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Author Correction: Targeted exon skipping with AAV-mediated split adenine base editors

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In the original publication of this article[1], Fig. 4 was labelled incorrectly. The second panel displaying *HSF1* Exon 10 should be labelled as *HSF1* Exon 11, while the third panel displaying *JUP* Exon 11 should be labelled as *JUP* Exon 10. The same labelling change should be applied to the corresponding panels in Fig. 5, as *HSF1* Exon 10 and JUP Exon 11 were incorrectly labelled in that figure as well and should be replaced with *HSF1* Exon 11 and *JUP* Exon 10, respectively.

All instances of *HSF1* exon 10 within the text should be corrected to *HSF1* exon 11 and all instances of *JUP* exon 11 should be corrected to JUP exon 10.

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References

1. Winter, J., Luu, A., Gapinske, M., Manandhar, S., Shirguppe, S., Woods, W.S., Song, J.S. & Perez-Pinera, P. Targeted exon skipping with AAV-mediated split adenine base editors. Cell Discov. **5**, 41 (2019).

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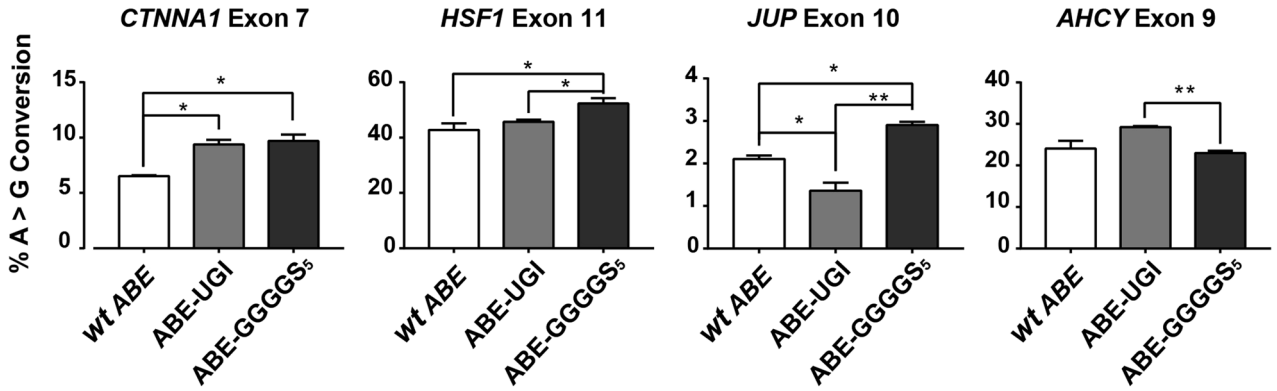

Fig. 4 Quantification of genomic DNA mutation rates created by several ABE constructs at multiple target sites. High-throughput sequencing was used to quantify rates of A > G genomic DNA mutation and rates of exon skipping across multiple targets using several ABE variants. * and ** correspond to $P < 0.05$ and $P < 0.01$, respectively by two-tailed unpaired Student's *t* test across two biological replicates

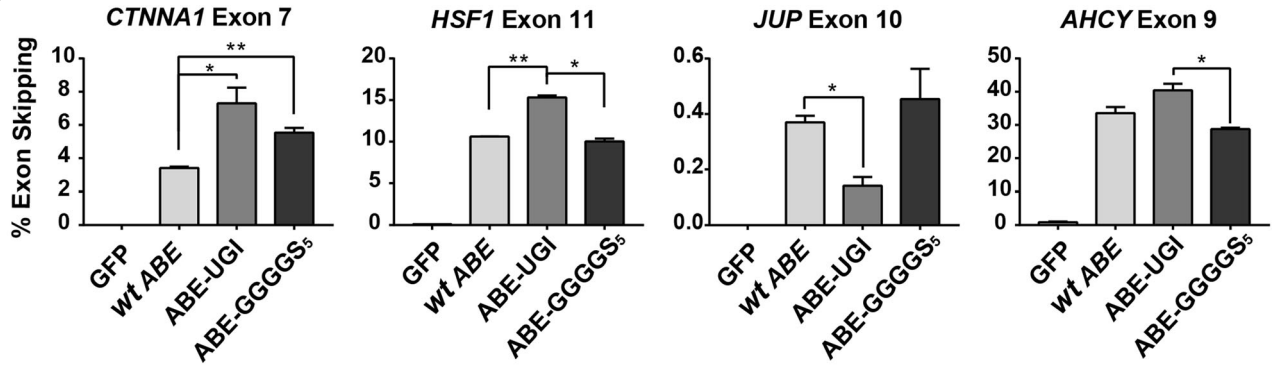

Fig. 5 Quantification of exon skipping rates at multiple gene targets induced by several ABE constructs. High-throughput sequencing of cDNA was used to quantify rates of exon skipping across multiple targets using several ABE variants. * and ** correspond to $P < 0.05$ and $P < 0.01$, respectively by two-tailed unpaired Student's *t* test across two biological replicates