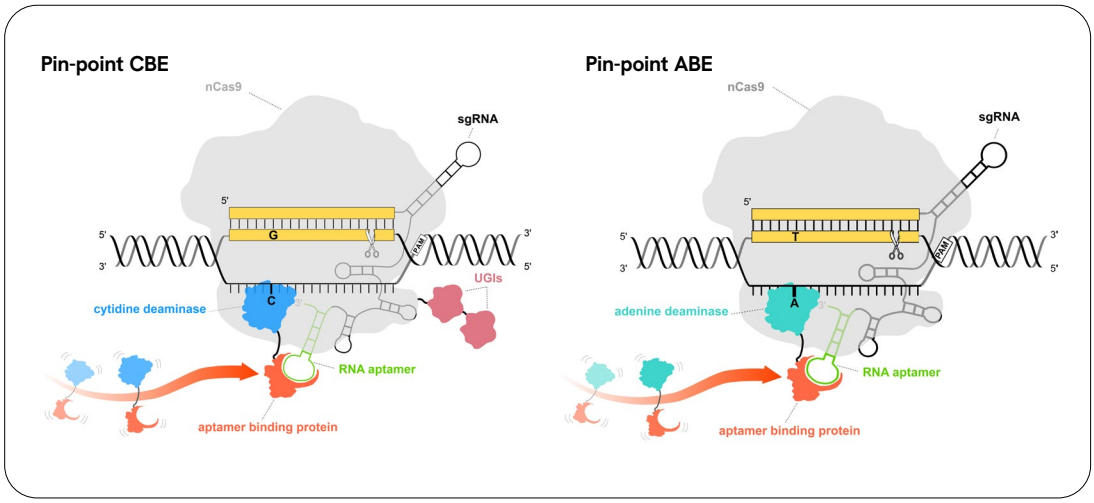
revvity

Precision, redefined.

Pin-point™ base editing ABE and CBE reagents

Base editing with the Pin-point platform induces specific nucleotide changes while avoiding the formation of DNA double-strand breaks or indels.

- Proven high editing efficiencies in clinically relevant iPSC, HSPCs, and T cells
- Reduced cytotoxicity, fewer off-targets, and lower risk of genomic aberrations than CRISPR/Cas9
- Multiplex gene editing including knock-in and knockout with high efficiency and safety
- A single platform to bring treatments to patients faster

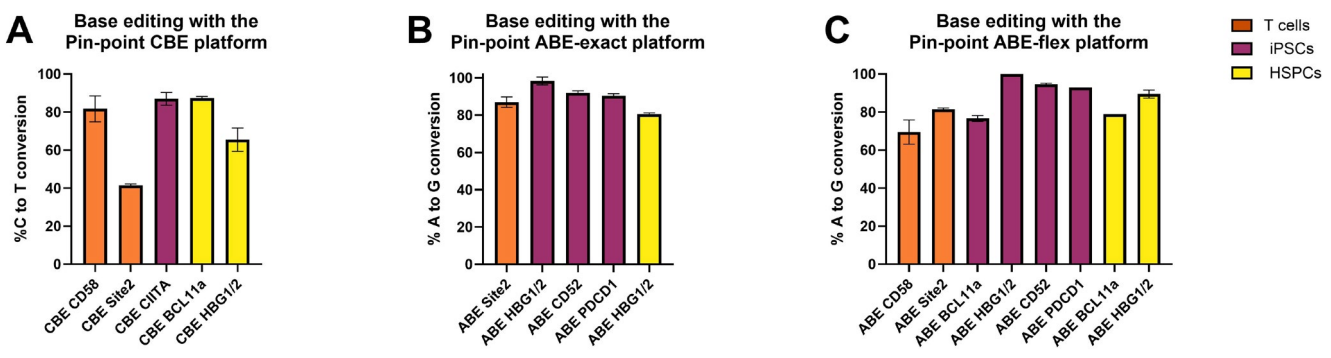


The Pin-point platform consists of three components: [1] a nuclease-defective "nickase" nCas9 that only cuts or "nicks" a single strand of DNA, [2] a cytidine deaminase (rAPOBEC) or an adenine deaminase (ABE-exact or ABE-flex) fused to an aptamer binding protein. The rAPOBEC enzyme converts C-G base pairs to T-A base pairs. ABE-exact and ABE-flex convert A-T base pairs to G-C base pairs, [3] an aptameric single guide RNA (sgRNA) that recruits the nCas9 and the aptamer-deaminase fusion to a specific DNA target site.

Pin-point base editing reagents – multiple product formats available to fit your experimental needs.

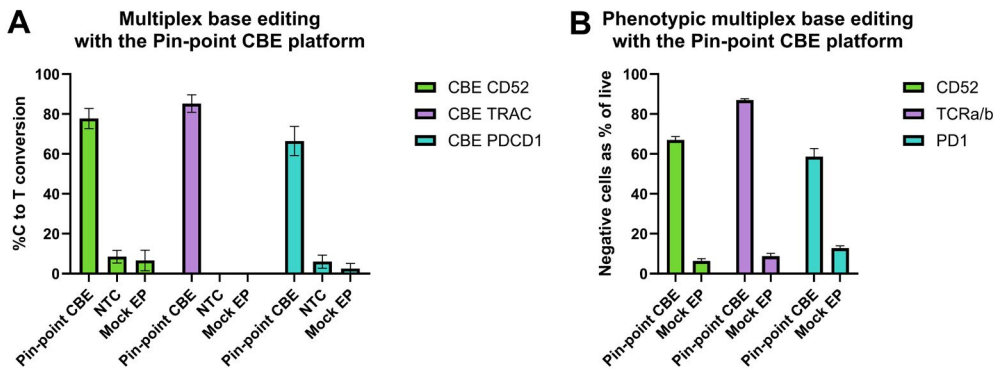
	Cytosine base editor (CBE)		Adenine base editor (ABE)	
Nickase (unmod or 5moU-modified mRNAs)	CBE nCas9		ABE nCas9	
Deaminase (unmod or 5moU-modified mRNAs)	CBE rAPOBEC deaminase		ABE-exact and ABE-flex deaminases designed using Profluent's frontier AI models	
sgRNAs + analysis primers	CBE CD52 CBE PDCD1 CBE TRAC CBE Site2 CBE PCSK9	CBE CD58 CBE CIITA CBE HBG1/2 CBE BCL11a	ABE CD52 ABE PDCD1 ABE TRAC ABE Site2	ABE CD58 ABE HBG1/2 ABE BCL11a
Custom sgRNA (Standard purification or HPLC)	Use our custom sgRNA design tool to target your gene of interest! https://horizondiscovery.com/en/ordering-and-calculation-tools/pin-point-base-editing-design-tool			

Efficient base editing using Pin-point mRNAs and control synthetic sgRNA reagents in various cell types.



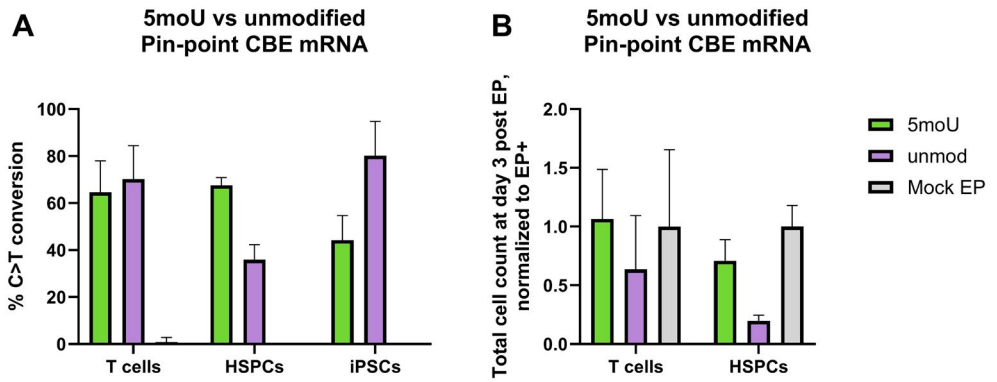
Base editing levels in activated T cells, iPSCs and HSPCs following electroporation with Pin-point base editing reagents: (A) Pin-point CBE nCas9 mRNA, CBE rAPOBEC deaminase mRNA and control synthetic sgRNAs (B) Pin-point ABE nCas9 mRNA, ABE-exact deaminase mRNA and control synthetic sgRNAs (C) Pin-point CBE nCas9 mRNA, CBE rAPOBEC deaminase mRNA and control synthetic. Base editing levels were assessed by Sanger sequencing.

Efficient multiplex base editing with Pin-point CBE platform in T cells.



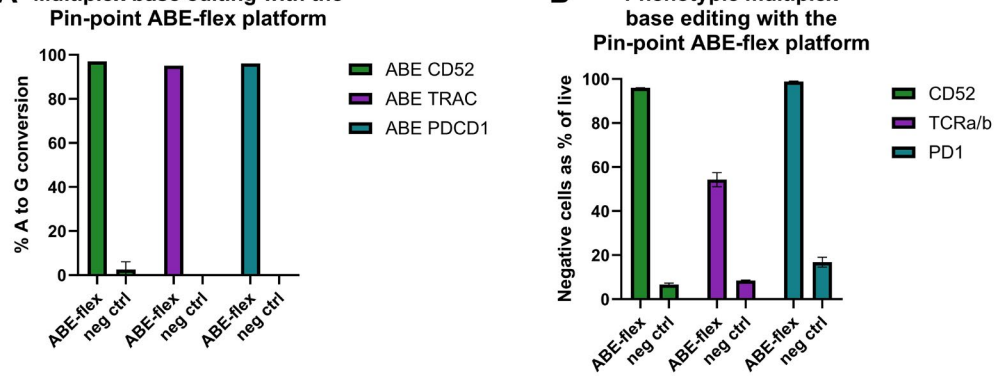
(A) Multiplex base editing levels and (B) protein knockout levels in activated T cells following electroporation with Pin-point CBE mRNAs and Pin-point synthetic sgRNAs for the 3 targets (CD52, PDCD1 and TRAC), or non-targeting control (NTC #1) sgRNA. Mock-electroporated (EP) cells were used as negative controls. Base editing levels were assessed by Sanger sequencing of PCR products, and protein knockout levels were evaluated by flow cytometry.

Base editing with the Pin-point CBE platform using unmodified or 5moU-modified mRNAs in T cells, HSPCs, and iPSCs.



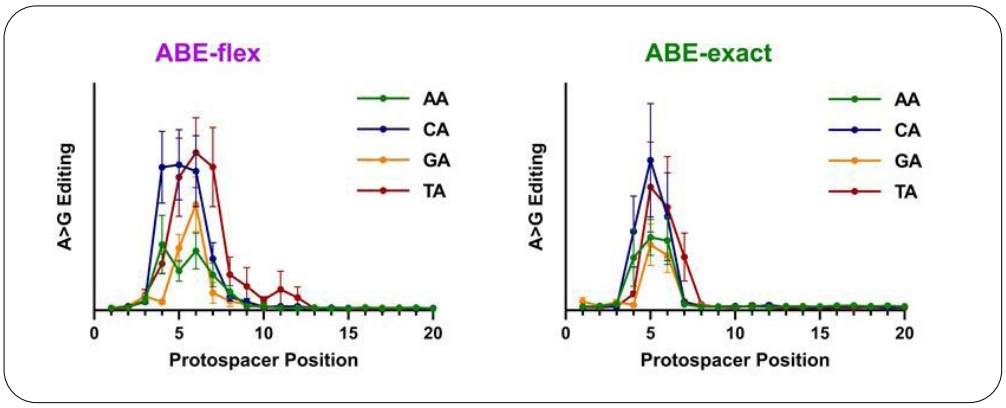
(A) Base editing levels and (B) total cell count 3 days post-EP when delivering a custom Pin-point synthetic sgRNA targeting a chain of the major histocompatibility complex class 1 and either Pin-point unmodified or Pin-point 5moU modified mRNAs in T cells, iPSCs, and HSPCs.

Efficient multiplex base editing with the Pin-point ABE platform in T cells.



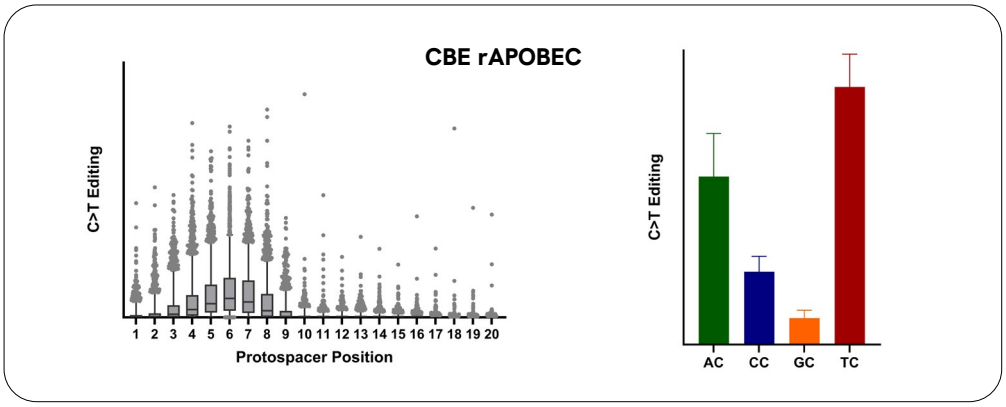
(A) Multiplex base editing levels and (B) protein knockout levels in activated T cells following electroporation with Pin-point nCas9 mRNA, ABE-flex deaminase mRNA and synthetic sgRNA controls targeting CD52, TRAC and PDCD1. Base editing levels were assessed by Sanger sequencing. Percent protein knockout was evaluated by flow cytometry.

Editing window and influence of the preceding base on ABE-flex and ABE-exact editing efficiency.



The nucleotide immediately upstream of the target adenine within the protospacer affects A→G editing outcomes. Both ABE-flex and ABE-exact show highest editing efficiency when the preceding base is C or T, whereas a preceding G or A base reduces target adenine editing. ABE-flex primarily edits positions 4–7, with lower-efficiency editing extending to positions 3 and 8–12. ABE-exact shows a narrower window centered on positions 5–6, with reduced editing at positions 4 and 7.

Editing window and influence of the preceding base on CBE rAPOBEC editing efficiency.



The Pin-point CBE rAPOBEC deaminase has a preferred editing window from positions 4-8, with extended editing possible at positions 2-9. Editing is optimal when the preceding base is an A or T, whereas a preceding C or G base reduces target cytosine editing.

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Pin-point™ base editing reagents are available for research use only and are not for diagnostic use or direct administration into humans or animals. The Pin-point™ base editing platform technology is available for clinical or diagnostic study and commercialization under a commercial license from Revvity.