ENGINEERED CELLS

CRISPR-Edited iPS Cells. Guaranteed.

High-efficiency, high-quality editing of iPS Cells to accelerate your research.

The ability to edit induced pluripotent stem (iPS) cells using CRISPR-Cas9 gives researchers a powerful discovery tool for many applications including disease modeling, therapeutic development, and regenerative medicine. However, these cells are notoriously difficult to work with and require special handling and expertise, especially when editing the genome.

Leveraging our history in automated genome engineering, EditCo has applied our editing expertise and high-throughput optimization to deliver high-quality CRISPR edits in iPS cells, guaranteed.

iPS Cell gene editing offerings

Knockouts

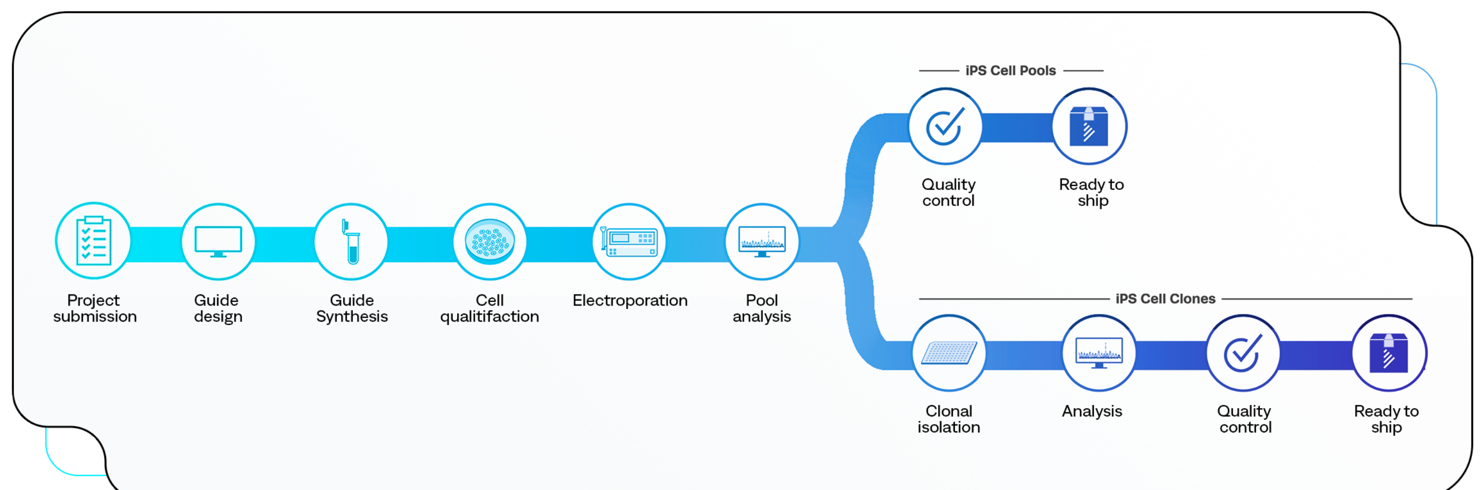
Single nucleotide variants

Tags

We offer knockouts, single nucleotide variants, and tag insertions in control or patient-derived iPS cell lines — available in homozygous or heterozygous clone or pool formats.

EditCo streamlines iPS Cell editing and quality process

EditCo achieves the highest efficiency of gene modifications in iPS cells by using modified sgRNA, proprietary high-throughput protocols, and robotic systems for cell culture and reliability.



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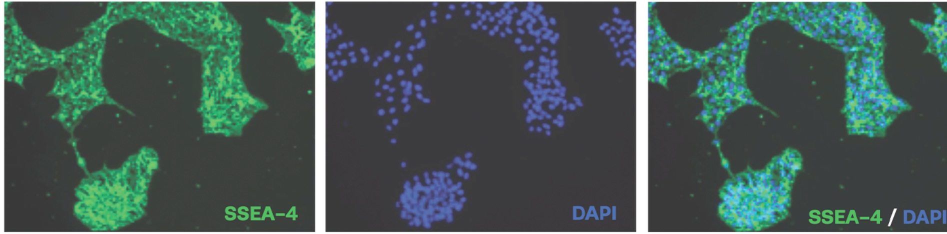
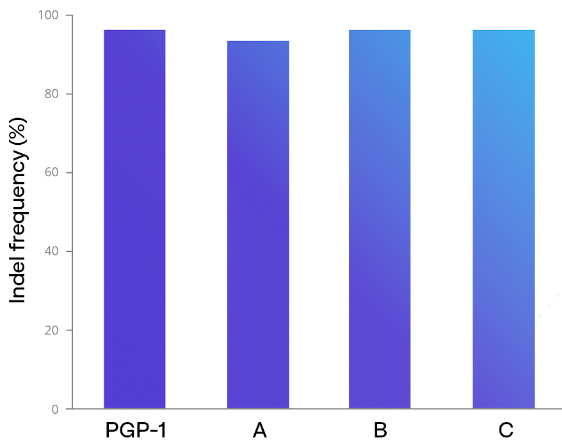
Maintaned pluripotency in edited iPS Cells



Immunofluorescence images of CRISPR-edited iPS cells demonstrate maintained pluripotency as measured by SSEA-4 protein expression (green). The nuclear stain DAPI (blue) used to show the presence of cells.

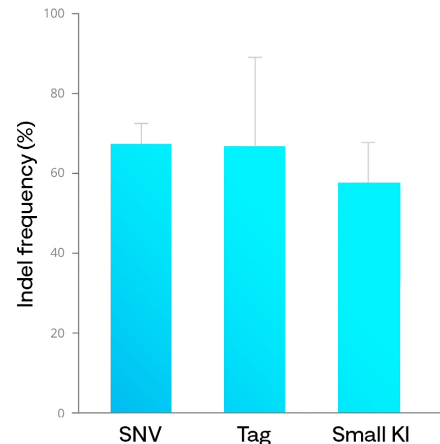
High-efficiency knockouts and knock-ins in iPS Cells

Knockouts



Modified sgRNAs were transfected along with Cas9 as RNPs to knock out RELA in four individual iPS cell lines. Each population of cells was PCR-amplified around the cut site, Sanger-sequenced, and submitted for ICE analysis to determine editing efficiency.

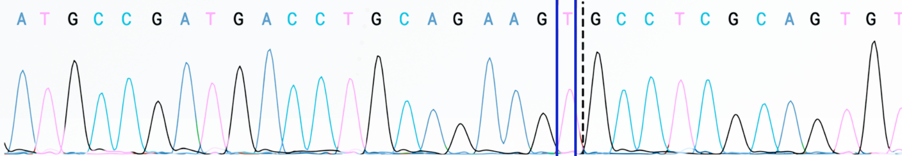
Knock-ins



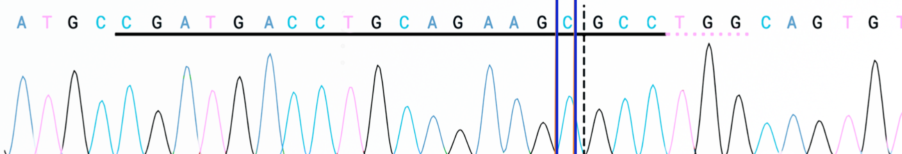
Average KI efficiency in a EditCo and customer supplied iPSC lines by type. Tags and Small KIs <100 bps. Edits were performed using RNPs and ssODNs. Editing efficiency assessed in the pool stage. Editing efficiency determined by DNA extraction, PCR-amplification, Sanger-sequencing, and ICE analysis.

Precision SNV editing in iPS Cells for your translational studies

Edited sample



Parental control



A CRISPR-edited homozygous clone containing a single nucleotide change (top) relative to the parental control (bottom). The single nucleotide change from cytosine (C) to thymine (T) in the control and edited trace, respectively, is enclosed by the orange box. The target sequence is underlined in black and the PAM site is underlined with a red dashed line in the control trace.

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