

# Knockout Primary Immune Cell Pools

## Knockout Primary Immune CD4+ T Cells

Made-to-order primary human T-cell pools in 28 days or faster. Multi-guide™ technology guarantees >80% knockout efficiency while still retaining high cell viability.

Donor ID	Donor 1	Donor 2	Donor 3
Race	White or Caucasian	White or Caucasian	White or Caucasian
Smoker	Non-Smoker	Non-Smoker	Non-Smoker
Age	59	24	52
Gender	Female	Male	Female

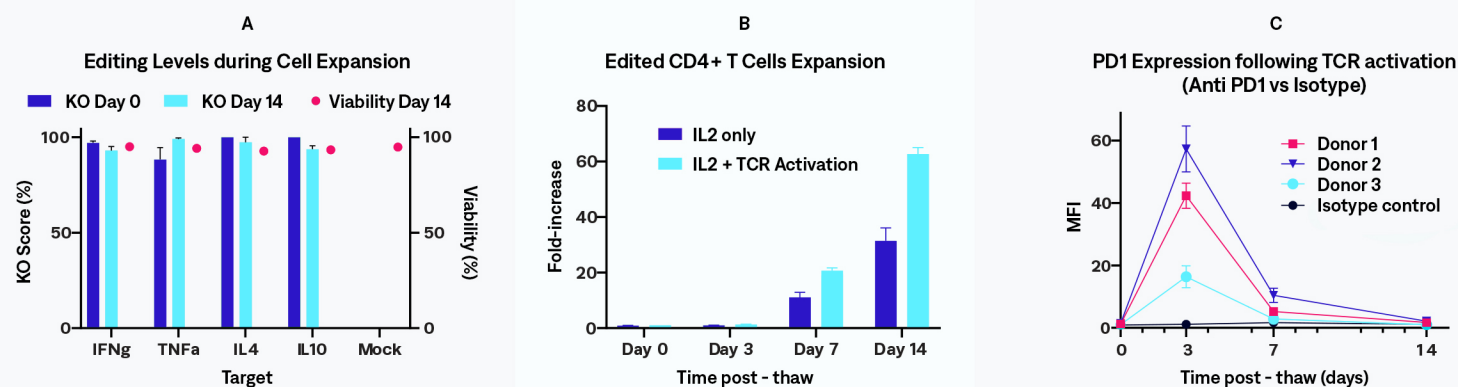
**Figure 1. Editing Efficiency and Viability for CD4+ T cell pools.** Three different donors (left table) show high editing efficiency, as determined by ICE analysis, across a variety of loci (green bars, mean KO scores ± SEM) without affecting viability at the time of freezing (blue dots).



## High-Quality Cell Results

The editing process and further expansion before freezing do not affect cell fitness. Cells can be thawed and expanded upon receiving to be used in any desired downstream assays, maintaining high cell viability and editing levels (Figure 2).

**Figure 2. CD4+ pool stability after thaw.** Panel A. Pools of 4 different edits from 3 separate donors showed >90% viability and no decrease in editing efficiency after 14 days in culture. Panel B. Relative fold expansion for edited pools and mock cultured with TCR activator or IL2 alone. Panel C. PD1 expression in TCR activator-treated cultures peaked on day 3 in all tested donors (edited and mock samples). Isotype control staining over the same period is shown for reference.



## Multi-Guide™ Technology Enables Target Protein Depletion

Multi-guide™ technology uses up to 3 sgRNAs to disrupt an early exon of the target protein-coding gene (Figure 3). The guides induce one or more fragment deletions by making concurrent double-strand breaks in the target gene. These deletions significantly increase the probability of a functional knockout while minimizing off-target effects.

**Figure 3.** The multi-guide approach employs up to 3 sgRNAs (green bars) that target a single gene of interest and are designed to yield fragment deletions within gene exons rather than smaller indels.

