Author Correction: Hypercompact adenine base editors based on a Cas12f variant guided by engineered RNA

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Two Matters Arising pieces pointed out that the nuclease used in our previous study[1] is a variant of Un1Cas12f1, not TnpB[2,3]. Because we fully accept their claims and also credit the authors for raising the issue, we changed "TnpB" to "a variant of Un1Cas12f1 from *Candidatus Woesearchaeota* archaeon (CWCas12f1)" in the article text, figures, extended data figures, supplementary information and source data. In the article title, we changed "transposase B" to "a Cas12f variant". Additionally, we renamed our technology to **T**iny nuclease/**a**ugment **R**NA-based **G**enome **E**diting **T**echnology-**A**denine **B**ase **E**ditor, preserving the former abbreviated name (TaRGET-ABE). We believe that this measure will clear the related arguments regarding the identity of the nuclease used in our ABE system. Despite the correction process, we believe that the nomenclature issue is not likely to detract from the quality and implications of the study based on the following points.

1. Head-to-head comparison of the base-editing efficiency of CWCas12f1 shows significantly higher base-editing efficiency compared to that of the previous Un1Cas12f1 (ref. [4]) (Fig. 2f, Extended Data Fig. 4).
2. The nuclease and deaminase were engineered to create different ABE versions, including TaRGET-ABE-C2.0, 3.0 and 3.1, with which specific and flexible base editing can be achieved in a sequence-context manner. Additionally, various PAM variants expanded the scope of this hypercompact base-editing system.
3. Although the nuclease is indeed a longer variant of Un1Cas12f1, this is the first report demonstrating the feasibility of a hypercompact adenine base-editing system in an in vivo system using AAV delivery.
4. Finally, we performed extensive analysis of specificity for the hypercompact base-editing system with respect to guide RNA-dependent and -independent off-target activity, which is also informative.

We believe that this corrective measure could provide accurate descriptions of the identity and utility of our TaRGET-ABE system to the scientific and research community.

References

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