

Supplementary Materials for

Internally inlaid SaCas9 base editors enable window specific base editing

Supplementary Text

Figure S1 to S22

Tables S1 to S9

Supplementary sequences1

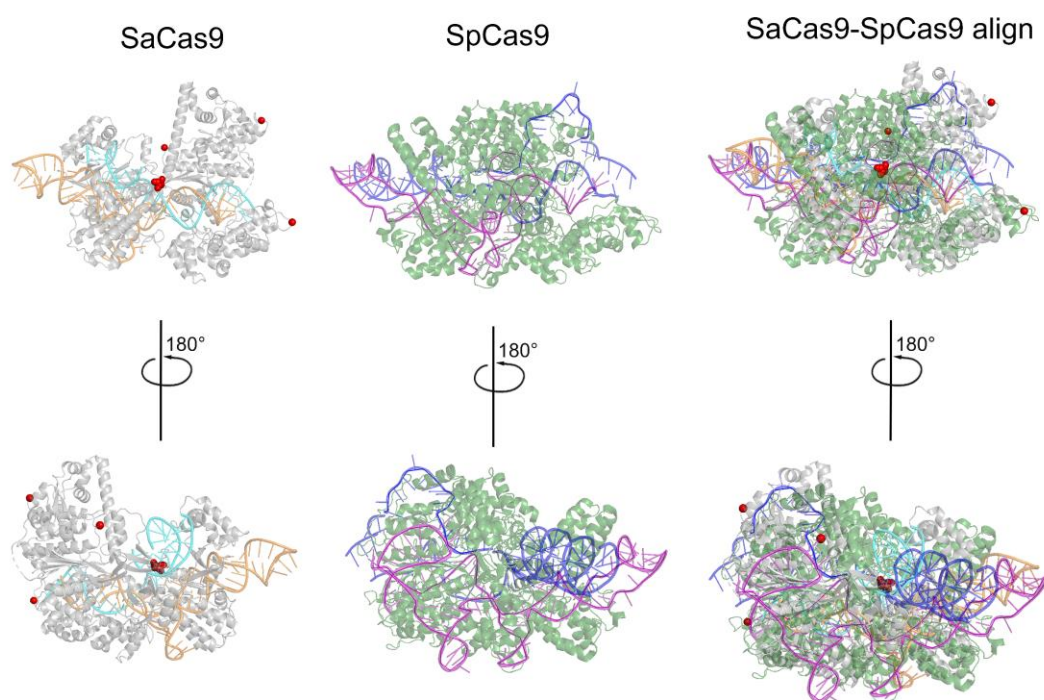


Figure S1. 3-dimensional structures of the SaCas9 complex and SpCas9 complex.

Cartoon representations of the structure SaCas9/RNA/DNA complex (PDB 5axw) (left), SpCas9/RNA/DNA complex (PDB 5y36) (middle) and alignment of SaCas9/SpCas9 complex (right). The amino acids E125, D269, S593 and R693 of SaCas9 are shown as red spheres.

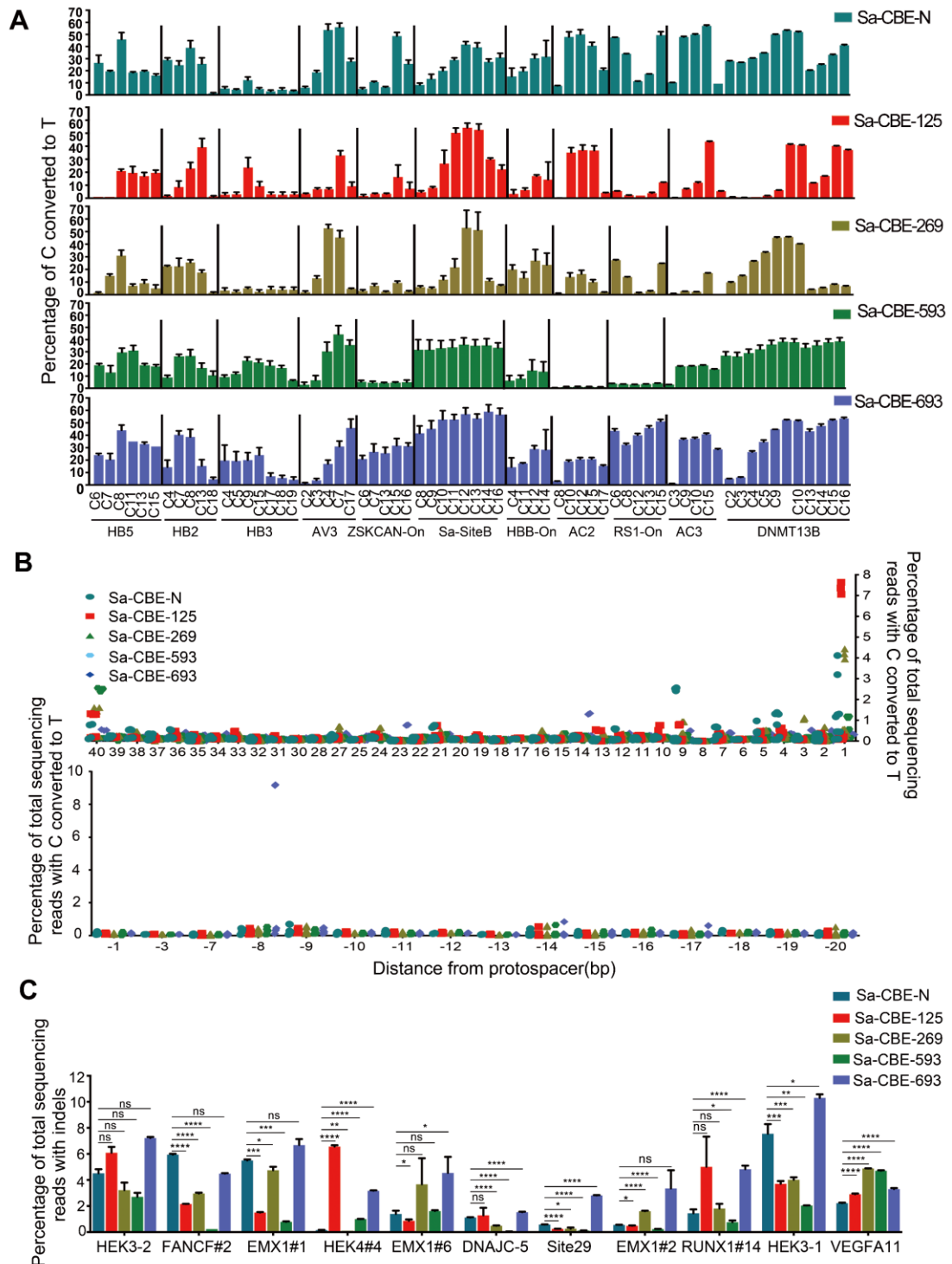


Figure S2. Additional data sets of Sa-CBE-N and inlaid-Sa-CBE editors editing outside of window and indel formation. A. Comparison of C-to-T editing efficiency produced by Sa-CBE-N and inlaid Sa-CBEs at additional 12 endogenous human genomic loci. Editing efficiencies were measured by Sanger sequencing and EditR

analysis. **B.** Cellular non-target C to T conversion percentages editing outside of window by Sa-CBE-N and inlaid-Sa-CBE editors are plotted individually against their positions relative to a protospacer for all 178 cytosines at 11 endogenous sites. The side of the protospacer distal to the PAM is designated with positive numbers, while the side that includes the PAM is designated with negative numbers. **C.** Indels frequencies following treatment of HEK293T cells with Sa-CBE-N and inlaid Sa-CBE editors at all 11 genomic loci. Indels frequencies were calculated as described in the Methods following treatment of HEK293T cells with Sa-CBE-N and inlaid Sa-CBE editors at all 11 genomic loci. Each experiment was repeated three times, data are represented as mean $\pm$ SD. Asterisks indicate statistically significant differences in editing efficiencies observed between Sa-CBE-N and inlaid Sa-CBEs at each site. ($P \geq 0.05$, * $P < 0.05$, ** $P < 0.01$, *** $P < 0.001$, **** $P < 0.0001$ by two-tailed Student's *t* test). Editing efficiencies were measured by HTS.

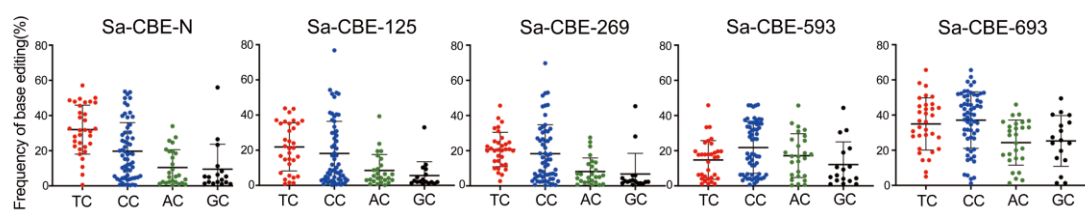


Figure S3. Comparison of base editing activity and sequence preference.

Frequencies of base editing of indicated motifs. Each dot represents the frequency of a specific. All Data were generated from three independent experiments and represented as mean $\pm$ SD.

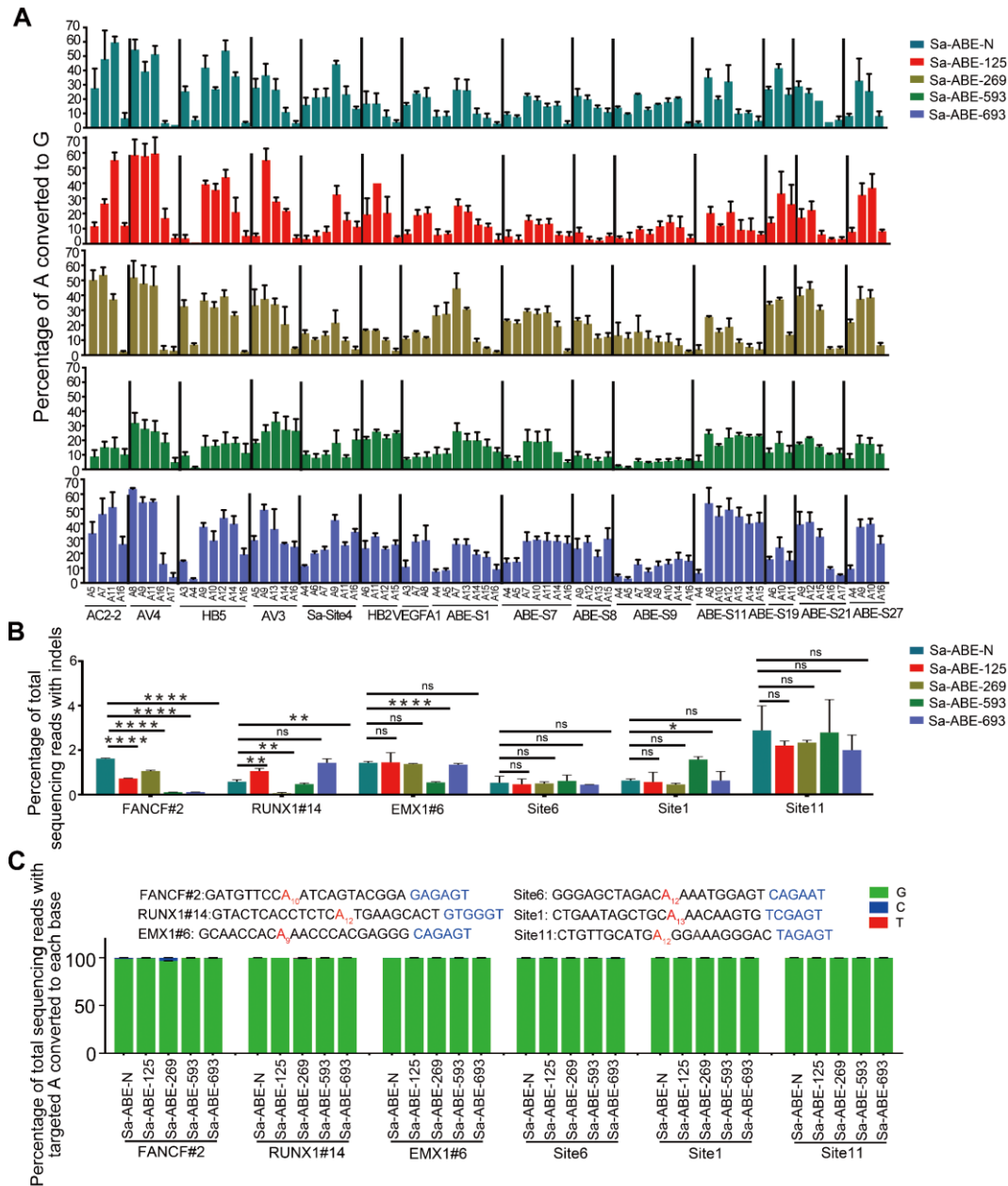


Figure S4. Indels frequencies and product purity following treatment of HEK293T cells with Sa-ABE-N and inlaid Sa-ABE editors at 6 genomic loci. A. Comparison of A-to-G editing efficiency produced by Sa-ABE-N and inlaid Sa-ABEs at additional 15 endogenous human genomic loci. Editing efficiencies were measured by Sanger sequencing and EditR analysis. **B.** Comparison of indels frequency produced by Sa-ABE-N and internally inlaid Sa-ABEs at 6 endogenous human genomic loci. Each experiment was repeated three times, data are represented as mean $\pm$ SD. Asterisks indicate statistically significant differences in editing efficiencies

observed between Sa-ABE-N and inlaid Sa-ABEs at each site. ($P \geq 0.05$, $*P < 0.05$, $**P < 0.01$, $***P < 0.001$, $****P < 0.0001$ by two-tailed Student's t test). Editing efficiencies were measured by HTS. **C.** The product distribution among edited DNA sequencing reads (reads in which the target A is converted) is shown for Sa-ABE-N and inlaid Sa-ABEs. The position that has A to Y conversion is indicated in red. Each experiment was repeated three times, data are represented as mean $\pm$ SD.

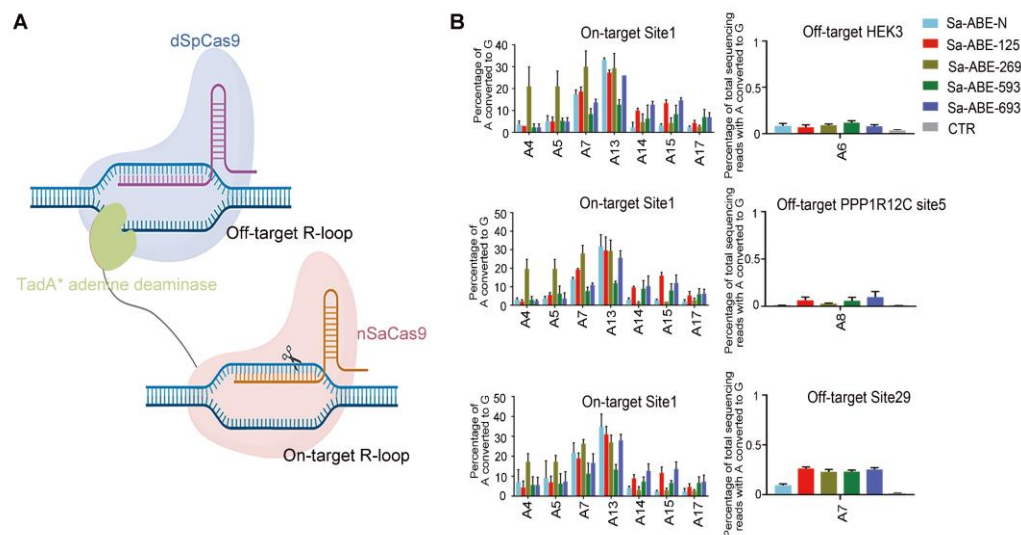


Figure S5. Cas9 independent DNA off-target editing of inlaid Sa-ABEs. A.

Schematic diagram showing the mechanism of artificial R-loop assays. Off-target R-Loop consisted of dead SpCas9 and corresponding sgRNAs. On-target R-Loop consisted of Sa-Cas9 derived ABEs and corresponding sgRNAs. **B.** Comparison of the DNA off-target editing produced by Sa-ABE-N and inlaid Sa-ABEs at three endogenous loci. Plasmids encoding paired R-loops were co-transfected into HEK293T cells and on-target editing efficiencies were determined by Sanger sequencing and off-target analysis efficiencies were determined by HTS. All Data were generated from three independent experiments and represented as mean $\pm$ SD.

Sa-CABE-N: HEK4#4 rep.1

bold Substitutions
 □ Insertions
 - Deletions

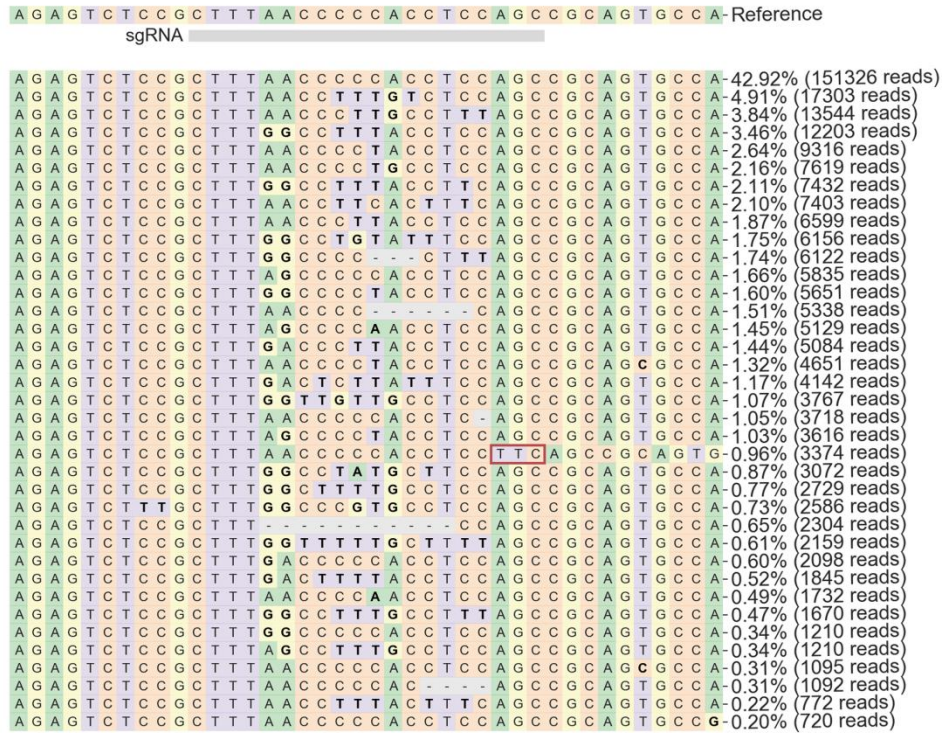


Figure S6. Allele frequencies following treatment with Sa-CABE-N at HEK4#4 genomic loci. Target site HEK4#4 is marked with a gray line. The percentile of unique sequencing read that represents a representative experiment from three independent experiments is listed on the right.

Sa-CABE-693: HEK4#4 rep.1

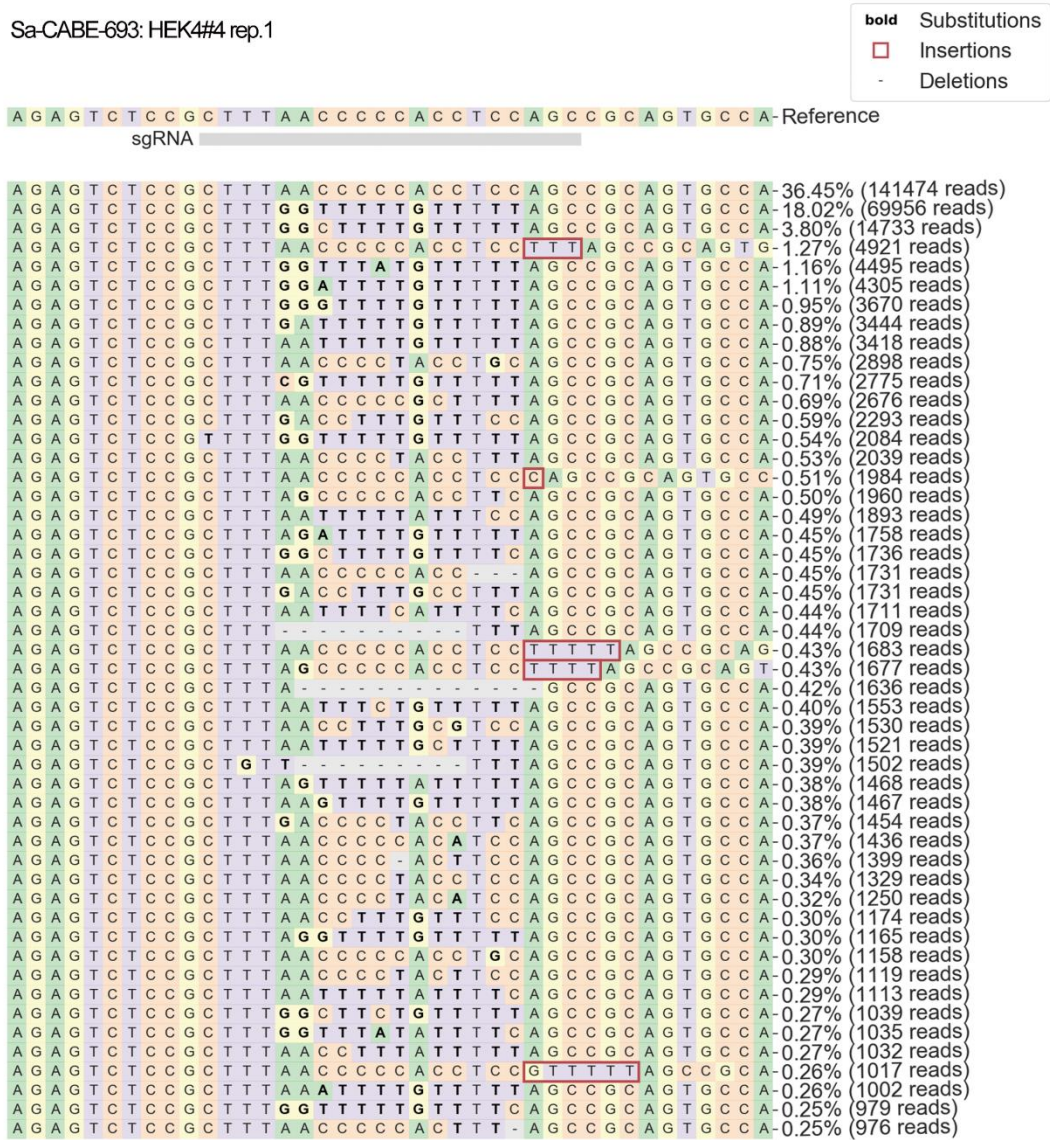


Figure S7.

Allele frequencies following treatment with Sa-CABE-693 at HEK4#4 genomic loci.

Sa-CABE-N: DNAJC-5 rep.1

bold Substitutions
 □ Insertions
 - Deletions

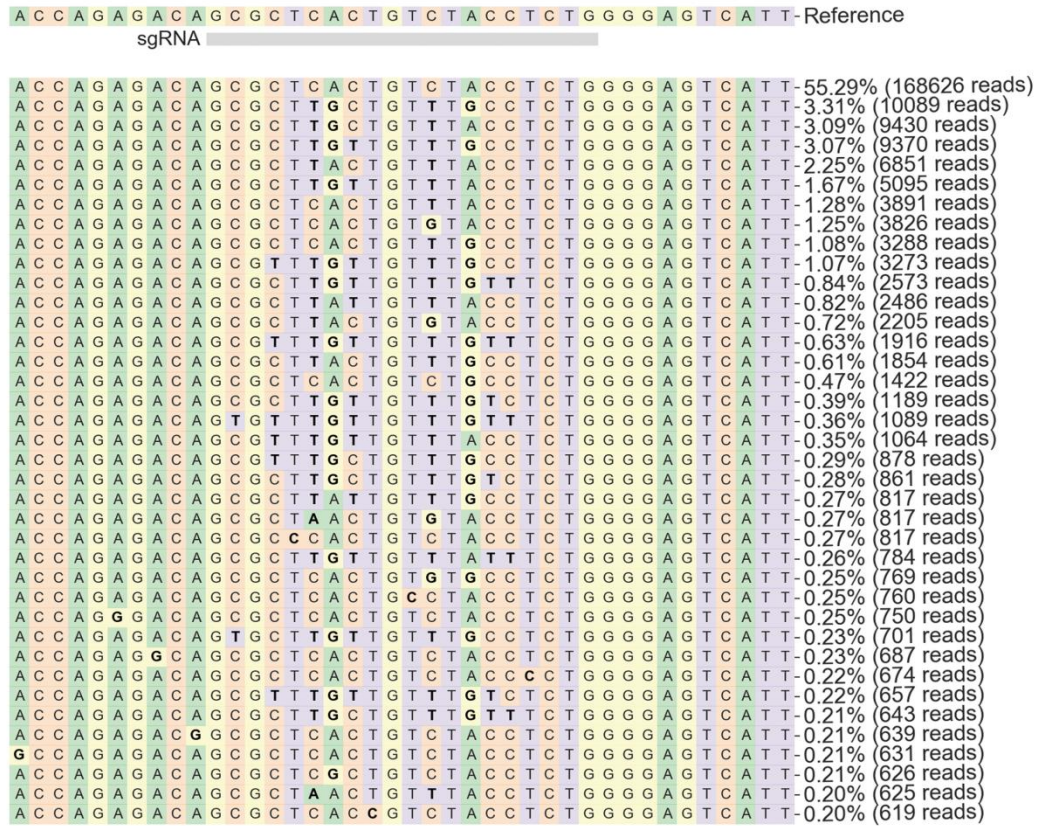


Figure S8.

Allele frequencies following treatment with Sa-CABE-N at DNAJC-5 genomic loci.

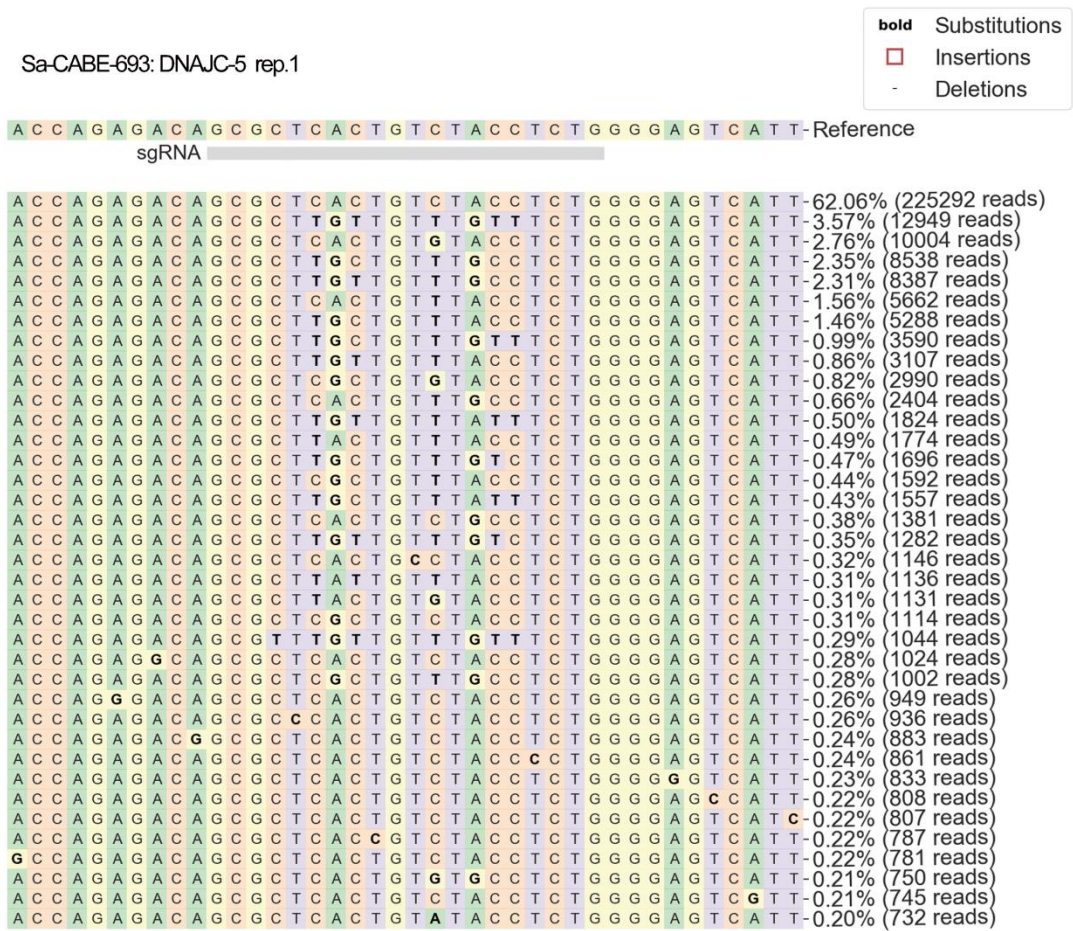


Figure S9

Allele frequencies following treatment with Sa-CABE-693 at DNAJC-5 genomic loci.



Figure S10.

Allele frequencies following treatment with Sa-CABE-N at EMX1#2 genomic loci.

Sa-CABE-693: EMX1#2 rep.1

bold Substitutions
 □ Insertions
 - Deletions

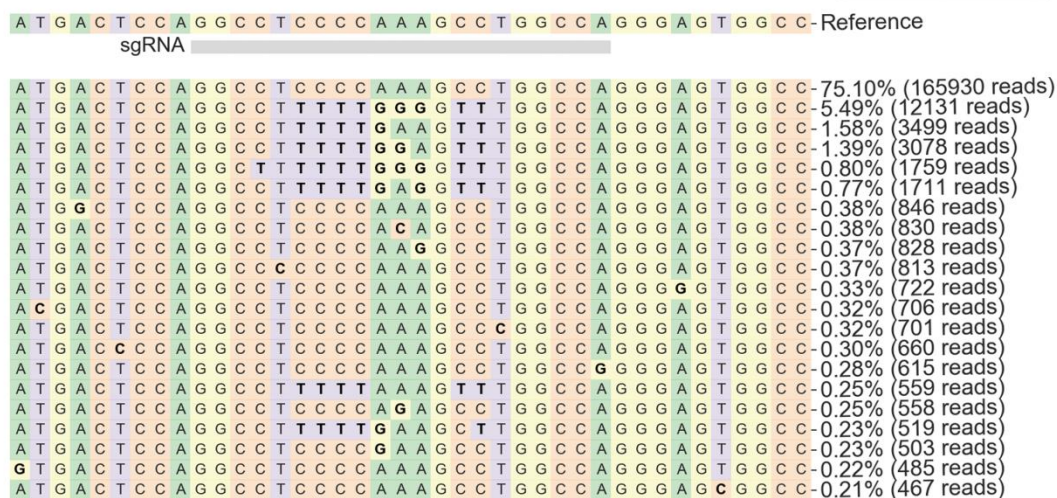


Figure S11.

Allele frequencies following treatment with Sa-CABE-693 at EMX1#2 genomic loci.



Figure S12.

Allele frequencies following treatment with Sa-CABE-N at EMX1#6 genomic loci.

Sa-CABE-693: EMX1#6 rep.1

bold Substitutions
 □ Insertions
 - Deletions

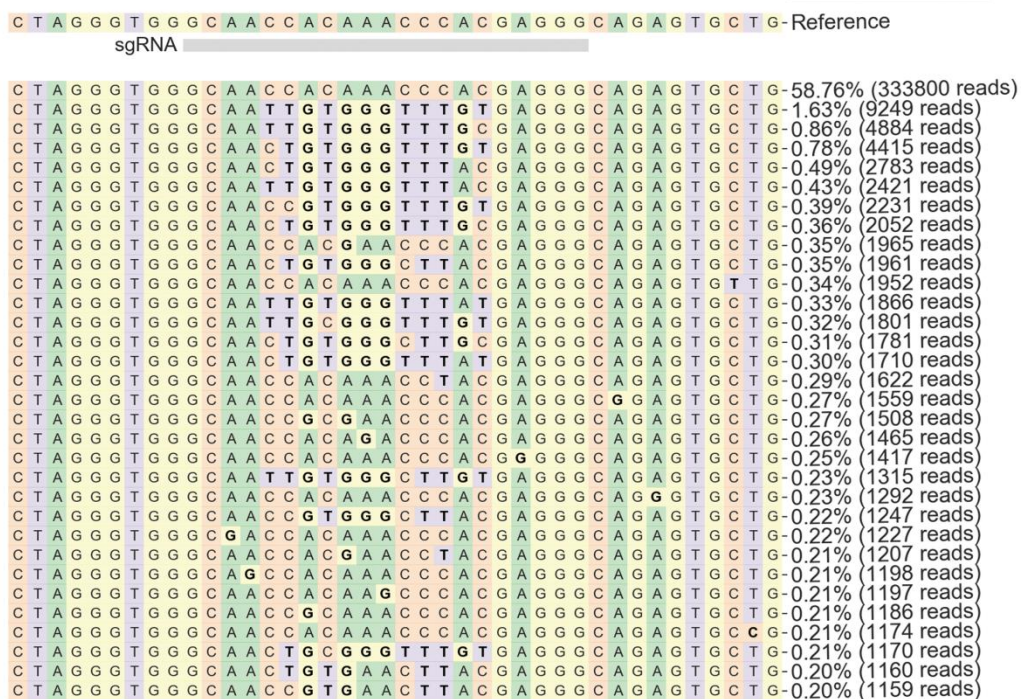


Figure S13.

Allele frequencies following treatment with Sa-CABE-693 at EMX1#6 genomic loci.

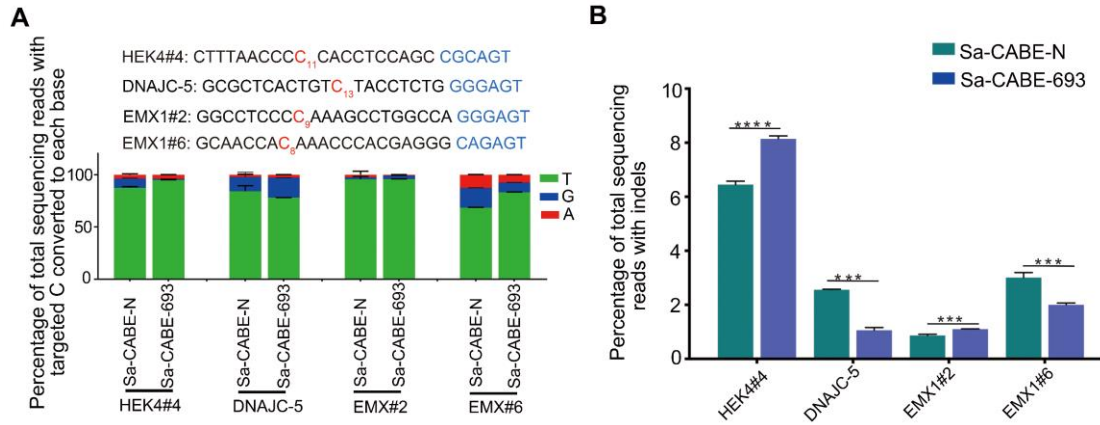


Figure S14.

Indels frequencies and product purity following treatment of HEK293T cells

with Sa-CABE-N and Sa-CABE-693 at all 4 genomic loci. A. The product distribution among edited DNA sequencing reads (reads in which the target C is converted) is shown for Sa-CABE-N and Sa-CABE-693. The position that has C to R conversion is indicated in red. Each experiment was repeated three times, data are represented as mean $\pm$ SD. **B.** Comparison of indels frequency produced by Sa-CABE-N and Sa-CABE-693 at 4 endogenous human genomic loci. Each experiment was repeated three times, data are represented as mean $\pm$ SD. Asterisks indicate statistically significant differences in editing efficiencies observed between Sa-CABE-N and Sa-CABE-693 at each site. ($P \geq 0.05$, $*P < 0.05$, $**P < 0.01$, $***P < 0.001$, $****P < 0.0001$ by two-tailed Student's t test). Editing efficiencies were measured by HTS.

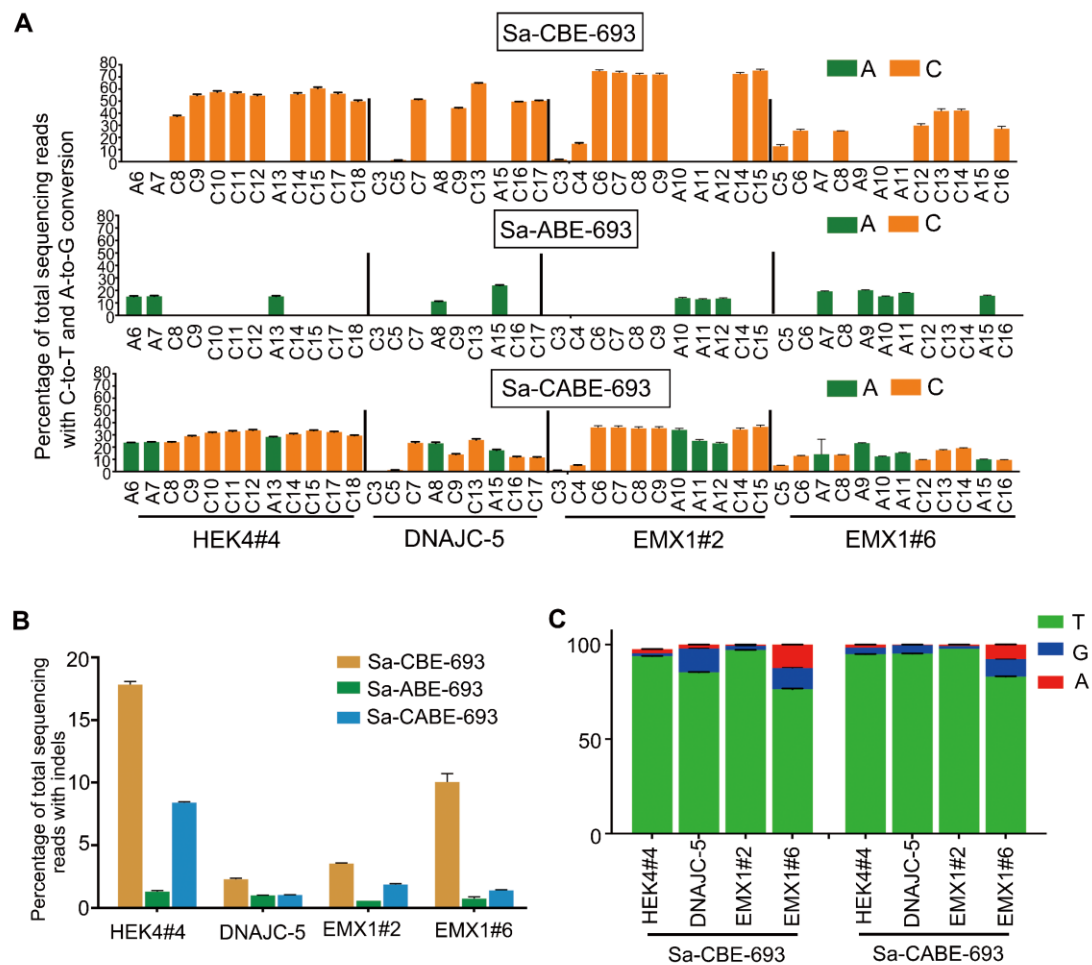


Figure S15. Comparison of base editing by Sa-CBE-693, Sa-ABE-693 and Sa-CABE-693.

A. Comparison of the C-to-T and A-to-G base-editing frequencies produced by Sa-CBE-693, Sa-ABE-693 and Sa-CABE-693 at 4 endogenous human genomic loci. **B.** Comparison of indels frequency produced by indicated editors. **C.** The product distribution among edited DNA sequencing reads (reads in which the target C is converted) is shown for Sa-CBE-693 and Sa-CABE-693. The position that has C to R conversion is indicated in red. Values and error bars reflect the mean $\pm$ SD of 3 independent experiments. Editing efficiencies were measured by HTS.

Sa-ABE-N: *BCL11A* rep.1

bold Substitutions
 Insertions
 - Deletions

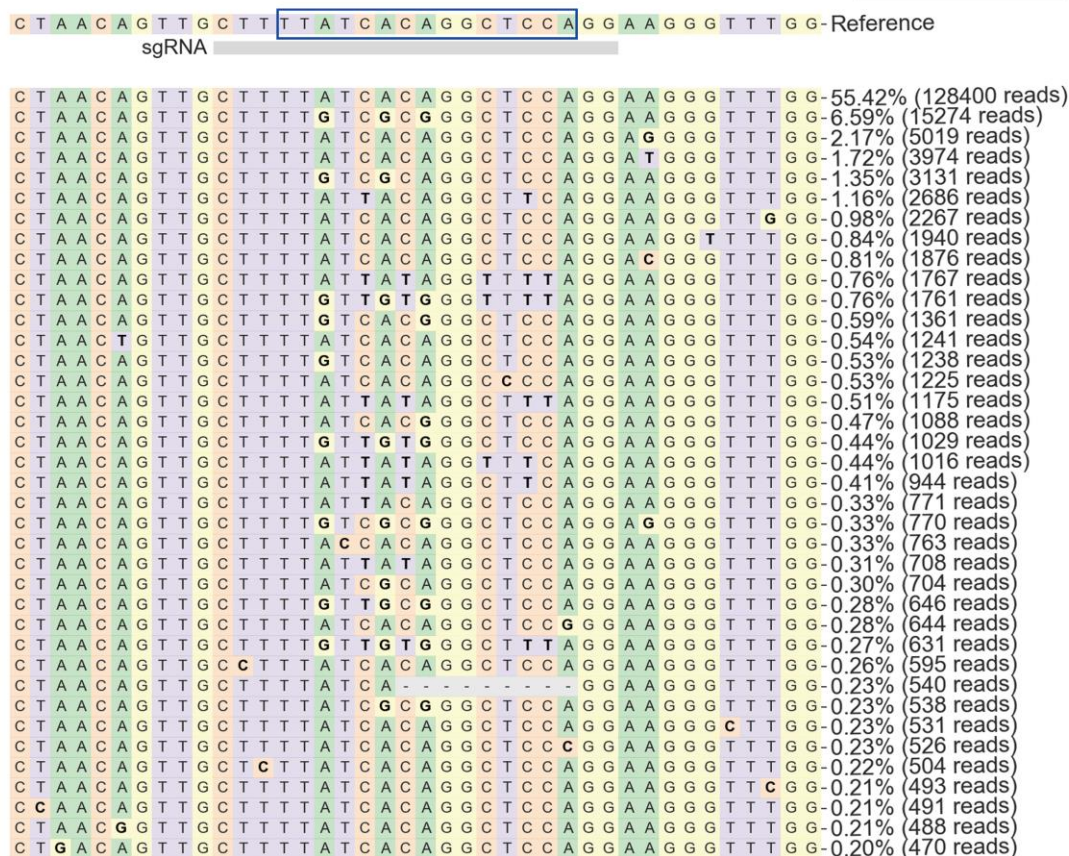


Figure S16.

Allele frequencies following treatment with Sa-ABE-N at a *BCL11A* enhancer. Target site is marked with a gray line. Consensus bases within a 15 bp fragment (TGN7-9WGATAR, where W=A or T and R=G or A) was framed with blue box. The percentile of unique sequencing read that represents a representative experiment from three independent experiments is listed on the right.

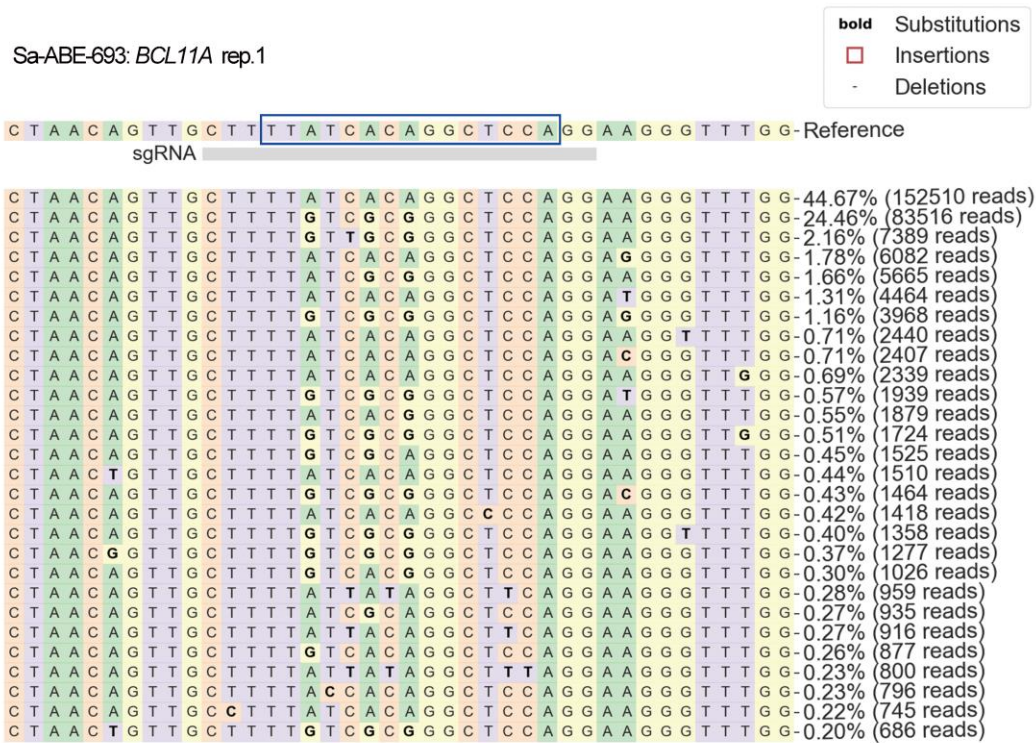


Figure S17.

Allele frequencies following treatment with Sa-ABE-693 at *BCL11A* enhancer.

Sa-CBE-N: *BCL11A* rep.1

bold Substitutions
 Insertions
 - Deletions

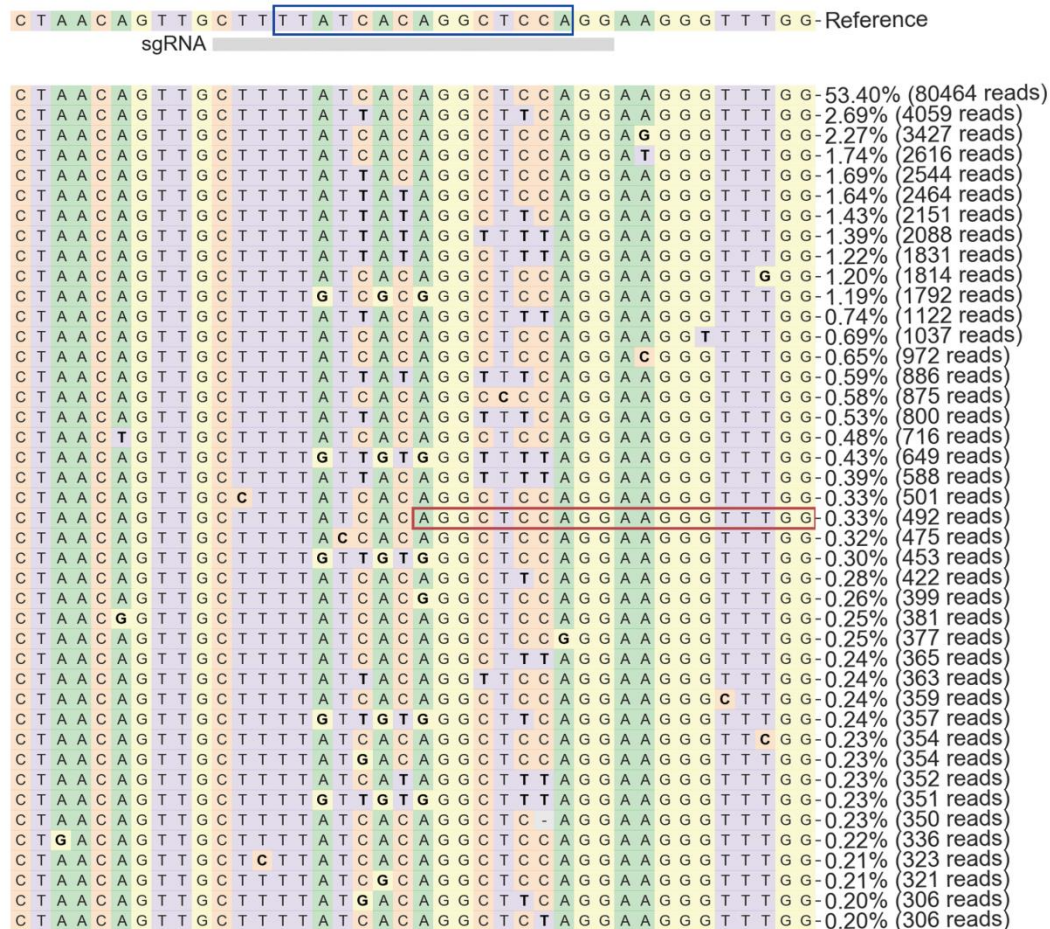


Figure S18.

Allele frequencies following treatment with Sa-CBE-N at *BCL11A* enhancer.

Sa-CBE-693: *BCL11A* rep.1

bold Substitutions
 Insertions
 - Deletions



Figure S19.

Allele frequencies following treatment with Sa-CBE-693 at *BCL11A* enhancer.

Sa-CABE-N: *BCL11A* rep.1

bold Substitutions
 Insertions
 - Deletions

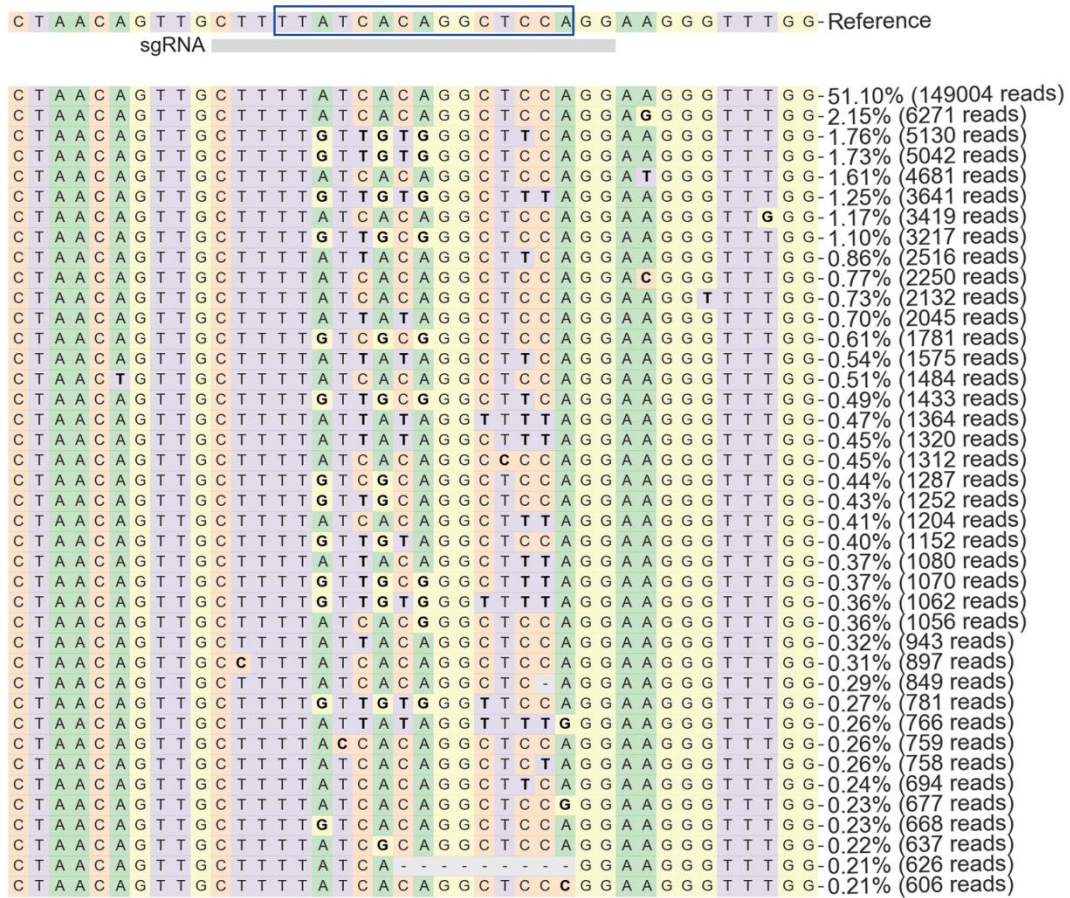


Figure S20.

Allele frequencies following treatment with Sa-CABE-N at *BCL11A* enhancer.

Sa-CABE-693: *BCL11A* rep.1

bold Substitutions
 Insertions
 - Deletions

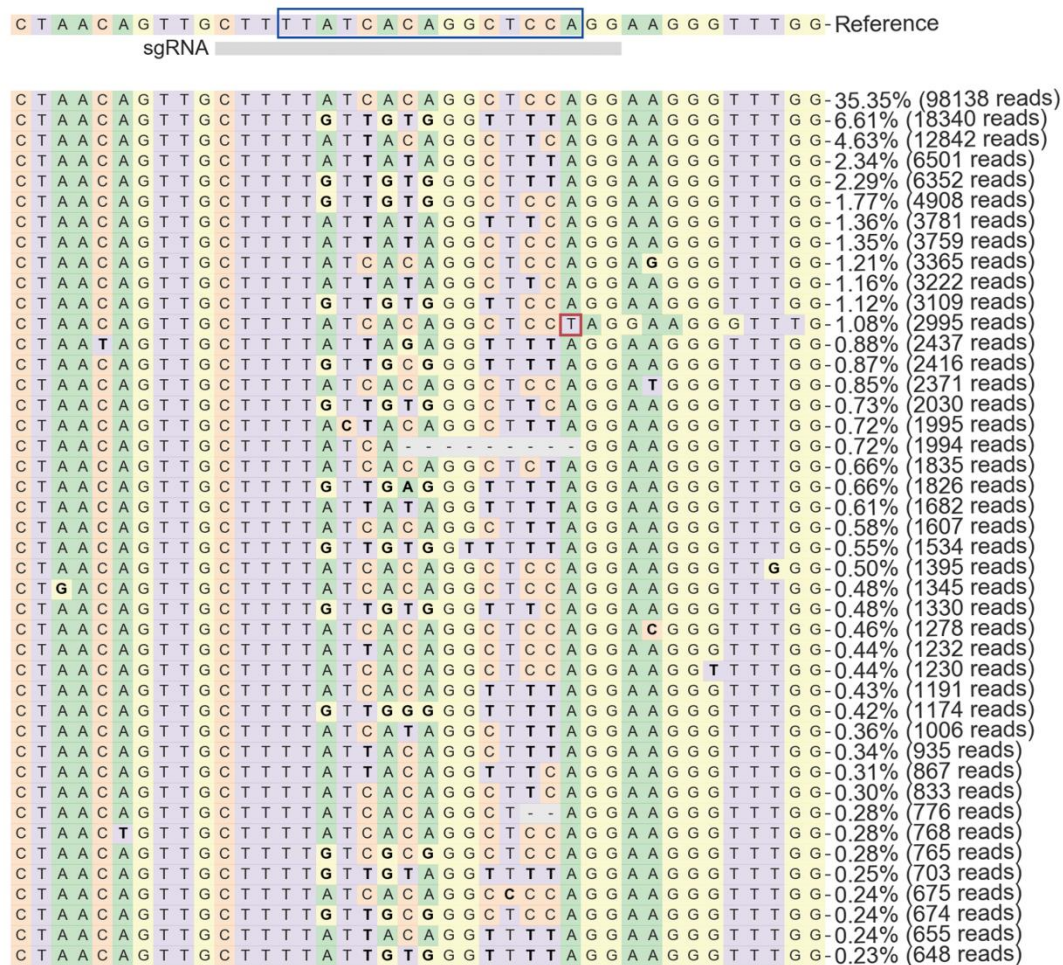


Figure S21.

Allele frequencies following treatment with Sa-CABE-693 at *BCL11A* enhancer.

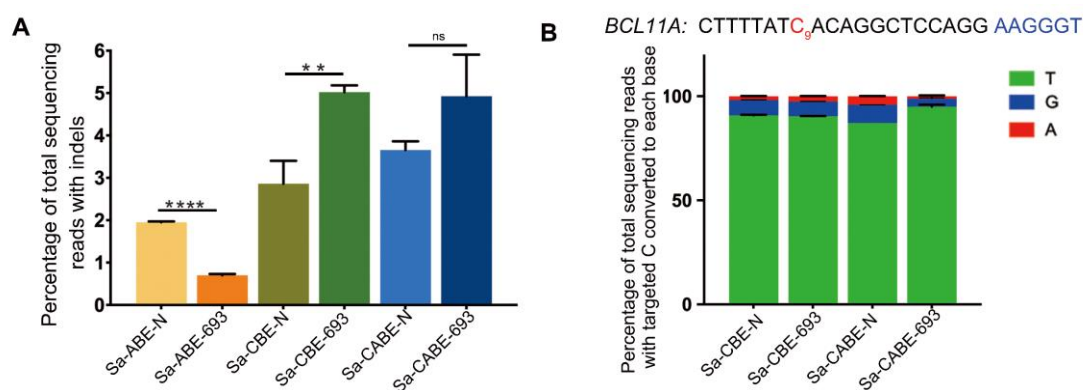


Figure S22.

Indels frequencies and product purity following treatment of HEK293T cells

with Sa-BEs-N and inlaid Sa-BEs-693 at *BCL11A* editing site. A. Indel frequencies following treatment of HEK293T cells with Sa-ABE-N, Sa-ABE-693, Sa-CBE-N, Sa-CBE-693, Sa-CABE-N and Sa-CABE-693. Each experiment was repeated three times, data are represented as mean $\pm$ SD. Asterisks indicate statistically significant differences in editing efficiencies observed among Sa-ABE-N, Sa-ABE-693, Sa-CBE-N, Sa-CBE-693, Sa-CABE-N and Sa-CABE-693 ($P \geq 0.05$, $*P < 0.05$, $**P < 0.01$, $***P < 0.001$, $****P < 0.0001$ by two-tailed Student's *t* test). Editing efficiencies were measured by HTS. **B.** The product distribution among edited DNA sequencing reads (reads in which the target C is converted) is shown for Sa-CBE-N, Sa-CBE-693, Sa-CABE-N and Sa-CABE-693. C₉ that has C to R conversion is labelled in red. Each experiment was repeated three times, data are represented as mean $\pm$ SD.

Table S1.**SgRNAs and Oligos sequence used for CBE editing window**

SgRNA	Target sequence	Oligo F	Oligo R	Reference
EMX1#1	CCTCCCTCCCTGGCCCA	CACCGCCTCCCTCC	AAACACCTGGGCCA	[1]
	GGT	CTGGCCCAGGT	GGGAGGGAGGC	
EMX1#2	GGCCTCCCCAAAGCCT	CACCGGCCTCCCCA	AAACTGGCCAGGCT	[1]
	GGCCA	AAGCCTGGCCA	TTGGGGAGGCC	
HEK4#4	CTTTAACCCCCACCTCC	CACCGCTTTAACCC	AAACGCTGGAGGTG	[2]
	AGC	CCACCTCCAGC	GGGGTTAAAGC	
DNMJC5-5	GCGCTCACTGTCTACCT	CACCGCGCTCACTG	AAACCAGAGGTAG	This study
	CTG	TCTACCTCTG	ACAGTGAGCGC	
Sa-Site29	GGGCCCTGCCTTCCTCA	CACCGGGCCCTGCC	AAACAGGTGAGGA	This study
	CCT	TTCCTCACCT	AGGCAGGGCCC	
EMX1#6	GCAACCACAAACCCAC	CACCGCAACCACAA	AAACCCCTCGTGGG	[1]
	GAGGG	ACCCACGAGGG	TTTGTGGTTGC	
RUNX1#14	GTACTCACCTCTCATGA	CACCGTACTCACCT	AAACAGTGCTTCAT	[1]
	AGCACT	CTCATGAAGCACT	GAGAGGTGAGTAC	
FANCF#2	GATGTTCCAATCAGTA	CACCGATGTTCCAA	AAACTGCGTACTGA	[3]
(Sasite6)	CGCA	TCAGTACGCA	TTGGAACATC	
HEK3-1	TCTGCTTCTCCAGCCCT	CACCGTCTGCTTCT	AAACGCCAGGGCTG	[3]
(Sasite5)	GGC	CCAGCCCTGGC	GAGAAGCAGAC	
HEK3-2	ACGTGCTCAGTCTGGG	CACCGACGTGCTCA	AAACGGGGCCCAG	[3]
	CCCC	GTCTGGGCCCC	ACTGAGCACGTC	
VEGFA11	GCTCCATTCACCCAGCT	CACCGCTCCATTCA	AAACGGGAAGCTG	This study
	TCCC	CCCAGCTTCCC	GGTGAATGGAGC	
HB5	CTAAGCCCCAACACACA	CACCGCTAAGCCCA	AAACCAGCATGTGT	This study
	TGCTG	ACACACATGCTG	GTTGGGCTTAGC	
HB2	GTTCTACCTTAACTATG	CACCGTTCTACCTT	AAACTCTGCATAGT	This study
	CAGA	AACTATGCAGA	TAAGGTAGAAC	

HB3	TAGCCTGACAGGAGCA	CACCGTAGCCTGAC	AAACATGGGTGCTC	This study
	CCCAT	AGGAGCACCCAT	CTGTCAGGCTAC	
AV3	ACCCAGCGAGTGAAGA	CACCGACCCAGCGA	AAACTGCCGTCTTC	This study
	CGGCA	GTGAAGACGGCA	ACTCGCTGGGTC	
ZKSCAN1-On	CCAGACCTGGAGCTCC	CACCGCCAGACCTG	AAACCCCAAGGAG	[4]
	TTGGG	GAGCTCCTTGGG	CTCCAGGTCTGGC	
Sa-SiteB	GacAGAGCCCCCCTCA	CACCGacAGAGCCC	CACCGacAGAGCCC	This study
	AAGA	CCCCTCAAAGA	CCCCTCAAAGA	
HBB-On	ACTCAAAGAACCTCTG	CACCGACTCAAAGA	AAACGGACCCAGA	[4]
	GGTCC	ACCTCTGGGTCC	GGTTCTTTGAGTC	
AC2	CGTAGGACTCTCTTCTC	CACCGCGTAGGACT	AAACGTCAGAGAA	This study
	TGAC	CTCTTCTCTGAC	GAGAGTCCTACGC	
RS1-On	CATATCACAAGCCTCT	CACCGCATATCACA	AAACAACCCAGAG	[4]
	GGGTT	AGCCTCTGGGTT	GCTTGTGATATGC	
AC3	ACCGGAGTCCATCACG	CACCGACCGGAGTC	AAACGGCATCGTGA	This study
	ATGCC	CATCACGATGCC	TGGACTCCGGTC	
DNMT13B	TCCCCCATCCTGCCCCA	CACCGTCCCCCATC	AAACCCTCTGGGGC	This study
	GAGG	CTGCCCCAGAGG	AGGATGGGGGAC	
V5	CCTGGACACTTCCCAA	CACCGCCTGGACAC	AAACGTCCTTTGGG	This study
	AGGAC	TTCCCAAAGGAC	AAGTGTCCAGGC	
PAH-1	GGGCACAGCGTTCAAG	CACCGGGCACAGC	AAACGAGTCTTGAA	This study
	ACTC	GTTCAAGACTC	CGCTGTGCCC	
PAH-2	GGGCCGAGGTACTGTG	CACCGGGCCGAGGT	AAACGGGCCGAGG	This study
	GCAG	ACTGTGGCAG	TACTGTGGCAG	

Table S2.**SgRNAs and Oligos sequence used for ABE editing window**

SgRNA	Target sequence	Oligo F	Oligo R	Reference
EMX1#6	GCAACCACAAACCCA	CACCGCAACCACAA	AAACCCCTCGTGGG	[1]
	CGAGGG	ACCCACGAGGG	TTTGTGGTTGC	
RUNX1#14	GTACTCACCTCTCATG	CACCGTACTCACCTC	AAACAGTGCTTCAT	[1]
	AAGCACT	TCATGAAGCACT	GAGAGGTGAGTAC	
FANCF#2	GATGTTCCAATCAGTA	CACCGATGTTCCAAT	AAACTGCGTACTGA	[3]
	CGCA	CAGTACGCA	TTGGAACATC	
Site1	CTGAATAGCTGCAAAC	CACCGCTGAATAGC	AAACCACTTGTTTG	[5]
	AAGTG	TGCAAACAAGTG	CAGCTATTCAGC	
Site6	GGGAGCTAGACAAAA	CACCGGGAGCTAGA	AAACACTCCATTTT	[5]
	TGGAGT	CAAAATGGAGT	GTCTAGCTCCC	
Site11	GCTGTTGCATGAGGAA	CACCGCTGTTGCATG	AAACGTCCTTTCC	[5]
	AGGGAC	AGGAAAGGGAC	TCATGCAACAGC	
AC2-2	AAGGAGACTCAGGTC	CACCGAAGGAGACT	AAACTTCTCTGACC	This study
	AGAGAA	CAGGTCAGAGAA	TGAGTCTCCTTC	
AV4	GGGGCTCAACATCGG	CACCGGGGCTCAAC	AAACCCCTCTCCGA	This study
	AAGAGG	ATCGGAAGAGG	TGTTGAGCCCC	
HB5	CTAAGCCCAACACAC	CACCGCTAAGCCCA	AAACCAGCATGTGT	This study
	ATGCTG	ACACACATGCTG	GTTGGGCTTAGC	
AV3	ACCCAGCGAGTGAAG	CACCGACCCAGCGA	AAACTGCCGTCTTC	This study
	ACGGCA	GTGAAGACGGCA	ACTCGCTGGGTC	
Sa-Site4	AAGAGAATAGACTGT	CACCGAAGAGAATA	AAACTTCCCTACAG	This study
	AGGGAAACCAGT	GACTGTAGGGAA	TCTATTCTCTTC	
HB2	GTTCTACCTTAACTAT	CACCGTTCTACCTTA	AAACTCTGCATAGT	This study
	GCAGA	ACTATGCAGA	TAAGGTAGAAC	
V1	AGAGGGAATGGGCTT	CACCGAGAGGGAAT	AAACTTTCCAAAGC	This study
	TGGAAG	GGGCTTTGGAAG	CCATTCCCTCTC	

ABE-S1	CTGAATAGCTGCAAAC	CACCGCTGAATAGC	AAACCACTTGTTTG	[5]
	AAGTG	TGCAAACAAGTG	CAGCTATTCAGC	
ABE-S7	AAGAATACTAAGCAT	CACCGAAGAATACT	AAACGAGTCTATGC	[5]
	AGACTC	AAGCATAGACTC	TTAGTATTCTTC	
ABE-S8	TGGGCTTTAGGAACAG	CACCGTGGGCTTTAG	AAACTACCCCTGTT	[5]
	GGGTA	GAACAGGGGTA	CCTAAAGCCCAC	
ABE-S9	AACAACAAAACGGAC	CACCGAACAACAAA	AAACTTCACTGTCC	[5]
	AGTGAA	ACGGACAGTGAA	GTTTTGTTGTTC	
ABE-S11	GGGAGCTAGACAAAA	CACCGGGAGCTAGA	AAACACTCCATTTT	[5]
	TGGAGT	CAAAATGGAGT	GTCTAGCTCCC	
ABE-S19	GTGTCAGGTAATGTGC	CACCGTGTCAAGTA	AAACTGTTTAGCAC	[5]
	TAAACA	ATGTGCTAAACA	ATTACCTGACAC	
ABE-S21	GCTGTTGCATGAGGAA	CACCGCTGTTGCATG	AAACGTCCCTTTCC	[5]
	AGGGAC	AGGAAAGGGAC	TCATGCAACAGC	
ABE-S27	GGGAGCTCAAGCCTG	CACCGGGAGCTCAA	AAACTTGGAATCAG	[5]
	ATTCCAA	GCCTGATTCCAA	GCTTGAGCTCCC	

Table S3.**SgRNAs and Oligos sequence used for testing DNA off-target editing**

SgRNA	Target sequence	Oligo F	Oligo R	Reference
HEK4	GGCACTGCGGCTGGA	CACCGGCACTGCGGC	AAACCCACCTCCAG	[3]
	GGTGG	TGGAGGTGG	CCGCAGTGCC	
SiteB	ACAGAGCCCCCCTC	CACCGACAGAGCCCC	AAACCTCTTTGAGG	[6]
	AAAGAG	CCCTCAAAGAG	GGGGGCTCTGTC	
PPP1R12C	GCTGACTCAGAGACC	CACCGCTGACTCAGA	AAACCTCAGGGTCT	[7]
site5	CTGAG	GACCCTGAG	CTGAGTCAGC	
FANCF	GGAATCCCTTCTGCA	CACCGGAATCCCTTCT	AAACGGTGCTGCAG	[6]
	GCACC	GCAGCACC	AAGGGATTCC	
FANCF#2	GATGTTCCAATCAGT	CACCGATGTTCCAATC	AAACTGCGTACTGA	[3]
	ACGCA	AGTACGCA	TTGGAACATC	
HEK3	GGCCCAGACTGAGCA	CACCGGCCCAGACTG	AAACTCACGTGCTC	[8]
	CGTGA	AGCACGTGA	AGTCTGGGCC	
Site29	G TTCACACCCATGAC	CACCGTTCACACCCAT	AAACTGTTGTCAT	[9]
	GAACA	GACGAACA	GGGTGTGAAC	
Site1	CTGAATAGCTGCAAA	CACCGCTGAATAGCT	AAACCACTTGTTTG	[5]
	CAAGTG	GCAAACAAGTG	CAGCTATTCAGC	

Table S4.**Primers used to amplify each target regions for Sanger sequencing**

Target site	Chrom	Forward primer	Reverse primer
	osome		
DNAJC5-5	Chr20	CTGTCTGTGCACGTGGCAA	AGCTGTGACCAGTTCAACGC
HEK4	Chr20	CAGCGAGGTCAAAGTCACC	TCCTTTCAACCCGAACGGAG
FANCF#2	Chr11	ATGACTGGCATCATCTCGCA	GGTGCTGACGTAGGTAGTGC
HEK3-1	Chr9	AGAATGGGTGACAGTGGCA	TAGGAAAAGCTGTCCTGCGA
EMX1#1	Chr2	CCCTATGTAGCCTCAGTCTT	GATGTGATGGGAGCCCTTCT
EMX1#2	Chr2	CGAGGAGAAGGCCAAGTGG	CCAATGACTAGGGTGGGCAA
EMX1#6	Chr2	AGCAGAAGAAGAAGGGCTC	ACTCCAGGCCTCCCCAAA
HEK4#4	Chr20	GGCTCCTTTCAACCCGAACG	GGCTGGGTGGAAGGAA
RUNX1#14	Chr21	CATCTCTGCACCGAGGTGAA	AGAAATCATTGAGTCCC
VEGFA11	Chr5	GGAACAAGGGCCTCTGTCTG	GCCGTTCCCTCTTTGCTAGG
HB5	Chr9	AGCAAAGCACCTATAAACA	TGCCCTGACTTTTATGCCACT
HB2	Chr9	AGCAAAGCACCTATAAACA	TGCCCTGACTTTTATGCCACT
HB3	Chr9	AGCAAAGCACCTATAAACA	TGCCCTGACTTTTATGCCACT
AV3	Chr19	ATCCTCTCTGGCTCCATCGT	GATGCTCTTTCCGGAGCACT
ZKSCAN1-On	Chr7	GTGAGCACAGACCCTGTTTG	TGGCTCCAGTTTCAACGTCT
Sa-SiteB	Chr20	GCCTGGAGGGAAATCTTAGG	GGGCTTCACTGAGTCTCCAC
HBB-On	Chr11	AAGGTGCCCTTGAGGTTGTC	AGGGTTGGCCAATCTACTCC
AC2	Chr7	GAGGCGTACAGGGATAGCAC	GCTCAGGGCTTCTTGTCCTT
RS1-On	ChrX	AGCCCACATACTGCTC	CGTTGAAGACACAGCTGTA
AC3	Chr7	GGGTAACCCTCATGTCAGGC	CCAAGACCCCAGCACACTTA
DNMT13B	Chr20	AGGCTTTAGCAGCTGGTGTC	TAGCTCCCTATTCCCATGCCTA
V5	Chr6	AGACTCCACAGTGCATACG	GAGCCGTTCCCTCTTTGCTA
Site1	Chr5	ACCTGGCTGAGCTAACTGTG	GAAGCCAGTGAATACAAA
Site6	Chr15	TGCTTCCTCCATGGAAAAAT	ATCGCTGACTCCAACCACCT
Site11	Chr1	ATGAATAGTTTAAGCAAGGC	CAGTGCCCCAAATTATTAC

AC2-2	Chr7	GAGGCGTACAGGGATAGCAC	GCTCAGGGCTTCTTGTCTT
AV4	Chr19	AGCGTTAGAGGGCAGAGTTC	ACTCTCTTCCGCATTGGAGTC
Sa-Site4	Chr19	CACTGTGTTAGCCAGGATGG	GAGCTGTCCAGAGGTGTTAAG
V1	Chr6	CCAGATGAGGGCTCCAGATG	GAAAGTGAGGTTACGTGCGG
ABE-S1	Chr5	TTCCCACGTATTGCACTGCC	GGGGAAAAATTGTCCAGCCC
ABE-S7	Chr4	GTGAGGGGCTCATGAACAGG	GCCACCTGAGACACATA
ABE-S8	Chr1	CCGACTCCGAAGACAGTCAG	CCTTCTACGGCAGAAACCACA
ABE-S9	Chr22	CACCTTTGGCCCAATGACAC	AGGATGAGCCTAGGGATTGGA
ABE-S11	Chr15	TAGGCTTAGGCCAACACAGC	TGTTGTGCTTCTGCTCCAT
ABE-S19	Chr19	TCTTTGCTCCAGATTTCCCTTCA	ATCCTTGCACTGAGACCGTG
ABE-S21	Chr1	CCGACTCCGAAGACAGTCAG	CCTTCTACGGCAGAAACCACA
ABE-S27	Chr6	AAAATTGTCCACCTGGCACG	CTTCCCTCCTCTGCGTGAAT
HEK3-2	Chr9	CAGTATCCCGGTGCAGGAGC	AACGCCCATGCAATTAGTCT
Sa-Site29	Chr12	AGCAGTTGGTGGTGCAGGA	GGGAGCCAAAAGGGTCATCA
Site29	Chr12	AGCAGTTGGTGGTGCAGGA	GGGAGCCAAAAGGGTCATCA
FANCF	Chr11	GGAGACGTTTCATGACTGGCA	GGGCCTGGAAGTTCGCTAAT
Sa-SiteB	Chr20	CCTGGAGGGAAATCTTAGGCA	GGGCTTCACTGAGTCTCCAC
SiteB	Chr20	CCTGGAGGGAAATCTTAGGCA	GGGCTTCACTGAGTCTCCAC
PPP1R12C site5	Chr19	CCCGGCCATGGTTTTAT	GACTTGCCCAGAGCTCTT
HEK3	Chr2	GTCTATTTCTGCTGCAAGTAAGCA	AGCCCCTGTCTAGGAAAAGC
BCL11A	Chr2	GGCCAGAAAAGAGATATGGC	AAACGGCCACCGATGGA
PAH-1		TGTAAAACGACGGCCAGT	CAGGAAACAGCTATGAC
PAH-2		TGTAAAACGACGGCCAGT	CAGGAAACAGCTATGAC

Table S5.**Sa-CBE HTS Primers used to amplify each target**

Sample name	Primer name	Sequence
Sa-CBE-HEK3-2-N	HEK3-2-1-Fwd	ACACAGTGCACATACTAGCCCCTGTCT
	HEK3-2-1-Rev	AGCATGCATTTGTAGGCTTGAT
Sa-CBE-HEK3-2-125	HEK3-2-2-Fwd	ACTGACTGCACATACTAGCCCCTGTCT
	HEK3-2-2-Rev	AGCATGCATTTGTAGGCTTGAT
Sa-CBE-HEK3-2-269	HEK3-2-3-Fwd	TCAGAGAGCACATACTAGCCCCTGTCT
	HEK3-2-3-Rev	AGCATGCATTTGTAGGCTTGAT
Sa-CBE-HEK3-2-593	HEK3-2-4-Fwd	TGTCAGTGCACATACTAGCCCCTGTCT
	HEK3-2-4-Rev	AGCATGCATTTGTAGGCTTGAT
Sa-CBE-HEK3-2-693	HEK3-2-5-Fwd	CATCAGAGCACATACTAGCCCCTGTCT
	HEK3-2-5-Rev	AGCATGCATTTGTAGGCTTGAT
Sa-CBE-FANCF#2-N	FANCF#2-1-Fwd	ACAGCATCCCAGAGTCAAGGAACACGG
	FANCF#2-1-Rev	CTCGGAAAAGCGATCCAGGT
Sa-CBE-FANCF#2-125	FANCF#2-2-Fwd	ACTTGCACCCAGAGTCAAGGAACACGG
	FANCF#2-2-Rev	CTCGGAAAAGCGATCCAGGT
Sa-CBE-FANCF#2-269	FANCF#2-3-Fwd	ACGTTCTCCCAGAGTCAAGGAACACGG
	FANCF#2-3-Rev	CTCGGAAAAGCGATCCAGGT
Sa-CBE-FANCF#2-593	FANCF#2-4-Fwd	AGATCACCCCAGAGTCAAGGAACACGG
	FANCF#2-4-Rev	CTCGGAAAAGCGATCCAGGT
Sa-CBE-FANCF#2-693	FANCF#2-5-Fwd	AGAGCTACCCAGAGTCAAGGAACACGG
	FANCF#2-5-Rev	CTCGGAAAAGCGATCCAGGT
Sa-CBE-EMX1#1-N	EMX1#1-1-Fwd	CAGATCATCAGTCTTCCCATCAGGCTC
	EMX1#1-1-Rev	CCCTTCTTCTTCTGCTCGGA
Sa-CBE-EMX1#1-125	EMX1#1-2-Fwd	CAGTACTTCAGTCTTCCCATCAGGCTC
	EMX1#1-2-Rev	CCCTTCTTCTTCTGCTCGGA
Sa-CBE-EMX1#1-269	EMX1#1-3-Fwd	CTTGAGTTCAGTCTTCCCATCAGGCTC
	EMX1#1-3-Rev	CCCTTCTTCTTCTGCTCGGA

Sa-CBE-EMX1#1-593	EMX1#1-4-Fwd	CTCTCAGTCAGTCTTCCCATCAGGCTC
	EMX1#1-4-Rev	CCCTTCTTCTTCTGCTCGGA
Sa-CBE-EMX1#1-693	EMX1#1-5-Fwd	CTGTAGATCAGTCTTCCCATCAGGCTC
	EMX1#1-5-Rev	CCCTTCTTCTTCTGCTCGGA
Sa-CBE-HEK4#4-N	HEK4#4-1-Fwd	GACTCACTTTCAACCCGAACGGAGACAC
	HEK4#4-1-Rev	GTCCAAAGCAGGATGACAGG
Sa-CBE-HEK4#4-125	HEK4#4-2-Fwd	GTAGTCTTTTCAACCCGAACGGAGACAC
	HEK4#4-2-Rev	GTCCAAAGCAGGATGACAGG
Sa-CBE-HEK4#4-269	HEK4#4-3-Fwd	GTCGTGATTTCAACCCGAACGGAGACAC
	HEK4#4-3-Rev	GTCCAAAGCAGGATGACAGG
Sa-CBE-HEK4#4-593	HEK4#4-4-Fwd	GTGTCAATTTCAACCCGAACGGAGACAC
	HEK4#4-4-Rev	GTCCAAAGCAGGATGACAGG
Sa-CBE-HEK4#4-693	HEK4#4-5-Fwd	AAGAGCTTTTCAACCCGAACGGAGACAC
	HEK4#4-5-Rev	GTCCAAAGCAGGATGACAGG
Sa-CBE-EMX1#6-N	EMX1#6-1-Fwd	GCCTCTACGAGCAGAAGAAGAAGGGCT
	EMX1#6-1-Rev	TTGTCCCTCTGTCAATGGCG
Sa-CBE-EMX1#6-125	EMX1#6-2-Fwd	AACCTAGCGAGCAGAAGAAGAAGGGCT
	EMX1#6-2-Rev	TTGTCCCTCTGTCAATGGCG
Sa-CBE-EMX1#6-269	EMX1#6-3-Fwd	ATTCTCGCGAGCAGAAGAAGAAGGGCT
	EMX1#6-3-Rev	TTGTCCCTCTGTCAATGGCG
Sa-CBE-EMX1#6-593	EMX1#6-4-Fwd	ATCCGGACGAGCAGAAGAAGAAGGGCT
	EMX1#6-4-Rev	TTGTCCCTCTGTCAATGGCG
Sa-CBE-EMX1#6-693	EMX1#6-5-Fwd	ATGCTTCCGAGCAGAAGAAGAAGGGCT
	EMX1#6-5-Rev	TTGTCCCTCTGTCAATGGCG
Sa-CBE-DNAJC-5-N	DNAJC-5-1-Fwd	ACAACTGAGCTCTGCCCTTGGTACTTTC
	DNAJC-5-1-Rev	CCACACTTGTCCACTTACCGA
Sa-CBE-DNAJC-5-125	DNAJC-5-2-Fwd	ACACGTAAGCTCTGCCCTTGGTACTTTC
	DNAJC-5-2-Rev	CCACACTTGTCCACTTACCGA

Sa-CBE-DNAJC-5-269	DNAJC-5-3-Fwd	ACTACGTAGCTCTGCCCTTGGTACTTTC
	DNAJC-5-3-Rev	CCACACTTGTCCACTTACCGA
Sa-CBE-DNAJC-5-593	DNAJC-5-4-Fwd	ACTCAAGAGCTCTGCCCTTGGTACTTTC
	DNAJC-5-4-Rev	CCACACTTGTCCACTTACCGA
Sa-CBE-DNAJC-5-693	DNAJC-5-5-Fwd	ACGTCTCAGCTCTGCCCTTGGTACTTTC
	DNAJC-5-5-Rev	CCACACTTGTCCACTTACCGA
Sa-CBE-Site29-N	Site29-1-Fwd	AGTACAGGCATTGCTGCAAAGAAAGAGGG
	Site29-1-Rev	TGATGCCCCCATGTTTCGTCAT
Sa-CBE-Site29-125	Site29-2-Fwd	AGTCGTTGCATTGCTGCAAAGAAAGAGGG
	Site29-2-Rev	TGATGCCCCCATGTTTCGTCAT
Sa-CBE-Site29-269	Site29-3-Fwd	AGCTCTGGCATTGCTGCAAAGAAAGAGGG
	Site29-3-Rev	TGATGCCCCCATGTTTCGTCAT
Sa-CBE-Site29-593	Site29-4-Fwd	TACAGAGGCATTGCTGCAAAGAAAGAGGG
	Site29-4-Rev	TGATGCCCCCATGTTTCGTCAT
Sa-CBE-Site29-693	Site29-5-Fwd	TAGCTCTGCATTGCTGCAAAGAAAGAGGG
	Site29-5-Rev	TGATGCCCCCATGTTTCGTCAT
Sa-CBE-EMX1#2-N	EMX1#2-1-Fwd	GATTGCTAGCCCATTGCTTGTCCCTC
	EMX1#2-1-Rev	CTAGGGTGGGCAACCACAAA
Sa-CBE-EMX1#2-125	EMX1#2-2-Fwd	GACCATCAGCCCATTGCTTGTCCCTC
	EMX1#2-2-Rev	CTAGGGTGGGCAACCACAAA
Sa-CBE-EMX1#2-269	EMX1#2-3-Fwd	GAGTTCGAGCCCATTGCTTGTCCCTC
	EMX1#2-3-Rev	CTAGGGTGGGCAACCACAAA
Sa-CBE-EMX1#2-593	EMX1#2-4-Fwd	GTACTTGAGCCCATTGCTTGTCCCTC
	EMX1#2-4-Rev	CTAGGGTGGGCAACCACAAA
Sa-CBE-EMX1#2-693	EMX1#2-5-Fwd	GTTGCCAAGCCCATTGCTTGTCCCTC
	EMX1#2-5-Rev	CTAGGGTGGGCAACCACAAA
Sa-CBE-RUNX14-N	RUNX14-1-Fwd	TATGCGTCACCGAGGTGAAACAAGCTG
	RUNX14-1-Rev	CAGAAGAGGGTGCATTTTCAGG

Sa-CBE-RUNX14-125	RUNX14-2-Fwd	TACGACCCACCGAGGTGAAACAAGCTG
	RUNX14-2-Rev	CAGAAGAGGGTGCATTTTCAGG
Sa-CBE-RUNX14-269	RUNX14-3-Fwd	TAGGTTCCACCGAGGTGAAACAAGCTG
	RUNX14-3-Rev	CAGAAGAGGGTGCATTTTCAGG
Sa-CBE-RUNX14-593	RUNX14-4-Fwd	TTCGCAACACCGAGGTGAAACAAGCTG
	RUNX14-4-Rev	CAGAAGAGGGTGCATTTTCAGG
Sa-CBE-RUNX14-693	RUNX14-5-Fwd	TTGCCTACACCGAGGTGAAACAAGCTG
	RUNX14-5-Rev	CAGAAGAGGGTGCATTTTCAGG
Sa-CBE-HEK3-1-N	HEK3-1-1-Fwd	AGCATGAGGCATGGATGAGAGAAGCCT
	HEK3-1-1-Rev	TAGGAAAAGCTGTCCTGCCA
Sa-CBE-HEK3-1-125	HEK3-1-2-Fwd	AGGACTTGGCATGGATGAGAGAAGCCT
	HEK3-1-2-Rev	TAGGAAAAGCTGTCCTGCCA
Sa-CBE-HEK3-1-269	HEK3-1-3-Fwd	TAGTGCAGGCATGGATGAGAGAAGCCT
	HEK3-1-3-Rev	TAGGAAAAGCTGTCCTGCCA
Sa-CBE-HEK3-1-593	HEK3-1-4-Fwd	TTGACAGGGCATGGATGAGAGAAGCCT
	HEK3-1-4-Rev	TAGGAAAAGCTGTCCTGCCA
Sa-CBE-HEK3-1-693	HEK3-1-5-Fwd	TCACACGGGCATGGATGAGAGAAGCCT
	HEK3-1-5-Rev	TAGGAAAAGCTGTCCTGCCA
Sa-CBE-VEGFA11-N	VEGFA11-1-Fwd	TGCATACACCCCTGGCCTTCTCCC
	VEGFA11-1-Rev	GCCCATTCCCTCTTTAGCCA
Sa-CBE-VEGFA11-125	VEGFA11-2-Fwd	CATACGCACCCCTGGCCTTCTCCC
	VEGFA11-2-Rev	GCCCATTCCCTCTTTAGCCA
Sa-CBE-VEGFA11-269	VEGFA11-3-Fwd	CCGCATAACCCCTGGCCTTCTCCC
	VEGFA11-3-Rev	GCCCATTCCCTCTTTAGCCA
Sa-CBE-VEGFA11-593	VEGFA11-4-Fwd	CGTAACCACCCCTGGCCTTCTCCC
	VEGFA11-4-Rev	GCCCATTCCCTCTTTAGCCA
Sa-CBE-VEGFA11-693	VEGFA11-5-Fwd	GTAATGCACCCCTGGCCTTCTCCC
	VEGFA11-5-Rev	GCCCATTCCCTCTTTAGCCA
Sa-CBE-RS1-On-N	RS1-On-1-Fwd	CACACTGTACTGCTCCGGGTTAGAGCA

	RS1-On-1-Rev	CGCAAAGCAGATGGGTTTGT
Sa-CBE-RS1-On-125	RS1-On-2-Fwd	CAGATCATACTGCTCCGGGTTAGAGCA
	RS1-On-2-Rev	CGCAAAGCAGATGGGTTTGT
Sa-CBE-RS1-On-269	RS1-On-3-Fwd	CAGTACTTACTGCTCCGGGTTAGAGCA
	RS1-On-3-Rev	CGCAAAGCAGATGGGTTTGT
Sa-CBE-RS1-On-593	RS1-On-4-Fwd	CTTGAGTTACTGCTCCGGGTTAGAGCA
	RS1-On-4-Rev	CGCAAAGCAGATGGGTTTGT
Sa-CBE-RS1-On-693	RS1-On-5-Fwd	CTCTCAGTACTGCTCCGGGTTAGAGCA
	RS1-On-5-Rev	CGCAAAGCAGATGGGTTTGT
Sa- CBE-DNMT13B-N	DNMT13B-1-Fwd	TCAGTACACTCAGTGAAGCCCACTCAT
	DNMT13B-1-Rev	GGATACAGCTGCAGAACACAC
Sa- CBE-DNMT13B-125	DNMT13B-2-Fwd	TCTCGAAACTCAGTGAAGCCCACTCAT
	DNMT13B-2-Rev	GGATACAGCTGCAGAACACAC
Sa- CBE-DNMT13B-269	DNMT13B-3-Fwd	TCCTGGAACTCAGTGAAGCCCACTCAT
	DNMT13B-3-Rev	GGATACAGCTGCAGAACACAC
Sa- CBE-DNMT13B-593	DNMT13B-4-Fwd	TGATCGTACTCAGTGAAGCCCACTCAT
	DNMT13B-4-Rev	GGATACAGCTGCAGAACACAC
Sa- CBE-DNMT13B-693	DNMT13B-5-Fwd	TGTACTCACTCAGTGAAGCCCACTCAT
	DNMT13B-5-Rev	GGATACAGCTGCAGAACACAC
Sa- CBE-V5-N	V5-1-Fwd	AGTCGTTGAACCACACAGCTTCCCGTT
	V5-1-Rev	TCCCTCTGACAATGTGCCATC
Sa- CBE-V5-125	V5-2-Fwd	AGCTCTGGAACCACACAGCTTCCCGTT
	V5-2-Rev	TCCCTCTGACAATGTGCCATC
Sa- CBE-V5-269	V5-3-Fwd	TACAGAGGAACCACACAGCTTCCCGTT
	V5-3-Rev	TCCCTCTGACAATGTGCCATC
Sa- CBE-V5-593	V5-4-Fwd	TAGCTCTGAACCACACAGCTTCCCGTT
	V5-4-Rev	TCCCTCTGACAATGTGCCATC
Sa- CBE-V5-693	V5-5-Fwd	TCAAGCTGAACCACACAGCTTCCCGTT
	V5-5-Rev	TCCCTCTGACAATGTGCCATC

Table S6.**Sa-ABE HTS Primers used to amplify each target**

Sample name	Primer name	Sequence
Sa-ABE-EMX1#6-N	EMX1#6-1-Fwd	GCCTCTACGAGCAGAAGAAGAAGGGCT
	EMX1#6-1-Rev	TTGTCCCTCTGTCAATGGCG
Sa-ABE-EMX1#6-125	EMX1#6-2-Fwd	AACCTAGCGAGCAGAAGAAGAAGGGCT
	EMX1#6-2-Rev	TTGTCCCTCTGTCAATGGCG
Sa-ABE-EMX1#6-269	EMX1#6-3-Fwd	ATTCTCGCGAGCAGAAGAAGAAGGGCT
	EMX1#6-3-Rev	TTGTCCCTCTGTCAATGGCG
Sa-ABE-EMX1#6-593	EMX1#6-4-Fwd	ATCCGGACGAGCAGAAGAAGAAGGGCT
	EMX1#6-4-Rev	TTGTCCCTCTGTCAATGGCG
Sa-ABE-EMX1#6-693	EMX1#6-5-Fwd	ATGCTTCCGAGCAGAAGAAGAAGGGCT
	EMX1#6-5-Rev	TTGTCCCTCTGTCAATGGCG
Sa-ABE-Site6-N	Site6-1-Fwd	CAGATCAAGATACAAGGACAGGCAGCATA
	Site6-1-Rev	AGAAATCGCTGACTCCAACCA
Sa-ABE-Site6-125	Site6-2-Fwd	CAGTACTAGATACAAGGACAGGCAGCATA
	Site6-2-Rev	AGAAATCGCTGACTCCAACCA
Sa-ABE-Site6-269	Site6-3-Fwd	CTTGAGTAGATACAAGGACAGGCAGCATA
	Site6-3-Rev	AGAAATCGCTGACTCCAACCA
Sa-ABE-Site6-593	Site6-4-Fwd	CTCTCAGAGATACAAGGACAGGCAGCATA
	Site6-4-Rev	AGAAATCGCTGACTCCAACCA
Sa-ABE-Site6-693	Site6-5-Fwd	CTGTAGAAGATACAAGGACAGGCAGCATA
	Site6-5-Rev	AGAAATCGCTGACTCCAACCA
Sa-ABE-Site1-N	Site1-1-Fwd	ACACAGTGCTAACTGTGACAGCATGTGG
	Site1-1-Rev	AAGAACACGTTTAAAGGGGGAA
Sa-ABE-Site1-125	Site1-2-Fwd	ACTGACTGCTAACTGTGACAGCATGTGG
	Site1-2-Rev	AAGAACACGTTTAAAGGGGGAA
Sa-ABE-Site1-269	Site1-3-Fwd	TCAGAGAGCTAACTGTGACAGCATGTGG
	Site1-3-Rev	AAGAACACGTTTAAAGGGGGAA

Sa-ABE-Site1-593	Site1-4-Fwd	TGTCAGTGCTAACTGTGACAGCATGTGG
	Site1-4-Rev	AAGAACACGTTTAAAGGGGGAA
Sa-ABE-Site1-693	Site1-5-Fwd	CATCAGAGCTAACTGTGACAGCATGTGG
	Site1-5-Rev	AAGAACACGTTTAAAGGGGGAA

Table S7.**Sa-CABE HTS Primers used to amplify each target**

Sample name	Primer name	Sequence
Sa-CBE-HEK4#4-N	HEK4#4-1-Fwd	GACTCACTTTCAACCCGAACGGAGACAC
	HEK4#4-1-Rev	GTCCAAAGCAGGATGACAGG
Sa-CBE-HEK4#4-693	HEK4#4-2-Fwd	GTAGTCTTTTCAACCCGAACGGAGACAC
	HEK4#4-2-Rev	GTCCAAAGCAGGATGACAGG
Sa-ABE-HEK4#4-N	HEK4#4-3-Fwd	GTCGTGATTTCAACCCGAACGGAGACAC
	HEK4#4-3-Rev	GTCCAAAGCAGGATGACAGG
Sa-ABE-HEK4#4-693	HEK4#4-4-Fwd	GTGTCAATTTCAACCCGAACGGAGACAC
	HEK4#4-4-Rev	GTCCAAAGCAGGATGACAGG
Sa-CABE-HEK4#4-N	HEK4#4-5-Fwd	AAGAGCTTTTCAACCCGAACGGAGACAC
	HEK4#4-5-Rev	GTCCAAAGCAGGATGACAGG
Sa-CABE-HEK4#4-693	HEK4#4-6-Fwd	ATCTGCTTTTCAACCCGAACGGAGACAC
	HEK4#4-6-Rev	GTCCAAAGCAGGATGACAGG
Sa-CBE-DNAJC-5-N	DNAJC-5-1-Fwd	ACAAGTCTGAGCTCTGCCCTTGGTACTTTC
	DNAJC-5-1-Rev	CCACACTTGTCCACTTACCGA
Sa-CBE-DNAJC-5-693	DNAJC-5-2-Fwd	ACACGTAAGCTCTGCCCTTGGTACTTTC
	DNAJC-5-2-Rev	CCACACTTGTCCACTTACCGA
Sa-ABE-DNAJC-5-N	DNAJC-5-3-Fwd	ACTACGTAGCTCTGCCCTTGGTACTTTC
	DNAJC-5-3-Rev	CCACACTTGTCCACTTACCGA
Sa-ABE-DNAJC-5-693	DNAJC-5-4-Fwd	ACTCAAGAGCTCTGCCCTTGGTACTTTC
	DNAJC-5-4-Rev	CCACACTTGTCCACTTACCGA
Sa-CABE-DNAJC-5-N	DNAJC-5-5-Fwd	ACGTCTCAGCTCTGCCCTTGGTACTTTC
	DNAJC-5-5-Rev	CCACACTTGTCCACTTACCGA
Sa-CABE-DNAJC-5-693	DNAJC-5-6-Fwd	AGACATGAGCTCTGCCCTTGGTACTTTC
	DNAJC-5-6-Rev	CCACACTTGTCCACTTACCGA
Sa-CBE-EMX1#2-N	EMX1#2-1-Fwd	GATTGCTAGCCCATTGCTTGTCCCTC
	EMX1#2-1-Rev	CTAGGGTGGGCAACCACAAA

Sa-CBE-EMX1#2-693	EMX1#2-2-Fwd	GACCATCAGCCCATTGCTTGTCCCTC
	EMX1#2-2-Rev	CTAGGGTGGGCAACCACAAA
Sa-ABE-EMX1#2-N	EMX1#2-3-Fwd	GAGTTCGAGCCCATTGCTTGTCCCTC
	EMX1#2-3-Rev	CTAGGGTGGGCAACCACAAA
Sa-ABE-EMX1#2-693	EMX1#2-4-Fwd	GTACTTGAGCCCATTGCTTGTCCCTC
	EMX1#2-4-Rev	CTAGGGTGGGCAACCACAAA
Sa-CABE-EMX1#2-N	EMX1#2-5-Fwd	GTTGCCAAGCCCATTGCTTGTCCCTC
	EMX1#2-5-Rev	CTAGGGTGGGCAACCACAAA
Sa-CABE-EMX1#2-693	EMX1#2-6-Fwd	GCTAAGAAGCCCATTGCTTGTCCCTC
	EMX1#2-6-Rev	CTAGGGTGGGCAACCACAAA
Sa-CBE-EMX1#6-N	EMX1#6-1-Fwd	GCCTCTACGAGCAGAAGAAGAAGGGCT
	EMX1#6-1-Rev	TTGTCCCTCTGTCAATGGCG
Sa-CBE-EMX1#6-693	EMX1#6-2-Fwd	AACCTAGCGAGCAGAAGAAGAAGGGCT
	EMX1#6-2-Rev	TTGTCCCTCTGTCAATGGCG
Sa-ABE-EMX1#6-N	EMX1#6-3-Fwd	ATTCTCGCGAGCAGAAGAAGAAGGGCT
	EMX1#6-3-Rev	TTGTCCCTCTGTCAATGGCG
Sa-ABE-EMX1#6-693	EMX1#6-4-Fwd	ATCCGGACGAGCAGAAGAAGAAGGGCT
	EMX1#6-4-Rev	TTGTCCCTCTGTCAATGGCG
Sa-CABE-EMX1#6-N	EMX1#6-5-Fwd	ATGCTTCCGAGCAGAAGAAGAAGGGCT
	EMX1#6-5-Rev	TTGTCCCTCTGTCAATGGCG
Sa-CABE-EMX1#6-693	EMX1#6-6-Fwd	ACCATCGCGAGCAGAAGAAGAAGGGCT
	EMX1#6-6-Rev	TTGTCCCTCTGTCAATGGCG

Table S8.**DNA off-target HTS Primers used to amplify each target**

Sample name	Primer name	Sequence
R-LOOP-HEK4-N	HEK4-1-Fwd	GAGCGATAGATGGCTGACAAAGGCCG
	HEK4-1-Rev	AACCCGAACGGAGACACAC
R-LOOP-HEK4-125	HEK4-2-Fwd	GTTCAACAGATGGCTGACAAAGGCCG
	HEK4-2-Rev	AACCCGAACGGAGACACAC
R-LOOP-HEK4-269	HEK4-3-Fwd	GTGGTACAGATGGCTGACAAAGGCCG
	HEK4-3-Rev	AACCCGAACGGAGACACAC
R-LOOP-HEK4-593	HEK4-4-Fwd	GCTCATTAGATGGCTGACAAAGGCCG
	HEK4-4-Rev	AACCCGAACGGAGACACAC
R-LOOP-HEK4-693	HEK4-5-Fwd	GCGAGTTAGATGGCTGACAAAGGCCG
	HEK4-5-Rev	AACCCGAACGGAGACACAC
R-LOOP-SiteB-N	SiteB-1-Fwd	ATTGCTCGTCTCCACACAGGTGCTGTT
	SiteB-1-Rev	AACTGCCAAAAGCCACAACC
R-LOOP-SiteB-125	SiteB-2-Fwd	ATCAAGCGTCTCCACACAGGTGCTGTT
	SiteB-2-Rev	AACTGCCAAAAGCCACAACC
R-LOOP-SiteB-269	SiteB-3-Fwd	ATCCGGAGTCTCCACACAGGTGCTGTT
	SiteB-3-Rev	AACTGCCAAAAGCCACAACC
R-LOOP-SiteB-593	SiteB-4-Fwd	ATCGAAGGTCTCCACACAGGTGCTGTT
	SiteB-4-Rev	AACTGCCAAAAGCCACAACC
R-LOOP-SiteB-693	SiteB-5-Fwd	ATCGTCCGTCTCCACACAGGTGCTGTT
	SiteB-5-Rev	AACTGCCAAAAGCCACAACC
R-LOOP-PPP-N	PPP-1-Fwd	CAATGTGTGCACCCGGCCATGGTTT
	PPP-1-Rev	CTGAGACTCAGGAGGCCCAGA
R-LOOP-PPP-125	PPP-2-Fwd	CATCTTGTGCACCCGGCCATGGTTT
	PPP-2-Rev	CTGAGACTCAGGAGGCCCAGA
R-LOOP-PPP-269	PPP-3-Fwd	CATGCAATGCACCCGGCCATGGTTT

	PPP-3-Rev	CTGAGACTCAGGAGGCCCAGA
R-LOOP-PPP-593	PPP-4-Fwd	CTACAAGTGCACCCGGCCATGGTTT
	PPP-4-Rev	CTGAGACTCAGGAGGCCCAGA
R-LOOP-PPP-693	PPP-5-Fwd	CTTAGCTTGCACCCGGCCATGGTTT
	PPP-5-Rev	CTGAGACTCAGGAGGCCCAGA
R-LOOP-FANCF-N	FANCF-1-Fwd	CCAATGACATTGCAGAGAGGCGTATCAT
	FANCF-1-Rev	GTGCTGACGTAGGTAGTGCT
R-LOOP-FANCF-125	FANCF-2-Fwd	CGATTACATTGCAGAGAGGCGTATCAT
	FANCF-2-Rev	GTGCTGACGTAGGTAGTGCT
R-LOOP-FANCF-269	FANCF-3-Fwd	CGTCCATCATTGCAGAGAGGCGTATCAT
	FANCF-3-Rev	GTGCTGACGTAGGTAGTGCT
R-LOOP-FANCF-593	FANCF-4-Fwd	GAAGGTCCATTGCAGAGAGGCGTATCAT
	FANCF-4-Rev	GTGCTGACGTAGGTAGTGCT
R-LOOP-FANCF-693	FANCF-5-Fwd	GATGACGCATTGCAGAGAGGCGTATCAT
	FANCF-5-Rev	GTGCTGACGTAGGTAGTGCT
R-LOOP-Site29-CTR	Site29-1-Fwd	ATTGCTCCAGGGGAGCGTGTCCATAGG
	Site29-1-Rev	CAGGACCCGGGTTCATAACT
R-LOOP-Site29-N	Site29-2-Fwd	ATCGAAGCAGGGGAGCGTGTCCATAGG
	Site29-2-Rev	CAGGACCCGGGTTCATAACT
R-LOOP-Site29-125	Site29-3-Fwd	ATGGCGACAGGGGAGCGTGTCCATAGG
	Site29-3-Rev	CAGGACCCGGGTTCATAACT
R-LOOP-Site29-269	Site29-4-Fwd	ACCGGTTTCAGGGGAGCGTGTCCATAGG
	Site29-4-Rev	CAGGACCCGGGTTCATAACT
R-LOOP-Site29-593	Site29-5-Fwd	TACTCCGCAGGGGAGCGTGTCCATAGG
	Site29-5-Rev	CAGGACCCGGGTTCATAACT
R-LOOP-Site29-693	Site29-6-Fwd	TAGAACGCAGGGGAGCGTGTCCATAGG
	Site29-6-Rev	CAGGACCCGGGTTCATAACT

R-LOOP-HEK3-CTR	HEK3-1-Fwd	TTCCGATTGCATTTGTAGGCTTGATGC
	HEK3-1-Rev	AGGAGCTGCACATACTAGCC
R-LOOP-HEK3-N	HEK3-2-Fwd	TTGCAGCTGCATTTGTAGGCTTGATGC
	HEK3-2-Rev	AGGAGCTGCACATACTAGCC
R-LOOP-HEK3-125	HEK3-3-Fwd	TCGAATCTGCATTTGTAGGCTTGATGC
	HEK3-3-Rev	AGGAGCTGCACATACTAGCC
R-LOOP-HEK3-269	HEK3-4-Fwd	TGCAAGGTGCATTTGTAGGCTTGATGC
	HEK3-4-Rev	AGGAGCTGCACATACTAGCC
R-LOOP-HEK3-593	HEK3-5-Fwd	CAATAGCTGCATTTGTAGGCTTGATGC
	HEK3-5-Rev	AGGAGCTGCACATACTAGCC
R-LOOP-HEK3-693	HEK3-6-Fwd	CCTTATGTGCATTTGTAGGCTTGATGC
	HEK3-6-Rev	AGGAGCTGCACATACTAGCC

Table S9.**BCL11A and PAH HTS Primers used to amplify each target**

Sample name	Primer name	Sequence
BCL11A-ABE-N	BCL11A-1-Fwd	TCAGTACCATAGGCCAGAAAAGAGATATGGCA
	BCL11A-1-Rev	AAACGGCCACCGATGGAG
BCL11A-CBE-N	BCL11A-2-Fwd	TCTCGAACATAGGCCAGAAAAGAGATATGGCA
	BCL11A-2-Rev	AAACGGCCACCGATGGAG
BCL11A-CABE-N	BCL11A-3-Fwd	TCCTGGACATAGGCCAGAAAAGAGATATGGCA
	BCL11A-3-Rev	AAACGGCCACCGATGGAG
BCL11A-ABE-693	BCL11A-4-Fwd	TGATCGTCATAGGCCAGAAAAGAGATATGGCA
	BCL11A-4-Rev	AAACGGCCACCGATGGAG
BCL11A-CBE-693	BCL11A-5-Fwd	TGTACTCCATAGGCCAGAAAAGAGATATGGCA
	BCL11A-5-Rev	AAACGGCCACCGATGGAG
BCL11A-CABE-693	BCL11A-6-Fwd	CAATGTGCATAGGCCAGAAAAGAGATATGGCA
	BCL11A-6-Rev	AAACGGCCACCGATGGAG
PAH-1-N	PAH-1-N-Fwd	GTAACCGTGTAACGACGGCCAGT
	PAH-1-N-Rev	ATGCCTTTATGGAGTATCA
PAH-1-125	PAH-1-125-Fwd	GCCAATGTGTAACGACGGCCAGT
	PAH-1-125-Rev	ATGCCTTTATGGAGTATCA
PAH-2-N	PAH-2-N-Fwd	GGCCTAAGCCACTGTCCGTGAGCT
	PAH-2-N-Rev	CAGGAAACAGCTATGAC
PAH-2-125	PAH-2-125-Fwd	ATACCGCGCCACTGTCCGTGAGCT
	PAH-2-125-Rev	CAGGAAACAGCTATGAC

Supplementary Sequences1.

Amino acid sequences of hA3A(130F), TadA-8e, Sa-CBE-N, SaCBE-125, SaCBE-269, SaCBE-593, SaCBE-693, Sa-ABE-N, SaABE-125, SaABE-269, SaABE-593, SaABE-693, Sa-CABE, Sa-CABE-693.

hA3A(130F)

MEASPASGPRHLMDPHIFTSNFNNGIGRHKTYLCYEVERLDNGTSVKMDQHRGFLHNQAKNL
LCGFYGRHAELRFLDLVPSLQLDPAQIYRVTFISWSPCFSWGCAGEVRAFLQENTHVRLRIF
AARIFDYDPLYKEALQMLRDAGAQVSIMTYDEFKHCWDTFVDHQGCPFQPWDGLDEHSQAL
SGRLRAILQNQGN

TadA-8e

SEVEFSHEYWMRHALTLAKRARDEREVPVGAVLVNLRVIGEGWNRAIGLHDPTAHAEIMA
LRQGGLVMQNYRLIDATLYVTFEPCVMCAGAMIHSRIGRVVFGVRNSKRGGAAGSLMNVLNY
PGMNHRVEITEGILADECAALLCDFYRMPRQVFNAQKKAQSSIN

Sa-CBE-N

MEASPASGPRHLMDPHIFTSNFNNGIGRHKTYLCYEVERLDNGTSVKMDQHRGFLHNQAKNL
LCGFYGRHAELRFLDLVPSLQLDPAQIYRVTFISWSPCFSWGCAGEVRAFLQENTHVRLRIF
AARIFDYDPLYKEALQMLRDAGAQVSIMTYDEFKHCWDTFVDHQGCPFQPWDGLDEHSQAL
SGRLRAILQNQNGSGSETPGTSESATPESGKRNYILGLAIGITSVGYGIIDYETRDVIDAGVRLFK
EANVENNEGRRSKRGARRLKRRRRRHRIQRVKLLFDYNLLTDHSELGINPYEARVKGLSQKL
SEEEFSAALLHLAKRRGVHNVNEVEEDTGNELSTKEQISRNSKALEEKYVAELQLERLKKDGE
VRGSINRFKTSYVKEAKQLLKVQKAYHQLDQSFIDTYIDLLETRRTYYEGPGEKSPFGWKDI
KEWYEMLMGHCTYFPEELRSVKYAYNADLYNALNDLNNLVITRDENEKLEYEYEFQIIENVF
KQKKKPTLKQIAKEILVNEEDIKGYRVSTGKPEFTNLKVYHDIKDITARKEIENAELLDQIAKI
LTIYQSSEDIQEELTNLSELQEEIEQISNLKGYTGTHNLSLKAINLILDELWHTNDNQIAIFNR
LKLVPKKVDLSQQKEIPTTLVDDFILSPVVKRSFIQSIKVINAIKKYGLPNDIIIELAREKNSKDA
QKMINEMQKRNRQTNERIEEIIRTTGKENAKYLIEKIKLHDMQEGKCLYSLEAIPLEDLLNPF
NYEVDHIIPRSVSFDNSFNKNVLVKQEENSKKGNRTPFQYLSSDSKISYETFKKHILNLAGKG
GRISKTKKEYLLEERDINRFSVQKDFINRNLVDTRYATRGLMNLLRSYFRVNNLDVKVKSING
GFTSFLRRKWKFKERNKGYKHHAEDALIINANADFIFKEWKKLDKAKKVMENQMFEKQAE

SMPEIETE QEYKEIFITPHQIKHIKDFKDYKYSHRVDKKPNRKLINDTL YSTRKDDKGNTLIVNN
LNGLYDKDNDKLLKLINKSPEKLLMYHHPQTYQKLKLIMEQYGDEKNPLYKYEEETGNYL
TKYSKKDNGPVIKKIKYYGNKLN AHL DITDDYPNSRNKVVKLSLKP YRFDVYLDNGVYKFVT
VKNLDVIKKENYYEVNSKCYEEAKKLLKISNQA EFIASFYKNDLIKINGEL YRVIGVNNDLLN
RIEVNMIDITYREYLENMNDKRPPHIIKTIASKTQSIKKYSTDILGNLYEVKSKKHPQIIKKGSS
GGSTNLSDIIEKETGKQLVIQESILMLPEEVEEVIGNKPESDILVHTAYDESTDENVMLLTSDAP
EYKPWALVIQDSNGENKIKMLSGGSPKKKRKV

Sa-CBE-125

KRNYILGLAIGITSVGYGIIDYETRDVIDAGVRLFKEANVENNEGRRSKRGARRLKRRRRHRIQ
RVKKLLFDYNLLTDHSELGINPYEARVKGLSQKLSEEFSAALLHLAKRRGVHNVNEVEESG
SETPGTSESATPESMEASPASGPRHLMDPHIFTSNFNNGIGRHKTYLCYEVERLDNGTSVKMD
QHRGFLHNQAKNLLCGFYGRHAELRFLDLVPSLQLDPAQIYRVTFISWSPCFSWGCAGEVR
AFLQENTHVRLRIFAARIFDYDPLYKEALQMLRDAGAQVSIMTYDEFKHCWDTFVDHQGCPF
QPWDGLDEHSQALSGRLRAILQNQGNSETPGTSESATPESDTGNELSTKEQISRNSKALEEK
YVAELQLERLKKDGEVRGSINRFKTS DYVKEAKQLLKVQKAYHQLDQSFIDTYIDLLETRRTY
YEGPGEGSPFGWKDIKEWYEMLMGHCTYFPEELRSVKYAYNADLYNALNDLNNLVITRDEN
EKLEYEKFQIIE NVFKQKKKPTLKQIAKEILVNEEDIKGYRVTSTGKPEFTNLKVYHDIKDITA
RKEIIEAELLDQIAKILTIYQSSEDIQEELTNL NSEL TQEEIEQISNLKGYTGTHNLSLKAINLILD
ELWHTNDNQIAIFNRLKLVPKKVDLSQQKEIPTTLVDDFILSPVVKRSFIQSIKVINAIKKYGLP
NDIIIELAREKNSKDAQKMINEMQKRNRQTNERIEEII RTTGKENAKYLIEKIKLHDMQEGKCL
YSLEAIPLEDLLNPNFNYEVDHII PRSVSFDNSFNKVLVKQEENSKKGNRTPFQYLSSSDSKIS
YETFKKHILNLAKGKGRISKTKKEYLLEERDINRFSVQKDFINRNLVDTRYATRGLMNLLRSYF
RVNNLDVKVKSINGGFTSFLRRKWKFKKERNKGYKHAEDALI IANADFIKWKKLDKAKK
VMENQMFEKQAESMPEIETE QEYKEIFITPHQIKHIKDFKDYKYSHRVDKKPNRKLINDTL YS
TRKDDKGNTLIVNNLNGLYDKDNDKLLKLINKSPEKLLMYHHPQTYQKLKLIMEQYGDEK
NPLYKYEEETGNYLTKYSKKDNGPVIKKIKYYGNKLN AHL DITDDYPNSRNKVVKLSLKP YR
FDVYLDNGVYKFVTVKNLDVIKKENYYEVNSKCYEEAKKLLKISNQA EFIASFYKNDLIKING
EL YRVIGVNNDLLNRIEVNMIDITYREYLENMNDKRPPHIIKTIASKTQSIKKYSTDILGNLYEV
KSKKHPQIIKKGSPKKKRKVSSDYKDHDGDYKDHDIDYKDDDDKSGGSTNLSDIIEKETGKQ

LVIQESILMLPEEVVEEVIGNKPESDILVHTAYDESTDENVMLLTSDAPEYKPWALVIQDSNGEN
KIKMLSGGSPKKKRKV

Sa-CBE-269

KRNYILGLAIGITSVGYGIIDYETRDVIDAGVRLFKEANVENNEGRRSKRGARRLKRRRRHRIQ
RVKKLLFDYNLLTDHSELGINPYEARVKGLSQKLSEEEFSAALLHLAKRRGVHNVNEVEEDT
GNELSTKEQISRNSKALEEKYVAELQLERLKKDGEVRGSINRFKTSDYVKEAKQLLKVQKAY
HQLDQSFIDTYIDLLETRRTYYEGPGEGSPFGWKDIKEWYEMLMGHCTYFPEELRSVKYAYN
ADLYNALNDLNNLVITRDSGSETPGTSESATPESMEASPASGPRHLMDFHFTSNFNNIGIRHK
TYLCYEVERLDNGTSVKMDQHRGFLHNQAKNLLCGFYGRHAELRFLDLVPSLQLDPAQIYRV
TWFISWSPCFSWGCAGEVRAFLQENTHVRLRIFAARIFDYDPLYKEALQMLRDAGAQVSIMTY
DEFKHCWDTFVDHQGCPFQPWDGLDEHSQALSGRLRAILQNQGNSGSETPGTSESATPESENE
KLEYEKFQIIENVFKQKKKPTLKQIAKEILVNEEDIKGYRVTSTGKPEFTNLKVYHDIKDITAR
KEIENAELLDQIAKILTIYQSSEDIQEELTNLNSLTQEEIEQISNLKGYTGTHNLSLKAINLILDE
LWHTNDNQIAIFNRLKLVKKVDLSQQKEIPTTLVDDFILSPVVKRSFIQSIKVINAIKKYGLPN
DIIIELAREKNSKDAQKMINEMQKRNRQTNERIEEIIRTTGKENAKYLIEKIKLHDMQEGKCLYS
LEAIPLEDLLNNPFNYEVDHIIPRSVSFDNSFNKNVLVKQEENSKKGNRTPFYLSSSDSKISYE
TFKKHILNLAGKGRISKTKKEYLLEERDINRFSVQKDFINRNLVDTRYATRGLMNLLRSYFR
VNNLDVKVKSINGGFTSFLRRKWKFKKERNKGYKHHAEDALIIANADFIFKEWKLDKAKKV
MENQMFEKQAESMPEIETEQEYKEIFITPHQIKHIKDFKDYKYSHRVDKKPNRKLINDTLYST
RKDDKGNTLIVNNLNGLYDKDNDKLLKLINKSPEKLLMYHHPQTYQKLKLIMEQYGDEKN
PLYKYYEETGNLYTKYSKKDNGPVIKKIKYYYGNKLNAHLDITDDYPNSRNKVVKLSLKPYRF
DVYLDNGVYKFVTVKNLDVIKKENYYEVNSKCYEEAKKLKKISNQAEFIASFYKNDLIKINGE
LYRVIGVNNDLLNRIEVNMIDITYREYLENMNDKRPPHIIKTIASKTQSIKKYSTDILGNLYEVK
SKKHPQIIKKGGSPKKKRKVSSDYKDHDGDYKDHDIDYKDDDDKSGGSTNLSDIIEKETGKQL
VIQESILMLPEEVVEEVIGNKPESDILVHTAYDESTDENVMLLTSDAPEYKPWALVIQDSNGENK
IKMLSGGSPKKKRKV

Sa-CBE-593

KRNYILGLAIGITSVGYGIIDYETRDVIDAGVRLFKEANVENNEGRRSKRGARRLKRRRRHRIQ
RVKKLLFDYNLLTDHSELGINPYEARVKGLSQKLSEEEFSAALLHLAKRRGVHNVNEVEEDT

GNELSTKEQISRNSKALEEKYVAELQLERLKKDGEVRGSINRFKTS DYVKEAKQLLKVQKAY
HQLDQSFIDTYIDLLETRRTYYEGPGE GSPFGWKDIKEWYEMLMGHCTYFPEELRSVKYAYN
ADLYNALNDLNNLVITRDENEKLEYEYEFQIIENVFKQKKKPTLKQIAKEILVNEEDIKGYRVT
STGKPEFTNLKVYHDIKDITARKEIENAELLDQIAKILTIYQSSEDIQEELTNLNSELTQEEIEQIS
NLKGYTGTHNLSLKAINLILDELWHTNDNQIAIFNRLKLVPKKVDLSQQKEIPTTLVDDFILSPV
VKRSFIQSIKVINAIKKYGLPNDIIELAREKNSKDAQKMINEMQKRNRQTNERIEEIIRTTGKE
NAKYLIEKIKLHDMQEGKCLYSLEAIPLEDLLNPNFNYEVDHIIPRSVSFDNSFNKNVLVKQEE
NSKKGNRTPFQYLSSSGSETPGTSESATPESMEASPASGPRHLMDPHIFTSNFNNGIGRHKTYLC
YEVERLDNGTSVKMDQHRGFLHNQAKNLLCGFYGRHAELRFLDLVPSLQLDPAQIYRVTWFI
SWSPCFSWGCAGEVRAFLQENTHVRLRIFAARIFDYDPLYKEALQMLRDAGAQVSIMTYDEF
KHCWDTFVDHQGCPFQPWDGLDEHSQALSGRLRAILQNQGN SGSETPGTSESATPESSDSKIS
YETFKKHILNLAKGKGRISKTKKEYLLEERDINRFSVQKDFINRNLVDTRYATRGLMNLLRSYF
RVNNLDVKVKSINGGFTSFLRRKWKFKKERNKGYKHHAE DALIIANADFIFKEWKKLDKAKK
VMENQMFE EKQAESMPEIETE QEYKEIFITPHQIKHIKDFKDYKYSHRVDKKPNRKLINDTLYS
TRKDDKGNTLIVNNLNGLYDKDNDKLLKLINKSPEKLLMYHHD PQTYQKLKLIMEQYGDEK
NPLYKYEEETGNYLTKYSKKDNGPVIKKIKYYGNKLN AHLDITDDYPNSRNKVVKLSLKPYR
FDVYLDNGVYKFVTVKNLDVIKKENYYEVNSKCYEEAKK LKKISNQAEFIASFYKNDLIKING
ELYRVIGVNNDLLNRIEVNMIDITYREYLENMNDKRPPHIKTIASKTQSIKKYSTDILGNLYEV
KSKKHPQIIKKGGSPKKKRKVSSDYKDHDGDYKDHDIDYK DDDDKSGGSTNLSDIIEKETGKQ
LVIQESILMLPEEVEEVIGNKPESDILVHTAYDESTDENVM LLTSDAPEYKPWALVIQDSNGEN
KIKMLSGGSPKKKRKV

Sa-CBE-693

KRNYILGLAIGITSVG YGIIDYETRDVIDAGVRLFKEANVENNEGRRSKRGARRLKRRRRHRIQ
RVKLLFDYNLLTDHSELGINPYEARVKGLSQKLSEEEFSAALLHLAKRRGVHNVNEVEEDT
GNELSTKEQISRNSKALEEKYVAELQLERLKKDGEVRGSINRFKTS DYVKEAKQLLKVQKAY
HQLDQSFIDTYIDLLETRRTYYEGPGE GSPFGWKDIKEWYEMLMGHCTYFPEELRSVKYAYN
ADLYNALNDLNNLVITRDENEKLEYEYEFQIIENVFKQKKKPTLKQIAKEILVNEEDIKGYRVT
STGKPEFTNLKVYHDIKDITARKEIENAELLDQIAKILTIYQSSEDIQEELTNLNSELTQEEIEQIS
NLKGYTGTHNLSLKAINLILDELWHTNDNQIAIFNRLKLVPKKVDLSQQKEIPTTLVDDFILSPV

VKRSFIQSIKVINAIKKYGLPNDIIIELAREKNSKDAQKMINEMQKRNQRQTNERIEEIIIRTTGKE
NAKYLIEKIKLHDMQEGKCLYSLEAIPLEDLLNPNFNYEVDHIIPRSVSFDNSFNKVLVKQEE
NSKKGNRTPFQYLSSSDSKISYETFKKHILNLAKGKGRISKTKKEYLLEERDINRFSVQKDFINR
NLVDTRYATRGLMNLRSYFRVNNLDVKVKSINGGFTSFLRRKWKFKKERSGSETPGTSESAT
PESMEASPASGPRHLMDPHIFTSNFNNGIGRHKTYLCYEVERLDNGTSVKMDQHRGFLHNQA
KNLLCGFYGRHAELRFLDLVPSLQLDPAQIYRVTWFIWSWPCFSWGCAGEVRAFLQENTHVRL
RIFAARIFDYDPLYKEALQMLRDAGAQVSIMTYDEFKHCWDTFVDHQQGCPFPWDGLDEHSQ
ALSGRLRAILQNQNGSGSETPGTSESATPESNKGKHHHAEDALIINANADFIFKEWKKLDAKK
VMENQMFEKQAESMPEIETEQEYKEIFITPHQIKHIKDFKDYKYSHRVDKKPNRKLINDTLYS
TRKDDKGNLTLIVNNLNGLYDKDNDKLLKLINKSPEKLLMYHHPQTYQKLKLIMEQYGDEK
NPLYKYEEETGNLYTKYSKKDNGPVIKKIKYYGNKLNHLADITDDYPNSRNKVVKLSLKPYP
FDVYLDNGVYKFVTVKNLDVIKKENYEEVNSKCYEEAKKLLKISNQAEFIASFYKNDLIKING
ELYRVIGVNNDLLNRIEVMIDITYREYLENMNDKRPPHIIKTIASKTQSIKKYSTDILGNLYEV
KSKKHPQIIKGGSPKKKRKVSSDYKDHDGDYKDHDIDYKDDDDKSGGSTNLSDIIEKETGKQ
LVIQESILMLPEEVEEVIGNKPESDILVHTAYDESTDENVMLLTSDAPEYKPWALVIQDSNGEN
KIKMLSGGSPKKKRKV

Sa-ABE-N

SEVEFSHEYWMRHALTLAKRARDEREVPVGAVLVLNNRVIGEGWNRAIGLHDPTAHAEIMA
LRQGGLVMQNYRLIDATLYVTFEPCVMCAGAMIHSRIGRVVFGVRNSKRGAAAGSLMNVLNY
PGMNRHVEITEGILADECAALLCDFYRMPRQVFNAQKKAQSSINSGSETPGTSESATPESGKRN
YILGLAIGITSVGYGIIDYETRDVIDAGVRLFKEANVENNEGRRSKRGARRLKRRRRRHRIQVRK
KLLFDYNLLTDHSELGINPYEARVKGLSQKLSEEEFSAALLHLAKRRGVHNVNEVEEDTGNE
LSTKEQISRNSKALEEKYVAELQLERLKKDGEVRGSINRFKTSYVKEAKQLLKVQKAYHQL
DQSFIDTYIDLLETRRTYYEGPGEPSFGWKDIKEWYEMLMGHCTYFPEELRSVKYAYNADL
YNALNDLNNLVITRDENEKLEYEYKFQIENVFKQKKKPTLKQIAKEILVNEEDIKGYRVTSTG
KPEFTNLKVYHDIKDITARKEIENAEELLDQIAKILTIYQSSEDIQEELTNLNSELTQEEIEQISNLK
GYTGTHNLSLKAINLILDELWHTNDNQIAIFNRLKLVKKVDLSQQKEIPTTLVDDFILSPVVKR
SFIQSIKVINAIKKYGLPNDIIIELAREKNSKDAQKMINEMQKRNQRQTNERIEEIIIRTTGKENAK
YLIEKIKLHDMQEGKCLYSLEAIPLEDLLNPNFNYEVDHIIPRSVSFDNSFNKVLVKQEENSK

KGNRTPFQYLSSSDSKISYETFKKHILNLA KGKGRISKTKKEYLLEERDINRFSVQKDFINRNLV
DTRYATRGLMNL LRSYFRVNNLDVKVKSINGGFTSFLRRKWKFKKERNKGYKHHAEDALIIA
NADFIFKEWK KLDKAKKVMENQMFE EKQAESMPEIETE QEYKEIFITPHQIKHIKDFKDYKYS
HRVDKKPNRKLINDTLYSTRKDDKGNTLIVNNLNGLYDKDNDK LKKLINKSPEKLLMYHHDP
QTYQKLKLIMEQYGDEKNPLYKY YEETGNYLTKY SKKDNGPVIKKIKYYGNKLNAHLDITDD
YPNSRNKVVKLSLKP YRFDVYLDNGVYKFVTVKNLDVIKKENYYEVNSKCYEEAKK LKKISN
QAEFIASFYKNDLIKINGEL YRVIGVNNDLLNRIEVNMIDITYREYLENMNDKRPPHIIKTIASKT
QSIKKYSTDILGNLYEVKSKHPQIIKKGSSGSGSTNLSDIIEKETGKQLVIQESILMLPEEVEEVI
GNKPESDILVHTAYDESTDENVMLLTSDAPEYKPWALVIQDSNGENKIKMLSGGSPKKKRKV

Sa-ABE-125

KRNYILGLAIGITSVGYGIIDYETRDVIDAGVRLFKEANVENNEGRRSKRGARRLKRRRRHRIQ
RVKLLFDYNLLTDHSELSGINPYEARVKGLSQKLSEEEFSAALLHLAKRRGVHNVNEVEESG
SETPGTSESATPES

SEVEFSHEYWMRHALTLAKRARDEREVPVGAVLV LNNRVIGEGWNRAIGLHDPTAHAEIMA
LRQGGLVMQNYRLIDATLYVTFEPCVMCAGAMIHSRIGRVVFGVRNSKRGAAAGSLMNV LNY
PGMNRHVEITEGILADECAALLCDFYRMPRQVFNAQKKAQSSINS GSETPGTSESATPESDTGN
ELSTKEQISRNSKALEEKYVAELQLERLKKDGEVRGSINRFKTS DYVKEAKQLLKVQKAYHQL
DQSFIDTYIDLLETRRTYYEGPGEGSPFGWKDIKEWYEMLMGHCTYFPEELRSVKYAYNADL
YNALNDLNNLVITRDENEKLEYEYEFQIEN VFQKKKPTLKQIAKEILVNEEDIKGYRVTSTG
KPEFTNLKVYHDIKDITARKEI IENAELLDQIAKILTIYQSSEDIQEELTNL NSELTQEEIEQISNLK
GYTGTHNLSLKAINLILDELWHTNDNQIAIFNRLKLVPKKVDLSQQKEIPTTLVDDFILSPVVKR
SFIQSIKVINAIIKKYGLPNDIIIELAREKNSKDAQKMINEMQKRNRQTNERIEEII RTTGKENAK
YLIEKIKLHDMQEGKCLYSLEAIPLEDLLNPNFNYEVDHII PRSVSFDNSFNKVLVKQEENSK
KGNRTPFQYLSSSDSKISYETFKKHILNLA KGKGRISKTKKEYLLEERDINRFSVQKDFINRNLV
DTRYATRGLMNL LRSYFRVNNLDVKVKSINGGFTSFLRRKWKFKKERNKGYKHHAEDALIIA
NADFIFKEWK KLDKAKKVMENQMFE EKQAESMPEIETE QEYKEIFITPHQIKHIKDFKDYKYS
HRVDKKPNRKLINDTLYSTRKDDKGNTLIVNNLNGLYDKDNDK LKKLINKSPEKLLMYHHDP
QTYQKLKLIMEQYGDEKNPLYKY YEETGNYLTKY SKKDNGPVIKKIKYYGNKLNAHLDITDD
YPNSRNKVVKLSLKP YRFDVYLDNGVYKFVTVKNLDVIKKENYYEVNSKCYEEAKK LKKISN

QAEFIASFYKNDLIKINGELYRVIGVNNDLLNRIEVMIDITYREYLENMNDKRPPHIIKTIASKT
QSIKKYSTDILGNLYEVKSKKHPQIIKKGGSPKKKRKVSSDYKDHDGDYKDHDIDYKDDDDK
SGGSTNLSDIIEKETGKQLVIQESILMLPEEVEEVIGNKPESDILVHTAYDESTDENVMMLLTSDA
PEYKPWALVIQDSNGENKIKMLSGGSPKKKRKV

Sa-ABE-269

KRNYILGLAIGITSVGYGIIDYETRDVIDAGVRLFKEANVENNEGRRSKRGARRLKRRRRHRIQ
RVKLLFDYNLLTDHSELGINPYEARVKGLSQKLSEEFSAALLHLAKRRGVHNVNEVEEDT
GNELSTKEQISRNSKALEEKYVAELQLERLKKDGEVRGSINRFKTSDYVKEAKQLLKVQKAY
HQLDQSFIDTYIDLLETRRTYYEGPGEGSPFGWKDIKEWYEMLMGHCTYFPEELRSVKYAYN
ADLYNALNDLNNLVITRDSGSETPGTSESATPESEVEFSHEYWMRHALTLAKRARDEREVPV
GAVLVLNNRVIGEGWNRAIGLHDPTAHAEIMALRQGGLVMQNYRLIDATLYVTFEPCVMCA
GAMIHSRIGRVVFGVRNSKRGAAAGSLMNVLNYPGMNHRVEITEGILADECAALLCDFYRMPR
QVFNAQKKAQSSINSGSETPGTSESATPESENEKLEYEKFQIENVFKQKKKPTLKQIAKEILV
NEEDIKGYRVTSTGKPEFTNLKVYHDIKDITARKEIENAELLDQIAKILTIYQSSEDIQEELTNL
NSELTQEEIEQISNLKGYTGTHNLSLKAINLILDELWHTNDNQIAIFNRLKLVKKVDSLQQKEI
PTTLVDDFILSPVVKRSFIQSIKVINAIIKKYGLPNDIIIELAREKNSKDAQKMINEMQKRNRQTN
ERIEEIIRTTGKENAKYLIEKIKLHDMQEGKCLYSLEAIPLEDLLNPNFNYEVDHIIPRSVSFDNS
FNNKVLVKQEENSKKGNRTPFQYLSSSDSKISYETFKKHILNLAGKGRISKTKKEYLLEERDI
NRFSVQKDFINRNLVDTRYATRGLMNLLRSYFRVNNLDVKVKSINGGFTSFLRRKWFKKER
NKGYKHHAEDALIIANADFIFKEWKLDKAKKVMENQMFEKQAESMPEIETEQEYKEIFITP
HQIKHIKDFKDYKYSHRVDKKPNRKLINDTLYSTRKDDKGNTLIVNNLNGLYDKDNDKLKKL
INKSPEKLLMYHHDQPQTYQKLKLIMEQYGDEKNPLYKYEEETGNYLTKYSKKDNGPVIKKIK
YYGNKLNAHLDITDDYPNSRNKVVKLSLKPFRFDVYLDNGVYKFVTVKNLDVIKKENYEEV
NSKCYEEAKKLKISNQAEFIASFYKNDLIKINGELYRVIGVNNDLLNRIEVMIDITYREYLEN
MNDKRPPHIIKTIASKTQSIKKYSTDILGNLYEVKSKKHPQIIKKGGSPKKKRKVSSDYKDHDG
DYKDHDIDYKDDDDKSGGSTNLSDIIEKETGKQLVIQESILMLPEEVEEVIGNKPESDILVHTAY
DESTDENVMMLLTSDAPEYKPWALVIQDSNGENKIKMLSGGSPKKKRKV

Sa-ABE-593

KRNYILGLAIGITSVGYGIIDYETRDVIDAGVRLFKEANVENNEGRRSKRGARRLKRRRRHRIQ
RVKKLLFDYNLLTDHSELGINPYEARVKGLSQKLSEEEFSAALLHLAKRRGVHNVNEVEEDT
GNELSTKEQISRNSKALEEKYVAELQLERLKKDGEVRGSINRFKTSDYVKEAKQLLKVQKAY
HQLDQSFIDTYIDLLETRRTYYEGPGEKSPFGWKDIKEWYEMLMGHCTYFPEELRSVKYAYN
ADLYNALNDLNNLVITRDENEKLEYEKFQIIENVFKQKKKPTLKQIAKEILVNEEDIKGYRVT
STGKPEFTNLKVYHDIKDITARKEIENAEELLDQIAKILTIYQSSEDIQEELTNLNSELTQEEIEQIS
NLKGYTGTHNLSLKAINLILDELWHTNDNQIAIFNRLKLVPKKVDLSQQKEIPTTLVDDFILSPV
VKRSFIQSIKVINAIKKYGLPNDIIELAREKNSKDAQKMINEMQKRNRQTNERIEEIIRTTGKE
NAKYLIEKIKLHDMQEGKCLYSLEAIPLEDLLNPNFNYEVDHIIPRSVSFDNSFNKVLVKQEE
NSKKGNRTPFQYLSSSGSETPGTSESATPESSEVEFSHEYWMRHALTLAKRARDEREVPVGAV
LVLNNRVIGEGWNRAIGLHDPTAHAEIMALRQGGLVMQNYRLIDATLYVTFEPCVMCAGAMI
HSRIGRVVFGVRNSKRGAAAGSLMNVLNYPGMNHRVEITEGILADECAALLCDFYRMPRQVFN
AQKKAQSSINSGSETPGTSESATPESSDSKISYETFKKHILNLAKGKGRISKTKKEYLLEERDINR
FSVQKDFINRNLVDTRYATRGLMNLLRSYFRVNNLDVKVKSINGGFTSFLRRKWKFKKERNK
GYKHAEDALIINANADFIFKEWKLDKAKKVMENQMFEKQAESMPEIETEQEYKEIFITPHQI
KHIKDFKDYKYSHRVDKKNRKLINDTLYSTRKDDKGNTLIVNNLNGLYDKDNDKLKLINK
SPEKLLMYHHPQTYQKLKLIMEQYGDEKNPLYKYEEETGNYLTKYSKKDNGPVIKKIKYYG
NKLNAHLDITDDYPNSRNKVVKLSLKPYRFDVYLDNGVYKFVTVKNLDVIKKENYYEVNSK
CYEEAKKLKKISNQAEFIASFYKNDLIKINGELYRVIGVNNDLLNRIEVNMIDITYREYLENMN
DKRPPHIIKTIASKTQSIKKYSTDILGNLYEVKSKKHPQIIKKGGSPKKKRKVSSDYKDHDGDY
KDHDIDYKDDDDKSGGSTNLSDIIEKETGKQLVIQESILMLPEEVVEEVIGNKPESDILVHTAYDE
STDENVMLLTSDAPEYKPWALVIQDSNGENKIKMLSGGSPKKKRKV

Sa-ABE-693

KRNYILGLAIGITSVGYGIIDYETRDVIDAGVRLFKEANVENNEGRRSKRGARRLKRRRRHRIQ
RVKKLLFDYNLLTDHSELGINPYEARVKGLSQKLSEEEFSAALLHLAKRRGVHNVNEVEEDT
GNELSTKEQISRNSKALEEKYVAELQLERLKKDGEVRGSINRFKTSDYVKEAKQLLKVQKAY
HQLDQSFIDTYIDLLETRRTYYEGPGEKSPFGWKDIKEWYEMLMGHCTYFPEELRSVKYAYN
ADLYNALNDLNNLVITRDENEKLEYEKFQIIENVFKQKKKPTLKQIAKEILVNEEDIKGYRVT
STGKPEFTNLKVYHDIKDITARKEIENAEELLDQIAKILTIYQSSEDIQEELTNLNSELTQEEIEQIS

NLKGYTGTHNLSLKAINLILDELWHTNDNQIAIFNRLKLVPKKVDLSQQKEIPTTLVDDFILSPV
VKRSFIQSIKVINAIKKYGLPNDIIIELAREKNSKDAQKMINEMQKRNRQTNERIEEIIIRTTGKE
NAKYLIEKIKLHDMQEGKCLYSLEAIPLEDLLNPNFYEVVDHIIPRSVSFDNSFNKVLVKQEE
NSKKGNRTPFQYLSSSDSKISYETFKKHILNLA KGKGRISKTKKEYLLEERDINRFSVQKDFINR
NLVDTRYATRGLMNLLRSYFRVNNLDVKVKSINGGFTSFLRRKWKFKKERSGSETPGTSESAT
PESSEVEFSHEYWMRHALTLAKRARDEREVPVGAVLVLNNRVIGEGWNRAIGLHDPTAHAEI
MALRQGGLVMQNYRLIDATLYVTFEPCVMCAGAMIHSRIGRVVFGVRNSKRGAAGSLMNVL
NYPGMNHRVEITEGILADECAALLCDFYRMPRQVFNAQKKAQSSINSGSETPGTSESATPESNK
GYKHAEDALIINANADFIFKEWKKLDKAKKVMENQMFEKQAESMPEIETE QEYKEIFITPHQI
KHIKDFKDYKYSHRVDKKPNRKLINDTLYSTRKDDKGNTLIVNNLNGLYDKDNDKLLKLINK
SPEKLLMYHHPQTYQKLKLIMEQYGDEKNPLYKYEEETGNYLTKYSKKDNGPVIKKIKYYG
NKLNAHLDDITDDYPNSRNKVVKLSLKPYRFDVYLDNGVYKFVTVKNLDVIKKENYYEVNSK
CYEEAKKLKKISNQAEFIASFYKNDLIKINGELYRVIGVNNDLLNRIEVMIDITYREYLENMN
DKRPPHIIKTIASKTQSIKKYSTDILGNLYEVKSKKHPQIIKKGGSPKKKRKVSSDYKDHDGDY
KDHDIDYKDDDDKSGGSTNLSDIIEKETGKQLVIQESILMLPEEVEEVIGNKPESDILVHTAYDE
STDENVMLLTSDAPEYKPWALVIQDSNGENKIKMLSGGSPKKKRKV

Sa-CABE-N

SEVEFSHEYWMRHALTLAKRARDEREVPVGAVLVLNNRVIGEGWNRAIGLHDPTAHAEIMA
LRQGGLVMQNYRLIDATLYVTFEPCVMCAGAMIHSRIGRVVFGVRNSKRGAAGSLMNVLN
PGMNHRVEITEGILADECAALLCDFYRMPRQVFNAQKKAQSSINSGSETPGTSESATPESMEAS
PASGPRHLMDPHIFTSNFNNGIGRHKTYLCYEVERLDNGTSVKMDQHRGFLHNQAKNLLCGF
YGRHAELRFLDLVPSLQLDPAQIYRVTFISWSPCFWGCAGEVRAFLQENTHVRLRIFAARIF
DYDPLYKEALQMLRDAGAQVSIMTYDEFKHCWDTFVDHQGCPFQPWDGLDEHSQALSGRLR
AILQNQGN SGSETPGTSESATPESGKRNYILGLAIGITSVGYGIIDYETRDVIDAGVRLFKEANV
ENNEGRRSKRGARRLKRRRRRHRIQRVKKLLFDYNLLTDHSELGINPYEARVKGLSQKLSEEE
FSAALLHLAKRRGVHNVNEVEEDTGNELSTKEQISRNSKALEEKYVAELQLERLKKDGEVRG
SINRFKTS DYVKEAKQLKVQKAYHQLDQSFIDTYIDLLETRRTYYEGPGE GSPFGWKDIKEW
YEMLMGHCTYFPEELRSVKYAYNADLYNALNDLNNLVITRDENEKLEYEYEFQIIENVFKQK
KKPTLKQIAKEILVNEEDIKGYRVTSTGKPEFTNLKVYHDIKDITARKEIENAELLDQIAKILTI

YQSSEDIQEELTNLNSLTQEEIEQISNLKGYTGTHNLSLKAINLILDELWHTNDNQIAIFNRLKL
VPKKVDLSQQKEIPTTLVDDFILSPVVKRSFIQSIKVINAIIKKYGLPNDIIIELAREKNSKDAQK
MINEMQKRNRQTNERIEEIIRTTGKENAKYLIEKIKLHDMQEGKCLYSLEAIPLEDLLNPNFNY
EVDHIIPRSVSFDNSFNKVLVKQEENSKKGNRTPFQYLSSSDSKISYETFKKHILNLAKGKGRI
SKTKKEYLLEERDINRFSVQKDFINRNLVDTRYATRGLMNLLRSYFRVNNLDVKVKSINGGFT
SFLRRKWKFKKERNKGYKHHAEDALIINANADFIFKEWKLDKAKKVMENQMFEEKQAESMP
EIETEQEYKEIFITPHQIKHIKDFKDYKYSHRVDKKPNRKLINDTLYSTRKDDKGNTLIVNNLNG
LYDKDNDKLLKLINKSPEKLLMYHHDPQTYQKLKLIMEQYGDEKNPLYKYEEETGNYLTKY
SKKDNGPVIKKIKYYGNKLNAHLDTDDYPNSRNKVVKLSLKPYPFDVYLDNGVYKFVTVKN
LDVIKKENYYEVNSKCYEEAKKLLKISNQAEFIASFYKNDLIKINGELYRVIGVNNDLLNRIEV
NMIDITYREYLENMNDKRPPHIIKTIASKTQSIKKYSTDILGNLYEVKSKKHPQIIKKGGSSGGST
NLSDIIEKETGKQLVIQESILMLPEEVEEVIGNKPESDILVHTAYDESTDENVMLLTSDAPEYKP
WALVIQDSNGENKIKMLSGGSPKKKRKV

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KRNYILGLAIGITSVGYGIIIDYETRDVIDAGVRLFKEANVENNEGRRSKRGARRLKRRRRHRIQ
RVKKLLFDYNLLTDHSELGINPYEARVKGLSQKLSEEEFSAALLHLAKRRGVHNVNEVEEDT
GNELSTKEQISRNSKALEEKYVAELQLERLKKDGEVRGSINRFKTSDYVKEAKQLLKVQKAY
HQLDQSFIDTYIDLLETRRTYYEGPGEGSPFGWKDIKEWYEMLMGHCTYFPEELRSVKYAYN
ADLYNALNDLNNLVITRDENEKLEYEYEFQIIEENVFKQKKKPTLKQIAKEILVNEEDIKGYRVT
STGKPEFTNLKVYHDIKDITARKEIIEAELLDQIAKILTIYQSSEDIQEELTNLNSLTQEEIEQIS
NLKGYTGTHNLSLKAINLILDELWHTNDNQIAIFNRLKLVPKKVDLSQQKEIPTTLVDDFILSPV
VKRSFIQSIKVINAIIKKYGLPNDIIIELAREKNSKDAQKMINEMQKRNRQTNERIEEIIRTTGKE
NAKYLIEKIKLHDMQEGKCLYSLEAIPLEDLLNPNFNYEVDHIIPRSVSFDNSFNKVLVKQEE
NSKKGNRTPFQYLSSSDSKISYETFKKHILNLAKGKGRIKTKKEYLLEERDINRFSVQKDFINR
NLVDTRYATRGLMNLLRSYFRVNNLDVKVKSINGGFTSFLRRKWKFKKERSGSETPGTSESAT
PESSEVEFSHEYWMRHALTLAKRARDEREVPVGAVLVLNNRVIGEGWNRAIGLHDPTAHAEI
MALRQGGLVMQNYRLIDATLYVTFEPCVMCAGAMIHSRIGRVVFGVRNSKRGAAAGSLMNVL
NYPGMNHRVEITEGILADECAALLCDFYRMPRQVFNAQKKAQSSINSGETPGTSESATPESM
EASPASGPRHLMDPHIFTSNFNNGIGRHKTYLCYEVERLDNGTSVKMDQHRGFLHNQAKNLL

CGFYGRHAELRFLDLVPSLQLDPAQIYRVTFISWSPCFSWGCAGEVRAFLQENTHVRLRIFA
 ARIFDYDPLYKEALQMLRDAGAQVSIMTYDEFKHCWDTFVDHQGCPFQPWDGLDEHSQALS
 GRLRAILQNQGNSETPGTSESATPESNKGKHHAEADALIINANADFIFKEWKKLDKAKKVME
 NQMFEKQAESMPEIETEQEYKEIFITPHQIKHIKDFKDYKYSHRVDKKPNRKLINDTLYSTRK
 DDKGNTLIVNNLNGLYDKDNDKLLKLINKSPEKLLMYHHDPQTYQKLKLIMEQYGDEKNPL
 YKYYEETGNYLTKYSKKDNGPVIKKIKYYGNKLNHLDDITDDYPNSRNKVVKLSLKPYPFDV
 YLDNGVYKFVTVKNLDVIKKENYYEVNSKCYEEAKKLKKISNQAEIFASFYKNDLIKINGELY
 RVIGVNNDLLNRIEVMIDITYREYLENMNDKRPPHIIKTIASKTQSIKKYSTDILGNLYEVKSK
 KHPQIIKKGSPKKRKVSSDYKDHDGDYKDHDIDYKDDDDKSGGSTNLSDIIEKETGKQLVI
 QESILMLPEEVEEVIGNKPESDILVHTAYDESTDENVMLLTSDAPEYKPWALVIQDSNGENKIK
 MLSGGSPKKKRKV

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