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Supplemental information

**Replacing the *SpCas9* HNH domain
by deaminases generates compact base
editors with an alternative targeting scope**

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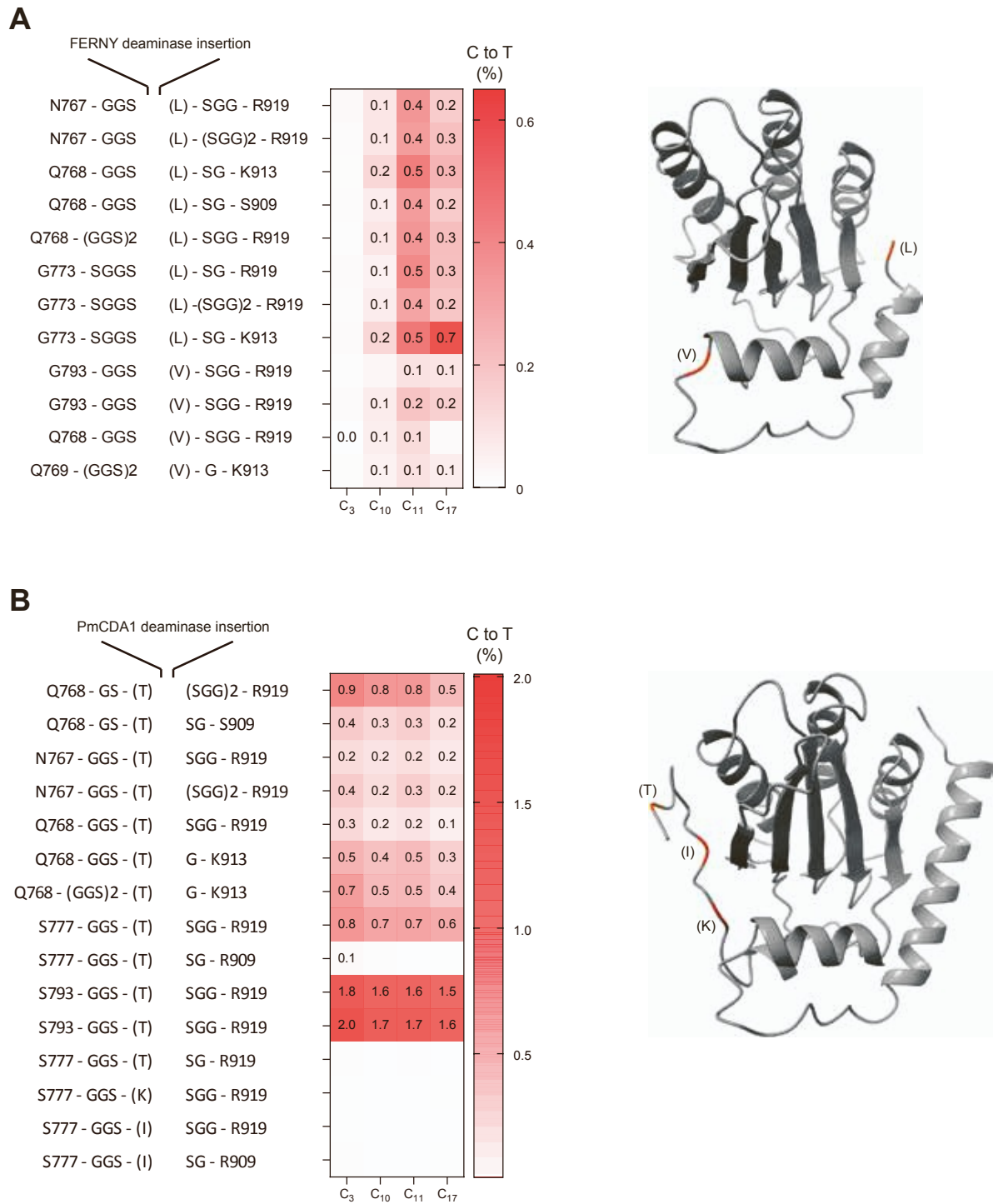


Figure S2. Linker optimization for FERNY and PmCDA1 integration (A, B) Heat map depicting different flanking amino acids of Cas9 and linkers to incorporate the FERNY (A) and PmCDA1 (B) deaminases in place of the HNH domain. The FERNY and PmCDA1 deaminase reading frames are listed in the Supplementary Information. Linkers that join Cas9 and deaminase at different amino acid positions within the deaminase are indicated in brackets.

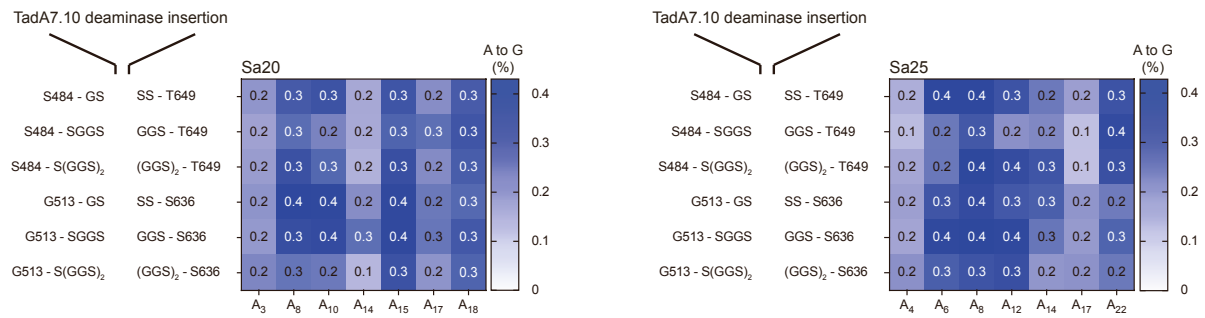


Figure S3. *Sa*KKH-HNHx-ABEmax7.10 constructs Heat map depicting editing efficiencies with *Sa*KKH-HNHx-ABEmax7.10 constructs, where different linkers were used to incorporate the TadA deaminase in place of the HNH domain of *Sa*Cas9-KKH. Editing efficiencies of different adenine bases within the protospacer region on endogenous loci Sa20 (left) and Sa25 (right) in HEK293T cells. Numbering starts with PAM-distal nucleotides. Values represent mean of two independent biological replicates performed on separate days \pm s.d. The TadA deaminase reading frame is listed in the Supplementary Information.

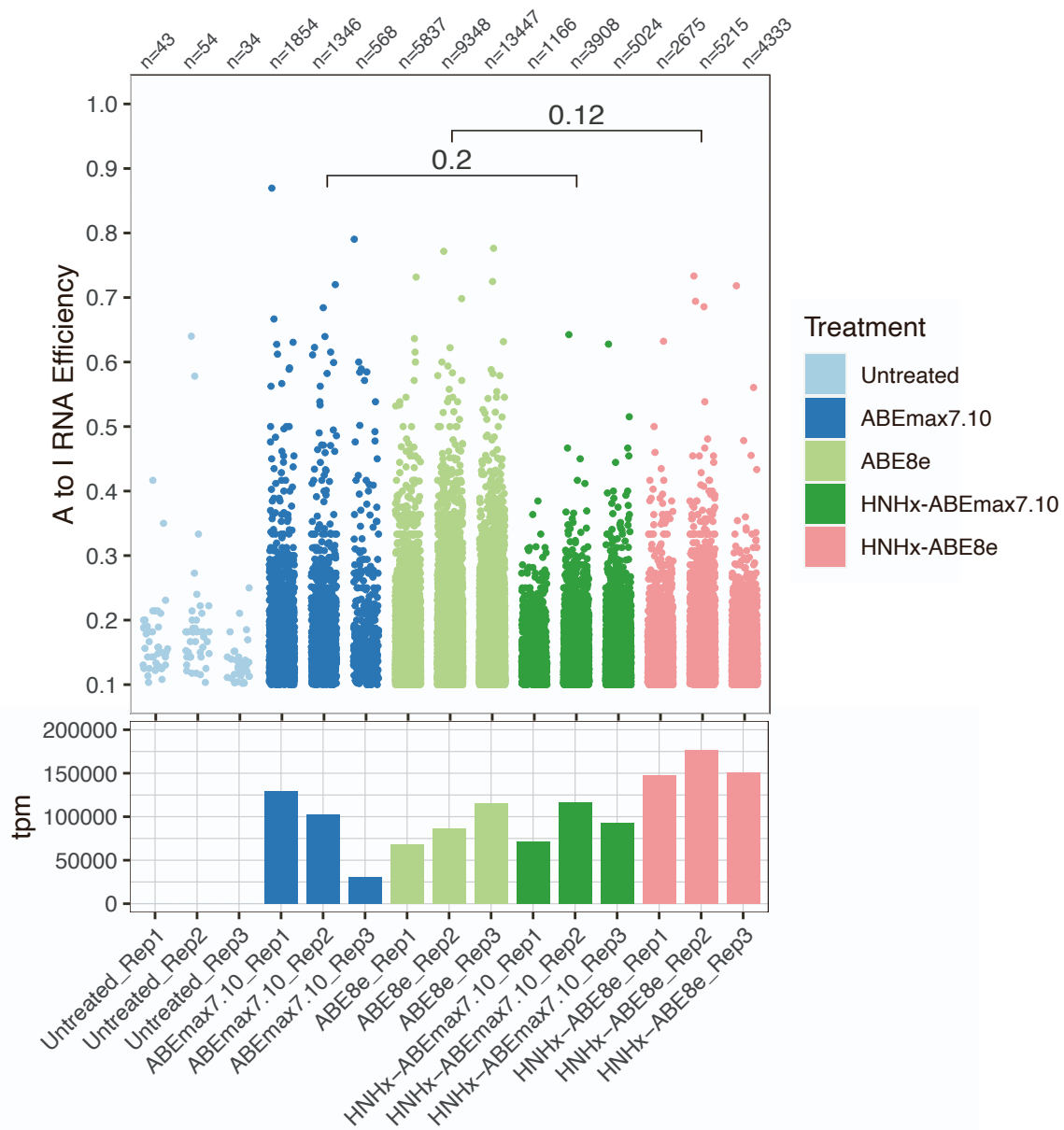


Figure S4. Transcriptome-wide RNA off-target deamination RNA-seq analysis of transcriptome-wide A to I RNA off-target editing after transfection of ABEmax7.10, ABE8e, HNHx-ABEmax7.10 and HNHx-ABE8e constructs. Indicated p-Values represent comparison of means of three independent biological replicates using two-tailed unpaired t-test.

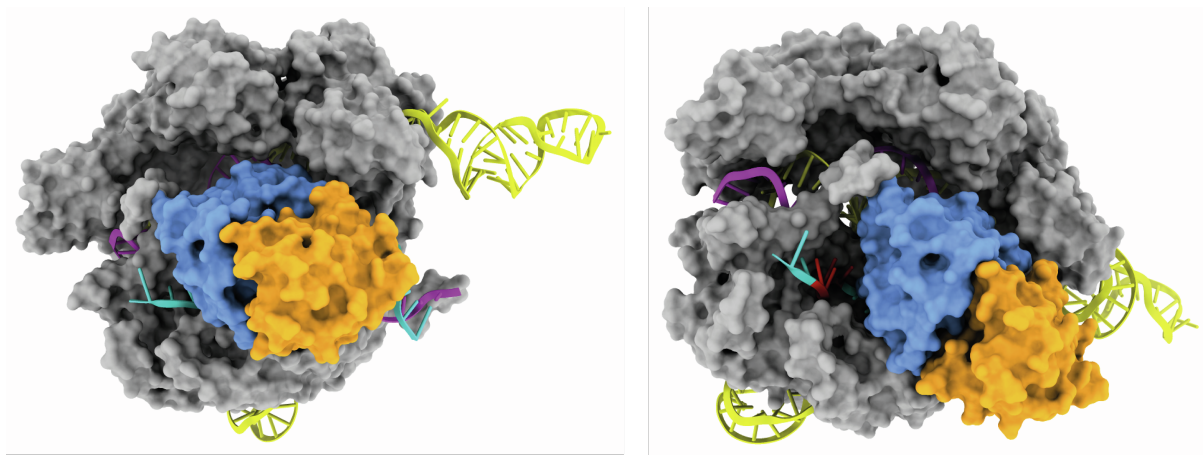


Figure S5. Different viewing angles of a hypothetical HNHx-ABE variant with a dimerized TadA Subunits are colored as follows: Cas9 Δ HNH, grey; TadA linked to Cas9, blue; TadA from another molecule dimerizes to Cas9-bound TadA for functional deamination, orange.



Figure S6. Schematic organisation of a self-targeting construct Each self-targeting construct consists of a human U6 promoter (red), a constant *SpCas9* scaffold (grey), a matching guide- and target sequence (green) and unique barcodes (orange). Sequences used are listed in Supplementary Table 2.

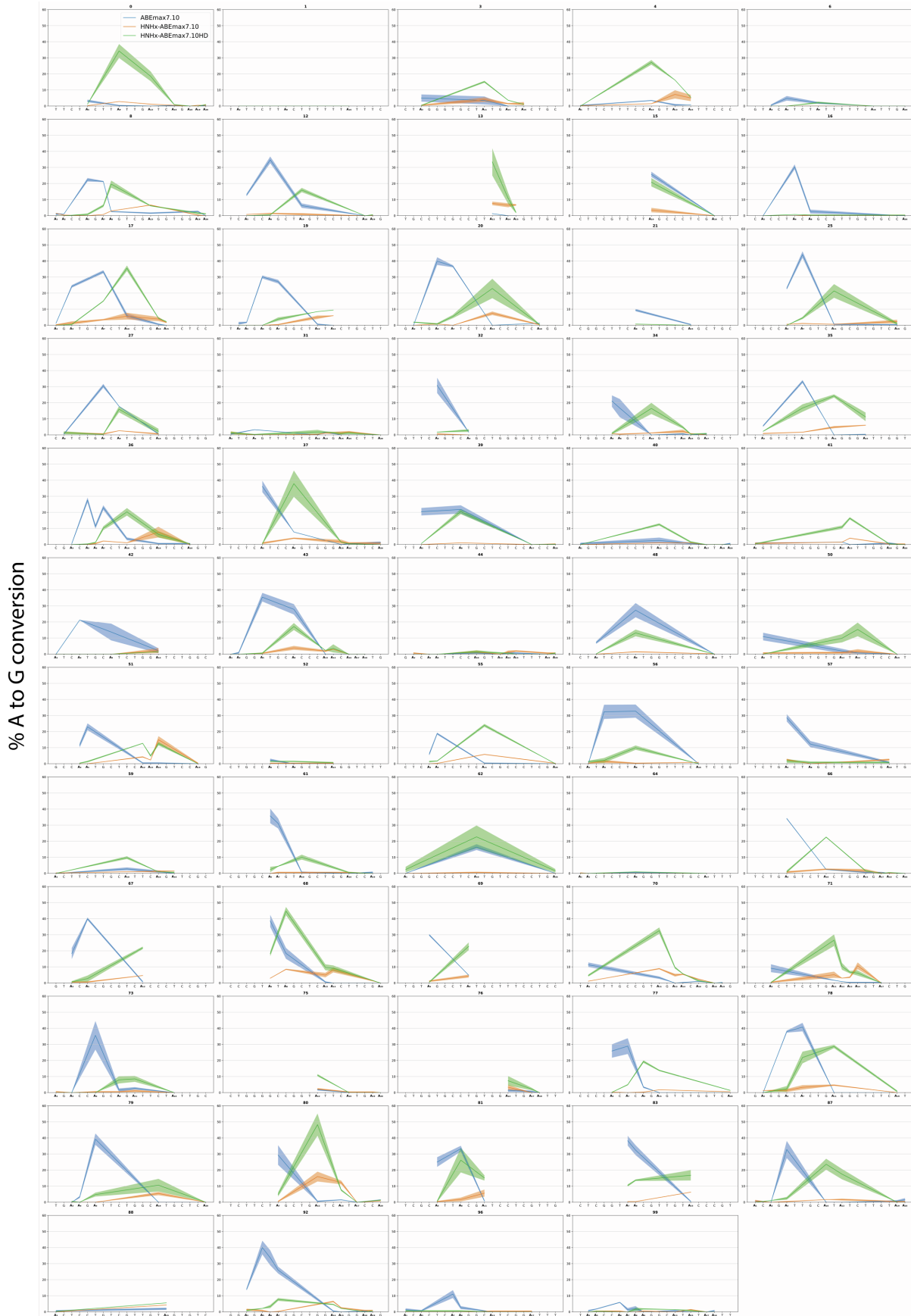


Figure S7. A to G conversions using Tada7.10-based constructs on self-targeting loci High throughput sequencing data compares editing efficiencies of ABEmax7.10, HNHx-

ABEmax7.10 and HNHx-ABEmax7.10HD on 59 self-targeting loci in HEK293T cells. Solid line represents mean of two independent biological replicates performed on separate days, with error band indicating \pm s.d.

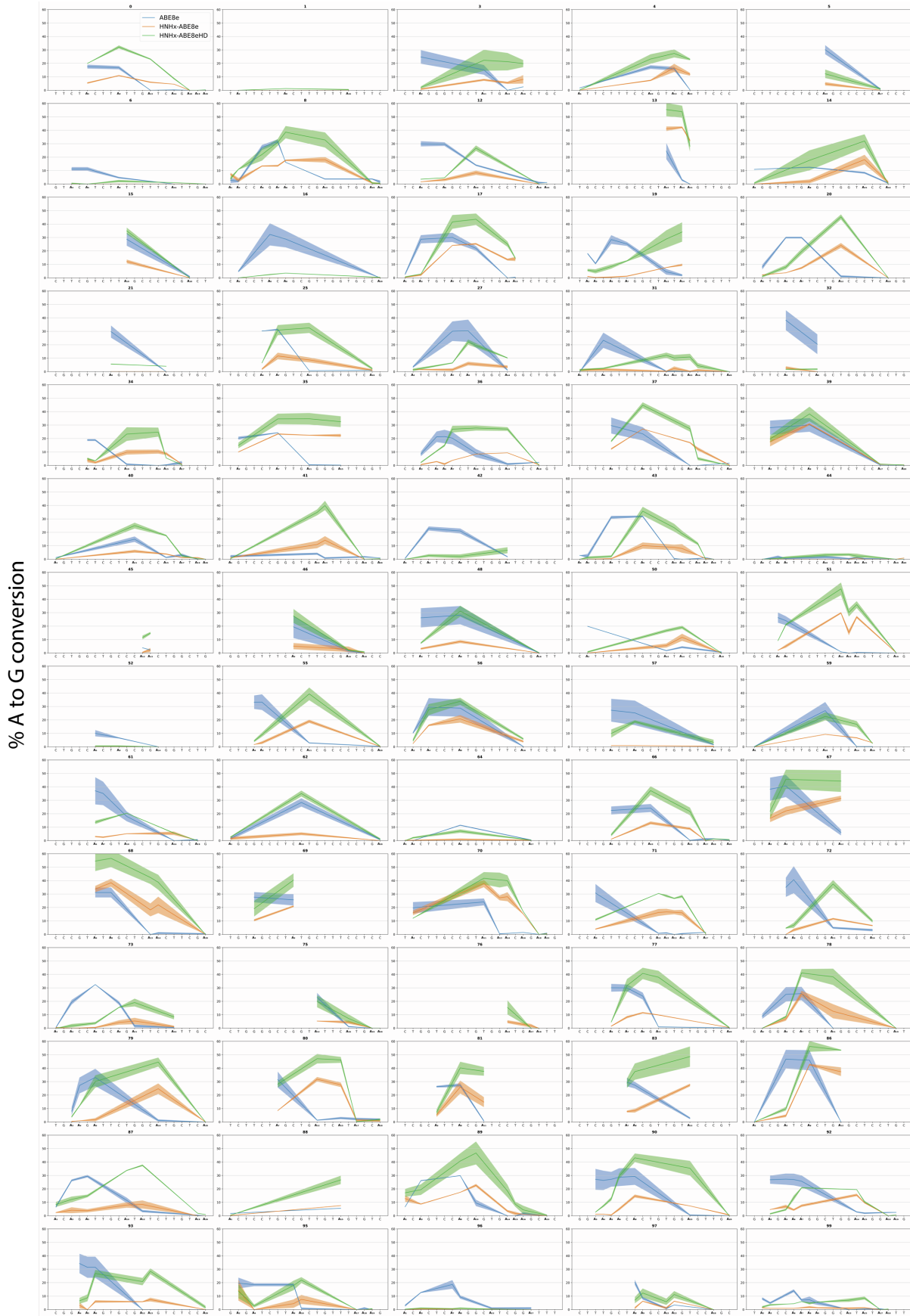


Figure S8. A to G conversions using TadA8e-based constructs on self-targeting loci. High throughput sequencing data compares editing efficiencies of ABE8e, HNHx-ABE8e and

HNHx-ABE8eHD on 70 self-targeting loci in HEK293T cells. Solid line represents mean of two independent biological replicates performed on separate days, with error band indicating \pm s.d.

PRIMER and gBLOCK SEQUENCES

See Supplemental tables 1 & 2.

AMINO ACID SEQUENCES OF BASE EDITOR CONSTRUCTS

HNHx-ABEmax7.10

MKRTADGSEFEFPKKKRKVGSDDKYSIGLAIGTNSVGWAVITDEYKVPSSKKFKVLGNTDRHSIKKNLI
GALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEMAKVDDSSFHRLSEESFLVEEDKKHERH
PIFGNIVDEVAYHEKYPTIYHLRKKLVSDTKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVKL
FIQLVQTYNQLFEEENPINASGVDAKAILSARLSKSRLENLIAQLPGEKKNGLFGNLIALSGLTPNF
KSNFDLAEDAQLQLSKDQYDDDLNLLAQIGDQYADLFLAAKNLSDAILLSDILRVNTEITKAPLSAS
MIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEE
LLVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYFPLKDNREKIEKILTFRIPYYVGPLA
RGNRSFAWMTRKSEETITPWNFEVVDKGSASQSFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNEL
TKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLG
TYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKYAHLFDDKVMKQLKRRRYTGWG
RLSRKLINGIRDKQSGKTILDFLKSDGFANRFMQLIHDDSLTFKEDIQKAQVSGQGDLSHEHIANLA
GSPAIIKKGILQTVKVVDELVKVMGRHKPENIVIAMARENQTTQKGQKNSRERMKRIEEGIKELSGGS
SEVEFSHEYWMRHALTLAKRARDEREVPGAVLVLNRRVIGEGWNRAIGLHDPTAHAEIMALRQGGLV
MQNYRLIDATLYVTFEPCVMCAGAMIHSRIGRVVFGVRNAKTGAAGSLMDVLHYPGMNRVEITEGIL
ADECAALLCYFFRMPRQVFNAQKKAQSSTDSGGRQLVETRQITKHVAQILD SRMNTKYDENDKLIREV
KVI TLKSKLVSDFRKDFQFYK VREINNYHHAHDAYLNAVVG TALIKKYPKLESEFVYGDYKVYDVRKM
IAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVL SM
PQVNIVKKTEVQTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKL
KSVKELLGITIMERSSEFKNPIDFLEAKGYKEVKKDLIIKLPKYSLFELENGRKRMLASAGELQKGNE
LALPSKYVNFLYLASHYEKLGKSPEDNEQKQLFVEQHKHYLDEIIIEQISEFSKRVI LADANLDKVL SA
YNKHRDKPIREQAENI IHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSI TGLYETRID
LSQLGGDSGGSKRTADGSEFEFPKKKRKV

Nuclear localization signal, SpCas9, Linker (Cas9), Linker (Gly-Gly-Ser, Ser-Gly-Gly), TadA (adenosine deaminase, 7.10)

HNHx-ABE8e

MKRTADGSEFE^SPKKKR^{KV}GS^DDKKYSIGLAIGTNSVGVAVITDEYKVPSKKFKVLGNTDRHSIKKNLI
GALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEMAKVDDSFHRLEESFLVEEDKKHERH
PIFGNIVDEVAYHEKYPTIYHLRKKLVSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVVKL
FIQLVQTYNQLFEEENPINASGVDAKAILSARLSKSRLENLIAQLPGEKKNGLFGNLIASLGLTPNF
KSNFDLAEDAQLQ^LSKD^TYDDDLNLLAQIGDQYADLFLAAKNLSDAILLSDILRVNTEITKAPLSAS
MIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEE
LLVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFY^PFLKDNREKIEKILTFRI^PYYVG^PLA
RGNSRFAMWTRKSEETITPWNFEEVVDK^GASQ^SFIERMTNFDKNLPNEKVL^PKHSL^LYEYFT^VYNEL
TKVKYVTEGMRKPAFLS^GEQK^AIVD^LL^LFK^TNR^KVT^VK^QLKEDY^FKKIE^CFDS^VEIS^GVED^RFNAS^LG
TYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKYAHLFDDKVMKQLKRRRYTGWG
RLSRKLINGIRDKQSGKTILD^FLKSD^GFAN^RN^FM^QL^IHDDSLTFKEDIQKAQVSGQGD^SLHEHIAN^LA
GSPA^IKK^GIL^QTV^KV^VDEL^VK^VM^GR^HK^PEN^IVIEMAREN^QTT^QK^GQ^KNS^RERM^KRIE^EG^IKEL^GSG^GS
^SE^VE^FS^HE^YW^MR^HA^LT^LA^KR^AR^DE^RE^VP^VG^AV^LV^LN^NR^VI^GE^GW^NR^AI^GL^HD^PT^AH^AE^IM^AL^RQ^GG^LV
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^IA^KS^EQ^EI^GK^AT^AK^YF^FY^SN^IM^NF^FK^TE^IT^LA^NG^EI^RK^RP^LI^ET^NG^ET^GE^IV^WD^KG^RD^FA^TV^RK^VL^SM
^PQ^VN^IV^KK^TE^VQ^TG^GF^SK^ES^IL^PK^RN^SD^KL^IA^RK^KD^WD^PK^KY^GG^FD^SP^TV^AY^SV^LV^VA^KV^EK^GK^SK^L
^KS^VK^EL^LG^IT^IM^ER^SS^FE^KN^PI^DF^LE^AK^YK^EV^KD^LI^IK^LP^KY^SL^FE^LE^NG^RK^RM^LA^SA^GE^LQ^KG^NE
^LA^LP^SK^YV^NF^LY^LA^SH^EK^LK^GS^PE^DN^EQ^QL^FV^EQ^HK^HY^LD^EI^IE^QI^SE^FS^KR^VI^LA^DA^NL^DK^VL^SA
^YN^KH^RD^KP^IR^EQ^AE^NI^IH^LF^TL^TN^LG^AP^AA^FK^YF^DT^TI^DR^KR^YT^ST^KE^VL^DA^TL^IH^QS^IT^GL^YE^TR^ID
^LS^QL^GG^DS^GG^SK^RT^AD^GS^EF^EP^KK^RK^V

Nuclear localization signal, SpCas9, Linker (Cas9), Linker (Gly-Gly-Ser, Ser-Gly-Gly), TadA (adenosine deaminase, 8e)

HNHx-ABEmax7.10HD

MKRTADGSEFE^SPKKKR^{KV}GS^DDKKYSIGLAIGTNSVGVAVITDEYKVPSKFKVLGNTDRHSIKKNLI
GALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEMAKVDDSFHRLEESFLVEEDKKHERH
PIFGNIVDEVAYHEKYPTIYHLRKKLVSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKL
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RGNSRFAMTRKSEETITPWNFEEVVDKGASAQSFIERMTNFDKNLPNEKVLPHKSLLYEYFTVYNEL
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EIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVL^{SMPQVNIV}
KKTEVQTGGFSKESILPKRNSDKLIAR^{KKDWDPKKYGGFDSPTVAYSVLVAKVEKGSKKLKSVKEL}
LGITIMERS^{SFEKNPIDFLEAKGYKEVKKDLIIKLPKYSLFELENGRKRMLASAGELQKGNELALPSK}
YVNFLYLASHYEKLK^{GSPEDNEQQLFVEQHKHYLDEII}EQISEFSKRVI^{LADANLDKVL}SAYNKHRD
KPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDR^{KRYTSTKEVLDATLIHQ}SITGLYETRIDLSQLGG
DSGGS^{KRTADGSEFE}PKKKR^{KV}

Nuclear localization signal, SpCas9, Linker (Cas9), Linker (Gly-Gly-Ser, Ser-Gly-Gly), TadA (adenosine deaminase, 7.10), Linker, TadA (WT)

HNHx-ABE8eHD

MKRTADGSEFE^SPKKKR^{KV}GS^{SD}KKYSIGLAIGTNSVGWAVITDEYKVPSK^KFKVLGNTDRHSIKKNLI
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KKTEVQTGGFSKESILPKRNSDKLIAR^{KK}DWDPKKYGGFDSPTVAYSVLVAKVEK^{GK}SKKLKSVKEL
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YVNFLYLASHYEKLK^GSPEDNEQQLFVEQHKHYLDEIEEQISEFSKR^{VIL}ADANLDKVL^{SAY}NKHRD
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DSGGS^{KRT}ADGSEFE^PPKKKR^{KV}

Nuclear localization signal, SpCas9, Linker (Cas9), Linker (Gly-Gly-Ser, Ser-Gly-Gly), TadA (adenosine deaminase, 7.10), Linker, TadA (WT)

HNHx - PmCDA1

MKRTADGSEFEFSPKKKRKVGSDDKKYSIGLAIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLI
GALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEMAKVDDSFHRLEESFLVEEDKKHERH
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EYVRIHEKLDIYTFKKQFSNNKKSVMHRCYVLFELKRRGERRACFWGYAVNKPQSGTERGIHAEI FSI
RKVEEYLRDNPQGFITINWYSSWSPCADCAEKILEWYNQELRGNHTLKIWVCKLYYEKNARNQIGLWN
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EQKQLFVEQHKHYLDEIEQISEFSKRVI LADANLDKVL SAYNKHRDKPIREQAENI IHLFTLTNLGA
PAAFKYFDTTIDRKRYTSTKEVLDATLIHQ SITGLYETRIDLSQLGGDSGGSGGSGGSTNLSDIIEKE
TGKQLVIQESILMLPEEVEEVIGNKPESDILVHTAYDESTDENVMLLTS DAPEYKPWALVIQDSNGEN
KIKMLSGGSGGSGGSTNLSDIIEKETGKQLVIQESILMLPEEVEEVIGNKPESDILVHTAYDESTDEN
VMLLTS DAPEYKPWALVIQDSNGENKIKMLSGGSKRTADGSEFEFPPKKKRKV

Nuclear localization signal, SpCas9, Linker (Cas9), Linker (Ser-Gly-Gly-Ser-Gly-Gly), PmCDA1, UGI

FERNY (=evolved APOBEC) Variant

MKRTADGSEFFESPKKKRKVGSDDKKYSIGLAIGTNSVGVAVITDEYKVPSKKFKVLGNTDRHSIKKNLI
GALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEMAKVDDSFHRLEESFLVEEDKKHERH
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RGNSRFAMTRKSEETITPWNFEEVVDKGASQSFIERMTNFDKNLPNEKVLPHKSLLYEYFTVYNEL
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GSPAIIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKSGSGSGSFERNYDPRELRKETYLL
YEIKWKGSGKLRHWCQNNRTQHAEVYFLENIFNARRFNPSTHCSITWYLSWSPCAECSQKIVDFLKE
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EKNPIDFLEAGYKEVKKDLIIKLPKYSLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHY
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TNLSDIIEKETGKQLVIQESILMLPEEVEEVIGNKPESDILVHTAYDESTDENVMLLTSDAPEYKPWA
LVIQDSNGENKIKMLSGSGSGSGSTNLSDIIEKETGKQLVIQESILMLPEEVEEVIGNKPESDILVH
TAYDESTDENVMLLTSDAPEYKPWALVIQDSNGENKIKMLSGGSKRTADGSEFFESPKKKRKV

Nuclear localization signal, SpCas9, Linker (Cas9), Linker (Ser-Gly-
Gly-Ser-Gly-Ser, Ser-Gly), FERNY (=evolved APOBEC), UGI

ABEmax7.10 PI1

MKRTADGSEFESPKKKRKVGSDDKKYSIGLAIGTNSVGVAVITDEYKVPSKKFKVLGNTDRHSIKKNLI
GALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEMAKVDDSFHRLEESFLVEEDKKHERH
PIFGNIVDEVAYHEKYPTIYHLRKKLVSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVKL
FIQLVQTYNQLFEEENPINASGVDAKAILSARLSKSRLENLIAQLPGEKKNGLFGNLIASLGLTPNF
KSNFDLAEDAQLQSKDQTYDDDLNLLAQIGDQYADLFLAAKNLSDAILLSDILRVNTEITKAPLSAS
MIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEE
LLVKNLREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYFPLKDNREKIEKILTFRIPIYYVGPLA
RGNSRFAMTRKSEETITPWNFEEVVDKGAQSFIERMTNFDKNLPNEKVLPHKSLLYEYFTVYNEL
TKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLG
TYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKYAHLFDDKVMKQLKRRRYTGWG
RLSRKLINGIRDKQSGKTILDFLKSDFANRNFQMQLIHDDSLTFKEDIQKAQVSGQGDLSHEHIANLA
GSPAIIKKGILQTVKVVDELVKVMGRHKPENIVIAMARENQTTQKGQKNSRERMKRIEEGKELGSQIL
KEHPVENTQLQNEKLYLYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKNR
GKSDNVPSEEVVKKMKNYWRQLLNAKLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVA
QILDSRMNTKYDENDKLIREVKVITLKSCLVSDFRKDFQFYKVVREINNYHHAHDAYLNAVVGTAIIKK
YPKLESEFVYGDYKVYDVRKMIKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGE
TGEIVWDKGRDFATVRKVLSPQVNIIVKKTVEVQTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDS
PTVAYSVLVAKVEKGGKSKLKSVEKLLGITIMERSSEFEKNPIDFLEAKGYKEVKKDLIIKLPKYSLE
ELENKRKRLASAGELQKGNELALPSKYVNFYLYLASHYEKLGGSGGSGSGSGSGSSEVEFSHEYWM
RHALTLAKRARDEREVPGAVLVLNNRVIGEGWNRAIGLHDPTAHAEIMALRQGGLVMQNYRLIDATL
YVTFEPCVMCAGAMIHSRIGRVVFGVRNAKTGAAGSLMDVLHYPGMNHRVEITEGILADECAALLCYF
FRMPRQVFNAQKKAQSSTDGGSGSGSGSGSGSPEDNEQKQLFVEQHKHYLDEIIIEQISEFSKRVIL
ADANLDKVL SAYNKHRDKPIREQAENI IHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVL DATLIHQ
SITGLYETRIDLSQLGGDSGGSKRTADGSEFEPKKKRKV

Nuclear localization signal, SpCas9, Linker (Gly-Gly-Ser), TadA
(adenosine deaminase, 7.10)

ABEmax7.10 PI2

MKRTADGSEFESPKKKRKVGSDDKYSIGLAIGTNSVGWAVITDEYKVPSSKKFKVLGNTDRHSIKKNLI
GALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEMAKVDDSFHRLEESFLVEEDKKHERH
PIFGNIVDEVAYHEKYPTIYHLRKKLVSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKL
FIQLVQTYNQLFEEENPINASGVDAKAILSARLSKSRLENLIAQLPGEKKNGLFGNLIASLGLTPNF
KSNFDLAEDAQLQSKDQYDDDLNLLAQIGDQYADLFLAAKNLSDAILLSDILRVNTEITKAPLSAS
MIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEE
LLVKNLREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYFPLKDNREKIEKILTFRIPIYYVGPLA
RGNSRFAMTRKSEETITPWNFEEVVDKGSASQSFIERMTNFDKNLPNEKVLPHKSLLYEYFTVYNEL
TKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLG
TYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKYAHLFDDKVMKQLKRRRYTGWG
RLSRKLINGIRDKQSGKTILDFLKSDFANRNFQMQLIHDDSLTFKEDIQKAQVSGQGDLSHEHIANLA
GSPAIAKKGILQTVKVVDELVKVMGRHKPENIVIEARENQTTQKGQKNSRERMKRIEEGKELGSQIL
KEHPVENTQLQNEKLYLYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKNR
GKSDNVPSEEVVKKMKNYWRQLLNAKLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVA
QILDSRMNTKYDENDKLIREVKVITLKSCLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTAIIKK
YPKLESEFVYGDYKVYDVRKMIKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGE
TGEIVWDKGRDFATVRKVLSPQVNIKKTEVQTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDS
PTVAYSVLVAKVEKGSKLLKSVKELLGITIMERSSEFKNPIDFLEAKGYKEVKKDLIIKLPKYSLE
ELENKRMLASAGELQKGNELALPSKYVNFYLYLASHYEKLGGSSGGSSEVEFSSHEYWMRHALTL
AKRARDEREVPVAVLVLNNRVIGEGWNRAIGLHDPTAHAEIMALRQGGLVMQNYRLIDATLYVTFEP
CVMCAGAMIHSRIGRVVFGVRNAKTGAAGSLMDVLHYPGMNRVEITEGILADECAALLCYFFRMPRQ
VFNAQKKAQSSTDGGSGSGSGSGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVL
SAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETR
IDLSQLGGDSSGSKRTADGSEFEPKKRKV

Nuclear localization signal, SpCas9, Linker (Gly-Gly-Ser), TadA
(adenosine deaminase, 7.10)

ABEmax7.10 PI3

MKRTADGSEFESPKKKRKVGSDDKYSIGLAIGTNSVGWAVITDEYKVPSSKKFKVLGNTDRHSIKKNLI
GALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEMAKVDDSFHRLEESFLVEEDKKHERH
PIFGNIVDEVAYHEKYPTIYHLRKKLVSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKL
FIQLVQTYNQLFEENPINASGVDAKAILSARLSKSRLENLIAQLPGEKKNGLFGNLIALSGLTPNF
KSNFDLAEDAQLQSKDTYDDDLNLLAQIGDQYADLFLAAKNLSDAILLSDILRVNTEITKAPLSAS
MIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEE
LLVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYFPLKDNREKIEKILTFRIPIYYVGPLA
RGNSRFAMTRKSEETITPWNFEEVVDKGASAQSFIERMNTNFDKNLPNEKVLPHKSHLLYEYFTVYNEL
TKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLG
TYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKYAHLFDDKVMKQLKRRRYTGWG
RLSRKLINGIRDKQSGKTILDFLKSDFANRNFQMQLIHDDSLTFKEDIQKAQVSGQGDLSHEHIANLA
GSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIKELGSQIL
KEHPVENTQLQNEKLYLYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKNR
GKSDNVPSEEVVKKMKNYWRQLLNAKLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVA
QILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTALIKK
YPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGE
TGEIVWDKGRDFATVRKVLSMPQVNIVKKTEVQTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDS
PTVAYSVLVAKVEKGKSKKLKSVKELLGITIMERSSSFEKNPIDFLEAKGYKEVKKDLIIKLPKYSLF
ELENGRKRLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSGSGSGSSEVEFSHEYWMRHALTL
AKRARDEREVPVGAVLVLNNRVIGEGWNRAIGLHDPTAHAEIMALRQGGLMQNYRLIDATLYVTFEP
CVMCAGAMIHSRIGRVVFGVRNAKTGAAGSLMDVLHYPGMNHRVEITEGILADECAALLCYFFRMPRQ
VFNAQKKAQSSTDGSGSGSGSPEDNEQKQLFVEQHKHYLDEIEEQISEFSKRVILADANLDKVLSAY
NKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDL
SQLGGDSGGSKRTADGSEFEPKKRKV

Nuclear localization signal, SpCas9, Linker (Gly-Gly-Ser), TadA
(adenosine deaminase, 7.10)

SaKKH-HNHx-ABEmax7.10 (S484)

MKRTADGSEFFESPKKKRKVGSKRNYILGLAIGITSVGYGIIDYETRDVIDAGVRLFKEANVENNEGR
SKRGARRLKRRRRHRIQRVKKLLFDYNLLTDHSELSGINPYEARVKGLSQKLSEEEFSAALLHLAKRR
GVHNVNEVEEDTGNELSTKEQISRNSKALEEKYVAELQLERLKKDGEVRGSINRFKTSDYVKEAKQLL
KVQKAYHQLDQSFIDTYIDLLETRRYYEGPGEPSFGWKDIKEWYEMLMGHCTYFPEELRSVKYAYN
ADLYNALNDLNNLVITRDENEKLEYEYKQI IENVFKQKKKPTLKQIAKEILVNEEDIKGYRVTSTGK
PEFTNLKVYHDIKDITARKEI IENAELLDQIAKILTIYQSSEDIQEELTNLNSELTQEEIEQISNLKG
YTGTHNLSLKAINLILDELWHTNDNQIAIFNRLKLVPKKVDLSQQKEIPTTLVDDFILSPVVKRSFIQ
SIKVINAI IKKYGLPNDII IELAREKNSGSSEVEFSHEYWMRHALTLAKRARDEREVPVGAVLVLNNR
VIGEGWNRAIGLHDPTAHAEIMALRQGGLVMQNYRLIDATLYVTFEPCVMCAGAMIHSRIGRVVFGVR
NAKTGAAGSLMDVLHYPGMNRVEITEGILADECAALLCYFFRMPRQVFNAQKKAQSSTDSSTRYATR
GLMNLRSYFRVNNLDVKVKSINGGFTSFLRRKWKFKKERNKGYKHAEDALI IANADFIKWKKLD
KAKVMENQMFEEKQAESMPEIETEQEYKEIFITPHQIKHIKDFKDYKYSHRVDKKPNRKLINDTLYS
TRKDDKGNTLIVNNLNGLYDKDNDKLLKLINKSPEKLLMYHHPQTYQKLKLIMEQYGDEKNPLYKYY
EETGNYLTKYSKKNPVIKIKYGNKLNALDITDDYPNSRNKVVKLSLKPYPFDVYLDNGVYKVV
TVKNLDVIKKNYEVNSKCYEEAKLKKISNQAEFIASFYKNDLIKINGELYRVIGVNNDLLNRIEV
NMIDITYREYLENMNDKRPPHI IKTIAKTQSIKYSTDILGNLYEVKSKKHPQIIKKGSGGSKRTAD
GSEFEPKKKRKV

Nuclear localization signal, SaKKH, Linker (Gly-Ser, Ser-Ser), TadA
(adenosine deaminase, 7.10)

SaKkH-HNHx-ABEmax7.10 (G513)

MKRTADGSEFFESPKKKRKVGSKRNYILGLAIGITSVGYGIIDYETRDVIDAGVRLFKEANVENNEGR
SKRGARRLKRRRRHRIQRVKKLLFDYNLLTDHSELSGINPYEARVKGLSQKLSEEEFSAALLHLAKRR
GVHNVNEVEEDTGNELSTKEQISRNSKALEEKYVAELQLERLKKDGEVRSINRFKTSDYVKEAKQLL
KVQKAYHQLDQSFIDTYIDLLETRRYYEGPGEKSPFGWKDIKEWYEMLMGHCTYFPEELRSVKYAYN
ADLYNALNDLNNLVITRDENEKLEYEYKQI IENVFKQKKKPTLKQIAKEILVNEEDIKGYRVTSTGK
PEFTNLKVYHDIKDITARKEI IENAELLDQIAKILTIYQSSEDIQEELTNLNSELTQEEIEQISNLKG
YTGTHNLSLKAINLILDELWHTNDNQIAIFNRLKLVPKKVDLSQQKEIPTTLVDDFILSPVVKRSFIQ
SIKVINAI IKKYGLPNDII IELAREKNSKDAQKMINEMQKRNRQTNERIEEII RTTGSSSEVEFSHEY
WMRHALTLAKRARDEREVPGAVLVLNNRVI GEGWNRAIGLHDPTAHAEIMALRQGGGLVMQNYRLIDA
TLYVTFEPCVMCAGAMIHSRIGRVVFGVRNAKTGAAGSLMDVLHYPGMNRVEITEGILADECAALLC
YFFRMPRQVFNAQKKAQSSTDSSSVQKDFINRNLVDTRYATRGLMNLRSYFRVNNLDVKVKSINGGF
TSFLRRKWKFKKERNKGYKHAEDALI IANADFIFKEWKKLDKAKKVMENQMFEKQAESMPEIETEQ
EYKEIFITPHQIKHIKDFKDYKYSRVDKKNRKLINDTLYSTRKDDKGNTLIVNNLNGLYDKDNDKL
KKLINKSPEKLLMYHHDPPQTYQKLKLIMEQYGDEKNPLYKYYEETGNYLTKYSKKDNGPVIKKIKYYG
NKLNAHLDITDDYPNSRNKVVKLSLKPFRFDVYLDNGVYKFVTVKNLDVIKENYYEVNSKCYEEAKK
LKKISNQAEFIASFYKNDLIKINGELYRVIGVNDLLNRIEVNMIDITYREYLENMNDKRPPIIKTI
ASKTQSIKKYSTDILGNLYEVKSKKHPQIIKKGSGGSKRTADGSEFFEPKKKRKV

Nuclear localization signal, SaKkH, Linker (Gly-Ser, Ser-Ser), TadA
(adenosine deaminase, 7.10)