

CRISPR base and prime editing

Achieve precise genome modifications without double-stranded DNA breaks using high-quality mRNA editors and guide RNAs



High on-target editing efficiency



Low off-target editing



High purity mRNA with enzymatic capping



New tool simplifies design and ordering

More precision. More possibilities.

From single-base changes to targeted insertions, deletions, and substitutions.

Base editing features:

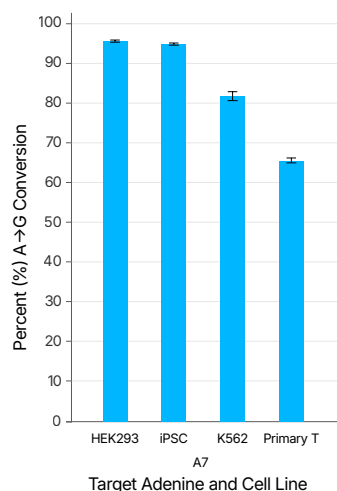
- Make precise A-to-G or T-to-C conversions without double-stranded breaks across a variety of cell types
- Choose base editor mRNA available in wild type and high specificity V106W variants
- Expand editable genomic regions with multiple PAM options
- Select one variant, or quickly test all six with the screening kit
- Alt-R™ Cas9 sgRNA XT are optimized for mRNA and LNP-based genome editing workflows

1 2 3 4 5 6 7 8 9 10 11 12 13 14 15 16 17 18 19 20
G A A C A C A A A G C A T A G A C T G C NGG

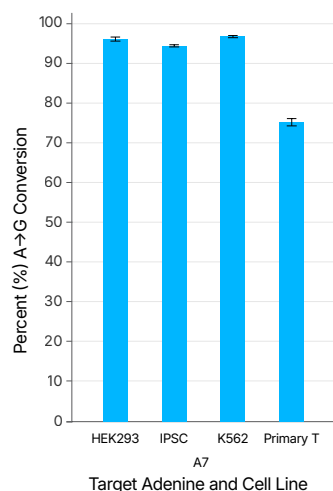
1 2 3 4 5 6 7 8 9 10 11 12 13 14 15 16 17 18 19 20
G C G A G C A G C G T C T T C G A G A G NGN

1 2 3 4 5 6 7 8 9 10 11 12 13 14 15 16 17 18 19 20
G C A G A C C C A G A T A G A C A G G A NRN

A. ABE8e-nCas9
Enhancer hs267



B. ABE8e-nSpG
VEGFA



C. ABE8e-nSPRY
FANCF

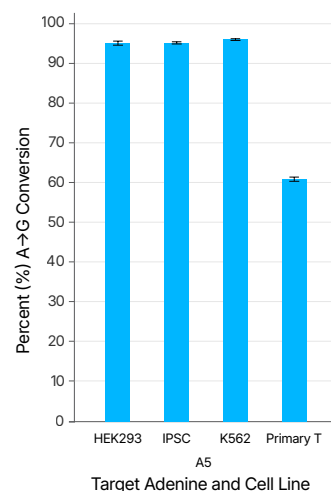


Figure 1. Target adenine editing efficiency across cell types for ABE8e-Cas variant combinations. Target adenine conversion at the indicated genomic loci was measured in HEK293, iPSC, K562, and primary T cells using ABE8e editors paired with nCas9, nSpG, or nSPRY. Data from ABE8e-WT and ABE8e-V106W were combined due to comparable on-target editing efficiencies and are presented as mean ± SEM (N = 6 biological replicates; 3 WT and 3 V106W). Cells were nucleofected using the Lonza nucleofection system with 1,000ng of base editor mRNA in HEK293, K562, and primary T cells or 500ng in iPSCs. gRNA was delivered at 2 μM in HEK293, K562, and iPSCs and 4 μM in primary T cells. High levels of target base conversion were observed across diverse cell types and Cas variants.

Prime editing

Prime editing unlocks the ability to make precise substitutions, insertions, and deletions without requiring double-strand breaks or donor DNA templates. However, developing an efficient editing workflow often requires careful design and optimization. Integrated DNA Technologies' (IDT) prime editing workflow combines an **optimized prime editor, modified synthetic pegRNAs, and a free design tool** to streamline experiment design and support successful editing outcomes.

Prime editing features:

- Optimized PE Ultra mRNA was engineered for improved activity vs commonly used PE editors
- Alt-R™ pegRNAs are highly modified for increased stability and editing efficiency
- Free pegRNA design tool simplifies selection and ordering
- Alt-R pegRNAs are chemically modified and engineered for use with mRNA to improve stability, cellular performance, and editing efficiency

Comparison of editing efficiency of PE Ultra mRNA to commercially available PEmax

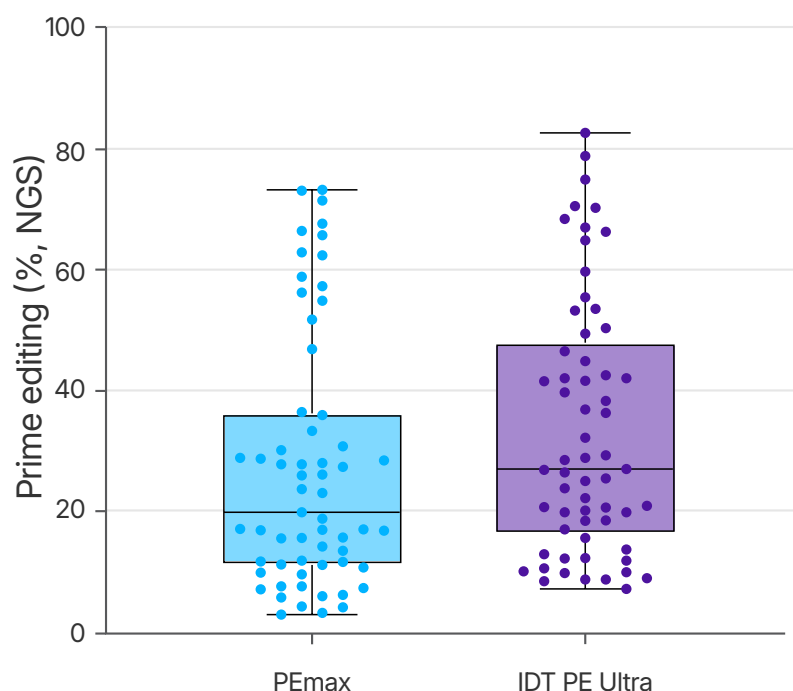


Figure 1. Editing efficiency of PE Ultra and PEmax in HEK293 cells PE Ultra and PEmax mRNA and Alt-R pegRNA (6 μ M) targeting a broad panel of sites (all 6 bp insertions) were delivered by nucleofection into HEK293 cells using the Lonza Nucleofection™ System. Genomic DNA (gDNA) was extracted 72 hours post nucleofection and editing was assessed by NGS.

For more information, visit idtdna.com/BasePrimeEditing



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