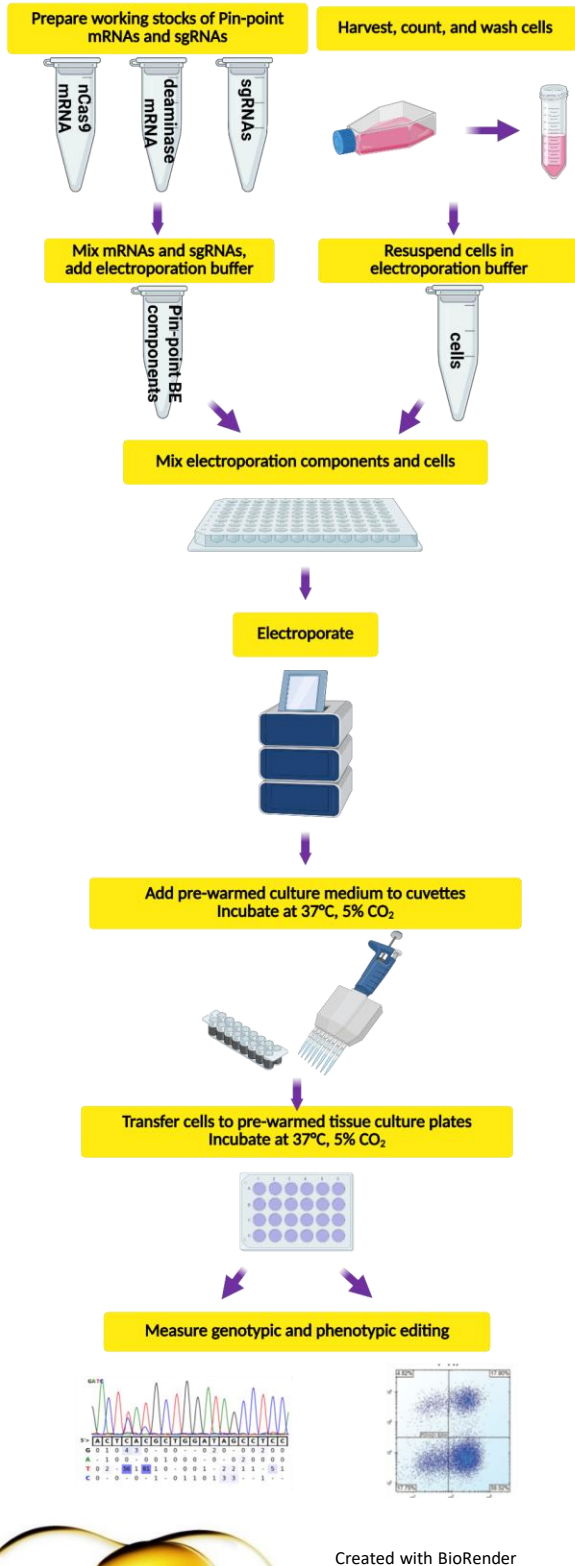


# Pin-point™ adenine base editing (ABE) platform

## Short protocol for electroporation of activated human T cells using the Lonza 4D-Nucleofector® System

### Experimental workflow:



The following is a protocol for delivering unmodified [Pin-point ABE nCas9 mRNA](#) (Cat # PNP13767, PNP13768, and PNP13769), [Pin-point ABE-exact deaminase mRNA](#) (Cat # PNP13781, PNP13782, and PNP13783) or [Pin-point ABE-flex deaminase mRNA](#) (Cat # PNP13773, PNP13774, and PNP13775), and Pin-point ABE sgRNAs ([validated controls](#) or [custom](#)) to activated human T cells using the Lonza 4D-Nucleofector System with the P3 Primary Cell 96-well Nucleofector® Kit. For more details, please refer to the [Pin-point platform ABE technical manual](#). (EP = electroporation)

Day -2	<b>Plate cells</b>	Seed cells at $1 \times 10^6$ cells/mL and activate using CD3/28 beads in T cell culture medium containing IL-2. Incubate at 37°C and 5% CO <sub>2</sub> .																												
	<b>Prepare post-EP plates</b>	Add 500 µL culture medium with cytokines (IL-2, IL-7, IL-15) to 24-well plates. Incubate at 37°C and 5% CO <sub>2</sub> .																												
	<b>Prepare Pin-point base editing components</b>	Prepare working stock solutions of mRNAs and sgRNAs on ice according to the table below.																												
	<b>Prepare the cells</b>	Harvest and count the cells. Transfer the desired number of cells for electroporation into a 15 mL conical tube. Wash with PBS, centrifuge at 200 x g for 5 - 10 mins. Resuspend cell pellet in P3 nucleofector solution: $1 \times 10^7$ cells/mL (250,000 cells per 20 µL EP).																												
Day 0	<b>Mix EP components</b>	Gently mix mRNAs + sgRNAs + cells:																												
		<table border="1"> <thead> <tr> <th></th> <th>Pin-point component</th> <th>Working stock*</th> <th>Final amount per 20 µL EP</th> <th>Volume per 20 µL EP</th> </tr> </thead> <tbody> <tr> <td rowspan="3">mRNA and sgRNA mix</td> <td>ABE nCas9 mRNA</td> <td>2 µg/µL</td> <td>1.5 µg</td> <td>0.75 µL</td> </tr> <tr> <td>ABE deaminase mRNA</td> <td>2 µg/µL ABE-exact, 0.2 µg/µL ABE-flex*</td> <td>1 µg ABE-exact, 0.1 µg ABE-flex</td> <td>0.5 µL</td> </tr> <tr> <td>Synthetic sgRNA</td> <td>200 µM</td> <td>40 pmol</td> <td>0.2 µL</td> </tr> <tr> <td>P3 nucleofector solution</td> <td>-</td> <td>-</td> <td>-</td> <td>to 10 µL</td> </tr> <tr> <td>Cells</td> <td>Cells in P3 nucleofector solution</td> <td>-</td> <td><math>2.5 \times 10^5</math> cells</td> <td>10 µL</td> </tr> </tbody> </table>		Pin-point component	Working stock*	Final amount per 20 µL EP	Volume per 20 µL EP	mRNA and sgRNA mix	ABE nCas9 mRNA	2 µg/µL	1.5 µg	0.75 µL	ABE deaminase mRNA	2 µg/µL ABE-exact, 0.2 µg/µL ABE-flex*	1 µg ABE-exact, 0.1 µg ABE-flex	0.5 µL	Synthetic sgRNA	200 µM	40 pmol	0.2 µL	P3 nucleofector solution	-	-	-	to 10 µL	Cells	Cells in P3 nucleofector solution	-	$2.5 \times 10^5$ cells	10 µL
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* ABE nCas9 mRNA and ABE deaminase mRNAs are shipped at 2 µg/µL																														
Day 0	<b>EP</b>	Electroporate 20 µL on Lonza 4D-Nucleofector System using program EO-115.																												
		Add 80 µL of pre-warmed culture medium without cytokines to the cuvette.																												
		Incubate at 37°C, 5% CO <sub>2</sub> for 15 - 30 mins.																												
Day 0	<b>EP</b>	Gently transfer 100 µL of electroporated cells into prepared plates and disperse evenly by tilting/rocking.																												
		Incubate at 37°C, 5% CO <sub>2</sub> .																												
Days 3 - 7	<b>Post-EP culture and analysis</b>	On day 3 post EP, adjust cell density to $1 \times 10^6$ cells/mL in culture medium with IL-2.																												
		Proceed with desired genotypic (Sanger sequencing) and/or phenotypic (flow cytometry) analyses of base editing levels.																												

If you have questions or comments, please reach out to [Scientific Support](#).