Supplementary information

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Fig. S1 Diagram maps for the donor plasmids used in the study. (a) *APP*.Donor (TPG); (b) *APP*.Donor (TZR).
(c) *PSEN1*.Donor (TPG); (d) *PSEN1*.Donor (TZR); (e) *APP*.Donor (PGT); (f) *APP*.Donor (ZRT); (g) *APP*.Donor (PT); h. *APP*.Donor (ZT).

a	Genome	PGT.I	Left arm	APP.target	t SP1.targe	t PGK
	1 MMMMMMM	MMM	MMMM		PAM MMMMMMM	www.www
	Genome	ZRT.I		APP.targe	t SP1.targe	et PGK
	MMMMM	MMM	MAMM	hummun	MAMAMAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA	MMMA
	SV40TpolyA SP	1.target	SSA	APP.target	Right arm	Genome
b	Genome	PT.Lef	t arm	APP.target	SP1.target	PGK
	MMMMMMMMMMMMMMMMMMMMMMMMMMMMMMMMMMMMMM	WMM (WWWW	muPA	MMMMMMM	WMMMM
	Genome	ZT.Lef	t arm	APP.target	SP1.target	PGK
	MMMMMMMMMMMMMMMMMMMMMMMMMMMMMMMMMMMMMM	MMM	MMMM	muP MMMMM	ам ИМ	MMM.MM
	SV40TpolyA SP1	.target	SSA	APP.target	Right arm	Genome

Fig. S2 Sanger sequencing result for optimized biallelic genome editing at the *APP* locus. Sequence alignment results of the three homologous arms of PGT/ZRT system (a) and PT/ZT system (b) confirming successful point mutation at the *APP* locus.