

Supplementary information

<https://doi.org/10.1631/jzus.B2100196>

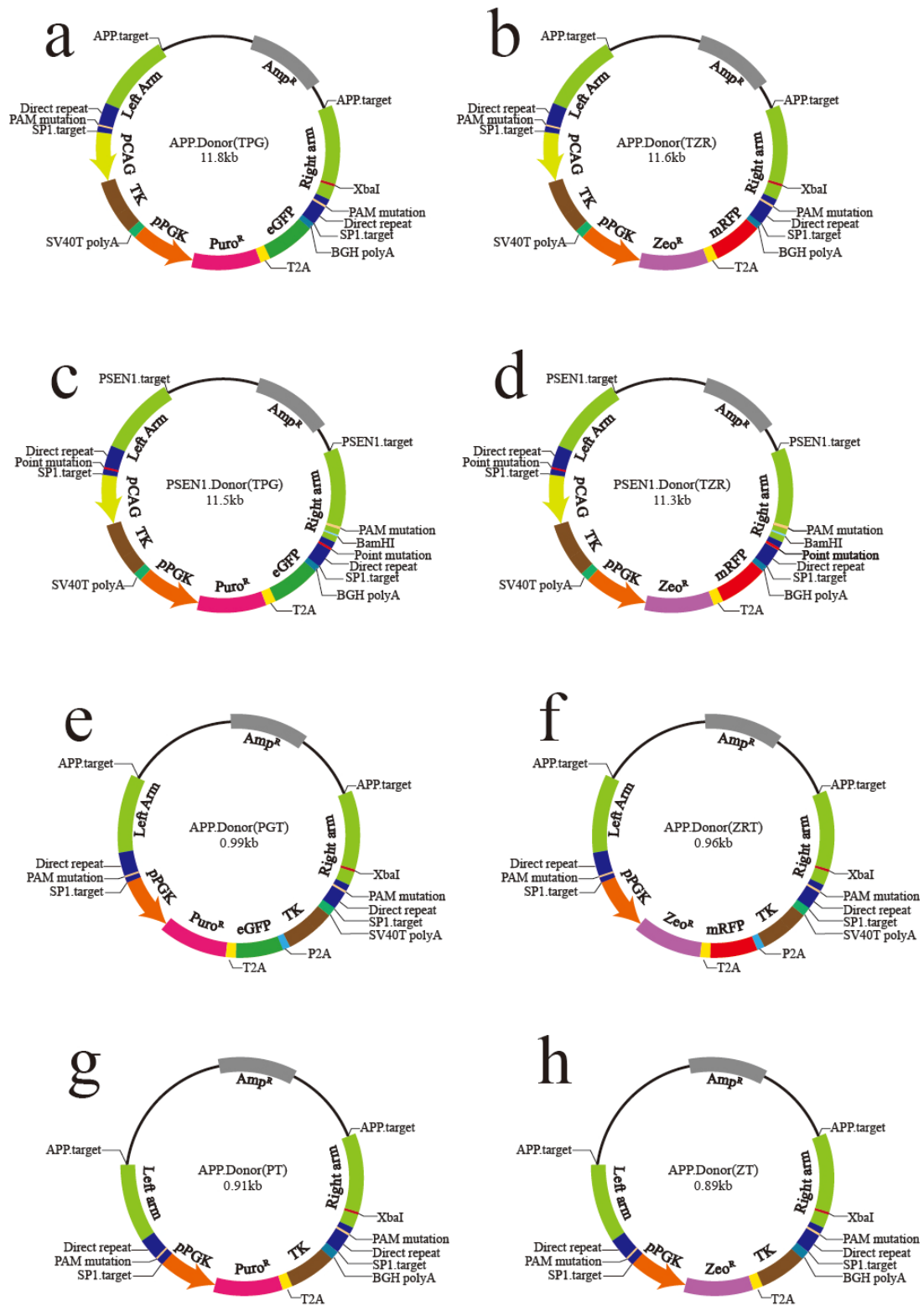


Fig. S1 Diagram maps for the donor plasmids used in the study. (a) *APP.Donor* (TPG); (b) *APP.Donor* (TZR); (c) *PSEN1.Donor* (TPG); (d) *PSEN1.Donor* (TZR); (e) *APP.Donor* (PGT); (f) *APP.Donor* (ZRT); (g) *APP.Donor* (PT); (h) *APP.Donor* (ZT).

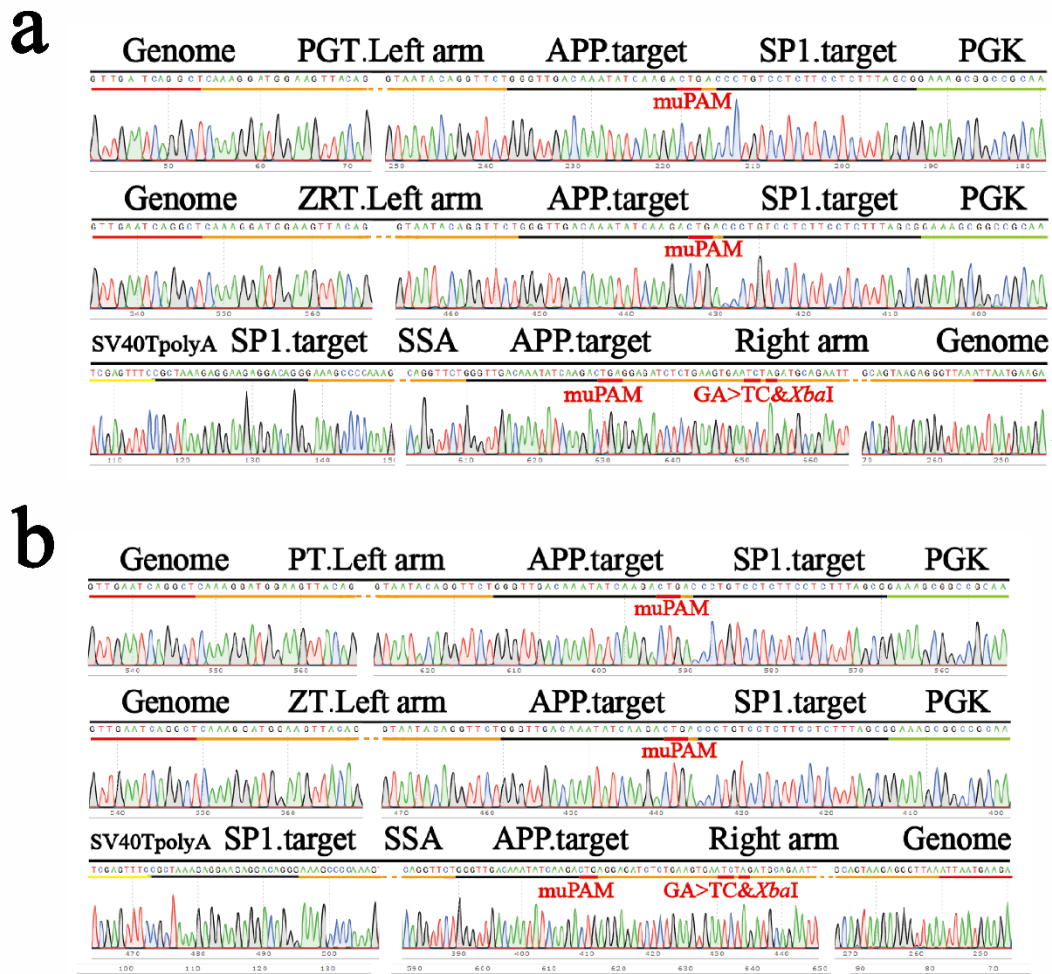


Fig. S2 Sanger sequencing result for optimized biallelic genome editing at the *APP* locus. Sequence alignment results of the three homologous arms of PGT/ZRT system (a) and PT/ZT system (b) confirming successful point mutation at the *APP* locus.