

Base editor	Substitution	Distance from PAM		PAM	Ref. #
		Major activity site	Minor activity site		
BE1, BE2, BE3, HF-BE3, BE4(max), BE4-Gam	C to T	13-17	10-12, 18-19	NGG	(1–4)
YE1-BE3	C to T	14-16	17	NGG	(5)
YEE-BE3	C to T	15	16	NGG	(5)
VQR-BE3	C to T	10-17		NGAN	(5)
VRER-BE3	C to T	11-18		NGCG	(5)
SaBE3, SaBE4, SaBE4-Gam (21nt gRNA)	C to T	10-19		NNGRRT	(3, 5)
Sa(KKH)-BE3 (21nt gRNA)	C to T	10-19		NNNRRT	(5)
Cas12a-BE	C to T	10-12 downstream	8-9, 13 downstream	TTTV	(6)
Target-AID	C to T	17-19	13-16	NGG	(7)
Target-AID-NG	C to T	17-19	13-16	NG	(8)
xBE3	C to T	13-17	10-12, 18-19	NG	(9)
eA3A-BE3	C to T when C comes after T	13-17	10-12, 18-19	NGG	(10)
BE-PLUS	C to T	7-17	5-6	NGG	(11)
CP-CBEmax variants	C to T	12-17	10-11* may exhibit editing upstream to the protospacer	NGG	(12, 13)
evoAPOBEC1-BE4max	C to T	13-18	19-20, 9-12	NGG	(14)
evoFERNY-BE4max	C to T	13-18	19-20	NGG	(14)
evoCDA1-BE4max	C to T	9-20	7-8* may exhibit editing upstream to the protospacer	NGG	(14)
ABE 7.9	A to G	13-16	12, 17	NGG	(15)
ABE 7.10	A to G	14-17	13	NGG	(15)
ABE 7.10*	A to G	13-17	12,18-19	NGG	(16)
xABE, NG-ABEmax	A to G	14-17	13	NG	(9, 13)
ABESa (21nt gRNA)	A to G	10-16		NNGRRT	(17)
VQR-ABE	A to G	15-17	13-14	NGA	(17, 18)
VRER-ABE	A to G	15-17	13-14	NGCG	(17)
Sa(KKH)-ABE (21nt gRNA)	A to G	10-16		NNNRRT	(17, 18)
CP-ABEmax variants	A to G	14-17	7-13	NGG	(12, 13)