

## Supplementary Information

### **Combined Lentiviral- and RNA-mediated CRISPR/Cas9 Delivery for Efficient and Traceable Gene Editing in Human Hematopoietic Stem and Progenitor Cells**

David Yudovich<sup>1,2</sup>, Alexandra Bäckström<sup>1,2</sup>, Ludwig Schmiderer<sup>1</sup>, Kristijonas Žemaitis<sup>1</sup>, Agatheeswaran Subramaniam<sup>1</sup> and Jonas Larsson<sup>1\*</sup>

<sup>1</sup>Division of Molecular Medicine and Gene Therapy, Lund Stem Cell Center, Lund University, Lund, Sweden

<sup>2</sup>Equal contribution

\*Correspondence to Jonas Larsson MD PhD, Molecular Medicine and Gene Therapy, BMC A12, 221 84, Lund, Sweden; phone: +46-46-2220580; fax: +46-46-2220568; e-mail: [jonas.larsson@med.lu.se](mailto:jonas.larsson@med.lu.se)

**Supplementary Table 1. List of unique predicted off-target sites for CD45 sg5**

Number	Chr position	Score	NGS
1	Chr2:28427250-28427271	0.97	Yes
2	Chr8:144448492-144448513	0.99	Yes
3	ChrX:153573824-153573845	2.43	Yes
4	Chr6:42935481-42935501	3.02	Yes
5	Chr15:90000801-90000821	3.02	PCR failed
6	Chr16:49494734-49494754	4.68	N/A
7	Chr7:98949526-98949547	4.7	N/A
8	Chr16:48447603-48447623	5.64	N/A
9	Chr18:76612153-76612173	5.86	N/A
10	Chr19:8903492-8903513	6.13	N/A

**Supplementary Table 2. Off-target editing (% modification normalized to on-target efficiency for each condition) for CD45 sg5**

Sample	Off-target site			
	#1 Chr2:28427250-28427271	#2 Chr8:144448492-144448513	#3 ChrX:153573824-153573845	#4 Chr6:42935481-42935501
Untreated	0.03	0.00	0.00	0.00
RNP (3 µg)	0.00	10.15	1.91	1.16
mRNA (1.5 µg)	0.58	4.47	0.63	0.29
LV sg5 + protein (3 µg)	0.00	0.00	0.00	0.00
LV sg5 + mRNA (1.5 µg)	0.13	2.00	0.00	0.00

**Supplementary Table 3. sgRNA sequences**

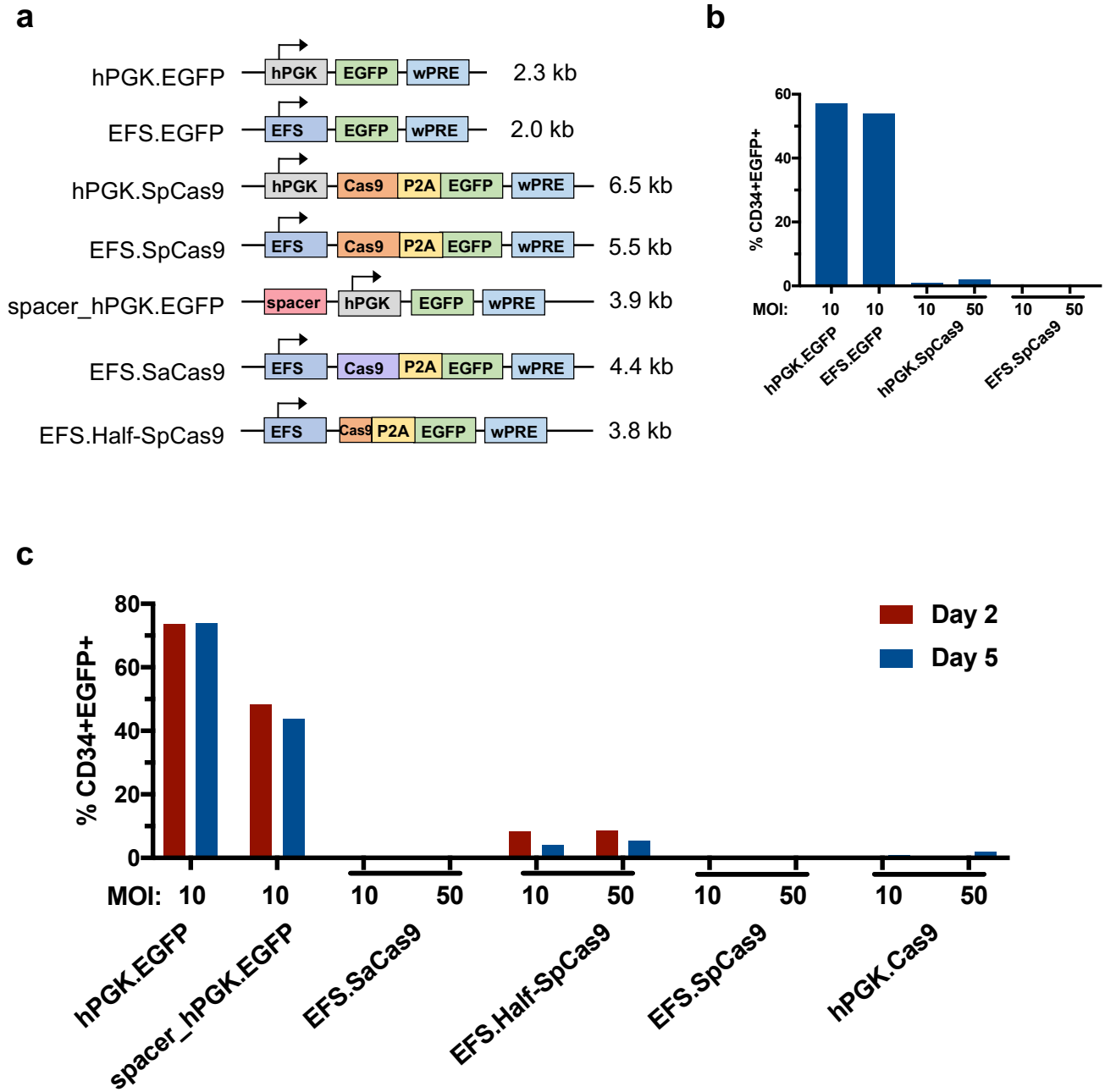
Gene target	Guide	Sequence
CD45	sg5*	GGTGCTGGTGTGGGCGCAC
CD45	sg8	GGGCGCACAGGAACCTATAT
Non-targeting	ntA	GACGGAGGCTAAGCGTCGCAA
CD44	sg1	GAAGGGCACGTGGTGATTCCC
CD44	sg2	GCAATATGTGTCATACTGGG
CD44	sg3	GTACAGGTATGGGTTCATAGA
CD44	sg4	GCCAGCTATTGTTAACCGTGA
CD29	sg1	GTCATCACATCGTGCAGAAGT
CD29	sg2	GAATGTAACCAACCGTAGCAA
CD29	sg3	GCATAAGGTAGTAGAGGTCAA
CD29	sg4	GACAGCGCATATCTGGAAATT

\*sgRNA sequence adapted from Gundry *et al.* 2016.

**Supplementary Table 4. Primer sequences**

Primer	Sequence 5'-3'
CD45_G5_Tag_FWD	CTGGGGCTGACTTTCCTCAG
CD45_G5_Tag_REV	TGAGCATCTCTCCAAACAGACA
CD44_G1t3_Tag_FWD	GTGGGGGAATGGGACATGAG
CD44_G1t3_Tag_REV	GCACTTTCCTGACCACCTT
CD44_G4_Tag_FWD	TCCTAGCCAGAAGTGGGTGT
CD44_G4_Tag_REV	AGGAGGGCTCTCCCCAAAAT
CD29_G1t2_Tag_FWD	AGCAGGATGAGGAGGAGAGG
CD29_G1t2_Tag_REV	ACACTTGGGTCAGTTCTGGG
CD29_G3_Tag_FWD	TTGGCACACCAGCTCTCAAT
CD29_G3_Tag_REV	GTGGCATCCCACTACACACA

## Supplementary Figure S1

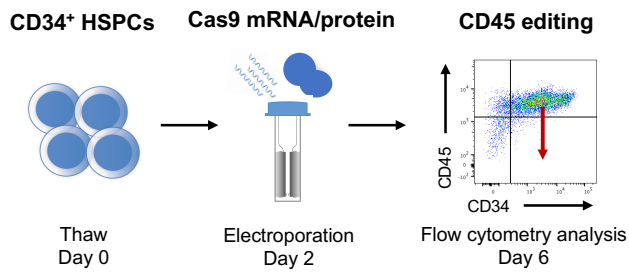


### Supplementary Figure S1. Challenge of lentiviral Cas9 delivery in human CD34<sup>+</sup> HSPCs

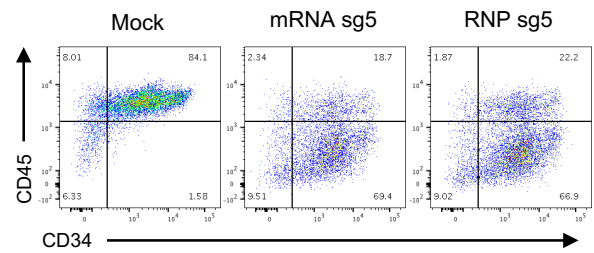
(a) Schematic outline of pLCv2 vectors. (b and c) CD34<sup>+</sup> HSPCs were transduced on day 2 post-thaw. EGFP and CD34 expression was analysed by flow cytometry on day 2 and/or day 5 post-transduction.

## Supplementary Figure S2

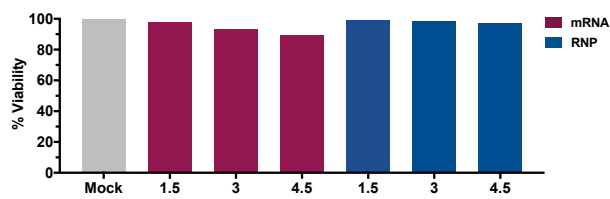
**a**



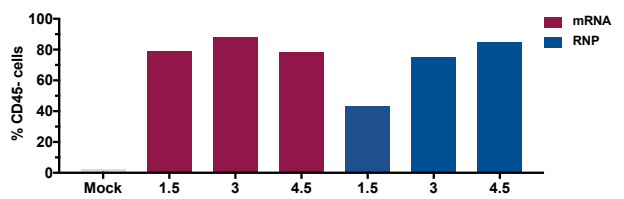
**b**



**c**



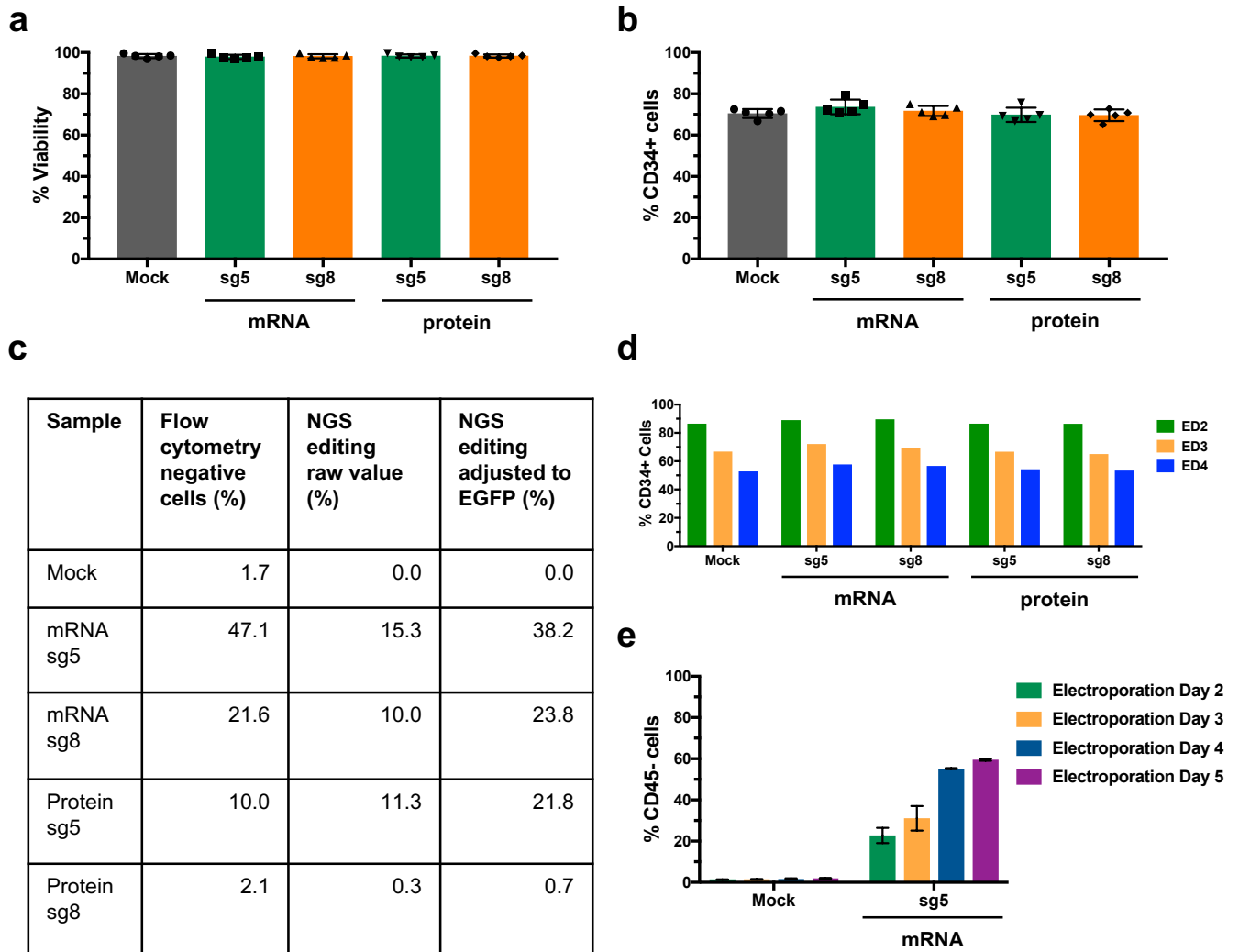
**d**



### Supplementary Figure S2. CD45 editing using Cas9 mRNA or protein with synthetic, modified sgRNA

CD34<sup>+</sup> HSPCs were treated with Cas9 mRNA or protein at various concentrations, in combination with co-electroporated modified, synthetic sgRNA targeting CD45 (sg5), and analysed by flow cytometry. **(a)** Overview of experimental outline. **(b)** Representative FACS plots of CD45 editing using 1.5  $\mu$ g Cas9 mRNA or 3  $\mu$ g Cas9 protein. **(c)** Viability analysis by flow cytometry 7AAD staining. **(d)** Frequency of CD45 edited cells.

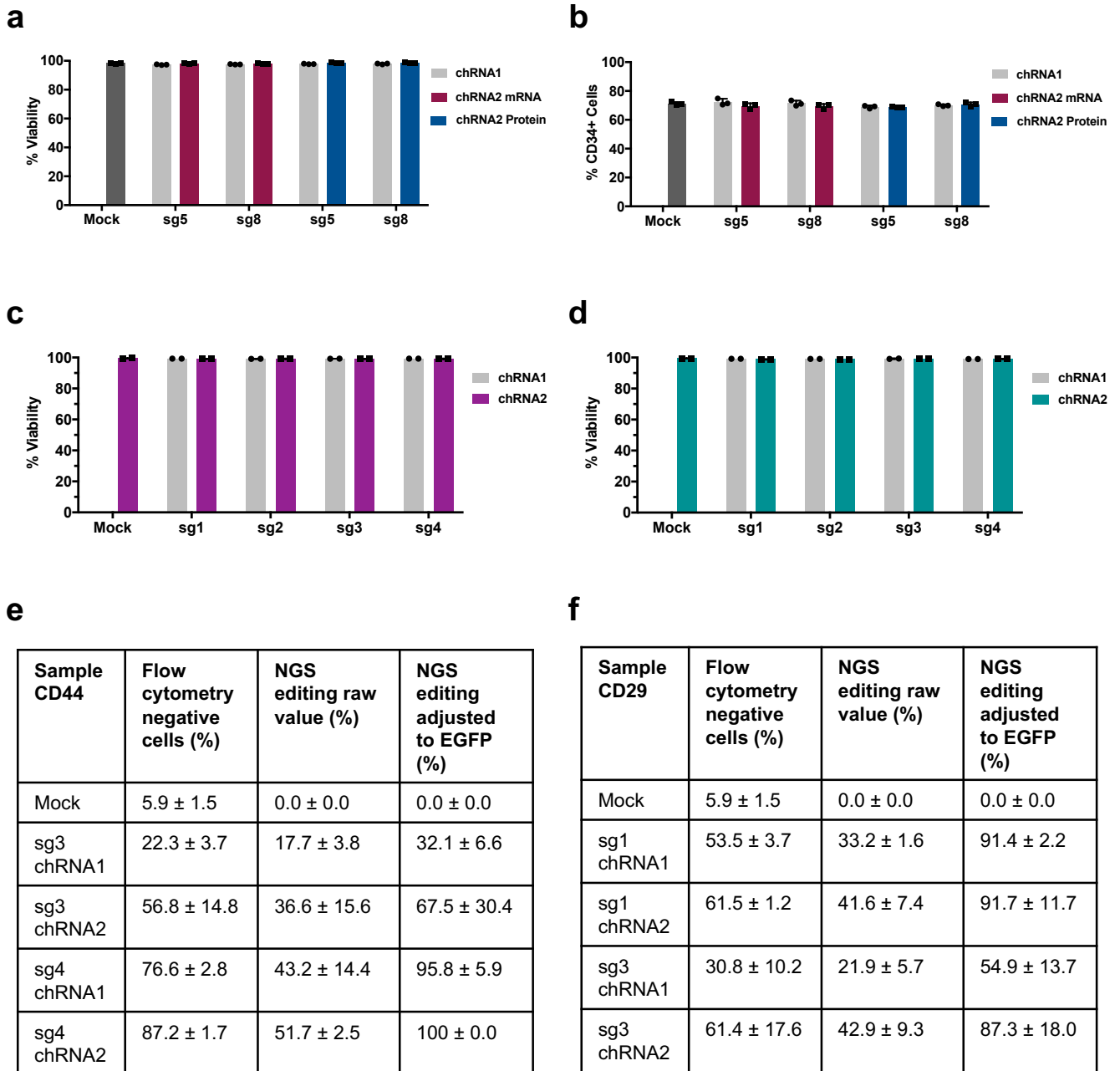
## Supplementary Figure S3



### Supplementary Figure S3. Effect on viability and CD34 expression from HSPC editing using Cas9 mRNA or protein with lentiviral sgRNA

(a and b) Primary CD34<sup>+</sup> HSPCs were transduced with sgRNA targeting CD45 (sg5 or sg8) and subsequently electroporated with Cas9 mRNA or protein (n=5). (a) Viability measured by 7AAD staining, (b) CD34<sup>+</sup> expression analysed by flow cytometry 4 days following the electroporation and (c) NGS analysis for representative samples, cells were collected 4 days following the electroporation. Note, raw gene editing efficiency scores were divided by percent EGFP<sup>+</sup> cells to provide an estimate of editing efficiency within the transduced population. (d) CD34<sup>+</sup> cells were transduced on day 1 with sgRNA targeting CD45, electroporated on either day 2, 3 or 4, and subsequently analysed by flow cytometry for CD34 expression 4 days following the electroporation. (e) CD34<sup>+</sup> cells were transduced on day 1 with sgRNA targeting CD45, electroporated with Cas9 mRNA on either day 2, 3, 4 or 5, and subsequently analysed by flow cytometry for CD45<sup>-</sup> cells 4 days following the electroporation.

## Supplementary Figure S4

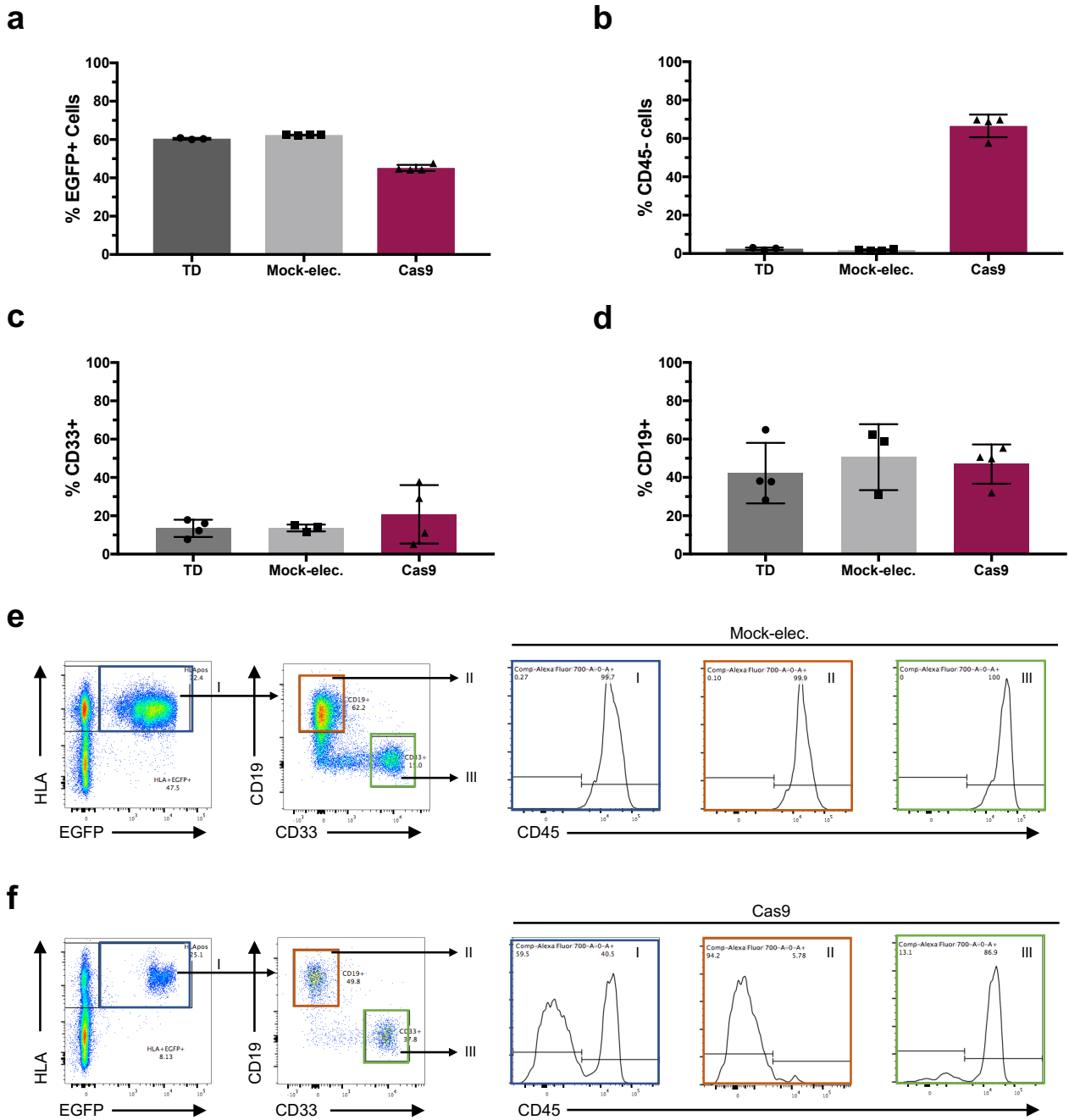


### Supplementary Figure S4. Modified chimeric guide RNA backbone enhances editing efficiency in HSPCs without compromising viability or CD34 expression

CD34<sup>+</sup> cells were transduced with sg5 or sg8 targeting CD45 encoding either chimeric guide RNA backbone 1 or 2 on day 1 post-thaw, electroporated with Cas9 mRNA or protein on day 4, and analysed by flow cytometry on day 8 (n=3). (a) Viability by 7AAD staining and (b) CD34<sup>+</sup> expression.

CD34<sup>+</sup> cells were transduced on day 1 post-thaw with 4 different lentiviral sgRNAs per target gene encoding either chimeric guide RNA backbone 1 or 2, electroporated with 2 µg Cas9 mRNA on day 4, and analysed by flow cytometry on day 8. At this time point, cells were also collected for NGS (n = 2). (c) Viability by 7AAD staining in CD44 edited cells and (d) in CD29 edited cells. (e) NGS analysis of the CD44 locus and (f) of the CD29 locus in edited cells ± standard deviation (s.d.). Note, raw gene editing efficiency scores were divided by percent EGFP<sup>+</sup> cells to provide an estimate of editing efficiency within the transduced population.

## Supplementary Figure S5



**Supplementary Figure S5. Edited CD34<sup>+</sup> HSPCs retain reconstitution capacity in vivo** (a and b) A portion of edited CD34<sup>+</sup> cells from each group was not used for transplantation and maintained in culture and analysed by flow cytometry 4 days after electroporation. (a) Frequency of EGFP<sup>+</sup> cells. (b) Frequency of CD45<sup>-</sup> cells in the EGFP<sup>+</sup> population. (c-f) BM from transplanted NSG mice harvested 9-12 weeks post-transplantation analysed by flow cytometry. n=3-4 mice per group. (c) Frequency of CD33<sup>+</sup> cells within the HLA<sup>+</sup>EGFP<sup>+</sup> population. (d) Frequency of CD19<sup>+</sup> cells within the HLA<sup>+</sup>EGFP<sup>+</sup> population. (e and f) Gating strategy to determine CD45 editing in the HLA<sup>+</sup>EGFP<sup>+</sup> population (I), CD19<sup>+</sup> population (II) and in the CD33<sup>+</sup> population (III), showing examples for (e) mock-electroporated and (f) Cas9-electroporated cells.