

**Supplementary Table 1. Unpaired two tailed Student's t-test p-values, t-values, and degrees of freedom for product purity comparisons. (a)** Unpaired two tailed Student's t-test p-values, t-values, and degrees of freedom (df) comparing CBEmax and CP-CBEmax variants at two genomic sites prone to non-C-to-T byproduct formation. **(b)** Unpaired two tailed Student's t-test p-values, t-values, and degrees of freedom (df) comparing CBEmax-B and CP-CBEmax-B variants at two genomic sites prone to non-C-to-T byproduct formation. Values and error bars reflect the mean±s.d. of three biological replicates performed on different days at each site. ns, P>0.05; \*P<0.05; \*\*P<0.01; \*\*\*P<0.001

**a**

	Site 28 (C7)					Site 30 (C6)				
	p-value	t value	df	significance		p-value	t value	df	significance	
CBEmax vs. CP1012-CBEmax	0.0041	5.9	4	**	CBEmax vs. CP1012-CBEmax	0.023	3.6	4	*	
CBEmax vs. CP1028-CBEmax	0.0029	6.5	4	**	CBEmax vs. CP1028-CBEmax	0.0010	8.5	4	**	
CBEmax vs. CP1041-CBEmax	0.0016	7.7	4	**	CBEmax vs. CP1041-CBEmax	0.00046	11	4	***	
CBEmax vs. CP1249-CBEmax	0.0050	5.6	4	**	CBEmax vs. CP1249-CBEmax	0.0064	5.2	4	**	

**b**

	Site 28 (C7)					Site 30 (C6)				
	p-value	t value	df	significance		p-value	t value	df	significance	
CBEmax-B vs. CP1012-CBEmax-B	0.00074	9.3	4	***	CBEmax-B vs. CP1012-CBEmax-B	0.21	1.5	4	ns	
CBEmax-B vs. CP1028-CBEmax-B	8.8E-05	16	4	***	CBEmax-B vs. CP1028-CBEmax-B	0.00082	9.1	4	***	
CBEmax-B vs. CP1041-CBEmax-B	0.0034	6.2	4	**	CBEmax-B vs. CP1041-CBEmax-B	2.3E-06	40	4	***	
CBEmax-B vs. CP1249-CBEmax-B	0.014	4.2	4	*	CBEmax-B vs. CP1249-CBEmax-B	0.00016	14	4	***	

**Supplementary Table 2.** Activities of CP-CBEmax variants versus CBEmax at the HEK2 on-target and off-target sites previously characterized for *S. pyogenes* Cas9 nuclease.

		% of total sequencing reads with C•G converted to T•A																				
Position		1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19	20	
<b>HEK2 on-target</b>		G	A	A	C	A	C	A	A	A	G	C	A	T	A	G	A	C	T	G	C	Indel%
CBEmax					58.6		59.9				0.2							0.1		0.1	0.9	
CP1012-CBEmax					21.6		53.0				2.9							0.4		0.1	0.4	
CP1028-CBEmax					32.7		63.1				15.5							1.1		0.1	0.5	
CP1041-CBEmax					12.9		20.1				0.6							0.3		0.1	0.1	
CP1249-CBEmax					14.5		60.7				3.9							0.4		0.0	0.6	
CP1300-CBEmax					0.5		16.4				0.6							0.1		0.0	0.1	

		% of total sequencing reads with C•G converted to T•A																				
Position		1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19	20	
<b>HEK2 off-target site 1</b>		G	A	A	C	A	C	A	A	T	G	C	A	T	A	G	A	T	T	G	C	Indel%
CBEmax					0.2		0.8				0.0									0.1	0.0	
CP1012-CBEmax					0.1		0.2				0.1									0.1	0.0	
CP1028-CBEmax					0.0		0.0				0.1									0.1	0.0	
CP1041-CBEmax					0.1		0.1				0.0									0.1	0.0	
CP1249-CBEmax					0.0		0.0				0.0									0.1	0.0	
CP1300-CBEmax					0.0		0.0				0.0									0.1	0.0	

		% of total sequencing reads with C•G converted to T•A																				
Position		1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19	20	
<b>HEK2 off-target site 2</b>		A	A	A	C	A	T	A	A	A	G	C	A	T	A	G	A	C	T	G	C	Indel%
CBEmax					0.0						0.0							0.0		0.0	0.0	
CP1012-CBEmax					0.0						0.0							0.0		0.0	0.0	
CP1028-CBEmax					0.0						0.0							0.0		0.0	0.0	
CP1041-CBEmax					0.0						0.0							0.0		0.0	0.0	
CP1249-CBEmax					0.0						0.0							0.0		0.0	0.0	
CP1300-CBEmax					0.0						0.0							0.0		0.0	0.0	

**Supplementary Table 3.** Activities of CP-ABEmax variants versus ABEmax at the HEK2 on-target and off-target sites previously characterized for *S. pyogenes* Cas9 nuclease.

Position	% of total sequencing reads with A•T converted to G•C																				Indel%
	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19	20	
<b>HEK2 on-target</b>	G	A	A	C	A	C	A	A	A	G	C	A	T	A	G	A	C	T	G	C	
ABEmax		0.1	0.8		78.0		27.3	1.0	1.0			0.1		0.0		0.0					0.9
CP1012-ABEmax		0.5	1.9		45.3		27.8	7.3	7.8			3.4		1.9		0.0					0.7
CP1028-ABEmax		0.1	1.1		80.6		8.5	3.1	4.7			6.3		1.6		0.0					0.6
CP1041-ABEmax		0.5	4.0		56.8		21.6	3.9	7.5			17.9		17.8		0.2					0.4
CP1249-ABEmax		0.0	0.8		84.9		33.0	7.5	12.4			2.7		2.0		0.0					0.4
CP1300-ABEmax		0.0	0.1		59.2		3.5	1.3	1.8			0.3		0.1		0.0					0.1

Position	% of total sequencing reads with A•T converted to G•C																				Indel%
	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19	20	
<b>HEK2 off-target site 1</b>	G	A	A	C	A	C	A	A	T	G	C	A	T	A	G	A	T	T	G	C	
ABEmax		0.0	0.0		1.7		0.1	0.1				0.0		0.0		0.0					0.1
CP1012-ABEmax		0.0	0.0		0.1		0.0	0.0				0.0		0.0		0.0					0.0
CP1028-ABEmax		0.0	0.0		0.5		0.1	0.0				0.0		0.1		0.0					0.0
CP1041-ABEmax		0.0	0.0		0.0		0.0	0.0				0.0		0.0		0.0					0.0
CP1249-ABEmax		0.0	0.0		0.1		0.1	0.1				0.0		0.1		0.0					0.0
CP1300-ABEmax		0.0	0.0		0.0		0.0	0.0				0.0		0.0		0.0					0.0

Position	% of total sequencing reads with A•T converted to G•C																				Indel%
	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19	20	
<b>HEK2 off-target site 2</b>	A	A	A	C	A	T	A	A	A	G	C	A	T	A	G	A	C	T	G	C	
ABEmax		0.0	0.0	0.0	0.0		0.0	0.0	0.0			0.0		0.0		0.0					0.0
CP1012-ABEmax		0.0	0.0	0.0	0.0		0.0	0.0	0.0			0.0		0.0		0.0					0.0
CP1028-ABEmax		0.0	0.0	0.0	0.0		0.0	0.0	0.0			0.0		0.0		0.0					0.0
CP1041-ABEmax		0.0	0.0	0.0	0.0		0.0	0.0	0.0			0.0		0.0		0.0					0.0
CP1249-ABEmax		0.0	0.0	0.0	0.0		0.0	0.0	0.0			0.0		0.0		0.0					0.0
CP1300-ABEmax		0.0	0.0	0.0	0.0		0.0	0.0	0.0			0.0		0.0		0.0					0.0



**Supplementary Table 5.** Activities of CP-ABEmax variants versus ABEmax at the EMX1 on-target and off-target sites previously characterized for *S. pyogenes* Cas9 nuclease.

Position	% of total sequencing reads with A•T converted to G•C																				Indel%
	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19	20	
<b>EMX on-target</b>	G	A	G	T	C	C	G	A	G	C	A	G	A	A	G	A	A	G	A	A	
ABEmax		2.5				0.0		2.2			1.0	0.2	0.1		1.1	0.3		0.1	0.2	7.0	
CP1012-ABEmax		4.1				0.0		23.1			22.4	0.7	0.4		1.2	0.4		0.2	0.3	1.0	
CP1028-ABEmax		3.0				0.0		7.1			15.7	0.6	0.4		1.3	0.4		0.2	0.3	2.8	
CP1041-ABEmax		7.2				0.0		15.7			24.4	2.7	2.2		1.3	0.4		0.2	0.3	0.7	
CP1249-ABEmax		2.7				0.0		23.8			11.2	0.5	0.4		1.1	0.5		0.2	0.3	4.0	
CP1300-ABEmax		2.5				0.0		3.4			1.5	0.2	0.1		1.1	0.4		0.1	0.3	0.2	

Position	% of total sequencing reads with A•T converted to G•C																				Indel%
	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19	20	
<b>EMX off-target site 1</b>	G	A	G	T	T	A	G	A	G	C	A	G	A	A	G	A	A	G	A	A	
ABEmax		0.2				19.5		0.9			0.1	0.0	0.0		0.0	0.0		0.0	0.0	0.0	
CP1012-ABEmax		0.2				3.9		2.0			2.6	0.2	0.1		0.0	0.0		0.0	0.0	0.0	
CP1028-ABEmax		0.8				14.9		4.4			12.7	0.5	0.4		0.0	0.0		0.0	0.0	0.2	
CP1041-ABEmax		0.2				2.0		2.5			3.8	3.2	5.0		0.1	0.0		0.0	0.0	0.0	
CP1249-ABEmax		0.1				11.6		2.7			2.4	0.5	0.6		0.0	0.0		0.0	0.0	0.0	
CP1300-ABEmax		0.0				0.5		0.2			0.2	0.0	0.1		0.0	0.0		0.0	0.0	0.0	

Position	% of total sequencing reads with A•T converted to G•C																				Indel%
	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19	20	
<b>EMX off-target site 2</b>	G	A	G	T	C	T	A	A	G	C	A	G	A	A	G	A	A	G	A	A	
ABEmax		0.1					1.1	0.1			0.0	0.0	0.0		0.0	0.0		0.0	0.0	0.1	
CP1012-ABEmax		0.1					0.1	0.1			0.1	0.0	0.0		0.0	0.0		0.0	0.0	0.0	
CP1028-ABEmax		0.2					0.8	0.4			1.9	0.1	0.1		0.0	0.0		0.0	0.0	0.0	
CP1041-ABEmax		0.0					0.1	0.0			0.0	0.0	0.0		0.0	0.0		0.0	0.0	0.0	
CP1249-ABEmax		0.0					1.3	1.1			0.6	0.1	0.1		0.0	0.0		0.0	0.0	0.0	
CP1300-ABEmax		0.0					0.0	0.0			0.0	0.0	0.0		0.0	0.0		0.0	0.0	0.0	

Position	% of total sequencing reads with A•T converted to G•C																				Indel%
	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19	20	
<b>EMX off-target site 3</b>	G	A	G	G	C	C	G	A	G	C	A	G	A	A	G	A	A	A	G	A	
ABEmax		0.0						0.0			0.0	0.0	0.0		0.0	0.0		0.0	0.0	0.0	
CP1012-ABEmax		0.0						0.0			0.0	0.0	0.0		0.0	0.0		0.0	0.0	0.0	
CP1028-ABEmax		0.0						0.1			0.1	0.1	0.0		0.0	0.0		0.0	0.0	0.0	
CP1041-ABEmax		0.0						0.0			0.0	0.0	0.0		0.0	0.0		0.0	0.0	0.0	
CP1249-ABEmax		0.0						0.1			0.1	0.0	0.0		0.0	0.0		0.0	0.0	0.0	
CP1300-ABEmax		0.0						0.0			0.0	0.0	0.0		0.0	0.0		0.0	0.0	0.0	



**Supplementary Table 7.** Activities of CP-ABEmax variants versus ABEmax at the HEK4 on-target and off-target sites previously characterized for *S. pyogenes* Cas9 nuclease

		% of total sequencing reads with A•T converted to G•C																				
		1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19	20	
<b>HEK4 on-target</b>		G	G	C	A	C	T	G	C	G	G	C	T	G	G	A	G	G	T	G	G	Indel%
ABEmax					9.7											0.8						4.8
CP1012-ABEmax					2.5											1.0						1.5
CP1028-ABEmax					9.5											0.2						2.1
CP1041-ABEmax					40.3											1.8						1.3
CP1249-ABEmax					2.4											0.8						4.3
CP1300-ABEmax					0.9											0.8						1.0

		% of total sequencing reads with A•T converted to G•C																				
		1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19	20	
<b>HEK4 off-target site 1</b>		T	G	C	A	C	T	G	C	G	G	C	C	G	G	A	G	G	A	G	G	Indel%
ABEmax					3.6											0.1			0.1			0.6
CP1012-ABEmax					1.3											0.1			0.2			0.3
CP1028-ABEmax					2.4											0.2			0.3			1.2
CP1041-ABEmax					1.1											0.1			0.2			0.3
CP1249-ABEmax					1.2											0.1			0.1			0.3
CP1300-ABEmax					0.1											0.1			0.1			0.3

		% of total sequencing reads with A•T converted to G•C																				
		1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19	20	
<b>HEK4 off-target site 2</b>		G	G	C	T	C	T	G	C	G	G	C	T	G	G	A	G	G	G	G	G	Indel%
ABEmax																0.0						0.3
CP1012-ABEmax																0.0						0.3
CP1028-ABEmax																0.0						0.2
CP1041-ABEmax																0.0						0.3
CP1249-ABEmax																0.0						0.1
CP1300-ABEmax																0.0						0.3

		% of total sequencing reads with A•T converted to G•C																				
		1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19	20	
<b>HEK4 off-target site 3</b>		G	G	C	A	C	G	A	C	G	G	C	T	G	G	A	G	G	T	G	G	Indel%
ABEmax					1.1			9.4								1.1						70.0
CP1012-ABEmax					0.3			2.7								2.4						12.0
CP1028-ABEmax					0.3			3.7								2.4						53.0
CP1041-ABEmax					0.2			0.4								6.1						4.0
CP1249-ABEmax					0.3			7.1								1.8						38.0
CP1300-ABEmax					0.0			0.4								2.2						0.4

		% of total sequencing reads with A•T converted to G•C																				
		1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19	20	
<b>HEK4 off-target site 4</b>		G	G	C	A	C	G	A	C	G	G	C	T	G	G	A	G	G	T	G	G	Indel%
ABEmax					0.0			0.0								0.0						0.1
CP1012-ABEmax					0.5			2.0								0.1						0.3
CP1028-ABEmax					3.6			6.2								0.6						0.5
CP1041-ABEmax					0.0			0.0								0.0						0.1
CP1249-ABEmax					0.1			1.8								0.2						0.3
CP1300-ABEmax					0.0			0.1								0.0						0.3

**Supplementary Table 8.** Protospacer sequences for 32 mammalian genomic sites

<b>Site #</b>	<b>Protospacer</b>	<b>PAM</b>
1	GGCAGAGAGCAGAACACTTT	TGA
2	GGGACAAGCAATGGGCTGGC	TGA
3	GTGGAACTCCTTGGGGGTAA	TGA
4	GATACAAGGACAGGCAGCAT	AGA
5	GTCTATTCTCTATCTTCATG	AGA
6	GCTCAAGCCTGATTCCAAGG	AGA
7	GCCGTACCCAAAGGTCCTC	AGCG
8	GGGGACTGAGCAGTAAACAA	GGCG
9	GATTTATGCAAACGGGTTGG	GGCG
10	GCGACAGGCCGAAGAGCTCAG	CGCG
11	GAAGGATGGAGAGGGCGGGG	CGCG
12	GAGAGAACCTGGCTAAGCAT	TGCG
13	GATCCAGGTGCTGCAGAAGG	GAT
14	GACAGGCAGGGGCACCGCGG	CGCC
15	GTGCCACCGGGGCGCCGCGG	TGCC
16	GTGGTAGACAGCATGTGTCCTA	AAGGGT
17	ATTTACAGCCTGGCCTTTGGGG	TCGGGT
18	GGAGAGAAAGAGAAGTTGATTG	ATGGGT
19	GTGTCAGGTAATGTGCTAAACA	GAGAGT
20	GCAGGGCACAGGGAAGAACCTC	TGGGAT
21	GCTGTTGCATGAGGAAAGGGAC	TAGAGT
22	GGCAGTCATCTTAGTCATTACC	TGAGGT
23	CCAACATACATGCCCTTTGCC	TCAAGT
24	GGACTAGAGTAGGATTGTACCC	CTCAGT
25	GTTAGACACGCACAGCATTTC	GGAAGT
26	GGCTGAGCTAACTGTGACAGCA	TGTGGT
27	GGGAGCTCAAGCCTGATTCCAA	GGAGAT
28	GACAAACCAGAAGCCGCTCC	TGG
29	GTTACACCCATGACGAACA	TGG
30	GAACACAAAGCATAGACTGC	GGG
31	GAGTCCGAGCAGAAGAAGAA	GGG
32	GAAGACCAAGGATAGACTGC	TGG



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

<b>Primer Name</b>	<b>Sequence</b>
HTS_fwd_site1	ACACTCTTTCCCTACACGACGCTCTCCGATCTNNNNACATGAGGGTGCCTGAGAAG
HTS_rev_site1	TGGAGTTCAGACGTGTGCTCTTCCGATCTGCAGGGCGCGTTGTAATTAG
HTS_fwd_site2	ACACTCTTTCCCTACACGACGCTCTCCGATCTNNNNCCAATGACTAGGGTGGGCAA
HTS_rev_site2	TGGAGTTCAGACGTGTGCTCTTCCGATCTGAGGAGAAGGCCAAGTGGTC
HTS_fwd_site3	ACACTCTTTCCCTACACGACGCTCTCCGATCTNNNNGAATATCAGGGGATGGCGCA
HTS_rev_site3	TGGAGTTCAGACGTGTGCTCTTCCGATCTTCCACACAGCCACAAGGATC
HTS_fwd_site4	ACACTCTTTCCCTACACGACGCTCTCCGATCTNNNNCCCTAAACCACCTGCAGAGG
HTS_rev_site4	TGGAGTTCAGACGTGTGCTCTTCCGATCTCAGCCCAGCCACATTCTAT
HTS_fwd_site5	TGGAGTTCAGACGTGTGCTCTTCCGATCTTCTCTTTCTCTCCCCACCC
HTS_rev_site5	ACACTCTTTCCCTACACGACGCTCTCCGATCTNNNNTCACTTCAGCCCAGGAGTAT
HTS_fwd_site6	ACACTCTTTCCCTACACGACGCTCTCCGATCTNNNNCGCGGGCTGAAGTAGATCAA
HTS_rev_site6	TGGAGTTCAGACGTGTGCTCTTCCGATCTCCTGTCTCTGCTCCTTTGTCCCC
HTS_fwd_site7	ACACTCTTTCCCTACACGACGCTCTTCCGATCTNNNNGAGGTTTCTGCCAGCTCTC
HTS_rev_site7	TGGAGTTCAGACGTGTGCTCTTCCGATCTGTCTGGCATCGAGTAGGCTG
HTS_fwd_site8	ACACTCTTTCCCTACACGACGCTCTTCCGATCTNNNNGATGCCCTCCATCTTCTCCG
HTS_rev_site8	TGGAGTTCAGACGTGTGCTCTTCCGATCTAGGTTTGCATAGACCTGCC
HTS_fwd_site9	ACACTCTTTCCCTACACGACGCTCTTCCGATCTNNNNGGAGATAGCCCCTTGGGGT
HTS_rev_site9	TGGAGTTCAGACGTGTGCTCTTCCGATCTGTGGCAGAGCTACACGTTCT
HTS_fwd_site10	ACACTCTTTCCCTACACGACGCTCTTCCGATCTNNNNCTCTCCATCCTTCACGCAG
HTS_rev_site10	TGGAGTTCAGACGTGTGCTCTTCCGATCTCTTTGAGGGCGGAGGTTAGG
HTS_fwd_site11	ACACTCTTTCCCTACACGACGCTCTTCCGATCTNNNNATCCAAGCCTCAAGCCTGTC
HTS_rev_site11	TGGAGTTCAGACGTGTGCTCTTCCGATCTCTTTGAGGGCGGAGGTTAGG
HTS_fwd_site12	ACACTCTTTCCCTACACGACGCTCTTCCGATCTNNNNGAACTCACAGAGCGGTGGAA
HTS_rev_site12	TGGAGTTCAGACGTGTGCTCTTCCGATCTACAAATCCTGGCACCAGACC
HTS_fwd_site13	ACACTCTTTCCCTACACGACGCTCTTCCGATCTNNNNCATTGCAGAGAGGCGTATCA
HTS_rev_site13	TGGAGTTCAGACGTGTGCTCTTCCGATCTGGGGTCCCAGGTGCTGAC
HTS_fwd_site14	ACACTCTTTCCCTACACGACGCTCTTCCGATCTNNNNGAACCAGGTAGCCAGAGAC
HTS_rev_site14	TGGAGTTCAGACGTGTGCTCTTCCGATCTTCTTTCAACCCGAACGGAG
HTS_fwd_site15	ACACTCTTTCCCTACACGACGCTCTTCCGATCTNNNNGAACCAGGTAGCCAGAGAC
HTS_rev_site15	TGGAGTTCAGACGTGTGCTCTTCCGATCTTCTTTCAACCCGAACGGAG
HTS_fwd_site16	ACACTCTTTCCCTACACGACGCTCTTCCGATCTNNNNTGCAGTCTCCTGCTTCTCTG
HTS_rev_site16	TGGAGTTCAGACGTGTGCTCTTCCGATTGGTGGAGTGCTCTGTGTTTG
HTS_fwd_site17	ACACTCTTTCCCTACACGACGCTCTTCCGATCTNNNNGGACATTTCCACCGCAAATG
HTS_rev_site17	TGGAGTTCAGACGTGTGCTCTTCCGATGCTACAGAAAGGTCAGCAGC
HTS_fwd_site18	ACACTCTTTCCCTACACGACGCTCTTCCGATCTNNNNTCACTTCAGCCCAGGAGTAT
HTS_rev_site18	TGGAGTTCAGACGTGTGCTCTTCCGATCTTGTGTATGGTGAGAGGTAGGGA
HTS_fwd_site19	ACACTCTTTCCCTACACGACGCTCTTCCGATCTNNNNCTGCACCTAGCCTCCATGTC

HTS_rev_site19	TGGAGTTCAGACGTGTGCTCTTCCGATCTGCTGTGGCATCCAGAGACAT
HTS_fwd_site20	ACACTCTTCCCTACACGACGCTCTTCCGATCTNNNNCTGGGAATAGAGGGTAGTTTC
HTS_rev_site20	TGGAGTTCAGACGTGTGCTCTTCCGATCTCACTCTGCACAGCTGGAGAA
HTS_fwd_site21	ACACTCTTCCCTACACGACGCTCTTCCGATCTNNNNCCCTGTTCCCTAAAGCCCACC
HTS_rev_site21	TGGAGTTCAGACGTGTGCTCTTCCGATCTACTGGTTCTGTTTGTGGCCA
HTS_fwd_site22	ACACTCTTCCCTACACGACGCTCTTCCGATCTNNNNACGTCTCATATGCCCTTGG
HTS_rev_site22	TGGAGTTCAGACGTGTGCTCTTCCGATCTACGTAGGAATTTTGGTGGGACA
HTS_fwd_site23	ACACTCTTCCCTACACGACGCTCTTCCGATCTNNNNTGCAGTCTCCTGCTTCTCTG
HTS_rev_site23	TGGAGTTCAGACGTGTGCTCTTCCGATTGGTGGAGTGCTCTGTGTTTG
HTS_fwd_site24	ACACTCTTCCCTACACGACGCTCTTCCGATCTNNNNCCCTGTTCCCTAAAGCCCACC
HTS_rev_site24	TGGAGTTCAGACGTGTGCTCTTCCGATCTACTGGTTCTGTTTGTGGCCA
HTS_fwd_site25	ACACTCTTCCCTACACGACGCTCTTCCGATCTNNNNAGAGACTGATTGCGTGGAGT
HTS_rev_site25	TGGAGTTCAGACGTGTGCTCTTCCGATCTCACTCCAGCCTAGGCAACAA
HTS_fwd_site26	ACACTCTTCCCTACACGACGCTCTTCCGATCTNNNNCCAGCCCCATCTGTCAAACCT
HTS_rev_site26	TGGAGTTCAGACGTGTGCTCTTCCGATCTTGAATGGATTCTTGGAAACAATGA
HTS_fwd_site27	ACACTCTTCCCTACACGACGCTCTTCCGATCTNNNNCGCGGGCTGAAGTAGATCAA
HTS_rev_site27	TGGAGTTCAGACGTGTGCTCTTCCGATCTCCTGTCTCTGCTCCTTTGTCCCC
HTS_fwd_site28	ACACTCTTCCCTACACGACGCTCTTCCGATCTNNNNAGCCCTCTTTTTATTGGAACCTGTG
HTS_rev_site28	TGGAGTTCAGACGTGTGCTCTTCCGATCTCCGACTGGTCCACTTACCTA
HTS_fwd_site29	ACACTCTTCCCTACACGACGCTCTTCCGATCTNNNNCTGACTCAGCCCTGCAAAGG
HTS_rev_site29	TGGAGTTCAGACGTGTGCTCTTCCGATCTCAAGTCAGGGGAGCGTGTC
HTS_fwd_site30	ACACTCTTCCCTACACGACGCTCTTCCGATCTNNNNCCAGCCCCATCTGTCAAACCT
HTS_rev_site30	TGGAGTTCAGACGTGTGCTCTTCCGATCTTGAATGGATTCTTGGAAACAATGA
HTS_fwd_site31	ACACTCTTCCCTACACGACGCTCTTCCGATCTNNNNCAGCTCAGCCTGAGTGTTGA
HTS_rev_site31	TGGAGTTCAGACGTGTGCTCTTCCGATCTCTCGTGGGTTTGTGGTTGC
HTS_fwd_site32	ACACTCTTCCCTACACGACGCTCTTCCGATCTNNNNTTGCTTATTGCTGAGGGGCA
HTS_rev_site32	TGGAGTTCAGACGTGTGCTCTTCCGATCTACCTCTCTCCTCCAGCTGAG

**Supplementary Sequences 1.** Amino acid sequences for each editor construct used in this study.

**VRQR-ABEmax**

MKRTADGSEFESPKKKRKRKRVSEVEFSHEYWMRHALTLAKRAWDEREVPVGAVLVHNN  
RVIGEGWNRPIGRHDPTAHAEIMALRQGGLVMQNYRLIDATLYVTLEPCVMCAGAMIH  
SRIGRVVFGARDAKTGAAGSLMDVLHHPGMNHRVEITEGILADECAALLSDFFRMRRQ  
EIKAQKKAQSSTDSSGGSSGGSSGSETPGTSESATPESSGGSSGGSSSEVEFSHEYWM  
RHALTLAKRARDEREVPVGAVLVLNNRVIGEGWNRAIGLHDPTAHAEIMALRQGGLVM  
QNYRLIDATLYVTFEPCVMCAGAMIHSRIGRVVFGVRNAKTGAAGSLMDVLHYPGMN  
HRVEITEGILADECAALLCYFFRMPRQVFNAQKKAQSSTDSSGGSSGGSSGSETPGTSE  
SATPESSGGSSGGSDKKYSIGLAIGTNSVGWAVITDEYKVPSSKFKVLGNTDRHSIKKN  
LIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEMAKVDDSSFFHRLEESFL  
VEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRG  
HFLIEGDLNPDNSDVKLFIQLVQTYNQLFEENPINASGVDKAILSARLSKSRLENLIA  
QLPGEKKNGLFGNLIASLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLNLLAQIGDQY  
ADLFLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKY  
KEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKNLREDLLRKQRTFD  
NGSIPHQIHLGELHAILRRQEDFYFPLKDNREKIEKILTRIPYYVGPLARGNSRFAMWT  
RKSEETITPWNFEVVDKGAQAQSFIERMTNFDKNLPNEKVLPHSLLYEYFTVYNELT  
KVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVE  
DRFNASLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDD  
KVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQLIHDDSLT  
FKEDIQKAQVSGQGDLSLHEHIANLAGSPAIKKILQTVKVVDELVKVMGRHKPENIVIEM  
ARENQTTQKGQKNSRERMKRIEEGKELGSQILKEHPVENTQLQNEKLYLYYLQNGRD  
MYVDQELDINRLSDYVDHIVPQSFLKDDSIDNKVLTRSDKNRGKSDNPSEEVVKKM  
KNYWRQLLNAKLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSR  
MNTKYDENDKLIREVKVITLKSCLVSDFRKDFQFYKVVREINNYHHAHDAYLNAVVGTAI  
KKYPKLESEFVYGDYKVYDVRKMIKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIR  
KRPLIETNGETGEIVWDKGRDFATVRKVLSPQVNIVKKTEVQTGGFSKESILPKRNSD  
KLIARKKDWDPKKYGGFVSPTVAYSVLVAKVEKGGKSKLKSVKELLGITIMERSSSF  
NPIDFLEAKGYKEVKKDLIIKLPKYSLFELENGRKRMLASARELQKGNELALPSKYVNF  
YLASHYEKLGKSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVL SAYNK  
HRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDRKQYRSTKEVLDATLIHQSI  
GLYE TRIDLSQLGGDSGGSSKRTADGSEFEPKKKRKV

**xABEmax**

MKRTADGSEFESPKKKRKRKRVSEVEFSHEYWMRHALTLAKRAWDEREVPVGAVLVHNN  
RVIGEGWNRPIGRHDPTAHAEIMALRQGGLVMQNYRLIDATLYVTLEPCVMCAGAMIH  
SRIGRVVFGARDAKTGAAGSLMDVLHHPGMNHRVEITEGILADECAALLSDFFRMRRQ  
EIKAQKKAQSSTDSSGGSSGGSSGSETPGTSESATPESSGGSSGGSSSEVEFSHEYWM  
RHALTLAKRARDEREVPVGAVLVLNNRVIGEGWNRAIGLHDPTAHAEIMALRQGGLVM  
QNYRLIDATLYVTFEPCVMCAGAMIHSRIGRVVFGVRNAKTGAAGSLMDVLHYPGMN  
HRVEITEGILADECAALLCYFFRMPRQVFNAQKKAQSSTDSSGGSSGGSSGSETPGTSE  
SATPESSGGSSGGSDKKYSIGLAIGTNSVGWAVITDEYKVPSSKFKVLGNTDRHSIKKN  
LIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEMAKVDDSSFFHRLEESFL

VEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRG  
HFLIEGDLNPDNSDVKLFIQLVQTYNQLFEENPINASGVDAKAILSARLSKSRLENLIA  
QLPGEKKNGLFGNLIASLGLTPNFKSNFDLAEDTKLQLSKDQYDDDLNLLAQIGDQY  
ADLFLAAKNLSDAILLSDILRVNTEITKAPLSASMIKLYDEHHQDLTLLKALVRQQLPEKY  
KEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKNLREDLLRKQRTFD  
NGIIPHQIHLGELHAILRRQEDFYFPLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTR  
KSEETITPWNFEKVVDKGASAQSFIERMTNFDKNLPNEKVLPHKSLLEYFTVYNELTK  
VKYVTEGMRKPAFLSGDQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVED  
RFNASLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDK  
VMKQLKRRRYTGWGRLSRKLINGIRDQKQSGKTILDFLKSDGFANRNFIQLIHDDSLTFK  
EDIQKAQVSGQGDSLHEHIANLAGSPAIKKILQTVKVVDELVKVMGRHHPENIVIEMA  
RENQTTQKGQKNSRERMKRIIEGKELGSQILKEHPVENTQLQNEKLYLYYLQNGRDM  
YVDQELDINRLSDYDHDHIVPQSFLKDDSIDNKVLTRSDKNRGSNDNPSEEVVKMMK  
NYWRQLLNAKLITQRKFDNLTKAERGGLSELDKAGFIKRLVETRQITKHVAQILD SRM  
NTKYDENDKLIREVKVITLKSCLVSDFRKDFQFYKREINNYHHAHDAYLNAVVG TALIK  
KYPKLESEFVYGDYKVYDVRKMIKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRK  
RPLIETNGETGEIVWDKGRDFATVRKVL SMPQVNIVKKT EVQTGGFSKESILPKRNSDK  
LIARKKDWDPKKYGGFDSPTVAYSVLVAKVEKGKSKKLKSVKELLGITIMERS SFEKN  
PIDFLEAKGYKEVKKDLIILPKYSLFEENGRKRMLASAGVLQKGNELALPSKYVNF LY  
LASHYEKLGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVLADANLDKVL SAYNKH  
RDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVL DATLIHQ SITGLYETR  
IDLSQLGGDSGGSKRTADGSEFEPKKKRKV

**VRER-ABEmax**

MKRTADGSEFESPKKKRKVSEVEFSHEYWMRHALTLAKRAWDEREVPVGAVLVHNN  
RVIGEGWNRPIGRHDPTAHAEIMALRQGGGLVMQNYRLIDATLYVTLEPCVMCAGAMIH  
SRIGRVVFGARDAKTGAAGSLMDVLHHPGMNHRVEITEGILADECAALLSDFFRMR RQ  
EIKAQKKAQSSTDSGGSSGGSSGSETPGTSESATPESSGGSSGGSSEVEFSHEYWM  
RHALTLAKRARDEREVPVGAVLVLNNRVIGEGWNRRAIGLHDPTAHAEIMALRQGGGLVM  
QNYRLIDATLYVTFEPCVMCAGAMIHSRIGRVVFGVRNAKTGAAGSLMDVLHYPGMN  
HRVEITEGILADECAALLCYFFRMPRQVFNAQKKAQSSTDSGGSSGGSSGSETPGTSE  
SATPESSGGSSGGSDKKYSIGLAIGTNSVGWAVITDEYKVPSKFKVLGNTDRHSIKKN  
LIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEMAKVDD SFFHRLEESFL  
VEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRG  
HFLIEGDLNPDNSDVKLFIQLVQTYNQLFEENPINASGVDAKAILSARLSKSRLENLIA  
QLPGEKKNGLFGNLIASLGLTPNFKSNFDLAEDA KLQLSKDQYDDDLNLLAQIGDQY  
ADLFLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKY  
KEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKNLREDLLRKQRTFD  
NGSIPHQIHLGELHAILRRQEDFYFPLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMT  
RKSEETITPWNFEVVDKGASAQSFIERMTNFDKNLPNEKVLPHKSLLEYFTVYNELT  
KVYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVE  
DRFNASLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDD  
KVMKQLKRRRYTGWGRLSRKLINGIRDQKQSGKTILDFLKSDGFANRNFMQLIHDDSLT  
FKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKILQTVKVVDELVKVMGRHHPENIVIEM  
ARENQTTQKGQKNSRERMKRIIEGKELGSQILKEHPVENTQLQNEKLYLYYLQNGRD

MYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKNRGKSDNVPSEEVVKKM  
KNYWRQLLNAKLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSR  
MNTKYDENDKLIREVKVITLKSCLVSDFRKDFQFYKREINNYHHAHDAYLNAVVGTAI  
KKYPKLESEFVYGDYKVYDVRKMIKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIR  
KRPLIETNGETGEIVWDKGRDFATVRKVLSPQVNIKKTEVQTGGFSKESILPKRNSD  
KLIARKKDWDPKKGFFVSPVAVSVLVAKVEKGGKSKKLSVKELLGITIMERSSSF  
NPIDFLEAKGYKEVKKDLIIKLPKYSLENGRKRMLASARELQKGNELALPSKYVNF  
YLASHYEKLGKSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVL  
SAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDRKEYRSTKEVLDATLIHQ  
SITGLYETRIDLSQLGGDSGGSKRTADGSEFEPKKKRKV

### **SaABEmax**

MKRTADGSEFESPKKKRKVSEVEFSHEYWMRHALTLAKRAWDEREVPVGAVLVHNN  
RVIGEGWNRPIGRHDPTAHAEIMALRQGGGLVMQNYRLIDATLYVTLEPCVMCAGAM  
IHSRIGRVVFGARDAKTGAAGSLMDVLHHPGMNHRVEITEGILADECAALLSDFFRM  
RREQEIKAKKAQSSTDSSGGSSGGSSGSETPGTSESATPESSGGSSGGSSSEVEFS  
HEYWMRHALTLAKRARDEREVPVGAVLVLNNRVIGEGWNRRAIGLHDPTAHAEIMA  
LRQGGGLVMQNYRLIDATLYVTLEPCVMCAGAMIHSRIGRVVFGVRNAKTGAAGSL  
MDVLHYPGMNHRVEITEGILADECAALLCYFFRMPRQVFNAQKKAQSSTDSSGGSS  
GGSSGSETPGTSESATPESSGGSSGGSGKRNILGLAIGITSVGYGIIDYETRDVID  
AGVRLFKEANVENNEGRRSKRGARLKRHHRIQRVKKLLFDYNLLTDHSELSGINPY  
EARVKGLSQKLSEEFSAALLHLAKRRGVHNVNEVEEDTGNELSTKEQISRNSKALEE  
KYVAELQLERLKKDGEVRGSINRFKTSYVKEAKQLLKVKAYHQLDQSFIDTYIDLL  
ETRRTYYEGPGEGSPFGWKDIKEWYEMLMGHCTYFPEELRSVKYAYNADLYNALND  
LNNLVITRDENEKLEYEFQIIENVFKQKKKPTLKQIAKEILVNEEDIKGYRVTSTGK  
PEFTNLKVYHDIKDITARKEIENAELLDQIAKILTIYQSSEDIQEELTNLNSELTQEE  
IEQISNLKGYTGTHNLSLKAINLILD ELWHTNDNQIAIFNRLKLVPKKVDLSQQKE  
IPTTLVDDFILSPVVKRSFIQSIVINAIKKYGLPNDIIELAREKNSKDAQKMINEMQ  
KRNQRQTNERIEEIIRTTGKENAKYLIEKIKLHDMQEGKCLYSLEAIPLEDLLNPF  
NYEVDHIIIPRSVSFDNSFNKVLVKQEENSKKGNRTPFQYLSSSDSKISYETFKKH  
ILNLAAGKGRISKTKKEYLLEERDINRFSVQKDFINRNLVDTRYATRGLMNLRSY  
FRVNNLDVKVKSINGGFTSFLRRKWKFKKERNKGYKHAEDALIIANADFIFKEWKK  
LDKAKKVMENQMFEEKQAESMPEIETEQEYKEIFITPHQIKHIKDFKDYKYSHRV  
DKKPNRELINDTLYSTRKDDKGNTLIVNNLNGLYDKDNDKLLKLINKSPEKLLMY  
HHDPQTYQKLKLIMEQYGDEKNPLYKYEEETGNLYTKYSKKDNGPVIKKIKYYGN  
KLNALHDITDDYPNSRNKVVKLSLKPYPYFDVYLDNGVYKFTVKNLVDVIKENY  
YEVNSKCYEEAKKLLKISNQAEFIASFYNNDLIKINGELYRVIGVNNDLLNRIE  
VNMIDITYREYLENMNDKRPPRIIKTIASKTQSIKKYSTDILGNLYEVKSKKHPQ  
IIKKGGSGGSKRTADGSEFEPKKKRKV

### **SaKKH-ABEmax**

MKRTADGSEFESPKKKRKVSEVEFSHEYWMRHALTLAKRAWDEREVPVGAVLVHNN  
RVIGEGWNRPIGRHDPTAHAEIMALRQGGGLVMQNYRLIDATLYVTLEPCVMCAGAM  
IHSRIGRVVFGARDAKTGAAGSLMDVLHHPGMNHRVEITEGILADECAALLSDFFRM  
RREQEIKAKKAQSSTDSSGGSSGGSSGSETPGTSESATPESSGGSSGGSSSEVEFS  
HEYWMRHALTLAKRARDEREVPVGAVLVLNNRVIGEGWNRRAIGLHDPTAHAEIMA  
LRQGGGLVMQNYRLIDATLYVTLEPCVMCAGAMIHSRIGRVVFGVRNAKTGAAGSL  
MDVLHYPGMN

HRVEITEGILADECAALLCYFFRMPRQVFNAQKKAQSSTDSGGSSGGSSGSETPGTSE  
SATPESSGGSSGGSGKRNYILGLAIGITSVGYGIIDYETRDVIDAGVRLFKEANVENNEG  
RRSKRGARRLKRRRRHRIQRVKKLLFDYNLLTDHSELSGINPYEARVKGLSQKLSEEE  
FSAALLHLAKRRGVHNVNEVEEDTGNELSTKEQISRNSKALEEKYVAELQLERLKKDG  
EVRGSINRFKTSDYVKEAKQLLKVKAYHQLDQSFIDTYIDLLETRRRTYYEGPGEPSF  
GWKDIKEWYEMLMGHCTYFPEELRSVKYAYNADLYNALNDLNNLVITRDENEKLEYE  
KFQIIENVFKQKKKPTLKQIAKEILVNEEDIKGYRVTSTGKPEFTNLKVYHDIKDITARKEI  
ENAELLDQIAKILTIYQSSEDIQEELTNLNSELTQEEIEQISNLKGYTGTHNLSLKAINLILD  
ELWHTNDNQIAIFNRLKLVPKKVDLSQQKEIPTTLVDDFILSPVVKRSFIQSIKVINAIKKY  
GLPNDIIIELAREKNSKDAQKMINEMQKRNRQTNERIEEIIRTTGKENAKYLIEKIKLHDM  
QEGKCLYSLEAIPLEDLLNPFNYEVDHIIPRSVSFDNSFNKVLVKQEENSKKGNRTP  
FQYLSSSDSKISYETFKKHILNLAAGKGRISKTKKEYLLEERDINRFSVQKDFINRNLVDT  
RYATRGLMNLRSYFRVNNLDVKVKSINGGFTSFLRRKWKFKKERNKGYKHHHAEDALII  
ANADFIFKEWKLDKAKKVMENQMFEEKQAESMPEIETEQEYKEIFITPHQIKHIKDFKD  
YKYSHRVDKKNRKLINDTLYSTRKDDKGNTLIVNNLNGLYDKDNDKLLKLINKSPEKLL  
MYHHDPQTYQKLLIMEQYGDENPLYKYEEETGNLYTKYSKKDNGPVIKKIKYYGNK  
LNAHLDITDDYPNSRNKVKLSLKPFRFDVYLDNGVYKFVTVKNLDVIKKENYYEVNSK  
CYEEAKLKKISNQAEFIASFYKNDLIKINGELRVIGVNNDLLNRIEVNMIDITYREYLEN  
MNDKRPPHIIKTIASKTQSIKKYSTDILGNLYEVKSKKHPQIIKKGGGSKRTADGSEFEP  
KKKRKV

**CP1012-CBEmax**

MKRTADGSEFESPCKKRKVSSETGPVAVDPTLRRRIEPHEFEVFFDPRELKRETCCLY  
EINWGGRRHSIWRHTSQNTNKHVEVNFIEKFTTERYFCPNTRCSITWFLSWSPCGECSR  
AITEFLSRYPHVTLFIYIARLYHHADPRNRQGLRDLISSGVTIQIMTEQESGYCWRNFVN  
YSPSNEAHWPYPHLLWVRLYVLELYCIILGLPCLNILRRKQPQLTFFTIALQSCHYQRL  
PPHILWATGLKSGGSSGGSSGSETPGTSESATPESSGGSSGGSDYKVYDVRKMIAS  
EQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRK  
VLSMPQVNIVKKTEVQTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSV  
LVVAKVEKGKSKKLKSVKELLGITIMERSSEFEKNPIDFLEAKGYKEVKKDLIILPKYSLF  
ELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLGKSPEDNEQKQLFVEQ  
HKHYLDEIIEQISEFSKRVLADANLDKVL SAYNKHARDKPIREQAENIIHLFTLTNLGAPAA  
FKYFDTTIDRKRYTSTKEVLDATLIHQ SITGLYETRIDLSQLGGDGGSSGGSSGGSSGG  
SGGSSGGDKKYSIGLAIGTNSVGWAVITDEYKVPSKFKVLGNTDRHSIKKNLIGALLFD  
SGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEMAKVDDSFHRLVESFLVEEDKK  
HERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGD  
LNPDNSDVKLFIQLVQTYNQLFEENPINASGVDAKAILSARLSKSRRLLENLIAQLPGEK  
KNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKD TYDDDLDNLLAQIGDQYADFLA  
AKNLSDAILSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPKEYKEIFFD  
QSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKNLREDLLRKQRTFDNGSIPH  
QIHLGELHAILRRQEDFYPLKDNREKIEKILTFRIPIYYVGPLARGNSRFAMTRKSEET  
ITPWNFEVVDKGASQAQSFIERMTNFDKNLPNEKVLPHKSLLYEYFTVYNELTKVKYVT  
EGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNAS  
LGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKYAHLFDDKVMKQL  
KRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDFANRNFMQLIHDDSLTFKEDIQK

AQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIAMARENQT  
TQKGQKNSRERMKRIEELGKELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQE  
LDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKNRGKSDNVPSEEVVKKMKNYWRQ  
LLNAKLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDE  
NDKLIREVKVITLKSCLVSDFRKDFQFYKREINNYHHAHDAYLNAVVG TALIKKYPKLE  
SEFVYGGSGGSKRTADGSEFEPKKKRKV

**CP1028-CBEmax**

MKRTADGSEFESPKKKRQVSSETGPVAVDPTLRRRIEPHEFEVFFDPRELKRETCCLY  
EINWGGRHSIWRHTSQNTNKHVEVNFIEKFTTERYFCPNTRCSITWFLSWSPCGECSR  
AITEFLSRYPHVTLFIYIARLYHHADPRNRQGLRDLISSGVTIQIMTEQESGYCWRNFVN  
YSPSNEAHWPYPHLLWVRLYVLELYCIIILGLPPCLNILRRKQPQLTFFTIALQSCHYQRL  
PPHILWATGLKSGGSSGGSSGSETPGTSESATPESGGSSGGSEIGKATAKYFFYSNI  
MNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSPQVNIVKTEVQ  
TGGFSKESILPKRNSDKLIARKKDWDPKKGFFDSPTVAYSVLVAKVEKKGSKKLKS  
VKELLGITIMERSSSFENPIDFLEAKGYKEVKKDLIIKLPKYSLFELENGRKRMLASAGEL  
QKGNELALPSKYVNFYLYLASHYEKLGSPEDNEQKQLFVEQHKKHYLDEIIEQISEFSKR  
VILADANLDKVL SAYNKHHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTK  
EVLDTLIHQSI TGLYETRIDLSQLGGDGGSGGSSGGSSGGSSGGSSGGSSGGMDKKYSIGL  
AIGTNSVGWAVITDEYKVPKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTAR  
RRYTRRKNRICYLQEIFSNEMAKVDDSSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAY  
HEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVKLFIQLV  
QTYNQLFEENPINASGVDAKILSARLSKSRLENLIAQLPGEKKNLFGNLIASLGLT  
PNFKSNFDLAEDAKLQLSKD TYDDDLDNLLAQIGDQYADLFLAAKNLSDAILLSDILRVN  
TEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGAS  
QEEFYKFIKPILEKMDGTEELLVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQED  
FYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDK GAS  
AQSFIERMTNFDKNLPNEKVL PKHSLLEYFTVYNELTKVKYVTEGMRKPAFLS GEQK  
KAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYHDLLKIIKDKDF  
LDNEENEDILEDIVLTLTLFEDREMIEERLKYAHLFDDKVMKQLKRRRYTGWGRLSRK  
LINGIRDKQSGKTILDFLKS DGFANRNFMLIHDDSLTFKEDIQKAQVSGQGDSLHEHIA  
NLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIAMARENQTTQKGQKNSRERMKRI  
EEGIKELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVP  
QSFLKDDSIDNKVLTRSDKNRGKSDNVPSEEVVKKMKNYWRQLLNAKLITQRKFDNLTKA  
ERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKS  
LVSDFRKDFQFYKREINNYHHAHDAYLNAVVG TALIKKYPKLESEFVYGDYKVYDVRK  
MIAKSEQSGGSKRTADGSEFEPKKKRKV

**CP1041-CBEmax**

MKRTADGSEFESPKKKRQVSSETGPVAVDPTLRRRIEPHEFEVFFDPRELKRETCCLY  
EINWGGRHSIWRHTSQNTNKHVEVNFIEKFTTERYFCPNTRCSITWFLSWSPCGECSR  
AITEFLSRYPHVTLFIYIARLYHHADPRNRQGLRDLISSGVTIQIMTEQESGYCWRNFVN  
YSPSNEAHWPYPHLLWVRLYVLELYCIIILGLPPCLNILRRKQPQLTFFTIALQSCHYQRL  
PPHILWATGLKSGGSSGGSSGSETPGTSESATPESGGSSGGSSNIMNFFKTEITLANG

EIRKRPLIETNGETGEIVWDKGRDFATVRKVL SMPQVNIVKKTEVQTGGFSKESILPKR  
NSDKLIARKKDWDPKKYGGFDSPTVAYSVLVAKVEKGKSKKLKSVKELLGITIMERS  
FEKNPIDFLEAKGYKEVKKDLIIKLPKYSLFELENGRKRMLASAGELQKGNELALPSKYV  
NFLYLASHYEKLGSPEDNEQKQLFVEQHKHYLDEIIIEQISEFSKRVLADANLDKVL  
SAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQ  
SITGLYETRIDLSQLGGDGGSGGSGGSGGSGGSGGSGGSGGDKKYSIGLAIGTNSV  
GWAVITDEYKVP SKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRY  
TRRKNRICYLQEIFS NEMAKVDD SFFHRLEESFLVEEDKKHERHPIFGNIVDEVAY  
HEKYPTIYHLRKKLVDSTDKADLR LIYLALAHMIKFRGHFLIEGDLNPDNSDVKLFI  
QLVQTYNQLFEENPINASGVDAKAILSARLSKSRRENLI AQLPGEKKNGLFGNLI  
ALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLAAKNLSDA  
ILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSK  
NGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKLNREDLLRKQRTFDNGSIPHQ  
IHGELHAILRRQEDFY PFLKDNREKIEKILTRIPYYVGPLARGNSRFAWMTRKSEE  
TITPWNFEEVVDKGASAQSFIERMTNFDKNLPNEKVL PKHSLLYEYFTVYNELTKV  
KYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISG  
VEDRFNASLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTFEDREMIEERLKYA  
HLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQ  
LIHDDSLTFKEDIQKAQVSGQGDLSLHEHIANLAGSPAIKKGILQTVKVVDELVKV  
MGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIKELGSQILKEHPVENTQL  
QNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRS  
DKNRGKSDNVPSEEVVKKMKNYWRQLLNAKLITQRKFDNLTKAERGGLSELDKAGFI  
K RQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKS KLVSDFRKDFQFYK  
VREINNYHHAHDAYLNAVVG TALIKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIG  
KATAKYFYSSGGSKRTADGSEFEPKKRKY

**CP1249-CBE<sub>max</sub>**

MKRTADGSEFESPKKKRKYVSSETGPVAVDPTLRRRIEPHEFEVFFDPREL  
RKETCLLYEINWGGRHSIWRHTSQNTNKHVEVNFIEKFTTERYFCPNTRCSITWFL  
SWSPCGECSR AITEFLSRYPHVTLFIYIARLYHHADPRNRQGLRDLISSGVTIQIMTE  
QESGYCWRNFVNYSPSNEAHWPYPHLLWVRLYVLELYCIILGLPCLNILRRKQPQLT  
FFTIALQSCHYQRLPPHILWATGLKSGGSSGGSSGSETPGTSESATPESSGGSSGG  
SPEDNEQKQLFVEQHKHYLDEIIIEQISEFSKRVLADANLDKVL SAYNKHRDKPI  
REQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQ  
SITGLYETRIDLSQLGGDGGSGGSGGSGGSGGSGGSGGMDKKYSIGLAIGTNSV  
GWAVITDEYKVP SKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRY  
TRRKNRICYLQEIFS NEMAKVDD SFFHRLEESFLVEEDKKHERHPIFGNIVDEVAY  
HEKYPTIYHLRKKLVDSTDKADLR LIYLALAHMIKFRGHFLIEGDLNPDNSDVKLFI  
QLVQTYNQLFEENPINASGVDAKAILSARLSKSRRENLI AQLPGEKKNGLFGNLI  
ALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLAAKNLSDA  
ILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSK  
NGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKLNREDLLRKQRTFDNGSIPHQ  
IHGELHAILRRQEDFY PFLKDNREKIEKILTRIPYYVGPLARGNSRFAWMTRKSEE  
TITPWNFEEVVDKGASAQSFIERMTNFDKNLPNEKVL PKHSLLYEYFTVYNELTKV  
KYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISG  
VEDRFNASLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTFEDREMIEERLKYA  
HLFDDKVMKQ



LKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQLIHDDSLTFKEDIQ  
KAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVDELVKVMGRHKPENIVEMARENQ  
TTQKGQKNSRERMKRIEEGIKELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQ  
ELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKNRGKSDNVPSEEVVKMKNYWR  
QLLNAKLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYD  
ENDKLIREVKVITLKSCLVSDFRKDFQFYKREINNYHHAHDAYLNAVVG TALIKKYPKL  
ESEFVYGDYKVYDVRKMIKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIET  
NGETGEIVWDKGRDFATVRKVL SMPQVNIVKKTEVQTGGFSKESILPKRNSDKLIARKK  
DWDPK KYGGFDSPTVAYSVLVAKVEK GKSKKLSVKELLGITIMERS SFEKNPIDFLE  
AKGYKEVKKDLIIKLPKYSLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHY  
EKLGSSGGSKRTADGSEFEPKKKRKV

**CP1300-CBE<sub>max</sub>**

MKRTADGSEFESPKKKRQVSSSETGPVAVDPTLRRRIEPHEFEVFFDPRELKRETCCLLY  
EINWGGRHSIWRHTSQNTNKHVEVNFIEKFTTERYFCPNTRCSITWFLSWSPCGECSR  
AITEFLSRYPHVTLFIYIARLYHHADPRNRQGLRDLISSGVTIQIMTEQESGYCWRNFVN  
YSPSNEAHWPYPHLLWVRLYVLELYCII LGLPPCLNLRKQPQLTFFTIALQSCHYQRL  
PPHILWATGLKSGGSSGGSSGSETPGTSESATPES SGGSSGGSKPIREQAENIIHLFTL  
TNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQ SITGLYETRIDLSQLGGDGGSSGS  
GGSSGGSSGGSSGGDKKYSIGLAIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKK  
NLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFS NEMAKVDDSFHRLEES  
FLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLR LIYLALAHMIKFR  
GHFLIEGDLNPDNSDVKLFIQLVQTYNQLFEENPINASGVDAKAILSARLSKSRRENL  
IAQLPGEKKNGLFGNLIASLGLTPNFKSNFDLAEDAKLQLSKD TYDDDLDNLLAQIGDQ  
YADLFLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEK  
YKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLV KLNREDLLRKQRTF  
DNGSIPHQIHLGELHAILRRQEDFY PFLKDNREKIEKILTFRIPYVVGPLARGNSRFAWM  
TRKSEETITPWNFEEVVDKGASAQSFIERMTNFDKNLPNEKVL PKHSLLYEYFTVYNEL  
TKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGV  
EDRFNASLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKYAHLFD  
DKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFANRNF MQLIHDDSL  
TFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVDELVKVMGRHKPENIVIE  
MARENQTTQKGQKNSRERMKRIEEGIKELGSQILKEHPVENTQLQNEKLYLYYLQNGR  
DMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKNRGKSDNVPSEEVVKK  
MKNYWRQLLNAKLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDS  
RMNTKYDENDKLIREVKVITLKSCLVSDFRKDFQFYKREINNYHHAHDAYLNAVVGTA  
LIKKYPKLESEFVYGDYKVYDVRKMIKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEI  
RKRPLIETNGETGEIVWDKGRDFATVRKVL SMPQVNIVKKTEVQTGGFSKESILPKRNS  
DKLIARKKDWDPK KYGGFDSPTVAYSVLVAKVEK GKSKKLSVKELLGITIMERS SFE  
KNPIDFLEAKGYKEVKKDLIIKLPKYSLFELENGRKRMLASAGELQKGNELALPSKYVNFL  
YLASHYEKLGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVL SAYN  
KHRDSGGSKRTADGSEFEPKKKRKV

**CP1012-ABE<sub>max</sub>**



DNEQKQLFVEQHKHYLDEIIEQISEFSKRVLADANLDKVL SAYNKHRDKPIREQAENIIH  
LFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQ SITGLYETRIDLSQLGGDGGG  
GGSGGSGGSGGSGGSGGMDKKYSIGLAIGTNSVGWAVITDEYKVPSKKFKVLGNTDR  
HSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFS NEMAKVDDSFHR  
LEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLR LIYLALAH  
MIKFRGHFLIEGDLNPDNSDVKLFIQLVQTYNQLFEENPINASGVDAKAILSARLSKSR  
RLENLIAQLPGEKKNGLFGNLIASLGLTPNFKSNFDLAEDA KLQLSKD TYDDDLDNLLA  
QIGDQYADLFLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQ  
QLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLV KLNREDLLRK  
QRTFDNGSIPHQIHLGELHAILRRQEDFY PFLKDNREKIEKILTFRIPYYVGPLARGNSRF  
AWMTRKSEETITPWNFEEVVDKGASAQSFIERMTNFDKNLPNEKVLPKHSLLYEYFTV  
YNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEI  
SGVEDRFNASLGTYHDLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKYAH  
LFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFANRNF MQLIHD  
DSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPEN  
IVIEMARENQTTQKGQKNSRERMKRIEEGIKELGSQILKEHPVENTQLQNEKLYLYLQ  
NGRDMYVDQELDINRLSDYVDHIVPQSFLKDDSIDNKVLTRSDKNRGKSDNVPSEEV  
VKKMKNYWRQLLNAKLITQRKFDNLTKAERGGLELKDAGFIKRQLVETRQITKHVAQI  
LDSRMNTKYDENDKLIREVKVITLKS KLVSDFRKDFQFYK VREINNYHHAHDAYLNAV  
GTALIKKYPKLESEFVYGDYKVYDVRKMIKSEQSGGSKRTADGSEFEPKKKRKV

**CP1041-ABEmax**

MKRTADGSEFESP KKKR KVSEVEFSHEYWMRHALTLAKRAWDEREVPVGAVLVHNN  
RVIGEGWNRPIGRHDPTAHAEIMALRQGG LVMQNYRLIDATLYVTLEPCVMCAGAMIH  
SRIGRVVFGARDAKTGAAGSLMDVLHHPGMNHRVEITEGILADECAALLSDFFRMRRQ  
EIKAKKAQSSTDSSGSSGGSSGSETPGTSESATPESSGGSSGGSSEVEFSHEYWM  
RHALTLAKRARDEREVPVGAVLVLNNRVIGEGWNRAIGLHDPTAHAEIMALRQGG LVM  
QNYRLIDATLYVTFEPCVMCAGAMIHSRIGRVVFGVRNAKTGAAGSLMDVLHYPGMN  
HRVEITEGILADECAALLCYFFRMPRQVFNAQKKAQSSTDSSGSSGGSSGSETPGTSE  
SATPESSGGSSGGSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRK  
VLSMPQVNIVKKTEVQTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSV  
LVVAKVEKGKSKKLKSVKELLGITIMERS SFEKNPIDFLEAKGYKEVKDLI IKLPKYSLF  
ELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLGSPEDNEQKQLFVEQ  
HKHYLDEIIEQISEFSKRVLADANLDKVL SAYNKHRDKPIREQAENIIHLFTLTNLGAPAA  
FKYFDTTIDRKRYTSTKEVLDATLIHQ SITGLYETRIDLSQLGGDGGSGGSGGSGGSGG  
SGGSGGDKKYSIGLAIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFD  
SGETAETRLKRTARRRYTRRKNRICYLQEIFS NEMAKVDDSFHRLEESFLVEEDKK  
HERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLR LIYLALAHMIKFRGHFLIEG  
LNPDNSDVKLFIQLVQTYNQLFEENPINASGVDAKAILSARLSKSRLENLIAQLPGEK  
KNGLFGNLIASLGLTPNFKSNFDLAEDA KLQLSKD TYDDDLDNLLAQIGDQYADLFLA  
AKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFD  
QSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLV KLNREDLLRKQRTFDNGSIPH  
QIHLGELHAILRRQEDFY PFLKDNREKIEKILTFRIPYYVGPLARGNSRF AWMTRKSEET  
ITPWNFEEVVDKGASAQSFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVT

EGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNAS  
LGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKYAHLFDDKVMKQL  
KRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFANRNFQMQLIHDDSLTFKEDIQK  
AQVSGQGDSLHEHIANLAGSPAIAKKGILQTVKVVDELVKVMGRHKPENIVIAMARENQT  
TQKGQKNSRERMKRIIEGKELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQE  
LDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKNRGKSDNVPSEEVVKMKMKNYWRQ  
LLNAKLITQRKFDNLTKAERGGELSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDE  
NDKLIREVKVITLKSCLVSDFRKDFQFYKVVREINNYHHAHDAYLNAVVG TALIKKYPKLE  
SEFVYGDYKVYDVRKMIKSEQEIGKATAKYFFYSSGGSKRTADGSEFEPKKRKY

**CP1249-ABEmax**

MKRTADGSEFESPKKKRKYSEVEFSHEYWMRHALTLAKRAWDEREVPVGAVLVHNN  
RVIGEGWNRPIGRHDPTAHAEIMALRQGGGLVMQNYRLIDATLYVTLEPCVMCAGAMIH  
SRIGRVVFGARDAKTGAAGSLMDVLHHPGMNHRVEITEGILADECAALLSDFFRMRQ  
EIKAKKAQSSTDSSGSSGSSGSETPGTSESATPESSGGSSGSSSEVEFSHEYWM  
RHALTLAKRARDEREVPVGAVLVLNRRVIGEGWNRRAIGLHDPTAHAEIMALRQGGGLVM  
QNYRLIDATLYVTFEPCVMCAGAMIHSRIGRVVFGVRNAKTGAAGSLMDVLHYPGMN  
HRVEITEGILADECAALLCYFFRMPRQVFNAQKKAQSSTDSSGSSGSSGSETPGTSE  
SATPESSGGSSGSSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVLADANLDKVLSA  
YKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSTGL  
YETRIDLSQLGGDGGSSGSSGSSGSSGSSGSSGSSGMDKKYSIGLAIGTNSVGWAVITDE  
YKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQ  
EIFSNEMAKVDDSFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLV  
DSTDKADRLIYLALAHMIKFRGHFLIEGDLNPDNSDVKLFIQLVQTYNQLFEENPINA  
SGVDAKAILSARLSKSRLENLIAQLPGEKKNLFGNLIASLGLTPNFKSNFDLAEDAK  
LQLSKDQYDDDLNLLAQIGDQYADLFLAAKNLSDAILLSDILRVNTEITKAPLSASMIKR  
YDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKM  
DGTEELLVKNLREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYFPLKDNREKIEKIL  
TFRIPYVYVGPLARGNSRFAMTRKSEETITPWNFEVVDKGGASQSFIERMTNFDKNL  
PNEKVLPHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTV  
KQLKEDYFKKIECFDSVEISGVEDRFNASLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTL  
TLFEDREMIEERLKYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDF  
LKSDGFANRNFQMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIAKKGILQTV  
KVVDELVKVMGRHKPENIVIAMARENQTTQKGQKNSRERMKRIIEGKELGSQILKEHP  
VENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTR  
SDKNRGKSDNVPSEEVVKMKMKNYWRQLLNAKLITQRKFDNLTKAERGGELSELDKAGFI  
KRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSCLVSDFRKDFQFYKVVRE  
INNYHHAHDAYLNAVVG TALIKKYPKLESEFVYGDYKVYDVRKMIKSEQEIGKATAKY  
FFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLVSMQVNIK  
KTEVQTGGFSKESILPKRNSDKLIARKKDWDPKKGFFSPTVAVSVLVVAKVEKGGKS  
KKLKSVELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIPKYSLELENGRKRMLA  
SAGELQKGNELALPSKYVNFLYLASHYEKLGSSGGSKRTADGSEFEPKKRKY



**Supplementary Note 1.** Representative batch file input with parameters for Crispresso2 HTS analysis

HTS analysis was performed using the batch function from Crispresso2<sup>39</sup>. Batch analysis was prepared using the following representative parameters. The parameters are as follows:

Parameter	Property
<i>fastq_r1</i>	.fastq file generated from miseq output
<i>a</i>	amplicon sequence of genomic site
<i>g</i>	protospacer sequence without PAM
<i>n</i>	name of Crispresso2 output file
<i>min_frequency_alleles_around_cut_to_plot</i>	minimum % for an outcome to be included in the allelic frequencies output figure
<i>w</i>	width of window around predicted cut site (3-nt 5' from start of PAM) for indel analysis
<i>q</i>	minimum average quality score (phred33) required to include a read for analysis

<i>fastq_r1</i>	<i>a</i>	<i>g</i>	<i>n</i>	<i>min_frequency_alleles_around_cut_to_plot</i>	<i>w</i>	<i>q</i>
TPH-210-unt-n1_S173	CCGACTG	GACAAACCAGAAGCCGCTCC	TPH-210-unt	0.05	10	30
TPH-210-unt-n2_S180	CCGACTG	GACAAACCAGAAGCCGCTCC	TPH-210-unt	0.05	10	30
TPH-ABE1012-210-n1	CCGACTG	GACAAACCAGAAGCCGCTCC	TPH-ABE10	0.05	10	30
TPH-ABE1012-210-n2	CCGACTG	GACAAACCAGAAGCCGCTCC	TPH-ABE10	0.05	10	30
TPH-ABE1028-210-n1	CCGACTG	GACAAACCAGAAGCCGCTCC	TPH-ABE10	0.05	10	30
TPH-ABE1028-210-n2	CCGACTG	GACAAACCAGAAGCCGCTCC	TPH-ABE10	0.05	10	30
TPH-ABE1041-210-n1	CCGACTG	GACAAACCAGAAGCCGCTCC	TPH-ABE10	0.05	10	30
TPH-ABE1041-210-n2	CCGACTG	GACAAACCAGAAGCCGCTCC	TPH-ABE10	0.05	10	30
TPH-ABE1249-210-n1	CCGACTG	GACAAACCAGAAGCCGCTCC	TPH-ABE12	0.05	10	30
TPH-ABE1249-210-n2	CCGACTG	GACAAACCAGAAGCCGCTCC	TPH-ABE12	0.05	10	30
TPH-ABE1300-210-n1	CCGACTG	GACAAACCAGAAGCCGCTCC	TPH-ABE12	0.05	10	30
TPH-ABE1300-210-n2	CCGACTG	GACAAACCAGAAGCCGCTCC	TPH-ABE12	0.05	10	30
TPH-ABEMAX-210-n1	CCGACTG	GACAAACCAGAAGCCGCTCC	TPH-ABEMA	0.05	10	30
TPH-ABEMAX-210-n2	CCGACTG	GACAAACCAGAAGCCGCTCC	TPH-ABEMA	0.05	10	30
TPH-CBE1012-210-n1	CCGACTG	GACAAACCAGAAGCCGCTCC	TPH-CBE10	0.05	10	30
TPH-CBE1012-210-n2	CCGACTG	GACAAACCAGAAGCCGCTCC	TPH-CBE10	0.05	10	30
TPH-CBE1028-210-n1	CCGACTG	GACAAACCAGAAGCCGCTCC	TPH-CBE10	0.05	10	30
TPH-CBE1028-210-n2	CCGACTG	GACAAACCAGAAGCCGCTCC	TPH-CBE10	0.05	10	30
TPH-CBE1041-210-n1	CCGACTG	GACAAACCAGAAGCCGCTCC	TPH-CBE10	0.05	10	30
TPH-CBE1041-210-n2	CCGACTG	GACAAACCAGAAGCCGCTCC	TPH-CBE10	0.05	10	30
TPH-CBE1249-210-n1	CCGACTG	GACAAACCAGAAGCCGCTCC	TPH-CBE12	0.05	10	30
TPH-CBE1249-210-n2	CCGACTG	GACAAACCAGAAGCCGCTCC	TPH-CBE12	0.05	10	30
TPH-CBE1300-210-n1	CCGACTG	GACAAACCAGAAGCCGCTCC	TPH-CBE12	0.05	10	30
TPH-CBE1300-210-n2	CCGACTG	GACAAACCAGAAGCCGCTCC	TPH-CBE12	0.05	10	30
TPH-CBEMAX-210-n1	CCGACTG	GACAAACCAGAAGCCGCTCC	TPH-CBEMA	0.05	10	30
TPH-CBEMAX-210-n2	CCGACTG	GACAAACCAGAAGCCGCTCC	TPH-CBEMA	0.05	10	30