

# Supplementary Information

## Inhibition of base editors with anti-deaminases derived from viruses

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**Supplementary Figure 1.** Base editing of RmA3Bctd-, mA3CDA1- and SsA3Bctd-CBE with Ades.

**Supplementary Figure 2.** Immunoblots of A3-CBEs in the presence or absence of corresponding Ades.

**Supplementary Figure 3.** Base editing of A3-CBE chimeras.

**Supplementary Figure 4.** Ade1 and Ade2 relocalized A3Bctd- and A3A-CBEs.

**Supplementary Figure 5.** *In vitro* deaminase activity assay of A3A and A3Bctd.

**Supplementary Figure 6.** Base editing of rA1-, eAID-, eCDA1-CBE and ABE8e with Ades.

**Supplementary Figure 7.** Comparison of base editing characteristics by rA1-, A3B- and A3Bctd-CBE.

**Supplementary Figure 8.** C-to-G base editing by rA1 variants-, A3A variants-, and A3Bctd variants-CGBEs.

**Supplementary Figure 9.** Evaluation of on-target and off-target editing by A3A- and A3Bctd-CBE in HEK site4.

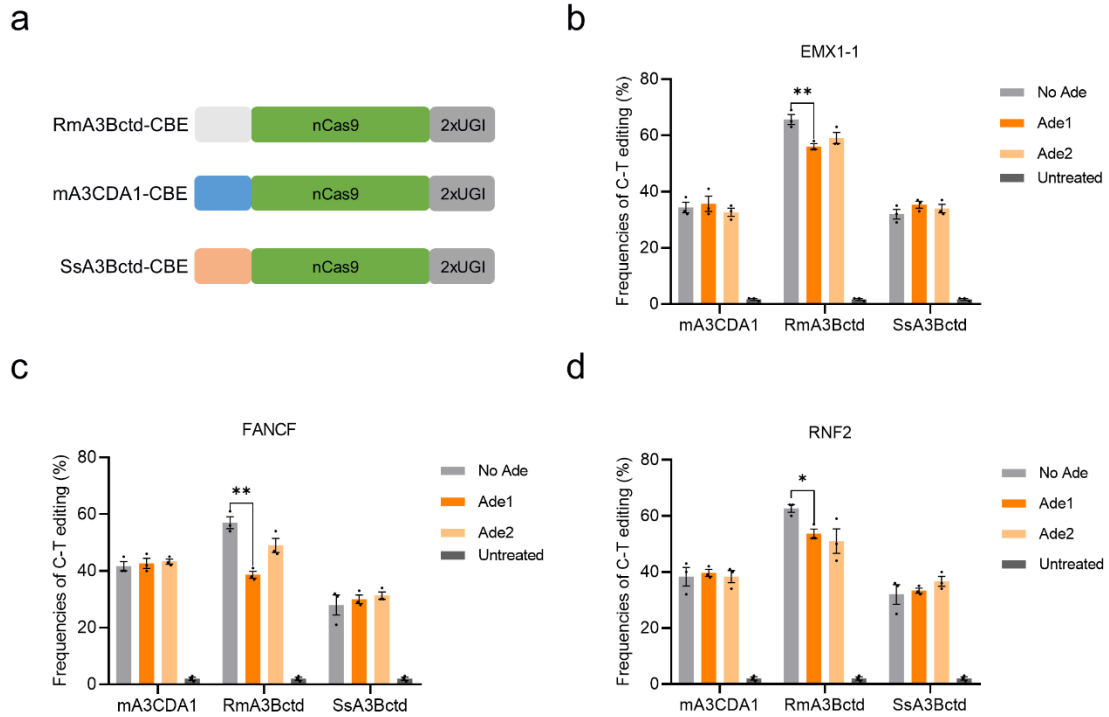
**Supplementary Figure 10.** Evaluation of on-target and off-target editing by A3G-CBE in EMX1-1.

**Supplementary Figure 11.** Ade2 moderately narrowed the C-to-T editing window of A3A-CBE.

**Supplementary Figure 12.** Base editing of A3A- and A3Bctd-CBE with both Acr and Ade.

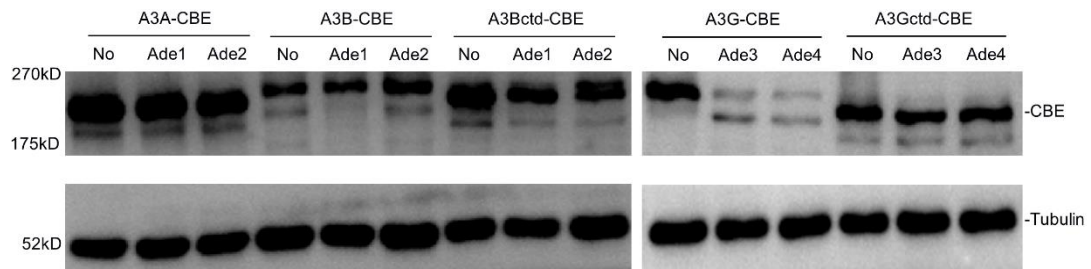
**Supplementary Table 1.** Target sites used in this study.

**Supplementary Table 2.** Primers used for genotyping in this study.

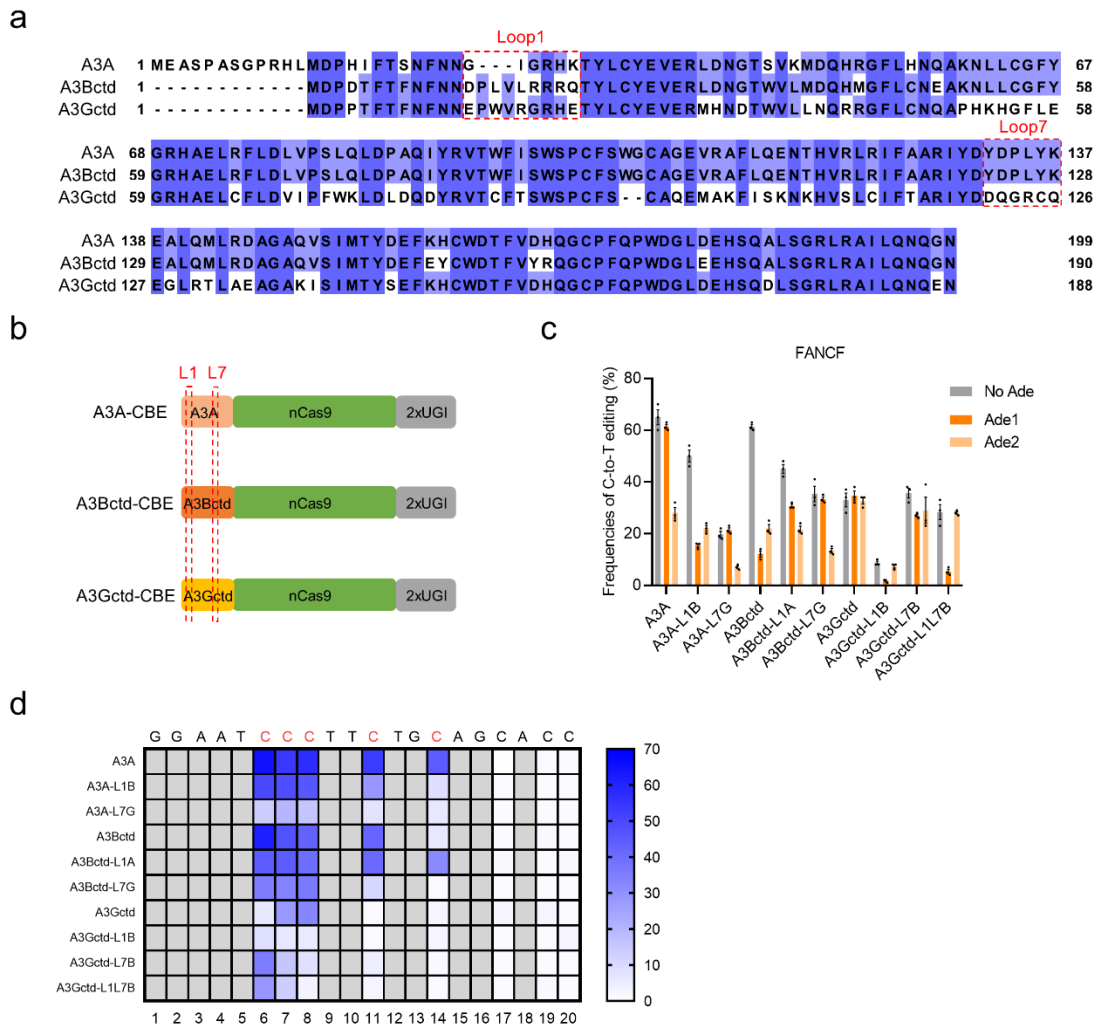


**Supplementary Figure 1.** Base editing of RmA3Bctd-, mA3CDA1- and SsA3Bctd-CBE with Ades.

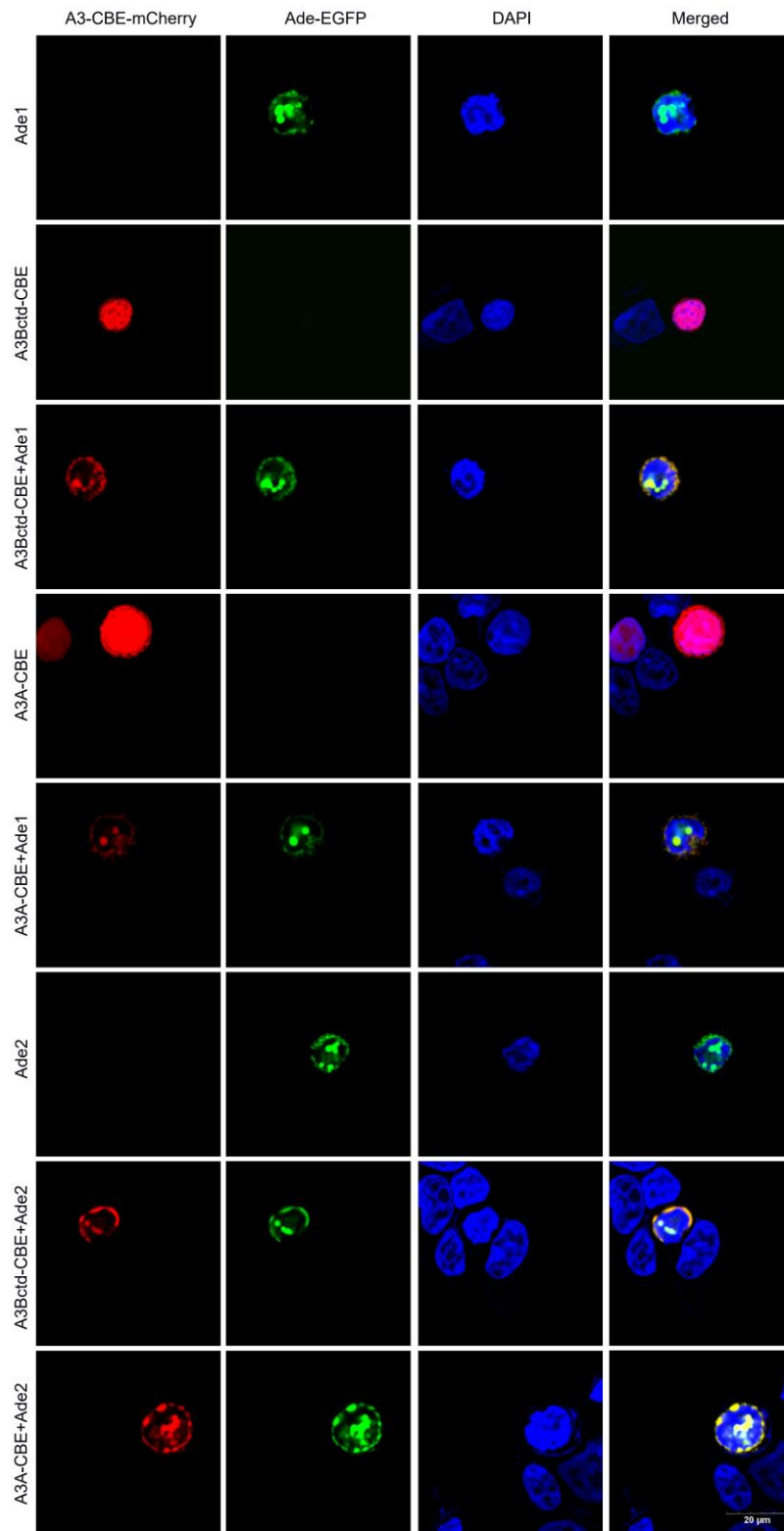
**a** Schematic representation of RmA3Bctd-, mA3CDA1- and SsA3Bctd-CBE. nCas9, D10A. **b-d** Base editing of these three CBEs in the presence or absence of the Ade1 and Ade2 at EMX1-1, FANCF and RNF2 site. Values and error bars reflect the mean  $\pm$  s.e.m. and  $n=3$  biologically independent experiments. All  $p$  values were calculated by two-sided t tests.  $*p < 0.05$ ,  $**p < 0.01$ . Source data are provided as a Source Data file.



**Supplementary Figure 2.** Immunoblots of A3-CBEs in the presence or absence of corresponding Ades. Tubulin was used as a loading control. The western blot experiments were repeated three times independently with similar results.

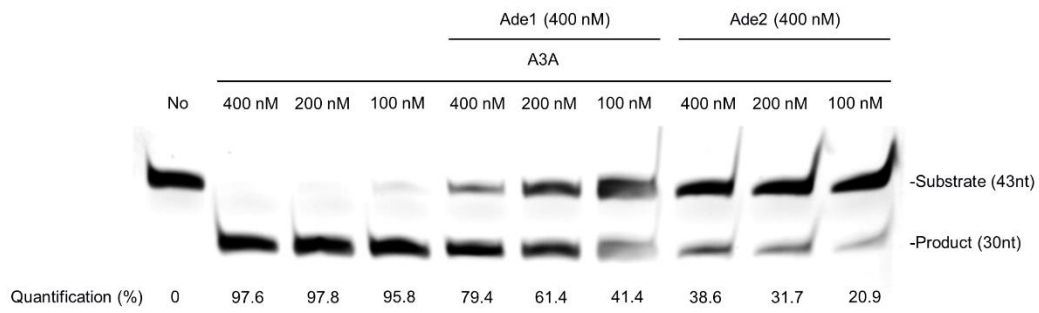


**Supplementary Figure 3.** Base editing of A3-CBE chimeras. **a** Amino acid sequence alignment of A3A, A3Bctd and A3Gctd. Alignment was performed with NCBI COBALT and rendered using Jalview. The L1 and L7 are shown in red rectangle. **b** Schematic representation of A3-CBE chimeras by exchanging L1 and L7 among A3A, A3Bctd and A3Gctd. nCas9, D10A. **c** Base editing of A3-CBE chimeras in the presence or absence of the Ade1 and Ade1 at FANCF site. **d** Heat map showing summary of C-to-T editing frequencies on each base for these A3-CBE chimeras at FANCF site. Values and error bars reflect the mean  $\pm$  s.e.m. and  $n=3$  biologically independent experiments. Source data are provided as a Source Data file.

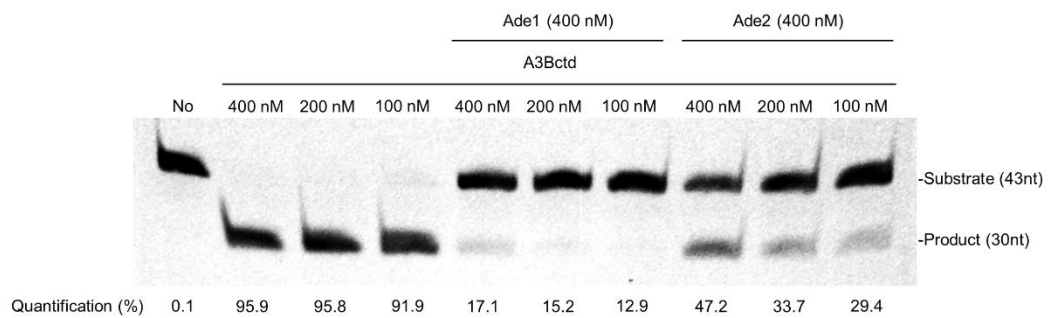


**Supplementary Figure 4.** Ade1 and Ade2 relocalized A3Bctd- and A3A-CBEs. Representative images of HEK293T cells expressing the indicated A3-CBE-mCherry constructs alone or in combination with Ade-EGFP constructs. The immunofluorescence microscopy experiments were repeated three times independently with similar results.

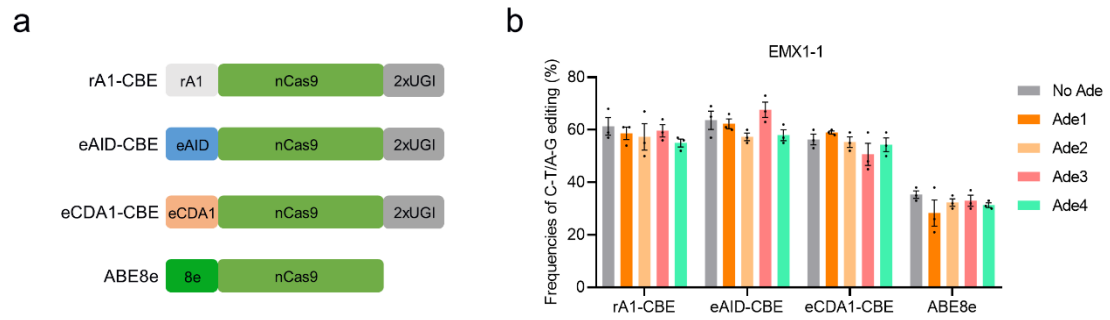
**a**



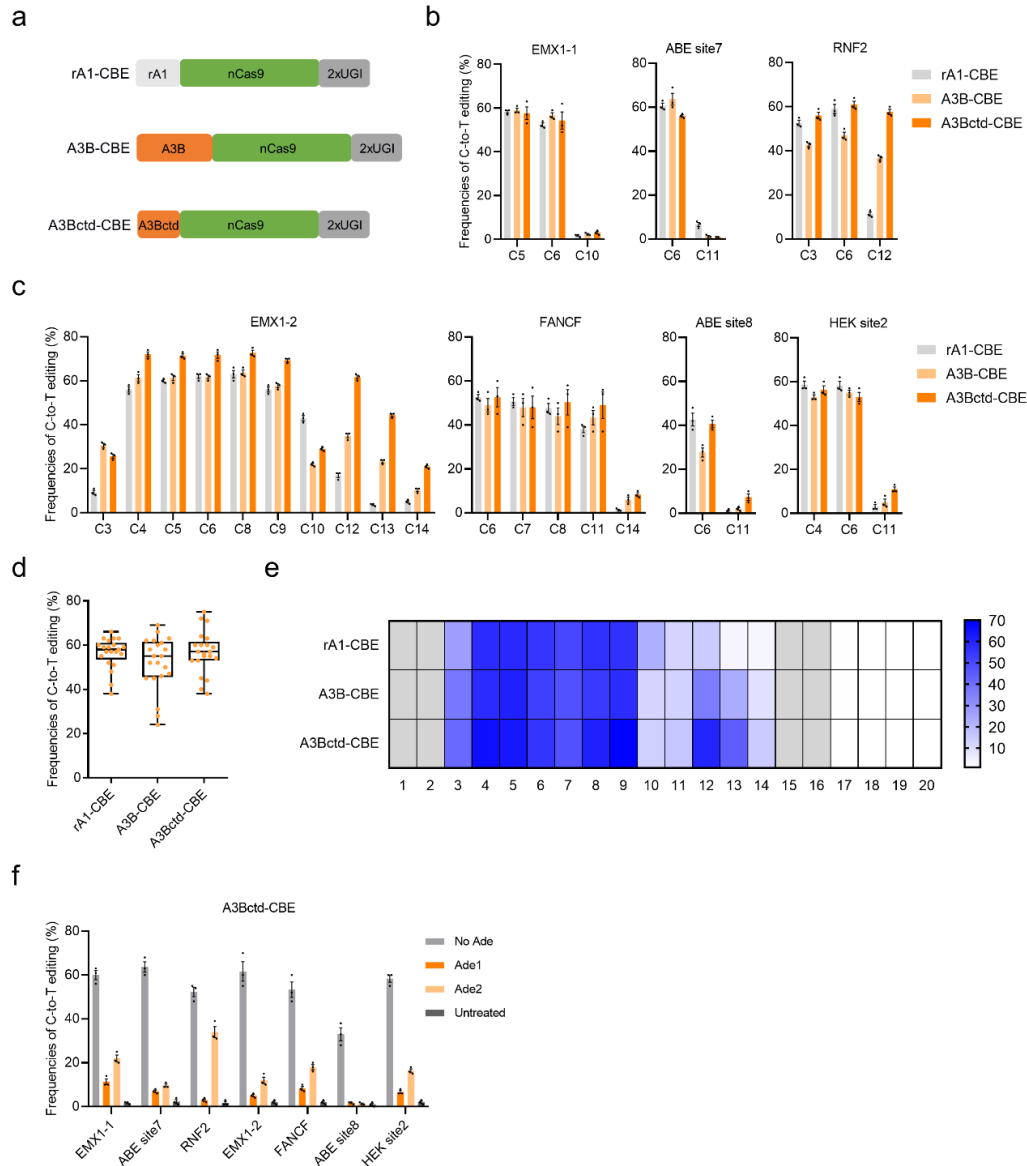
**b**



**Supplementary Figure 5.** *In vitro* deaminase activity assay of A3A and A3Bctd. TBE-urea PAGE analysis of A3A (**a**) and A3Bctd (**b**) deaminase activity in the presence of Ade1 or Ade2 (product percentage indicated below each lane). The experiment was repeated three times independently with similar results.

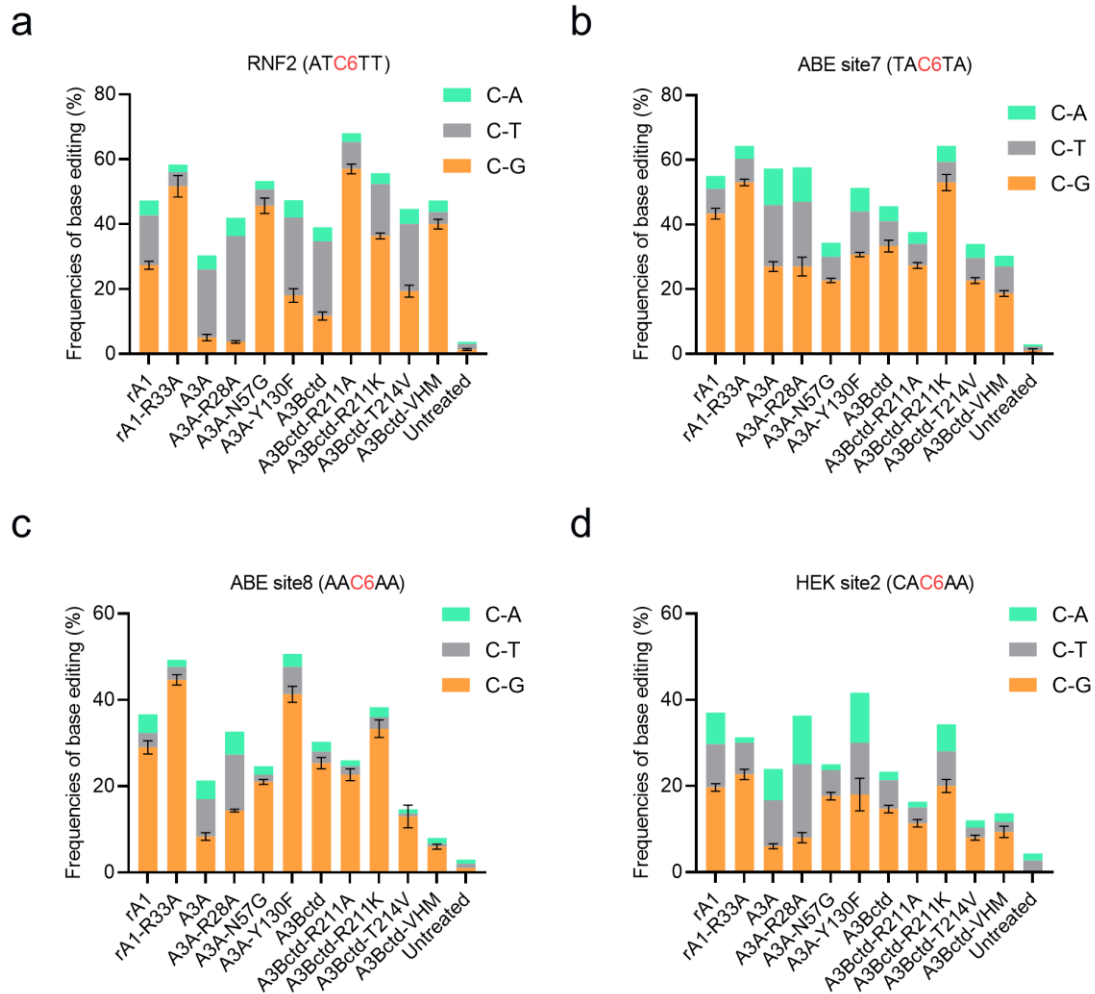


**Supplementary Figure 6.** Base editing of rA1-, eAID-, eCDA1-CBE and ABE8e with Ades. **a** Schematic representation of rA1-, eAID-, eCDA1-CBE and ABE8e. nCas9, D10A. **b** Base editing of these four BEs in the presence or absence of the Ade1-Ade4 at EMX1-1 site. Values and error bars reflect the mean  $\pm$  s.e.m. and  $n=3$  biologically independent experiments. Source data are provided as a Source Data file.

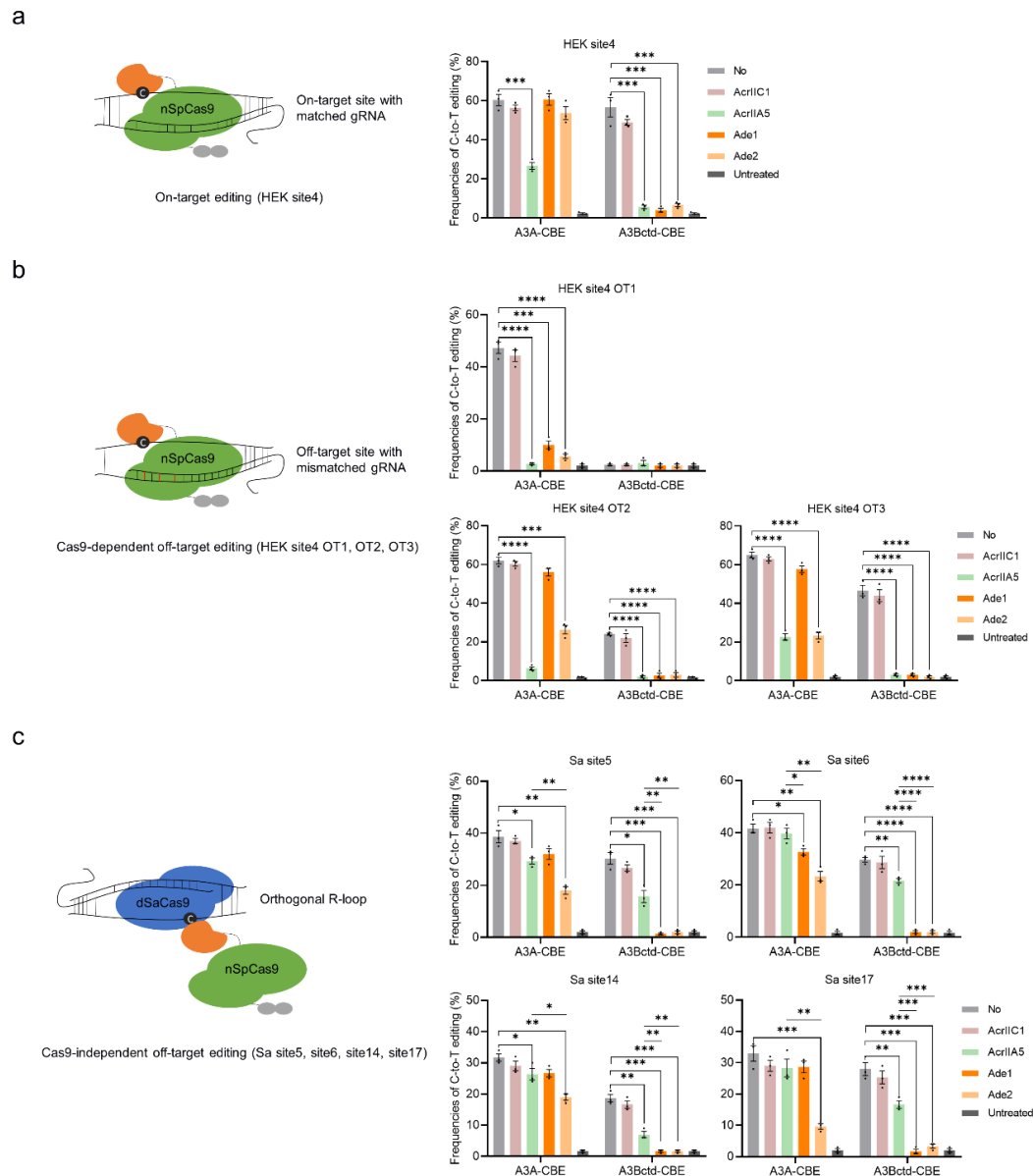


**Supplementary Figure 7.** Comparison of base editing characteristics by rA1-, A3B- and A3Bctd-CBE. **a** Schematic representation of rA1-, A3B- and A3Bctd-CBE. nCas9, D10A. **b-c** Summary of C-to-T editing frequencies induced by rA1-, A3B- and A3Bctd-CBE systems on each cytosine at seven target sites. **d** Summary of average C-to-T editing frequencies induced by rA1-, A3B- and A3Bctd-CBE systems at seven target sites in **(b)** and **(c)**. The center line indicates the median, and the bottom and top lines of the box represent the minima and maxima, respectively. **e** Heat map showing summary of C-to-T editing frequencies on each base for rA1-, A3B- and A3Bctd-CBE. **f** Base editing of A3Bctd-CBE in the presence or absence of the Ade1 and Ade2 at seven sites. Values and error bars reflect the mean  $\pm$  s.e.m. and  $n=3$  biologically independent experiments. Source data are provided as a Source Data file.

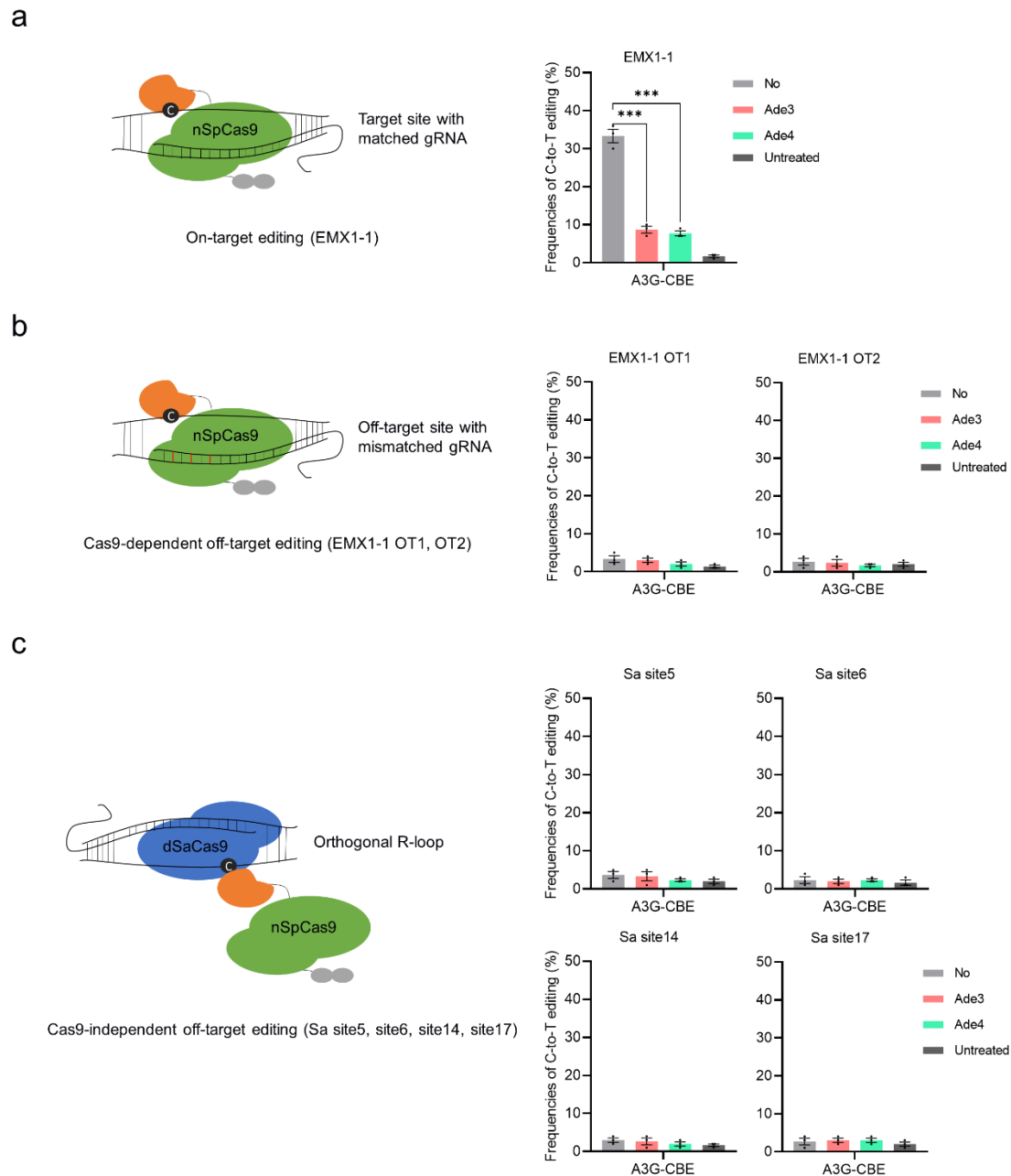




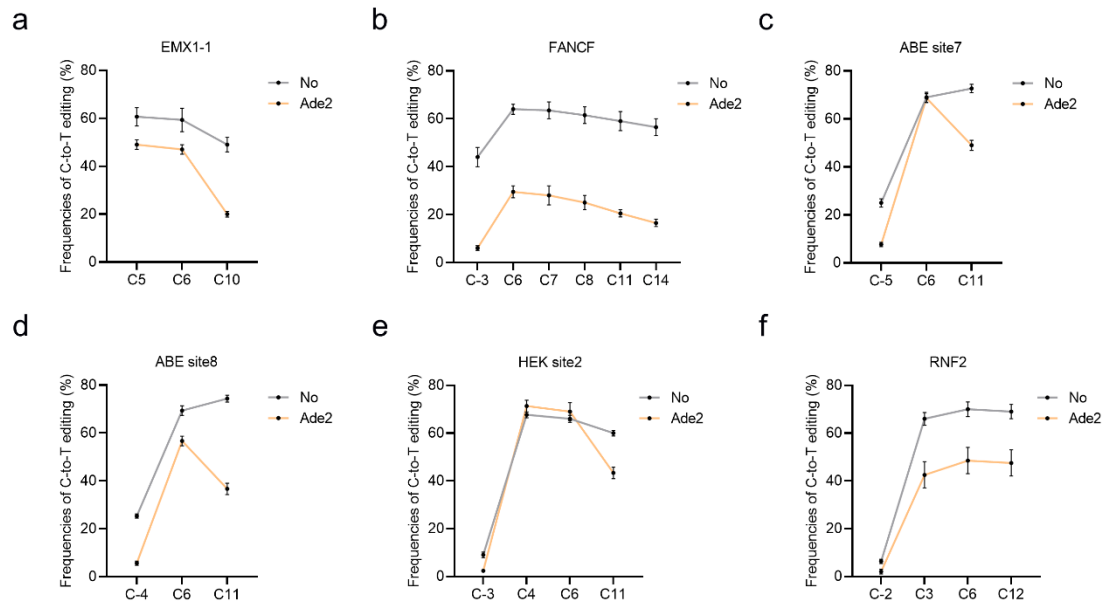
**Supplementary Figure 8.** C-to-G base editing by rA1 variants-, A3A variants-, and A3Bctd variants-CGBEs. **a-d** Bar plots showing the base editing frequencies induced by rA1 variants-, A3A variants-, and A3Bctd variants-CGBEs at RNF2, ABE site7, ABE site8 and HEK site2. Target C, red. Plasmids expressing CGBE, sgRNA, and Ade (1:1:1) were co-transfected into HEK293T cells. Values and error bars reflect the mean  $\pm$  s.e.m. and  $n=3$  biologically independent experiments. Source data are provided as a Source Data file.



**Supplementary Figure 9.** Evaluation of on-target and off-target editing by A3A- and A3Bctd-CBE in HEK site4. **a** On-target editing frequencies of A3A and A3Bctd-CBE in the presence or absence of the AcrlIC1 (as a negative control), AcrlIA5, Ade1 and Ade2 at HEK site4. **b** The Cas9-dependent OT editing frequencies of A3A and A3Bctd-CBE in the presence or absence of the AcrlIC1 (as a negative control), AcrlIA5, Ade1 and Ade2 at OT1-OT3 sites. **c** The Cas9-independent OT editing frequencies of A3A and A3Bctd-CBE in the presence or absence of the AcrlIC1 (as a negative control), AcrlIA5, Ade1 and Ade2 at Sa site5, site6, site14 and site17. Values and error bars reflect the mean  $\pm$  s.e.m. and  $n=3$  biologically independent experiments. All  $p$  values were calculated by two-sided  $t$  tests.  $*p < 0.05$ ,  $**p < 0.01$ ,  $***p < 0.001$ ,  $****p < 0.0001$ . Source data are provided as a Source Data file.

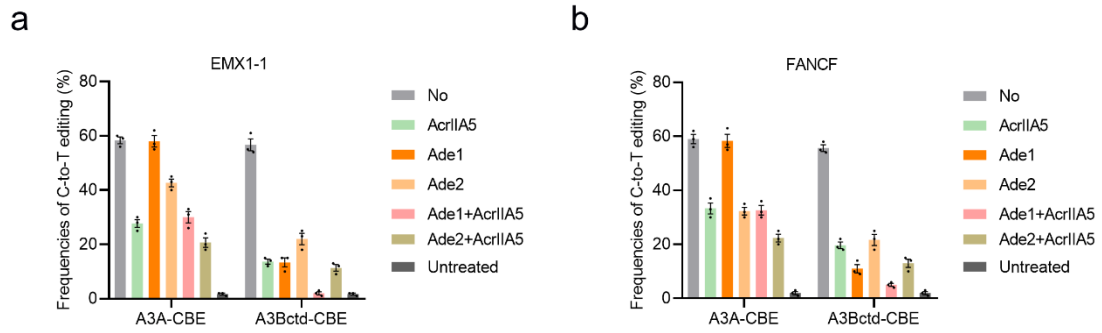


**Supplementary Figure 10.** Evaluation of on-target and off-target editing by A3G-CBE in EMX1-1. **a** On-target editing frequencies of A3G-CBE in the presence or absence of the Ade3 and Ade4 at EMX1-1 site. **b** The Cas9-dependent OT editing frequencies of A3G-CBE in the presence or absence of the Ade3 and Ade4 at EMX1-1 OT1 and OT2 site. **c** The Cas9-independent OT editing frequencies of A3G-CBE in the presence or absence of the Ade3 and Ade4 at Sa site5, site6, site14 and site17. Values and error bars reflect the mean  $\pm$  s.e.m. and  $n=3$  biologically independent experiments. All  $p$  values were calculated by two-sided t tests.  $*p < 0.05$ ,  $**p < 0.01$ ,  $***p < 0.001$ ,  $****p < 0.0001$ . Source data are provided as a Source Data file.



**Supplementary Figure 11.** Ade2 moderately narrowed the C-to-T editing window of A3A-CBE.

**a-f** Frequencies of single C-to-T conversions using A3A-CBE in the presence or absence of Ade2 at six target sites. Values and error bars reflect the mean  $\pm$  s.e.m. and  $n=3$  biologically independent experiments. Source data are provided as a Source Data file.



**Supplementary Figure 12.** Base editing of A3A- and A3Bctd-CBE with both Acr and Ade. **a-b** Base editing of A3A- and A3Bctd-CBE in the presence or absence of the AcrIIA5 alone, Ade1 alone, Ade2 alone, Ade1+AcrIIA5 and Ade2+AcrIIA5 at EMX1-1 and FANCF site. Values and error bars reflect the mean  $\pm$  s.e.m. and n=3 biologically independent experiments. Source data are provided as a Source Data file.

**Supplementary Table 1.** Target sites used in this study. Target sequence (black), PAM region (green).

Target site	Sequence (5'-3')
EMX1-1	GAGTCCGAGCAGAAGAAGAAGGG
FANCF	GGAATCCCTTCTGCAGCACCTGG
EMX1-2	TGCCCTCCCTCCCTGGCCAGG
RNF2	GTCATCTTAGTCATTACCTGAGG
ABE site7	GAATACTAAGCATAGACTCCAGG
ABE site7	GTAACAAAAGCATAGACTGAGGG
HEK site2	GAACACAAAAGCATAGACTGC GGG
HEK site4	GGCACTGCGGCTGGAGGTGGGG
EMX1-1 OT1	GAGTCTAAGCAGAAGAAGAAGAG
EMX1-1 OT2	GAATCCAAGCAGAAGAAGAGAAG
HEK site4 OT1	GCACTGCAGCTGGAGGTGGGG
HEK site4 OT2	GGCACGACGGCTGGAGGTGGGG
HEK site4 OT3	GGCATCACGGCTGGAGGTGGAGG
Sa site5	TCTGCTTCTCCAGCCCTGGCCTGGGT
Sa site6	GATGTTCCAATCAGTACGCAGAGAGT
Sa site14	GGCCTCCGTATCACTCTCTGACTGGGGT
Sa site17	GGTCGTAGCCAGTCCGAACCCGGAGT

**Supplementary Table 2.** Primers used for genotyping in this study.

Primers	Sequence (5'-3')	Product size (bp)	Target sites
EMX1-F: EMX1-R:	CCTTCTGTGAATGTTAGACCCA TGCTTGTCCCTCTGTCAATG	520	EMX1-1, EMX1-2
FANCF-F: FANCF-R:	ATCTGCTCTCCCTCCACTAA GGCCTGGAAGTTCGCTAAT	483	FANCF
RNF2-F: RNF2-R:	GTCTTCCTTGGTGCCTTATCA TGGTGGGACACATACATTCAAG	524	RNF2
AS7-F: AS7-R:	CATCTTCTCCGCAGACAGAAATA TCCTGCCCTTAGGTCAAATAAC	465	ABE site7
AS8-F: AS8-R:	CATACTTAAAGTAAAGCAGAAGGAATAACAGTGC GAAGTTTCATTCCACTATAGAACTGGTTCTG	225	ABE site8
HS2-F: HS2-R:	GGACGTCTGCCCAATATGTAA GCATTAATCCACAGCAACACC	455	HEK site2
HS4-F: HS4-R:	CCCTTCAAGATGGCTGACAA TTTCAACCCGAACGGAGAC	230	HEK site4
E-OT1-F: E-OT1-R:	GCTTCTTGTCTTTGGCTTTCT AGGGTATAGTTGAGGTGGGATA	476	EMX1-1 OT1
E-OT2-F: E-OT2-R:	CATCTTCTGCTGGTCCGATTA GATCAGGGCGAGATTAGAGTTG	407	EMX1-1 OT2
H-OT1-F: H-OT1-R:	CAGTGGCTCATCCCTGTAATTC CCACACACAATCCAAACAAAGG	407	HEK site4 OT1
H-OT2-F: H-OT2-R:	GGTTGCCTTTCTCCTTGGT GTCCAGATTCTCTGGTGTGTG	403	HEK site4 OT2
H-OT3-F: H-OT3-R:	GTATCCTGTTATCTGTTGCTGAAATG CAGGTGTGGAAGAGAAATGAAATG	409	HEK site4 OT3
Sa5-F: Sa5-R:	ATGTGGGCTGCCTAGAAAGG CCCAGCCAAACTTGTC AAC	297	Sa site5
Sa6-F: Sa6-R:	TAGGATGCCCTACATCTGCTCTC CGGAAAAGCGATCCAGGTGC	278	Sa site6
Sa14-F: Sa14-R:	CCCACAGACTAGCCAAGAAAC CCTTCTCTTGAACCAACTCCTATAC	401	Sa site14
Sa17-F: Sa17-R:	GGCTGTCTTGGGATGTTTCT GGCCAGTGGAGGATCTTTATTAG	271	Sa site17

## Supplementary sequence

### A3A:

MEASPASGPRHLMDPHIFTSNFNNGIGRHKTYLCYEVERLDNGTSVKMDQHRGFLHNQA  
KNLLCGFYGRHAELRFLDLVPSLQLDPAQIYRVTFWISWSPCFSWGCAGEVRAFLQENTH  
VRLRIFAARIYDYDPLYKEALQMLRDAGAQVSIMTYDEFKHCWDTFVDHQGCPFQPWDG  
LDEHSQALSGLRRAILQNQGN

### A3B:

MNPQIRNPMERMYRDTFYDNFENEPILYGRSYTWLCYEVKIKRGRSNLLWDTGVFRGQV  
YFKPQYHAEMCFLSWFCGNQLPAYKCFQITWFVSWTPCPCVAKLAEFLSEHPNVTLTIS  
AARLYYYWERDYRRALCRLSQAGARVKIMDYEEFAYCWENFVYNEGQQFMPWYKFNDE  
NYAFLHRTLKEILRYLMDPDTFTFNFNNDPLVLRRRQTYLCYEVERLDNGTWVLMQHM  
GFLCNEAKNLLCGFYGRHAELRFLDLVPSLQLDPAQIYRVTFWISWSPCFSWGCAGEVRA  
FLQENTHVRLRIFAARIYDYDPLYKEALQMLRDAGAQVSIMTYDEFEYCWDTFVYRQGC  
PFQPWDGLEEHSQALSGLRRAILQNQGN

### A3Bctd:

MDPDTFTFNFNNDPLVLRRRQTYLCYEVERLDNGTWVLMQHMFLCNEAKNLLCGFY  
GRHAELRFLDLVPSLQLDPAQIYRVTFWISWSPCFSWGCAGEVRAFLQENTHVRLRIFAAR  
IYDYDPLYKEALQMLRDAGAQVSIMTYDEFEYCWDTFVYRQGC PFQPWDGLEEHSQALS  
GRLRAILQNQGN

### A3G:

MKPHFRNTVERMYRDTFSYNFYNRPILSRRNTVWLCYEVKTKGPSRPPLDAKIFRGQVYS  
ELKYHPEMRFFHWFSKWRKLHRDQEYEV TWYISWSPCTKCTRDMATFLAEDPKVTLTIF  
VARLYYFWDPDYQEALRSLCQKRDGPRATMKIMNYDEFQHCWSKFVYSQRELFEPWNN  
LPKYIILLHIMLGEILRHSMDPPTFTFNFNNEPWVRGRHETYLCYEVERMHNDTWVLLN  
QRRGFLCNQAPHKHGFLEGRHAELCFLDVIPFWKLDLDQDYRVTCFTSWSPCFSCAQEM  
AKFISKKNKHVSLCIFTARIYDDQGRCQEGLRTLAEAGAKISIMTYSEFKHCWDTFVDHQGC  
PFQPWDGLDEHSQDLSGRLRAILQNQEN

### A3Gctd:

MDPPTFTFNFNNEPWVRGRHETYLCYEVERMHNDTWVLLNQRRGFLCNQAPHKHGFLE  
GRHAELCFLDVIPFWKLDLDQDYRVTCFTSWSPCFSCAQEMAKFISKKNKHVSLCIFTARIY  
DDQGRCQEGLRTLAEAGAKISIMTYSEFKHCWDTFVDHQGCPFQPWDGLDEHSQDLSGR  
LRAILQNQEN

### Ade1 (EBV-BORF2):

MATTSHVEHELLSKLIDELKVKANS DPEADVLAGRLLHRLKAESVTHTVAEYLEVFSDFK  
YDEEFFQMHRDELETRVSAFAQSPAYERIVSSGYLSALRYDYTYLYVGRSGKQESVQHFY  
MRLAGFCASTTCLYAGLRAALQRARPEIESDMEVFDYFEHLTSQTVCCSTPFMRFAGVE  
NSTLASCILTPDLSSEWDVTQALYRHLGRYLFQRAGVGVGVTGAGQDGKHISLLMRMIN  
SHVEYHNYGCKRPVSVAAYMEPWHSQIFKFLETCLPENHERCPGIFTGLFVPELFFKLFRD  
TPWSDWYLFDPKDAGDLERLYGEEFEREYRLV TAGKFCGRVSIKSLMFSIVNCAVKAGS  
PFILLKEACNAHFWRDLQGEAMNAANLCAEVLQPSRKS VATCNLANICLPRCLVNAPLAV



RAQRADTQGDELLLALPRLSVTLPGEGAVGDGFSLARLRDATQCATFVVACSILQGSPTYD  
SRDMASMLGVQGLADVFDLWQYTDPPSRSLNKEIFEHMYFTALCTSSLIHLHTRKIF  
PGFKQSKYAGGWFWHDWAGTDLSPREIWSRLSERIVRDGLFNSQFIALMPTSGCAQVT  
GCSDAFYFPYANASTKVTNKEEALRPNRSFWRHVRLDDREALNLVGGRRVSLPEALRQR  
YLRFQTAFDYNQEDLIQMSRDRAPFVDQSQSHSLFLREEDAARASTLANLLVRSYELGLK  
TIMYYCRIEKAADLGVMECKASAALSVPREEQNERSPAEQMPPRMEPAQVAGPVDIMSK  
GPGEPPGGWCVPGGLEVCYKYRQLFSEDDLLETGDFTERACESCQ

**Ade2 (KSHV-ORF61):**

MSVRTFCQVHLGAVPPERRGSQVSAGQLSDFDMCAQSLIDFLKVRVGVWDVRANAMAGR  
LWHQIMEARCPATLKQYLGIFRGVLGHRVESFIQKNIDALEDMLCAYRRSKAYEDTLNCG  
YLSAVRLYDITYVLRTMGTEPVYESVAQMFMRVSVFVACQCLEHECLYWLARDLIEDAKS  
VSEMAIVEYVFGYLAQAHVCCATPILRSAGVEGGQLASCFILQPSMMNEPGTLDALYHD  
MSPLLASKSGVGLDVTSFSHQKNIASCLKLVDAQVHYFNDNNIRPVGASAYMELWHSQIC  
DFLNAKLPENPDRCHSLFQGVCIPTLFFRMYEKDPSKLWYLFDPATAPNLIKLYGAAFDNE  
YERLVRAGKYVSCMPLKSMFTLIHTIITGSPYVLLKEALNEHHWTDQTQMAINCSNLC  
AEIVQLPGRNTSVCNLANICLPKCLRTVESARVGTDDANRPFFCFEALGDAVRVAVLVINA  
CILGGSHPTPGVERGQKERSMGIGVQGLADVFAELGYGYLDAESAELDKNIFQSMYYTAV  
ETSHNLVLEGQGVPHGWEVSNFAKGRFWQWEGEDASFVPRHRWDALGKSIAEHGIF  
NSQFLAVMPTAGTSQVTGYAESVYPPFANISSKVTNKEEVLRPNVTFFKKVLPDDLRRVVRQ  
YGGDVSTFPKHHRERYRVFLTAFDYCPFKLLDRARARAPFVDQSQSMSFFLKEDRVRNAS  
YLRDLLLHGYYRLGLKTLMYYCRVQKQSSLTALQCLADPGSPPHSGMKQDGAWLPGPKNP  
EEESCAADPECLVCQ

**Ade3 (HIV-1-Vif):**

MENRWQVMIVWQVDRMRIRTWKSLVKHHMYVSGKARGWFWYRHHYESPHPRISSEVHIP  
LGDARLVITTYWGLHTGERDWHLGQGVSIERWKKRYSTQVDPPELADQLIHLYYFDCFS  
SAIRKALLGHIVSPRCEYQAGHNKVGSLQYLALALITPKKIKPPLPSVTKLTEDRWKPKQ  
KTKGHRGSHTMNGH

**Ade4 (SIVmac239-Vif):**

MEEEKRWIAVPTWRIPERLERWHSLIKYLKYKTKDLQKVCYVPHFKVGVWAWWTCSRVI  
PLQEGSHLEVQGYWHLTPEKGWLSYAVRITWYSKNFWTDVTPNYADILLHSTYFPCFTA  
GEVRRAIRGEQLLSCCRFPRAHKYQVPSLQYLALKVSDVRSQGENPTWKQWRRDNRR  
GLRMAKQNSRGDKQRGGKPPTKGANFPGLAKVLGILA

**Ade5 (HSV-1-ICP6):**

MASRPAASSPVEARAPVGGQEAGGPSAATQGEAAGAPLAHGHVYVCQRVNGVMVLSK  
TPGSASYRISDSNFVQCGSNCTMIIDGDVVRGRPDGAAASPAPFVAVTNIGAGSDGGTA  
VVAFGGTPRRSAGTSTGTQTADVPTALGGPPPPRFTLGGGCCSCRDRRRSAVFGGED  
PVGPAEFVSDDRSSDSDDSEDTDSETLSHASSDVSGGATYDDALDSSSSDDSLQIDG  
PVCRPWSNDTAPLDVCPGTPGADAGGPSAVDPHAPTPEAGAGLAADPAVARDDAEG  
SDPRPRLGTGTAYPVPLELTPENAEAVARFLGDVNNREPALMLEYFCRCAREETKRVPPRT  
GSPPRLTEDDFGLLNYALVEMQRLCLDVPPVPPNAYMPYYLREYVTRLVNGFKPLVSRSA

RLYRILGVLVHLRIRTREASFEEWLSKEVALDFGLTERLREHEAQLVILAQALDHYDCLIH  
STPHTLVERGLQSALKYEEFYLKRFGGHYMESVFMQMYTRIAGFLACRATRGMRHIALGRE  
GSWWEMFKFFFHRLYDHQIVPSTPAMLNLGTRNYTSSCYLVNPQATTNKATLRAITSNV  
SAILARNGGIGLCVQAFNDSGPGTASVMPALKVLDSLVAAHNKESARPTGACVYLEPWHT  
DVRAVLRMKGVLAGEEAQRCDNIFSAWMPDLFFKRLIRHLDGKENVTWTLFDRDTSMS  
LADFHGEEFEKLYQHLEVMGFGEQIPIQELAYGIVRSAATTGSPFVMFKDAVNRHYIYDTQ  
GAAIAGSNLCTEIVHPASKRSSGVCNLGVSNLARCVSRQTFDFGRLRDAVQACVLMVNIM  
IDSTLQPTPQCTRGNLNRSMGIGMQGLHTACLKGLDLESAEFQDLNKHIAEVMLLSAM  
KTSNALCVRGARPFNFHFKRSMYRAGRFRHWERFPDARPRYEGEWEMLRQSMMKHGLRN  
SQFVALMPTAASAQISDVSEGFAPLFTNLFSKVTRDGETLRPNTLLLKELERTFSGKRLLLEV  
MDSLDAKQWSVAQALPCLEPHPLRRFKTAFDYDQKLLIDLCADRAPYVDHSQSMTLYV  
TEKADGTLPASTLVRLLVHAYKRGLKTGMYYCKVRKATNSGVFGGDDNIVCMSCAL

**Ade6 (EV71-2C):**

MSASWLKKFNDMANAAKGLEWISSKISKFIDWLKEKIIPAAREKVEFLNNLKQLPLENQI  
SNLEQSAASQEDLEAMFGNVSYLAHFRCRKFQPLYATEAKRVYALEKRMNNYMQFKSKHR  
IEPVCLIRGSPGTGKSLATGIIARAIADKYHSSVYSLPPDPDHFHDGYKQQVVMVMDDLCQ  
NPDGKDISLFCQMVSTVDFIPPMASLEEKGVSTSKFVIASTNSSNIIVPTVSDSDAIRRRFY  
MDCDIEVTDSYKTDLGRDLAAGRAAKLCSNNTANFKRCSPLVCGKAIQLRDRKSKVRYS  
VDTVVSSELIREYNNRSAIGNTIEALFQ

**Ade7 (HBV-HBx):**

MAARLCCQLDPARDVLCLRPVGAESRGRPLAGPLGALPPASPPVLPTDHGAHLSLRGLPV  
CAFSSAGPCALRFTSARRMETTVNAHRNLPKVLHKRTLGLSAMSTTDLEAYFKDCVFNE  
WEELGEEVRLKVFVLGGCRHKLVCSPAPCNFF TSA

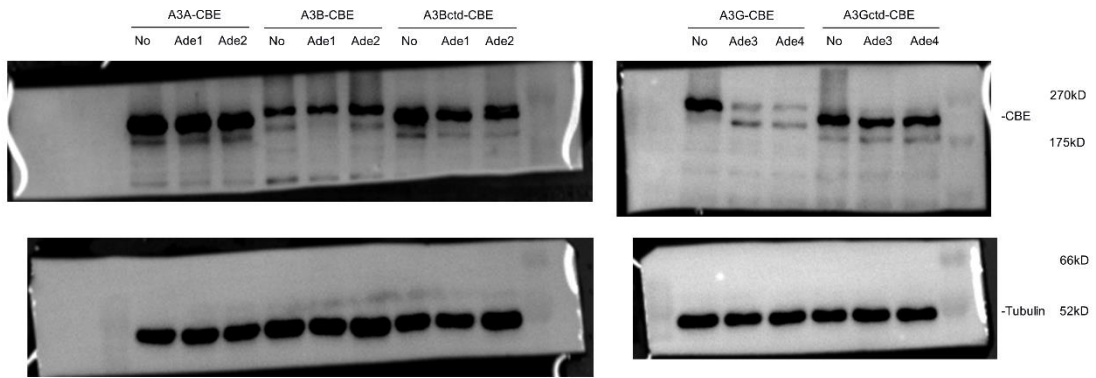
**AcrIIC1:**

MANKTYKIGKNAGYDGCGLCLAAISENEAIKVKYLRDPCPDYDGDDKAEDWLRWGTDS  
RVKAAALEMEQYAYTSVGMASCWEFVEL

**AcrIIA5:**

MAYGKSRYNSYRKRSFNRSNKQRREYAQEMDRLEKAFENLDGWYLSMKDSAYKDFGK  
YEIRLSNHSADNKYHDLENGRLIVNIKASKLNFVDIIENKLDKIIKIDKLDLTKYRFINATN  
LEHDIKCYYKGFKTKKEVI

## Raw Images for Supplementary Figure 2



## Raw Images for Supplementary Figure 5a



## Raw Images for Supplementary Figure 5b

