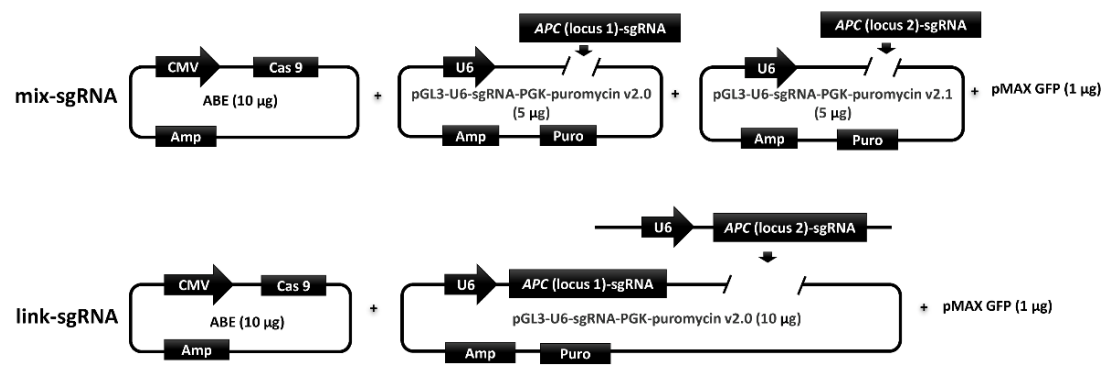


## **Supplementary information**

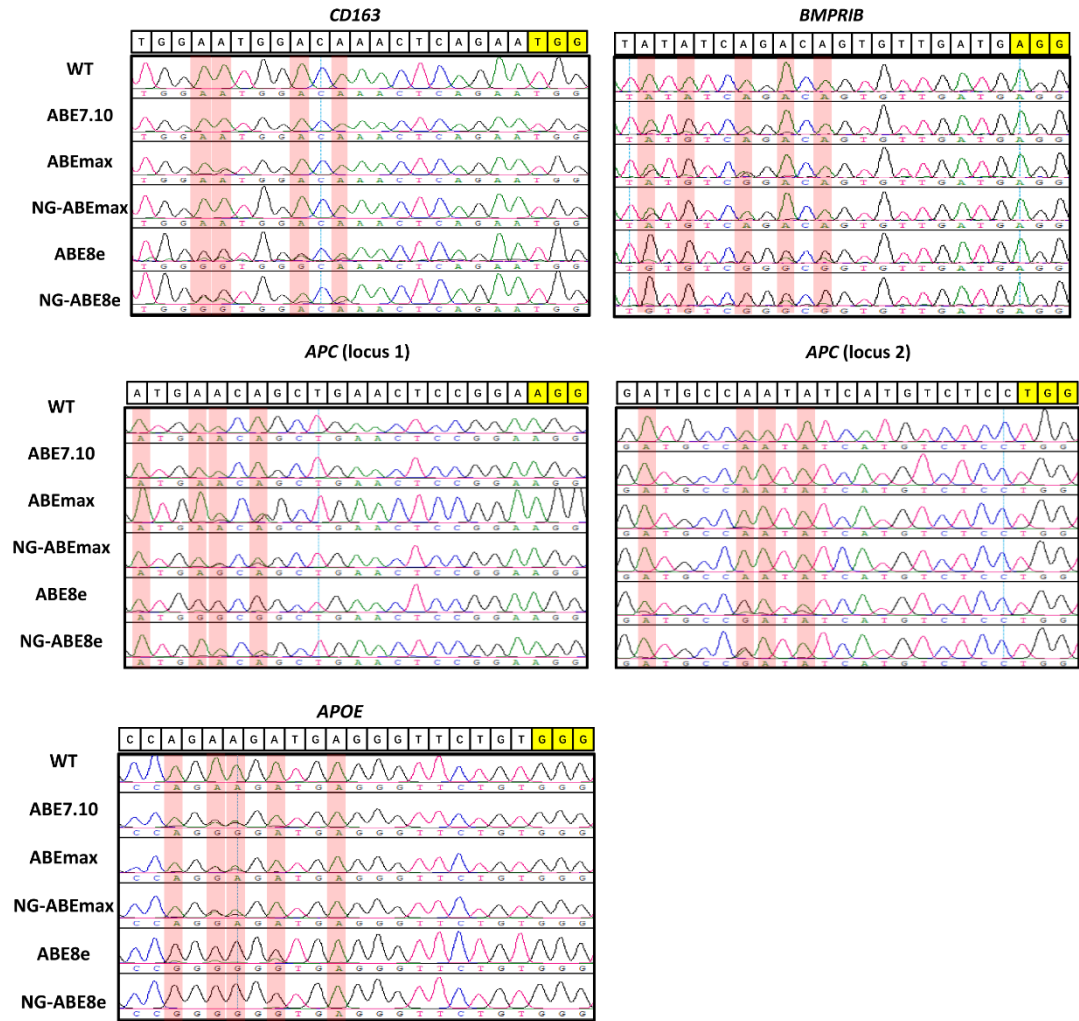
### **Highly efficient A-to-G editing in PFFs via multiple ABE**

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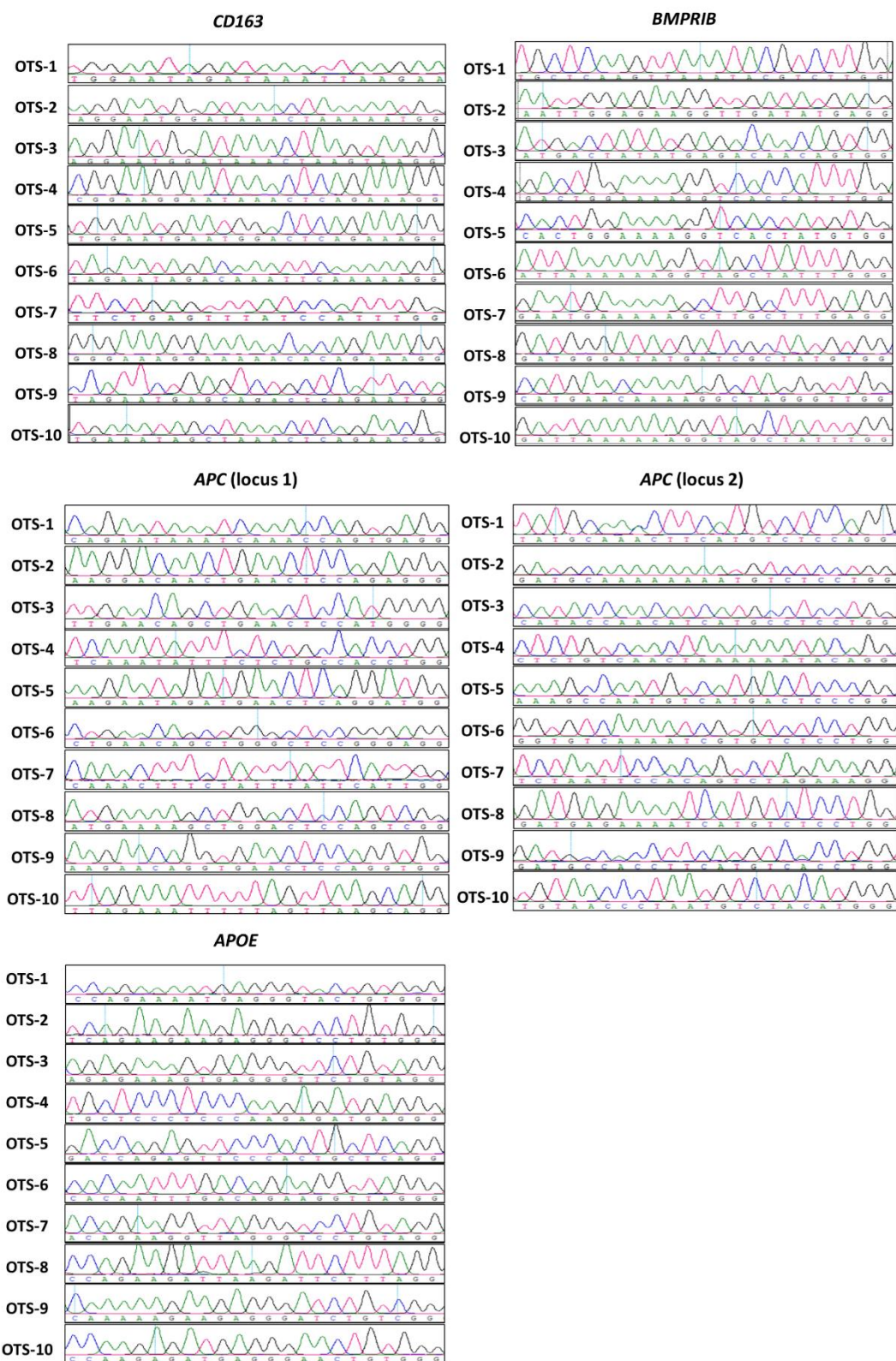
<sup>1</sup>State Key Laboratory of Pig Genetic Improvement and Production Technology,  
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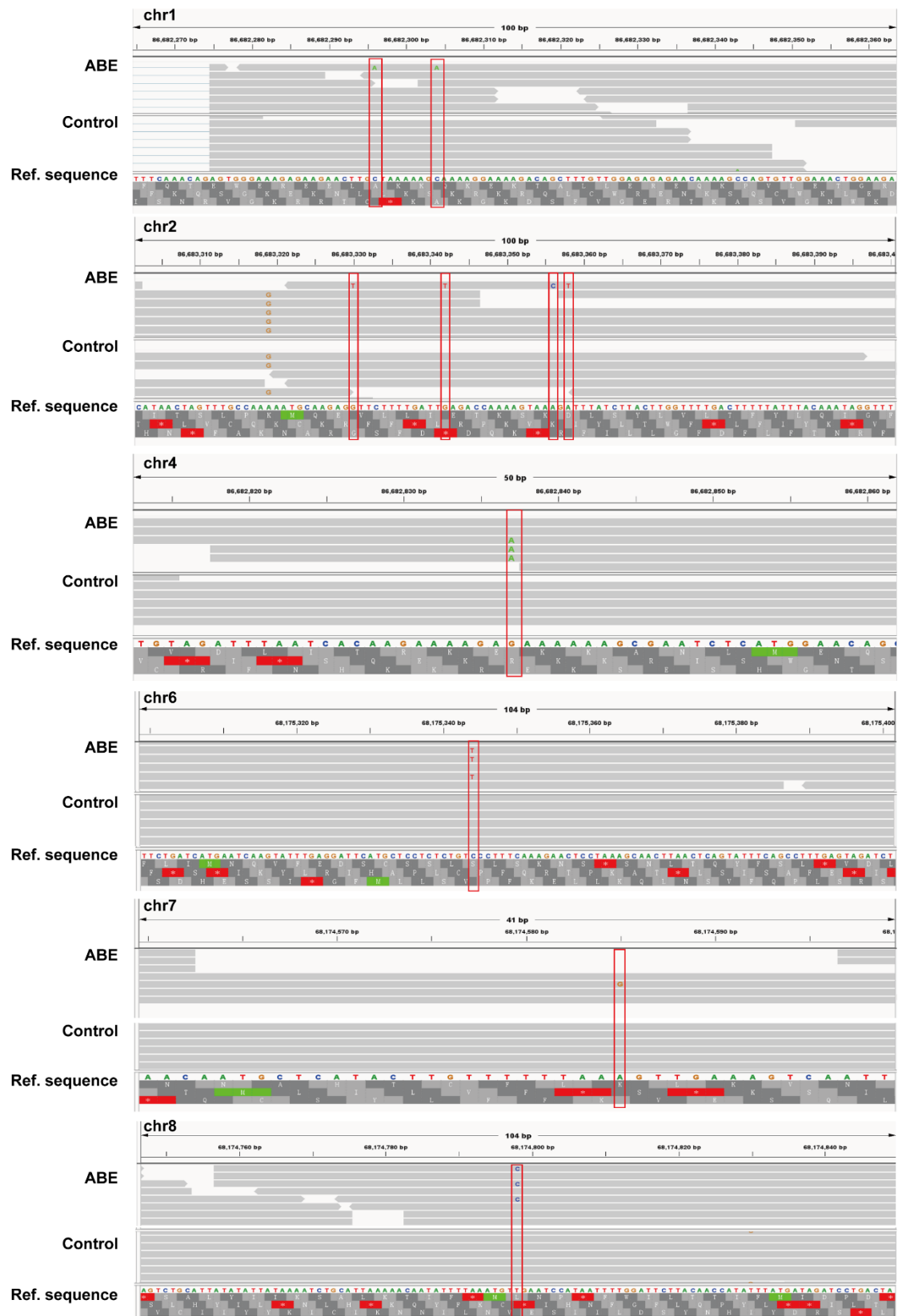
**Figure S1:** The schematic diagrams of mix-sgRNA and link-sgRNA strategies.



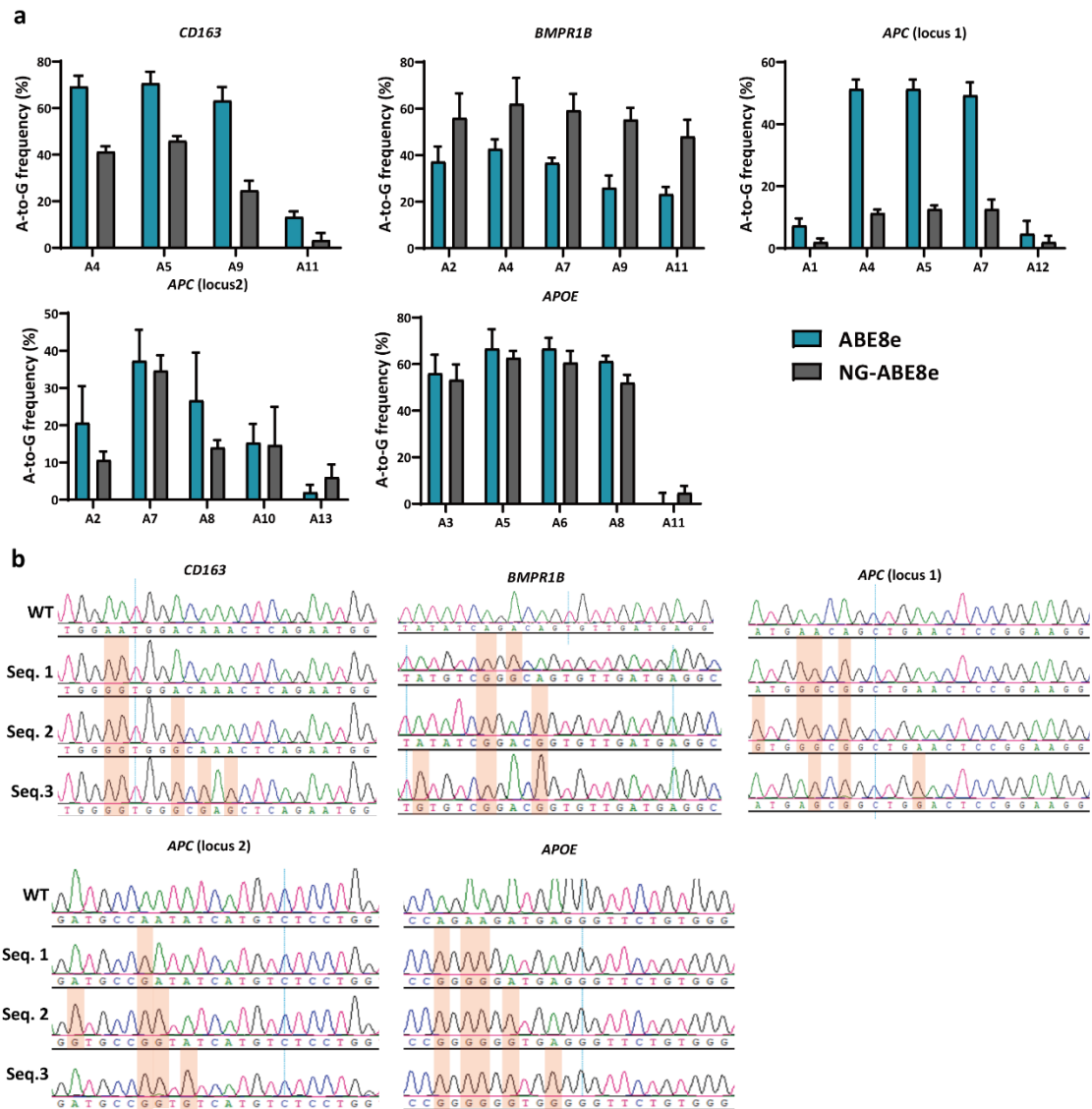
**Figure S2:** Representative sanger sequencing chromatograms of PFFs transfected with ABEs targeting *CD163*, *BMPR1B*, *APC* and *APOE* loci.

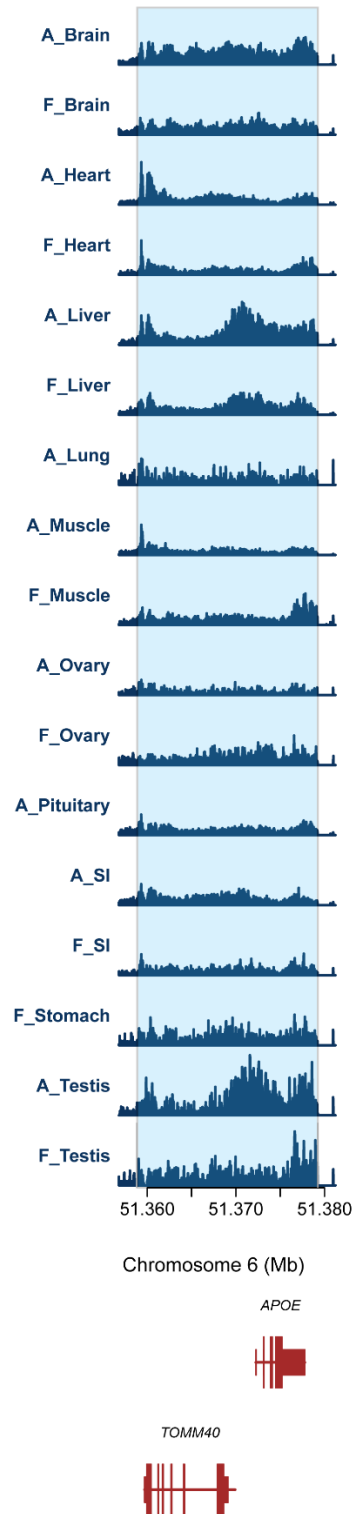


**Figure S3:** Representative sequencing chromatograms of top 10 predicted OTS for each sgRNA.



**Figure S4:** Comparison situation of RNA editing sites between RNA-seq reads and reference genome sequence. The red box represents the RNA editing sites identified.





**Figure S6:** Distribution of H3K27ac modification in chromosome 6. Shaded areas indicate the H3K27ac modification. A: Adult; F: Fetal.