## SUPPLEMENTAL MATERIAL



Seki and Rutz, https://doi.org/10.1084/jem.20171626





Figure S2. Electroporation of in vitro transcribed sgRNA and recombinant Cas9 protein leads to highly efficient gene KO in primary T cells. (A) Schematic depiction of RNP components, in vitro-transcribed sgRNA, and recombinant Cas9 protein. (B) Titration of amount and ratio of sgRNA/Cas9 targeting CD90 in activated mouse CD8<sup>+</sup> T cells. Data are representative of two independent experiments. (C) KO efficiency as measured by flow cytometry 3 d after RNP transfection targeting CD90, CTLA4, and PD1 in activated mouse CD8<sup>+</sup> T cells. Data are representative of two independent experiments. (D) Titration of number of activated mouse CD8<sup>+</sup> T cells transfected with sgRNA targeting CD90. Data are representative of two independent experiments.





Figure S3. **KO of Foxp3 in expanded human regulatory T cells.** KO efficiency of targeting FoxP3 in human regulatory T cells expanded in vitro for 7 d was analyzed by flow cytometry 72 h after RNP transfection. Data are presented as mean  $\pm$  SD (n = 2) and representative of two independent experiments. \*\*\*\*, P < 0.001 by one-way ANOVA.



Figure S4. **Optimization of RNP transfection conditions in nonactivated mouse T cells. (A–C)** Systematic optimization of nucleofection parameters for RNP transfection of nonactivated mouse CD8<sup>+</sup> T cells. Cell viability (A), transfection efficiency as determined by tracrRNA positive cells (B), and KO efficiency (%; C) of mouse CD8<sup>+</sup> T cells transfected with RNP targeting CD90 and cultured for 2 d either without any stimulation or with anti-CD3/anti-CD28 stimulation. Data are from one experiment. **(D and E)** Analysis by flow cytometry of viable cells and CD25 and CD69 expression after 3 d of culture and titration of IL-2, IL-7, or IL-15 in CD8<sup>+</sup> (D) or CD4<sup>+</sup> mouse T cells (E). Data are presented as mean  $\pm$  SD (n = 2) and representative of two independent experiments.



## Table S1. gRNA sequences

Name	Sequence (5'-3')	Name	Sequence (5'-3')
sgRNA (plasmid constructs	s)		
mCd4_1	ACTCCTAGCTGTCACTCAA	mCd90_1	ATGGCGGCAGTCCAGGCGA
mCd4_2	AAGGGAAGACGCTGGTGCT	mCd90_2	CTTGGTGTTATTCTCATGG
mCd4_3	TAAGTTTATTGATGATGAG	mCd90_3	TGCTGGATGGAGTTATCCT
mCd4_4	AGAGTTGCTATCCAAGGTC	mCd90_4	CTTCCTCTTCTCGGGTC
sgRNA (IVT)			
mCd90_1	GGCGAAGGTTTTGGTTCACC	mCtla4_1	GACCCAACCTTCAGTGGTGT
mCd90_2	AAAGTAGTCGCCCTCATCCT	mCtla4_2	ATGGAAAGCTGGCGACACCA
mPd1_1	CGGAGGATCTTATGCTGAAC		
mPd1_2	GACACACGGCGCAATGACAG		
crRNA			
mPd1_1	ACAGCCCAAGTGAATGACCA	hCXCR4_1	GAAGCGTGATGACAAAGAGG
mPd1_2	TGAATGACCAGGGTACCTGC	hCXCR4_2	AGGGAAGCGTGATGACAAAG
mPd1_3	AGTTGAGCTGGCAATCAGGG	hCXCR4_3	ACGGCATCAACTGCCCAGAA
mCtla4_1	AGGTCCGGGTGACTGTGCTG	hCCR7_1	TACCTACCTGCTCAACCTGG
mCtla4_2	GACAAATGACCAAATGACTG	hCCR7_2	CATCAGCATTGACCGCTACG
mCtla4_3	ATGGAAAGCTGGCGACACCA	hCCR7_3	AAAGTGGACACCGAAGACCC
mCd90_1	CCGCCATGAGAATAACACCA	hCD127_1	TCAGGCACTTTACCTCCACG
mCd90_2	CCTTGGTGTTATTCTCATGG	hCD127_2	CAGGCACTTTACCTCCACGA
mCd90_3	GAGCAGGAGAGCGACGCTGA	hCD127_3	CAAGTCGTTTCTGGAGAAAG
mCd8a_1	ATCCCACAACAAGATAACGT	hIFNG_1	CCAGAGCATCCAAAAGAGTG
mCd8a_2	TGAAGCCATATAGACAACGA	hIFNG_2	AAAGAGTGTGGAGACCATCA
mCd8a_3	TGGGTGAGTCGATTATCCTG	hIFNG_3	TGCAGGTCATTCAGATGTAG
mFoxp3_1	TGGACGCACTTGGAGCACAG	hFOXP3_1	CTTGAGGGAGAAGACCCCAG
mFoxp3_2	TCTACCCACAGGGATCAATG	hFOXP3_2	GAGGGAGAAGACCCCAGTGG
mFoxp3_3	CTTGAGGGAGAAGACCCCAG	hFOXP3_3	GGGGTGCACCTGCAGCACAG
		hPD1_1	CTGCAGCTTCTCCAACACAT
NTC	Negative control crRNA #1 (IDT 1072544)	hPD1_2	CGTGTCACACAACTGCCCAA
		hPD1_3	GCCCTGGCCAGTCGTCTGGG
		hCTLA4_1	CCAGGTGACTGAAGTCTGTG
		hCTLA4_2	CACTGTCACCCGGACCTCAG
		hCTLA4_3	GCACGTGGCCCAGCCTGCTG
		hTIGIT_1	CAGGCACAATAGAAACAACG
		hTIGIT_2	GACCTGGGTCACTTGTGCCG
		hTIGIT_3	CAGCGCATGCTTCTGCCCAG