 0.0 0.0 0.0 0.0 3.0 0.0 Ag 98.7 0.0 1.3 0.0 0.0 Ag 98.7 0.0 1.3 0.0 99.7 0.0 0.0 1.3 0.0 Ag 99.7 0.0 0.0 1.3 0.0	G ₁₀ 0.0 99.9 0.1 G ₁₀ 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0	A11 100.0 0.0 0.0 0.0 0.0 0.0 0.0 11 98.5 0.0 1.5 0.0 0.0 1.5 0.0 0.0 0.3 0.0 0.3 0.0 0.2 0.0 0.2 0.0 0.2 0.0 0.1	A12 100.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 A12 0.0 0.3 0.0 A12 0.0 0.2 0.0 0.2 0.0 0.1 0.0 99.9 0.0 0.1 0.0 0.1 0.0 0.0 0.0 0.0 0.0	T ₁₃ 0.0 1 0.0 0.0 100.0 100.0 T ₁₃ 0.0 0.0 0.0 99.9 T ₁₃ 0.0 100.0 T ₁₃ 0.0 100.0 100.0	A ₁₄ 00.0 0.0 0.0 0.0 1 0.0 1 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 A ₁₄ 0.0 0.0 0.0	G15 0.0 1 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 G15 0.0 0.0 0.0 0.0 G15 1 0.0 0.0 0.0 G15 0.0 0.0 0.0 0.0 G15 1 0.0 0.0 0.0 0.0 G15 1 0.0	A ₁₆ 00.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 1 0.0 0.0 0.0 1 0.0 0.0 A ₁₆ 0.0 0.0 0.0	C ₁₇ 0.0 99.9 0.0 0.0 0.0 0.0 1 C ₁₇ 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 9 C ₁₇ 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0	T18 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.2 2 99.8 1 118 0.0 0.0 0.2 99.8 1 118 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0	G ₁₉ 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.	$\begin{array}{c} T_{20} \\ 0.0 \\ 0.0 \\ 0.0 \\ 0.0 \\ 99.9 \end{array}$	A 100.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0	G 0.0 0.1 99.8 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 100.0	G 0.0 0.0 100.0 0.0	Indel% 0.033 0.16 0.16 0.12 Indel% 0.10 Indel% 0.27

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 | 0.0 | 0.0 | 0.0
 | 0.0
 | 99.7 | 0.0
 | 0.0 | 100.0
 | 0.0
 | 0.0 | 99.7 | 0.0 | 0.0 | 0.0 | 99.7
 | 0.0 | 0.0 | 0.0 | J 0. | J 0.0 | | |
| ABE6.3 | | |
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 | | | | | | Inde | 1% |
| Site 5 | G₁ | A ₂ | T₂
 | G₄ | A۶ | Ge
 | A ₇
 | T. | A
 | A10 | T11
 | G12
 | A12 | T14 | G15 | A ₁₆ | G17 | T19
 | C10 | A20 | G | G | G | 0.05 | 57 |
| A | 0.0 | 99.9 | 0.0
 | 0.0 | 51.4 | 0.0
 | 75.1
 | 0.0 | 93.5
 | 96.6 | 0.0
 | 0.0
 | 100.0 | 0.0 | 0.0 | 100.0 | 0.0 | 0.0
 | 0.0 | 100.0 | 0.0 | 0. | 0.0 | | |
| C | 0.0 | 0.0 | 0.0
 | 0.0 | 0.0 | 0.0
 | 0.0
 | 0.0 | 0.0
 | 0.0 | 0.0
 | 0.0
 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0
 | 99.9 | 0.0 | 0.0 | 0.0 | 0.0 | | |
| G | 100.0 | 0.1 | 0.0
 | 99.9 | 48.6 | 100.0
 | 24.9
 | 0.0 | 6.5
 | 3.4 | 0.0
 | 100.0
 | 0.0 | 0.0 | 100.0 | 0.0 | 100.0 | 0.0
 | 0.0 | 0.0 | 100 | .0 100 | .0 100. | 0 | |
| Т | 0.0 | 0.0 | 100.0
 | 0.0 | 0.0 | 0.0
 | 0.0
 | 100.0 | 0.0
 | 0.0 | 100.0
 | 0.0
 | 0.0 | 100.0 | 0.0 | 0.0 | 0.0 | 100.0
 | 0.1 | 0.0 | 0.0 | 0.0 | 0.0 C | | |
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| ABE7.8 | | | -
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 | T |
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 | ~ | | | | | Inde | 1% |
| Site 5 | G ₁ | A ₂ | 13
 | G ₄ | A ₅ | G ₆
 | A ₇
 | 18 | A ₉
 | A ₁₀ | I ₁₁
 | G ₁₂
 | A ₁₃ | I ₁₄ | G ₁₅ | A ₁₆ | G ₁₇ | I ₁₈
 | C ₁₉ | A ₂₀ | G | G | G | 0.04 | 15 |
| A | 0.0 | 99.4 | 0.0
 | 0.0 | 60.0 | 0.0
 | 55.3
 | 0.0 | 96.2
 | 97.1 | 0.0
 | 0.1
 | 100.0 | 0.0 | 0.1 | 100.0 | 0.0 | 0.0
 | 0.0 | 100.0 | 0.0 | 0.0 | 0.0 | | |
| G | 100.0 | 0.0 | 0.0
 | 0.0
QQ Q | 40.0 | 100.0
 | 44.7
 | 0.0 | 3.8
 | 2.0 | 0.0
 | 0.0
 | 0.0 | 0.0 | 0.0 | 0.0 | 100.0 | 0.0
 | 99.9 | 0.0 | 100 | 0 100 | 0.0 | 0 | |
| т | 0.0 | 0.0 | 100.0
 | 0.0 | 0.0 | 0.0
 | 0.0
 | 100.0 | 0.0
 | 0.0 | 100.0
 | 0.0
 | 0.0 | 100.0 | 0.0 | 0.0 | 0.0 | 100.0
 | 0.0 | 0.0 | 0.0 | | 0.0100 | • | |
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| ABE7.9 | | |
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 | | | | | | Inde | 1% |
| Site 5 | G ₁ | A ₂ | T ₃
 | G ₄ | A ₅ | G ₆
 | A ₇
 | T ₈ | A ₉
 | A ₁₀ | T ₁₁
 | G ₁₂
 | A ₁₃ | T ₁₄ | G ₁₅ | A ₁₆ | G ₁₇ | T ₁₈
 | C ₁₉ | A ₂₀ | G | G | G | 0.03 | 30 |
| A | 0.0 | 99.8 | 0.0
 | 0.1 | 60.2 | 0.0
 | 49.0
 | 0.0 | 98.0
 | 98.3 | 0.0
 | 0.0
 | 100.0 | 0.0 | 0.1 | 100.0 | 0.0 | 0.0
 | 0.0 | 100.0 | 0.0 | 0.0 | 0.0 C | | |
| С | 0.0 | 0.0 | 0.0
 | 0.0 | 0.0 | 0.0
 | 0.0
 | 0.0 | 0.0
 | 0.0 | 0.0
 | 0.0
 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0
 | 99.9 | 0.0 | 0.0 | 0.0 | 0.0 C | | |
| G | 100.0 | 0.2 | 0.0
 | 99.9 | 39.7 | 100.0
 | 51.0
 | 0.0 | 2.0
 | 1.7 | 0.0
 | 99.9
 | 0.0 | 0.0 | 99.9 | 0.0 | 100.0 | 0.0
 | 0.0 | 0.0 | 100 | .0 100 | .0 100. | 0 | |
| Т | 0.0 | 0.0 | 100.0
 | 0.0 | 0.0 | 0.0
 | 0.0
 | 100.0 | 0.0
 | 0.0 | 100.0
 | 0.0
 | 0.0 | 100.0 | 0.0 | 0.0 | 0.0 | 100.0
 | 0.1 | 0.0 | 0.0 | 0.0 | 0.0 C | | |
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| ABE7.10 | | | -
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 | ~ | | | | | Inde | 1% |
| Site 5 | G ₁ | A ₂ | I ₃
 | G ₄ | A ₅ | G ₆
 | A ₇
 | 1 ₈ | A ₉
 | A ₁₀ | I ₁₁
 | G ₁₂
 | A ₁₃ | I ₁₄ | G ₁₅ | A ₁₆ | G ₁₇ | I ₁₈
 | C ₁₉ | A ₂₀ | G | G | G | 0.0 | 8 |
| A | 0.1 | 100.0 | 0.0
 | 0.1 | 39.5 | 0.0
 | 39.4
 | 0.0 | 86.2
 | 98.1 | 0.0
 | 0.2
 | 99.8 | 0.0 | 0.2 | 100.0 | 0.0 | 0.0
 | 0.0 | 100.0 | 0.0 | 0.0 | J 0.0 | | |
| C | 0.0 | 0.0 | 0.0
 | 0.0 | 0.0 | 100.0
 | 0.0
 | 0.0 | 12.7
 | 1.0 | 0.0
 | 0.0
 | 0.0 | 0.0 | 0.0 | 0.0 | 100.0 | 0.0
 | 99.9 | 0.0 | 0.0 | 0 100 | J 0.0 | 0 | |
| т | 99.9 | 0.0 | 100.0
 | 99.9 | 0.0 | 0.0
 | 0.0
 | 100.0 | 0.0
 | 0.0 | 100.0
 | 99.8
 | 0.2 | 100.0 | 99.8 | 0.0 | 0.0 | 100.0
 | 0.0 | 0.0 | 99. | | 100100 | U | |
| | 0.0 | 0.0 | 100.0
 | 0.0 | 0.0 | 0.0
 | 0.0
 | 100.0 | 0.0
 | 0.0 | 100.0
 | 0.0
 | 0.0 | 100.0 | 0.0 | 0.0 | 0.0 | 100.0
 | 0.1 | 0.0 | 0.0 | . 0. | 0.0 | | |
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| Untreated
Site 6
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C | G ₁
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0.0 | G ₂
0.0
0.0 | A ₃
100.0
0.0
 | T ₄
0.0
0.0 | T ₅
0.0
0.0 | G ₆
0.1
0.0
 | A ₇
99.8
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 | C ₈
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100. | Cg
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 | C
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0.0 0
 | 11 G
0.0 0
 | G ₁₂ G
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.0 0
.0 10 | 14 C
.0 0
0.0 99 | | 16 G
0.0 0
0 0 | 6 ₁₇ G
 | 6 ₁₈
1.0
0.0 | G ₁₉
0.0
0.0 | C ₂₀
0.0
100.0 | T
0.0
0.0 | G
0.0
0.0 | G
0.0
0.0 | Indel%
0.011 |
| Untreated
Site 6
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G | G ₁
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0.0
100.0 | G ₂
0.0
0.0
100.0 | A ₃
100.0
0.0
0.0
 | T ₄
0.0
0.0
0.0 | T ₅
0.0
0.0
0.0 | G ₆
0.1
0.0
99.9
 | A ₇
99.8
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9 0.2
 | C ₈
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100.
0.0 | C ₉
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0 100
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 | C
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 | G ₁₂ G
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0.0 10 | 13 C
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| Untreated
Site 6
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99 9 | T
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G
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0.0 | Indel%
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Indel%
0.024 |
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ABE6.3
Site 6
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G ₁
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0.0 | T₅ 0.0 0.0 0.0 100.0 T₅ 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 | $\begin{array}{c c} G_6 \\ 0.1 \\ 0.0 \\ 99.9 \\ 0 \\ 0.0 \\ \hline \\ G_6 \\ 0.0 \\ 0.0 \\ 99.5 \\ \end{array}$
 | A ₇
99.8
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9 39.2
 | C ₈
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C ₈
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99.5
2 0.0 | C ₉
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C | Image: 10 min. A .0 100 0.0 0. .0 0. .0 0. .0 0. .0 0. .0 99 0.0 0. .0 0.
 | 11 G
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 | 12 G
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0 0 | 15 A .0 100 .0.9 0. .0 0. .15 A .15 99 .0.9 0. .0 99 .0.9 0. | 16 G 0.0 0 0 10 0 0 16 G 16 G 19 0 0 9 0 9 | 6 ₁₇ 6
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Site 6
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 | 11 G 0.0 0 0 10 0 10 11 G 15 0 0 0 5 98 0 0
 | I2 G 0.0 0.0 0.0 100 0.0 0 12 G 0.0 0 0.0 0 0.0 0 0.0 0 0.0 0 0.0 0 0.0 0 0.0 0 | 13 C 0 0 0 10 0.0 0 13 C 0 0 13 C 0 0 0 0 0 0 0 0 0 0 0.0 0 | 14 C 0 0 95 0 0 0 14 C 0 14 C 0 0 0 0 0 0 0 0.0 95 0 0.0 0 0 0.0 0 0 | 15 A 0.0 100 0.9 0. .0 0. .15 A .0 99 0.0 0. .0 0.0 .11 0. | 16 G 0 0 0 0 10 0 16 G 0 16 G 0 16 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 | 6 ₁₇ C
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C ₂₀ | T
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| Untreated
Site 6
A
C
G
T
ABE6.3
Site 6
A
C
G
T
ABE7.8
Site 6
A | G ₁
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6 ₁
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0.0 | $\begin{array}{c} G_2 \\ 0.0 \\ 0.0 \\ 100.0 \\ 0.0 \\ \hline \\ 0.0 \\ 0.0 \\ 100.0 \\ 0.0 \\ \hline \\ G_2 \\ 0.0 \\ \hline \\ \end{array}$ | A ₃
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4
3
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 | T ₄
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T ₄
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T ₄
0.0 | $\begin{array}{c c} T_5 \\ 0.0 \\ 0.0 \\ 0.0 \\ 100.0 \\ \hline T_5 \\ 0.0 \\$ | G ₆
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0
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99.3
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99.3
0 0.0
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0 0.0
99.3
0 0.0
 | A ₇
99.8
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9 0.2
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 | C ₈ 0.0 100. 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 99.5 0.0 0.1 C ₈ 0.0 0.1 | Cg 0 0.0 0 100 0.0 0.0 0 0.0 0 0.0 0 0.0 0 0.0 0 0.0 0 0.0 0 0.0 0 0.0 0 0.0 0 0.0 0 0.0
 | C
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C
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C
C | IO A .0 100 0.0 0. .0 0. .0 0. .0 0. .0 99 0.0 0. .0 0. .0 0. .0 0. .0 0. .0 0. .0 0. .0 0. .0 0. | 11 G 0.0 0 0.0 10 0.0 0 11 G 0.5 98 0.0 0 11 G 0.5 98 0.0 0 11 G 0.5 98 0.0 0 0.1 0
 | input G 0 0 0 0 0 0 0 0 0 input G 0 input G 0 0 0 0 0 0 0 0 0 0 input G 0 input G 0
 | $\begin{array}{c ccccccccccccccccccccccccccccccccccc$ | $\begin{array}{c ccccccccccccccccccccccccccccccccccc$ | 15 A 0 100 0.9 0. 0 0.0 .0 0.0 .0 0.0 .0 0.0 .0 0.0 .0 0.0 .0 0.0 .0 0.0 .0 0.0 .1 0.0 .15 A .15 A | $ \begin{array}{cccccccccccccccccccccccccccccccccccc$ | \hat{s}_{17} \hat{c}_{0}
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\hat{c}_{17} \hat{c}_{0}
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\hat{c}_{17} \hat{c}_{0}
\hat{c}_{17} \hat{c}_{0} | 3_{18}
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 | G ₁₉
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Indel%
0.024
Indel%
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| Untreated
Site 6
A
C
G
T
ABE6.3
Site 6
A
C
G
T
ABE7.8
Site 6
A
C | G ₁
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 | A ₇
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 | 11 G 0.0 0 0.0 10 0.0 10 0.0 0 11 G 0.5 98 0.0 0 11 G 12.5 98 0.0 0 11 G 12.5 98 0.0 0
 | it2 G .0 0 .0 0 .0 0 .12 G .12 G .0 0 .0 0 .0 0 .0 0 .12 G .0 0 .0 0 .12 G .0 0 .12 G .0 0 .12 G .0 0 .12 G .12 .12 .12 .12 .13 .12 .14 .12 .15 .12 .15 .12 .15 | 13 C 0 0 0 10 0 0 13 C 0 0 13 C 0 0 0 0 13 C 13 C 10 0 13 C 13 C 13 C 13 C 10 0 | 14 C 00 0 00.0 95 00.0 0 00 0 14 C 00 0 00 0 00 0 14 C 14 C 14 C 14 C 14 C 14 C 00 0 14 C 14 C 14 C 14 C 00 0 14 C 00 0 14 C 10 0 | 15 A 0 100 0.9 0. 0 0.0 .0 0.0 .0 0.0 .0 0.0 .0 0.0 .0 99 .0 0.0 .1 0.0 .15 A .15 A .15 A .0 100 .0 0.0 | $ \begin{array}{cccccccccccccccccccccccccccccccccccc$ |
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Site 6
A
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Site 6
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G | G ₁
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4 ₃
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 | CONTRACTOR | A .0 100 .0 0.0 .0 0.0 .0 0.0 .0 0.0 .0 98 .0 98 .0 98 .0 98 .0 99 .0 0 | 11 G 0.0 0 0.0 0 0.0 10 0.0 0 11 G 0.5 98 0.0 0 11 G 12 98 0.0 0 13 G 14 G 15 98 0 0 14 G 15 98 16 0 17 G 18 0 10 0
 | International International International International <t< td=""><td>13 C 0 0 0 10 0 0 13 C 0 0 13 C 0 0 0 0 13 C 13 C 13 C 0 0 0 0 0 0 0 0 0 0 0 0 0 0</td><td>14 C 0 0 0.0 98 0.0 0 0 0 0 0 0 0 0 0 0 0 14 C 0 0 14 C 0 0 14 C 0 0 0 0 0 0</td><td>15 A .0 100 .9 0. .0 0. .0 0. .0 0. .15 A .0 99 .0 0. .1 0. .1 0. .1 0. .1 0. .10 0.0 .0 0.0</td><td>16 C 0 0 0 0 10 0 16 C 0 19 0 0 0 98 0 0 16 C 0 0 16 C 0 0 16 0 0 0 16 0 0 0 16 0 0 0 16 0 0 0 0 0 0 0 0</td><td></td><td>\hat{S}_{18} .0
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| Untreated
Site 6
A
C
G
T
ABE6.3
Site 6
A
C
G
T
ABE7.8
Site 6
A
C
G
T | G1 0.0 100.0 0.0 100.0 0.0 100.0 0.0 100.0 0.0 100.0 0.0 100.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 | $\begin{array}{c} G_2 \\ 0.0 \\ 0.0 \\ 100.0 \\ 0.0 \\ \hline \\ 0.0 \\ 0.0 \\ 100.0 \\ \hline \\ 0.0 \\ \hline \\ 0.0 \\ 0.0 \\ \hline \\ 0.0 \\ 100.0 \\ 0.0 \\ \hline \end{array}$ | A ₃
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0.0
0.0
98.4
0.0
1.6
0.0
1.6
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1.6
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6.7
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 | T ₄
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0.0 | T ₅ 0.0 0.0 0.0 100.0 T ₅ 0.0 | G ₆ 0.1 0.0 99.9 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0
 | A ₇
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 | CODE CODE CODE CODE CODE CODE CODE CODE | 10 A .0 100 .0 0 .0 0 .0 0 .0 0 .0 0 .0 0 .0 0 .0 0 .0 0 .0 0 .0 0 .0 0 .0 0 .0 0 .0 0 .0 0
 | 11 G 0.0 0 0 10 0 10 0 0 11 G 0.5 0 0.5 98 0 0 11 G 12 10 0 0 0 0
 | i12 G .0 0 .0 0 0.0 100 .0 0 .12 G .0 0 .0 0 .0 0 .0 0 .0 0 .0 0 .0 0 .0 0 .0 0 .0 0 .0 0 | $\begin{array}{c ccccccccccccccccccccccccccccccccccc$ | $\begin{array}{c ccccccccccccccccccccccccccccccccccc$ | 15 A .0 100 .0 0 .0 0 .0 0 .0 0 .15 A .0 99 .0 0 .1 0 .1 0 .1 0 .1 0 .1 0 .0 0 .0 0 .0 0 | 16 G 0.0 0 0 0 0 0 0 0 0 16 G 0 0 0 0 16 0 0 0 0 0 | s_{17} C
0 | 3_{18}
 | G19 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 | C ₂₀ 0.0 100.0 | T
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| Untreated
Site 6
A
C
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ABE6.3
Site 6
A
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G
G
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ABE7.8
Site 6
A
C
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G
T | G1 0.0 0.0 0.0 100.0 0.0 0.0 0.0 100.0 0.0 100.0 0.0 100.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 | G ₂
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100.0
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4 ₃
98.4
0.0
1.6
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1.6
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4 ₃
93.3
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 | T ₄
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100.0 | $\begin{array}{ c c c c }\hline T_{5} & 0.0 \\ 0.0 & 0.0 \\ 0.0 & 0.0 \\ \hline 0.0 & 0.0 \\ 0.0 & 0.0 \\ 0.0 & 0.0 \\ \hline 0.0 & 0.0 \\ \hline 0.0 & 0.0 \\ 0.0 & $ | G ₆ 0.1 99.3 0 0.0 99.3 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0
 | A ₇
99.8
0.00
9.0.2
0.00
9.0.2
0.00
9.0.2
0.00
9.0.0
9.39.2
0.00
9.39.2
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9.34.8
0.00
0.65.2
0.00
 | Cg Cg 0.00 100. 0.00 0.00 0.00 99.9 2 0.00 99.9 0.0 0.1 0.0 0.0 99.9 2 0.00 0.01 0.00 0.02 0.00 0.00 0.00 | Cg
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Untreated																								Indel%
Site 7	G ₁	A ₂	A ₃	T ₄	A ₅	C ₆	T ₇	A ₈	A ₉	G ₁₀	C ₁₁	A ₁₂	T ₁₃	A ₁₄	G ₁₅	A ₁₆	C ₁₇	T ₁₈	C ₁₉	C ₂₀	А	G	G	0.093
A	0.0	100.0	100.0	0.0	99.9	0.0	0.0	99.9	100.0	0.0	0.0	100.0	0.0	100.0	0.1	100.0	0.0	0.0	0.0	0.0	100.0	0.0	0.0	
G	100.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	100.0	0.0	0.0	0.0	0.0	0.0	0.0	100.0	0.0	100.0	100.0	0.0	100.0	100.0	
T	0.0	0.0	0.0	100.0	0.0	0.0	100.0	0.0	0.0	0.0	0.0	0.0	100.0	0.0	0.0	0.0	0.0	100.0	0.0	0.0	0.0	0.0	0.0	
ABE6.3				1	1																			Indel%
Site 7	G1	A ₂	A ₃	T ₄	A ₅	C ₆	T ₇	A ₈	A ₉	G ₁₀	C ₁₁	A ₁₂	T ₁₃	A ₁₄	G ₁₅	A ₁₆	C ₁₇	T ₁₈	C ₁₉	C ₂₀	A	G	G	0.12
C	0.0	0.0	0.0	0.0	0.0	99.8	0.0	0.0	0.0	0.0	100.0	0.0	0.0	0.0	0.0	0.0	100.0	0.0	99.9	99.9	0.0	0.0	0.0	
G	100.0	0.9	1.3	0.0	42.9	0.1	0.0	2.3	1.1	100.0	0.0	0.0	0.0	0.0	99.9	0.0	0.0	0.0	0.0	0.0	0.0	100.0	100.0	
т	0.0	0.0	0.0	100.0	0.0	0.1	100.0	0.0	0.0	0.0	0.0	0.0	100.0	0.0	0.1	0.0	0.0	100.0	0.1	0.1	0.0	0.0	0.0	
4057.0																								l1 - 10/
ABE7.8		^	٨	т	٨	C	т	^	٨	C	<u> </u>	٨	т	٨	C	^	C	т	C	C	^	C	C	0.075
	G ₁	98.7	98.5	0.0	A ₅		0.0	99.2	A ₉	G ₁₀	0.0	99 9	0.0	A ₁₄	0.0	A ₁₆	0.0	1 ₁₈	0.0	0.0	99.9	0.0	0.0	0.075
c	0.0	0.0	0.0	0.0	0.0	99.8	0.0	0.0	0.0	0.0	99.9	0.0	0.0	0.0	0.0	0.0	100.0	0.0	99.9	99.9	0.1	0.0	0.0	
G	100.0	1.3	1.5	0.0	48.7	0.1	0.0	0.8	0.7	100.0	0.0	0.1	0.0	0.0	100.0	0.0	0.0	0.0	0.0	0.0	0.0	100.0	100.0	
т	0.0	0.0	0.0	100.0	0.0	0.1	100.0	0.0	0.0	0.0	0.0	0.0	100.0	0.0	0.0	0.0	0.0	100.0	0.1	0.0	0.0	0.0	0.0	
																								Indel%
Site 7	G.	A	Δ.	т.	Δ.	Ca	Т.	Δ.	A.	Gu	C.,	Δ	Tua	Δ.,	Gu	A.a	Cur	Tra	Cue	Cas	Δ	G	G	0.077
A	0.0	99.8	99.4	0.0	49.3	0.1	0.0	99.4	99.4	0.0	0.0	99.9	0.0	100.0	0.0	100.0	0.0	0.0	0.0	0.0	99.9	0.0	0.0	0.077
С	0.0	0.0	0.0	0.0	0.0	99.6	0.0	0.0	0.0	0.0	100.0	0.0	0.0	0.0	0.0	0.0	100.0	0.0	100.0	100.0	0.1	0.0	0.0	
G	100.0	0.2	0.5	0.0	50.7	0.3	0.0	0.6	0.6	100.0	0.0	0.0	0.0	0.0	99.9	0.0	0.0	0.0	0.0	0.0	0.0	100.0	100.0	
I	0.0	0.0	0.0	100.0	0.0	0.1	100.0	0.0	0.0	0.0	0.0	0.0	100.0	0.0	0.0	0.0	0.0	100.0	0.0	0.0	0.0	0.0	0.0	
ABE7.10																								Indel%
Site 7	G1	A ₂	A ₃	T₄	A ₅	C ₆	T ₇	A ₈	Aq	G ₁₀	C ₁₁	A ₁₂	T ₁₃	A ₁₄	G ₁₅	A ₁₆	C ₁₇	T ₁₈	C19	C ₂₀	Α	G	G	0.10
А	0.0	99.9	99.5	0.0	45.9	0.0	0.0	93.9	99.5	0.0	0.0	99.9	0.0	100.0	0.0	100.0	0.0	0.0	0.0	0.0	100.0	0.0	0.0	
С	0.0	0.0	0.0	0.0	0.0	99.6	0.0	0.0	0.0	0.0	100.0	0.0	0.0	0.0	0.0	0.0	100.0	0.0	99.9	99.9	0.0	0.0	0.0	
G	99.9	0.1	0.5	0.0	54.0	0.3	0.0	6.1	0.5	100.0	0.0	0.1	0.0	0.0	99.9	0.0	0.0	0.0	0.0	0.0	0.0	99.9	99.9	
Untreated																								Indel%
Untreated Site 8	G ₁	T ₂	A ₃	A ₄	A ₅	C ₆	A ₇	A ₈	A ₉	G ₁₀	C ₁₁	A ₁₂	T ₁₃	A ₁₄	G ₁₅	A ₁₆	C ₁₇	T ₁₈	G ₁₉	A ₂₀	G	G	G	Indel% 0.02
Untreated Site 8 A	G ₁ 0.0	T ₂ 0.0	A ₃ 100.0	A ₄ 100.0	A ₅ 99.9	C ₆ 0.0	A ₇ 100.0	A ₈ 100.0	A ₉ 100.0	G ₁₀ 0.0	C ₁₁ 0.0	A ₁₂ 100.0	T ₁₃ 0.0	A ₁₄ 100.0	G ₁₅ 0.1	A ₁₆ 100.0	C ₁₇ 0.0	T ₁₈ 0.0	G ₁₉ 0.1	A ₂₀ 100.0	G 0.0	G 0.0	G 0.0	Indel% 0.02
Untreated Site 8 A C G	G ₁ 0.0 0.0	T ₂ 0.0 0.0 0.0	A ₃ 100.0 0.0 0.0	A ₄ 100.0 0.0 0.0	A ₅ 99.9 0.0 0.1	C ₆ 0.0 100.0 0.0	A ₇ 100.0 0.0 0.0	A ₈ 100.0 0.0 0.0	A ₉ 100.0 0.0 0.0	G ₁₀ 0.0 0.0	C ₁₁ 0.0 100.0	A ₁₂ 100.0 0.0 0.0	T ₁₃ 0.0 0.0 0.0	A ₁₄ 100.0 0.0 0.0	G ₁₅ 0.1 0.0 99 9	A ₁₆ 100.0 0.0 0.0	C ₁₇ 0.0 100.0 0.0	T ₁₈ 0.0 0.0 0.0	G ₁₉ 0.1 0.0	A ₂₀ 100.0 0.0 0.0	G 0.0 0.0	G 0.0 0.0 99 9	G 0.0 0.0 100 0	Indel% 0.02
Untreated Site 8 A C G T	G ₁ 0.0 0.0 100.0 0.0	T ₂ 0.0 0.0 0.0 100.0	A ₃ 100.0 0.0 0.0 0.0	A ₄ 100.0 0.0 0.0 0.0	A ₅ 99.9 0.0 0.1 0.0	C ₆ 0.0 100.0 0.0 0.0	A ₇ 100.0 0.0 0.0 0.0	A ₈ 100.0 0.0 0.0 0.0	A ₉ 100.0 0.0 0.0 0.0	G ₁₀ 0.0 0.0 100.0 0.0	C ₁₁ 0.0 100.0 0.0 0.0	A ₁₂ 100.0 0.0 0.0 0.0	T ₁₃ 0.0 0.0 0.0 100.0	A ₁₄ 100.0 0.0 0.0 0.0	G ₁₅ 0.1 0.0 99.9 0.0	A ₁₆ 100.0 0.0 0.0 0.0	C ₁₇ 0.0 100.0 0.0 0.0	T ₁₈ 0.0 0.0 0.0 100.0	G ₁₉ 0.1 0.0 99.8 0.0	A ₂₀ 100.0 0.0 0.0 0.0	G 0.0 0.0 100.0 0.0	G 0.0 0.0 99.9 0.0	G 0.0 0.0 100.0 0.0	Indel% 0.02
Untreated Site 8 A C G T	G ₁ 0.0 0.0 100.0 0.0	T ₂ 0.0 0.0 0.0 100.0	A ₃ 100.0 0.0 0.0 0.0	A ₄ 100.0 0.0 0.0 0.0	A ₅ 99.9 0.0 0.1 0.0	C ₆ 0.0 100.0 0.0 0.0	A ₇ 100.0 0.0 0.0 0.0	A ₈ 100.0 0.0 0.0 0.0	A ₉ 100.0 0.0 0.0 0.0	G ₁₀ 0.0 0.0 100.0 0.0	C ₁₁ 0.0 100.0 0.0 0.0	A ₁₂ 100.0 0.0 0.0 0.0	T ₁₃ 0.0 0.0 0.0 100.0	A ₁₄ 100.0 0.0 0.0 0.0	G ₁₅ 0.1 0.0 99.9 0.0	A ₁₆ 100.0 0.0 0.0 0.0	C ₁₇ 0.0 100.0 0.0 0.0	T ₁₈ 0.0 0.0 0.0 100.0	G ₁₉ 0.1 0.0 99.8 0.0	A ₂₀ 100.0 0.0 0.0 0.0	G 0.0 0.0 100.0 0.0	G 0.0 0.0 99.9 0.0	G 0.0 0.0 100.0 0.0	Indel% 0.02
Untreated Site 8 A C G T ABE6.3	G ₁ 0.0 0.0 100.0 0.0	T ₂ 0.0 0.0 0.0 100.0	A ₃ 100.0 0.0 0.0 0.0	A ₄ 100.0 0.0 0.0 0.0	A ₅ 99.9 0.0 0.1 0.0	C ₆ 0.0 100.0 0.0 0.0	A ₇ 100.0 0.0 0.0 0.0	A ₈ 100.0 0.0 0.0 0.0	A ₉ 100.0 0.0 0.0	G ₁₀ 0.0 0.0 100.0 0.0	C ₁₁ 0.0 100.0 0.0 0.0	A ₁₂ 100.0 0.0 0.0 0.0	T ₁₃ 0.0 0.0 100.0	A ₁₄ 100.0 0.0 0.0 0.0	G ₁₅ 0.1 0.0 99.9 0.0	A ₁₆ 100.0 0.0 0.0 0.0	C ₁₇ 0.0 100.0 0.0 0.0	T ₁₈ 0.0 0.0 100.0	G ₁₉ 0.1 0.0 99.8 0.0	A ₂₀ 100.0 0.0 0.0 0.0	G 0.0 0.0 100.0 0.0	G 0.0 0.0 99.9 0.0	G 0.0 0.0 100.0 0.0	Indel%
Untreated Site 8 A C G T ABE6.3 Site 8	G ₁ 0.0 0.0 100.0 0.0 G ₁	T ₂ 0.0 0.0 100.0 T ₂	A ₃ 100.0 0.0 0.0 0.0 0.0	A ₄ 100.0 0.0 0.0 0.0 A ₄	A ₅ 99.9 0.0 0.1 0.0 A ₅ 71.7	C ₆ 0.0 100.0 0.0 0.0	A ₇ 100.0 0.0 0.0 0.0 A ₇ 96.0	A ₈ 100.0 0.0 0.0 0.0 0.0	A ₉ 100.0 0.0 0.0 0.0 A ₉ 98.4	G ₁₀ 0.0 100.0 0.0 G ₁₀ 0.0	C ₁₁ 0.0 100.0 0.0 0.0 C ₁₁	A ₁₂ 100.0 0.0 0.0 0.0 0.0	T ₁₃ 0.0 0.0 100.0 T ₁₃	A ₁₄ 100.0 0.0 0.0 0.0 A ₁₄	G ₁₅ 0.1 0.0 99.9 0.0 G ₁₅	A ₁₆ 100.0 0.0 0.0 0.0 A ₁₆	C ₁₇ 0.0 100.0 0.0 0.0 C ₁₇	T ₁₈ 0.0 0.0 100.0 T ₁₈	G ₁₉ 0.1 0.0 99.8 0.0 G ₁₉ 0.2	A ₂₀ 100.0 0.0 0.0 0.0 0.0	G 0.0 0.0 100.0 0.0 G 0.0	G 0.0 0.0 99.9 0.0 G 0.0	G 0.0 0.0 100.0 0.0 G	Indel% 0.02 Indel% 0.027
Untreated Site 8 A C G T ABE6.3 Site 8 A C	G ₁ 0.0 100.0 0.0 G ₁ 0.0 0.0	T ₂ 0.0 0.0 100.0 T ₂ 0.0 0.0	A ₃ 100.0 0.0 0.0 0.0 0.0 A ₃ 98.8 0.0	A ₄ 100.0 0.0 0.0 0.0 8.0 98.0 0.0	A ₅ 99.9 0.0 0.1 0.0 A ₅ 71.7 0.0	C ₆ 0.0 100.0 0.0 0.0 C ₆ 0.0 99.9	Α ₇ 100.0 0.0 0.0 0.0 96.9 0.1	A ₈ 100.0 0.0 0.0 0.0 0.0 94.0 0.0	A ₉ 100.0 0.0 0.0 0.0 A ₉ 98.4 0.0	G ₁₀ 0.0 100.0 0.0 G ₁₀ 0.0	C ₁₁ 0.0 100.0 0.0 0.0 C ₁₁ 0.0	A ₁₂ 100.0 0.0 0.0 0.0 A ₁₂ 99.9 0.0	T ₁₃ 0.0 0.0 100.0 T ₁₃ 0.0 0.0	A ₁₄ 100.0 0.0 0.0 0.0 A ₁₄ 100.0 0.0	G ₁₅ 0.1 0.0 99.9 0.0 G ₁₅ 0.1 0.0	A ₁₆ 100.0 0.0 0.0 0.0 A ₁₆ 100.0 0.0	C ₁₇ 0.0 100.0 0.0 0.0 C ₁₇ 0.0	T ₁₈ 0.0 0.0 100.0 T <u>18</u> 0.0	G ₁₉ 0.1 0.0 99.8 0.0 G ₁₉ 0.2 0.0	A ₂₀ 100.0 0.0 0.0 0.0 100.0	G 0.0 100.0 0.0 0.0 0.0 0.0	G 0.0 99.9 0.0 G 0.0 0.0	G 0.0 0.0 100.0 0.0 G 0.0 0.0	Indel% 0.02 Indel% 0.027
Untreated Site 8 A C G T ABE6.3 Site 8 A C G	G ₁ 0.0 100.0 0.0 G ₁ 0.0 0.0 100.0	T ₂ 0.0 0.0 100.0 T ₂ 0.0 0.0 0.0 0.0	A ₃ 100.0 0.0 0.0 0.0 0.0 A ₃ 98.8 0.0 1.2	A ₄ 100.0 0.0 0.0 0.0 A ₄ 98.0 0.0 2.0	A ₅ 99.9 0.0 0.1 0.0 A ₅ 71.7 0.0 28.3	C ₆ 0.0 100.0 0.0 0.0 C ₆ 0.0 99.9 0.0	A ₇ 100.0 0.0 0.0 0.0 96.9 0.1 3.1	A ₈ 100.0 0.0 0.0 0.0 0.0 A ₈ 94.0 0.0 5.9	A ₉ 100.0 0.0 0.0 0.0 98.4 0.0 1.6	G ₁₀ 0.0 100.0 0.0 G ₁₀ 0.0 99.9	C ₁₁ 0.0 100.0 0.0 0.0 C ₁₁ 0.0 100.0	A ₁₂ 100.0 0.0 0.0 0.0 99.9 0.0 0.1	T ₁₃ 0.0 0.0 100.0 T ₁₃ 0.0 0.0 0.0	A ₁₄ 100.0 0.0 0.0 0.0 A ₁₄ 100.0 0.0	G ₁₅ 0.1 0.0 99.9 0.0 G ₁₅ 0.1 0.0 99.9	A ₁₆ 100.0 0.0 0.0 0.0 A ₁₆ 100.0 0.0	C ₁₇ 0.0 100.0 0.0 0.0 C ₁₇ 0.0 100.0 0.0	T ₁₈ 0.0 0.0 100.0 T <u>18</u> 0.0 0.0 0.0	G ₁₉ 0.1 0.0 99.8 0.0 G ₁₉ 0.2 0.0 99.7	A ₂₀ 100.0 0.0 0.0 0.0 A ₂₀ 100.0 0.0	G 0.0 100.0 0.0 G 0.0 0.0 99.9	G 0.0 99.9 0.0 G 0.0 0.0 99.9	G 0.0 100.0 0.0 0.0 0.0 0.0 0.0 0.0 99.9	Indel% 0.02 Indel% 0.027
Untreated Site 8 A C G T ABE6.3 Site 8 A C G T	G ₁ 0.0 0.0 100.0 0.0 G ₁ 0.0 0.0 100.0 0.0	T ₂ 0.0 0.0 100.0 T ₂ 0.0 0.0 0.0 0.0 99.9	A ₃ 100.0 0.0 0.0 0.0 98.8 0.0 1.2 0.0	A ₄ 100.0 0.0 0.0 0.0 4 98.0 0.0 2.0 0.0	A ₅ 99.9 0.0 0.1 0.0 A ₅ 71.7 0.0 28.3 0.0	C ₆ 0.0 100.0 0.0 0.0 99.9 0.0 0.0	A ₇ 100.0 0.0 0.0 0.0 96.9 0.1 3.1 0.0	A ₈ 100.0 0.0 0.0 0.0 A ₈ 94.0 0.0 5.9 0.0	A ₉ 100.0 0.0 0.0 0.0 98.4 0.0 1.6 0.0	G ₁₀ 0.0 100.0 0.0 G ₁₀ 0.0 99.9 0.0	C ₁₁ 0.0 100.0 0.0 0.0 0.0 100.0 100.0 0.0	A ₁₂ 100.0 0.0 0.0 0.0 0.0 99.9 0.0 0.1 0.0	T ₁₃ 0.0 0.0 100.0 T ₁₃ 0.0 0.0 0.0 100.0	A ₁₄ 100.0 0.0 0.0 0.0 A ₁₄ 100.0 0.0 0.0 0.0	G ₁₅ 0.1 0.0 99.9 0.0 G ₁₅ 0.1 0.0 99.9 0.0	A ₁₆ 100.0 0.0 0.0 0.0 A ₁₆ 100.0 0.0 0.0 0.0	C ₁₇ 0.0 100.0 0.0 0.0 C ₁₇ 0.0 100.0 0.0	T ₁₈ 0.0 0.0 100.0 100.0 T ₁₈ 0.0 0.0 0.0 100.0	G ₁₉ 0.1 0.0 99.8 0.0 G ₁₉ 0.2 0.0 99.7 0.0	A ₂₀ 100.0 0.0 0.0 0.0 100.0 0.0 0.0 0.0	G 0.0 100.0 0.0 0.0 99.9 0.0	G 0.0 99.9 0.0 G 0.0 0.0 99.9 0.1	G 0.0 0.0 100.0 0.0 G 0.0 0.0 99.9 0.0	Indel% 0.02 Indel% 0.027
Untreated Site 8 A C G T ABE6.3 Site 8 A C G T	G ₁ 0.0 100.0 0.0 G ₁ 0.0 0.0 100.0 0.0	T ₂ 0.0 0.0 100.0 100.0 T ₂ 0.0 0.0 0.0 99.9	A ₃ 100.0 0.0 0.0 0.0 0.0 98.8 0.0 1.2 0.0	A ₄ 100.0 0.0 0.0 0.0 98.0 0.0 2.0 0.0	A ₅ 99.9 0.0 0.1 0.0 A ₅ 71.7 0.0 28.3 0.0	$\begin{array}{c} C_6 \\ 0.0 \\ 100.0 \\ 0.0 \\ 0.0 \\ \end{array}$	Α ₇ 100.0 0.0 0.0 0.0 96.9 0.1 3.1 0.0	A ₈ 100.0 0.0 0.0 0.0 48 94.0 0.0 5.9 0.0	A ₉ 100.0 0.0 0.0 0.0 98.4 0.0 1.6 0.0	G ₁₀ 0.0 100.0 0.0 G ₁₀ 0.0 99.9 0.0	C ₁₁ 0.0 100.0 0.0 0.0 0.0 100.0 100.0 0.0	A ₁₂ 100.0 0.0 0.0 0.0 99.9 0.0 0.1 0.0	T ₁₃ 0.0 0.0 100.0 100.0 T ₁₃ 0.0 0.0 0.0 100.0	A ₁₄ 100.0 0.0 0.0 0.0 A ₁₄ 100.0 0.0 0.0 0.0	G ₁₅ 0.1 0.0 99.9 0.0 G ₁₅ 0.1 0.0 99.9 0.0	A ₁₆ 100.0 0.0 0.0 0.0 100.0 0.0 0.0 0.0 0.0	C ₁₇ 0.0 100.0 0.0 0.0 C ₁₇ 0.0 100.0 0.0	T ₁₈ 0.0 0.0 100.0 100.0 T ₁₈ 0.0 0.0 0.0 100.0	G ₁₉ 0.1 0.0 99.8 0.0 G ₁₉ 0.2 0.0 99.7 0.0	A ₂₀ 100.0 0.0 0.0 0.0 100.0 0.0 0.0 0.0 0.0	G 0.0 100.0 0.0 0.0 0.0 99.9 0.0	G 0.0 99.9 0.0 G 0.0 0.0 99.9 0.1	G 0.0 0.0 100.0 0.0 G 0.0 0.0 99.9 0.0	Indel% 0.02 Indel% 0.027
Untreated Site 8 A C G T ABE6.3 Site 8 A C G T T ABE7.8	G ₁ 0.0 100.0 0.0 G ₁ 0.0 0.0 100.0 0.0	T ₂ 0.0 0.0 100.0 100.0 T ₂ 0.0 0.0 0.0 99.9	A ₃ 100.0 0.0 0.0 0.0 0.0 98.8 0.0 1.2 0.0	A ₄ 100.0 0.0 0.0 0.0 98.0 0.0 2.0 0.0	A ₅ 99.9 0.0 0.1 0.0 Α ₅ 71.7 0.0 28.3 0.0	C ₆ 0.0 100.0 0.0 0.0 0.0 99.9 0.0 0.0	A ₇ 100.0 0.0 0.0 96.9 0.1 3.1 0.0	A ₈ 100.0 0.0 0.0 0.0 48 94.0 0.0 5.9 0.0	A ₉ 100.0 0.0 0.0 0.0 98.4 0.0 1.6 0.0	G ₁₀ 0.0 100.0 0.0 G ₁₀ 0.0 99.9 0.0	C ₁₁ 0.0 100.0 0.0 0.0 0.0 100.0 100.0 0.0	A ₁₂ 100.0 0.0 0.0 0.0 99.9 0.0 0.1 0.0	$\begin{array}{c} T_{13} \\ 0.0 \\ 0.0 \\ 100.0 \\ \hline \end{array}$	A ₁₄ 100.0 0.0 0.0 0.0 A ₁₄ 100.0 0.0 0.0 0.0	G ₁₅ 0.1 0.0 99.9 0.0 G ₁₅ 0.1 0.1 0.0 99.9 0.0	A ₁₆ 100.0 0.0 0.0 100.0 0.0 0.0 0.0	C ₁₇ 0.0 100.0 0.0 0.0 C ₁₇ 0.0 100.0 0.0	T ₁₈ 0.0 0.0 100.0 100.0 T ₁₈ 0.0 0.0 0.0 100.0	G ₁₉ 0.1 0.0 99.8 0.0 G ₁₉ 0.2 0.0 99.7 0.0	A ₂₀ 100.0 0.0 0.0 100.0 0.0 0.0 0.0	G 0.0 0.0 100.0 0.0 0.0 99.9 0.0	G 0.0 99.9 0.0 G 0.0 99.9 0.1	G 0.0 0.0 100.0 0.0 G 0.0 99.9 0.0	Indel% 0.02 Indel% 0.027
Untreated Site 8 A C G T ABE6.3 Site 8 A C G T ABE7.8 Site 8 A	G ₁ 0.0 100.0 0.0 G ₁ 0.0 0.0 100.0 0.0	T ₂ 0.0 0.0 100.0 T ₂ 0.0 0.0 0.0 99.9 T ₂ 0.0	A ₃ 100.0 0.0 0.0 0.0 98.8 0.0 1.2 0.0 4 3 98.4	A ₄ 100.0 0.0 0.0 98.0 0.0 2.0 0.0 2.0 0.0 2.0 0.0	A ₅ 99.9 0.0 0.1 0.0 A ₅ 71.7 0.0 28.3 0.0 A ₅ 85.2	C ₆ 0.0 100.0 0.0 0.0 99.9 0.0 0.0 0.0 0.0	A ₇ 100.0 0.0 0.0 96.9 0.1 3.1 0.0 A ₇ 98.5	A ₈ 100.0 0.0 0.0 94.0 0.0 5.9 0.0 48 99.1	A ₉ 100.0 0.0 0.0 98.4 0.0 1.6 0.0 A ₉ 99.2	G ₁₀ 0.0 100.0 0.0 500 0.0 99.9 0.0 6 ₁₀ 0.0	C ₁₁ 0.0 100.0 0.0 0.0 100.0 100.0 0.0 0.0 0	A ₁₂ 100.0 0.0 0.0 0.0 99.9 0.0 0.1 0.0 0.1 0.0 99.8	$\begin{array}{c} T_{13} \\ 0.0 \\ 0.0 \\ 100.0 \\ \hline \end{array}$	A ₁₄ 100.0 0.0 0.0 100.0 0.0 0.0 0.0 0.0 0.0	G ₁₅ 0.1 0.0 99.9 0.0 G ₁₅ 0.1 0.0 99.9 0.0 G ₁₅ 0.0	A ₁₆ 100.0 0.0 0.0 100.0 0.0 0.0 0.0 0.0 0.0	C ₁₇ 0.0 100.0 0.0 0.0 100.0 100.0 0.0 0.0 0	T ₁₈ 0.0 0.0 100.0 100.0 0.0 0.0 100.0 100.0 100.0	G ₁₉ 0.1 0.0 99.8 0.0 G ₁₉ 0.2 0.0 99.7 0.0 99.7 0.0	A ₂₀ 100.0 0.0 0.0 100.0 0.0 0.0 0.0 0.0 0.0	G 0.0 0.0 100.0 0.0 0.0 99.9 0.0 G G 0.0	G 0.0 99.9 0.0 G 0.0 99.9 0.1 G G 0.0	G 0.0 0.0 100.0 0.0 G 0.0 99.9 0.0 G 0.0	Indel% 0.02 Indel% 0.027 Indel% 0.024
Untreated Site 8 A C G T ABE6.3 Site 8 A C G T ABE7.8 Site 8 A C	$\begin{array}{c} G_1 \\ 0.0 \\ 0.0 \\ 100.0 \\ 0.0 \\ \hline \\ G_1 \\ 0.0 \\ 0.0 \\ \hline \\ G_0 \\ 0.0 \\ \hline \\ G_1 \\ 0.0 \\ \hline \\ 0.0 \\ \hline \end{array}$	T2 0.0 0.0 0.0 100.0 T2 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0	A ₃ 100.0 0.0 0.0 0.0 98.8 0.0 1.2 0.0 1.2 0.0 4 ₃ 98.4 0.0	A ₄ 100.0 0.0 0.0 98.0 0.0 2.0 0.0 2.0 0.0 4 4 97.7 0.0	A ₅ 99.9 0.0 0.1 0.0 28.3 0.0 28.3 0.0 A ₅ 85.2 0.0	C ₆ 0.0 100.0 0.0 0.0 99.9 0.0 0.0 0.0 0.0 99.9	A ₇ 100.0 0.0 0.0 96.9 0.1 3.1 0.0 4 ₇ 98.5 0.0	A ₈ 100.0 0.0 0.0 0.0 48 94.0 0.0 5.9 0.0 48 99.1 0.0	A ₉ 100.0 0.0 0.0 98.4 0.0 1.6 0.0 4.9 99.2 0.0	G ₁₀ 0.0 100.0 0.0 0.0 99.9 0.0 G ₁₀ 0.0 99.9 0.0	C ₁₁ 0.0 100.0 0.0 0.0 100.0 0.0 0.0 0.0 0.0	A ₁₂ 100.0 0.0 0.0 0.0 99.9 0.0 0.1 0.0 0.1 0.0 99.8 0.0	$\begin{array}{c} T_{13} \\ 0.0 \\ 0.0 \\ 100.0 \\ \hline \end{array}$	A ₁₄ 100.0 0.0 0.0 100.0 0.0 0.0 0.0	$\begin{array}{c} G_{15} \\ 0.1 \\ 0.0 \\ 99.9 \\ 0.0 \\ \end{array}$	A ₁₆ 100.0 0.0 0.0 100.0 0.0 0.0 0.0 0.0 0.0	C ₁₇ 0.0 100.0 0.0 0.0 100.0 100.0 0.0 0.0 0	T ₁₈ 0.0 0.0 100.0 T ₁₈ 0.0 0.0 100.0 T _{0.0} T ₁₈ 0.0 0.0	G ₁₉ 0.1 0.0 99.8 0.0 6 <u>19</u> 0.2 0.0 99.7 0.0 99.7 0.0	A ₂₀ 100.0 0.0 0.0 100.0 0.0 0.0 0.0 0.0 0.0	G 0.0 100.0 0.0 G 0.0 99.9 0.0 G G.0 0.0 0.0	G 0.0 99.9 0.0 G 0.0 99.9 0.1 G G 0.0 0.0	G 0.0 100.0 0.0 0.0 0.0 99.9 0.0 G 0.0 0.0 0.0	Indel% 0.02 Indel% 0.027 Indel% 0.024
Untreated Site 8 A C G T ABE6.3 Site 8 A C G T ABE7.8 Site 8 A C G T	G ₁ 0.0 100.0 0.0 G ₁ 0.0 100.0 0.0 100.0 G ₁ 0.0 100.0 100.0	T2 0.0	A ₃ 100.0 0.0 0.0 0.0 4 3 98.8 0.0 1.2 0.0 4 3 98.4 0.0 1.5	A ₄ 100.0 0.0 0.0 98.0 0.0 2.0 0.0 2.0 0.0 4 4 97.7 0.0 2.2	A ₅ 99.9 0.0 0.1 0.0 71.7 0.0 28.3 0.0 85.2 0.0 14.8	C6 0.0 100.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 99.9 0.0 99.9 0.0	A ₇ 100.0 0.0 0.0 96.9 0.1 3.1 0.0 4 ₇ 98.5 0.0 1.5	A ₈ 100.0 0.0 0.0 94.0 0.0 5.9 0.0 5.9 0.0 4.8 99.1 99.1 9.0 0.0 0.9	A ₉ 100.0 0.0 0.0 98.4 0.0 1.6 0.0 4.9 99.2 0.0 0.8	G ₁₀ 0.0 100.0 0.0 0.0 99.9 0.0 G ₁₀ 0.0 99.9 9.0 0.0 99.9	C ₁₁ 0.0 100.0 0.0 0.0 100.0 0.0 0.0 0.0 0.0	A ₁₂ 100.0 0.0 0.0 99.9 0.0 0.1 0.0 0.1 99.8 9.0 0.0 0.1	$\begin{array}{c c} T_{13} \\ 0.0 \\ 0.0 \\ 100.0 \\ \hline \end{array}$	A ₁₄ 100.0 0.0 0.0 0.0 100.0 0.0 0.0 0.0 0.0	G15 0.1 0.9.9 0.0 G15 0.1 0.0 G15 0.1 0.0 G9.9 0.0 G15 0.0 G15 0.0 99.9	A ₁₆ 100.0 0.0 0.0 100.0 0.0 0.0 0.0 0.0 0.0	C ₁₇ 0.0 100.0 0.0 C ₁₇ 0.0 100.0 0.0 0.0 C ₁₇ 0.0 99.9 0.0	T ₁₈ 0.0 100.0 100.0 T ₁₈ 0.0 0.0 100.0 100.0 100.0	G ₁₉ 0.1 0.0 99.8 0.0 G ₁₉ 0.0 G ₁₉ 0.1 0.0 99.7 0.0 99.7 0.0 99.7 0.0 99.7 0.0	A ₂₀ 100.0 0.0 0.0 100.0 0.0 0.0 0.0 0.0 0.0	G 0.0 0.0 100.0 0.0 99.9 9.9 0.0 G G 0.0 0.0 100.0	G 0.0 99.9 0.0 G 0.0 99.9 0.1 G G 0.0 0.0 99.9 9.9	G 0.0 100.0 0.0 0.0 0.0 99.9 0.0 G 0.0 0.0 0.0 0.0 100.0	Indel% 0.02 Indel% 0.027 Indel% 0.024
Untreated Site 8 A C G T ABE6.3 Site 8 A C G T ABE7.8 Site 8 A C G T	G ₁ 0.0 100.0 0.0 0.0 100.0 0.0 100.0 0.0 100.0 0.0	T2 0.0 0.0 0.0 0.0 100.0 T2 0.0	A ₃ 100.0 0.0 0.0 0.0 98.8 0.0 1.2 0.0 98.4 0.0 1.5 0.0	A ₄ 100.0 0.0 0.0 98.0 0.0 2.0 0.0 2.0 0.0 2.0 0.0 2.2 0.0	A ₅ 99.9 0.0 0.1 0.0 71.7 0.0 28.3 0.0 85.2 0.0 14.8 0.0	$\begin{array}{c} C_6 \\ \hline 0.0 \\ 100.0 \\ 0.0 \\ 0.0 \\ \hline 0.0 \\ 99.9 \\ 0.0 \\ 0.0 \\ \hline 0.0 \\ 99.9 \\ 0.0 \\ 0.0 \\ 99.9 \\ 90.9 \\ 0.0 \\ 0.0 \\ 0.0 \\ \hline \end{array}$	A ₇ 100.0 0.0 0.0 96.9 0.1 3.1 0.0 A ₇ 986.9 0.1 3.1 0.0	A ₈ 100.0 0.0 0.0 94.0 0.0 5.9 0.0 A ₈ 99.1 0.0 0.9 0.0	A ₉ 100.0 0.0 0.0 0.0 98.4 0.0 1.6 0.0 99.2 0.0 0.8 0.0	G10 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 99.9 0.0 0.0 99.9 0.0 0.0 99.9 0.1	C ₁₁ 0.0 100.0 0.0 0.0 100.0 100.0 0.0 0.0 0	A ₁₂ 100.0 0.0 0.0 0.0 0.0 0.0 0.1 0.0 0.1 0.0 0.1 0.1	T ₁₃ 0.0 0.0 100.0 100.0 100.0 T ₁₃ 0.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0	A ₁₄ 100.0 0.0 0.0 0.0 0.0 0.0 0.0 0	$\begin{array}{c} G_{15} \\ 0.1 \\ 0.0 \\ 99.9 \\ 0.0 \\ \end{array}$	A ₁₆ 100.0 0.0 0.0 100.0 0.0 0.0 0.0 0.0 0.0	C ₁₇ 0.0 100.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0	T ₁₈ 0.0 0.0 100.0 100.0 100.0 100.0 100.0 T ₁₈ 0.0 0.0 100.0 100.0	G19 0.1 0.0 99.8 0.0 G19 0.2 0.0 99.7 0.0 99.7 0.0 99.7 0.0 99.7 0.0 99.7 0.0 99.7 0.0	A ₂₀ 100.0 0.0 0.0 100.0 0.0 0.0 0.0 0.0 0.0	G 0.0 0.0 100.0 0.0 99.9 0.0 G G 0.0 100.0 100.0	G 0.0 99.9 0.0 G 0.0 99.9 0.1 G 0.0 99.9 0.1	G 0.0 0.0 100.0 0.0 99.9 0.0 99.9 0.0 G G 0.0 0.0 100.0 0.0	Indel% 0.02 Indel% 0.027 Indel% 0.024
Untreated Site 8 A C G T ABE6.3 Site 8 A C G G T ABE7.8 Site 8 A C G G T	G ₁ 0.0 100.0 0.0 100.0 0.0 100.0 100.0 0.0	T2 0.0 0.0 0.0 100.0 T2 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 100.0	A ₃ 100.0 0.0 0.0 0.0 98.8 0.0 1.2 0.0 4 3 98.4 0.0 1.2 0.0 1.5 0.0	A4 100.0 0.0	A ₅ 99.9 0.0 0.1 0.0 A ₅ 71.7 0.0 28.3 0.0 A ₅ 85.2 0.0 14.8 0.0	$\begin{array}{c} C_6 \\ 0.0 \\ 100.0 \\ 0.0 \\ 0.0 \\ 0.0 \\ 99.9 \\ 0.0 \\ 0.$	A ₇ 100.0 0.0 0.0 96.9 0.1 3.1 0.0 98.5 0.0 1.5 0.0	A ₈ 100.0 0.0 0.0 94.0 0.0 5.9 0.0 A ₈ 99.1 0.0 99.1 0.9 0.9	A ₉ 100.0 0.0 0.0 0.0 98.4 0.0 1.6 0.0 1.6 0.0 99.2 0.0 0.8 0.0	$\begin{bmatrix} G_{10} \\ 0.0 \\$	C11 O.0 100.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 100.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0	A ₁₂ 100.0 0.0 0.0 0.0 0.0 0.0 0.0 0	T ₁₃ 0.0 0.0 100.0 100.0 T ₁₃ 0.0 0.0 100.0 T ₁₃ 0.0 100.0 100.0 100.0 100.0 100.0	A ₁₄ 100.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0	$\begin{array}{c} G_{15} \\ 0.1 \\ 0.0 \\ 99.9 \\ 0.0 \\ \hline \\ 0.1 \\ 0.0 \\ 99.9 \\ 0.0 \\ \hline \\ 0.0 \\ 0.0 \\ 99.9 \\ 0.0 \\ \hline \\ 0.0 \\ 99.9 \\ 0.0 \\ \hline \end{array}$	A ₁₆ 100.0 0.0 0.0 0.0 0.0 0.0 0.0 0	C ₁₇ 0.0 0.0 0.0 0.0 100.0 0.0 100.0 0.0 0.0	T ₁₈ 0.0 0.0 0.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 100.0	G19 0.1 0.0 99.8 0.0 G19 0.0 99.7 0.0 99.7 0.0 99.7 0.0 99.7 0.0 99.7 0.0 99.7 0.0	A ₂₀ 100.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0	G 0.0 100.0 0.0 0.0 99.9 0.0 G G 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0	G 0.0 99.9 0.0 0.0 99.9 0.0 0.0 99.9 0.1	G 0.0 0.0 100.0 0.0 0.0 99.9 0.0 G 0.0 0.0 0.0 100.0 0.0	Indel% 0.02 Indel% 0.027 Indel%
Untreated Site 8 A C G T ABE6.3 Site 8 A C G T ABE7.8 Site 8 A C G G T ABE7.9 Site 8	$ \begin{array}{c} G_{1} \\ 0.0 \\ 0.0 \\ 100.0 \\ 0.0 \\ \hline G_{1} \\ 0.0 \\ 0.0 \\ \hline G_{1} \\ 0.0 \\ 0.0 \\ \hline 0.0 \\ $	T ₂ 0.0 0.0 100.0 100.0 T ₂ 0.0 0.0 99.9 T ₂ 0.0 0.0 0.0 100.0	A ₃ 100.0 0.0 0.0 0.0 1.2 0.0 1.2 0.0 1.2 0.0 4 3 88.4 0.0 1.5 0.0	A4 100.0 0.0	A ₅ 99.9 0.0 0.1 0.0 71.7 0.0 28.3 0.0 A ₅ 85.2 0.0 14.8 0.0	C ₆ 0.0 100.0 0.0 0.0 99.9 0.0 0.0 0.0 0.0 99.9 0.0 0.0	A ₇ 100.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 96.9 0.1 3.1 0.0 4.7 98.5 0.0 1.5 0.0 4.5	A ₈ 100.0 0.0 0.0 94.0 0.0 5.9 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0	A ₉ 100.0 0.0 0.0 0.0 1.6 0.0 1.6 0.0 4.9 99.2 0.0 0.0 0.0 0.0	$ \begin{array}{c} G_{10} \\ 0.0 \\ 0.0 \\ 100.0 \\ 0.0 \\ 0.0 \\ 0.0 \\ 99.9 \\ 0.0 $	C11 0.0 100.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 100.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0	A ₁₂ 100.0 0.0 0.0 0.0 0.0 0.0 0.0 0	T ₁₃ 0.0 0.0 0.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0	A ₁₄ 100.0 0.0 0.0 100.0 0.0 0.0 0.0	G16 O.1 0.0 99.9 0.0 0.0 G15 0.1 0.0 99.9 0.0 0.0 99.9 0.0 G15 0.1 0.0 99.9 0.0 0.0 99.9 0.0	A ₁₆ 100.0 0.0 0.0 A ₁₆ 100.0 0.0 A ₁₆ 100.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0	C ₁₇ 0.0 100.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0	T ₁₈ 0.0 0.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0	G19 0.1 0.0 99.8 0.0 G19 0.2 0.0 99.7 0.0 99.7 0.0 99.7 0.0 99.7 0.0 99.9 0.0 99.9 0.0	A ₂₀ 100.0 0.0 0.0 100.0 0.0 0.0 0.0 0.0 100.0 0.0	G 0.0 100.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0	G 0.0 99.9 0.0 99.9 0.0 0.0 0.0 0.0 0.0 99.9 0.0 0.0	G 0.0 0.0 100.0 0.0 0.0 99.9 0.0 G 0.0 0.0 0.0 100.0 0.0 100.0 0.0	Indel% 0.02 Indel% 0.027 Indel% 0.024
Untreated Site 8 A C G T ABE6.3 Site 8 A C G T ABE7.8 Site 8 A C G T ABE7.9 Site 8 A A ABE7.9 Site 8 A	$\begin{array}{c} G_1 \\ 0.0 \\ 0.0 \\ 100.0 \\ 0.0 \\ \hline \\ 0.0 0.0$	T₂ 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 100.0 T₂ 0.0 0.0	A ₃ 100.0 0.0 0.0 98.8 0.0 1.2 0.0 1.2 0.0 1.5 0.0 1.5 0.0 99.5	A4 100.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 2.0 0.0 0.0 2.2 0.0 2.2 0.0 2.2 0.0 2.2 0.0 2.4 99.0	A ₅ 99.9 0.0 0.1 0.0 71.7 0.0 28.3 0.0 A ₅ 85.2 0.0 14.8 0.0 A ₅ 73.7	C ₆ 0.0 100.0 0.0	A ₇ 100.0 0.0 0.0 0.0 0.0 0.1 3.1 0.0 4.7 98.5 0.0 A ₇ 98.5	A ₈ 100.0 0.0 0.0 94.0 0.0 5.9 0.0 0.0 A ₈ 99.1 0.0 0.9 0.0 8 99.1	A ₃ 100.0 0.0 0.0 0.0 0.0 0.0 98.4 0.0 1.6 0.0 1.6 0.0 99.2 0.0 0.8 0.0 8 0.0 8 99.2 99.4 99.4	G10 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 99.9 0.1 G10.0 0.0 90.9 0.1	C11 0.0 100.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0	A ₁₂ 100.0 0.0 0.0 0.0 99.9 0.0 0.1 0.1 A ₁₂ 99.8 0.0 0.1 0.1 99.9 9.9	T ₁₃ 0.0 0.0 0.0 100.0 100.0 100.0 0.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0	A ₁₄ 100.0 0.0 0.0 A ₁₄ 100.0 0.0 0.0 A ₁₄ 99.9 0.0 0.0 0.0 A ₁₄ 100.0 A ₁₄ 100.0 A ₁₄ 100.0 A ₁₄ 100.0 A ₁₄ 100.0 A ₁₆ 100.0 A ₁₆ 100.0 A ₁₆ 100.0 A ₁₆ 100.0 A ₁₆ 100.0 A ₁₆ 100.0 A ₁₆ 100.0 A ₁₆ 100.0 0 .0 0 .0 1 .	$\begin{array}{c} G_{16} \\ 0.1 \\ 0.0 \\ 99.9 \\ 0.0 \\ \hline \\ 0.1 \\ 0.1 \\ 0.0 \\ 99.9 \\ 0.0 \\ \hline \\ 0.0 \\ \hline \\ 99.9 \\ 0.0 \\ \hline 0.0 \\ 0.0 \\ \hline 0$	A ₁₆ 100.0 0.0 0.0 0.0 100.0 0.0 0.0 0.0 0.0	C ₁₇ 0.0 100.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0	T ₁₆ 0.0 0.0 0.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0	G ₁₉ 0.1 0.0 99.8 0.0 0.2 0.0 0.2 0.0 0.0 99.7 0.0 0.0 0.0 99.9 0.0 0.0	A ₂₀ 100.0 0.0 0.0 100.0 0.0 0.0 0.0 0.0 0.0	G 0.0 0.0 100.0 0.0 0.0 0.0 0.0 0.0 0.0 0	G 0.0 99.9 0.0 99.9 0.0 0.0 0.0 0.0 0.0 0	G 0.0 0.0 100.0 0.0 0.0 99.9 0.0 0.0 0.0 0.0 0.0 0.	Indel% 0.02 0.027 0.027 Indel% 0.024 Indel% 0.034
Untreated Site 8 A C G T ABE6.3 Site 8 A C G T ABE7.8 Site 8 A C G T T ABE7.9 Site 8 A C C G T T	$\begin{array}{c} G_1 \\ 0.0 \\ 0.0 \\ 100.0 \\ 0.0 \\ \hline \\ 0.0 \\ 0.0 \\ \hline \\ 0.0 \\ 0.0 \\ \hline \\ 0.0 \\ \hline \\ 0.0 \\ \hline \\ 0.0 \\ \hline \\ G_1 \\ 0.0 \\ \hline \\ 0.0 \\ \hline \\ 0.0 \\ \hline \\ 0.0 \\ \hline \end{array}$	T₂ 0.0 0.0 0.0 100.0 100.0 T₂ 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 100.0 T₂ 0.0 0.0 0.0	A ₃ 100.0 0.0 0.0 0.0 98.8 0.0 1.2 0.0 1.2 0.0 4 3 98.4 0.0 1.5 0.0 99.5 0.0	A4 100.0 0.0 0.0 0.0 0.0 98.0 0.0 2.0 0.0 97.7 0.0 2.2 0.0 2.2 0.0 2.2 0.0 99.0 0.0	A ₅ 99.9 0.0 0.1 0.0 71.7 0.0 28.3 0.0 A ₅ 85.2 0.0 14.8 0.0 14.8 0.0 4.5 73.7 0.0	C6 0.0 100.0 0.0 0.0 0.0 0.0 0.0 99.9 0.0 0.0 0.0 99.9 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0	A ₇ 100.0 0.0 0.0 0.0 0.0 0.1 3.1 0.0 47 98.5 0.0 1.5 0.0 98.5 0.0	A ₆ 100.0 0.0 0.0 94.0 0.0 5.9 0.0 899.1 0.0 0.9 0.0 99.3 0.0	A ₃ 100.0 0.0 0.0 0.0 98.4 0.0 1.6 0.0 1.6 0.0 99.2 0.0 0.8 0.0 8 0.0 0.8 0.0 99.4 0.0	G10 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 99.9 0.0 0.0 99.9 0.1 G10 0.0 0.0	C11 0.0 100.0 0.0 0.0 0.0 100.0 0.0 100.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 100.0 0.0 0.0 0.0 0.0 0.0 100.0 100.0	A12 100.0 0.0 0.0 0.1 0.0 0.1 0.0 0.1 0.0 0.1 0.0 0.1 0.0 0.1 0.1 0.1 0.1 0.1 0.1 0.1	T ₁₃ 0.0 0.0 0.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 0.0 0.0 0.0 0.0 0.0	A ₁₄ 100.0 0.0 0.0 100.0 0.0 0.0 0.0	G ₁₅ 0.1 0.0 99.9 0.0 0.1 0.1 0.0 99.9 0.0 G ₁₅ 0.1 0.0 0.0 99.9 0.0 G ₁₅ 0.0 G ₁₅ 0.0 0.0 0.0	A ₁₆ 100.0 0.0 0.0 100.0 0.0 0.0 0.0	C ₁₇ 0.0 00.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0	T ₁₈ 0.0 0.0 0.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 0.0 0.0 0.0 0.0	G ₁₉ 0.1 0.0 99.8 0.0 G ₁₉ 0.2 0.0 99.7 0.0 99.7 0.0 99.7 0.0 G ₁₉ 0.1 0.0 G ₁₉ 0.0 G ₁₉ 0.0	A ₂₀ 100.0 0.0 0.0 100.0 0.0 0.0 0.0 0.0 0.0	G 0.0 0.0 100.0 0.0 0.0 99.9 0.0 6 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0	G 0.0 0.0 99.9 0.0 0.0 0.0 0.0 0.0 0.0 0.	G 0.0 0.0 100.0 0.0 0.0 99.9 0.0 G 0.0 0.0 100.0 0.0 100.0 0.0 0.0	Indel% 0.02 Indel% 0.027 Indel% 0.024
Untreated Site 8 A C G T ABE6.3 Site 8 A C G T ABE7.8 Site 8 A C G T ABE7.9 Site 8 A C G G T	G1 0.0 100.0 0.0 100.0 0.0 100.0 0.0 100.0 0.0 100.0 0.0 100.0 0.0 100.0 0.0 100.0 0.0 100.0 0.0 100.0 100.0	$\begin{array}{c} T_2 \\ 0.0 \\ 0.0 \\ 0.0 \\ 100.0 \\ \hline \\ \hline \\ T_2 \\ 0.0 \\ 0.0 \\ 99.9 \\ \hline \\ \hline \\ T_2 \\ 0.0 \\ 0.0 \\ 0.0 \\ \hline \\ \hline \\ \hline \\ T_2 \\ 0.0 \\ 0.0 \\ \hline \end{array}$	A3 100.0 0.0 0.0 0.0 0.0 101.2 0.0 1.2 0.0 1.2 0.0 1.2 0.0 1.5 0.0 1.5 0.0 43 99.5 0.0 0.0 0.4	A ₄ 100.0 0.0 0.0 98.0 0.0 2.0 0.0 2.0 0.0 2.2 0.0 2.2 0.0 2.2 0.0 2.2 0.0 1.0	A ₅ 99.9 0.0 0.1 0.0 8.3 0.0 A ₅ 85.2 0.0 14.8 0.0 14.8 0.0 28.3 0.0 26.3	C6 0.0 100.0 0.0 0.0 0.0 0.0 0.0 99.9 0.0 0.0 0.0 99.9 0.0 0.0 0.0 99.9 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0	A7 100.0 0.0 0.0 0.0 0.0 0.1 3.1 0.0 98.5 0.0 1.5 0.0 98.5 0.0 1.5 0.0 1.5	Ag 100.0 0.0 0.0 0.0 94.0 0.0 5.9 0.0 99.1 0.0 0.9 0.0 99.1 0.0 99.1 0.0 0.9 0.0 0.0 0.0 0.0 0.7	A ₉ 100.0 0.0 0.0 0.0 98.4 0.0 1.6 0.0 99.2 0.0 0.8 0.0 0.8 0.0 0.8 0.0 0.8 0.0 0.8 0.0 0.8 0.0 0.6	G10 0.0	C11 0.0 100.0 0.0 0.0 0.0 0.0 100.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0	A ₁₂ 100.0 0.0 0.0 0.0 0.0 0.0 0.1 0.0 0.1 0.0 0.1 0.1 0.1 0.1 0.1 0.1 0.1 0.1 0.1 0.1 0.1 0.1	T ₁₃ 0.0 0.0 0.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 0.0 0.0 0.0 0.0 0.0 0.0	A ₁₄ 100.0 0.0 0.0 0.0 0.0 0.0 0.0 0	G ₁₅ 0.1 0.0 99.9 0.0 0.1 0.0 0.1 0.0 99.9 0.0 99.9 0.0 99.9 0.0 99.9 0.0 99.9 0.0 99.9 0.0 9.0 0.0 0.0 0.0 0.0 100.0	A ₁₆ 100.0 0.0 0.0 0.0 0.0 0.0 0.0 0	C ₁₇ 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.	T ₁₈ 0.0 0.0 0.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0	G19 0.1 0.0 99.8 0.0 G19 0.0 99.7 0.0 99.9 0.1 0.0 99.9 0.0 G19 0.1 0.0 99.9 0.0 99.9 0.0 99.9 0.0 99.9	A ₂₀ 100.0 0.0 0.0 100.0 0.0 0.0 0.0 0.0 0.0	G 0.0 0.0 100.0 0.0 99.9 0.0 0.0 0.0 0.0 0.0 0.0 0.	G 0.0 0.0 99.9 0.0 0.0 0.0 0.0 0.0 0.0 0.	G 0.0 0.0 100.0 0.0 0.0 99.9 0.0 99.9 0.0 100.0 0.0 100.0 0.0 0.0 0.0 0.0 99.9	Indel% 0.02 Indel% 0.027 Indel% 0.024 Indel% 0.034
Untreated Site 8 A C G T ABE6.3 Site 8 A C G T ABE7.8 Site 8 A C G T ABE7.9 Site 8 A C G T T	G1 0.0 100.0 0.0 100.0 0.0 100.0 0.0 100.0 0.0 100.0 0.0 100.0 0.0 G1 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0	$\begin{array}{c} T_2 \\ 0.0 \\ 0.0 \\ 0.0 \\ 100.0 \\ \hline \end{array}$ $\begin{array}{c} T_2 \\ 0.0 \\ 0.0 \\ 0.0 \\ 99.9 \\ \hline \end{array}$ $\begin{array}{c} T_2 \\ 0.0 \\ 0.0 \\ 0.0 \\ 100.0 \\ \hline \end{array}$	A3 100.0 0.0 0.0 0.0 0.0 101.0 98.8 0.0 1.2 0.0 1.2 0.0 1.2 0.0 1.2 0.0 1.2 0.0 1.2 0.0 A3 98.4 0.0 A3 99.5 0.0 0.4 0.0	A ₄ 100.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 2.0 0.0 2.2 0.0 2.2 0.0 2.2 0.0 2.2 0.0 2.2 0.0 A ₄ 99.0 1.0 0.0	A ₅ 99.9 0.0 0.1 0.0 28.3 0.0 28.3 0.0 28.3 0.0 28.3 0.0 A ₅ 85.2 0.0 14.8 0.0 26.3 0.0	C ₆ 0.0 100.0 0.0	Α ₇ 100.0 0.0 0.0 0.0 0.0 0.1 3.1 0.0 88.5 0.0 4.7 98.5 0.0 1.5 0.0 1.5 0.0	A8 100.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 5.9 0.0 5.9 0.0 99.1 0.0 0.0 99.3 0.0 99.3 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0	A ₉ 100.0 0.0	G10 0.0	C11 0.0 00.0 0.0	A ₁₂ 100.0 0.0 0.0 0.0 0.0 0.0 99.9 0.0 0.1 0.0 9.9 0.0 0.1 0.0 9.9 0.0 0.1 0.1 9.9 0.0 0.1 0.1 0.1 0.1	$\begin{array}{c} T_{13} \\ 0.0 \\ 0.0 \\ 0.0 \\ 100.0 \\ \hline \end{array}$	A ₁₄ 100.0 0.0 0.0 A ₁₄ 100.0 0.0 A ₁₄ 99.9 0.0 0.0 A ₁₄ 100.0 0.0 A ₁₄ 100.0 0.0 A ₁₄ 100.0 0 .0 0	G ₁₅ G 0.1 0.0 99.9 0.0 G ₁₆ 0.1 0.0 99.9 0.0 G ₁₆ 0.1 0.0 99.9 0.0 0.0 99.9 0.0 G ₁₆ 0.0 0.0 99.9 0.0 0.0 99.9 0.0 0.0 99.9 0.0 0.0 99.9 0.0 0.0 99.9 0.0 0.0 99.9 0.0 0.0 99.9 0.0 0.0 99.9 0.0 0.0 99.9 0.0 0.0 99.9 0.0 0.0 99.9 0.0 0.0 10.0 0.0 0.0 100.0 0.0 100.0 0.0	A ₁₆ (00.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0	C ₁₇ 0.0 100.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0	T18 0.0 0.0 0.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0	G10 0.1 0.0 99.8 0.0 99.8 0.0 99.8 0.0 99.7 0.0 99.7 0.0 99.7 0.0 99.7 0.0 99.7 0.0 99.9 0.0 99.9 0.0 99.9 0.0	A ₂₀ 100.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0	G 0.0 100.0 0.0 0.0 99.9 0.0 100.0 0.0 100.0 0.0 0.0 100.0 0.0 99.9 0.0	G 0.0 99.9 0.0 99.9 0.0 99.9 0.1 6 0.0 99.9 0.0 99.9 0.0 99.9 0.0 99.9 0.0 0.0	G 0.0 0.0 100.0 0.0 99.9 0.0 G 0.0 0.0 100.0 0.0 0.0 0.0 0.0	Indel% 0.02 Indel% 0.027 Indel% 0.024 Indel% 0.034
Untreated Site 8 A C G T ABE6.3 Site 8 A C G T ABE7.8 Site 8 A C G T ABE7.9 Site 8 A C G T ABE7.9	$\begin{array}{c} G_1 \\ 0.0 \\ 0.0 \\ 100.0 \\ 0.0 \\ \hline \\ 0.0 \\ 100.0 \\ 0.0 \\ \hline \\ \hline \\ 0.0 \\ \hline \\ 0.0 \\ \hline \\ \hline \\ \hline \\ 0.0 \\ \hline \\ $	$\begin{array}{c} T_2 \\ 0.0 \\ 0.0 \\ 0.0 \\ 100.0 \\ \hline \end{array} \\ \hline T_2 \\ 0.0 \\ 0.0 \\ 0.0 \\ 99.9 \\ \hline T_2 \\ 0.0 \\ 0.0 \\ 0.0 \\ 100.0 \\ \hline \end{array} \\ \hline \begin{array}{c} T_2 \\ 0.0 \\ 0$	A ₃ 100.0 0.0 0.0 0.0 10.0 0.0 10.0 A ₃ 98.8 0.0 1.2 0.0 A ₃ 98.4 0.0 1.2 0.0 A ₃ 98.5 0.0 A ₃ 99.5 0.4 0.0	A4 100.0 0.0	A ₅ 99.9 0.0 0.1 0.0 71.7 0.0 A ₅ 85.2 0.0 A ₅ 73.7 0.0 26.3 0.0	Ce 0.0 100.0 0.0	Α ₇ 100.0 0.0 0.0 0.0 0.0 96.9 0.1 3.1 0.0 98.5 0.0 1.5 0.0 1.5 0.0	A8 100.0 0.0 0.0 0.0 0.0 0.0 0.0 99.1 0.0 99.1 0.0 99.1 0.0 99.1 0.0 99.3 0.0 0.7 0.0	A ₉ 100.0 0.0	$\begin{array}{c} G_{10} \\ 0.0 \\ 0.$	C11 0.0 100.0 0.0	A12 100.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.1 0.0 0.1 0.1 0.1 0.1 0.1 0.1 0.1 0.1 0.1 0.1 0.1 0.1 0.1	T ₁₃ 0.0 0.0 0.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 0.0 100.0 0.0 100.0 0.0 100.0 0.0	A ₁₄ 100.0 0.0 0.0 100.0 0.0 A ₁₄ 100.0 0.0 A ₁₄ 99.9 0.0 0.0 A ₁₄ 100.0 0.0 A ₁₄ 100.0 0.0 A ₁₄ 100.0 0.0 A ₁₄ 100.0 0.0 A ₁₄ 100.0 0.0 A ₁₅ 100.0 0 .0 0	G ₁₅ 0.1 0.0 99.9 0.0 G ₁₅ 0.1 0.0 99.9 0.0 99.9 0.0 99.9 0.0 99.9 0.0 99.9 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0	A ₁₆ 100.0 0.0 0.0 100.0 0.0 100.0 0.0 0.0 A₁₆ 99.9 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0	C ₁₇ 0.0 100.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0	T18 0.0 0.0 0.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0	G ₁₀ 0.1 0.0 99.8 0.0 G ₁₀ 0.2 0.0 99.7 0.0 99.7 0.0 G ₁₉ 0.1 0.0 99.7 0.0 G ₁₉ 0.1 0.0 99.9 0.0 0.0 0.0 0.0 0.0 0.0 0.0	A ₂₀ 100.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0	G 0.0 100.0 0.0 0.0 99.9 0.0 0.0 0.0 0.0 0.0 0.	G 0.0 99.9 0.0 99.9 0.0 99.9 0.1 G 0.0 99.9 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.	G 0.0 0.0 0.0 100.0 0.0 0.0 99.9 0.0 0.0 G 0.0 100.0 0.0 G 0.0 G 0.0 G 0.0 0.0 0.0 0.0 99.9 0.0 99.9 0.0 0.0	Indel% 0.02 Indel% 0.027 Indel% 0.024 Indel%
Untreated Site 8 A C G T ABE6.3 Site 8 A C G T ABE7.8 Site 8 A C G G T ABE7.9 Site 8 A C G G T ABE7.9 Site 8 A C G G T ABE6.3 Site 8 A C G G T A ABE6.3 Site 8 A C G G T A ABE6.3 Site 8 A C G G T A ABE6.3 Site 8 A C G G T A ABE6.3 Site 8 A C G G T A ABE6.3 Site 8 A C G G T A ABE6.3 Site 8 A C G G T A ABE6.3 Site 8 A C G G T A ABE7.8 A C G G T A ABE7.8 A C G G T A ABE7.8 A C G G T A ABE7.8 A C G G T A ABE7.8 A C G G G T A ABE7.8 A C G G G T A ABE7.8 A C G G G A A C G G G A A C Site 8 A C G G G A A C Site 8 A C G G G A A A C Site 8 A C G G G A A A C Site 8 A C G G G G Site 8 A C Site 8 A C G G Site 8 A C G G G Site 8 A C G Site 8 A C G G Site 8 A C Site 8 A C G Site 8 A C Site 8 A C Site 8 A C Site 8 A C Site 8 A C Site 8 A C Site 8 A C Site 8 A C Site 8 A C Site 8 C Site 8 Site 8 C Site 8 C Site 8 Site 8 C Site 8 C Site 8 Site 8 C Si Site 8 Si Si Site 8 Site 8 Site 8 Site 8 Site 8 Si Site 8 Site 8 Site 8 C Si Si Si Si Si Si Si Si Si Si Si Si Si	$ \begin{array}{c} G_{1} \\ 0.0 \\ 0.0 \\ 100.0 \\ 0.0 \\ \hline G_{1} \\ 0.0 \\ \hline G_{1} \\ 0.0 \\ \hline G_{1} \\ \hline G_{2} \\ \hline G_{3} \\ \hline G_{4} \\ \hline G_{5} \\ \hline G_$	$\begin{array}{c} T_2 \\ 0.0 \\ 0.0 \\ 0.0 \\ 100.0 \\ \hline \\ T_2 \\ 0.0 \\ 0.0 \\ 0.0 \\ 99.9 \\ \hline \\ T_2 \\ 0.0 \\ 0.0 \\ 100.0 \\ \hline \\ \hline \\ T_2 \\ 0.0 \\ 0.0 \\ 100.0 \\ \hline \\ \hline \\ T_2 \\ 0.0 \\ 0.0 \\ 100.0 \\ \hline \\ \hline \\ T_2 \\ 0.0 \\ 0.0 \\ \hline \\ \hline \\ T_2 \\ 0.0 \\ 0.0 \\ \hline \\ \hline \\ T_2 \\ 0.0 \\ 0.0 \\ \hline \\ \hline \\ T_2 \\ 0.0 \\ 0.0 \\ \hline \\ \hline \\ \hline \\ \hline \\ T_2 \\ 0.0 \\ 0.0 \\ \hline \\ $	A ₃ 100.0 0.0 0.0 98.8 0.0 1.2 0.0 4 3 98.4 0.0 1.5 0.0 99.5 0.0 0.4 0.0 2 99.5	A4 100.0 0.0	A ₅ 99.9 0.0 0.1 0.0 71.7 0.0 28.3 0.0 4.5 85.2 0.0 14.8 0.0 26.3 0.0 26.3 0.0	C6 0.0 100.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0	A ₇ 100.0 0.0 0.0 0.0 96.9 0.1 3.1 0.0 98.5 0.0 1.5 0.0 1.5 0.0 1.5 0.0	A ₈ 100.0 0.0 0.0 0.0 94.0 0.0 5.9 0.0 0.0 0.0 0.9 0.0 0.9 0.0 0.9 0.0 0.0	A ₉ 100.0 0.0 0.0 0.0 0.0 98.4 0.0 99.2 0.0 0.0 99.2 0.0 99.2 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0	G ₁₀ 0.0 0.0 0.0	C11 0.0 100.0 0.0	A ₁₂ 100.0 0.0 0.0 0.0 0.0 0.0 0.0 0	T ₁₃ 0.0 0.0 0.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0	A ₁₄ 100.0 0.0 0.0 0.0 A ₁₄ 100.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0	G ₁₆ 0.1 0.1 0.0 99.9 0.0 G15 0.1 0.0 99.9 0.0 0.0 G15 0.0 0.0 99.9 0.0 0.0 G15 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0	A ₁₆ 100.0 0.0 0.0 100.0 0.0 0.0 0.0 0.0 0.0	C ₁₇ 0.0 100.0 0.0 0.0 100.0 0.0 0.0 0.0 0.0	T18 0.0 0.0 0.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0	G19 0.1 0.0 99.8 0.0 G19 0.2 0.0 99.7 0.0 G19 0.1 0.99.7 0.0 G19 0.1 0.0	A ₂₀ 100.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 100.0 0.0	G 0.0 0.0 100.0 0.0 99.9 0.0 0.0 0.0 0.0 0.0 0.0 0.	G 0.0 99.9 0.0 0.0 99.9 0.0 0.0 99.9 0.1 G 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0	G 0.0 0.0 100.0 0.0 99.9 0.0 G 0.0 0.0 100.0 0.0 0.0 0.0 99.9 0.0	Indel% 0.02 Indel% 0.027 Indel% 0.024 Indel% 0.034
Untreated Site 8 A C G T ABE6.3 Site 8 A C G T ABE7.8 Site 8 A C G T ABE7.9 Site 8 A C G T ABE7.10 Site 8 A C G T	$\begin{array}{c} G_1 \\ 0.0 \\ 0.0 \\ 100.0 \\ 0.0 \\ \hline 0.0 \\ \hline \\ 0.0 \\ \hline 0.0 \\$	T2 0.0 0.0 0.0 0.0 100.0 T2 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 100.0 T2 0.0 0.0 0.0 0.0 0.0 0.0	A ₃ 100.0 0.0 0.0 98.8 0.0 1.2 0.0 98.4 0.0 1.5 0.0 1.5 0.0 4.3 99.5 0.0 0.4 0.0 0.4 0.0 0.4 0.0	A4 100.0 0.0 0.0 0.0 0.0 0.0 0.0 98.0 0.0	A ₅ 99.9 0.0 0.1 0.0 71.7 0.0 28.3 0.0 A ₅ 85.2 0.0 14.8 0.0 26.3 0.0 26.3 0.0 26.3 0.0 48.3	C6 0.0 100.0 0.0	A ₇ 100.0 0.0 0.0 0.0 0.0 0.0 96.9 0.1 3.1 0.0 98.5 0.0 1.5 0.0 1.5 0.0 1.5 0.0 4.7 90.9	A8 100.0 0.0 0.0 0.0 0.0 94.0 0.0 99.1 0.0 0.0 99.1 0.0 99.1 0.0	A ₉ 100.0 0.0 0.0 0.0 0.0 0.0 98.4 0.0 1.6 0.0 99.2 0.0 0.8 99.2 0.0 0.8 99.2 0.0 0.8 99.4 0.0 0.8 99.4 0.0 0.6 0.0 99.4 0.0 A ₉ 99.4 0.0 A ₉ 99.5	G ₁₀ 0.0 0.0	C11 0.0 100.0 0.0	A ₁₂ 100.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.1 99.9 0.0 0.1 0.1 0.1 0.0	T ₁₃ 0.0 0.0 0.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0	A ₁₄ 100.0 0.0	$\begin{array}{c} G_{16} \\ 0.1 \\ 0.1 \\ 0.0 \\ 99.9 \\ 0.0 \\ \end{array}$	A ₁₆ 100.0 0.0 0.0 A ₁₆ 100.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0	C ₁₇ 0.0 100.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0	T ₁₈ 0.0 0.0 0.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0	G19 0.1 0.0 0.0 0.1 0.0 0.1 0.0 0.1 0.2 0.0 0.1 0.2 0.0 0.1 0.0 0.1 0.0 0.1 0.0	A ₂₀ 100.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0	G 0.0 0.0 100.0 0.0 99.9 0.0 0.0 0.0 0.0 0.0 0.0 0.	G 0.0 99.9 0.0 99.9 0.0 0.0 99.9 0.1 G 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0	G 0.0 0.0 100.0 0.0 0.0 99.9 0.0 6 0.0 100.0 0.0 100.0 0.0 99.9 0.0 100.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0	Indel% 0.02 Indel% 0.027 Indel% 0.024 Indel% 0.034 Indel% 0.062
Untreated Site 8 A C G T ABE6.3 Site 8 A C G T ABE7.8 Site 8 A C G T ABE7.9 Site 8 A C G T ABE7.10 Site 8 A C G T	$\begin{array}{c} G_1 \\ 0.0 \\ 0.0 \\ 100.0 \\ 0.0 \\ \hline \end{array} \\ \hline \\ G_1 \\ 0.0 \\ 0.0 \\ \hline \\ 0.0 \\ 0.0 \\ \hline \\ 0.0 \\ 0.0 \\ \hline 0.0 \\ \hline \\ 0.0 \\ \hline 0.0 \\ \hline 0.0 \\ \hline \\ 0.0 \\ \hline 0.0$	T2 0.0 T2 0.0 100.0	A ₃ 100.0 0.0 0.0 98.8 0.0 1.2 0.0 98.4 0.0 1.5 0.0 0.4 0.0 0.4 0.0 0.4 0.0 0.4 0.0 0.4 0.0 0.4 0.0	A4 100.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 2.0 0.0 0.0 2.0 0.0 2.0 0.0 2.0 0.0 2.2 0.0 2.2 0.0 1.0 0.0 1.0 0.0 4.4 99.0 0.0	A ₅ 99.9 0.0 0.1 0.0 71.7 0.0 28.3 0.0 As 85.2 0.0 14.8 0.0 26.3 0.0 26.3 0.0 26.3 0.0 26.3 0.0	C6 0.0 100.0 0.0	A ₇ 100.0 0.0 0.0 0.0 0.0 0.1 3.1 0.0 A ₇ 98.5 0.0 1.5 0.0 1.5 0.0 1.5 0.0 1.5 0.0 1.5 0.0 1.5 0.0	A ₈ 100.0 0.0 0.0 94.0 0.0 5.9 0.0 0.0 99.1 0.0 0.9 0.0 0.9 0.0 0.0 0.9 0.0 0.0 0.9 0.0 0.0	A ₉ 100.0 0.0 0.0 0.0 0.0 98.4 0.0 1.6 0.0 99.2 0.0 99.2 0.0 0.0 99.2 0.0 0.8 0.0 0.8 0.0 0.8 0.0 A ₉ 99.4 0.0 A ₉ 99.4 0.0	G ₁₀ 0.0 0.0	C11 0.0 100.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0	A ₁₂ 100.0 0.0 0.0 0.0 0.0 99.9 0.0 0.1 0.0 0.1 0.1 0.1 0.0 0.1 0.1 0.1 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0	T ₁₃ 0.0 0.0 0.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 0.0 100.0 0.0 100.0 0.0	A ₁₄ 100.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0	G16 0.1 0.0 99.9 0.0 0.0 G15 0.1 0.0 0.0 G16 0.0 0.0 0.0 G16 0.0 0.0 0.0 G16 0.0 0.0 0.0 G15 0.0 G15 0.0 0.0 0.0	A ₁₆ 100.0 0.0 0.0 100.0 0.0 0.0 100.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0	C ₁₇ 0.0 100.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0	T ₁₈ 0.0 0.0 0.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0	G ₁₉ 0.1 0.0 99.8 0.0 0.2 0.0 0.1 0.2 0.0 0.1 0.2 0.0 99.7 0.0 G ₁₉ 0.0 99.9 0.0 G ₁₉ 0.0 99.9 0.0 G ₁₉ 0.0 0.0	A ₂₀ 100.0 0.0 0.0 100.0 0.0 0.0 0.0 0.0 100.0 0.0	G 0.0 0.0 100.0 0.0 99.9 0.0 0.0 0.0 0.0 0.0 0.0 0.	G 0.0 99.9 0.0 99.9 0.0 0.0 0.0 0.0 0.0 0	G 0.0 G 0.0 G 0.0 0.0 0.0 0.0	Indel% 0.02 Indel% 0.027 Indel% 0.024 Indel% 0.034 Indel% 0.062
Untreated Site 8 A C G T ABE6.3 Site 8 A C G T ABE7.8 Site 8 A C G T ABE7.9 Site 8 A C G T ABE7.10 Site 8 A C G T T ABE7.10 Site 8 A C G T	$\begin{array}{c} G_1 \\ 0.0 \\ 0.0 \\ 100.0 \\ 0.0 \\ \hline \\ 0.0 0$	T2 0.0	A ₃ 100.0 0.0 0.0 98.8 0.0 1.2 0.0 1.2 0.0 1.2 0.0 1.5 0.0 0.4 0.0 0.4 0.0 0.4 0.0 0.4 0.0 0.4 0.0 0.0 0.0 0.0 0.0	A4 100.0 0.0 0.0 0.0 0.0 0.0 0.0 2.0 0.0 2.0 0.0 2.0 0.0 2.0 0.0 2.0 0.0 2.1 0.0 2.2 0.0 2.2 0.0 1.0 0.0 1.0 0.0 1.0 0.0 2.6 0.0 2.6 0.0	A ₅ 99.9 0.0 0.1 0.0 71.7 0.0 28.3 0.0 85.2 0.0 48.5 0.0 14.8 0.0 26.3 0.0 26.3 0.0 26.3 0.0 26.3 0.0 26.3 0.0 26.3 0.0 26.3 0.0 26.3 0.0 26.3 0.0	C6 0.0 100.0 0.0	A ₇ 100.0 0.0 0.0 0.0 0.0 0.1 3.1 0.0 4.7 98.5 0.0 1.5 0.0 1.5 0.0 1.5 0.0 1.5 0.0 1.5 0.0 1.5 0.0 98.5 0.0 9.0 9.0	A ₈ 100.0 0.0 0.0 94.0 0.0 5.9 0.0 5.9 0.0 0.9 0.0 0.9 0.0 0.9 0.0 0.7 0.0 0.7 0.0 0.7 0.0 0.0 0.7 0.0	A ₉ 100.0 0.0 0.0 0.0 0.0 98.4 0.0 1.6 0.0 99.2 0.0 0.8 0.0 0.8 0.0 0.8 0.0 A ₉ 99.4 0.0 0.8 0.0 0.6 0.0 A ₉ 99.4 0.0 0.5 0.0 0.5	G10 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 99.9 0.1 G10.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0	C11 0.0 100.0 0.0 0.0 0.0	A ₁₂ 100.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.1 0.1 0.1 0.1 0.1 0.0 0.0 0.0 0.0 0.0 0.0 0.1	T ₁₃ 0.0 0.0 0.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0	A ₁₄ 100.0 0.0	G15 0.1 0.0 99.9 0.0 G15 0.1 0.0 0.1 0.0 99.9 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0	A ₁₆ 100.0 0.0 0.0 100.0 0.0 0.0 0.0	C ₁₇ 0.0 100.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0	T ₁₈ 0.0 0.0 0.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0	G19 0.1 0.0 99.8 0.0 0.1 0.2 0.0 99.7 0.0 G19 0.1 0.0 99.7 0.0 G19 0.1 0.0 G19 0.0 0.0 0.0 0.0 99.9 0.0 G19 0.0 G19 0.0 99.9 0.0 99.9 0.0 99.9 0.0 99.9 0.0 9.0	A ₂₀ 100.0 0.0 0.0 100.0 0.0 0.0 0.0 0.0 0.0	G 0.0 0.0 100.0 0.0 99.9 0.0 0.0 0.0 0.0 0.0 0.0 0.	G 0.0 99.9 0.0 99.9 0.0 0.0 0.0 0.0 0.0 0	G 0.0 0.0 100.0 0.0 0.0 99.9 0.0 100.0 0.0 100.0 0.0 0.0 0.0 0.0 0.0	Indel% 0.02 Indel% 0.027 Indel% 0.024 Indel% 0.034

Untreated																								Indel%
Site 9	G ₁	A ₂	A ₃	G ₄	A ₅	C ₆	C ₇	A ₈	A ₉	G ₁₀	G ₁₁	A ₁₂	T ₁₃	A ₁₄	G ₁₅	A ₁₆	C ₁₇	T ₁₈	G ₁₉	C ₂₀	Т	G	G	0.027
A	0.0	100.0	100.0	0.0	100.0	0.0	0.0	100.0	100.0	0.0	0.0	100.0	0.0	100.0	0.0	100.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	
C	0.0	0.0	0.0	0.0	0.0	100.	0 100.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	100.0	0.0	0.0	100.0	0.0	0.0	0.0	
G T	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	100.0	0.0	0.0	0.0	0.0	100.0	0.0	0.0	100.0	0.0	0.0	
'	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	100.0	0.0	0.0	0.0	0.0	100.0	0.0	0.0	100.0	0.0	0.0	
ABE6.3																								Indel%
Site 9	G ₁	A ₂	A ₃	G ₄	A ₅	C ₆	C ₇	A ₈	A ₉	G ₁₀	G ₁₁	A ₁₂	T ₁₃	A ₁₄	G ₁₅	A ₁₆	C ₁₇	T ₁₈	G ₁₉	C ₂₀	Т	G	G	0.029
A	0.0	99.9	99.9	0.0	83.8	0.0	0.0	98.2	99.0	0.0	0.0	99.9	0.0	100.0	0.0	99.9	0.0	0.0	0.0	0.0	0.0	0.0	0.0	
С	0.0	0.0	0.0	0.0	0.0	99.9	99.9	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	100.0	0.0	0.0	100.0	0.0	0.0	0.0	
G	99.9	0.1	0.1	99.9	16.1	0.0	0.0	1.8	0.9	100.0	99.8	0.0	0.0	0.0	99.9	0.0	0.0	0.0	99.9	0.0	0.0	99.9	99.9	
I	0.0	0.0	0.0	0.1	0.1	0.0	0.1	0.0	0.0	0.0	0.1	0.0	100.0	0.0	0.0	0.0	0.0	100.0	0.1	0.0	99.9	0.1	0.1	
ABE7.8																								Indel%
Site 9	G	A	A ₂	G,	Ac	Co	C-	A	A	Gto	Gu	A	Tan	Α.,	Ger	A	Cur	Tro	Gia	Coo	Т	G	G	0.036
A	0.0	99.8	99.2	0.0	87.9	0.0	0.0	98.7	99.0	0.0	0.0	99.8	0.0	100.0	0.0	100.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	
С	0.0	0.0	0.4	0.0	0.0	100.	0 100.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	100.0	0.0	0.0	100.0	0.0	0.0	0.0	
G	99.9	0.2	0.3	100.0	12.0	0.0	0.0	1.2	1.0	100.0	99.9	0.2	0.0	0.0	100.0	0.0	0.0	0.0	99.9	0.0	0.0	99.9	99.9	
Т	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.1	0.0	100.0	0.0	0.0	0.0	0.0	100.0	0.1	0.0	100.0	0.0	0.1	
40570																								1
ABE7.9		•							•	0		•	-	٨	0		0	-	0		-		0	indel%
Site 9	G1	A ₂	A ₃	G ₄	A5	C ₆	C7	A ₈	A ₉	G ₁₀	G ₁₁	A ₁₂	I ₁₃	A ₁₄	G ₁₅	A ₁₆	C ₁₇	I 18	G ₁₉	C ₂₀	0.0	G	G	0.027
ĉ	0.0	0.0	0.1	0.0	0.0	99.0	9 99 9	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	100.0	0.0	0.0	99.9	0.0	0.0	0.0	
Ğ	99.9	0.1	0.1	100.0	13.2	0.0	0.0	0.6	0.7	100.0	99.8	0.1	0.0	0.0	99.9	0.0	0.0	0.0	99.9	0.0	0.0	99.9	99.8	
Т	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.1	0.0	100.0	0.0	0.0	0.0	0.0	100.0	0.0	0.0	100.0	0.0	0.2	
ABE7.10				r	1	1			r	r	-					-				-	-	1	r	Indel%
Site 9	G1	A ₂	A ₃	G ₄	A ₅	C ₆	C ₇	A ₈	A ₉	G ₁₀	G ₁₁	A ₁₂	T ₁₃	A ₁₄	G ₁₅	A ₁₆	C ₁₇	T ₁₈	G ₁₉	C ₂₀	T	G	G	0.051
A	0.1	99.9	99.8	0.0	61.8	0.0	0.0	95.5	98.7	0.0	0.0	99.9	0.0	99.9	0.0	100.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	
G	99.9	0.0	0.0	100.0	38.2	0.0	0 99.9	4.4	1.2	99.9	100.0	0.0	0.0	0.0	99.9	0.0	0.0	0.0	99.9	0.0	0.0	99.8	99.8	
т	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	100.0	0.0	0.1	0.0	0.0	100.0	0.1	0.0	100.0	0.1	0.2	
Untreated						_							_							-	_ 1	- 1	In	del%
Site 10	G ₁	A ₂	A ₃	C ₄	A ₅	1 ₆	A ₇	A ₈ /	A ₉ G	6 ₁₀ A	A ₁₁ A	12	I ₁₃ A	· ₁₄ (·	6 ₁₅ A	A ₁₆ A	Λ ₁₇ Ι	18 G	19 A	A ₂₀		G	G 0	.034
A	0.2	0.0	0.0	100.0	99.7	0.0	99.8			.0 10			0.0 10	0.0 0				0.0 0.					1.0	
G	99.8	0.0	0.0	0.0	0.0	0.0	0.0	0.0 0	0 10	0 0	0 0		0.0 0	0 9	99 0			0 99	9 (5.0 (5.0 (0 0 10	0.0	
т	0.0	0.0	0.0	0.0	0.0	100.0	0.0	0.0 0	0.0 0	.0 C	0.0 0	0.0 10	0.0	.0 0	.0 0	0.0 0	0.0 10	0.0 0.	0 0	D.0 10	00.0	0.0 0	0.0	
ABE6.3																							In	del%
Site 10	G ₁	A ₂	A ₃	C_4	A ₅	T ₆	A ₇	A ₈	A ₉ G	i ₁₀ A	A ₁₁ A	12	Г ₁₃ А	14	6 ₁₅ A	A ₁₆ A	Λ ₁₇ Τ	18 G	19 A	A ₂₀	Т	G	G 0	.026
A	0.2	98.4	97.7	0.0	57.6	0.0	79.8	93.4 9	7.2 0	.0 9	8.6 99	9.9 0	0.0 10	0.0 0	0.0 10	0.0 10		0.0 0.	1 10	0.00	0.0 0	0.0 0	0.0	
G	99.8	0.0	2.3	0.0	42.4	0.0	20.1	6.6 2	0.0 0	0 1	4 0	1.0 0	0.0 0	0 10				1.0 0. 1.0 99	9 (J.U (0.0 0		
т	0.0	0.0	0.0	0.0	0.0	100.0	0.0	0.0 0	0.0 0	.0 0	0.0	0.0 10	0.0 0	.0 0	0.0 0	0.0 0	0.0 10	0.0 0.	0 0	0.0 10	00.0 0	0.0 0	0.0	
ABE7.8																							In	del%
Site 10	G ₁	A ₂	A ₃	C_4	A ₅	T ₆	A ₇	A ₈	A ₉ G	i ₁₀ A	A ₁₁ A	12 7	Г ₁₃ А	- ₁₄ G	6 ₁₅ A	A ₁₆ A	Λ ₁₇ Τ	18 G	19 A	A ₂₀	Т	G	G 0	.023
Α	0.1	97.8	97.9	0.0	64.9	0.0	92.8	96.3 9	8.1 0	.0 9	9.2 99	9.9 0	0.0 10	0.0 0	.0 10	0.0 10	0.0	0.0 0.	0 10	0.00	0.0 C	0.0 0	0.0	
С	0.0	0.0	0.1	99.9	0.0	0.0	0.0	0.0 0	0.0	.0 0	0.0 0	0.0	0.0 0	.0 0	0.0	0.0 0	0.0 0	0.0 0.	0 0	0.0	0.0 0	0.0 0	0.0	
G	99.9	2.2	2.1	0.0	35.1	0.0	7.2	3.7	.9 9	9.9 0	0.8 0		0 0	.0 10				0.2 100	0.0				0.0	
'	0.0	0.0	0.0	0.0	0.0	100.0	0.0	0.0 0	.0 0	.0 0	.0 0	.0 9	9.9 0	.0 0	.0 0		.0 9.	9.0 0.	0 (5.0	00.0	.0 0	.0	
ABE7.9																							In	del%
Site 10	G₁	A ₂	A ₃	C4	As	Te	A ₇	A ₈	A. G	i10 A	A11 A	12	T13 A	14 0	A	A16 A	17 T	18 G	10	A ₂₀	Т	G	G 0	.021
A	0.1	99.6	99.3	0.0	51.9	0.0	86.5	95.8 9	8.1 0	.1 9	9.3 99	9.9 0	0.0 10	0.0 0	.0 10	0.0 10	0.0 0	0.0 0.	0 10	0.00	0.0 0.0	0.0	.0	
С	0.0	0.0	0.1	100.0	0.0	0.0	0.0	0.0 0	0.0	.0 0	0.0	0.0 (0.0 0	.0_0	.0 0	0.0 0	0.0 0	.0 _0.	0 0	0.0	0.0 0.0	0.0	.0	
G	99.9	0.4	0.6	0.0	48.1	0.0	13.5	4.2 1	.9 99	9.9 0).7 0	.1 (0.0 0	.0 10	0.0 0	0.0 0	.0 0	.2 100	0.0	0.0	0.0 10	0.0 10	0.0	
T	0.0	0.0	0.0	0.0	0.0	100.0	0.0	0.0 0	0.0 0	.0 0	0.0 0	0.0 9	9.9 0	.0 0	.0 0	0.0 0	0.0 99	9.8 0.	0 0	J.O 10	0.00	0.0 0	0.0	
ARE7 10																							In	del%
Sito 10	G	Δ.	Δ.	<u> </u>	Δ.	т.	Δ_	Δ.	A. C								Т			Δ	т	G	in G O	040
A	0.2	99.9	99.4	0.0	46.9	0.0	49.5	97.9 9	⁻⁹ 0	.0 9	9.8 10	0.0	0.0 10	0.0 0	0 10	16 P	0.0 0	18 G.	19 / 1 10	²⁰	0.0	0.0 0	0	
c	0.0	0.0	0.0	100.0	0.0	0.0	0.1	0.0 0	0.0 0	.0 0	0.0 0	0.0 (0.0 0	.0 0	.0 0	0.0 0	0.0 0	0.0 0.	0 0	0.0	0.0 C).0 O	.0	
G	99.8	0.1	0.6	0.0	53.1	0.0	50.4	2.1 1	.5 10	0.0 0).2 0	0.0 0	0.0 0	.0 10	0.0 0).O 0	0.0 0	.0 99	.9 0	0.0	0.0 10	0.0 10	0.0	
т	0 0	0.0	0.0	0.0	0.0	100.0	0.0	0.0 0		0 0		0 10		0 0			10 10		n n	10 10			0	

Untreated	l																							Indel%
Site 11	G ₁	G ₂	A_3	C ₄	A ₅	G ₆	G ₇	C ₈	A ₉	G ₁₀	C ₁₁	A ₁₂	T ₁₃	A ₁₄	G ₁₅	A ₁₆	C ₇	T ₁₈	G ₁₉	T ₂₀	G	G	G	0.023
A	0.0	0.0	100.0	0.0	100.0	0.0	0.0	0.0	100.0	0.0	0.0	100.0	0.0	100.0	0.0	100.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	-
С	0.0	0.0	0.0	100.0	0.0	0.0	0.0	100.0	0.0	0.0	100.0	0.0	0.0	0.0	0.0	0.0	100.0	0.0	0.0	0.0	0.0	0.0	0.0	
G	100.0	100.0	0.0	0.0	0.0	100.0	0.0	0.0	0.0	100.0	0.0	0.0	100.0	0.0	0.0	0.0	0.0	100.0	100.0	100.0	100.	0 100.0	0.0	
	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	100.0	0.0	0.0	0.0	0.0	100.0	0.0	100.0	0.0	0.0	0.0	
ABE6.3																								Indel%
Site 11	G ₁	G ₂	A ₃	C ₄	A ₅	G ₆	G7	C ₈	A ₉	G ₁₀	C ₁₁	A ₁₂	T ₁₃	A ₁₄	G ₁₅	A ₁₆	C ₇	T ₁₈	G ₁₉	T ₂₀	G	G	G	0.027
А	0.0	0.0	91.7	0.0	45.7	0.0	0.0	0.0	97.1	0.1	0.0	99.8	0.0	100.0	0.0	100.0	0.1	0.0	0.0	0.0	0.1	0.0	0.0	•
С	0.0	0.0	0.0	99.9	0.0	0.0	0.0	99.9	0.0	0.0	100.0	0.0	0.0	0.0	0.0	0.0	99.9	0.0	0.0	0.0	0.0	0.0	0.1	
G	100.0	100.0	8.3	0.0	54.2	99.9	99.9	0.0	2.8	99.9	0.0	0.2	0.0	0.0	99.9	0.0	0.0	0.0	99.9	0.0	99.9	99.9	99.9	
	0.0	0.0	0.0	0.1	0.0	0.0	0.0	0.1	0.0	0.0	0.0	0.0	100.0	0.0	0.1	0.0	0.0	100.0	0.0	100.0	0.0	0.0	0.0	
ABE7.8																								Indel%
Site 11	G1	G ₂	A3	C₄	A ₅	G ₆	G7	C ₈	Ag	G10	C11	A12	T13	A14	G15	A16	C ₇	T ₁₈	G19	T20	G	G	G	0.025
А	0.0	0.0	95.7	0.0	66.8	0.0	0.0	0.0	96.8	0.0	0.0	100.0	0.0	100.0	0.0	100.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	1
С	0.0	0.0	0.0	100.0	0.0	0.0	0.0	100.0	0.0	0.0	99.9	0.0	0.0	0.0	0.0	0.0	99.9	0.0	0.0	0.0	0.0	0.0	0.0	_
G	99.9	100.0	4.3	0.0	33.2	100.0	100.0	0.0	3.2	100.0	0.0	0.0	0.0	0.0	100.0	0.0	0.0	0.0	100.0	0.0	99.9	9 100.0) 99.9	
I	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	100.0	0.0	0.0	0.0	0.0	100.0	0.0	100.0	0.0	0.0	0.0	
ABE7 9																								Indel%
Site 11	Gı	Ga	A ₂	C4	A	Ge	Gz	C.	A	G10	C11	A12	T12	A14	G15	A ₁₆	C ₇	T10	G10	T20	G	G	G	0.018
A	0.0	0.0	99.1	0.0	53.7	0.0	0.0	0.0	94.4	0.0	0.0	99.9	0.0	100.0	0.0	100.0	0.1	0.0	0.0	0.0	0.0	0.0	0.0	0.010
С	0.0	0.0	0.0	99.9	0.1	0.0	0.0	99.9	0.0	0.0	100.0	0.0	0.0	0.0	0.0	0.0	99.9	0.0	0.0	0.0	0.0	0.0	0.1	
G	99.9	100.0	0.9	0.0	46.2	100.0	99.9	0.0	5.6	100.0	0.0	0.1	0.0	0.0	99.9	0.0	0.0	0.0	100.0	0.1	100.	0 100.0) 99.9	
т	0.0	0.0	0.0	0.0	0.0	0.0	0.1	0.0	0.0	0.0	0.0	0.0	100.0	0.0	0.0	0.0	0.0	100.0	0.0	99.9	0.0	0.0	0.0	
ABE7 10																								Indol%
Sito 11	G	G	۸.	C.	Δ.	G.	G-	C.	۸.	Gu	C	Δ	Т.,	Δ	Gu	Δ	C-	т.,	Gu	Т.,	G	G	G	0.051
A	0.0	0.0	97.9	0.0	50.4	0.0	0.0	0.0	95.6	0.0	0.0	99.8	0.0	99.9	0.0	100.0	0.1	0.0	0.0	0.0	0.0	0.0	0.0	0.051
С	0.0	0.0	0.0	99.9	0.1	0.0	0.0	99.9	0.0	0.0	99.9	0.0	0.0	0.0	0.0	0.0	99.9	0.0	0.0	0.0	0.0	0.0	0.1	
G	99.9	99.9	2.1	0.0	49.5	99.9	99.9	0.0	4.4	99.9	0.0	0.1	0.0	0.0	100.0	0.0	0.0	0.0	99.9	0.0	99.9	99.9	99.8	
т	0.0	0.0	0.0	0.1	0.1	0.0	0.0	0.0	0.0	0.0	0.0	0.0	100.0	0.0	0.0	0.0	0.0	100.0	0.1	100.0	0.1	0.1	0.1	
Untreated	I																							Indel%
Site 12	G ₁	T ₂	A ₃	G ₄	A ₅	A ₆	A ₇	A ₈	A ₉	G ₁₀	T ₁₁	A ₁₂	T ₁₃	A ₁₄	G ₁₅	A ₁₆	C ₇	T ₁₈	G ₁₉	C ₂₀	А	G	G	0.061
Α	0.0	0.0	99.9	0.0	100.0	100.0	100.0	100.0	100.0	0.0	0.0	99.9	0.0	99.9	0.0 1	00.0	0.0	0.0	0.1	0.0	99.9	0.1	0.0	
С	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	100.0	0.0	0.0	99.9	0.0	0.0	0.0	
G	100.0	0.0	0.0	99.9	0.0	0.0	0.0	0.0	0.0	100.0	100.0	0.0	0.0	0.0	99.9	0.0	0.0	0.0	99.9	0.0	0.0	99.9	99.9	
	0.0	100.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	100.0	0.0	33.5	0.0	0.0	0.0	0.0	00.0	0.1	0.1	0.0	0.0	0.0	
ABE6.3																								Indel%
Site 12	G ₁	T ₂	A ₃	G ₄	A ₅	A ₆	A ₇	A ₈	A ₉	G ₁₀	T ₁₁	A ₁₂	T ₁₃	A ₁₄	G ₁₅	A ₁₆	C ₇	T ₁₈	G ₁₉	C ₂₀	Α	G	G	0.12
А	0.0	0.0	98.1	0.1	74.3	88.2	93.9	94.6	94.6	0.0	0.0	99.9	0.0 1	00.0	0.1 1	00.0	0.0	0.0	0.0	0.0	99.9	0.1	0.0	
С	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	100.0	0.0	0.0	100.0	0.0	0.0	0.0	
G	100.0	0.0	1.9	99.9	25.7	11.8	6.1	5.4	5.4	100.0	0.0	0.1	0.0	0.0	99.9	0.0	0.0	0.0	99.9	0.0	0.0	99.9	99.9	
	0.0	100.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	100.0	0.0	100.0	0.0	0.0	0.0	0.0	00.0	0.0	0.0	0.0	0.0	0.0	
ABE7.8																								Indel%
Site 12	G1	T ₂	A ₃	G4	A ₅	A ₆	A ₇	A ₈	A ₉	G ₁₀	T ₁₁	A ₁₂	T ₁₃	A ₁₄	G ₁₅	A ₁₆	C ₇	T ₁₈	G ₁₉	C ₂₀	А	G	G	0.075
А	0.0	0.0	97.5	0.0	75.7	84.8	92.1	96.0	96.0	0.0	0.0	99.8	0.0 1	0.00	0.0 1	00.0	0.0	0.0	0.0	0.0	100.0	0.0	0.0	
С	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.001	0.0	0.0	100.0	0.0	0.0	0.0	
G	100.0	0.0	2.5	100.0	24.3	15.2	7.9	4.0	3.9	100.0	0.0	0.1	0.0	0.0 1	100.0	0.0	0.0	0.0 1	0.001	0.0	0.0	100.0	100.0	
I	0.0	100.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	100.0	0.0	100.0	0.0	0.0	0.0	0.0	00.0	0.0	0.0	0.0	0.0	0.0	
ARE7 9																								Indel%
Site 12	G.	Ta	A ₂	G	Ac	Ac	Α.	A	A	Gra	Tu	A ₄₀	Tra	A.,	Ger	A	C ₇	Tra	G	Con	А	G	G	0.090
A	0.0	0.0	98.9	0.0	71.2	82.1	91.0	97.5	98.1	0.0	0.0	99.9	0.0 1	00.0	0.0 1	00.0	0.0	0.0	0.1	0.0	100.0	0.0	0.0	0.000
С	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.001	0.0	0.0	99.9	0.0	0.0	0.0	
G	100.0	0.0	1.1	100.0	28.7	17.8	9.0	2.5	1.9	100.0	0.0	0.1	0.0	0.0 1	0.001	0.0	0.0	0.0	99.9	0.0	0.0	100.0	99.9	
Т	0.0	100.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	100.0	0.0	100.0	0.0	0.0	0.0	0.0 1	00.0	0.0	0.0	0.0	0.0	0.0	
ADE7 40																								Indol%
Site 12	G	т	Δ	G	Δ	Δ	Δ	Δ	Δ	G	т.	Δ.	т., Г	Δ	Gu	Δ.,	C-	т.,	Gu	C.	Δ	G	G	0 150
A	0.0	0.0	96.2	0.0	41.6	57.9	81.5	97.3	97.9	0.0	0.0	98.6	0.1 1	00.0	0.0 1	00.0	0.0	0.0	0.0	0.1	99.9	0.0	0.0	0.100
C	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	99.9	0.0	0.0	99.9	0.0	0.0	0.0	
				00.0	50.4	40.4	10 E	27	21	100.0	0.0	1 2	0.0	00	00.0	00	0.0	00	99 9	0.0	00	100.0	00.0	
G	100.0	0.0	3.8	99.9	58.4	42.1	10.5	2.1	2.1	100.0	0.0	1.5	0.0	0.0	55.5	0.0	0.0	0.0	00.0	0.0	0.0	100.0	99.9	

Untreated																								Indel%
Site 13	G ₁	A ₂	A ₃	G ₄	A ₅	T ₆	A ₇	G ₈	A ₉	G ₁₀	A ₁₁	A ₁₂	T ₁₃	A ₁₄	G ₁₅	A ₁₆	C ₇	T ₁₈	G ₁₉	C ₂₀	T	G	G	0.063
c	0.1	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	100.0	0.0	0.0	99.9	0.0	0.0	0.0	
G	99.8	0.0	0.0	99.9	0.0	0.0	0.0	99.9	0.0	99.9	0.0	0.0	0.0	0.0	99.9	0.0	0.0	0.0	99.9	0.0	0.0	99.9	100.0	
Т	0.0	0.0	0.0	0.0	0.0	100.0	0.0	0.0	0.0	0.0	0.0	0.0	100.0	0.0	0.0	0.0	0.0	100.0	0.1	0.0	100.0	0.1	0.0	
ABE6.3																								Indel%
Site 13	G ₁	A_2	A ₃	G ₄	A ₅	T ₆	A ₇	G ₈	A ₉	G ₁₀	A ₁₁	A ₁₂	T ₁₃	A ₁₄	G ₁₅	A ₁₆	C ₇	T ₁₈	G ₁₉	C ₂₀	Т	G	G	0.12
A	0.1	98.1	99.3	0.0	71.4	0.0	85.3	0.0	97.1	0.0	98.8	100.0	0.0	100.0	0.0	100.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	
G	99.9	1.8	0.7	100.0	28.6	0.0	14.7	100.0	2.9	100.0	1.1	0.0	0.0	0.0	100.0	0.0	0.0	0.0	100.0	0.0	0.0	100.0	100.0	
Т	0.0	0.0	0.0	0.0	0.0	100.0	0.0	0.0	0.0	0.0	0.0	0.0	100.0	0.0	0.0	0.0	0.0	100.0	0.0	0.0	100.0	0.0	0.0	
ABE7.8																								Indel%
Site 13	G ₁	A ₂	A ₃	G ₄	A ₅	T ₆	A ₇	G ₈	A ₉	G ₁₀	A ₁₁	A ₁₂	T ₁₃	A ₁₄	G ₁₅	A ₁₆	C ₇	T ₁₈	G ₁₉	C ₂₀	Т	G	G	0.11
A	0.0	97.9	99.1	0.0	74.4	0.0	92.8	0.0	96.2	0.0	99.4	99.9	0.0	100.0	0.0	100.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	
G	0.0	2.1	0.0	0.0	25.5	0.0	7.1	0.0	3.8	100.0	0.0	0.0	0.0	0.0	0.0	0.0	100.0	0.0	100.0	100.0	0.0	0.0	0.0	
T	0.0	0.0	0.0	0.0	0.0	100.0	0.0	0.0	0.0	0.0	0.0	0.0	100.0	0.0	0.0	0.0	0.0	100.0	0.0	0.0	100.0	0.0	0.0	
																								Indel%
Site 13	G1	A ₂	A ₃	G₄	As	Te	A ₇	Ga	A۹	G10	A11	A12	T13	A14	G15	A ₁₆	C ₇	T18	G10	C20	Т	G	G	0.150
A	0.1	99.6	99.5	0.0	66.6	0.0	83.1	0.0	96.9	0.0	99.6	99.9	0.0	100.0	0.0	100.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.100
C	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	100.0	0.0	0.0	99.9	0.0	0.0	0.0	
Т	0.0	0.4	0.0	0.0	0.0	100.0	0.0	0.0	0.0	0.0	0.4	0.1	100.0	0.0	0.0	0.0	0.0	100.0	0.0	0.0	100.0	0.0	0.0	
ABE7.10 Site 12		٨	٨	C	٨	т	٨	C	٨	<u> </u>	٨	٨	т	^	C	۸	C	т	C	C	т	C		Indel%
A	0.2	99.9	99.6	0.0	49.3	0.0	52.2	0.0	97.9	0.0	99.7	99.9	0.0	99.9	0.0	A ₁₆	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.160
С	0.0	0.0	0.0	0.0	0.0	0.0	0.1	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	99.9	0.0	0.0	100.0	0.0	0.0	0.0	
G T	99.8	0.1	0.3	99.9	50.7	0.0	47.6	99.9	2.1	99.9	0.3	0.0	0.0	0.0	99.9	0.0	0.0	0.0	99.9	0.0	0.0	99.9	99.9	
	0.0	0.0	0.0	0.1	0.1	100.0	0.1	0.0	0.0	0.0	0.0	0.0	100.0	0.0	0.0	0.0	0.0	100.0	0.1	0.0	100.0	0.1	0.0	
Untreated							•		1.				↓ -				0	-	0	Ŧ				Indel%
Untreated Site 14 A	G ₁ 0.0	G ₂ 0.0	C ₃	T ₄ 0.0	A ₅ 99.8	A ₆ 100.0	A ₇ 100.0	G ₈	A ₉ 100.0	C ₁₀ 0.0	C ₁₁ 0.0	A ₁₂ 99.9	T ₁₃	A ₁₄ 100.0	G ₁₅	A ₁₆	C ₇ 0.0	T ₁₈	G ₁₉ 0.0	T ₂₀	G 0.0	G 0.0	G 0.0	Indel% 0.029
Untreated Site 14 A C	G ₁ 0.0 0.0	G ₂ 0.0 0.0	C ₃ 0.0 99.9	T ₄ 0.0 0.0	A ₅ 99.8 0.0	A ₆ 100.0 0.0	A ₇ 100.0 0.0	G ₈ 0.0 0.0	A ₉ 100.0 0.0	C ₁₀ 0.0 100.0	C ₁₁ 0.0 99.9	A ₁₂ 99.9 0.0	T ₁₃ 0.1 2.8	A ₁₄ 100.0 0.0	G ₁₅ 0.0 0.0	A ₁₆ 100.0 0.0	C ₇ 0.0 100.0	T ₁₈ 0.0 0.0	G ₁₉ 0.0 0.0	T ₂₀ 0.0 0.0	G 0.0 0.0	G 0.0 0.0	G 0.0 0.0	Indel% 0.029
Untreated Site 14 A C G T	G ₁ 0.0 0.0 99.9	G ₂ 0.0 0.0 99.9	C ₃ 0.0 99.9 0.0	T ₄ 0.0 0.0 0.0	A ₅ 99.8 0.0 0.1	A ₆ 100.0 0.0 0.0	A ₇ 100.0 0.0 0.0	G ₈ 0.0 0.0 99.9	A ₉ 100.0 0.0 0.0	C ₁₀ 0.0 100.0 0.0	C ₁₁ 0.0 99.9 0.0	A ₁₂ 99.9 0.0 0.0 0.1	T ₁₃ 0.1 2.8 0.0 97 1	A ₁₄ 100.0 0.0 0.0 0.0	G ₁₅ 0.0 0.0 99.9	A ₁₆ 100.0 0.0 0.0	C ₇ 0.0 100.0 0.0 0.0	T ₁₈ 0.0 0.0 0.0	G ₁₉ 0.0 0.0 99.9	T ₂₀ 0.0 0.0 0.0	G 0.0 0.0 99.9	G 0.0 0.0 99.9 0.1	G 0.0 0.0 99.9	Indel% 0.029
Untreated Site 14 A C G T	G ₁ 0.0 0.0 99.9 0.0	G ₂ 0.0 0.0 99.9 0.0	C ₃ 0.0 99.9 0.0 0.0	T ₄ 0.0 0.0 0.0 100.0	A ₅ 99.8 0.0 0.1 0.0	A ₆ 100.0 0.0 0.0 0.0	A ₇ 100.0 0.0 0.0 0.0	G ₈ 0.0 0.0 99.9 0.0	A ₉ 100.0 0.0 0.0 0.0	C ₁₀ 0.0 100.0 0.0 0.0	C ₁₁ 0.0 99.9 0.0 0.0	A ₁₂ 99.9 0.0 0.0 0.1	T ₁₃ 0.1 2.8 0.0 97.1	A ₁₄ 100.0 0.0 0.0 0.0	G ₁₅ 0.0 0.0 99.9 0.0	A ₁₆ 100.0 0.0 0.0 0.0	C ₇ 0.0 100.0 0.0 0.0	T ₁₈ 0.0 0.0 0.0 100.0	G ₁₉ 0.0 0.0 99.9 0.1	T ₂₀ 0.0 0.0 0.0 100.0	G 0.0 0.0 99.9 0.1	G 0.0 0.0 99.9 0.1	G 0.0 0.0 99.9 0.0	Indel% 0.029
Untreated Site 14 A C G T ABE6.3	G ₁ 0.0 0.0 99.9 0.0	G ₂ 0.0 0.0 99.9 0.0	C ₃ 0.0 99.9 0.0 0.0	T ₄ 0.0 0.0 0.0 100.0	A ₅ 99.8 0.0 0.1 0.0	A ₆ 100.0 0.0 0.0 0.0	A ₇ 100.0 0.0 0.0	G ₈ 0.0 99.9 0.0	A ₉ 100.0 0.0 0.0 0.0	C ₁₀ 0.0 100.0 0.0 0.0	C ₁₁ 0.0 99.9 0.0 0.0	A ₁₂ 99.9 0.0 0.0 0.1	T ₁₃ 0.1 2.8 0.0 97.1	A ₁₄ 100.0 0.0 0.0 0.0	G ₁₅ 0.0 0.0 99.9 0.0	A ₁₆ 100.0 0.0 0.0 0.0	C ₇ 0.0 100.0 0.0 0.0	T ₁₈ 0.0 0.0 0.0 100.0	G ₁₉ 0.0 0.0 99.9 0.1	T ₂₀ 0.0 0.0 0.0 100.0	G 0.0 0.0 99.9 0.1	G 0.0 0.0 99.9 0.1	G 0.0 0.0 99.9 0.0	Indel%
Untreated Site 14 A C G T ABE6.3 Site 14 A	G ₁ 0.0 99.9 0.0 G ₁	G ₂ 0.0 0.0 99.9 0.0 G ₂	C ₃ 0.0 99.9 0.0 0.0 C ₃	T ₄ 0.0 0.0 100.0 T ₄	A₅ 99.8 0.0 0.1 0.0 A₅	A ₆ 100.0 0.0 0.0 0.0 A ₆ 95.1	A ₇ 100.0 0.0 0.0 0.0 A ₇ 98.6	G ₈ 0.0 99.9 0.0 G ₈ 0.0	A ₉ 100.0 0.0 0.0 0.0 0.0	C ₁₀ 0.0 100.0 0.0 0.0 C ₁₀	C ₁₁ 0.0 99.9 0.0 0.0 C ₁₁ 0.0	A ₁₂ 99.9 0.0 0.0 0.1 A ₁₂	T ₁₃ 0.1 2.8 0.0 97.1 T ₁₃	A ₁₄ 100.0 0.0 0.0 0.0 0.0	G ₁₅ 0.0 99.9 0.0 G ₁₅	A ₁₆ 100.0 0.0 0.0 0.0 A ₁₆	C ₇ 0.0 100.0 0.0 0.0 C ₇	T ₁₈ 0.0 0.0 100.0 T ₁₈	G ₁₉ 0.0 0.0 99.9 0.1 G ₁₉	T ₂₀ 0.0 0.0 100.0 T ₂₀	G 0.0 99.9 0.1 G 0.0	G 0.0 99.9 0.1 G 0.0	G 0.0 0.0 99.9 0.0 G	Indel% 0.029 Indel% 0.11
Untreated Site 14 A C G T ABE6.3 Site 14 A C	G ₁ 0.0 99.9 0.0 G ₁ 0.1	G ₂ 0.0 99.9 0.0 G ₂ 0.1 0.0	C ₃ 0.0 99.9 0.0 0.0 C ₃ 0.0 100.0	T ₄ 0.0 0.0 100.0 T ₄ 0.0 0.0	A ₅ 99.8 0.0 0.1 0.0 A ₅ 70.5 0.0	A ₆ 100.0 0.0 0.0 0.0 0.0 95.1	A ₇ 100.0 0.0 0.0 0.0 A ₇ 98.6 0.0	G ₈ 0.0 99.9 0.0 G ₈ 0.0 0.0	A ₉ 100.0 0.0 0.0 0.0 0.0 8 95.8 0.0	C ₁₀ 0.0 100.0 0.0 0.0 C ₁₀ 0.0 100.0	C ₁₁ 0.0 99.9 0.0 0.0 C ₁₁ 0.0 99.9	A ₁₂ 99.9 0.0 0.1 A ₁₂ 100.0 0.0	T ₁₃ 0.1 2.8 0.0 97.1 T ₁₃ 0.0 4.3	A ₁₄ 100.0 0.0 0.0 0.0 A ₁₄ 100.0 0.0	G ₁₅ 0.0 99.9 0.0 G ₁₅ 0.0 0.0	A ₁₆ 100.0 0.0 0.0 0.0 A ₁₆ 100.0 0.0	C ₇ 0.0 100.0 0.0 0.0 C ₇ 0.0 100.0	T ₁₈ 0.0 0.0 100.0 T ₁₈ 0.0 0.0	G ₁₉ 0.0 99.9 0.1 G ₁₉ 0.0 0.0	T ₂₀ 0.0 0.0 100.0 T ₂₀ 0.0	G 0.0 99.9 0.1 G 0.0 0.0	G 0.0 99.9 0.1 G 0.0 0.0	G 0.0 0.0 99.9 0.0 G 0.0 0.0	Indel% 0.029 Indel% 0.11
Untreated Site 14 A C G T ABE6.3 Site 14 A C G	$ \begin{array}{c} G_{1} \\ 0.0 \\ 99.9 \\ 0.0 \\ \hline G_{1} \\ 0.1 \\ 0.0 \\ 99.9 \\ 9.4 \\ \hline \end{array} $	G_2 0.0 99.9 0.0 G_2 0.1 0.0 99.9	C ₃ 0.0 99.9 0.0 0.0 C ₃ 0.0 100.0 0.0	T ₄ 0.0 0.0 100.0 T ₄ 0.0 0.0 0.0	A₅ 99.8 0.0 0.1 0.0 A₅ 70.5 0.0 29.5	A ₆ 100.0 0.0 0.0 0.0 4.6 95.1 0.0 4.9	A ₇ 100.0 0.0 0.0 0.0 A ₇ 98.6 0.0 1.4	G ₈ 0.0 99.9 0.0 G ₈ 0.0 0.0 99.9	A ₉ 100.0 0.0 0.0 0.0 4.9 95.8 0.0 4.2	C ₁₀ 0.0 100.0 0.0 0.0 C ₁₀ 0.0 100.0 0.0	C ₁₁ 0.0 99.9 0.0 0.0 C ₁₁ 0.0 99.9 0.0	A ₁₂ 99.9 0.0 0.1 A ₁₂ 100.0 0.0 0.0 0.0	T ₁₃ 0.1 2.8 0.0 97.1 T ₁₃ 0.0 4.3 0.0	A ₁₄ 100.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0	$\begin{array}{c} G_{15} \\ 0.0 \\ 0.0 \\ 99.9 \\ 0.0 \\ \end{array}$	A ₁₆ 100.0 0.0 0.0 0.0 A ₁₆ 100.0 0.0 0.0	C ₇ 0.0 100.0 0.0 0.0 C ₇ 0.0 100.0 0.0	T ₁₈ 0.0 0.0 100.0 100.0 T ₁₈ 0.0 0.0 0.0	G ₁₉ 0.0 99.9 0.1 G ₁₉ 0.0 0.0 99.9	T ₂₀ 0.0 0.0 100.0 T ₂₀ 0.0 0.0 0.0 0.0	G 0.0 99.9 0.1 G 0.0 0.0 99.9	G 0.0 99.9 0.1 G 0.0 0.0 100.0	G 0.0 99.9 0.0 G 0.0 0.0 100.0	Indel% 0.029 Indel% 0.11
Untreated Site 14 A C G T ABE6.3 Site 14 A C G T	$\begin{array}{c} G_1 \\ 0.0 \\ 0.0 \\ 99.9 \\ 0.0 \\ \hline \\ G_1 \\ 0.1 \\ 0.0 \\ 99.9 \\ 0.1 \\ \end{array}$	G ₂ 0.0 99.9 0.0 G ₂ 0.1 0.0 99.9 0.0	C ₃ 0.0 99.9 0.0 0.0 C ₃ 0.0 100.0 0.0	T ₄ 0.0 0.0 100.0 T ₄ 0.0 0.0 0.0 100.0	A ₅ 99.8 0.0 0.1 0.0 A ₅ 70.5 0.0 29.5 0.0	$\begin{array}{c} A_6 \\ 100.0 \\ 0.0 \\ 0.0 \\ 0.0 \\ 95.1 \\ 0.0 \\ 4.9 \\ 0.0 \\ \end{array}$	A ₇ 100.0 0.0 0.0 0.0 A ₇ 98.6 0.0 1.4 0.0	G ₈ 0.0 99.9 0.0 99.9 0.0 99.9 0.0 99.9 0.0 99.9 0.0 99.9 0.0 99.9 0.0 99.9 0.0	A ₉ 100.0 0.0 0.0 95.8 0.0 4.2 0.0	C ₁₀ 0.0 100.0 0.0 0.0 100.0 0.0 0.0 0.0	C ₁₁ 0.0 99.9 0.0 0.0 C ₁₁ 0.0 99.9 0.0 0.0	A ₁₂ 99.9 0.0 0.1 A ₁₂ 100.0 0.0 0.0 0.0	T ₁₃ 0.1 2.8 0.0 97.1 T ₁₃ 0.0 4.3 0.0 95.7	A ₁₄ 100.0 0.0 0.0 0.0 0.0 100.0 0.0 0.0	G ₁₅ 0.0 99.9 0.0 G ₁₅ 0.0 99.9 0.0	A ₁₆ 100.0 0.0 0.0 0.0 100.0 0.0 0.0 0.0 0.0	C7 0.0 100.0 0.0 0.0 C7 0.0 100.0 0.0 0.0	T ₁₈ 0.0 0.0 100.0 T ₁₈ 0.0 0.0 0.0 100.0	G ₁₉ 0.0 99.9 0.1 G ₁₉ 0.0 0.0 99.9 0.0	T ₂₀ 0.0 0.0 100.0 T ₂₀ 0.0 0.0 0.0 100.0	G 0.0 99.9 0.1 G 0.0 0.0 99.9 0.0	G 0.0 99.9 0.1 G 0.0 0.0 0.0 0.0	G 0.0 99.9 0.0 G 0.0 0.0 100.0 0.0	Indel% 0.029 Indel% 0.11
Untreated Site 14 A C G T ABE6.3 Site 14 A C G T T ABE7.8	$ \begin{array}{c} G_1 \\ 0.0 \\ 99.9 \\ 0.0 \\ \hline G_1 \\ 0.1 \\ 0.9 \\ 99.9 \\ 0.1 \\ \end{array} $	G ₂ 0.0 99.9 0.0 G ₂ 0.1 0.0 99.9 0.0	C ₃ 0.0 99.9 0.0 0.0 C ₃ 100.0 0.0 0.0	T ₄ 0.0 0.0 100.0 T ₄ 0.0 0.0 0.0 100.0	A₅ 99.8 0.0 0.1 0.0 A₅ 70.5 0.0 29.5 0.0	A ₆ 100.0 0.0 0.0 0.0 95.1 0.0 4.9 0.0	A ₇ 100.0 0.0 0.0 0.0 A ₇ 98.6 0.0 1.4 0.0	G ₈ 0.0 99.9 0.0 G ₈ 0.0 99.9 0.0	A ₉ 100.0 0.0 0.0 95.8 0.0 4.2 0.0	C ₁₀ 0.0 100.0 0.0 0.0 C ₁₀ 0.0 100.0 0.0	C ₁₁ 0.0 99.9 0.0 0.0 0.0 99.9 0.0 0.0	A ₁₂ 99.9 0.0 0.1 A ₁₂ 100.0 0.0 0.0 0.0	T ₁₃ 0.1 2.8 0.0 97.1 T ₁₃ 0.0 4.3 0.0 95.7	A ₁₄ 100.0 0.0 0.0 0.0 100.0 0.0 0.0 0.0	G ₁₅ 0.0 99.9 0.0 G ₁₅ 0.0 99.9 0.0	A ₁₆ 100.0 0.0 0.0 0.0 100.0 0.0 0.0 0.0	C7 0.0 100.0 0.0 0.0 C7 0.0 100.0 0.0	T ₁₈ 0.0 0.0 100.0 T ₁₈ 0.0 0.0 0.0 100.0	G ₁₉ 0.0 99.9 0.1 G ₁₉ 0.0 0.0 99.9 0.0	T ₂₀ 0.0 0.0 100.0 100.0 0.0 0.0 0.0 100.0	G 0.0 99.9 0.1 G 0.0 99.9 0.0	G 0.0 99.9 0.1 G 0.0 0.0 100.0	G 0.0 99.9 0.0 G 0.0 0.0 100.0 0.0	Indel% 0.029 Indel% 0.11 Indel%
Untreated Site 14 A C G T ABE6.3 Site 14 A C G T T ABE7.8 Site 14	$ \begin{array}{c} G_{1} \\ 0.0 \\ 99.9 \\ 0.0 \\ \hline G_{1} \\ 0.1 \\ 99.9 \\ 0.1 \\ \hline G_{1} \\ 0.0 \\ \hline 0.1 \\ \hline 0.1 \\ \hline 0.0 \\ \hline 0.1 \\ \hline 0.1 \\ \hline 0.0 \\ \hline 0.1 \\ \hline 0.0 \\ \hline 0.1 $	G ₂ 0.0 99.9 0.0 G ₂ 0.1 0.0 99.9 0.0 G ₂	C ₃ 0.0 99.9 0.0 0.0 C ₃ 0.0 100.0 0.0 0.0 0.0	T ₄ 0.0 0.0 100.0 T ₄ 0.0 0.0 100.0 T ₄ 0.0 100.0	A ₅ 99.8 0.0 0.1 0.0 70.5 0.0 29.5 0.0 29.5 0.0	A ₆ 100.0 0.0 0.0 95.1 0.0 4.9 0.0 A ₆ 0.0	A ₇ 100.0 0.0 0.0 0.0 98.6 0.0 1.4 0.0 1.4 0.0	G ₈ 0.0 99.9 0.0 G ₈ 0.0 99.9 0.0 99.9 0.0 99.9 0.0	A ₉ 100.0 0.0 0.0 95.8 0.0 4.2 0.0 4.2 0.0	C ₁₀ 0.0 100.0 0.0 0.0 100.0 0.0 0.0 0.0 C ₁₀ 0.0 0.0	C ₁₁ 0.0 99.9 0.0 0.0 C ₁₁ 0.0 99.9 0.0 0.0 C ₁₁	A ₁₂ 99.9 0.0 0.1 100.0 0.0 0.0 0.0 0.0 0.0	T ₁₃ 0.1 2.8 0.0 97.1 T ₁₃ 0.0 4.3 0.0 95.7 T ₁₃	A ₁₄ 100.0 0.0 0.0 0.0 100.0 0.0 0.0 0.0 0.0	$\begin{array}{c} G_{15} \\ 0.0 \\ 0.0 \\ 99.9 \\ 0.0 \\ \end{array}$	A ₁₆ 100.0 0.0 0.0 0.0 100.0 0.0 0.0 0.0 0.0	C ₇ 0.0 100.0 0.0 0.0 C ₇ 0.0 100.0 0.0 0.0	T ₁₈ 0.0 0.0 100.0 T ₁₈ 0.0 0.0 100.0 T ₁₈	G ₁₉ 0.0 99.9 0.1 G ₁₉ 0.0 0.0 99.9 0.0 G ₁₉	T ₂₀ 0.0 0.0 100.0 T ₂₀ 0.0 0.0 100.0 T ₂₀	G 0.0 99.9 0.1 G 0.0 99.9 0.0 99.9 0.0	G 0.0 99.9 0.1 G 0.0 0.0 100.0 0.0	G 0.0 99.9 0.0 G 0.0 0.0 100.0 0.0	Indel% 0.029 Indel% 0.11 Indel% 0.096
Untreated Site 14 A C G T ABE6.3 Site 14 A C G T T ABE7.8 Site 14 A C C G T C G T C G T C G T C G T C Site 14 C C G C C C C C C C C C C C C C C C C	$\begin{array}{c} G_1 \\ 0.0 \\ 0.0 \\ 99.9 \\ 0.0 \\ \hline \\ 0.1 \\ 0.1 \\ 0.0 \\ 99.9 \\ 0.1 \\ \hline \\ G_1 \\ 0.0 \\ 0.0 \\ \hline \end{array}$	G ₂ 0.0 99.9 0.0 G ₂ 0.1 0.0 99.9 0.0 G ₂ 0.0 0.0	C ₃ 0.0 99.9 0.0 0.0 100.0 100.0 0.0 0.0 0.0 100.0 100.0	$\begin{array}{c} T_4 \\ 0.0 \\ 0.0 \\ 100.0 \\ \hline 100.0 \\ \hline 100.0 \\ 0.0 \\ 100.0 \\ \hline 100.0 \\ \hline T_4 \\ 0.0 \\ 0.0 \\ \hline 0.0 \\ 0.0 \\ \hline \end{array}$	A ₅ 99.8 0.0 0.1 0.0 70.5 0.0 29.5 0.0 92.5 0.0 92.5 0.0	A ₆ 100.0 0.0 0.0 0.0 4.9 0.0 4.9 0.0 A ₆ 94.9 0.0	A ₇ 100.0 0.0 0.0 0.0 98.6 0.0 1.4 0.0 A ₇ 98.4 0.0	G ₈ 0.0 99.9 0.0 G ₈ 0.0 99.9 0.0 99.9 0.0 99.9 0.0	A ₉ 100.0 0.0 0.0 0.0 0.0 0.0 4.2 0.0 4.2 0.0 4.2 0.0 4.2 0.0	C ₁₀ 0.0 100.0 0.0 0.0 100.0 0.0 100.0 0.0 0	C11 0.0 99.9 0.0	A ₁₂ 99.9 0.0 0.1 100.0 0.0 0.0 0.0 0.0 0.0 100.0 0.0	T ₁₃ 0.1 2.8 0.0 97.1 T ₁₃ 0.0 4.3 0.0 95.7 T ₁₃ 0.0 4.3	A ₁₄ 100.0 0.0 0.0 0.0 A ₁₄ 100.0 0.0 0.0 A ₁₄ 100.0 0.0	$\begin{array}{c} G_{15} \\ 0.0 \\ 0.0 \\ 99.9 \\ 0.0 \\ \hline \\ G_{15} \\ 0.0 \\ 0.0 \\ \hline \\ 99.9 \\ 0.0 \\ \hline \\ G_{15} \\ 0.0 \\ \hline \\ 0.0 \\ 0.0 \\ \hline \end{array}$	A ₁₆ 100.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0	C ₇ 0.0 100.0 0.0 0.0 100.0 0.0 100.0 0.0 C ₇ C ₇ 0.0 100.0	T ₁₈ 0.0 0.0 100.0 T ₁₈ 0.0 0.0 100.0 T ₁₈ 0.0 0.0 0.0	G ₁₉ 0.0 99.9 0.1 G ₁₉ 0.0 99.9 0.0 99.9 0.0 G ₁₉ 0.0 0.0	T ₂₀ 0.0 0.0 100.0 T ₂₀ 0.0 0.0 100.0 T ₂₀ 0.0 0.0	G 0.0 99.9 0.1 G 0.0 99.9 0.0 99.9 0.0	G 0.0 99.9 0.1 G 0.0 0.0 100.0 0.0 G 0.0 0.0	G 0.0 99.9 0.0 99.9 0.0 0.0 100.0 0.0 0.0 0.0	Indel% 0.029 0.11 0.11 Indel% 0.096
Untreated Site 14 A C G T ABE6.3 Site 14 A C G T T ABE7.8 Site 14 A C G T C G G T	$\begin{array}{c} G_1 \\ 0.0 \\ 0.0 \\ 99.9 \\ 0.0 \\ \hline \\ 0.1 \\ 0.0 \\ 99.9 \\ 0.1 \\ \hline \\ G_1 \\ 0.0 \\ 0.0 \\ 100.0 \\ \end{array}$	$\begin{array}{c} G_2 \\ 0.0 \\ 0.0 \\ 99.9 \\ 0.0 \\ \end{array}$ $\begin{array}{c} G_2 \\ 0.1 \\ 0.0 \\ 99.9 \\ 0.0 \\ \end{array}$ $\begin{array}{c} G_2 \\ 0.0 \\ 0.0 \\ 0.0 \\ 100.0 \\ \end{array}$	C3 0.0 99.9 0.0	T4 0.0 0.0 0.0 100.0 T4 0.0 0.0 100.0 T4 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0	A ₅ 99.8 0.0 0.1 0.0 70.5 0.0 29.5 0.0 99.5 0.0 29.5 0.0 70.5 0.0 29.5 0.0 7.5	A ₆ 100.0 0.0 0.0 0.0 0.0 0.0 4.9 0.0 4.9 0.0 4.9 0.0 5.1	A ₇ 100.0 0.0 0.0 98.6 0.0 1.4 0.0 A ₇ 98.4 0.0 1.6	G ₈ 0.0 99.9 0.0 99.9 0.0 99.9 0.0 99.9 0.0 99.9 0.0 99.9 0.0 90.0 0.0	A ₉ 100.0 0.0 0.0 0.0 0.0 0.0 4.2 0.0 4.2 0.0 4.2 0.0 3.4	C ₁₀ 0.0 100.0 0.0 0.0 100.0 0.0 100.0 0.0 0	C11 0.0 99.9 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0	A ₁₂ 99.9 0.0 0.1 A ₁₂ 100.0 0.0 0.0 0.0 100.0 0.0 0.0	T ₁₃ 0.1 2.8 0.0 97.1 T ₁₃ 0.0 4.3 0.0 95.7 T ₁₃ 0.0 4.3 0.0 4.3 0.0 4.3 0.0	A ₁₄ 100.0 0.0 0.0 0.0 A ₁₄ 100.0 0.0 0.0 0.0 0.0 0.0 0.0 0	G ₁₅ 0.0 99.9 0.0 G ₁₅ 0.0 99.9 0.0 G ₁₅ 0.0 G ₁₅ 0.0 0.0	A ₁₆ 100.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0	C ₇ 0.0 100.0 0.0 0.0 0.0 100.0 0.0 0.0 0.0	T ₁₈ 0.0 0.0 0.0 100.0 T ₁₈ 0.0 0.0 0.0 0.0 0.0 0.0 0.0 T ₁₈ 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0	G ₁₉ 0.0 99.9 0.1 G ₁₉ 0.0 99.9 0.0 99.9 0.0 99.9 0.0 90.0 0.0	T ₂₀ 0.0 0.0 100.0 100.0 100.0 100.0 100.0 100.0	G 0.0 99.9 0.1 G 0.0 99.9 0.0 99.9 0.0 G G 0.0 99.9	G 0.0 99.9 0.1 G 0.0 0.0 100.0 0.0 G 0.0 0.0 100.0	G 0.0 99.9 0.0 G 0.0 0.0 100.0 0.0 G 0.0 0.0 100.0 100.0	Indel% 0.029 0.11 0.11 Indel% 0.096
Untreated Site 14 A C G T ABE6.3 Site 14 A C G T ABE7.8 Site 14 A C G T	G1 0.0 0.0 99.9 0.0 99.9 0.0 99.9 0.1 0.1 0.1 0.1 0.1 0.0 100.0 0.0	G2 0.0 0.0 99.9 0.0 0.0 99.9 0.0 99.9 0.0 99.9 0.0 99.9 0.0 90.0 0.0 90.0 0.0 0.0 0.0 0.0 0.0 0.0	C3 0.0 99.9 0.0	T4 0.0 0.0 0.0 100.0 T4 0.0 100.0 T4 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 100.0	A ₅ 99.8 0.0 0.1 0.0 70.5 0.0 29.5 0.0 7.5 0.0 7.5 0.0	A ₆ 100.0 0.0 0.0 0.0 95.1 0.0 4.9 0.0 4.9 0.0 4.9 0.0 5.1 0.0	A ₇ 100.0 0.0 0.0 0.0 0.0 98.6 0.0 1.4 0.0 1.4 0.0 1.4 0.0 1.4 0.0	G ₈ 0.0 99.9 0.0 99.9 0.0 99.9 0.0 99.9 0.0 99.9 0.0 99.9 0.0 90.0 0.0	A ₉ 100.0 0.0 0.0 0.0 0.0 0.0 4.2 0.0 4.2 0.0 4.2 0.0 3.4 0.0	C ₁₀ 0.0 100.0 0.0 0.0 100.0 0.0 100.0 0.0 0	C11 0.0 99.9 0.0	A ₁₂ 99.9 0.0 0.1 100.0 0.0 0.1 412 100.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0	T ₁₃ 0.1 2.8 0.0 97.1 T ₁₃ 0.0 4.3 0.0 95.7 T ₁₃ 0.0 4.3 0.0 4.3 0.0 95.7	A ₁₄ 100.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0	$\begin{array}{c} G_{15} \\ 0.0 \\ 99.9 \\ 0.0 \\ \end{array}$	A ₁₆ 100.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0	C7 0.0 100.0 0.0 0.0 100.0 0.0 100.0 0.0 C7 0.0 100.0 0.0 0.0 0.0	T ₁₈ 0.0 0.0 0.0 100.0 T ₁₈ 0.0 0.0 0.0 0.0 0.0 0.0 0.0 100.0 T ₁₈ 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0	G ₁₉ 0.0 99.9 0.1 G ₁₉ 0.0 99.9 0.0 99.9 0.0 0.0 0.0 0.0 0.0 0	T ₂₀ 0.0 0.0 100.0 T ₂₀ 0.0 0.0 0.0 100.0 100.0 100.0 100.0	G 0.0 99.9 0.1 G 0.0 99.9 0.0 99.9 0.0 G G 0.0 99.9 0.0	G 0.0 99.9 0.1 G 0.0 0.0 100.0 0.0 G 0.0 0.0 100.0 0.0	G 0.0 99.9 0.0 G 0.0 100.0 0.0 G 0.0 0.0 100.0 0.0 100.0 0.0	Indel% 0.029 0.11 0.11 Indel% 0.096
Untreated Site 14 A C G T ABE6.3 Site 14 A C G T ABE7.8 Site 14 A C G T ABE7.9	$\begin{array}{c} G_1 \\ 0.0 \\ 0.0 \\ 99.9 \\ 0.0 \\ \hline \\ 0.1 \\ 0.0 \\ 99.9 \\ 0.1 \\ \hline \\ G_1 \\ 0.0 \\ 0.0 \\ 100.0 \\ 0.0 \\ \hline \end{array}$	G2 0.0 99.9 0.0 99.9 0.0 99.9 0.0 99.9 0.0 99.9 0.0 99.9 0.0 0.0 0.0 0.0 0.0 0.0 0.0	C ₃ 0.0 99.9 0.0 0.0 0.0 0.0 100.0 0.0 C ₃ 0.0 100.0 0.0 100.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0	T ₄ 0.0 0.0 0.0 100.0 T ₄ 0.0 0.0 100.0 T ₄ 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0	A ₅ 99.8 0.0 0.1 0.0 70.5 0.0 29.5 0.0 7.5 0.0 7.5 0.0	A ₆ 100.0 0.0 0.0 0.0 95.1 0.0 4.9 0.0 94.9 0.0 5.1 0.0 5.1 0.0	A ₇ 100.0 0.0 0.0 0.0 98.6 0.0 1.4 0.0 1.4 0.0 1.6 0.0	G8 0.0 0.0 99.9 0.0 99.9 0.0 99.9 0.0 99.9 0.0 99.9 0.0 99.9 0.0 99.9 0.0 99.9 0.0 90.0 100.0 0.0 0.0	Ag 100.0 0.0 0.0 0.0 0.0 0.0 95.8 0.0 4.2 0.0 4.2 0.0 96.6 0.0 3.4 0.0	C ₁₀ 0.0 100.0 0.0 0.0 100.0 0.0 100.0 0.0 0	C11 0.0 99.9 0.0	A12 99.9 0.0 0.0 0.0 0.1 100.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0	T ₁₃ 0.1 2.8 0.0 97.1 T ₁₃ 0.0 95.7 T ₁₃ 0.0 4.3 0.0 95.7	A ₁₄ 100.0 0.0 0.0 0.0 100.0 0.0 0.0 0.0 0.0	$\begin{array}{c} G_{15} \\ 0.0 \\ 0.0 \\ 99.9 \\ 0.0 \\ \hline \\ 0.0 \\ 99.9 \\ 0.0 \\ \hline \\ 99.9 \\ 0.0 \\ \hline \\ G_{15} \\ 0.0 \\ 0.0 \\ \hline \\ 100.0 \\ 0.0 \\ \hline \end{array}$	A ₁₆ 100.0 0.0 0.0 100.0 0.0 0.0 0.0 0.0 0.0	C ₇ 0.0 100.0 0.0 0.0 100.0 0.0 0.0 0.0 0.0	T ₁₈ 0.0 0.0 100.0 T ₁₈ 0.0 0.0 0.0 100.0 T ₁₈ 0.0 0.0 0.0 100.0	G ₁₉ 0.0 99.9 0.1 G ₁₉ 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.	T ₂₀ 0.0 0.0 0.0 100.0 100.0 100.0 100.0 100.0 0.0	G 0.0 99.9 0.1 G 0.0 99.9 0.0 99.9 0.0 G G 0.0 99.9 0.0	G 0.0 99.9 0.1 G 0.0 100.0 0.0 100.0 0.0 100.0 0.0	G 0.0 99.9 0.0 0.0 100.0 0.0 100.0 0.0 100.0 0.0 100.0 0.0	Indel% 0.029 0.11 0.11 Indel% 0.096
Untreated Site 14 A C G T ABE6.3 Site 14 A C G T ABE7.8 Site 14 A C G T ABE7.9 Site 14	$\begin{array}{c} G_1 \\ 0.0 \\ 0.0 \\ 99.9 \\ 0.0 \\ \hline \\ 0.1 \\ 0.0 \\ 99.9 \\ 0.1 \\ \hline \\ G_1 \\ 0.0 \\ 100.0 \\ 0.0 \\ \hline \\ G_1 \\ \hline \end{array}$	G2 0.0 99.9 0.0 99.9 0.0 99.9 0.0 99.9 0.0 99.9 0.0 90.0 0.0	C3 0.0 99.9 0.0	T4 0.0 0.0 0.0 0.0 100.0 T4 0.0 0.0 100.0 T4 0.0 0.0 100.0 T4 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 100.0 T4	A ₅ 99.8 0.0 0.1 0.0 70.5 0.0 29.5 0.0 7.5 0.0 7.5 0.0 7.5 0.0	A ₆ 100.0 0.0 0.0 95.1 0.0 4.9 0.0 5.1 0.0 5.1 0.0	A ₇ 100.0 0.0 0.0 98.6 0.0 1.4 0.0 1.4 0.0 1.6 0.0 1.6 0.0	G8 0.0 0.0 99.9 0.0 99.9 0.0 99.9 0.0 99.9 0.0 99.9 0.0 99.9 0.0 99.9 0.0 90.0 90.0 90.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0	A _g 100.0 0.0 0.0 0.0 0.0 95.8 0.0 4.2 0.0 4.2 0.0 4.2 0.0 4.2 0.0 4.2 0.0 4.2 0.0 4.2 0.0 4.2 0.0 4.2 0.0 A _g 96.6 0.0 3.4 0.0 A _g	C10 0.0 100.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0	C ₁₁ 0.0 99.9 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.	A12 99.9 0.0 0.0 0.0 0.1 100.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0	T ₁₃ 0.1 2.8 0.0 97.1 T ₁₃ 0.0 95.7 T ₁₃ 0.0 95.7 T ₁₃ 0.0 95.7 T ₁₃ 0.0 95.7	A ₁₄ 100.0 0.0 0.0 0.0 100.0 0.0 0.0 0.0 0.0	G ₁₅ 0.0 99.9 0.0 G ₁₅ 0.0 G ₁₅ 0.0 G ₁₅ 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.	A ₁₆ 100.0 0.0 0.0 100.0 0.0 0.0 0.0	C7 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.	T ₁₈ 0.0 0.0 100.0 100.0 T ₁₈ 0.0 0.0 100.0 T ₁₈ T ₁₈ T ₁₈	G ₁₉ 0.0 99.9 0.1 G ₁₉ 0.0 99.9 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.	T ₂₀ 0.0 0.0 0.0 100.0 0.0 0.0 0.0 0.0 0.0 0	G 0.0 0.0 99.9 0.1 G 0.0 99.9 0.0 G G 0.0 0.0 99.9 0.0	G 0.0 99.9 0.1 6 0.0 0.0 100.0 0.0 100.0 0.0 100.0 0.0 100.0 0.0	G 0.0 99.9 0.0 0.0 100.0 0.0 100.0 0.0 100.0 0.0 100.0 0.0	Indel% 0.029 0.11 0.11 Indel% 0.096
Untreated Site 14 A C G T ABE6.3 Site 14 A C G T ABE7.8 Site 14 A C G T ABE7.9 Site 14 A C G T ABE7.9 Site 14	$\begin{array}{c} G_1 \\ 0.0 \\ 0.0 \\ 99.9 \\ 0.0 \\ \hline \\ 0.1 \\ 0.0 \\ 99.9 \\ 0.1 \\ \hline \\ G_1 \\ 0.0 \\ 100.0 \\ 0.0 \\ \hline \\ G_1 \\ 0.0 \\ \hline \end{array}$	G2 0.0 0.0 99.9 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 99.9 0.0 99.9 0.0 90.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0	C3 0.0 99.9 0.0	T4 0.0 0.0 0.0 0.0 100.0 T4 0.0 0.0 100.0 T4 0.0 0.0 100.0 T4 0.0 0.0 100.0 T4 0.0 0.0 100.0	A ₅ 99.8 0.0 0.1 0.0 29.5 0.0 7.5 0.0 7.5 0.0 7.5 0.0 7.5 0.0	A ₆ 100.0 0.0 0.0 95.1 0.0 4.9 0.0 5.1 0.0 5.1 0.0 5.1 0.0 5.1 0.0	A7 100.0 0.0 0.0 0.0 0.0 98.6 0.0 1.4 0.0 1.6 0.0 1.6 0.0 A7 98.4 0.0	G8 0.0 0.0 99.9 0.0 99.9 0.0 99.9 0.0 99.9 0.0 99.9 0.0 99.9 0.0 99.9 0.0 90.0 90.0 90.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0	A ₀ 100.0 0.0 0.0 0.0 0.0 0.0 95.8 0.0 4.2 0.0 4.2 0.0 4.2 0.0 4.2 0.0 4.2 0.0 4.2 0.0 4.2 0.0 4.2 0.0 4.2 0.0 A ₀ 96.6 0.0 3.4 0.0 A ₀ 98.5 0.0	C10 0.0 100.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0	C11 0.0 99.9 0.0	A12 99.9 0.0 0.1 100.0 0.0 0.1 A12 100.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0	T ₁₃ 0.1 2.8 0.0 97.1 T ₁₃ 0.0 95.7 T ₁₃ 0.0 95.7 T ₁₃ 0.0 95.7	A ₁₄ 100.0 0.0 0.0 100.0 0.0 0.0 0.0	G ₁₅ 0.0 0.0 99.9 0.0 G ₁₅ 0.0 0.0 G ₁₅ 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.	A ₁₆ 100.0 0.0 0.0 100.0 0.0 0.0 0.0	C7 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.	T ₁₈ 0.0 0.0 100.0 T ₁₈ 0.0 0.0 100.0 T ₁₈ 0.0 0.0 0.0 0.0 0.0 100.0 T ₁₈ 0.0 0.0 100.0 T ₁₈ 0.0 0.0	G ₁₉ 0.0 0.0 99.9 0.1 G ₁₉ 0.0 99.9 0.0 G ₁₉ 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.	T ₂₀ 0.0 0.0 100.0 T ₂₀ 0.0 0.0 0.0 100.0 T ₂₀ 0.0 0.0 0.0 100.0 100.0	G 0.0 0.0 99.9 0.1 G 0.0 99.9 0.0 99.9 0.0 G G 0.0 0.0 99.9 0.0 0.0 99.9 0.0 0.0 0.0 0	G 0.0 99.9 0.1 G 0.0 0.0 100.0 0.0 100.0 0.0 100.0 0.0 0	G 0.0 99.9 0.0 0.0 0.0 100.0 0.0 100.0 0.0 100.0 0.0	Indel% 0.029 0.11 0.11 Indel% 0.096 Indel% 0.078
Untreated Site 14 A C G T ABE6.3 Site 14 A C G T ABE7.8 Site 14 A C G T ABE7.9 Site 14 A C G G T ABE7.9 Site 14 G G G T	G1 0.0 0.0 99.9 0.0 99.9 0.0 99.9 0.1 0.1 0.1 0.1 0.1 0.0 100.0 0.0 0.0 99.9	G2 0.0 0.0 99.9 0.0 0.0 99.9 0.0 0.0 99.9 0.0 99.9 0.0 99.9 0.0 99.9 0.0 90.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0	C3 0.0 99.9 0.0	T4 0.0 0.0 0.0 100.0 T4 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 100.0 T4 0.0 0.0 100.0	A ₅ 99.8 0.0 0.1 0.0 29.5 0.0 7.5 0.0 7.5 0.0 7.5 0.0 7.5 0.0 7.5 0.0	A ₆ 100.0 0.0 0.0 95.1 0.0 4.9 0.0 4.9 0.0 5.1 0.0 4.9 0.0 5.1 0.0 4.9 7.9	A7 100.0 0.0 0.0 0.0 0.0 98.6 0.0 1.4 0.0 1.6 0.0 1.6 0.0 A7 98.4 0.0 2.6	G8 0.0 0.0 99.9 0.0 99.9 0.0 99.9 0.0 99.9 0.0 99.9 0.0 99.9 0.0 99.9 0.0 90.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0	Ag 100.0 0.0 0.0 0.0 0.0 0.0 95.8 0.0 4.2 0.0 4.2 0.0 4.2 0.0 4.2 0.0 4.2 0.0 4.2 0.0 4.2 0.0 4.2 0.0 4.2 0.0 4.2 0.0 4.2 0.0 4.2 0.0 4.2 0.0 4.2 0.0 4.2 0.0 3.4 0.0 4.3 0.0 4.4 0.0 3.4 0.0 1.5	C10 0.0 100.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0	C11 99.9 0.0	A12 99.9 0.0 0.1 100.0 0.0 0.1 A12 100.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0	T ₁₃ 0.1 2.8 0.0 97.1 713 0.0 97.1 713 0.0 95.7 713 0.0 95.7 713 0.0 95.7 713 0.0 95.7 713 0.0 95.7 713 0.0 95.7 713 0.0 95.7 714 713 0.0 95.7 714 714 715 715 716 717 717 713 716 717 716 717 716 717 716 717 716 717 717 713 716 717 717 713 716 717 716 717 716 717 717 717 713 716 717	A ₁₄ 100.0 0.0 0.0 0.0 100.0 0.0 0.0 0.0 0.0	G ₁₅ 0.0 99.9 0.0 G ₁₅ 0.0 99.9 0.0 G ₁₅ 0.0 0.0 100.0 0.0 0.0 100.0	A ₁₆ 100.0 0.0 0.0 100.0 0.0 0.0 0.0 0.0 0.0	C ₇ 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.	T18 0.0 0.0 0.0 100.0 0.0 100.0 0.0 100.0 0.0 100.0 0.0 100.0 0.0 100.0 0.0 100.0 0.0 100.0 0.0 100.0 0.0 100.0 0.0 100.0 0.0	G ₁₉ 0.0 0.0 99.9 0.1 G ₁₉ 0.0 99.9 0.0 99.9 0.0 0.0 100.0 0.0 0.0 0.0 0.0 0.0 0.0 0	T ₂₀ 0.0 0.0 0.0 100.0 0.0 0.0 0.0 100.0 T ₂₀ 0.0 0.0 0.0 100.0 100.0	G 0.0 0.0 99.9 0.1 G 0.0 99.9 0.0 G 0.0 99.9 0.0 G 0.0 0.0 99.9 0.0	G 0.0 99.9 0.1 6 0.0 0.0 100.0 0.0 100.0 0.0 100.0 0.0 100.0 0.0	G 0.0 99.9 0.0 0.0 100.0 0.0 100.0 0.0 100.0 0.0 100.0 0.0	Indel% 0.029 0.11 0.11 Indel% 0.096 Indel% 0.078
Untreated Site 14 A C G T ABE6.3 Site 14 A C G T ABE7.8 Site 14 A C G G T ABE7.9 Site 14 A C G G T ABE7.9 Site 14 A C G T	$ \begin{array}{c} G_1 \\ 0.0 \\ 0.0 \\ 99.9 \\ 0.0 \\ \end{array} \\ \begin{array}{c} G_1 \\ 0.1 \\ 0.0 \\ 99.9 \\ 0.1 \\ \end{array} \\ \begin{array}{c} G_1 \\ 0.0 \\ 100.0 \\ 0.0 \\ \end{array} \\ \begin{array}{c} G_1 \\ 0.0 \\ 0.0 \\ \end{array} \\ \end{array} $	G2 0.0 0.0 99.9 0.0 0.0 0.0 99.9 0.0 99.9 0.0 99.9 0.0 99.9 0.0 99.9 0.0 90.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0	C3 0.0 99.9 0.0	T ₄ 0.0 0.0 0.0 100.0 T ₄ 0.0 0.0 100.0 T ₄ 0.0 0.0 0.0 100.0 T ₄ 0.0 0.0 0.0 0.0 0.0 0.0 0.0 100.0	A ₅ 99.8 0.0 0.1 0.0 29.5 0.0 70.5 0.0 70.5 0.0 7.5 0.0 7.5 0.0 7.5 0.0 7.5 0.0	A ₆ 100.0 0.0 0.0 0.0 95.1 0.0 4.9 0.0 5.1 0.0 5.1 0.0 5.1 0.0 94.9 0.0 5.1 0.0	A7 100.0 0.0 0.0 0.0 0.0 0.0 1.4 0.0 1.4 0.0 1.4 0.0 1.4 0.0 A7 98.4 0.0 A7 97.4 0.0 2.6 0.0	G8 0.0 0.0 99.9 0.0 99.9 0.0 99.9 0.0 99.9 0.0 99.9 0.0 99.9 0.0 90.0 90.0 90.0 0.0	A ₀ 100.0 0.0 0.0 0.0 0.0 0.0 95.8 0.0 4.2 0.0 4.2 0.0 4.2 0.0 4.2 0.0 4.2 0.0 4.2 0.0 4.2 0.0 4.2 0.0 4.2 0.0 4.2 0.0 4.2 0.0 4.2 0.0 4.2 0.0	C10 0.0 100.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0	C11 99.9 0.0 99.9 0.0	A12 99.9 0.0 0.1 100.0 0.0 0.1 A12 100.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0	T ₁₃ 0.1 2.8 0.0 97.1 T ₁₃ 0.0 95.7 T ₁₃ 0.0 95.7 T ₁₃ 0.0 95.7 T ₁₃ 0.0 95.7	A ₁₄ 100.0 0.0 0.0 0.0 100.0 0.0 0.0 0.0 0.0	G ₁₅ 0.0 99.9 0.0 G ₁₅ 0.0 G ₁₅ 0.0 G ₁₅ 0.0 0.0 100.0 0.0 100.0 0.0	A ₁₆ 100.0 0.0 0.0 100.0 0.0 0.0 0.0 0.0 0.0	C7 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.	T ₁₈ 0.0 0.0 100.0 T ₁₈ 0.0 0.0 100.0 T ₁₈ 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 100.0	G ₁₉ 0.0 0.0 99.9 0.1 G ₁₉ 0.0 99.9 0.0 99.9 0.0 0.0 100.0 0.0 100.0 0.0	T ₂₀ 0.0 0.0 0.0 100.0 7 20 0.0 0.0 100.0 100.0 100.0 100.0 100.0	G 0.0 0.0 99.9 0.1 G 0.0 99.9 0.0 G 0.0 99.9 0.0 G 0.0 0.0 99.9 0.0	G 0.0 99.9 0.1 6 0.0 0.0 100.0 0.0 100.0 0.0 100.0 0.0 0	G 0.0 99.9 0.0 0.0 100.0 0.0 100.0 0.0 100.0 0.0 100.0 0.0	Indel% 0.029 0.11 0.11 Indel% 0.096 Indel% 0.078
Untreated Site 14 A C G T ABE6.3 Site 14 A C G T ABE7.8 Site 14 A C G G T ABE7.9 Site 14 A C G G T ABE7.9 Site 14 A C G T A A C G Site 14 A A C G Site 14 A A C G Site 14 A A C G Site 14 A A C G Site 14 A A C G Site 14 A C G G T T A A BE6.3 Site 14 A C G G T T A A BE6.3 Site 14 A C G G T T A A BE6.3 Site 14 A C G G T T A A BE6.3 Site 14 A C G G T T A A C G G T T A A C G G T T A A C G G T T A A C G G T T A A C G G T T A C G G T T A A C Site 14 A C C G Site 14 A A C C G G T T A A BE7.8 Site 14 A A C C G Site 14 A C C G T T A A A C C G G T T A A A A C C G G T T A A A A C C Site 14 A C C G Site 14 A C C Site 14 C C Site 14 C Site 14 C C Site 14 C Site 14 C C Site 14 C C Site 14 C C Site 14 C C Site 14 C C Site 14 C C Site 14 C C C C C Site 14 C C Site 14 C C C C C C Site 14 C C C C C C C C C C C C C C C C C C C	$ \begin{array}{c} G_1 \\ 0.0 \\ 0.0 \\ 99.9 \\ 0.0 \\ \end{array} \\ \begin{array}{c} G_1 \\ 0.1 \\ 0.0 \\ 99.9 \\ 0.1 \\ \end{array} \\ \begin{array}{c} G_1 \\ 0.0 \\ 0.0 \\ \end{array} \\ \end{array} $	G2 0.0 0.0 99.9 0.0 0.0 99.9 0.0 99.9 0.0 99.9 0.0 99.9 0.0 90.0 90.0 90.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0	C3 99.9 0.0 90.9 0.0	T4 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 100.0 T4 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 100.0	A ₅ 99.8 0.0 0.1 0.0 29.5 0.0 70.5 0.0 70.5 0.0 7.5 0.0 7.5 0.0 7.5 0.0 7.5 0.0	A ₆ 100.0 0.0 0.0 95.1 0.0 94.9 0.0 5.1 0.0 5.1 0.0 5.1 0.0 94.9 0.0	A7 100.0 0.0 0.0 0.0 0.0 1.4 0.0 1.4 0.0 1.4 0.0 1.4 0.0 A7 98.4 0.0 A7 98.4 0.0 2.6 0.0	G8 0.0 0.0 99.9 0.0 99.9 0.0 99.9 0.0 99.9 0.0 99.9 0.0 99.9 0.0 99.9 0.0 90.0 90.0 90.0 90.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0	A ₀ 100.0 0.0 0.0 0.0 0.0 0.0 95.8 0.0 4.2 0.0 4.2 0.0 4.2 0.0 4.2 0.0 4.2 0.0 3.4 0.0 3.4 0.0 1.5 0.0	$\begin{tabular}{ c c c c c } \hline C_{10} & 0.0 \\ \hline 0.0 & 0.$	C11 0.0 99.9 0.0	A12 99.9 0.0 0.1 100.0 0.0 0.1 A12 100.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0	T ₁₃ 0.1 2.8 0.0 97.1 T ₁₃ 0.0 95.7 T ₁₃ 0.0 95.7 T ₁₃ 0.0 95.7 T ₁₃ 0.0 95.7 0.0 95.7	A ₁₄ 100.0 0.0 0.0 100.0 0.0 0.0 0.0	G ₁₅ 0.0 99.9 0.0 G ₁₅ 0.0 99.9 0.0 G ₁₅ 0.0 0.0 100.0 0.0 100.0 0.0	A ₁₆ 100.0 0.0 0.0 100.0 0.0 0.0 0.0	C7 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.	$\begin{array}{c} T_{18} \\ 0.0 \\ 0.0 \\ 0.0 \\ 100.0 \\ \hline \end{array}$	G ₁₉ 0.0 0.0 99.9 0.1 G ₁₉ 0.0 99.9 0.0 99.9 0.0 G ₁₉ 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.	T ₂₀ 0.0 0.0 0.0 0.0 100.0 T ₂₀ 0.0 0.0	G 0.0 0.0 99.9 0.1 G 0.0 99.9 0.1 G 0.0 99.9 0.0 99.9 0.0 99.9 0.0 99.9 0.0 99.9 0.0 99.9 0.0 99.9 0.0 99.9 0.0	G 0.0 99.9 0.1 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0	G 0.0 99.9 0.0 0.0 100.0 0.0 100.0 0.0 100.0 0.0 100.0 0.0	Indel% 0.029 0.11 0.11 Indel% 0.096 0.078
Untreated Site 14 A C G T ABE6.3 Site 14 A C G T ABE7.8 Site 14 A C G T ABE7.9 Site 14 A C G T ABE7.9 Site 14 A C G T ABE6.3 Site 14 A C G T T ABE6.3 Site 14 A C G T T ABE6.3 Site 14 A C G T T ABE6.3 Site 14 A C G G T T ABE6.3 Site 14 A C G G T T ABE6.3 Site 14 A C G G T T ABE6.3 Site 14 A C G G T T ABE6.3 Site 14 A C G G T T ABE6.3 Site 14 A C G G T T ABE7.8 Site 14 A C G G T T A ABE7.8 Site 14 A C G G T T A ABE7.8 Site 14 A C G G T T A ABE7.8 Site 14 A C G G T T A ABE7.8 Site 14 A C G G T T ABE7.8 Site 14 A C G G T T A ABE7.8 Site 14 A C G G T A ABE7.8 Site 14 A C G G T A ABE7.8 Site 14 A C G G T A A C C G G T A A C C G Site 14 A C C G G T C A Site 14 A C C G G T C C Site 14 C C Site 14 C C Site 14 C C Site 14 C C Site 14 C Site 14 C C Site 14 C Site 14 C C Site 14 C Site 14 C C Site 14 C Site 14 Site 14 C Site 14 C Si Si Site 14 Site 14 Si Site 14 C Site 14 Site 14 Si Si	$\begin{array}{c} G_{1} \\ 0.0 \\ 0.0 \\ 99.9 \\ 0.0 \\ \end{array}$ $\begin{array}{c} G_{1} \\ 0.1 \\ 0.0 \\ 99.9 \\ 0.1 \\ \end{array}$ $\begin{array}{c} G_{1} \\ 0.0 \\ 0.0 \\ \end{array}$ $\begin{array}{c} G_{1} \\ 0.0 \\ 0.0 \\ \end{array}$ $\begin{array}{c} G_{1} \\ 0.0 \\ 0.0 \\ \end{array}$	G2 0.0 0.0 99.9 0.0 0.0 99.9 0.0 99.9 0.0 99.9 0.0 99.9 0.0 90.0 0.0	C3 0.0 99.9 0.0	T ₄ 0.0 0.0 0.0 100.0 T ₄ 0.0 0.0 100.0 T ₄ 0.0 0.0 0.0 100.0 T ₄ 0.0 0.0 0.0 0.0 0.0 0.0 100.0 100.0 T ₄	A ₅ 99.8 0.0 0.1 0.0 29.5 0.0 70.5 0.0 70.5 0.0 7.5 0.0 7.5 0.0 7.5 0.0 7.5 0.0 7.5 0.0 7.5 0.0	A ₆ 100.0 0.0 0.0 95.1 0.0 4.9 0.0 5.1 0.0 5.1 0.0 5.1 0.0 5.1 0.0 5.1 0.0 5.1 0.0 5.1 0.0 5.1 0.0 5.1 0.0 0.0 5.1 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0	A7 100.0 0.0 0.0 0.0 0.0 1.4 0.0 1.4 0.0 1.4 0.0 1.4 0.0 A7 98.46 0.0 A7 97.4 0.0 2.6 0.0 A7	G ₈ 0.0 0.0 99.9 0.0 99.9 0.0 99.9 0.0 99.9 0.0 99.9 0.0 99.9 0.0 99.9 0.0 90.0 0.0	A ₀ 100.0 0.0 0.0 0.0 0.0 0.0 95.8 0.0 4.2 0.0 4.2 0.0 4.2 0.0 4.2 0.0 4.2 0.0 4.2 0.0 4.2 0.0 4.2 0.0 4.2 0.0 4.2 0.0 4.2 0.0 1.5 0.0 1.5 0.0	C10 0.0 100.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0	C11 0.0 99.9 0.0	A12 99.9 0.0 0.1 100.0 0.0 0.1 A12 100.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0	T ₁₃ 0.1 2.8 0.0 97.1 T ₁₃ 0.0 95.7	A ₁₄ 100.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0	G ₁₅ 0.0 99.9 0.0 G ₁₅ 0.0 G ₁₅ 0.0 0.0 100.0 0.0 100.0 0.0 0.0 0.0 100.0 0.0	A ₁₆ 100.0 0.0 0.0 100.0 0.0 0.0 0.0 0.0 0.0	C7 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.	T18 0.0 0.0 0.0 100.0 0.0 100.0 0.0 100.0 0.0 100.0 0.0 100.0 0.0 100.0 0.0 100.0 0.0 100.0 0.0 100.0 0.0 100.0 0.0 100.0 0.0 100.0 100.0	G ₁₉ 0.0 0.0 99.9 0.1 G ₁₉ 0.0 99.9 0.0 99.9 0.0 0.0 100.0 0.0 100.0 0.0 100.0 0.0 0	T ₂₀ 0.0 0.0 0.0 0.0 100.0 T ₂₀ 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 100.0 T ₂₀	G 0.0 0.0 99.9 0.1 G 0.0 99.9 0.0 G G 0.0 0.0 99.9 0.0 0.0 99.9 0.0 0.0 0.0 99.9 0.0 0.0	G 0.0 99.9 0.1 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0	G 0.0 0.0 99.9 0.0 0.0 100.0 0.0 100.0 0.0 100.0 0.0 100.0 0.0	Indel% 0.029 0.11 0.11 Indel% 0.096 0.078 Indel% 0.095
Untreated Site 14 A C G T ABE6.3 Site 14 A C G T ABE7.8 Site 14 A C G G T ABE7.9 Site 14 A C G G T ABE7.9 Site 14 A C G T ABE6.3 Site 14 A A C G S T T ABE6.3 Site 14 A C G S T T ABE6.3 Site 14 A C G S T T ABE6.3 Site 14 A C G S T T ABE6.3 Site 14 A C G S T T ABE6.3 Site 14 A C G G T T ABE6.3 Site 14 A C G G T T ABE6.3 Site 14 A C G G T T ABE7.8 Site 14 A C G G T T A ABE7.8 Site 14 A C G G T T A ABE7.8 Site 14 A C G G T T A ABE7.8 Site 14 A C C G G T A ABE7.8 Site 14 A C C G G T Site 14 A C C G G T Site 14 A C C G G T Site 14 A C C G G T Site 14 A C C G G T Site 14 A C C G G T Site 14 A C C G G T Site 14 A C C G G T Site 14 A C C G G T Site 14 A C C Site 14 A C C G G T Site 14 C C Site 14 C C Site 14 C C Site 14 C C Site 14 C Site 14 C C Site 14 C Site 14 C C Site 14 C C Site 14 C C Site 14 C Site 14 Site 14 C Site 14 C Site 14 Site 14 C Site 14 Site 14 C Site 14 C Site 14 C Site 14 C Site 14 Site 14 C Site 14 C Si Site 14 C Si Si Site 14 Si Si Si Si Si Site 14 Si Si Si Si	$\begin{array}{c} G_1 \\ 0.0 \\ 0.0 \\ 99.9 \\ 0.0 \\ \end{array}$ $\begin{array}{c} G_1 \\ 0.1 \\ 0.0 \\ 99.9 \\ 0.1 \\ \end{array}$ $\begin{array}{c} G_1 \\ 0.0 \\ 0.0 \\ 100.0 \\ 0.0 \\ \end{array}$ $\begin{array}{c} G_1 \\ 0.0 \\ 99.9 \\ 0.0 \\ \end{array}$ $\begin{array}{c} G_1 \\ 0.0 \\ 0.0 \\ \end{array}$	G2 0.0 0.0 99.9 0.0 0.0 99.9 0.0 99.9 0.0 99.9 0.0 99.9 0.0 99.9 0.0 90.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0	C3 0.0 99.9 0.0	T ₄ 0.0 0.0 0.0 100.0 T ₄ 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 100.0 T ₄ 0.0 100.0 T ₄ 0.0 100.0	A ₅ 99.8 0.0 0.1 0.0 29.5 0.0 29.5 0.0 7.5 0.0 7.5 0.0 7.5 0.0 7.5 0.0 7.5 0.0 7.5 0.0 7.5 0.0 7.5 0.0 7.5 0.0 7.5 0.0 7.5 0.0 7.5 88.7 1.3 8.8.7 0.0 92.8 8.8.7 9.8.8 9.8.8 9.8.8 9.8.8 9.8.8 9.8.8 9.8.8 9.8.8 9.8.7 9.0.0 9.8.7 9.0.0 9.0.0 7.5 7.5 9.0.0 7.5 9.0.0 7.5 7.5 9.0.0 7.5 7.5 7.5 7.5 7.5 7.5 7.5 7.5 7.5 7.5	A ₆ 100.0 0.0 0.0 95.1 0.0 4.9 0.0 4.9 0.0 5.1 0.0 4.9 0.0 5.1 0.0 94.9 0.0 5.1 0.0 94.9 0.0 5.1 0.0 94.9 0.0 9.0 9.0 9.0 9.0 9.0 9.0 0.0 0.0 0	A7 100.0 0.0 0.0 0.0 0.0 0.0 1.4 0.0 1.4 0.0 1.4 0.0 1.4 0.0 A7 98.4 0.0 A7 97.4 0.0 A7 95.2	G8 0.0 0.0 99.9 0.0 99.9 0.0 99.9 0.0 99.9 0.0 99.9 0.0 99.9 0.0 99.9 0.0 90.0 100.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0	A ₀ 100.0 0.0 0.0 0.0 0.0 0.0 95.8 0.0 4.2 0.0 4.2 0.0 4.2 0.0 4.2 0.0 4.2 0.0 4.2 0.0 4.2 0.0 4.2 0.0 4.2 0.0 4.2 0.0 4.2 0.0 1.5 0.0 4.3 98.8	C10 0.0 100.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0	C11 0.0 99.9 0.0	A12 99.9 0.0 0.1 100.0 0.0 0.1 A12 100.0 0.0	T ₁₃ 0.1 2.8 0.0 97.1 T ₁₃ 0.0 95.7 T ₁₃ 0.0 94.9 T ₁₃ 0.0 94.9	A ₁₄ 100.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0	G ₁₅ 0.0 99.9 0.0 G ₁₅ 0.0 99.9 0.0 G ₁₅ 0.0 0.0 100.0 0.0 0.0 100.0 0.0 0.0 0.0	A ₁₆ 100.0 0.0 0.0 100.0 0.0 0.0 0.0 0.0 0.0	C7 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.	T ₁₈ 0.0 0.0 100.0 T ₁₈ 0.0 100.0 T ₁₈ 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 100.0 T ₁₈ 0.0 100.0 T ₁₈ 0.0 0.0	G ₁₉ 0.0 0.0 99.9 0.1 G ₁₉ 0.0 99.9 0.0 99.9 0.0 0.0 100.0 0.0 100.0 0.0 100.0 0.0 0	T ₂₀ 0.0 0.0 0.0 0.0 100.0 T ₂₀ 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 100.0 T ₂₀ 0.0 100.0 T ₂₀	G 0.0 0.0 99.9 0.1 G 0.0 99.9 0.0 G 0.0 99.9 0.0 G 0.1 0.0 99.9 0.0 G 0.1 0.0 0.0 0.0 99.9 0.0 0.0 0.0 0.0 0.0 0.	G 0.0 99.9 0.1 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0	G 0.0 0.0 99.9 0.0 0.0 100.0 0.0 100.0 0.0 100.0 0.0 100.0 0.0	Indel% 0.029 0.11 0.11 Indel% 0.096 0.078 Indel% 0.095
Untreated Site 14 A C G T ABE6.3 Site 14 A C G T ABE7.8 Site 14 A C G T ABE7.9 Site 14 A C G T ABE7.9 Site 14 A C G T ABE7.9 Site 14 A C G T T ABE6.1 Site 14 A C G T T ABE6.3 Site 14 A C G T T ABE6.3 Site 14 A C G T T ABE6.3 Site 14 A C G G T T ABE6.3 Site 14 A C G G T T ABE6.3 Site 14 A C G G T T ABE6.3 Site 14 A C G G T T ABE7.8 Site 14 A C G G T T ABE7.8 Site 14 A C G G T T ABE7.8 Site 14 A C G G T T ABE7.8 Site 14 A C C G G T T ABE7.8 Site 14 A C C G G T T ABE7.8 Site 14 A C C G G T T ABE7.8 Site 14 A C C G G T T ABE7.8 Site 14 A C C G G T Site 14 A C C G G T Site 14 A C C G G T Site 14 A C C G G T Site 14 A C C G G T Site 14 A C C G G C C Site 14 C C C G G C C C C C C C C C C C C C C	$\begin{array}{c} G_{1} \\ 0.0 \\ 0.0 \\ 99.9 \\ 0.0 \\ \hline \\ 0.1 \\ 0.0 \\ 99.9 \\ 0.1 \\ \hline \\ 0.1 \\ 0.0 \\ 99.9 \\ 0.1 \\ \hline \\ 0.0 \\ 0.0 \\ 0.0 \\ \hline \\ 0.0 $	G2 0.0 0.0 99.9 0.0 99.9 0.0 99.9 0.0 99.9 0.0 99.9 0.0 99.9 0.0 99.9 0.0 90.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0	C3 0.0 99.9 0.0	T ₄ 0.0 0.0 100.0 T ₄ 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 100.0 100.0 0.0 0.0 0.0	A ₅ 99.8 0.0 0.1 0.0 29.5 0.0 29.5 0.0 7.5 0.0 7.5 0.0 7.5 0.0 7.5 0.0 7.5 0.0 7.5 0.0 7.5 0.0 7.5 0.0 7.5 0.0 7.5 0.0 7.5 88.7 0.0 0.0 7.5 8.7 7.5 7.5 7.5 7.5 7.5 7.5 7.5 7.5 7.5 7	A ₆ 100.0 0.0 0.0 95.1 0.0 4.9 0.0 4.9 0.0 5.1 0.0 4.9 0.0 5.1 0.0 92.1 0.0 9.0 9.1 9.0 9.0 9.0 9.0 9.0 9.0 9.0 9.0 9.0 9.0	A7 100.0 0.0 0.0 0.0 0.0 0.0 1.4 0.0 1.4 0.0 1.4 0.0 1.4 0.0 A7 98.4 0.0 A7 97.4 0.0 A7 97.4 0.0 A7 95.2 0.0	G8 0.0 0.0 99.9 0.0 99.9 0.0 99.9 0.0 99.9 0.0 99.9 0.0 99.9 0.0 90.0 90.0 90.0 0.0	Ag 100.0 0.0 0.0 0.0 0.0 0.0 95.8 0.0 4.2 0.0 4.2 0.0 4.2 0.0 4.2 0.0 4.2 0.0 4.2 0.0 4.2 0.0 4.2 0.0 4.2 0.0 4.2 0.0 4.2 0.0 1.5 0.0 1.5 0.0 1.5 0.0 1.2	C10 0.0 100.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0	C11 0.0 99.9 0.0	A12 99.9 0.0 0.1 100.0 0.0 0.1 A12 100.0 0.0	T ₁₃ 0.1 2.8 0.0 97.1 T ₁₃ 0.0 95.7	A ₁₄ 100.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0	G ₁₅ 0.0 99.9 0.0 G ₁₅ 0.0 99.9 0.0 G ₁₅ 0.0 0.0 100.0 0.0 0.0 100.0 0.0 0.0 0.0	A ₁₆ 100.0 0.0 0.0 0.0 100.0 0.0 0.0 0.0 0.0	C7 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.	T18 0.0 0.0 0.0 100.0 0.0 100.0 0.0 100.0 0.0 100.0 0.0 100.0 0.0 100.0 0.0 100.0 0.0 100.0 0.0 100.0 0.0 100.0 0.0 100.0 0.0 100.0 0.0 100.0 0.0	G ₁₉ 0.0 99.9 0.1 G ₁₉ 0.0 99.9 0.0 99.9 0.0 99.9 0.0 0.0 100.0 0.0 0.0 0.0 0.0 0.0 0.0 0	T ₂₀ 0.0 0.0 0.0 0.0 100.0 T ₂₀ 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 100.0 100.0 0.0 0.0	G 0.0 0.0 99.9 0.1 G 0.0 99.9 0.0 G 0.0 99.9 0.0 G 0.1 0.0 99.9 0.0 G 0.0 0.0 0.0 99.9 0.0 0.0 0.0 0.0 0.0 0.	G 0.0 99.9 0.1 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0	G 0.0 0.0 99.9 0.0 0.0 100.0 0.0 100.0 0.0 100.0 0.0 100.0 0.0	Indel% 0.029 0.11 0.11 Indel% 0.096 0.078 Indel% 0.095

Untreated																								Indel%
Site 15	G ₁	T ₂	C ₃	T ₄	A ₅	G ₆	A ₇	A ₈	A ₉	G ₁₀	C ₁₁	T ₁₂	T ₁₃	A ₁₄	G ₁₅	A ₁₆	C ₇	T ₁₈	G ₁₉	C ₂₀	Т	G	G	0.032
A	0.0	0.0	0.0	0.0	99.9	0.0	100.0	100.0 1	0.001	0.0	0.0	0.0	0.0	100.0	0.0	100.0	0.0	0.0	0.0	0.0	0.0	0.1	0.0	
C	0.0	0.0	99.9	0.0	0.0	0.0	0.0	0.0	0.0	0.0 1	100.0	0.0	0.0	0.0	0.0	0.0	100.0	0.0	0.0	100.0	0.0	0.0	0.0	
т	99.9	100.0	0.0	100.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	100.0	100.0	0.0	99.9	0.0	0.0	100.0	99.9	0.0	100.0	99.9	99.9	
•	0.1	100.0	0.0	100.0	0.1	0.0	0.0	0.0	0.0	0.0	0.0	100.0	100.0	0.0	0.0	0.0	0.0	100.0	0.1	0.0	100.0	0.0	0.0	
ABE6.3																								Indel%
Site 15	G ₁	T ₂	C ₃	T ₄	A ₅	G ₆	A ₇	A ₈	A ₉	G ₁₀	C ₁₁	T ₁₂	T ₁₃	A ₁₄	G ₁₅	A ₁₆	C ₇	T ₁₈	G ₁₉	C ₂₀	Т	G	G	0.034
A	0.0	0.0	0.0	0.0	63.5	0.0	95.3	81.5	98.1	0.0	0.0	0.0	0.0	100.0	0.0	100.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	
С	0.0	0.0	99.9	0.0	0.0	0.0	0.0	0.0	0.0	0.0	100.0	0.0	0.0	0.0	0.0	0.0	100.0	0.0	0.0	100.0	0.0	0.0	0.0	
G	100.0	0.0	0.1	0.0	36.4	100.0	4.6	18.5	1.9	100.0	0.0	0.0	0.0	0.0	100.0	0.0	0.0	0.0	100.0	0.0	0.0	100.0	100.0	
	0.0	100.0	0.1	100.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	100.0	100.0	0.0	0.0	0.0	0.0	100.0	0.0	0.0	100.0	0.0	0.0	
ABE7.8																								Indel%
Site 15	G ₁	T ₂	C ₃	T ₄	A ₅	G ₆	A ₇	A ₈	A ₉	G ₁₀	C ₁₁	T ₁₂	T ₁₃	A ₁₄	G ₁₅	A ₁₆	C ₇	T ₁₈	G ₁₉	C ₂₀	Т	G	G	0.022
Α	0.0	0.0	0.0	0.0	69.4	0.1	87.8	97.4	98.8	0.0	0.0	0.0	0.0	100.0	0.0	100.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	
С	0.0	0.0	99.9	0.0	0.0	0.0	0.0	0.0	0.0	0.0	99.9	0.0	0.0	0.0	0.0	0.0	100.0	0.0	0.0	100.0	0.0	0.0	0.0	
G	100.0	0.0	0.0	0.0	30.6	99.9	12.2	2.6	1.2	100.0	0.0	0.0	0.0	0.0	100.0	0.0	0.0	0.0	100.0	0.0	0.0	100.0	100.0	
	0.0	100.0	0.0	100.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	100.0	100.0	0.0	0.0	0.0	0.0	100.0	0.0	0.0	100.0	0.0	0.0	
ABE7.9																								Indel%
Site 15	G ₁	T ₂	C ₃	T4	A ₅	G ₆	A ₇	A ₈	A9	G ₁₀	C ₁₁	T ₁₂	T ₁₃	A ₁₄	G ₁₅	A ₁₆	C ₇	T ₁₈	G ₁₉	C ₂₀	Т	G	G	0.023
А	0.0	0.0	0.0	0.0	56.6	0.0	85.7	98.7	99.0	0.0	0.0	0.0	0.0	100.0	0.0	100.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	
С	0.0	0.0	99.9	0.0	0.0	0.0	0.0	0.0	0.0	0.0	99.9	0.0	0.0	0.0	0.0	0.0	99.9	0.0	0.0	100.0	0.0	0.0	0.0	
G	100.0	0.0	0.0	0.0	43.4	100.0	14.3	1.3	1.0	100.0	0.0	0.0	0.0	0.0	100.0	0.0	0.0	0.0	100.0	0.0	0.0	100.0	100.0	
I	0.0	100.0	0.1	100.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	100.0	100.0	0.0	0.0	0.0	0.0	100.0	0.0	0.0	100.0	0.0	0.0	
ABE7.10																								Indel%
Site 15	G1	T ₂	C ₃	Τı	A ₅	Ge	A ₇	Aa	Aa	G10	C11	T12	T13	A14	G15	A ₁₆	C ₇	T18	G10	C20	Т	G	G	0.056
A	0.0	0.0	0.0	0.0	50.0	0.0	86.8	98.2	99.3	0.0	0.0	0.0	0.0	100.0	0.0	100.0	0.0	0.0	0.1	0.0	0.0	0.1	0.0	
С	0.0	0.0	99.9	0.0	0.0	0.0	0.0	0.0	0.0	0.0	100.0	0.0	0.0	0.0	0.0	0.0	100.0	0.0	0.0	99.9	0.0	0.0	0.0	
G	99.9	0.0	0.0	0.0	49.9	99.9	13.2	1.8	0.7	100.0	0.0	0.0	0.0	0.0	99.9	0.0	0.0	0.0	99.9	0.0	0.0	99.9	99.9	
I	0.1	100.0	0.0	100.0	0.1	0.0	0.0	0.0	0.0	0.0	0.0	100.0	100.0	0.0	0.0	0.0	0.0	100.0	0.1	0.0	100.0	0.1	0.1	
Untreated Site 16	G ₁	G ₂	G ₃	A ₄	A ₅	T ₆	A ₇	A ₈	A ₉	T ₁₀	C ₁₁	A ₁₂	T ₁₃	A ₁₄	G ₁₅	A ₁₆	A7	T ₁₈	C ₁	9 C ₂	20 T	G	G	Indel% 0.028
A	0.0	0.0	0.0	100.0	100.0	0.0	100.0	100.0	100.0	0.0	0.0	99.9	0.0	100.0	0.0	100.	.0 100.	0 0.0	0.0	0.0	0 0.0	0.0	0.0	
G	99.9	99.9	99.9	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	99.9	0.0	0.0	0.0	0.0	0 99	0 0.0) 99.9	99.9	
Т	0.1	0.1	0.0	0.0	0.0	100.0	0.0	0.0	0.0	100.0	0.1	0.0	100.0	0.0	0.0	0.0	0.0	100.0	0.0	0.0	0 100	.0 0.1	0.0	
ABE6.3					_	-																		Indel%
Site 16	G ₁	G ₂	G ₃	A ₄	A ₅	T ₆	A ₇	A ₈	A ₉	T ₁₀	C ₁₁	A ₁₂	T ₁₃	A ₁₄	G ₁₅	A ₁₆	6 A ₇	T ₁₈	C ₁	9 C ₂	20 T	G	G	0.14
A	0.0	0.0	0.0	95.8	58.9	0.0	89.6	97.3	97.8	0.0	0.0	99.9	0.0	100.0	0.1	100.	.0 100.	0 0.0	0.0	0.0	0 0.0	0.0	0.0	
G	99.9	100.0	99.9	4.2	41 1	0.0	10.4	2.7	2.1	0.0	99.8	0.0	0.0	0.0	99.0	0.0	0.0	0.0	0.0				0.0 100.0	
Т	0.1	0.0	0.0	0.0	0.0	100.0	0.0	0.0	0.0	100.0	0.2	0.0	100.0	0.0	0.0	0.0	0.0	100.0	0.0	0.0	0 100	.0 0.0	0.0	
ABE7.8						_									-									Indel%
Site 16	G ₁	G ₂	G ₃	A ₄	A ₅	T ₆	A ₇	A ₈	A ₉	T ₁₀	C ₁₁	A ₁₂	T ₁₃	A ₁₄	G ₁₅	A ₁₆	A7	T ₁₈	C ₁	9 C ₂	20 T	G	G	0.16
A	0.0	0.0	0.0	88.4	56.0	0.0	93.9	96.1	96.3	0.0	0.0	100.0	0.0	99.7	0.0	99.	7 99.1	0.0	0.0) 0.0	U 0.0	0.0	0.0	
G	100.0	100.0	100.0	0.0	44.0	0.0	0.0	0.2	3.5	0.0	99.7	0.0	0.0	0.0	100 (0.1	0.2	0.0	100		0.0		0.0	
Т	0.0	0.0	0.0	0.0	0.0	100.0	0.0	0.0	0.0	100.0	0.1	0.0	100.0	0.0	0.0	0.0	0.0	100.0	0.0	0.0	0 100	.0 0.0	0.0	
		••••			••••												•••	_						
ABE7.9																								
Site 16																								Indel%
	G ₁	G ₂	G ₃	A ₄	A ₅	T ₆	A ₇	A ₈	A ₉	T ₁₀	C ₁₁	A ₁₂	T ₁₃	A ₁₄	G ₁₅	A ₁₆	A7	T ₁₈	C ₁	9 C ₂	20 T	G	G	Indel% 0.130
A	G ₁ 0.0	G ₂ 0.0	G ₃	A ₄ 93.8	A ₅ 49.5	T ₆ 0.0	A ₇ 86.4	A ₈ 94.7	A ₉ 98.0	T ₁₀	C ₁₁ 0.0	A ₁₂ 99.9	T ₁₃ 0.0	A ₁₄ 100.0	G ₁₅ 0 0.0	A ₁₆	A ₇	T ₁₈ 0 0.0	C ₁ 0.0	9 C ₂	20 T	G 0 0.0	G 0.0	Indel% 0.130
A C	G ₁ 0.0 0.0	G ₂ 0.0 0.0	G ₃ 0.0 0.0	A ₄ 93.8 0.0	A ₅ 49.5 0.0	T ₆ 0.0 0.0	A ₇ 86.4 0.0	A ₈ 94.7 0.0	A ₉ 98.0 0.0	T ₁₀ 0.0 0.0	C ₁₁ 0.0 100.0	A ₁₂ 99.9 0.0	T ₁₃ 0.0 0.0	A ₁₄ 100.0	G ₁₅ 0.0 0.0	A ₁₆ 100. 0.0	A ₇ 0 100.	T ₁₈ 0 0.0 0.0	C ₁ 0.0	$\frac{9}{100} \frac{C_2}{0.01}$	20 T 0 0.0	G 0 0.0 0 0.0	G 0.0 0.0	Indel% 0.130
A C G T	G ₁ 0.0 0.0 100.0	G ₂ 0.0 0.0 100.0	G ₃ 0.0 0.0 100.0	A₄ 93.8 0.0 6.2	A₅ 49.5 0.0 50.5	T ₆ 0.0 0.0 0.0	A ₇ 86.4 0.0 13.6	A ₈ 94.7 0.0 5.3	A ₉ 98.0 0.0 2.0	T ₁₀ 0.0 0.0 0.0	C ₁₁ 0.0 100.0 0.0	A ₁₂ 99.9 0.0 0.0 0.0	T ₁₃ 0.0 0.0 0.0	A ₁₄ 100.0 0.0 0.0	G ₁₅ 0 0.0 0.0 100.0	A ₁₆ 100. 0.0 0.0	A ₇ 0 100.	T ₁₈ 0 0.0 0.0 0.0	C ₁ 0.0 100 0.0	$ \begin{array}{c c} 9 & C_2 \\ 0 & 0.0 \\ 1.0 & 100 \\ 0 & 0.0 \\ 0 & 0.1 \\ $	20 T 0 0.0 0.0 0.0 0 0.0 0 0.0	G 0 0.0 0 0.0 0 100.	G 0.0 0.0 0 100.0	Indel% 0.130
A C G T	G ₁ 0.0 0.0 100.0 0.0	G ₂ 0.0 0.0 100.0 0.0	G ₃ 0.0 0.0 100.0 0.0	A ₄ 93.8 0.0 6.2 0.0	A ₅ 49.5 0.0 50.5 0.0	T ₆ 0.0 0.0 0.0 100.0	A ₇ 86.4 0.0 13.6 0.0	A ₈ 94.7 0.0 5.3 0.0	A ₉ 98.0 0.0 2.0 0.0	T ₁₀ 0.0 0.0 0.0 100.0	C ₁₁ 0.0 100.0 0.0 0.0	A ₁₂ 99.9 0.0 0.0 0.0	T ₁₃ 0.0 0.0 0.0 100.0	A ₁₄ 100.0 0.0 0.0 0.0	G ₁₅ 0 0.0 0.0 100.0 0.0	A ₁₆ 100. 0.0 0.0 0.0	A ₇ 0 100. 0 0.0 0 0.0 0 0.0	T ₁₈ 0 0.0 0.0 0.0 100.0	C ₁ 0.0 100 0.0 0.0	9 C2 0 0.1 1.0 100 0 0.1 0 0.1 0 0.1	20 T 0 0.0 0.0 0.0 0 0.0 0 0.0 0 100	G 0 0.0 0 0.0 0 100. 0 0.0	G 0.0 0.0 0 100.0 0.0	Indel% 0.130
A C G T ABE7.10	G ₁ 0.0 0.0 100.0 0.0	G ₂ 0.0 0.0 100.0 0.0	G ₃ 0.0 0.0 100.0 0.0	A ₄ 93.8 0.0 6.2 0.0	A ₅ 49.5 0.0 50.5 0.0	T ₆ 0.0 0.0 0.0 100.0	A ₇ 86.4 0.0 13.6 0.0	A ₈ 94.7 0.0 5.3 0.0	A ₉ 98.0 0.0 2.0 0.0	T ₁₀ 0.0 0.0 0.0 100.0	C ₁₁ 0.0 100.0 0.0 0.0	A ₁₂ 99.9 0.0 0.0 0.0	T ₁₃ 0.0 0.0 0.0 100.0	A ₁₄ 100.0 0.0 0.0 0.0	G ₁₅ 0 0.0 0.0 100.0 0.0	A ₁₆ 100. 0.0 0.0 0.0	A ₇ 0 100. 0 0.0 0 0.0 0 0.0	T ₁₈ 0 0.0 0.0 0.0 100.0	C ₁ 0.0 100 0.0 0.0	9 C ₂ 0 0.1 0 100 0 0.1 0 0.1	Z0 T 0 0.0 0.0 0.0 0 0.0 0 0.0 0 100	G 0 0.0 0 0.0 0 100. 0 0.0	G 0.0 0.0 100.0 0.0	Indel% 0.130 Indel%
A C G T ABE7.10 Site 16	G ₁ 0.0 0.0 100.0 0.0	G ₂ 0.0 0.0 100.0 0.0 G ₂	G ₃ 0.0 0.0 100.0 0.0 G ₃	A ₄ 93.8 0.0 6.2 0.0	A ₅ 49.5 0.0 50.5 0.0 A ₅	T ₆ 0.0 0.0 100.0 T ₆	A ₇ 86.4 0.0 13.6 0.0	A ₈ 94.7 0.0 5.3 0.0	A ₉ 98.0 0.0 2.0 0.0 A ₉	T ₁₀ 0.0 0.0 100.0 T ₁₀	C ₁₁ 0.0 100.0 0.0 0.0 C ₁₁	A ₁₂ 99.9 0.0 0.0 0.0 0.0 A ₁₂	T ₁₃ 0.0 0.0 100.0 T ₁₃	A ₁₄ 100.0 0.0 0.0 0.0 A ₁₄	G ₁₅ 0 0.0 0.0 100.0 0.0 G ₁₅	A ₁₆ 100. 0.0 0.0 0.0 0.0	$\begin{array}{c c} $	T ₁₈ 0 0.0 0.0 0.0 100.0 T ₁₈	C ₁ 0.0 100 0.0 0.0 C ₁	$\begin{array}{c c} 9 & C_2 \\ 0 & 0.1 \\ 1.0 & 100 \\ 0 & 0.1 \\ 0 & 0.1 \\ 9 & C_2 \end{array}$	20 T 0 0.0 0.0 0.0 0 0.0 0 100 20 T	G 0 0.0 0 0.0 0 100. 0 0.0 G	G 0.0 0.0 0 100.0 0.0 G	Indel% 0.130 Indel% 0.150
A C G T ABE7.10 Site 16 A	$ \begin{array}{c} G_{1} \\ 0.0 \\ 0.0 \\ 100.0 \\ \hline 0.0 \\ \hline G_{1} \\ 0.0 \\ \hline \end{array} $	G ₂ 0.0 100.0 0.0 G ₂ 0.0	G ₃ 0.0 100.0 0.0 G ₃ 0.0	A ₄ 93.8 0.0 6.2 0.0 A ₄ 83.6	A₅ 49.5 0.0 50.5 0.0 A₅ 34.5	$ \begin{array}{r} T_6 \\ 0.0 \\ 0.0 \\ 100.0 \\ \hline T_6 \\ 0.0 \\ 0.0 \\ \hline T_6 \\ 0.0 \\ $	A ₇ 86.4 0.0 13.6 0.0 A ₇ 44.1	A ₈ 94.7 0.0 5.3 0.0 A ₈ 97.1	A ₉ 98.0 0.0 2.0 0.0 A ₉ 98.3	$ \begin{array}{c c} T_{10} \\ 0.0 \\ 0.0 \\ 100.0 \\ \hline T_{10} \\ 0.0 \\ \hline \end{array} $	C ₁₁ 0.0 100.0 0.0 0.0 C ₁₁ 0.0	A ₁₂ 99.9 0 0.0 0.0 0.0 0.0 0.0 A ₁₂ 99.8	$ \begin{array}{c} T_{13} \\ 0.0 \\ 0.0 \\ 0.0 \\ 100.0 \\ \hline T_{13} \\ 0.0 \\ 0.0 \\ \hline T_{13} \\ 0.0 \\ 0.0 \\ \hline T_{13} \\ 0.0 \\ 0.0 \\ T_{13} \\ $	A ₁₄ 100.0 0.0 0.0 0.0 A ₁₄ 99.9	G ₁₅ 0 0.0 100.0 0.0 G ₁₅ 0.0	A ₁₆ 100. 0.0 0.0 0.0 0.0 0.0 0.0	$\begin{array}{c c} $	T ₁₈ 0 0.0 0.0 100.0 T ₁₈ 0 0.0	C ₁ 0.0 100 0.0 0.0 0 0.0	$\frac{9}{100} \frac{C_2}{0.01}$	20 T 0 0.0 0.0 0.0 0 0.0 0 100 20 T 0 0.0	G 0 0.0 0 0.0 0 100. .0 0.0 G 0 0.0	G 0.0 0.0 0 100.0 0.0 G 0.1	Indel% 0.130 Indel% 0.150
A C G T ABE7.10 Site 16 A C	G ₁ 0.0 100.0 0.0 G ₁ 0.0	G ₂ 0.0 100.0 0.0 G ₂ 0.0 0.0 0.0	G ₃ 0.0 100.0 0.0 G ₃ 0.0 0.0	A ₄ 93.8 0.0 6.2 0.0 A ₄ 83.6 0.0	A ₅ 49.5 0.0 50.5 0.0 A ₅ 34.5 0.0	T ₆ 0.0 0.0 100.0 T ₆ 0.0 0.0	A ₇ 86.4 0.0 13.6 0.0 A ₇ 44.1 0.1	A ₈ 94.7 0.0 5.3 0.0 A ₈ 97.1 0.0	A ₉ 98.0 0.0 2.0 0.0 A ₉ 98.3 0.0	T ₁₀ 0.0 0.0 100.0 T ₁₀ 0.0 0.0	C ₁₁ 0.0 100.0 0.0 0.0 C ₁₁ 0.0 99.8	A ₁₂ 99.9 0.0 0.0 0.0 0.0 0.0 99.8 0.0 0.2	T ₁₃ 0.0 0.0 100.0 T ₁₃ 0.0 0.0	A ₁₄ 100.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0	G ₁₅) 0.0 100.0 0.0 G ₁₅ 0.0 0.0	A ₁₆ 100. 0.0 0.0 0.0 0.0 0.0 A ₁₆ 100. 0.0	A_7 A_7	T ₁₈ 0 0.0 0.0 100.0 T ₁₈ 0 0.0 0.0	$\begin{array}{c} C_{1} \\ 0.0 \\ 100 \\ 0.0 \\ 0 \\ 0 \\ 0 \\ 0 \\ 0 \\ 0 \\ 0 \\ 0$	$\begin{array}{c c} 9 & C_2 \\ \hline 0 & 0.1 \\ 0.0 & 100 \\ \hline 0 & 0.1 \\ 0 & 0.1 \\ \hline 0 & 0.1 \\ \hline 0 & 0.1 \\ \hline 9 & C_2 \\ \hline 0 & 0.1 \\ \hline 9 & 99 \\ \hline 0 & 0.1 \\ \hline \end{array}$	20 T 0 0.0 0 0.0 0 0.0 0 0.0 0 100 20 T 20 T 0 0.0 0 0.0	G 0 0.0 0 100 .0 0.0 0 0.0 G 0 0.0 0 0.0	G 0.0 0.0 0 100.0 0.0 G 0.1 0.0	Indel% 0.130 Indel% 0.150
A C G T ABE7.10 Site 16 A C G T	$ \begin{array}{r} G_1 \\ 0.0 \\ 0.0 \\ 100.0 \\ 0.0 \\ \hline G_1 \\ 0.0 \\ 0.0 \\ 99.9 \\ 0.1 \\ \end{array} $	G ₂ 0.0 100.0 0.0 G ₂ 0.0 0.0 99.9 0.1	G ₃ 0.0 100.0 0.0 G ₃ 0.0 0.0 99.9 0.0	A ₄ 93.8 0.0 6.2 0.0 A ₄ 83.6 0.0 16.4 0.0	A ₅ 49.5 0.0 50.5 0.0 A ₅ 34.5 0.0 65.4 0.0	T ₆ 0.0 0.0 100.0 T ₆ 0.0 0.0 0.0	A ₇ 86.4 0.0 13.6 0.0 A ₇ 44.1 0.1 55.7 0.1	A ₈ 94.7 0.0 5.3 0.0 A ₈ 97.1 0.0 2.8 0 0	A ₉ 98.0 0.0 2.0 0.0 A ₉ 98.3 0.0 1.7 0.0	T ₁₀ 0.0 0.0 100.0 T ₁₀ 0.0 0.0 0.0 100.0	C ₁₁ 0.0 100.0 0.0 0.0 C ₁₁ 0.0 99.8 0.0	A ₁₂ 99.9 0.0 0.0 0.0 0.0 0.0 99.8 0.0 0.2 0.0	T ₁₃ 0.0 0.0 100.0 T ₁₃ 0.0 0.0 0.0 0.0	A ₁₄ 100.0 0.0 0.0 0.0 1 0.0 0.0 0.0 0.0	G ₁₅) 0.0 100.0 0.0 G ₁₅ 0.0 99.9 0.0	A ₁₆ 100. 0.0 0.0 0.0 0.0 100. 0.0 0.0	$3 A_7$ 0 100. 0 0.0 0 0.0	T ₁₈ 0 0.0 0.0 100.0 T <u>18</u> 0 0.0 0.0 0.0 0.0	$\begin{array}{c} C_{1} \\ 0.0 \\ 100 \\ 0.0 \\ 0 \\ 0 \\ 0 \\ 0 \\ 0 \\ 0 \\ 0 \\ 0$	$\begin{array}{c c} 9 & C_2 \\ 0 & 0.1 \\ 0 & 100 \\ 0 & 0.1 \\ 0 & 0.1 \\ 0 & 0.1 \\ 9 & 0.1 \\ 9 & 99 \\ 0 & 0.1 \\ 9 & 99 \\ 0 & 0.1 \\ 0 & 0$	20 T 0 0.0 0.0 0.0 0 0.0 0 100 20 T 20 0.0 20 0.0 0 0.0 0 0.0 0 0.0 0 0.0 0 0.0	G 0 0.0 0 100 0 100 0 0.0 0 0.0 0 0.0 0 0.0 0 99.9 0 1	G 0.0 0.00 0.00 0.0 0.0 G 0.1 0.0 9.99.9 0.0	Indel% 0.130 Indel% 0.150

Untreated																								Indel%
Site 17	G ₁	A ₂	C ₃	A ₄	A ₅	A ₆	G ₇	A ₈	G ₉	G ₁₀	A ₁₁	A ₁₂	G ₁₃	A ₁₄	G ₁₅	A ₁₆	G ₇	A ₁₈	C ₁₉	G ₂₀	G	G	G	0.077
А	0.0	100.0	0.0	99.9	99.6	99.6	0.0	99.9	0.0	0.0	100.0	100.0	0.0	100.0	0.0	100.0	0.0	100.0	0.0	0.0	0.0	0.0	0.0	
С	0.0	0.0	100.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	99.9	0.0	0.0	0.0	0.0	
G	100.0	0.0	0.0	0.1	0.4	0.4	100.0	0.1	100.0	100.0	0.0	0.0	100.0	0.0	100.0	0.0	100.0	0.0	0.0	99.9	100.0	99.9	100.0	
Т	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	
ABE6.3																								Indel%
Site 17	G	A	Ca	Δ.	Ar	A۵	Gr	A.	Ga	Guo	Δ.,	Δ	Gua	Δ.,	Gu	Arc	Gr	A.0	Cuo	Gaa	G	G	G	0.072
A	0.0	99.3	0.0	96.9	83.8	86.7	01	97.4	0.0	0.0	99.7	99.8	0.0	100.0	0.0	100.0	0.0	100.0	0.0	0.1	0.0	0.0	0.0	0.012
C C	0.0	0.0	99.9	0.0	0.1	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	99.9	0.1	0.0	0.0	0.0	
G	100.0	0.7	0.1	3.1	16.1	13.3	99.9	2.6	100.0	100.0	0.2	0.2	99.9	0.0	100.0	0.0	100.0	0.0	0.0	99.8	100.0	100.0	100.0	
Ť	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.1	0.0	0.0	0.0	0.0	
ABE7.8																								Indel%
Site 17	G	A ₂	C2	A4	A۶	Ac	G ₇	A.	Go	G10	A11	A12	G12	A14	G15	A ₁₆	G ₇	A10	C10	Gao	G	G	G	0.06
A	0.0	99.0	0.0	96.8	88.0	88.5	0.1	92.9	0.0	0.0	99.8	99.9	0.0	100.0	0.0	100.0	0.0	100.0	0.0	0.1	0.0	0.0	0.0	
C	0.0	0.0	99.9	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	100.0	0.0	0.0	0.0	0.0	
G	100.0	0.9	0.1	3.2	12.0	11.5	99.9	7.0	100.0	100.0	0.2	0.1	99.9	0.0	100.0	0.0	100.0	0.0	0.0	99.9	100.0	100.0	100.0	
т	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	
ABE7.9																								Indel%
Site 17	G1	A ₂	C3	A₄	A ₅	A	G7	A ₈	G۹	G10	A11	A12	G13	A14	G15	A16	G7	A ₁₈	C19	G ₂₀	G	G	G	0.053
Α	0.0	99.5	0.0	97.8	84.1	77.9	0.1	90.4	0.0	0.0	99.7	99.9	0.0	100.0	0.0	100.0	0.0	100.0	0.0	0.1	0.0	0.0	0.0	
С	0.0	0.0	99.9	0.0	0.1	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.1	0.0	0.0	0.0	0.0	0.0	99.9	0.0	0.0	0.0	0.0	
G	100.0	0.5	0.1	2.2	15.8	22.1	99.9	9.6	100.0	100.0	0.3	0.1	99.9	0.0	100.0	0.0	100.0	0.0	0.0	99.9	100.0	100.0	100.0	
Т	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	
ARE7 10																								Indel%
Site 17	G	Δ.	C.	Δ.	Δ.	Δ.	G	Δ.	G.	Gu	Δ	Δ.,	Gu	Δ	Gu	Δ.,	G.	Δ.,	C	Gu	G	G	G	0.130
Δ	0.0	00.7	0.0	83.1	45.6	45.3	0.1	95.6	0.0	0 1	99.6	00.0	0.0	100.0	0.0	100.0	0.0	100.0	0.0	0.1	0.0	0.1	0.0	0.130
ĉ	0.0	0.0	0.0 00 0	0.0	-0.1	-0.0	0.1	0.0	0.0	0.1	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0 00.0		0.0	0.1	0.0	
G	100.0	0.0	0.1	16.8	54.3	54.7	0.0 00 0	4.4	100.0	0.0 00.0	0.0	0.0	0.1	0.0	100.0	0.0	100.0	0.0	0.0	0.0	0.0 00 0	0.0 00 0	100.0	
Т	0.0	0.0	0.1	0.0	0.0	0.0	0.0	4	0.0	0.0	0.0	0.1	0.0	0.0	0.0	0.0	0.0	0.0	0.1	0.0	0.0	0.0	0.0	
	0.0	0.0	0.1	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.1	0.0	0.0	0.0	0.0	

Supplementary Table 2. Activities of ABE7.8, ABE7.9, and ABE7.10 at the HEK2 on-target and off-target sites previously characterized for *S. pyogenes* Cas9 nuclease.¹

	-																				
						%	of total	seque	encing	reads w	ith targe	et A•T b	ase pair	convei	ted to G	•C					
HEK2 (on-target site)	G1	A2	A3	C4	A5	C6	A7	A8	A9	G10	C11	A12	T13	A14	G15	A16	C17	T18	G19	C20	Indel%
ABE 7.8		0.2	1.8		77.2		2.7	1.0	0.8			0.1		0.0		0.0				-	0.2
ABE 7.9		0.1	0.5		79.4		2.5	0.5	0.5			0.0		0.0		0.0					0.1
ABE 7.10		0.0	0.5		87.6		23.0	1.0	1.0			0.1		0.0		0.0					0.3
Cas9 nuclease		0.0	0.7		0.0	_	0.0	0.0	0.0			0.3		0.1		0.1				I	54.5
D10A Cas9 nickase		0.0	0.0		0.0		0.0	0.0	0.0			0.0		0.0		0.0					0.2
H840A Cas9 nickase		0.0	0.1		0.0		0.0	0.0	0.0			0.2		0.0		0.0					5.3
dCas9 (D10A + H840A)		0.0	0.0		0.0		0.0	0.0	0.0			0.0		0.0		0.0					0.0
no treatment		0.0	0.0		0.0		0.0	0.0	0.0			0.0		0.0		0.0					0.0
						%	of total	seque	encing	reads w	ith targe	et A•T b	ase pair	conve	ted to G	•C					
HEK2 off-target site 1	G1	A2	A3	C4	A5	C6	A7	A8	T9	G10	C11	A12	T13	A14	G15	A16	T17	T18	G19	C20	Indel%
ABE 7.8		0.0	0.0		0.0		0.0	0.0				0.0		0.0		0.0					0.0
ABE 7.9		0.0	0.0		0.0		0.0	0.0				0.0		0.0		0.0					0.0
ABE 7.10		0.0	0.0		0.3		0.1	0.0				0.0		0.0		0.0					0.0
Cas9 nuclease		0.0	0.0		0.0		0.0	0.0				0.0		0.0		0.0					0.5
D10A Cas9 nickase		0.0	0.0		0.0		0.0	0.0				0.0		0.0		0.0					0.0
H840A Cas9 nickase		0.0	0.0		0.0		0.0	0.0				0.0		0.0		0.0					0.0
dCas9 (D10A + H840A)		0.0	0.0		0.0		0.0	0.0				0.0		0.0		0.0					0.0
no treatment		0.0	0.0		0.0		0.0	0.0				0.0		0.0		0.0					0.0
						%	of total	seque	ncing	reads w	ith targe	et A•T b	ase pair	convei	ted to G	•C					
HEK2 off-target site 2	A1	A2	A3	C4	A5	T6	A7	A8	A9	G10	C11	A12	T13	A14	G15	A16	C17	T18	G19	C20	Indel%
ABE 7.8	0.0	0.0	0.0		0.0		0.1	0.0	0.0			0.0		0.0		0.0					0.0
ABE 7.9	0.0	0.0	0.0		0.0		0.0	0.0	0.0			0.0		0.0		0.0					0.0
ABE 7.10	0.0	0.0	0.0		0.0		0.0	0.0	0.0			0.0		0.0		0.0					0.0
Cas9 nuclease	0.0	0.0	0.0		0.0		0.0	0.0	0.0			0.0		0.0		0.0					0.0
D10A Cas9 nickase	0.0	0.0	0.0		0.0		0.0	0.0	0.0			0.0		0.0		0.0					0.0
H840A Cas9 nickase	0.0	0.0	0.0		0.0		0.0	0.0	0.0			0.0		0.0		0.0					0.0
dCas9 (D10A + H840A)	0.0	0.0	0.0		0.0		0.0	0.0	0.0			0.0		0.0		0.0					0.0
no treatment	0.0	0.0	0.0		0.0		0.1	0.0	0.0			0.0		0.0		0.0					0.0

Supplementary Table 3. Activities of ABE7.8, ABE7.9, and ABE7.10 at the HEK3 site previously characterized for on-target and off-target modification by *S. pyogenes* Cas9 nuclease.¹

		%	of total seque	encing reads	with target A	T base pa	ir converted to	G•C				
HEK3 (on-target site)	G1 G2 C3 C	C4 C5 A6	G7 A8	C9 T10	G11 A'	2 G13	C14 A15	C16	G17 1	G19 G19	A20	Indel%
ABE 7.8		8.4	14.7		0.	1	0.0				0.0	0.1
ABE 7.9		12.2	9.4		0.	2	0.0				0.0	0.2
ABE 7.10		62.7	18.6		0.	2	0.0				0.0	0.2
Cas9 nuclease		0.0	0.0		0.	2	0.2				0.2	64.8
D10A Cas9 nickase		0.0	0.0		0.	2	0.0				0.0	2.0
H840A Cas9 nickase		0.0	0.0		0.	0	0.0				0.0	0.4
dCas9 (D10A + H840A)		0.0	0.0		0.)	0.0				0.0	0.0
no treatment		0.0	0.0		0.)	0.0				0.0	0.0
		%	of total seque	encing reads	with target A	T base pa	ir converted to (G•C				
HEK3 off-target site 1	C1 A2 C3 C	C4 C5 A6	G7 A8	C9 T10	G11 A ²	2 G13	C14 A15	C16	G17 1	F18 G19	C20	Indel%
ABE 7.8	0.0	0.0	0.0		0.)	0.0					0.0
ABE 7.9	0.0	0.0	0.0		0.)	0.0					0.0
ABE 7.10	0.0	0.0	0.0		0.)	0.0					0.0
Cas9 nuclease	0.0	0.0	0.0		0.	2	0.0					1.0
D10A Cas9 nickase	0.0	0.0	0.0		0.))	0.0					0.0
H840A Cas9 nickase	0.0	0.0	0.0		0.))	0.0					0.0
	0.0	0.0	0.0		0.))	0.0					0.0
no treatment	0.0	0.0	0.0		0.	J	0.0					0.0
		0/			with terest A	T		2.0				1
HEK2 off target site 2	G1 A2 C3 /	×		encing reads	G11 C1	1 base pa	C14 A15		G17 1	C10	A20	Indol%
			01 A0	03 010	011 0	2 013		010		019	A20	
	0.0 0	0.0 0.0	0.1				0.0				0.0	0.0
ABE 7.9	0.0 0		0.0				0.0				0.0	0.0
	0.0 0	0.0 0.0	0.0				0.0				0.0	1.6
	0.0 0	0.0 0.0	0.0				0.0				0.0	0.0
	0.0 0	0.0 0.0	0.0				0.0				0.0	0.0
	0.0 0	0 00	0.0				0.0				0.0	0.0
no treatment	0.0 0	0 00	0.0				0.0				0.0	0.0
no doution.												
		%	of total seque	encing reads	with target A	T base pa	ir converted to	G•C				1
HEK3 off-target site 3	A1 G2 C3 1	[4 C5 A6	G7 A8	C9 T10	G11 A	2 G13	C14 A15	A16	G17 1	[18 G19	A20	Indel%
ABE 7.8	0.0	0.0	0.0		0.)	0.0	0.0			0.0	0.0
ABE 7.9	0.0	0.0	0.0		0.	C	0.0	0.0			0.0	0.0
ABE 7.10	0.0	0.0	0.0		0.	C	0.0	0.0			0.0	0.0
Cas9 nuclease	0.0	0.0	0.0		0.	C	0.0	0.0			0.0	0.2
D10A Cas9 nickase	0.0	0.0	0.0		0.	C	0.0	0.0			0.0	0.0
H840A Cas9 nickase	0.0	0.0	0.0		0.	C	0.0	0.0			0.0	0.0
dCas9 (D10A + H840A)	0.0	0.0	0.0		0.	D	0.0	0.0			0.0	0.0
no treatment	0.0	0.0	0.0		0.	C	0.0	0.0			0.0	0.0
												_
		%	of total seque	encing reads	with target A	T base pa	ir converted to	G•C				
HEK3 off-target site 4	A1 G2 A3 C	C4 C5 A6	G7 A8	C9 T10	G11 A ²	2 G13	C14 A15	A16	G17 A	A18 G19	A20	Indel%
ABE 7.8	0.0 0.0	0.0	0.0		0.	0	0.0	0.0	(0.0	0.0	0.0
ABE 7.9	0.0 0.0	0.0	0.0		0.	D	0.0	0.0	(0.0	0.0	0.0
ABE 7.10	0.0 0.0	0.0	0.0		0.)	0.0	0.0	(0.0	0.0	0.0
Cas9 nuclease	0.0 0.0	0.0	0.0		0.)	0.0	0.0	(0.0	0.0	0.0
D10A Cas9 nickase	0.0 0.0	0.0	0.0		0.	2	0.0	0.0	(0.0	0.0	0.0
H840A Cas9 nickase	0.0 0.0	0.0	0.0		0.)	0.0	0.0	(0.0	0.0	0.0
dCas9 (D10A + H840A)	0.0 0.0	0.0	0.0		0.)	0.0	0.0	(0.0	0.0	0.0
no treatment	0.0 0.0	0.0	0.0		0.)	0.0	0.0	(0.0	0.0	0.0
		%	of total seque	encing reads	with target A	I base pa	ir converted to	ن ور	o (= 1 -		1.67	
HEK3 off-target site 5	G1 A2 G3 C	C4 C5 A6	G7 A8	A9 T10	G11 A	2 G13	C14 A15	C16	G17 1	18 G19	A20	Indel%
ABE 7.8	0.0	0.0	0.0	0.0	0.	J	0.0				0.0	0.1
ABE 7.9	0.0	0.0	0.0	0.0	0.	J	0.0				0.0	0.1
ABE 7.10	0.0	0.0	0.0	0.0	0.	J	0.0				0.0	0.0
Case nuclease	0.0	0.0	0.0	0.0	0.		0.0				0.0	0.1
UTUA Case nickase	0.0	0.0	0.0	0.0	0.		0.0				0.0	0.0
	0.0	0.0	0.0	0.0	0.	1	0.0				0.0	0.1
ucase (D10A + 11640A)	0.0	0.0	0.0	0.0	0.	, 1	0.0				0.0	0.1
no treatment	0.0											

Supplementary Table 4. Activities of ABE7.8, ABE7.9, and ABE7.10 at the HEK4 site previously characterized for on-target and off-target modification by *S. pyogenes* Cas9 nuclease.¹ Although HEK4 off-target site 3 showed appreciable indel formation upon ABE treatment, this locus also showed unusually high (89%) indel formation by Cas9 nuclease and was the only tested off-target site exhibiting indel formation upon treatment with Cas9 nickases. We speculate that this locus is unusually fragile, and that indel formation here arises from simply nicking the site, rather than from ABE-mediated adenine deamination.

	% of total sequencing reads with target A•1 base pair converted to G•C	1
HEK4 (on-target site)	G1 G2 C3 A4 C5 T6 G7 C8 G9 G10 C11 T12 G13 G14 A15 G16 G17 T18 G19 G20	Indel%
ABE 7.8	4.8 0.0	0.2
ABE 7.9	1.5 0.0	0.1
ABE 7.10	16.0 0.0	0.2
Cas9 nuclease	0.1 0.0	36.5
D10A Cas9 nickase	0.0	0.8
H840A Cas9 nickase		0.7
		0.7
dCas9 (DT0A + H840A)		0.0
no treatment	0.0	0.0
	% of total sequencing reads with target A•T base pair converted to G•C	1
HEK4 off-target site 1	T1 G2 C3 A4 C5 T6 G7 C8 G9 G10 C11 C12 G13 G14 A15 G16 G17 A18 G19 G20	Indel%
ABE 7.8	0.0 0.0	0.1
ABE 7.9	0.2 0.0 0.0	0.0
ABE 7.10	1.2 0.0 0.0	0.0
Cas9 nuclease	00 02	12.3
		0.0
		0.0
		0.0
dCas9 (D10A + H840A)		0.0
no treatment	0.0 0.0 0.0	0.0
		1
	% of total sequencing reads with target A•T base pair converted to G•C	1
HEK4 off-target site 2	G1 G2 C3 T4 C5 T6 G7 C8 G9 G10 C11 T12 G13 G14 A15 G16 G17 G18 G19 G20	Indel%
ABE 7.8	0.0	0.0
ABE 7.9	0.0	0.0
ABE 7 10	0.0	0.0
	00	4.8
		4.0
DTUA Case nickase		0.0
H840A Cas9 hickase	0.0	0.0
dCas9 (D10A + H840A)	0.0	0.0
no trootmont	0.0	0.0
no treatment	0.0	
no treatment		
no treatment	% of total sequencing reads with target A+T base pair converted to G+C	I
HEK4 off-target site 3	% of total sequencing reads with target A•T base pair converted to G•C G1 G2 C3 A4 C5 G6 A7 C8 G9 G10 C11 T12 G13 G14 A15 G16 G17 T18 G19 G20	Indel%
HEK4 off-target site 3 ABE 7.8	% of total sequencing reads with target A•T base pair converted to G•C G1 G2 C3 A4 C5 G6 A7 C8 G9 G10 C11 T12 G13 G14 A15 G16 G17 T18 G19 G20 0.5 16.8 0.0	Indel% 1.1
HEK4 off-target site 3 ABE 7.8 ABE 7.9	% of total sequencing reads with target A•T base pair converted to G•C G1 G2 C3 A4 C5 G6 A7 C8 G9 G10 C11 T12 G13 G14 A15 G16 G17 T18 G19 G20 0.5 16.8 0.0 0.0 0.0 0.0 0.0	Indel% 1.1 1.7
HEK4 off-target site 3 ABE 7.8 ABE 7.9 ABE 7.10	% of total sequencing reads with target A+T base pair converted to G+C G1 G2 C3 A4 C5 G6 A7 C8 G9 G10 C11 T12 G13 G14 A15 G16 G17 T18 G19 G20 0.5 16.8 0.0	Indel% 1.1 1.7 3.7
HEK4 off-target site 3 ABE 7.8 ABE 7.9 ABE 7.10 Cas9 nuclease	% of total sequencing reads with target A*T base pair converted to G*C G1 G2 C3 A4 C5 G6 A7 C8 G9 G10 C11 T12 G13 G14 A15 G16 G17 T18 G19 G20 0.5 16.8 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.1	Indel% 1.1 1.7 3.7 89.1
HEK4 off-target site 3 ABE 7.8 ABE 7.9 ABE 7.10 Cas9 nuclease D104 Cas9 nickase	% of total sequencing reads with target A+T base pair converted to G+C G1 G2 C3 A4 C5 G6 A7 C8 G9 G10 C11 T12 G13 G14 A15 G16 G17 T18 G19 G20 0.5 16.8 0.2 21.9 0.0	Indel% 1.1 1.7 3.7 89.1 0.6
HEK4 off-target site 3 ABE 7.8 ABE 7.9 ABE 7.10 Cas9 nuclease D10A Cas9 nickase	% of total sequencing reads with target A*T base pair converted to G*C G1 G2 C3 A4 C5 G6 A7 C8 G9 G10 C11 T12 G13 G14 A15 G16 G17 T18 G19 G20 0.5 16.8 0.2 21.9 0.0	Indel% 1.1 1.7 3.7 89.1 0.6 1.4
HEK4 off-target site 3 ABE 7.8 ABE 7.9 ABE 7.10 Cas9 nuclease D10A Cas9 nickase H840A Cas9 nickase	% of total sequencing reads with target A*T base pair converted to G*C G1 G2 C3 A4 C5 G6 A7 C8 G9 G10 C11 T12 G13 G14 A15 G16 G17 T18 G19 G20 0.5 16.8 0.0	Indel% 1.1 1.7 3.7 89.1 0.6 1.4 0.0
HEK4 off-target site 3 ABE 7.8 ABE 7.9 ABE 7.10 Cas9 nuclease D10A Cas9 nickase H840A Cas9 nickase dCas9 (D10A + H840A)	% of total sequencing reads with target A*T base pair converted to G*C G1 G2 C3 A4 C5 G6 A7 C8 G9 G10 C11 T12 G13 G14 A15 G16 G17 T18 G19 G20 0.5 16.8 0.2 21.9 0.0	Indel% 1.1 1.7 3.7 89.1 0.6 1.4 0.0 0.0
HEK4 off-target site 3 ABE 7.8 ABE 7.9 ABE 7.10 Cas9 nuclease D10A Cas9 nickase H840A Cas9 nickase dCas9 (D10A + H840A) no treatment	% of total sequencing reads with target A*T base pair converted to G*C G1 G2 C3 A4 C5 G6 A7 C8 G9 G10 C11 T12 G13 G14 A15 G16 G17 T18 G19 G20 0.2 21.9 0.0	Indel% 1.1 1.7 3.7 89.1 0.6 1.4 0.0 0.0
HEK4 off-target site 3 ABE 7.8 ABE 7.9 ABE 7.10 Cas9 nuclease D10A Cas9 nickase H840A Cas9 nickase dCas9 (D10A + H840A) no treatment	% of total sequencing reads with target A*T base pair converted to G*C G1 G2 C3 A4 C5 G6 A7 C8 G9 G10 C11 T12 G13 G14 A15 G16 G17 T18 G19 G20 0.5 16.8 0.0	Indel% 1.1 1.7 3.7 89.1 0.6 1.4 0.0 0.0
HEK4 off-target site 3 ABE 7.8 ABE 7.9 ABE 7.10 Cas9 nuclease D10A Cas9 nickase H840A Cas9 nickase dCas9 (D10A + H840A) no treatment	% of total sequencing reads with target A*T base pair converted to G*C G1 G2 C3 A4 C5 G6 A7 C8 G9 G10 C11 T12 G13 G14 A15 G16 G17 T18 G19 G20 0.5 16.8 0.0	Indel% 1.1 1.7 3.7 89.1 0.6 1.4 0.0 0.0
HEK4 off-target site 3 ABE 7.8 ABE 7.9 ABE 7.10 Cas9 nuclease D10A Cas9 nickase H840A Cas9 nickase dCas9 (D10A + H840A) no treatment HEK4 off-target site 4	% of total sequencing reads with target A*T base pair converted to G*C G1 G2 C3 A4 C5 G6 A7 C8 G9 G10 C11 T12 G13 G14 A15 G16 G17 T18 G19 G20 0.5 16.8 0.2 21.9 0.0	Indel% 1.1 1.7 3.7 89.1 0.6 1.4 0.0 0.0 Indel%
HEK4 off-target site 3 ABE 7.8 ABE 7.9 ABE 7.10 Cas9 nuclease D10A Cas9 nickase H840A Cas9 nickase dCas9 (D10A + H840A) no treatment HEK4 off-target site 4 ABE 7.8	% of total sequencing reads with target A*T base pair converted to G*C G1 G2 C3 A4 C5 G6 A7 C8 G9 G10 C11 T12 G13 G14 A15 G16 G17 T18 G19 G20 0.5 16.8 0.0	Indel% 1.1 1.7 3.7 89.1 0.6 1.4 0.0 0.0 Indel% 0.0
HEK4 off-target site 3 ABE 7.8 ABE 7.9 ABE 7.10 Cas9 nuclease D10A Cas9 nickase H840A Cas9 nickase dCas9 (D10A + H840A) no treatment HEK4 off-target site 4 ABE 7.8 ABE 7.9	% of total sequencing reads with target A*T base pair converted to G*C G1 G2 C3 A4 C5 G6 A7 C8 G9 G10 C11 T12 G13 G14 A15 G16 G17 T18 G19 G20 0.5 16.8 0.0	Indel% 1.1 1.7 3.7 89.1 0.6 1.4 0.0 0.0 Indel% 0.0 0.0
HEK4 off-target site 3 ABE 7.8 ABE 7.9 ABE 7.10 Cas9 nuclease D10A Cas9 nickase H840A Cas9 nickase dCas9 (D10A + H840A) no treatment HEK4 off-target site 4 ABE 7.8 ABE 7.9 ABE 7.10	% of total sequencing reads with target A*T base pair converted to G*C G1 G2 G3 A4 C5 G6 A7 C8 G9 G10 C11 T12 G13 G14 A15 G16 G17 T18 G19 G20 0.5 16.8 0.0	Indel% 1.1 1.7 3.7 89.1 0.6 1.4 0.0 0.0 Indel% 0.0 0.0 0.0
HEK4 off-target site 3 ABE 7.8 ABE 7.9 ABE 7.10 Cas9 nuclease D10A Cas9 nickase H840A Cas9 nickase dCas9 (D10A + H840A) no treatment HEK4 off-target site 4 ABE 7.8 ABE 7.9 ABE 7.10 Cas9 nuclease	% of total sequencing reads with target A*T base pair converted to G*C G1 G2 C3 A4 C5 G6 A7 C8 G9 G10 C11 T12 G13 G14 A15 G16 G17 T18 G19 G20 0.5 16.8 0.0	Indel% 1.1 1.7 3.7 89.1 0.6 1.4 0.0 0.0 0.0 0.0 0.0 0.0 0.0 2.5
HEK4 off-target site 3 ABE 7.8 ABE 7.9 ABE 7.10 Cas9 nuclease D10A Cas9 nickase H840A Cas9 nickase dCas9 (D10A + H840A) no treatment HEK4 off-target site 4 ABE 7.8 ABE 7.9 ABE 7.10 Cas9 nuclease D10A Cas9 nickase	% of total sequencing reads with target A*T base pair converted to G*C G1 G2 G3 A4 C5 G6 A7 C8 G9 G10 C11 T12 G13 G14 A15 G16 G17 T18 G19 G20 0.5 16.8 0.0	Indel% 1.1 1.7 3.7 89.1 0.6 1.4 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0
HEK4 off-target site 3 ABE 7.8 ABE 7.9 ABE 7.10 Cas9 nuclease D10A Cas9 nickase H840A Cas9 nickase dCas9 (D10A + H840A) no treatment HEK4 off-target site 4 ABE 7.8 ABE 7.9 ABE 7.10 Cas9 nuclease D10A Cas9 nickase H840A Cas9 nickase H840A Cas9 nickase	% of total sequencing reads with target A*T base pair converted to G*C G1 G2 G3 A4 C5 G6 A7 C8 G9 G10 C11 T12 G13 G14 A15 G16 G17 T18 G19 G20 0.5 16.8 0.0	Indel% 1.1 1.7 3.7 89.1 0.6 1.4 0.0 0.0 Indel% 0.0 0.0 0.0 2.5 0.0 0.0
HEK4 off-target site 3 ABE 7.8 ABE 7.9 ABE 7.10 Cas9 nuclease D10A Cas9 nickase H840A Cas9 nickase dCas9 (D10A + H840A) no treatment HEK4 off-target site 4 ABE 7.8 ABE 7.9 ABE 7.10 Cas9 nuclease D10A Cas9 nickase H840A Cas9 nickase H840A Cas9 nickase	% of total sequencing reads with target A*T base pair converted to G*C G1 G2 C3 A4 C5 G6 A7 C8 G9 G10 C11 T12 G13 G14 A15 G16 G17 T18 G19 G20 0.5 16.8 0.2 21.9 0.0	Indel% 1.1 1.7 3.7 89.1 0.6 1.4 0.0 0.0 0.0 1ndel% 0.0 0.0 2.5 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0
HEK4 off-target site 3 ABE 7.8 ABE 7.9 ABE 7.10 Cas9 nuclease D10A Cas9 nickase dCas9 (D10A + H840A) no treatment HEK4 off-target site 4 ABE 7.8 ABE 7.9 ABE 7.10 Cas9 nuclease D10A Cas9 nickase H840A Cas9 nickase dCas9 (D10A + H840A)	% of total sequencing reads with target A*T base pair converted to G*C G1 G2 C3 A4 C5 G6 A7 C8 G9 G10 C11 T12 G13 G14 A15 G16 G17 T18 G19 G20 0.5 16.8 0.0	Indel% 1.1 1.7 3.7 89.1 0.6 1.4 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0
HEK4 off-target site 3 ABE 7.8 ABE 7.9 ABE 7.10 Cas9 nuclease D10A Cas9 nickase H840A Cas9 nickase dCas9 (D10A + H840A) no treatment HEK4 off-target site 4 ABE 7.8 ABE 7.9 ABE 7.10 Cas9 nuclease D10A Cas9 nickase H840A Cas9 nickase dCas9 (D10A + H840A) no treatment	% of total sequencing reads with target A*T base pair converted to G*C G1 G2 C3 A4 C5 G6 A7 C8 G9 G10 C11 T12 G13 G14 A15 G16 G17 T18 G19 G20 0.5 16.8 0.0	Indel% 1.1 1.7 3.7 89.1 0.6 1.4 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0
HEK4 off-target site 3 ABE 7.8 ABE 7.9 ABE 7.10 Cas9 nuclease D10A Cas9 nickase H840A Cas9 nickase dCas9 (D10A + H840A) no treatment HEK4 off-target site 4 ABE 7.8 ABE 7.9 ABE 7.10 Cas9 nuclease D10A Cas9 nickase H840A Cas9 nickase dCas9 (D10A + H840A) no treatment	% of total sequencing reads with target A*T base pair converted to G*C G1 G2 C3 A4 C5 G6 A7 C8 G9 G10 C11 T12 G13 G14 A15 G16 G17 T18 G19 G20 0.5 16.8 0.2 21.9 0.0	Indel% 1.1 1.7 3.7 89.1 0.6 1.4 0.0 0.0 Indel% 0.0 0.0 2.5 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0
HEK4 off-target site 3 ABE 7.8 ABE 7.9 ABE 7.10 Cas9 nuclease D10A Cas9 nickase H840A Cas9 nickase dCas9 (D10A + H840A) no treatment HEK4 off-target site 4 ABE 7.8 ABE 7.9 ABE 7.10 Cas9 nuclease D10A Cas9 nickase H840A Cas9 nickase dCas9 (D10A + H840A) no treatment	% of total sequencing reads with target A+T base pair converted to G+C G1 G2 C3 A4 C5 G6 A7 C8 G9 G10 C11 T12 G13 G14 A15 G16 G17 T18 G19 G20 0.5 16.8 0.2 21.9 0.0	Indel% 1.1 1.7 3.7 89.1 0.6 1.4 0.0 0.0 Indel% 0.0 0.0 0.0 2.5 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0
HEK4 off-target site 3 ABE 7.8 ABE 7.9 ABE 7.10 Cas9 nuclease D10A Cas9 nickase dCas9 (D10A + H840A) no treatment HEK4 off-target site 4 ABE 7.8 ABE 7.9 ABE 7.10 Cas9 nuclease D10A Cas9 nickase H840A Cas9 nickase dCas9 (D10A + H840A) no treatment	% of total sequencing reads with target A*T base pair converted to G*C G1 G2 C3 A4 C5 G6 A7 C8 G9 G10 C11 T12 G13 G14 A15 G16 G17 T18 G19 G20 0.5 16.8 0.2 21.9 0.0	Indel% 1.1 1.7 3.7 89.1 0.6 1.4 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0
HEK4 off-target site 3 ABE 7.8 ABE 7.9 ABE 7.10 Cas9 nuclease D10A Cas9 nickase H840A Cas9 nickase dCas9 (D10A + H840A) no treatment HEK4 off-target site 4 ABE 7.8 ABE 7.9 ABE 7.10 Cas9 nuclease D10A Cas9 nickase H840A Cas9 nickase dCas9 (D10A + H840A) no treatment HEK4 off-target site 5 ABE 7.8	% of total sequencing reads with target A+T base pair converted to G+C G1 G2 C3 A4 C5 G6 A7 C8 G9 G10 C11 T12 G13 G14 A15 G16 G17 T18 G19 G20 0.5 16.8 0.0	Indel% 1.1 1.7 3.7 89.1 0.6 1.4 0.0 0.0 Indel% 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.
HEK4 off-target site 3 ABE 7.8 ABE 7.9 ABE 7.10 Cas9 nuclease D10A Cas9 nickase H840A Cas9 nickase dCas9 (D10A + H840A) no treatment HEK4 off-target site 4 ABE 7.8 ABE 7.9 ABE 7.10 Cas9 nuclease D10A Cas9 nickase H840A Cas9 nickase dCas9 (D10A + H840A) no treatment HEK4 off-target site 5 ABE 7.8 ABE 7.9 ABE 7.9	% of total sequencing reads with target A+T base pair converted to G+C G1 G2 G3 A4 C5 G6 A7 C8 G9 G10 C11 T12 G13 G14 A15 G16 G17 T18 G19 G20 0.5 16.8 0.2 21.9 0.0	Indel% 1.1 1.7 3.7 89.1 0.6 1.4 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0
HEK4 off-target site 3 ABE 7.8 ABE 7.9 ABE 7.10 Cas9 nuclease D10A Cas9 nickase H840A Cas9 nickase dCas9 (D10A + H840A) no treatment HEK4 off-target site 4 ABE 7.8 ABE 7.9 ABE 7.10 Cas9 nuclease D10A Cas9 nickase H840A Cas9 nickase dCas9 (D10A + H840A) no treatment HEK4 off-target site 5 ABE 7.8 ABE 7.9 ABE 7.10	% of total sequencing reads with target A*T base pair converted to G*C G1 G2 G3 A4 C5 G6 AT C8 G9 G10 C11 T12 G13 G14 A15 G16 G17 T18 G19 G20 0.5 16.8 0.0	Indel% 1.1 1.7 3.7 89.1 0.6 1.4 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0
HEK4 off-target site 3 ABE 7.8 ABE 7.9 ABE 7.10 Cas9 nuclease D10A Cas9 nickase H840A Cas9 nickase dCas9 (D10A + H840A) no treatment HEK4 off-target site 4 ABE 7.8 ABE 7.9 ABE 7.10 Cas9 nuclease D10A Cas9 nickase H840A Cas9 nickase dCas9 (D10A + H840A) no treatment HEK4 off-target site 5 ABE 7.8 ABE 7.9 ABE 7.10 Cas9 nuclease	% of total sequencing reads with target A*T base pair converted to G*C G1 G2 G3 A4 C5 G6 A7 C8 G9 G10 C11 T12 G13 G14 A15 G16 G17 T18 G19 G20 0.5 16.8 0.0	Indel% 1.1 1.7 3.7 89.1 0.6 1.4 0.0 0.0 Indel% 0.0 0.0 2.5 0.0 0.0 0.0 Indel% 0.0 0.0 Indel% 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.
HEK4 off-target site 3 ABE 7.8 ABE 7.9 ABE 7.10 Cas9 nuclease D10A Cas9 nickase H840A Cas9 nickase dCas9 (D10A + H840A) no treatment HEK4 off-target site 4 ABE 7.8 ABE 7.9 ABE 7.10 Cas9 nuclease D10A Cas9 nickase dCas9 (D10A + H840A) no treatment HEK4 off-target site 5 ABE 7.9 ABE 7.9 ABE 7.10 Cas9 nuclease D10A Cas9 nickase dCas9 (D10A + H840A)	% of total sequencing reads with target A+T base pair converted to G+C G1 G2 C3 A4 C5 G6 A7 C8 G9 G10 C11 T12 G13 G14 A15 G16 G17 T18 G19 G20 0.5 0.5 0.6 A7 C8 G9 G10 C11 T12 G13 G14 A15 G16 G17 T18 G19 G20 0.2 21.9 0.0 <	Indel% 1.1 1.7 3.7 89.1 0.6 1.4 0.0 0.0 Indel% 0.0 0.0 2.5 0.0 0.0 0.0 Indel% 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.
HEK4 off-target site 3 ABE 7.8 ABE 7.9 ABE 7.10 Cas9 nuclease D10A Cas9 nickase H840A Cas9 nickase dCas9 (D10A + H840A) no treatment HEK4 off-target site 4 ABE 7.8 ABE 7.9 ABE 7.10 Cas9 nuclease D10A Cas9 nickase H840A Cas9 nickase dCas9 (D10A + H840A) no treatment HEK4 off-target site 5 ABE 7.8 ABE 7.9 ABE 7.10 Cas9 nuclease D10A Cas9 nickase H840A Cas9 nickase dCas9 (D10A + H840A) no treatment	% of total sequencing reads with target A-T base pair converted to G-C G1 G2 C3 A4 C5 G1 G2 G1	Indel% 1.1 1.7 3.7 89.1 0.6 1.4 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0
HEK4 off-target site 3 ABE 7.8 ABE 7.9 ABE 7.10 Cas9 nuclease D10A Cas9 nickase dCas9 (D10A + H840A) no treatment HEK4 off-target site 4 ABE 7.8 ABE 7.9 ABE 7.10 Cas9 nuclease D10A Cas9 nickase dCas9 (D10A + H840A) no treatment HEK4 off-target site 5 ABE 7.8 ABE 7.9 ABE 7.10 Cas9 nuclease D10A Cas9 nickase H840A Cas9 nickase dCas9 (D10A + H840A) no treatment	% of total sequencing reads with target A*T base pair converted to G*C G1 G2 C3 A4 C5 G6 A7 C8 G9 G10 C11 T12 G13 G14 A15 G16 G17 T18 G19 G20 0.5 16.8 0.0	Indel% 1.1 1.7 3.7 89.1 0.6 1.4 0.0 0.0 Indel% 0.0 0.0 2.5 0.0 0.0 0.0 0.0 Indel% 0.0 0.0 0.0 Indel% 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.
HEK4 off-target site 3 ABE 7.8 ABE 7.9 ABE 7.10 Cas9 nuclease D10A Cas9 nickase H840A Cas9 nickase dCas9 (D10A + H840A) no treatment HEK4 off-target site 4 ABE 7.8 ABE 7.9 ABE 7.10 Cas9 nuclease D10A Cas9 nickase H840A Cas9 nickase dCas9 (D10A + H840A) no treatment HEK4 off-target site 5 ABE 7.9 ABE 7.9 ABE 7.10 Cas9 nuclease D10A Cas9 nickase dCas9 nuclease D10A Cas9 nickase dCas9 (D10A + H840A)	% of total sequencing reads with target A-T base pair converted to G-C G1 G2 C3 A4 C5 G6 A7 C8 G9 G1 C11 T12 G13 G14 A15 G16 G17 T18 G19 G20 0.5 16.8 0.0	Indel% 1.1 1.7 3.7 89.1 0.6 1.4 0.0 0.0 Indel% 0.0 0.0 2.5 0.0 0.0 0.0 Indel% 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.

Supplementary Table 5. Primers used for generating sgRNA plasmids. The 20-nt target protospacer is shown in red. When a target DNA sequence did not start with a 'G', a 'G' was added to the 5' end of the primer since the human U6 promoter prefers a 'G' at the transcription start site²⁻⁴. The pFYF sgRNA plasmid described previously⁵ was used as a template for PCR amplification.

Primer	Sequence
R-sgRNA	5'-GGTGTTTCGTCCTTTCCACAAG-3'
F-site 1	5'-GAACACAAAGCATAGACTGCGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC-3'
F-site 2	5'-GAGTATGAGGCATAGACTGCGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC-3'
F-site 3	5'-GTCAAGAAAGCAGAGACTGCGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC-3'
F-site 4	5'-GAGCAAAGAGAATAGACTGTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC-3'
F-site 5	5'-GATGAGATAATGATGAGTCAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC-3'
F-site 6	5'-GGATTGACCCAGGCCAGGGCGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC-3'
F-site 7	5'-GAATACTAAGCATAGACTCCGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC-3'
F-site 8	5'-GTAAACAAAGCATAGACTGAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC-3'
F-site 9	5'-GAAGACCAAGGATAGACTGCGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC-3'
F-site 10	5'-GAACATAAAGAATAGAATGAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC-3'
F-site 11	5'-GGACAGGCAGCATAGACTGTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC-3'
F-site 12	5'-GTAGAAAAGTATAGACTGCGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC-3'
F-site 13	5'-GAAGATAGAGAATAGACTGCGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC-3'
F-site 14	5'-GGCTAAAGACCATAGACTGTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC-3'
F-site 15	5'-GTCTAGAAAGCTTAGACTGCGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC-3'
F-site 16	5'-GGGAATAAATCATAGAATCCGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC-3'
F-site 17	5'-GACAAAGAGGAAGAGAGAGGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC-3'
F-site 18	5'-GACACACACACTTAGAATCTGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC-3'
F-site 19	5'- GCACACACACTTAGAATCTGTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC-3'
F- hbg1/2	5'-GTGGGGAAGGGGCCCCCAAGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC-3'
F-HFE	5'- GACGTACCAGGTGGAGCACCCGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC-3'

Supplementary Table 6. Primers used for generating bacterial TadA* libraries.

Primer	Sequence
NMG-799	AGTTGTACGCG/ideoxyU/CCAAAAAACGGG
NMG-822	AGATTAGCGGATCCTACCTGAC
NMG-823	GCGGTCTGTATTTCCCAGAAC
NMG-824	ACCGGGGACTTCAGAA/ideoxyU/CGGC
NMG-825	ATTCTGAAGTCCCCGG/ideoxyU/GTTTCG
NMG-826	ACGCGTACAAC/ideoxyU/CAAAGGAGGAAAAAAAAAGG
NMG-1197	ACGCTGGCGAAACG/ideoxyU/GCCTGGGATNNKNNKGAAGTGCCGGTCGGCGC
NMG-1198	ACGTTTCGCCAGCG/ideoxyU/CAGCGCGTGACG
NMG-1199	ACGCGAAAACTGGCGC/ideoxyU/GCG
NMG-1200	AGCGCCAGTTTTCGCG/ideoxyU/TMNNCACACCAAAGACCACGCGACC
NMG-1201	ACTGGCGGATGAG/ideoxyU/GCNNKNNKTTGCTCAGTTACTTCTTTCGCATGCG
NMG-1202	ACTCATCCGCCAG/ideoxyU/ATTCCTTCCG

Supplementary Table 7. Starting constructs used for each round of TadA* mutagenesis and selection in *E. coli*. All plasmids contain an SC101 origin of replication, a β -lactamase gene for plasmid maintenance with carbenicillin, a P_{BAD} promoter driving TadA*–dCas9 expression, and a lac promoter driving sgRNA transcription. The architecture of the base editors used during bacterial selection is: TadA*–linker(16 aa)–dCas9.

Round	Template used for mutagenesis	TadA mutations	Guide RNA protospacer 1	Guide RNA protospacer 2
1	nNMG-104	wild-type	TACGGCGTAGTGCACCTGGA	n/a
2	pNMG-128	H8Y, D108N, N127S	TACGGCGTAGTGCACCTGGA	n/a
3	pNMG-288	A106V, D108N, D147Y, E155V	ATCTTATTCGATCATGCGAA	GCTTAGGTGGAGCGCCTATT
4	pNMG-343	A106V, D108N, D147Y, E155V	CAATGATGACTTCTACAGCG	n/a
5	pNMG-381	L84F, A106V, D108N, H123Y, D147Y, E155V, I156F	CAATGATGACTTCTACAGCG	TACGGCGTAGTGCACCTGGA
6	round 1-5 plasmids + pNMG-104	all mutations accumulated	CAATGATGACTTCTACAGCG	TACGGCGTAGTGCACCTGGA
7	multiple round 6 plasmids	H36L, P48S, L84P, S97C, A106V, D108N, H123Y, S146C, D147Y, E155V, I156F, K157N, K161T	TTCATTAACTGTGGCCGGCT	ATCTTATTCGATCATGCGAA

Supplementary Table 8. Antibiotic selection plasmids and their corresponding *E. coli* antibiotic minimum inhibitory concentrations (MICs).

Round	Antibiotic resistance	Target sequence	Inactivating mutation	Position of target A in protospacer	MIC in S1030 cells (µg/mL)	Selection antibiotic concentration (µg/mL)	Library c.f.u. after USER assembly
1	Cam ^R	TACGGCGTAGTGCACCTGGA	H193Y	9	1	2, 4, 8, 16	2 x 10 ⁶
2	Cam ^R	TACGGCGTAGTGCACCTGGA	H193Y	9	1	16, 32, 64, 128	2 x 10 ⁶
3	Kan ^R	ATCTTATTCGATCATGCGAA GCTTAGGTGGAGCGCCTATT	Q4* and W15*	6, 5	8	16, 32, 64, 128	5 x 10 ⁶
4	Spect ^R	CAATGATGACTTCTACAGCG	T89I	6	32	64, 128, 256, 512	5 x 10 ⁶
5	Spect ^R Cam ^R	CAATGATGACTTCTACAGCG TACGGCGTAGTGCACCTGGA	T89I (spect) H193Y (chlor)	6, 9	32(spect) 1 (chlor)	64, 128, 256, 512 (spect) 16, 32, 64, 128 (chlor)	5 x 10 ⁶
6	Spect ^R	CAATGATGACTTCTACAGCG	T89I	6, 9	32	128, 256, 384, 512	5 x 10 ⁶
7	Kan ^ĸ	ATCTTATTCGATCATGCGAA TTCATTAACTGTGGCCGGCT	Q4* and D208N	6, 7	8	64, 128, 256, 384	8 x 10 ⁶

Supplementary Table 9. Primers used for mammalian cell genomic DNA and RNA amplification.

Primer name	Sequence
fwd_site 1_HTS	ACACTCTTTCCCTACACGACGCTCTTCCGATCTNNNNCCAGCCCCATCTGTCAAACT
rev_site 1_HTS	TGGAGTTCAGACGTGTGCTCTTCCGATCTTGAATGGATTCCTTGGAAACAATGA
fwd_site 2_HTS	ACACTCTTTCCCTACACGACGCTCTTCCGATCTNNNNAGAGACTGATTGCGTGGAGT
rev_site 2_HTS	TGGAGTTCAGACGTGTGCTCTTCCGATCTCACTCCAGCCTAGGCAACAA
fwd_site 3_HTS	ACACTCTTTCCCTACACGACGCTCTTCCGATCTNNNNCCGACAGCCAGTGGTTAAGT
rev_site 3_HTS	TGGAGTTCAGACGTGTGCTCTTCCGATCTGCTTTTCACCGACTGCACAG
fwd_site 4_HTS	ACACTCTTTCCCTACACGACGCTCTTCCGATCTNNNNCTGCACCTAGCCTCCATGTC
rev_site 4_HTS	TGGAGTTCAGACGTGTGCTCTTCCGATCTCCTTGCACTGAGACCGTGAA
fwd_site 5_HTS	ACACTCTTTCCCTACACGACGCTCTTCCGATCTNNNNGTCTGAGGTCACACAGTGGG
rev_site 5_HTS	TGGAGTTCAGACGTGTGCTCTTCCGATCTCTGAGAGCAGGGACCACATC
fwd_site 6_HTS	ACACTCTTTCCCTACACGACGCTCTTCCGATCTNNNNATGTGGGCTGCCTAGAAAGG
rev_site 6_HTS	TGGAGTTCAGACGTGTGCTCTTCCGATCTCCCAGCCAAACTTGTCAACC
fwd_site 7_HTS	ACACTCTTTCCCTACACGACGCTCTTCCGATCTNNNNGATGCCCTCCATCTTCTCCG
rev_site 7_HTS	TGGAGTTCAGACGTGTGCTCTTCCGATCTAGGTTTGCATAGACCTGCCC
fwd_site 8_HTS	ACACTCTTTCCCTACACGACGCTCTTCCGATCTNNNNCCCTGTTCCTAAAGCCCACC
rev_site 8_HTS	TGGAGTTCAGACGTGTGCTCTTCCGATCTACTGGTTCTGTTTGTGGCCA
fwd_site 9_HTS	ACACTCTTTCCCTACACGACGCTCTTCCGATCTNNNNTTGCTTATTGCTGAGGGGGCA
rev_site 9_HTS	TGGAGTTCAGACGTGTGCTCTTCCGATCTACCTCTCTCCCAGCTGAG
fwd_site 10_HTS	ACACTCTTTCCCTACACGACGCTCTTCCGATCTNNNNTCCACCTCCCCACTTCTCTT
rev_site 10_HTS	TGGAGTTCAGACGTGTGCTCTTCCGATCTGGTGAAATGAGCAAGGCACA
fwd_site 11_HTS	ACACTCTTTCCCTACACGACGCTCTTCCGATCTNNNNCCCTAAACCACCTGCAGAGG
rev_site 11_HTS	TGGAGTTCAGACGTGTGCTCTTCCGATCTCAGCCCCAGCCACATTCTAT
fwd_site 12_HTS	ACACTCTTTCCCTACACGACGCTCTTCCGATCTNNNNACCCATGTGCCTGACATAGG
rev_site 12_HTS	TGGAGTTCAGACGTGTGCTCTTCCGATCTTGGTGATTATGGTTACACAGCG
fwd_site 13_HTS	ACACTCTTTCCCTACACGACGCTCTTCCGATCTNNNNTCACTTCAGCCCAGGAGTAT
rev_site 13_HTS	TGGAGTTCAGACGTGTGCTCTTCCGATCTTCTCTCTCTCCCCCACCC
fwd_site 14_HTS	ACACTCTTTCCCTACACGACGCTCTTCCGATCTNNNNGAACCTGAAGCCTTTCCCCA
rev_site 14_HTS	TGGAGTTCAGACGTGTGCTCTTCCGATCTAACCTGTGTGACACTTGGCA
fwd_site 15_HTS	ACACTCTTTCCCTACACGACGCTCTTCCGATCTNNNNGCAGACACCCACAACTGTCT
rev_site 15_HTS	TGGAGTTCAGACGTGTGCTCTTCCGATCTGCACTCAGCTAGACTTAACTCCC
fwd_site 16_HTS	ACACTCTTTCCCTACACGACGCTCTTCCGATCTNNNNGGGAGGTGGAGAGAGGATGT
rev_site 16_HTS	TGGAGTTCAGACGTGTGCTCTTCCGATCTTCCTGAGGTCTAGGAACCCG
fwd_site 17_HTS	ACACTCTTTCCCTACACGACGCTCTTCCGATCTNNNNCGCGGGCTGAAGTAGATCAA

rev_site 17_HTS	TGGAGTTCAGACGTGTGCTCTTCCGATCTCCTGTCTCTGCTCCTTTGTCCCC
fwd_site 18/19_HTS	ACACTCTTTCCCTACACGACGCTCTTCCGATCTNNNNGCATTACCTGGGAGCCTGTT
rev_site 18/19_HTS	TGGAGTTCAGACGTGTGCTCTTCCGATCTAACTTCAGCGGGCATCAGAA
fwd_site HGB1/2_HTS	ACACTCTTTCCCTACACGACGCTCTTCCGATCTNNNNGTGGAGTTTAGCCAGGGACC
rev_site HGB1/2_HTS	TGGAGTTCAGACGTGTGCTCTTCCGATCTTACAGGCCTCACTGGAGCTA
fwd_site HFE_HTS	ACACTCTTTCCCTACACGACGCTCTTCCGATCTNNNNGGCTGGATAACCTTGGCTGT
rev_site HFE_HTS	TGGAGTTCAGACGTGTGCTCTTCCGATCTTCCTCAGGCACTCCTCTAA
fwd_HEK2_HTS	ACACTCTTTCCCTACACGACGCTCTTCCGATCTNNNNCCAGCCCCATCTGTCAAACT
rev_HEK2_HTS	TGGAGTTCAGACGTGTGCTCTTCCGATCTTGAATGGATTCCTTGGAAACAATGA
fwd_HEK3_HTS	ACACTCTTTCCCTACACGACGCTCTTCCGATCTNNNNATGTGGGCTGCCTAGAAAGG
rev_HEK3_HTS	TGGAGTTCAGACGTGTGCTCTTCCGATCTCCCAGCCAAACTTGTCAACC
fwd_HEK4_HTS	ACACTCTTTCCCTACACGACGCTCTTCCGATCTNNNNGAACCCAGGTAGCCAGAGAC
rev_HEK4_HTS	TGGAGTTCAGACGTGTGCTCTTCCGATCTTCCTTTCAACCCGAACGGAG
fwd_HEK2_off1_HTS	ACACTCTTTCCCTACACGACGCTCTTCCGATCTNNNNGTGTGGAGAGTGAGTAAGCCA
rev_HEK2_off1_HTS	TGGAGTTCAGACGTGTGCTCTTCCGATCTACGGTAGGATGATTTCAGGCA
fwd_HEK2_off2_HTS	ACACTCTTTCCCTACACGACGCTCTTCCGATCTNNNNCACAAAGCAGTGTAGCTCAGG
rev_HEK2_off2_HTS	TGGAGTTCAGACGTGTGCTCTTCCGATCTTTTTGGTACTCGAGTGTTATTCAG
fwd_HEK3 off1_HTS	ACACTCTTTCCCTACACGACGCTCTTCCGATCTNNNNTCCCCTGTTGACCTGGAGAA
rev_HEK3_off1_HTS	TGGAGTTCAGACGTGTGCTCTTCCGATCTCACTGTACTTGCCCTGACCA
fwd_HEK3_off2_HTS	ACACTCTTTCCCTACACGACGCTCTTCCGATCTNNNNTTGGTGTTGACAGGGAGCAA
rev_HEK3_off2_HTS	TGGAGTTCAGACGTGTGCTCTTCCGATCTCTGAGATGTGGGCAGAAGGG
fwd_HEK3_off3_HTS	ACACTCTTTCCCTACACGACGCTCTTCCGATCTNNNNTGAGAGGGAACAGAAGGGCT
rev_HEK3_off3_HTS	TGGAGTTCAGACGTGTGCTCTTCCGATCTGTCCAAAGGCCCAAGAACCT
fwd_HEK3_off4_HTS	ACACTCTTTCCCTACACGACGCTCTTCCGATCTNNNNTCCTAGCACTTTGGAAGGTCG
rev_HEK3_off4_HTS	TGGAGTTCAGACGTGTGCTCTTCCGATCTGCTCATCTTAATCTGCTCAGCC
fwd_HEK3_off5_HTS	ACACTCTTTCCCTACACGACGCTCTTCCGATCTNNNNAAAGGAGCAGCTCTTCCTGG
rev_HEK3_off5_HTS	TGGAGTTCAGACGTGTGCTCTTCCGATCTGTCTGCACCATCTCCCACAA
fwd_HEK4_off1_HTS	ACACTCTTTCCCTACACGACGCTCTTCCGATCTNNNNGGCATGGCTTCTGAGACTCA
rev_HEK4_off1_HTS	TGGAGTTCAGACGTGTGCTCTTCCGATCTGTCTCCCTTGCACTCCCTGTCTTT
fwd_HEK4_off2_HTS	ACACTCTTTCCCTACACGACGCTCTTCCGATCTNNNNTTTGGCAATGGAGGCATTGG
rev_HEK4_off2_HTS	TGGAGTTCAGACGTGTGCTCTTCCGATCTGAAGAGGCTGCCCATGAGAG
fwd_HEK4_off3_HTS	ACACTCTTTCCCTACACGACGCTCTTCCGATCTNNNNGGTCTGAGGCTCGAATCCTG
rev_HEK4_off3_HTS	TGGAGTTCAGACGTGTGCTCTTCCGATCTCTGTGGCCTCCATATCCCTG
fwd_HEK4_off4_HTS	ACACTCTTTCCCTACACGACGCTCTTCCGATCTNNNNTTTCCACCAGAACTCAGCCC
rev_HEK4_off4_HTS	TGGAGTTCAGACGTGTGCTCTTCCGATCTCCTCGGTTCCTCCACAACAC

fwd_HEK4_off5_HTS	ACACTCTTTCCCTACACGACGCTCTTCCGATCTNNNNCACGGGAAGGACAGGAGAAG
rev_HEK4_off5_HTS	TGGAGTTCAGACGTGTGCTCTTCCGATCTGCAGGGGGGGG
fwd_site 1_HDR_HTS	ACACTCTTTCCCTACACGACGCTCTTCCGATCTNNNNCCAGCCCCATCTGTCAAACT
rev_site 1_HDR_HTS	TGGAGTTCAGACGTGTGCTCTTCCGATCTTGAATGGATTCCTTGGAAACAATGA
fwd_site 2_HDR_HTS	ACACTCTTTCCCTACACGACGCTCTTCCGATCTNNNNCCCTGAGATACAGTCACGAGGT
rev_site 2_HDR_HTS	TGGAGTTCAGACGTGTGCTCTTCCGATCTCCTGAAATGCTGTGCGTGTCTA
fwd_site 3_HDR_HTS	ACACTCTTTCCCTACACGACGCTCTTCCGATCTNNNNGCCCACATTACCTTGGTGCATA
rev_site 3_HDR_HTS	TGGAGTTCAGACGTGTGCTCTTCCGATCTGGCAGGCAGATTATCATTCCCA
fwd_site 4_HDR_HTS	ACACTCTTTCCCTACACGACGCTCTTCCGATCTNNNNAAAGTGCTGCGATTACAGGC
rev_site 4_HDR_HTS	TGGAGTTCAGACGTGTGCTCTTCCGATCTGTGGCATCCAGAGACATGGT
fwd_site 6_HDR_HTS	ACACTCTTTCCCTACACGACGCTCTTCCGATCTNNNNATGTGGGCTGCCTAGAAAGG
rev_site 6_HDR_HTS	TGGAGTTCAGACGTGTGCTCTTCCGATCTCCCAGCCAAACTTGTCAACC
B_Catenin_mRNA _fwd	ACACTCTTTCCCTACACGACGCTCTTCCGATCTNNNNATTTGATGGAGTTGGACATGGCC
B_Catenin_mRNA _rev	TGGAGTTCAGACGTGTGCTCCCAGCTACTTGTTCTTGAGTGAAGG
B_Actin_mRNA_fwd	ACACTCTTTCCCTACACGACGCTCTTCCGATCTNNNNGACAAAACCTAACTTGCGCAGAAAACAAGATG
B_Actin_mRNA_rev	TGGAGTTCAGACGTGTGCTCTGCTTTTAGGATGGCAAGGGACTTCCTG
GAPDH_mRNA_fwd	ACACTCTTTCCCTACACGACGCTCTTCCGATCTNNNNGGCTACAGCAACAGGGTGGTGGAC
GAPDH_mRNA_rev	TGGAGTTCAGACGTGTGCTCTCCATCAATAAAGTACCCTGTGCTCAACC
RB1_mRNA_fwd	ACACTCTTTCCCTACACGACGCTCTTCCGATCTNNNNGGAAGGATTATGATAGGGACAAGG
RB1_mRNA_rev	TGGAGTTCAGACGTGTGCTCTCCACAATTTCCTTCATATGTTCAAAC

Supplementary Table 10. 100-mer single-stranded oligonucleotide donor templates (ssODNs) used in HDR experiments.

Target site	Sequence
1	5'-TTTTCCAGCCCGCTGGCCCTGTAAAGGAAACTGGAACGCAAAGCATAGACTGCGCGGCGG GCCAGCCTGAATAGCTGCAAACAAGTGCAGAATATCTGAT-3'
2	5'-CATGAAAAAGAGACTGATTGCGTGGAGTTCATGGAGTGTGAGGCATAGACTGCACGAGACA TAAACCATGACTTGCAGATGAAGAAGCATTTTAAAAGT-3'
3	5'-GACAGCCAGTGGTTAAGTCAGAACCCGACTCAGGTCAGG
4	5'-ATTTTAAGCTGTAGTATTATGAAGGGAAATCTGGAGCGAAGAGAATAGACTGTACGGAAACC AGTTAAGAAATAGGACATGGAGGCTAGGTGCAGTGGCT-3'
6	5'-CCTCTGCCATCACGTGCTCAGTCTGGGCCCCAAGGATTGGCCCAGGCCAGGGCTCGAGAA GCAGAAAAAAGCATCAAGCCTACAAATGCATGCTTACTT-3'

Supplementary Sequences 1. DNA sequences of adenine deaminases used in this study.

Bacterial codon-optimized ecTadA (wild-type):

ATGTCTGAAGTCGAATTTAGCCACGAATACTGGATGCGTCACGCGCTGACGCTGGCGAAACGTGCCTGGGATGAGC GGGAAGTGCCGGTCGGCGCGGTATTAGTGCATAACAATCGGGTAATCGGCGAAGGCTGGAACCGCCCGATTGGTC GCCATGATCCCACCGCACATGCAGAAATCATGGCCCTGCGGGCAGGGTGGTCTGGTGATGCAAAATTATCGTCTGATC GACGCCACGTTGTATGTCACGCTTGAACCATGTGTAATGTGTGCCGGAGCGATGATCCACAGTCGCATTGGTCGCGT GGTCTTTGGTGCGCGTGACGCGAAAACTGGCGCTGCGGGATCTTTAATGGATGTGCTGCATCATCCGGGTATGAATC ACCGAGTGGAAATTACGGAAGGAATACTGGCCGGATGAGTGCGCGGCGTTGCTCAGTGACTTCTTTCGCATGCGCCG CCAGGAAATTAAAGCGCAGAAAAAGCGCCAATCCTCGACGGAT

Mammalian codon-optimized ecTadA (wild-type):

Mammalian codon-optimized mADA:

Mammalian codon optimized hADAR2 (catalytic domain):

ATGCATCTCGATCAAACCCCGAGCCGCCAACCAATCCCGAGTGAAGGCCTGCAACTGCATCTGCCACAAGTTCTGGC AGGTGCTGGCTGGCGTTGTGATGACCACAGGTACAGACGTCAAAGATGCTAAAGTGATTTCTGTGTCTACTGGCACG AAGTGCATTAACGGCGAATATATGTCTGACCGTGGCTTAGCGCTTAACGATTGTCATGCCGAAATCATCTCCCGTCGT TCATTGCTTCGCTTCCTGTACACGCAGTTGGAACTGTATCTGAATAACAAAGACGATCAGAAGCGTTCTATTTTCCAG AAGTCTGAGCGCGGCGGGTTCCGTCTTAAAGAGAATGTGCAGTTTCACCTTTATATTTCAACCTCTCCTTGTGGTGAT GCCCGTATTTTTTCACCACGAACCTATTTTAGAGGAACCGGCCGATCGTCATCCGAACCGCAAAGCCCGTGGGCA GCTGCGTACGAAAATCGAATCAGGTGAAGGCACCATTCCCGTCCGCTCCAATGCGAGCATTCAAACGTGGGACGGT GTGTTACAGGGCGAACGCCTGTTAACCATGAGCTGCTCAGACAAAATTGCACGTTGGAACGTGGTAGGCATCCAGG GCTCGTTATTGAGCATTTTCGTGGAGCCGATTTATTTTAGTTCCATCATTTTGGGCTCACTCTACCACGGCGATCACCT TAGCCGCGCGATGTACCAGCGCATTAGTAACATCGAAGATTTACCGCCCCTGTATACCCCTGAACAAACCACTGTTAA GCGGTATTTCTAACGCGGAGGCGCGTCAGCCTGGTAAAGCCCCGAACTTCAGTGTGAACTGGACTGTGGGTGATTC TGCAATTGAGGTAATTAACGCGACGACGGGTAAAGATGAACTGGGCCGTGCCTCTCGTCTGTGTAAACACGCGCTGT ACTGTCGTTGGATGCGCGTGCACGGTAAAGTTCCCAGTCATCTGTTACGTAGCAAGATCACCAAGCCAAATGTCTAC AGGGGCCTGGGTGGAAAAACCAACCGAGCAAGATCAATTCAGTCTGACCCCG

Mammalian codon optimized hADAT2:

ATGGAGGCGAAGGCGGCACCCAAGCCAGCTGCAAGCGGCGCGTGCTCGGTGTCGGCAGAGAGGAGACCGAAAAGTG GATGGAGGAGGCGATGCACATGGCCAAAGAAGCCCTCGAAAATACTGAAGTTCCTGTTGGCTGTCTTATGGTCTACA ACAATGAAGTTGTAGGGAAGGGGAGAAATGAAGTTAACCAAACCAAAAATGCTACTCGACATGCAGAAATGGTGGCC ATCGATCAGGTCCTCGATTGGTGTCGTCAAAGTGGCAAGAGTCCCTCTGAAGTATTTGAACACACTGTGTTGTATGTC ACTGTGGAGCCGTGCATTATGTGTGCAGCTGCTCTCCGCCTGATGAAAATCCCGCTGGTTGTATATGGCTGTCAGAA TGAACGATTTGGTGGTTGTGGCTCTGTTCTAAATATTGCCTCTGCTGACCTACCAAACACTGGGAGACCATTTCAGTG **Supplementary Sequences 2.** DNA sequences of antibiotic resistance genes used in this study. Inactivating mutations are shown in red.

Chloramphenicol resistance gene (Cam^R) H193Y:

Kanamycin resistance gene (Kan^R) Q4STOP and W15STOP:

Spectinomycin resistance gene (Spect^R) T89I:

Kanamycin resistance gene (Kan^R) Q4STOP and D208N:

Supplementary Sequences 3. Amino acid sequences of late-stage ABEs developed in this study.

Color coding is as follows: green = ecTadA (wt), monomer 1 of 2 orange = linker black + red = evolved ecTadA* internal monomer 2 of 2, with mutations highlighted in red blue = Cas9 nickase (D10A mutation underlined) purple = NLS

ABE6.3 (ecTadA(wt)–linker(32 aa)–ecTadA*(6.3)–linker(32 aa)–Cas9 nickase–NLS):

MSEVEFSHEYWMRHALTLAKRAWDEREVPVGAVLVHNNRVIGEGWNRPIGRHDPTAHAEIMALRQGGLVMQNYRLIDAT LYVTLEPCVMCAGAMIHSRIGRVVFGARDAKTGAAGSLMDVLHHPGMNHRVEITEGILADECAALLSDFFRMRRQEIKAQK KAQSSTDSGGSSGGSSGSETPGTSESATPESSGGSSGGSSEVEFSHEYWMRHALTLAKRAWDEREVPVGAVLVLNNRV IGEGWNR<mark>S</mark>IGLHDPTAHAEIMALRQGGLVMQNYRLIDATLYVTFEPCVMCAGAMIHSRIGRVVFG<mark>V</mark>RNAKTGAAGSLMDV LHYPGMNHRVEITEGILADECAALLCYFRMRRQVFNAQKKAQSSTDSGGSSGGSSGSETPGTSESATPESSGGSSGGS DKKYSIGLAIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQE IFSNEMAKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGH FLIEGDLNPDNSDVDKLFIQLVQTYNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPN FKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLL KALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKLNREDLLRKQRTFDNGSIPHQIHLG ELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIERMTNFD KNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISG VEDRFNASLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRK LINGIRDKQSGKTILDFLKSDGFANRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELV KVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIKELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQEL DINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKNRGKSDNVPSEEVVKKMKNYWRQLLNAKLITQRKFDNLTKAERGGLS ELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAV VGTALIKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDK GRDFATVRKVLSMPQVNIVKKTEVQTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKL KSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKYSLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASH YEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFK YFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDSGGSPKKKRKV*

ABE7.8 (ecTadA(wt)-linker(32 aa)-ecTadA*(7.8)-linker(32 aa)-Cas9 nickase-NLS):

MSEVEFSHEYWMRHALTLAKRAWDEREVPVGAVLVHNNRVIGEGWNRPIGRHDPTAHAEIMALRQGGLVMQNYRLIDAT LYVTLEPCVMCAGAMIHSRIGRVVFGARDAKTGAAGSLMDVLHHPGMNHRVEITEGILADECAALLSDFFRMRRQEIKAQK KAQSSTDSGGSSGGSSGSETPGTSESATPESSGGSSGGSSEVEFSHEYWMRHALTLAKRALDEREVPVGAVLVLNNRVI GEGWNRAIGLHDPTAHAEIMALRQGGLVMQNYRLIDATLYVTFEPCVMCAGAMIHSRIGRVVFGVRNAKTGAAGSLMDVL HYPGMNHRVEITEGILADECNALLCYFFRMRRQVFNAQKKAQSSTDSGGSSGGSSGSETPGTSESATPESSGGSSGGSD KKYSIGLAIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEI FSNEMAKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHF LIEGDLNPDNSDVDKLFIQLVQTYNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNF KSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLK ALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKLNREDLLRKQRTFDNGSIPHQIHLGEL HAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIERMTNFDKN LPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVE DRFNASLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLI NGIRDKQSGKTILDFLKSDGFANRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKV MGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIKELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDIN RLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKNRGKSDNVPSEEVVKKMKNYWRQLLNAKLITQRKFDNLTKAERGGLSELD KAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGT ALIKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRD FATVRKVLSMPQVNIVKKTEVQTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSV KELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKYSLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEK LKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFD TTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDSGGSPKKKRKV*

ABE7.9 (ecTadA(wt)–linker(32 aa)–ecTadA*(7.9)–linker(32 aa)–Cas9 nickase–NLS):

MSEVEFSHEYWMRHALTLAKRAWDEREVPVGAVLVHNNRVIGEGWNRPIGRHDPTAHAEIMALRQGGLVMQNYRLIDAT LYVTLEPCVMCAGAMIHSRIGRVVFGARDAKTGAAGSLMDVLHHPGMNHRVEITEGILADECAALLSDFFRMRRQEIKAQK KAQSSTD<mark>SGGSSGGSSGSETPGTSESATPESSGGSSGGSSEVEFSHEYWMRHALTLAKRALDEREVPVGAVLVLNNRVI</mark> GEGWNRAIGLHDPTAHAEIMALRQGGLVMQNYRLIDATLYVTFEPCVMCAGAMIHSRIGRVVFGVRNAKTGAAGSLMDVL HYPGMNHRVEITEGILADECNALLCYFFRMPRQVFNAQKKAQSSTDSGGSSGGSSGSETPGTSESATPESSGGSSGGSD KKYSIGLAIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEI FSNEMAKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHF LIEGDLNPDNSDVDKLFIQLVQTYNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNF KSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLK ALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKLNREDLLRKQRTFDNGSIPHQIHLGEL HAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIERMTNFDKN LPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVE DRFNASLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLI NGIRDKQSGKTILDFLKSDGFANRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKV MGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIKELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDIN RLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKNRGKSDNVPSEEVVKKMKNYWRQLLNAKLITQRKFDNLTKAERGGLSELD KAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGT ALIKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRD FATVRKVLSMPQVNIVKKTEVQTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSV KELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKYSLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEK LKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFD TTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDSGGSPKKKRKV*

ABE7.10 (ecTadA(wt)-linker(32 aa)-ecTadA*(7.10)-linker(32 aa)-Cas9 nickase-NLS):

MSEVEFSHEYWMRHALTLAKRAWDEREVPVGAVLVHNNRVIGEGWNRPIGRHDPTAHAEIMALRQGGLVMQNYRLIDAT LYVTLEPCVMCAGAMIHSRIGRVVFGARDAKTGAAGSLMDVLHHPGMNHRVEITEGILADECAALLSDFFRMRRQEIKAQK KAQSSTDSGGSSGGSSGSETPGTSESATPESSGGSSGGSSEVEFSHEYWMRHALTLAKRARDEREVPVGAVLVLNNRVI GEGWNRAIGLHDPTAHAEIMALRQGGLVMQNYRLIDATLYVTFEPCVMCAGAMIHSRIGRVVFGVRNAKTGAAGSLMDVL HYPGMNHRVEITEGILADECAALLCYFFRMPRQVFNAQKKAQSSTDSGGSSGGSSGSETPGTSESATPESSGGSSGGSD KKYSIGLAIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEI FSNEMAKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHF LIEGDLNPDNSDVDKLFIQLVQTYNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNF KSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLK ALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKLNREDLLRKQRTFDNGSIPHQIHLGEL HAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIERMTNFDKN LPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVE DRFNASLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLI NGIRDKQSGKTILDFLKSDGFANRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKV MGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIKELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDIN RLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKNRGKSDNVPSEEVVKKMKNYWRQLLNAKLITQRKFDNLTKAERGGLSELD KAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGT ALIKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRD FATVRKVLSMPQVNIVKKTEVQTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSV KELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKYSLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEK LKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFD TTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDSGGSPKKKRKV*

Supplementary Note 1. Matlab script for base calling.

```
function basecall(WTnuc, directory)
%cycle through fastq files for different samples
cd directory
files=dir('*.fastq');
for d=1:2
    filename=files(d).name;
    %read fastq file
    [header,seqs,gscore] = fastgread(filename);
    seqsLength = length(seqs);
                                        % number of sequences
    seqsFile = strrep(filename, '.fastq', '');
                                                  % trims off .fastq
    %create a directory with the same name as fastq file
    if exist(seqsFile,'dir');
        error('Directory already exists. Please rename or move it before moving on.');
    end
   mkdir(seqsFile);
                                         % make directory
   wtLength = length(WTnuc);
                                           % length of wildtype sequence
    %% aligning back to the wildtype nucleotide sequence
    8
    % AlN is a matrix of the nucleotide alignment
   window=1:wtLength;
   sBLength = length(seqs);
                                      % number of sequences
    % counts number of skips
   nSkips = 0;
   ALN=repmat(' ',[sBLength wtLength]);
    % iterate through each sequencing read
    for i = 1:sBLength
        %If you only have forward read fastq files leave as is
        %If you have R1 foward and R2 is reverse fastq files uncomment the
        %next four lines of code and the subsequent end statement
웅
          if mod(d, 2) == 0;
웅
              reverse = segrcomplement(seqs{i});
옹
              [score,alignment,start] = swalign(reverse,WTnuc,'Alphabet','NT');
8
          else
        [score,alignment,start] = swalign(seqs{i},WTnuc,'Alphabet','NT');
8
          end
        % length of the sequencing read
        len = length(alignment(3,:));
        % if there is a gap in the alignment , skip = 1 and we will
        % throw away the entire read
        skip = 0;
        for j = 1:len
            if (alignment(3,j) == '-' || alignment(1,j) == '-')
                skip = 1;
                break;
            end
            %in addition if the qscore for any given base in the read is
            %below 31 the nucleotide is turned into an N (fastq qscores that are not
letters)
            if isletter(qscore{i}(start(1)+j-1))
            else
                alignment(1,j) = 'N';
            end
        end
        if skip == 0 && len>10
            ALN(i, start(2):(start(2)+length(alignment)-1))=alignment(1,:);
        end
    end
    % with the alignment matrices we can simply tally up the occurrences of
```

```
doi:10.1038/nature24644
```

```
% each nucleotide at each column in the alignment these
    % tallies ignore bases annotated as N
    % due to low qscores
   TallyNTD=zeros(5,wtLength);
   FreqNTD=zeros(4,wtLength);
    SUM=zeros(1,wtLength);
    for i=1:wtLength
TallyNTD(:,i)=[sum(ALN(:,i)=='A'),sum(ALN(:,i)=='C'),sum(ALN(:,i)=='G'),sum(ALN(:,i)=='T'
), sum(ALN(:,i)=='N')];
    end
    for i=1:wtLength
        FreqNTD(:,i)=100*TallyNTD(1:4,i)/sum(TallyNTD(1:4,i));
    end
    for i=1:wtLength
        SUM(:,i)=sum(TallyNTD(1:4,i));
    end
    % we then save these tally matrices in the respective folder for
    % further processing
    save(strcat(seqsFile, '/TallyNTD'), 'TallyNTD');
    dlmwrite(strcat(seqsFile, '/TallyNTD.csv'), TallyNTD, 'precision', '%.3f', 'newline',
'pc');
    save(strcat(seqsFile, '/FreqNTD'), 'FreqNTD');
    dlmwrite(strcat(seqsFile, '/FreqNTD.csv'), FreqNTD, 'precision', '%.3f', 'newline',
'pc');
    fid = fopen('FrequencySummary.csv', 'a');
    fprintf(fid, '\n \n');
    fprintf(fid, filename);
    fprintf(fid, '\n \n');
    dlmwrite('FrequencySummary.csv', FreqNTD, 'precision', '%.3f', 'newline', 'pc', '-
append');
    dlmwrite('FrequencySummary.csv', SUM, 'precision', '%.3f', 'newline', 'pc', '-
append');
end
% set up queue of basecalling runs
% change directory to folder of fastq files for a given target site
cd('/Users/michaelpacker/Documents/MATLAB/BaseCallingWithSummary')
cd PUTFOLDERNAMEHERE
% call upon the basecall program
basecall(PUTWTSEQUENCEHERE)
% and repeat
cd('/Users/michaelpacker/Documents/MATLAB/BaseCallingWithSummary')
cd PUTFOLDERNAMEHERE
basecall(PUTWTSEQUENCEHERE)
```

```
% and repeat ...
```

end

Supplementary Note 2. Matlab script for indel analysis.

```
%WTnuc='CGGTGGGAGGTCTATATAAGCAGAGCTGGTTTAGTGAACCGTCAGATCCGCTAGAGATCCGCGGCCGCTAATACGACTCAC
CCTAGGGAGAGCCGCCACCGTGGTGAGCAAGGGCGAGGAGCTGTTCACCGGGGTGGTGCCCATCCTGGTCGAGCTGGACGGCGACGTAA
ACGGCCACAAGTTCAGCGTGTCCGGCGAG';
%cycle through fastq files for different samples
files=dir('*.fastq');
indelstart=55;
width=30;
flank=10;
for d=1:2
    filename=files(d).name;
    %read fastq file
    [header,seqs,qscore] = fastqread(filename);
    seqsLength = length(seqs);
                                        % number of sequences
    seqsFile = strcat(strrep(filename, '.fastq', ''), '_INDELS');
                                                                     % trims off .fastq
    %create a directory with the same name as fastq file+_INDELS
    if exist(seqsFile,'dir');
        error('Directory already exists. Please rename or move it before moving on.');
    end
                                         % make directory
   mkdir(seqsFile);
   wtLength = length(WTnuc);
                                        % length of wildtype sequence
                                        % number of sequences
   sBLength = length(seqs);
    % initialize counters and cell arrays
   nSkips = 0;
    notINDEL=0;
    ins={};
    dels={};
   NumIns=0;
   NumDels=0;
    % iterate through each sequencing read
    for i = 1:sBLength
    %search for 10BP sequences that should flank both sides of the "INDEL WINDOW"
       windowstart=strfind(seqs{i},WTnuc(indelstart-flank:indelstart));
       windowend=strfind(seqs{i},WTnuc(indelstart+width:indelstart+width+flank));
        %if these flanks are found and more than half of base calls
        %are above Q31 THEN proceed OTHERWISE save as a skip
        if length(windowstart)==1 && length(windowend)==1 &&
(sum(isletter(qscore{i}))/length(qscore{i}))>=0.5
            %if the sequence length matches the INDEL window length save as
            %not INDEL
            if windowend-windowstart==width+flank
                notINDEL=notINDEL+1;
            %if the sequence is ONE or more baseslonger than the INDEL
            %window length save as an Insertion
            elseif windowend-windowstart>=width+flank+1
                NumIns=NumIns+1;
                ins{NumIns}=seqs{i};
            %if the sequence is ONE or more bases shorter than the INDEL
            %window length save as a Deletion
            elseif windowend-windowstart<=width+flank-1</pre>
                NumDels=NumDels+1;
                dels{NumDels}=seqs{i};
            end
        %keep track of skipped sequences that do not posess matching flank
        %sequences and do not pass quality cutoff
        else
            nSkips=nSkips+1;
```

```
doi:10.1038/nature24644
```

```
end
     INDELrate=(NumIns+NumDels)/(NumIns+NumDels+notINDEL)*100.;
    FID = fopen('INDELSummary.csv', 'a');
     fprintf(FID, '\n \n');
     fprintf(FID, filename);
     fprintf(FID, '\n');
     fprintf(FID, num2str(INDELrate));
    fid=fopen(strcat(seqsFile, '/summary.txt'), 'wt');
fprintf(fid, 'Skipped reads %i\n not INDEL %i\n Insertions %i\n Deletions %i\n INDEL
percent %e\n', [nSkips, notINDEL, NumIns, NumDels, INDELrate]);
     fclose(fid);
    save(strcat(seqsFile, '/nSkips'), 'nSkips');
save(strcat(seqsFile, '/notINDEL'), 'notINDEL');
save(strcat(seqsFile, '/NumIns'), 'NumIns');
save(strcat(seqsFile, '/NumDels'), 'NumDels');
    save(strcat(seqsFile, '/INDELrate'), 'INDELrate');
    save(strcat(seqsFile, '/dels'), 'dels');
     C = dels;
     fid = fopen(strcat(seqsFile, '/dels.txt'), 'wt');
     fprintf(fid, '"%s"\n', C{:});
     fclose(fid);
     save(strcat(seqsFile, '/ins'), 'ins');
     C = ins;
     fid = fopen(strcat(seqsFile, '/ins.txt'), 'wt');
     fprintf(fid, '"%s"\n', C{:});
     fclose(fid);
```

```
doi:10.1038/nature24644
```

Supplementary Note 3. Python script for analysis of HBG1 and HBG2 base editing and indels.

```
%matplotlib inline
import numpy as np
import scipy as sp
import matplotlib as mpl
import matplotlib.cm as cm
import matplotlib.pyplot as plt
import pandas as pd
pd.set option('display.width', 500)
pd.set option('display.max columns', 100)
pd.set_option('display.notebook_repr_html', True)
import seaborn as sns
sns.set style("whitegrid")
sns.set_context("poster")
import requests
import time
from bs4 import BeautifulSoup
import regex
import re
import os
from Bio import SeqIO
import Bio
from Bio import motifs
from Bio import pairwise2
from Bio.pairwise2 import format alignment
from Bio.Alphabet import IUPAC
from sklearn import preprocessing
basecall analysis with 50% Q31 cutoff on protospacer region (as defined by flanks)
#includes a check for match with two HBG1 SNPs
#inputs:
#directory, working directory folder containing all fastq files
#site, genomic site name as it appears in the fastq filenames
#orientation, 'FWD' if you want output in the same direction as the sequencing read or
'REV' if you want reverse complement output,
#flank1, sequence that is used to define the 5' end of protospacer in the sequencing read
direction,
#flank2, sequence that is used to define the 5' end of protospacer in the sequencing read
direction,
#width, expected bp length of basecalling window
#outputs:
#' counts.csv', all base editing product sequences with corresponding number of
occurences
#' rawsummary.csv', summarizes base call counts for all samples
#'
  normalizedsummary.csv', summarizes base call percentages for all samples
def basecallhbg1(directory, site, orientation, flank1, flank2, width):
    indir=directory
    outdir=directory
    filenames=os.listdir(indir)
    for i in range(len(filenames)):
        seqs={}
        if (filenames[i][-5:]=='fastq') and (site in filenames[i]):
            for record in SeqIO.parse(indir+filenames[i], "fastq") :
                recordqual=[x>31 for x in record.letter_annotations['phred_quality']]
                #only process reads that have more than half of basecalls >Q31 and
contain two HBG1 specific SNPs at 3' end of read
                if (record.seq.find('GTTTTTCTCTAATTTATTCTTCCCTTTAGCTAGTTTC')>0) and
(float(sum(recordqual))/float(len(recordqual))>=.5):
                    recordseq="".join([y if x else 'N' for (x,y) in zip(recordqual,
record.seq)])
```

recordseq="".join([y if x else 'N' for (x,y) in zip(recordqual, record.seq)]) #split prior to spacer window split1=recordseq.split(flank1) if len(split1)==2: #take second item in first split #split again at the sequence right after the protospacer and take first item split2=split1[1].split(flank2)[0] #keep only entries with exact width if (len(split2)==width): if orientation=='FWD': seqs[record.id]=split2 elif orientation=='REV': seqs[record.id]=Bio.Seq.reverse complement(split2) frame=pd.DataFrame({'Spacer':seqs.values()}, index=seqs.keys()) Motif=motifs.create(frame.Spacer.values, alphabet=IUPAC.IUPACAmbiguousDNA()) raw=pd.DataFrame(Motif.counts, index=[str(s+1) for s in range(width)])[['A','C','G','T','N']].transpose() normalized=pd.DataFrame(Motif.counts, index=[str(s+1) for s in range(width)])[['A','C','G','T']].transpose() normalized=normalized/normalized.sum(axis=0)*100. normalized=normalized.round(2) Counts=pd.DataFrame(seqs.items(), columns=['ID', 'Window']) Counts=Counts[['N' not in x for x in Counts.Window]] Counts=Counts.groupby('Window').count().sort values('ID', ascending=False) Counts.to csv(outdir+filenames[i].strip('.fastq')+' hbgl.csv') fd=open(directory+site+' normalizedsummary hbg1.csv','a') fd.write('\n'+filenames[i]+'\n') normalized.to_csv(fd) fd.close() fd=open(directory+site+' rawsummary hbg1.csv','a') fd.write('\n'+filenames[i]+'\n') raw.to_csv(fd) fd.close() return #basecall analysis with 50% Q31 cutoff on protospacer region (as defined by flanks) #includes a check for match with two HBG2 SNPs #inputs: #directory, working directory folder containing all fastq files #site, genomic site name as it appears in the fastq filenames #orientation, 'FWD' if you want output in the same direction as the sequencing read or 'REV' if you want reverse complement output, #flank1, sequence that is used to define the 5' end of protospacer in the sequencing read direction, #flank2, sequence that is used to define the 5' end of protospacer in the sequencing read direction, #width, expected bp length of basecalling window # #outputs: #' counts.csv', all base editing product sequences with corresponding number of occurences _rawsummary.csv', summarizes base call counts for all samples #' _normalizedsummary.csv', summarizes base call percentages for all samples def basecallhbg2(directory, site, orientation, flank1, flank2, width): indir=directory outdir=directory filenames=os.listdir(indir) for i in range(len(filenames)): seqs={} if (filenames[i][-5:]=='fastq') and (site in filenames[i]):

for record in SeqIO.parse(indir+filenames[i], "fastq") : recordqual=[x>31 for x in record.letter_annotations['phred_quality']] #only process reads that have more than half of basecalls >Q31 and contain two HBG2 specific SNPs at 3' end of read if (record.seq.find('ATTTTTCTCTAATTTATTCTTCCCTTTAGCTAGTTTT')>0) and (float(sum(recordqual))/float(len(recordqual))>=.5): recordseq="".join([y if x else 'N' for (x,y) in zip(recordqual, record.seq)]) #split prior to spacer window split1=recordseq.split(flank1) if len(split1)==2: #take second item in first split #split again at the sequence right after the protospacer and take first item split2=split1[1].split(flank2)[0] #keep only entries with exact width if (len(split2)==width): if orientation=='FWD': seqs[record.id]=split2 elif orientation=='REV': seqs[record.id]=Bio.Seq.reverse complement(split2) frame=pd.DataFrame({'Spacer':seqs.values()}, index=seqs.keys()) Motif=motifs.create(frame.Spacer.values, alphabet=IUPAC.IUPACAmbiguousDNA()) raw=pd.DataFrame(Motif.counts, index=[str(s+1) for s in range(width)])[['A','C','G','T','N']].transpose() normalized=pd.DataFrame(Motif.counts, index=[str(s+1) for s in range(width)])[['A','C','G','T']].transpose() normalized=normalized/normalized.sum(axis=0)*100. normalized=normalized.round(2) Counts=pd.DataFrame(seqs.items(), columns=['ID', 'Window']) Counts=Counts[['N' not in x for x in Counts.Window]] Counts=Counts.groupby('Window').count().sort values('ID', ascending=False) Counts.to csv(outdir+filenames[i].strip('.fastq')+' hbg2.csv') fd=open(directory+site+'_normalizedsummary_hbg2.csv','a') fd.write('\n'+filenames[i]+'\n') normalized.to csv(fd) fd.close() fd=open(directory+site+' rawsummary hbg2.csv','a') fd.write('\n'+filenames[i]+'\n') raw.to_csv(fd) fd.close() return #indel analysis #includes a check for match with two HBG1 SNPs #inputs: #directory, working directory folder containing all fastq files #site, genomic site name as it appears in the fastq filenames #orientation, 'FWD' if you want output in the same direction as the sequencing read or 'REV' if you want reverse complement output, #flank1, sequence that is used to define the 5' end of protospacer in the sequencing read direction, #flank2, sequence that is used to define the 5' end of protospacer in the sequencing read direction, #width, expected bp length of basecalling window #ouputs: #"_Insertions_hbg1.csv", sequences of all insertion reads #" deletions hbg1.csv", sequences of all deletion reads #'indelsummary hbgl.csv', contains all indel stats for all fastq files def indelshbg1(directory, site, flank1, flank2, width): indir=directory outdir=directory

```
filenames=os.listdir(indir)
    for i in range(len(filenames)):
        seqs={}
        if (filenames[i][-5:]=='fastq') and (site in filenames[i]):
            skips=0
            ins=0
            insertions=[]
            dels=0
            deletions=[]
            notindel=0
            for record in SeqIO.parse(indir+filenames[i], "fastq") :
                recordqual=[x>31 for x in record.letter_annotations['phred_quality']]
                #only process reads that have more than half of basecalls >Q31 and
contain two HBG1 specific SNPs at 3' end of read
                if (record.seq.find('GTTTTTCTCTAATTTATTCTTCCCTTTAGCTAGTTTC')>0) and
(float(sum(recordqual))/float(len(recordqual))>=.5):
                    #split prior to indel window
                    split1=record.seq.split(flank1)
                    if len(split1)==2:
                        #take second item in first split
                        #split again at the sequence right after the indel window
                        if len(split1[1].split(flank2))==2:
                            split2=split1[1].split(flank2)[0]
                        #if INDEL window is +1 add to Insertions
                            if (len(split2)>=width+1):
                                ins=ins+1
                                insertions.append(split2)
                        #if INDEL window is -1 add to Deletions
                            if (len(split2)<=width-1):</pre>
                                dels=dels+1
                                deletions.append(split2)
                            if len(split2)==width:
                                notindel=notindel+1
                        else:
                            skips=skips+1
                    else:
                        skips=skips+1
                else:
                    skips=skips+1
            fd=open(directory+'indelsummary hbg1.csv','a')
            fd.write('\n'+filenames[i]+'\n')
            fd.write('skipped reads: '+str(skips)+'\n')
            fd.write('insertions: '+str(ins)+'\n')
            fd.write('deletions: '+str(dels)+'\n')
            fd.write('notindels: '+str(notindel)+'\n')
            fd.write('indel rate:
'+str(float(ins+dels)/float(ins+dels+notindel)*100.)+'%'+'\n')
            fd.close()
            pd.DataFrame(insertions).to csv(directory+filenames[i]+'Insertions hbg1.csv')
            pd.DataFrame(deletions).to csv(directory+filenames[i]+'Deletions hbg1.csv')
    return
```

#indel analysis
#includes a check for match with two HBG2 SNPs
#inputs:
#directory, working directory folder containing all fastq files
#site, genomic site name as it appears in the fastq filenames
#orientation, 'FWD' if you want output in the same direction as the sequencing read or
'REV' if you want reverse complement output,

```
#flank1, sequence that is used to define the 5' end of protospacer in the sequencing read
direction,
#flank2, sequence that is used to define the 5' end of protospacer in the sequencing read
direction,
#width, expected bp length of basecalling window
#ouputs:
#"_Insertions_hbg2.csv", sequences of all insertion reads
#"_deletions_hbg2.csv", sequences of all deletion reads
#'indelsummary_hbg2.csv', contains all indel stats for all fastq files
def indelshbg2(directory, site, flank1, flank2, width):
    indir=directory
    outdir=directory
    filenames=os.listdir(indir)
    for i in range(len(filenames)):
        seqs={}
        if (filenames[i][-5:]=='fastq') and (site in filenames[i]):
            skips=0
            ins=0
            insertions=[]
            dels=0
            deletions=[]
            notindel=0
            for record in SeqIO.parse(indir+filenames[i], "fastq") :
                recordqual=[x>31 for x in record.letter_annotations['phred_quality']]
                #only process reads that have more than half of basecalls >Q31 and
contain two HBG2 specific SNPs at 3' end of read
                if (record.seq.find('ATTTTTCTCTAATTTATTCTTCCCTTTAGCTAGTTTT')>0) and
(float(sum(recordqual))/float(len(recordqual))>=.5):
                    #split prior to indel window
                    split1=record.seq.split(flank1)
                    if len(split1)==2:
                        #take second item in first split
                        #split again at the sequence right after the indel window
                        if len(split1[1].split(flank2))==2:
                             split2=split1[1].split(flank2)[0]
                        #if INDEL window is +1 add to Insertions
                             if (len(split2)>=width+1):
                                 ins=ins+1
                                 insertions.append(split2)
                        #if INDEL window is -1 add to Deletions
                             if (len(split2)<=width-1):</pre>
                                 dels=dels+1
                                 deletions.append(split2)
                             if len(split2)==width:
                                 notindel=notindel+1
                        else:
                             skips=skips+1
                    else:
                        skips=skips+1
                else:
                    skips=skips+1
            fd=open(directory+'indelsummary_hbg2.csv','a')
            fd.write('\n'+filenames[i]+'\n')
fd.write('skipped reads: '+str(skips)+'\n')
            fd.write('insertions: '+str(ins)+'\n')
            fd.write('deletions: '+str(dels)+'\n')
            fd.write('notindels: '+str(notindel)+'\n')
            fd.write('indel rate:
'+str(float(ins+dels)/float(ins+dels+notindel)*100.)+'%'+'\n')
            fd.close()
            pd.DataFrame(insertions).to csv(directory+filenames[i]+'Insertions hbg2.csv')
            pd.DataFrame(deletions).to csv(directory+filenames[i]+'Deletions hbg2.csv')
    return
```

directory1='/Users/michaelpacker/Desktop/Liu_Lab/MiSeqData/y-globin_632/'
basecallhbg1(directory1, '632', 'FWD','ATTTGCA','TTAATTTTTT', 43)
indelshbg1(directory1, '632', 'ATTTGCA','TTAATTTTTT',43)
indelshbg2(directory1, '632','ATTTGCA','TTAATTTTTT',43)

```
doi:10.1038/nature24644
```

Supplementary Note 4. Python script for analysis of base editing linkage disequilibrium.

```
%matplotlib inline
import numpy as np
import scipy as sp
import matplotlib as mpl
import matplotlib.cm as cm
import matplotlib.pyplot as plt
import pandas as pd
pd.set option('display.width', 500)
pd.set option('display.max columns', 100)
pd.set_option('display.notebook_repr_html', True)
import seaborn as sns
sns.set style("whitegrid")
sns.set_context("poster")
import requests
import time
from bs4 import BeautifulSoup
import regex
import re
import os
from Bio import SeqIO
import Bio
from Bio import motifs
#ABE processivity analysis
#inputs:
#directory, working directory folder containing all fastq files for a single ABE
#site, genomic site name as it appears in the fastq filenames
#orientation, 'FWD' if you want output in the same direction as the sequencing read or
'REV' if you want reverse complement output,
#flank1, sequence that is used to define the 5' end of protospacer in the sequencing read
direction,
#flank2, sequence that is used to define the 5' end of protospacer in the sequencing read
direction,
#primaryposition, site of primary target A in protospacer with the position furthest from
the PAM as 0
#secondaryposition, site of secondary target A in protospacer with the position furthest
from the PAM as 0
#outputs:
#' counts.csv', all base editing product sequences with corresponding number of
occurrences
#' RawMotifs.csv', unnormalized nucleotide counts at all 20 positions of protospacer as
well as counts conditional on the identity of the primary target position
#'_NormalizedMotifs.csv' normalized nucleotide frequencies at all 20 positions of
protospacer as well as frequencies conditional on the identity of the primary target
position
#'_probability.csv', summary containing editing probabilities at both positions as well
as observed probability of double editing
def processivity(directory, site, orientation, flank1, flank2, primaryposition,
secondaryposition):
    indir=directory
    outdir=directory
    filenames=os.listdir(indir)
    probabilities=pd.DataFrame({'P1':[],'P2':[],'P21':[], 'P2P1':[]})
    for i in range(len(filenames)):
        seqs={}
        if (filenames[i][-5:]=='fastq') and (site in filenames[i]):
            for record in SeqIO.parse(indir+filenames[i], "fastq") :
                #split prior to spacer window
                split1=record.seq.tostring().split(flank1)
                if len(split1)==2:
                    #take second item in first split
```

```
#split again at the sequence right after the protospacer and take
first item
                    split2=split1[1].split(flank2)[0]
                    #keep only 20 basepair long protospacers
                    if (len(split2)==20) & (split2.find('N')==-1):
                        if orientation=='FWD':
                            seqs[record.id]=split2
                        elif orientation=='REV':
                            seqs[record.id]=Bio.Seq.reverse_complement(split2)
            frame=pd.DataFrame({'Spacer':seqs.values(),
'Primary Position':[x[primaryposition] for x in seqs.values()]}, index=seqs.keys())
            MotifAll=motifs.create(frame.Spacer.values)
            #in the event that no reads have a given base call at the primary position we
will save a dummy motif for a polyA sequence
            if len(frame[frame.Primary Position=='A'])>0:
                MotifA=motifs.create(frame[frame.Primary_Position=='A'].Spacer.values)
            else:
                MotifA=motifs.create(['A'*20])
            if len(frame[frame.Primary Position=='C'])>0:
                MotifC=motifs.create(frame[frame.Primary_Position=='C'].Spacer.values)
            else:
                MotifC=motifs.create(['A'*20])
            if len(frame[frame.Primary_Position=='G'])>0:
                MotifG=motifs.create(frame[frame.Primary_Position=='G'].Spacer.values)
            else:
                MotifG=motifs.create(['A'*20])
            if len(frame[frame.Primary Position=='T'])>0:
                MotifT=motifs.create(frame[frame.Primary Position=='T'].Spacer.values)
            else:
                MotifT=motifs.create(['A'*20])
            #save motifs both raw and normalized conditional on the primary position
being each of the four bases
            a=pd.DataFrame(MotifA.counts, index=['A'+str(s) for s in range(20)])
            A=pd.DataFrame(MotifA.counts.normalize(),index=['A'+str(s) for s in
range(20)])
            c=pd.DataFrame(MotifC.counts, index=['C'+str(s) for s in range(20)])
            C=pd.DataFrame(MotifC.counts.normalize(), index=['C'+str(s) for s in
range(20)])
            g=pd.DataFrame(MotifG.counts, index=['G'+str(s) for s in range(20)])
            G=pd.DataFrame(MotifG.counts.normalize(), index=['G'+str(s) for s in
range(20)])
            t=pd.DataFrame(MotifT.counts, index=['T'+str(s) for s in range(20)])
            T=pd.DataFrame(MotifT.counts.normalize(), index=['T'+str(s) for s in
range(20)])
            #save motifs both raw and normalized for all base editing products
            All=pd.DataFrame(MotifAll.counts, index=['All'+str(s) for s in range(20)])
            ALL=pd.DataFrame(MotifAll.counts.normalize(),index=['All'+str(s) for s in
range(20)])
            #append all motifs and export, indices contain protospacer position as well
as an identifier for the primary position
All.append(a).append(c).append(g).append(t).to_csv(outdir+filenames[i].strip('.fastq')+'R
awMotifs.csv')
ALL.append(A).append(C).append(G).append(T).to_csv(outdir+filenames[i].strip('.fastq')+'N
ormalizedMotifs.csv')
            #save the base editing product sequences and corresponding number of
occurrences
            Counts=pd.DataFrame(seqs.items(),
columns=['ID', 'Window']).groupby('Window').count().sort values('ID', ascending=False)
            Counts.to csv(outdir+filenames[i].strip('.fastq')+'.csv')
            #evaluate editing probability at both primary and secondary positions
            P1=ALL['G'].iloc[primaryposition]
```

```
P2=ALL['G'].iloc[secondaryposition]
            #evaluate observed probability of joint editing as P(2|1)*P(1)
            P21=G['G'].iloc[secondaryposition]*P1
            #evaluate expected probability of joint editing given statistical
independence as P(1)*P(2)
            P2P1=P1*P2
            #export probabilities
probabilities=probabilities.append(pd.DataFrame({'P1':[P1],'P2':[P2],'P21':[P21],
'P2P1':[P2P1]}, index=[site]))
            probabilities.to csv(outdir+site+' probabilities.csv')
    return
#ABE processivity analysis, for when flank1 needs to be short, we instead split on flank2
first and then find flank1
#program is otherwise identical to processivity
def processivity2(directory, site, orientation, flank1, flank2, primaryposition,
secondaryposition):
    indir=directory
    outdir=directory
    filenames=os.listdir(indir)
    probabilities=pd.DataFrame({'P1':[],'P2':[],'P21':[], 'P2P1':[]})
    for i in range(len(filenames)):
        seqs={}
        if (filenames[i][-5:]=='fastq') and (site in filenames[i]):
            for record in SeqIO.parse(indir+filenames[i], "fastq") :
                #split prior to spacer window
                split1=record.seq.tostring().split(flank2)
                if len(split1)==2:
                    #take second item in first split
                    #split again at the sequence right after the protospacer and take
first item
                    if len(split1[0].split(flank1))==2:
                        split2=split1[0].split(flank1)[1]
                    #keep only 20 basepair long protospacers
                        if (len(split2)==20) & (split2.find('N')==-1):
                            if orientation=='FWD':
                                seqs[record.id]=split2
                            elif orientation=='REV':
                                seqs[record.id]=Bio.Seq.reverse_complement(split2)
            frame=pd.DataFrame({'Spacer':seqs.values(),
'Primary Position':[x[primaryposition] for x in seqs.values()]}, index=seqs.keys())
            MotifAll=motifs.create(frame.Spacer.values)
            if len(frame[frame.Primary_Position=='A'])>0:
                MotifA=motifs.create(frame[frame.Primary_Position=='A'].Spacer.values)
            else:
                MotifA=motifs.create(['A'*20])
            if len(frame[frame.Primary Position=='C'])>0:
                MotifC=motifs.create(frame[frame.Primary Position=='C'].Spacer.values)
            else:
                MotifC=motifs.create(['A'*20])
            if len(frame[frame.Primary_Position=='G'])>0:
                MotifG=motifs.create(frame[frame.Primary Position=='G'].Spacer.values)
            else:
                MotifG=motifs.create(['A'*20])
            if len(frame[frame.Primary Position=='T'])>0:
                MotifT=motifs.create(frame[frame.Primary Position=='T'].Spacer.values)
            else:
                MotifT=motifs.create(['A'*20])
            a=pd.DataFrame(MotifA.counts, index=['A'+str(s) for s in range(20)])
            A=pd.DataFrame(MotifA.counts.normalize(),index=['A'+str(s) for s in
range(20)])
```

```
doi:10.1038/nature24644
```

```
c=pd.DataFrame(MotifC.counts, index=['C'+str(s) for s in range(20)])
             C=pd.DataFrame(MotifC.counts.normalize(), index=['C'+str(s) for s in
range(20)])
             g=pd.DataFrame(MotifG.counts, index=['G'+str(s) for s in range(20)])
             G=pd.DataFrame(MotifG.counts.normalize(), index=['G'+str(s) for s in
range(20)])
             t=pd.DataFrame(MotifT.counts, index=['T'+str(s) for s in range(20)])
             T=pd.DataFrame(MotifT.counts.normalize(), index=['T'+str(s) for s in
range(20)])
             All=pd.DataFrame(MotifAll.counts, index=['All'+str(s) for s in range(20)])
             ALL=pd.DataFrame(MotifAll.counts.normalize(),index=['All'+str(s) for s in
range(20)])
All.append(a).append(c).append(g).append(t).to_csv(outdir+filenames[i].strip('.fastq')+'R
awMotifs.csv')
ALL.append(A).append(C).append(G).append(T).to_csv(outdir+filenames[i].strip('.fastq')+'N
ormalizedMotifs.csv')
             Counts=pd.DataFrame(seqs.items(),
columns=['ID','Window']).groupby('Window').count().sort_values('ID', ascending=False)
             Counts.to csv(outdir+filenames[i].strip('.fastq')+'.csv')
             P1=ALL['G'].iloc[primaryposition]
             P2=ALL['G'].iloc[secondaryposition]
             P21=G['G'].iloc[secondaryposition]*P1
             P2P1=P1*P2
probabilities=probabilities.append(pd.DataFrame({'P1':[P1],'P2':[P2],'P21':[P21],
'P2P1':[P2P1]}, index=[site]))
             probabilities.to_csv(outdir+site+' probabilities.csv')
    return
directory1='/Users/michaelpacker/Desktop/Liu Lab/MiSeqData/2017 0824 MSP/144/'
processivity(directory1, '299', 'REV', 'CCGCCCC','CAGTTTC',5-1, 7-1)
                                     'FWD', 'ATCGAAA','AGGATAA', 5-1,8-1)
'FWD', 'ACTCAGA','GGGGTAC', 5-1,8-1)
processivity(directory1, '310',
processivity(directory1, '311',
                                    'FWD',
                                             'AAGT', 'TGGGCTTG', 5-1, 8-1)
processivity2(directory1, '314',
processivity(directory1, '318', 'REV','GTAACCA','ATGAGTTCA',5-1,7-1)
processivity(directory1, '463',
                                    'FWD', 'GATACAA','GGGT', 5-1, 3-1)
processivity(directory1, '464',
                                    'FWD', 'ACCAGGA', 'AGGCAAA', 5-1, 6-1)
                                    FWD , ACCAGGA , AGGCAAA , 5-1, 6-1)
'FWD', 'ATCTCAT', 'TGGTTAC', 5-1, 7-1)
'FWD', 'GAGACTG', 'GGGAATG', 5-1, 6-1)
'FWD', 'AACGACT', 'TGGTATC', 5-1, 8-1)
'FWD', 'GACTCAG', 'CGGGGGGT', 5-1, 7-1)
'FWD', 'GCCTCAG', 'TGGACAA', 5-1, 7-1)
processivity(directory1, '466',
processivity(directory1, '467',
processivity(directory1, '468',
processivity(directory1, '469',
processivity(directory1, '470',
                                     'FWD', 'GCCTCAG', 'TGGACAA', 5-1, 7-1)
processivity(directory1, '471',
processivity(directory1, '472', 'REV', 'TGGTTTCCCT', 'CAGATTT', 5-1, 6-1)
processivity(directory1, '501',
                                     'FWD', 'CTGAGAG', 'GGGAGA', 5-1, 6-1)
processivity2(directory1, '505',
                                    'FWD', 'AGT','GGGTCGCTGAAAA', 5-1, 8-1)
'FWD', 'GGTGAGG','GGGCTTC', 5-1, 7-1)
processivity(directory1, '508',
processivity(directory1, '536', 'REV', 'TTCTCCA', 'TTGGGGC', 7-1, 3-1)
processivity(directory1, '601',
                                    'FWD', 'CACAGAC', 'TGGGAGT', 5-1, 7-1)
processivity(directory1, '602', 'FWD', 'ACAGACA', 'GGGAGTG', 6-1, 8-1)
#script to combine all sites into one summary file for each ABE
indir=directory1
filenames=os.listdir(indir)
summary=pd.DataFrame({'P1':[],'P2':[],'P21':[], 'P2P1':[]})
for i in range(len(filenames)):
    if 'probabilities' in filenames[i]:
        summary=summary.append(pd.read csv(indir+filenames[i], index col=0))
summary.to_csv(indir+'summary.csv')
```

Supplementary References

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