

Supplementary information

Rh D blood group conversion using transcription activator-like effector nucleases

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Supplementary information:

Supplementary Figures 1 – 15

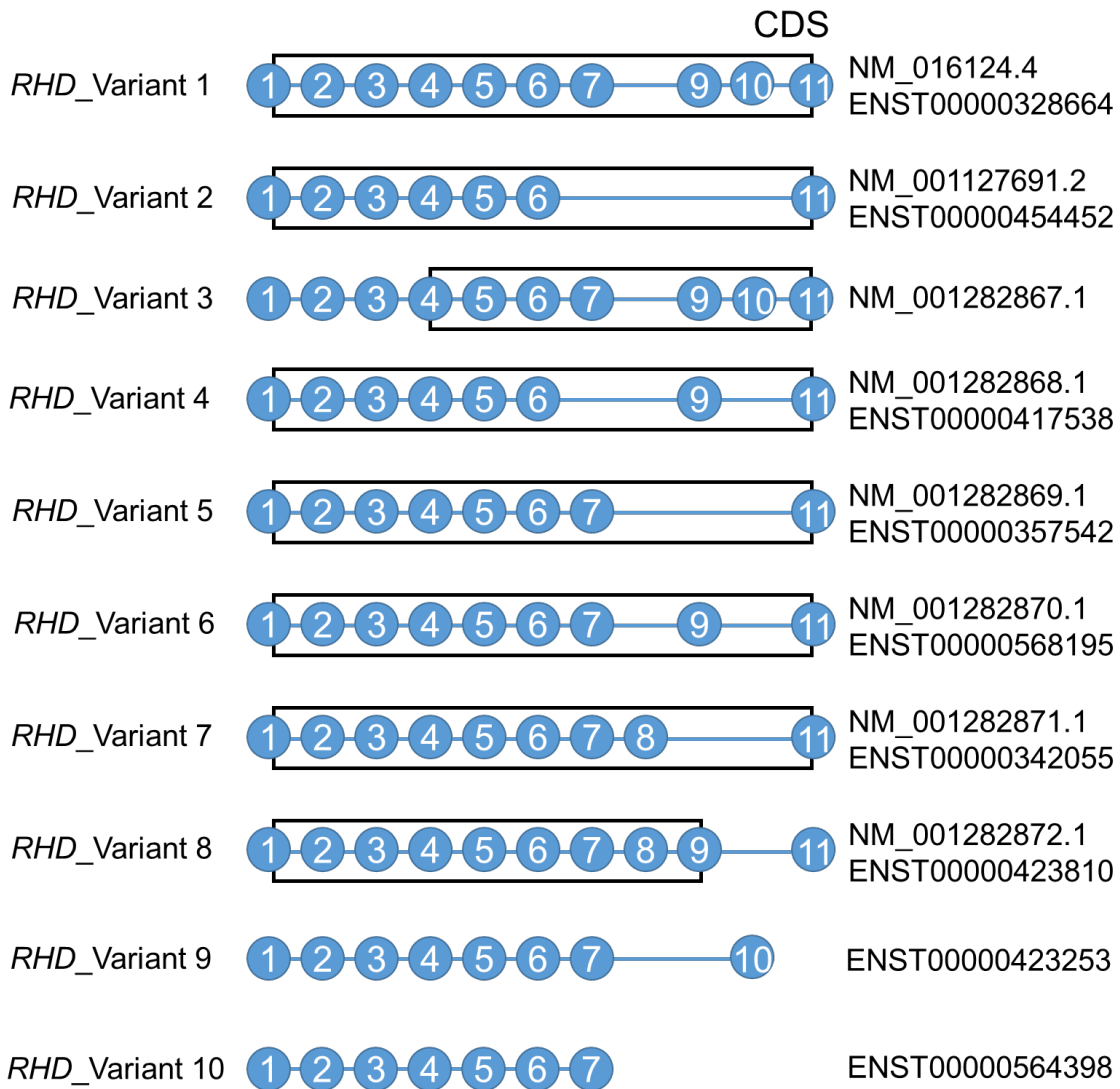
Supplementary Table 1

Supplementary Note 1

Supplementary Reference

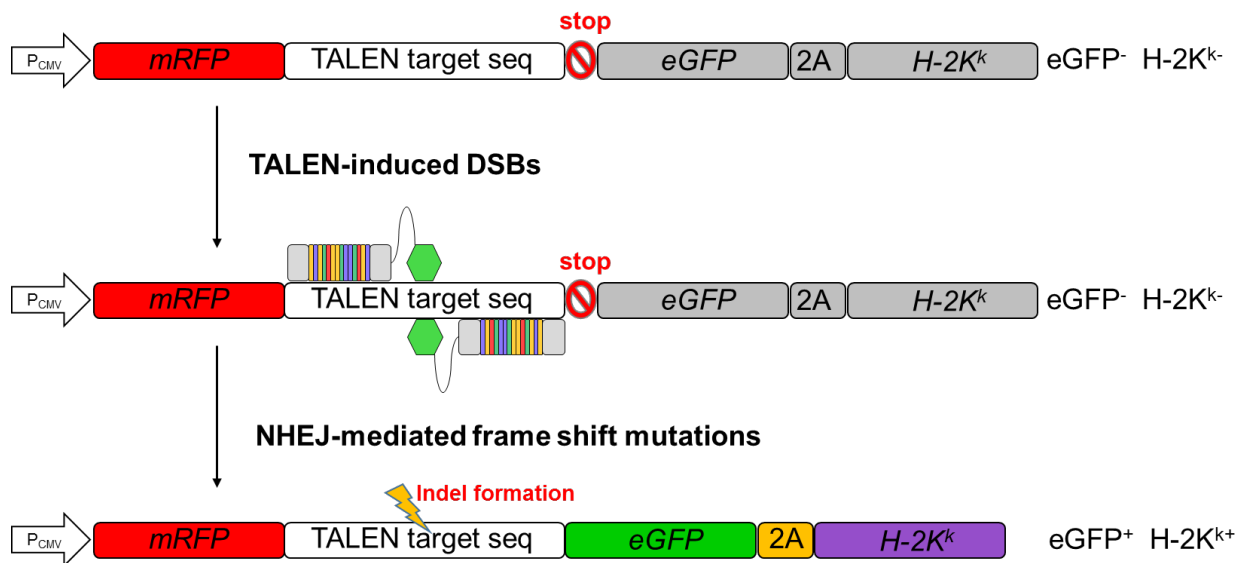
Supplementary Figure 1. The reported transcript variants of the *RHD* gene

The transcript variants of *RHD* reported in NCBI and Ensembl are shown with their accession numbers and transcript IDs, respectively, on the right. All of the variants have the start codon in exon 1 except variant 3, which has the start codon in exon 4. Blue circles and black boxes indicate exons and coding sequence (CDS), respectively.



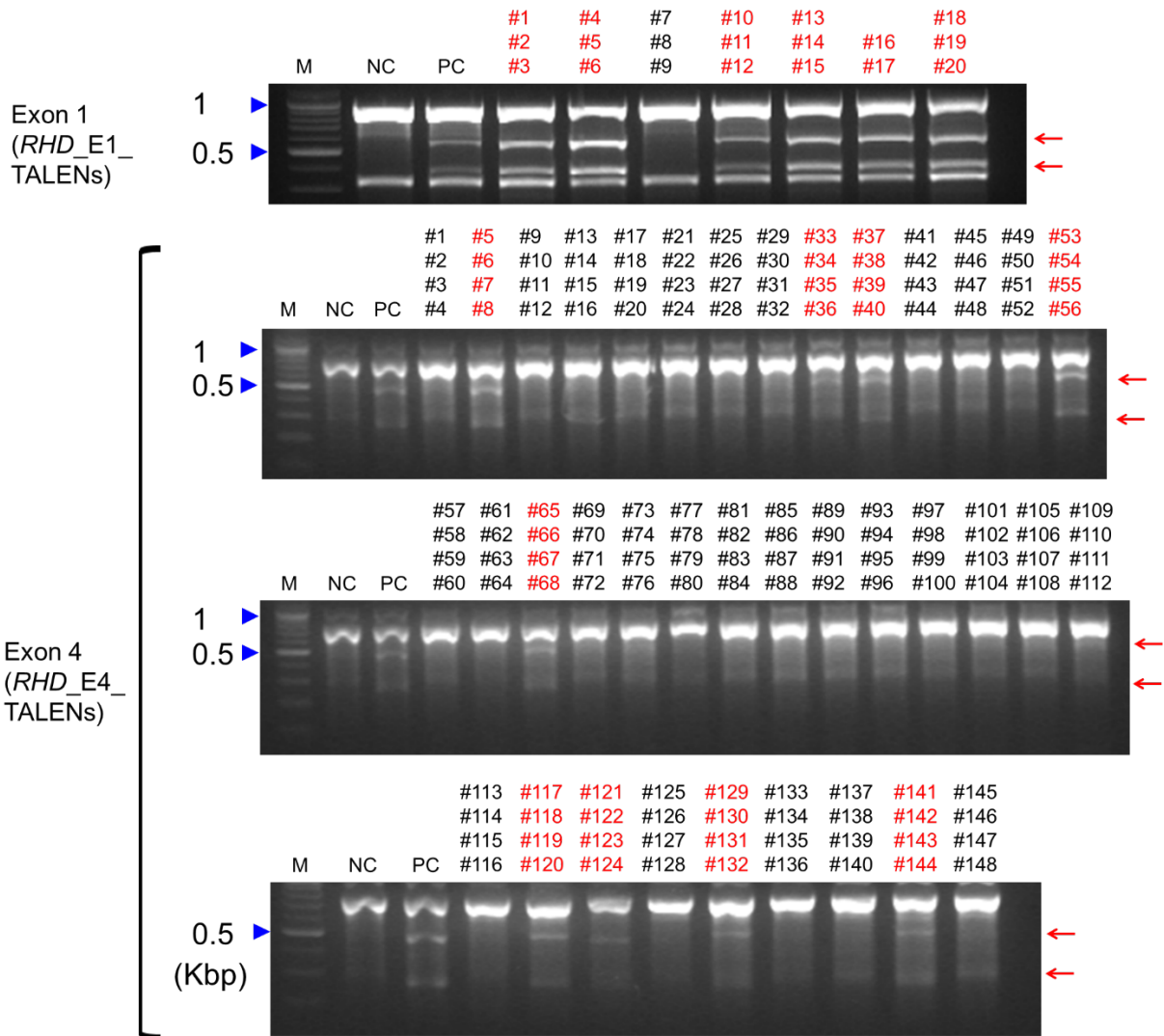
Supplementary Figure 2. The structure and working mechanism of the episomal reporters

mRFP is constitutively expressed by the CMV promoter (P_{CMV}), whereas eGFP and H-2K^k are not expressed without the activity of TALENs because i) the sequences are out of frame and ii) there is a stop codon before the eGFP gene. When a double-strand break is introduced into the target sequence by TALENs, the break is repaired by nonhomologous end-joining (NHEJ) which often results in indels. Indel generation can cause frame shifts, which can render eGFP and H-2K^k genes in frame and lead to the expression of eGFP and H-2K^k.



Supplementary Figure 3. T7E1 assay to screen mutant clones

Clonal culture of HiDEP-1 erythroid progenitor cells was initiated three days after transfection with plasmids encoding TALENs that target *RHD*. Genomic DNA from each clone was analyzed 17 days after the initiation of clonal culture. Genomic DNA from four clones was mixed at a 1:1:1:1 weight ratio and subjected to the T7E1 assay to determine whether at least one of the four clones contains mutations. The identities of the clones in each DNA mixture are shown. Arrows indicate the expected position of DNA bands cleaved by T7E1. Genomic DNA mixtures containing mutations at the target sites are marked with red clone numbers. Untransfected cells and a cell population transfected with the TALENs were used as the negative control (NC) and positive control (PC), respectively. The sizes of marker (M) bands are shown on the left (Kbp, kilobase pairs).



Supplementary Figure 4. DNA sequences of *RHD*-mutated clones

HiDEP-1 cells were co-transfected with the reporter plasmid and plasmids encoding TALENs that target *RHD* exon 1 (a, b) or exon 4 (c). After magnetic separation, cells were subjected to clonal culture. Genomic DNA was isolated from each clone, PCR-amplified, and cloned into T vectors; individual cloned amplicons were then subjected to sequencing. The *RHD* gene DNA sequences in the wild-type cells and selected clones (#number) are shown with TALE binding sequences in a red font. Clone #7 (a) was subjected to another cycle of transfection, magnetic separation, and clonal culture; subclones derived from clone #7 are indicated by a number following #7 (b). Deleted bases are indicated by dashes and inserted bases are shown in a blue font. The number of occurrences is shown in parentheses (e.g., x2 and x4 indicate the number of each sequence). Clones that were selected for further experiments are indicated with the clone name in a red color.

a Exon 1

GGGCCCTAACACTGGAAGCAGCTCTCATTCTCCTCTTCTATTTTTTTTACCCACTATGACGCTTC (Wild type)

#1 GGGCCCTAACACTGGAAGCAGCTCTCATTCTCCTCTTCTATTTTTTTTACCCACTATGACGCTTC (x2) ← Wild type
GGGCCCTAACACTGGAAGCAGCTCTCAT--TCCTCTTCTATTTTTTTTACCCACTATGACGCTTC (x3) ← 2nt deletion; out of frame

#3 GGGCCCTAACACTGGAAGCAGCTCTCATTCTCCTCTTCTATTTTTTTTACCCACTATGACGCTTC (x3) ← Wild type
GGGCCCTAACACTGGAAGCAGCTCTCATTCT--TCTTCTATTTTTTTTACCCACTATGACGCTTC (x2) ← 2nt deletion; out of frame

#4 GGGCCCTAACACTGGAAGCAGCTCTCATTCTCC-----ATTTTTTTTACCCACTATGACGCTTC (x3) ← 6nt deletion; inframe
GGGCCCTAACACTGGAAGCAGCTCTCATTCTC--CTTCTATTTTTTTTACCCACTATGACGCTTC (x2) ← 2nt deletion; out of frame

#6 GGGCCCTAACACTGGAAGCAGCTCTCATTCTCCTCTTCTATTTTTTTTACCCACTATGACGCTTC (x1) ← Wild type
GGGCCCTAACACTGGAAGCAGCTCTCAT-----TCTTCTATTTTTTTTACCCACTATGACGCTTC (x11) ← 5nt deletion; out of frame

#11 GGGCCCTAACACTGGAAGCAGCTCTCATTCTCCTCTTCTATTTTTTTTACCCACTATGACGCTTC (x2) ← Wild type
GGGCCCTAACACTGGAAGCAGCTCTCAT-----TCTTCTATTTTTTTTACCCACTATGACGCTTC (x3) ← 5nt deletion; out of frame

#15 GGGCCCTAACACTGGAAGCAGCTCTCATTCTCCTCTTCTATTTTTTTTACCCACTATGACGCTTC (x3) ← Wild type
GGGCCCTAACACTGGAAGCAGCTCTCATTCTCC---TCTATTTTTTTTACCCACTATGACGCTTC (x2) ← 3nt deletion; inframe

#17 GGGCCCTAACACTGGAAGCAGCTCTCATTCTCCTCTTCTATTTTTTTTACCCACTATGACGCTTC (x1) ← Wild type
GGGCCCTAACACTGGAAGCAGCTCTCATTCTC--CTTCTATTTTTTTTACCCACTATGACGCTTC (x4) ← 2nt deletion; out of frame

#19 GGGCCCTAACACTGGAAGCAGCTCTCATTCTCCTCTTCTATTTTTTTTACCCACTATGACGCTTC (x2) ← Wild type
GGGCCCTAACACTGGAAGCAGCTCTCATTCTCCTC--CTATTTTTTTTACCCACTATGACGCTTC (x2) ← 2nt deletion; out of frame

#20 GGGCCCTAACACTGGAAGCAGCTCTCATTCTCCTCTTCTATTTTTTTTACCCACTATGACGCTTC (x3) ← Wild type
GGGCCCTAACACTGGAAGCAGCTCTCA-----TTCTATTTTTTTTACCCACTATGACGCTTC (x1) ← 8nt deletion; out of frame

b Exon 1

GGGCCCTAACACTGGAAGCAGCTCTCATTCTCCTCTTCTATTTTTTTTACCCACTATGACGCTTC (Wild type)

- #17-1 GGGCCCTAACACTGGAAGCAGCTCTCATTCTCCTCTTCTATTTTTTTTACCCACTATGACGCTTC (x2) ← Wild type
GGGCCCTAACACTGGAAGCAGCTCTCATTCTC--CTTCTATTTTTTTTACCCACTATGACGCTTC (x4) ← 2nt deletion; out of frame
- #17-2 GGGCCCTAACACTGGAAGCAGCTCTCATTCTCCTCTTCTATTTTTTTTACCCACTATGACGCTTC (x2) ← Wild type
GGGCCCTAACACTGGAAGCAGCTCTCATTCTC--CTTCTATTTTTTTTACCCACTATGACGCTTC (x3) ← 2nt deletion; out of frame
- #17-3 (E1_B) GGGCCCTAACACTGGAAGCAGCTCTCATTCTCCT--TTCTATTTTTTTTACCCACTATGACGCTTC (x7) ← 1nt deletion; out of frame
GGGCCCTAACACTGGAAGCAGCTCTCATTCTC--CTTCTATTTTTTTTACCCACTATGACGCTTC (x5) ← 2nt deletion; out of frame
- #17-4 GGGCCCTAACACTGGAAGCAGCTCTCATTCTCCTCTTCTATTTTTTTTACCCACTATGACGCTTC (x1) ← Wild type
GGGCCCTAACACTGGAAGCAGCTCTCATTCTC--CTTCTATTTTTTTTACCCACTATGACGCTTC (x4) ← 2nt deletion; out of frame
- #17-5 GGGCCCTAACACTGGAAGCAGCTCTCATTCTCCTCTTCTATTTTTTTTACCCACTATGACGCTTC (x2) ← Wild type
GGGCCCTAACACTGGAAGCAGCTCTCATTCTC--CTTCTATTTTTTTTACCCACTATGACGCTTC (x4) ← 2nt deletion; out of frame
- #17-6 GGGCCCTAACACTGGAAGCAGCTCTCATTCTCCTCTTCTATTTTTTTTACCCACTATGACGCTTC (x3) ← Wild type
GGGCCCTAACACTGGAAGCAGCTCTCATTCTC--CTTCTATTTTTTTTACCCACTATGACGCTTC (x3) ← 2nt deletion; out of frame
- #17-7 GGGCCCTAACACTGGAAGCAGCTCTCATTCTCCTCTTCTATTTTTTTTACCCACTATGACGCTTC (x2) ← Wild type
GGGCCCTAACACTGGAAGCAGCTCTCATTCTC--CTTCTATTTTTTTTACCCACTATGACGCTTC (x4) ← 2nt deletion; out of frame

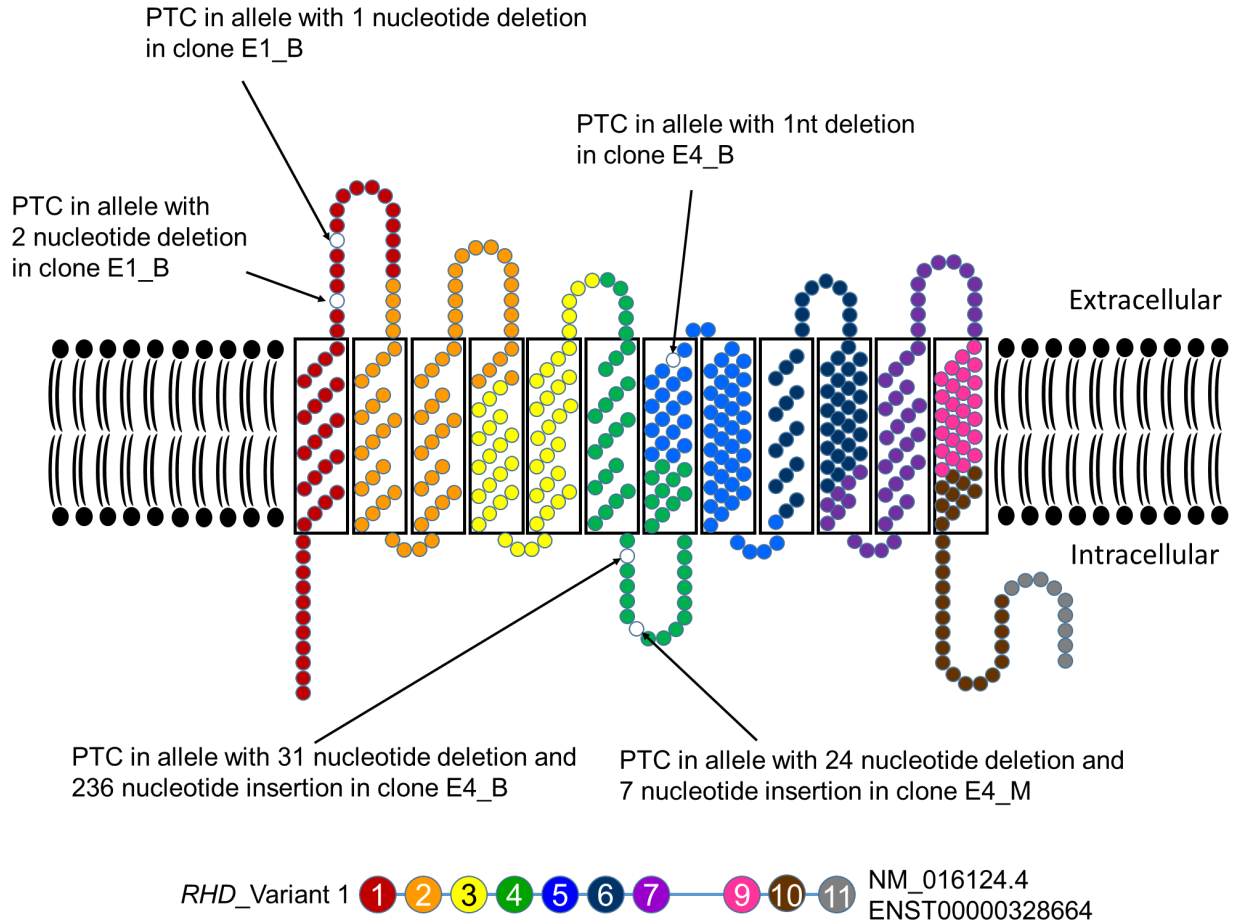
c Exon 4

TTGGGCTGTCTGTGGCCTGGTGCCTGCCAAAGCCTCTACCCGAGGGAACGGAGGATAAAGATCA (Wild type)

- #5 (E4_B) TTTCCTCCACTCCACACACCCCTAAGACTCTGGATCCTGCGAGGGAACGGAGGATAAAGATCA (x2) ← 31nt deletion, 236nt insertion; out of frame
TTGGGCTGTCTGTGGCCTGGTGCCTGCCAAAG-CTCTACCCGAGGGAACGGAGGATAAAGATCA (x17) ← 1nt deletion; out of frame
- #8 (E4_M) TTGGGCTGTCTGTGGCCTGGTGCCTGCCAAAGCCTCTACCCGAGGGAACGGAGGATAAAGATCA (x1) ← Wild type
TTGGGCTGTCTGTGGCCT-----CTACCCAAGGGAACGGAGGATAAAGATCA (x5) ← 24nt deletion, 7nt insertion; out of frame
- #33 TTGGGCTGTCTGTGGCCTGGTGCCTGCCAAAGCCTCTACCCGAGGGAACGGAGGATAAAGATCA (x2) ← Wild type
TTGGGCTGTCTGTGGCCTGGT-----CGGAGGATAAAGATCA (x4) ← 27nt deletion; inframe
- #37 TTGGGCTGTCTGTGGCCTGGTGCCTGCCAAAGCCTCTACCCGAGGGAACGGAGGATAAAGATCA (x3) ← Wild type
TTGGGCTGTCTGTGGCCTGGTGCCTGCCAAAG-----GAACGGAGGATAAAGATCA (x3) ← 12nt deletion; inframe
- #53 TTGGGCTGTCTGTGGCCTGGTGCCTGCCAAAGCCTCTACCCGAGGGAACGGAGGATAAAGATCA (x3) ← Wild type
TTGGGCTGTCTGTGGCCTGGTGCCTGCCAA---CTCTACCCGAGGGAACGGAGGATAAAGATCA (x3) ← 3nt deletion; inframe
- #118 TTGGGCTGTCTGTGGCCTGGTGC-----TCTACCCGAGGGAACGGAGGATAAAGATCA (x9) ← 11nt deletion; out of frame
TTGGGCTGTCTGTGGCCTGGTGCCTGCCAAAG-CTCTACCCGAGGGAACGGAGGATAAAGATCA (x4) ← 1nt deletion; out of frame
- #122 TTGGGCTGTCTGTGGCCTGGTGCCTGCCAAAGCCTCTACCCGAGGGAACGGAGGATAAAGATCA (x1) ← Wild type
-----GAACGGAGGATAAAGATCA (x5) ← 54nt deletion; inframe

Supplementary Figure 5. Two dimensional representation of the RHD protein structure

A two dimensional structure of the RHD protein translated from transcript variant 1 is shown. The positions of premature termination codons (PTCs) observed in E1_B and E4_B are indicated with arrows. The picture was re-drawn based on a previous presentation⁴⁷ (<http://www.uniulm.de/~wflegel/RH/SympDGTI2004/4WagnerDGTI2004MA>).



b Off target (RHCE)

Clone E1_B: sequences (10/10)

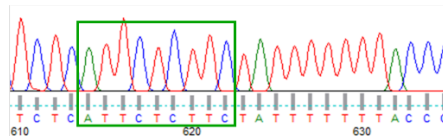
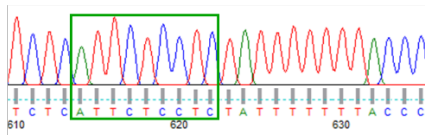
```

GGGCCCTAACACTGGAAGCAGCTCTCATTCTCCTCTTCTATTTTTTTACCCACTATGACGCTTC (RHD Wild-type)
GCGCCCTAACACTGGAAGCAGCTCTCATTCTCCTCTTCTATTTTTTTACCCACTATGACGCTTC (RHCE Wild-type)
GCGCCCTAACACTGGAAGCAGCTCTCATTCTCC---TCTATTTTTTTACCCACTATGACGCTTC (x6)
GCGCCCTAACACTGGAAGCAGCTCTCATTCTC---TCTATTTTTTTACCCACTATGACGCTTC (x4)
    
```

← 3nt deletion
← 3nt deletion

Allele with 3nt deletion

Allele with 3nt deletion



C

RHD_E4_TALEN_L

```

TGTCTGTGGCCTGGTGCCTG
: : : : : : : : : : : :
    
```

On-Target (RHD_exon4)

```

5' TGTCTGTGGCCTGGTGCCTGN12CCCAGGGAACGGAGGATAA3'
3' ACAGACACCGGACCACGGACN12GGGCTCCCTTGCCCTCCTATT5'
: : : : : : : : : : : :
GGGCTCCCTTGCCCTCCTATT
RHD_E4_TALEN_R
    
```

RHD_E4_TALEN_L

```

TGTCTGTGGCCTGGTGCCTG
: : : : : : : : : : : :
    
```

Off-Target (RHCE)

```

5' TGACTTGTGGCCTGGTGCCTGN12CCAGAGGGAACGGAGGATAA3'
3' ACTGACACCGGACCACGGACN12GGTTCTCCCTTGCCCTCCTATT5'
: : : : : : : : : : : :
GGGCTCCCTTGCCCTCCTATT
RHD_E4_TALEN_R
    
```

RHD_E4_TALEN_L

```

TGTCTGTGGCCTGGTGCCTG
: : : : : : : : : : : :
    
```

Off-Target (PMEPA1)

```

5' TCCCTGTGGCCTGGTGCCTGN24CAGGCCAAAAGCCACAAAGA3'
3' AGGGACACCGGACCACGGACN24GTCCGGTTTTCGGTGTTC5'
: : : : : : : : : : : :
GTCCGTGGTCCGGTGTCTGT
RHD_E4_TALEN_L
    
```

RHD_E4_TALEN_R

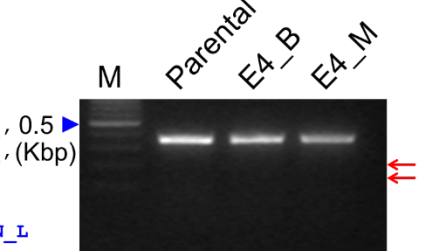
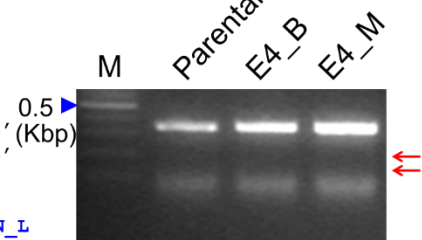
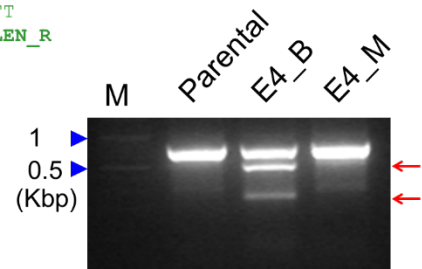
```

TGTCTGTGGCCTGGTGCCTG
: : : : : : : : : : : :
    
```

Off-Target (PPP3CA)

```

5' TGTCTGTGGCCTGGGGTGN10CCCTAGAGAACCAAGTATAA3'
3' ACAGACACCGGACCCCAACN10GGGATCTCTTGGTTCATAT5'
: : : : : : : : : : : :
GGGCTCCCTTGCCCTCCTATT
RHD_E4_TALEN_L
    
```



d Off target (RHCE)

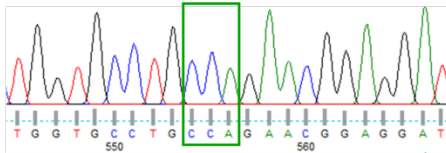
Clone E4_B: sequences (10/10)

```

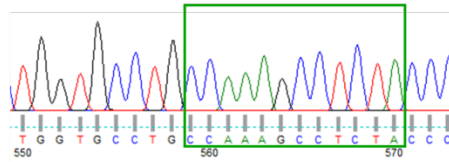
TTGGGCTGTCTGTGGCCTGGTGCCTGCCAAAGCCTCTACCCGAGGGAACGGAGGATAAAGATCA (RHD Wild-type)
TTGGGCTGACTGTGGCCTGGTGCCTGCCAAAGCCTCTACCCAGGGAACGGAGGATAATGATCA (RHCE Wild-type)
TTGGGCTGACTGTGGCCTGGTGCCTGCCA-----GAACGGAGGATAATGATCA (x5)
TTGGGCTGACTGTGGCCTGGTGCCTGCCAAAGCCTCTACCCAGGGAACGGAGGATAATGATCA (x5)
    
```

← 16nt deletion

Allele with 3nt deletion



Allele with Wild type sequence

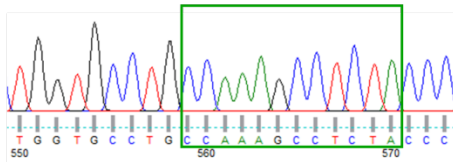


Clone E4_M: sequences (10/10)

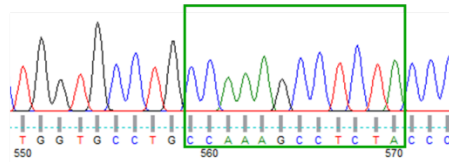
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TTGGGCTGTCTGTGGCCTGGTGCCTGCCAAAGCCTCTACCCGAGGGAACGGAGGATAAAGATCA (RHD Wild-type)
TTGGGCTGACTGTGGCCTGGTGCCTGCCAAAGCCTCTACCCAGGGAACGGAGGATAATGATCA (RHCE Wild-type)
TTGGGCTGACTGTGGCCTGGTGCCTGCCAAAGCCTCTACCCAGGGAACGGAGGATAATGATCA (x10)
    
```

Allele with Wild type sequence



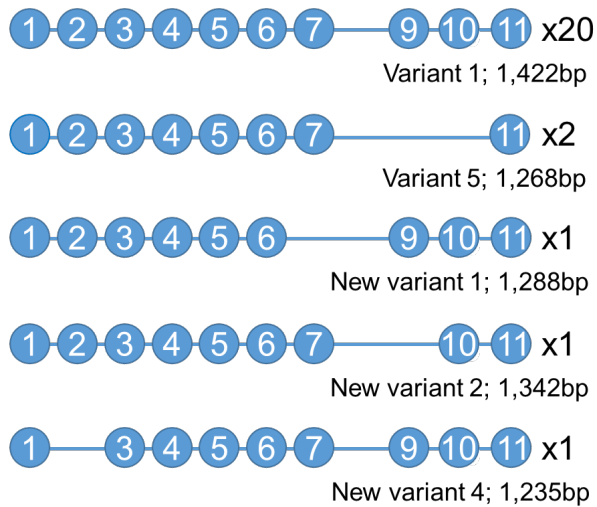
Allele with Wild type sequence



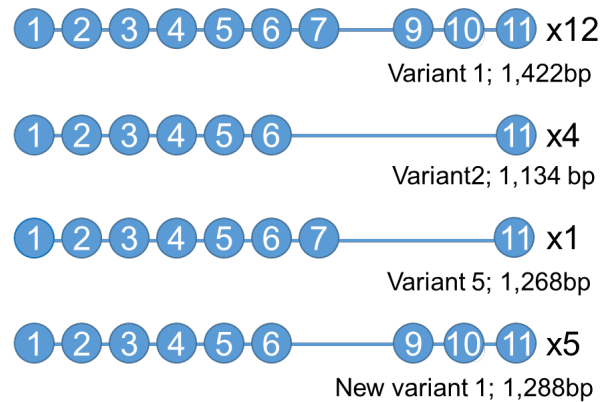
Supplementary Figure 7. Schematic representation of *RHD* mRNA variants in erythroid cells derived from cord blood CD34⁺ cells and HUDEP-2 cells.

RT-PCR was performed to detect *RHD* mRNA in each cell type; the amplicons were then subjected to sequencing. The number of occurrences is shown on the right of each transcript. The blue circles indicate exons.

**Erythroid cells
from cord blood CD34⁺ cells**

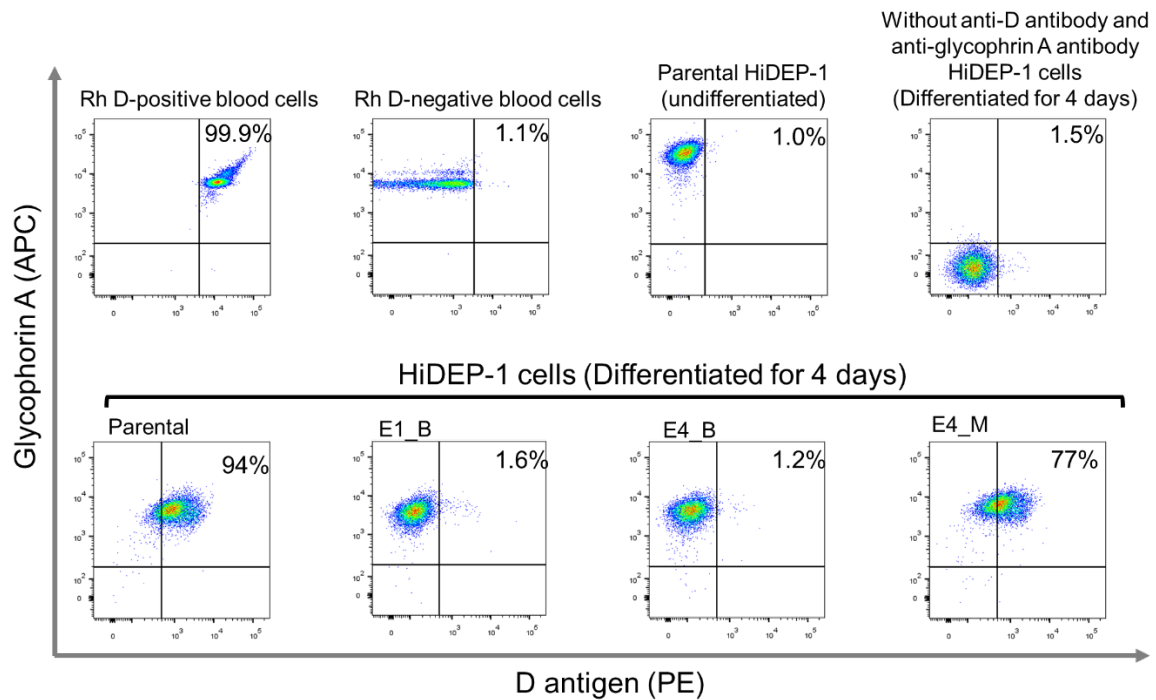


HUDEP-2



Supplementary Figure 8. Flow cytometric analysis of D antigen expression in mutated cells

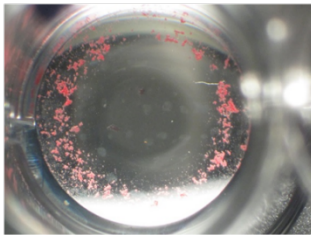
Parental and *RHD*-mutated (biallelic, E1_B, E4_B; monoallelic, E4_M) HiDEP-1 cells were induced for differentiation for four days and subjected to flow cytometry. Dot plots show that D antigen is expressed in parental and monoallelic mutated cells, but not in biallelic mutated cells. Rh D-positive and D-negative peripheral blood cells were used as positive and negative controls, respectively.



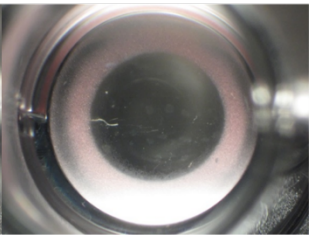
Supplementary Figure 9. Absence of Rh D antigen-mediated agglutination in *RHD*-knockout cell lines

Parental, *RHD*-knockout (E1_B, E4_B), and *RHD*-monoallelic mutant (E4_M) HiDEP-1 cells were induced for differentiation for four days and subjected to an agglutination test using anti-D blood grouping reagents in 96 well plates. Rh D-positive and D-negative blood cells were used as positive and negative controls, respectively. Pictures of the agglutination test covering whole test wells are shown.

Rh D-positive
blood cells

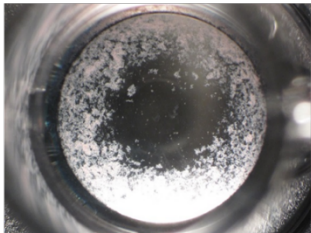


Rh D-negative
blood cells

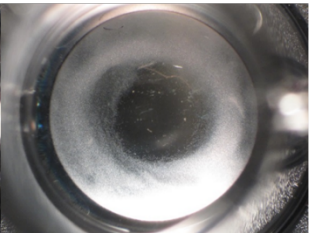


HiDEP-1 cells (Differentiated for 4 days)

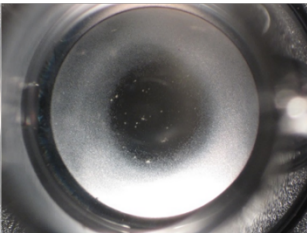
Parental



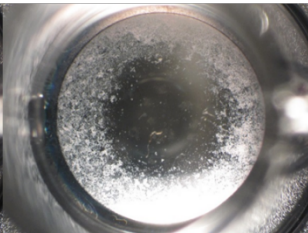
E1_B



E4_B

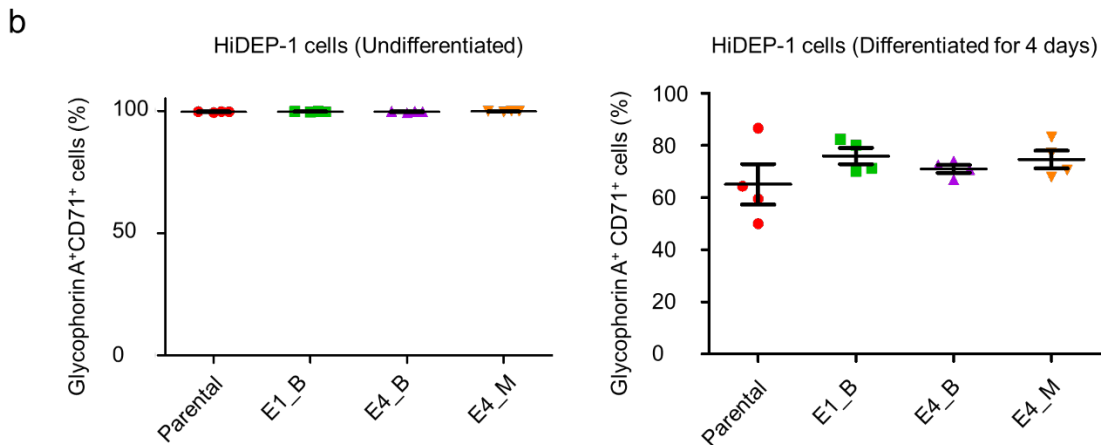
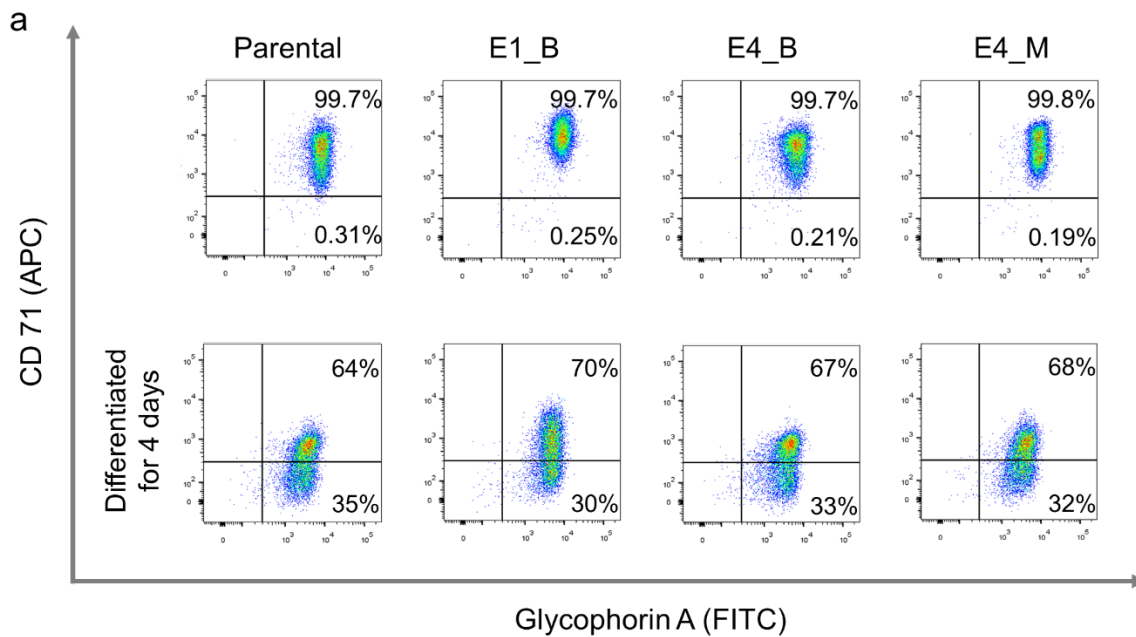


E4_M

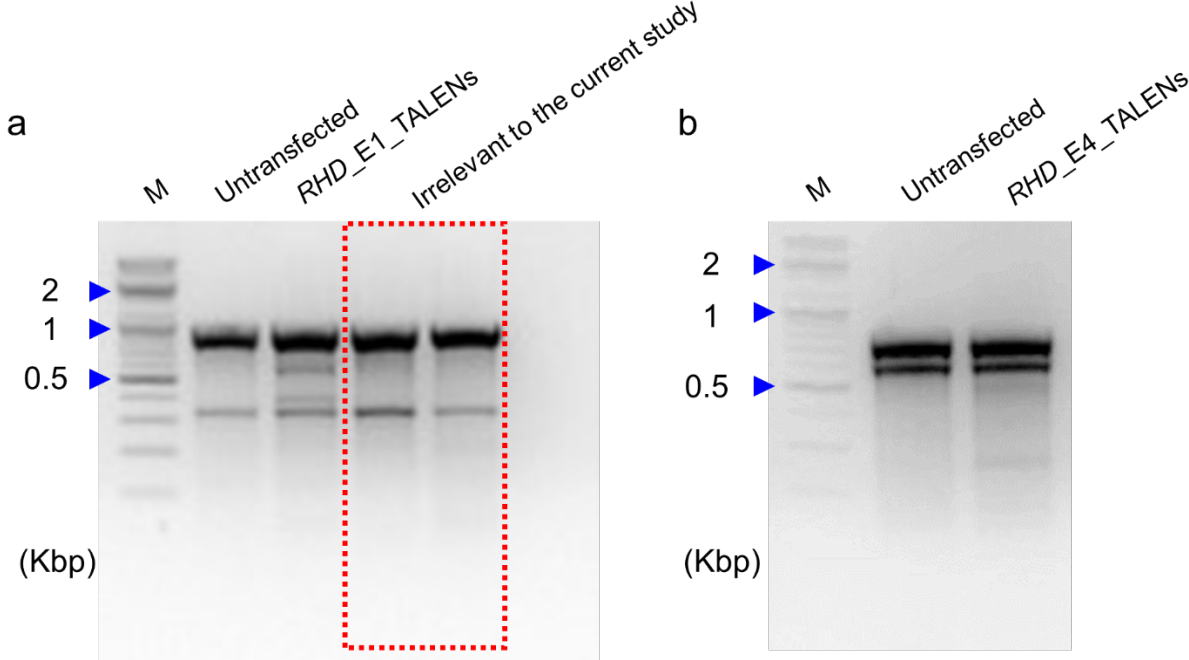


Supplementary Figure 10. Expression of erythroblast specific markers in parental and mutant cells.

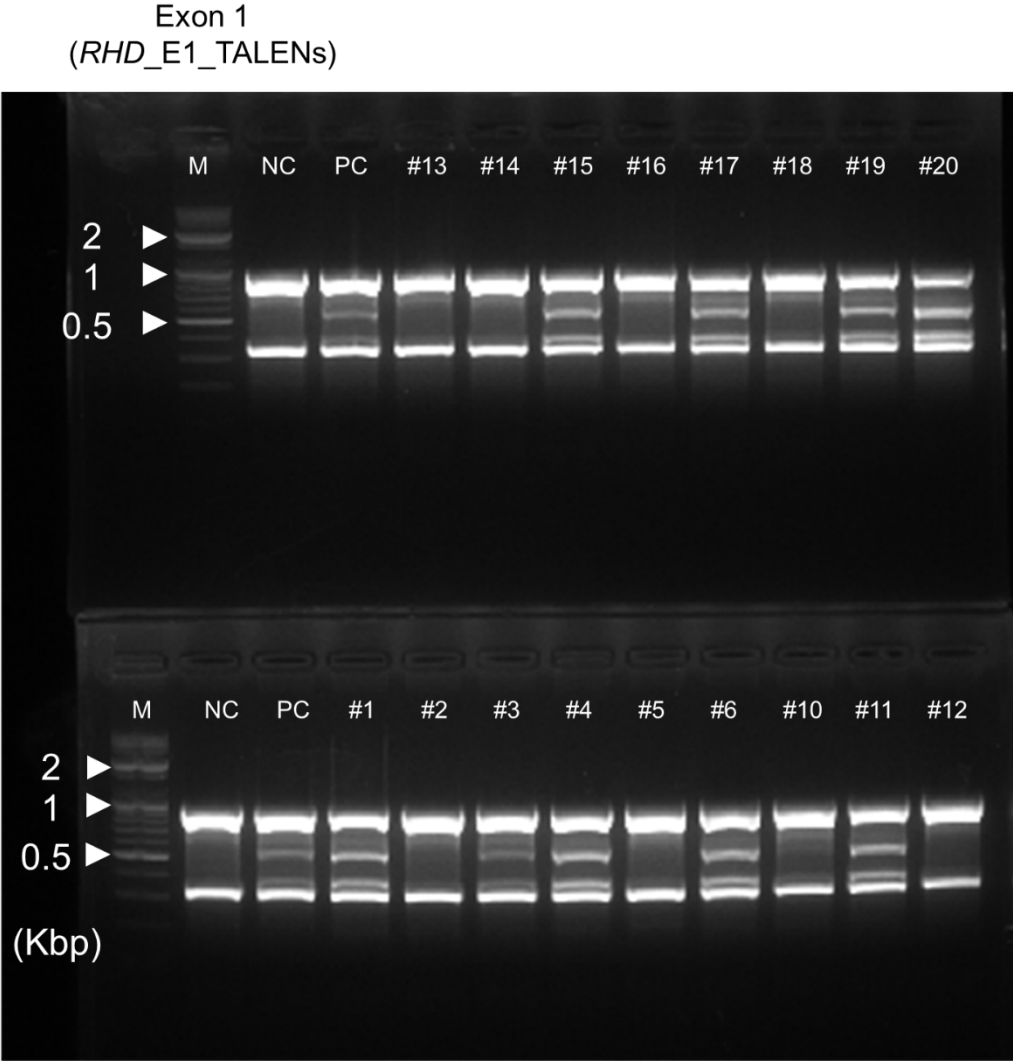
Parental and *RHD*-mutated (biallelic, E1_B, E4_B; monoallelic, E4_M) HiDEP-1 cells were induced for differentiation for four days and subjected to flow cytometry to evaluate glycophorin A and CD71 expression. (a) Representative flow cytometry. (b) The expression levels of glycophorin A and CD71. The percentage of glycophorin A⁺CD71⁺ cells was the same in the parental and *RHD*-mutant clones (n = 4, ANOVA was performed). Error bars represent the standard error of the mean (S.E.M.).



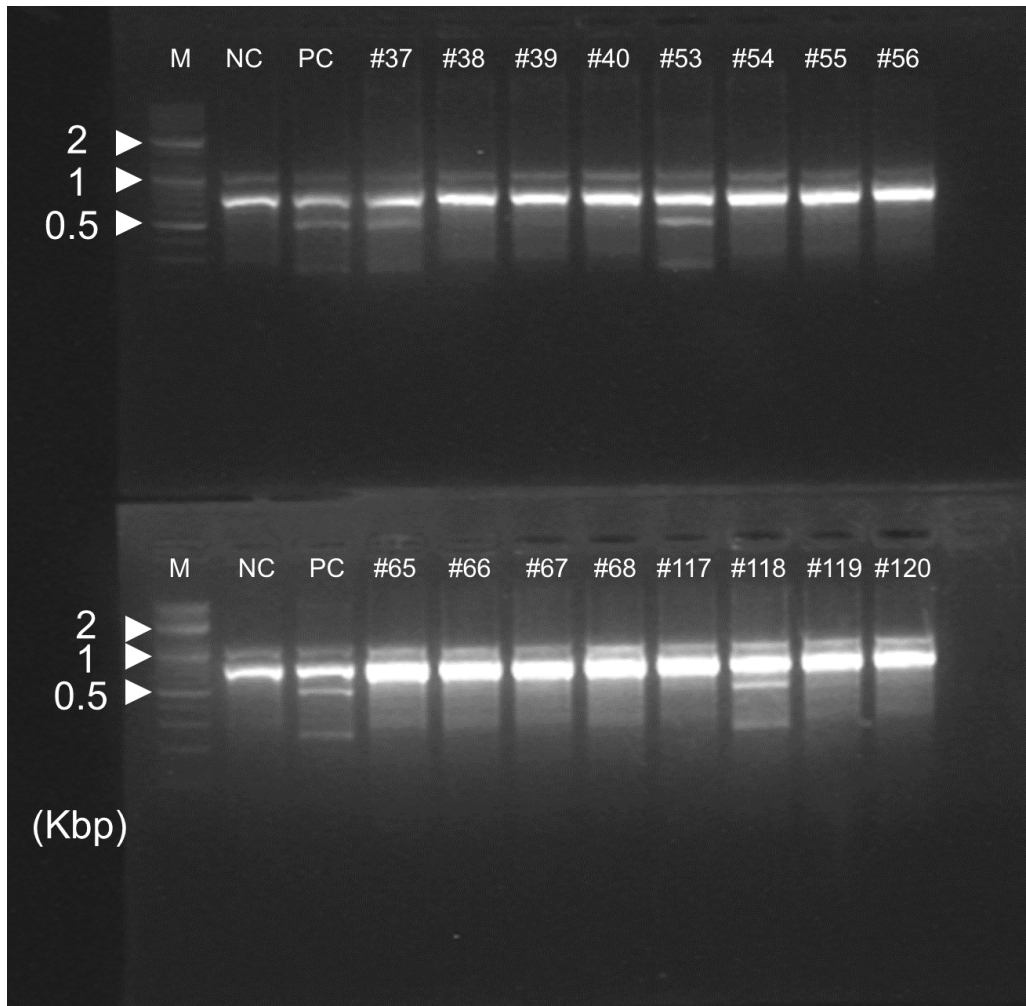
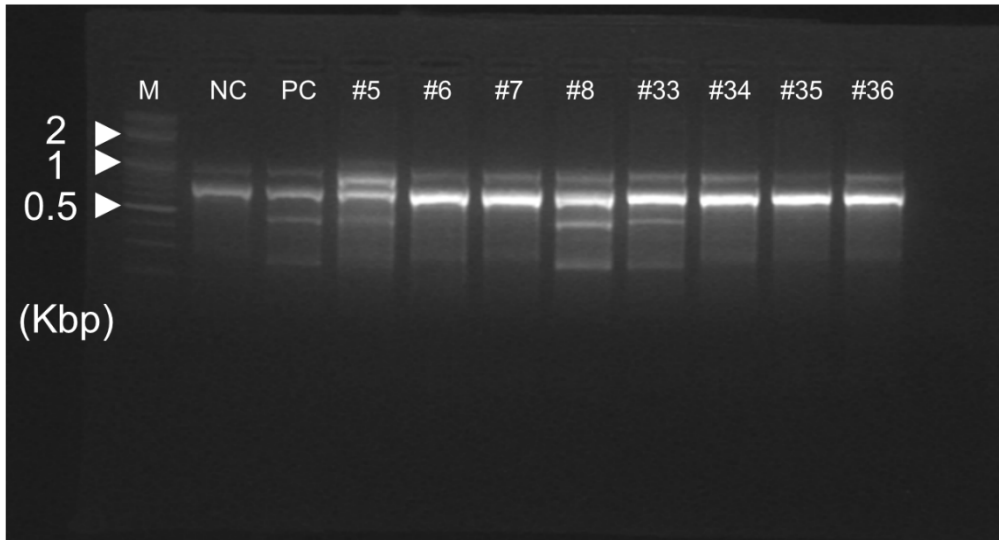
Supplementary Figure 11. Uncropped images of gels shown in Fig. 1b (a) and 1c (b).

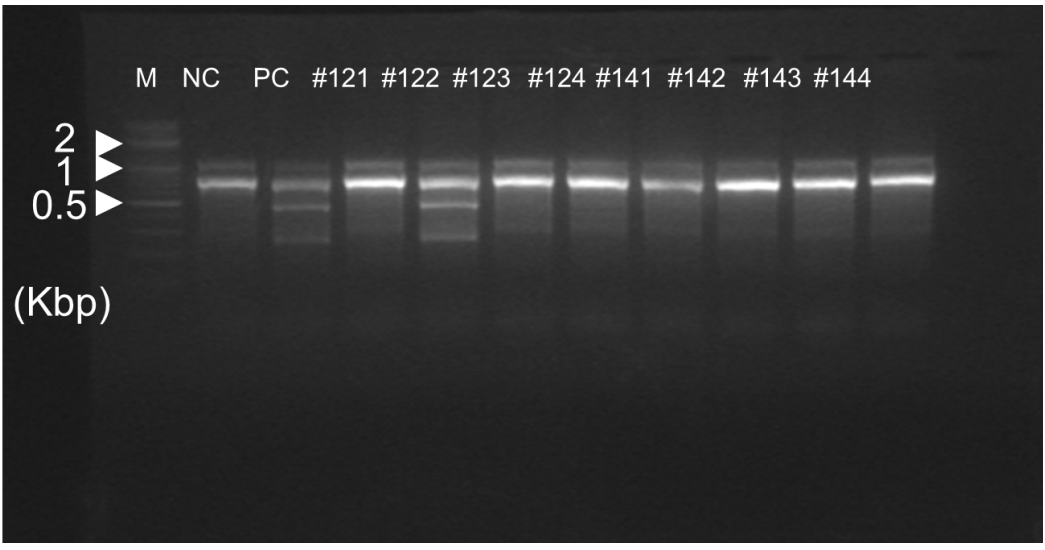


Supplementary Figure 12. Uncropped images of gels shown in Fig. 2b.

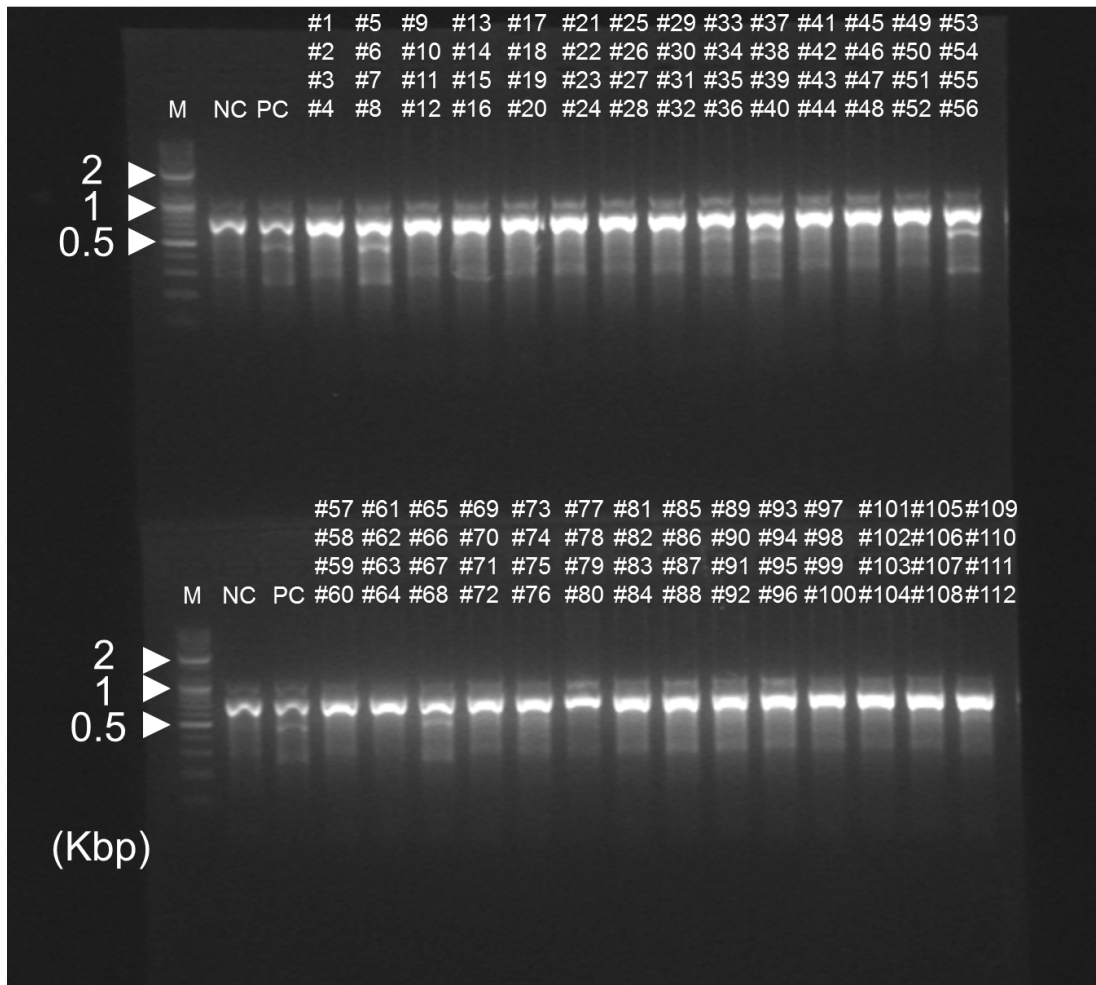
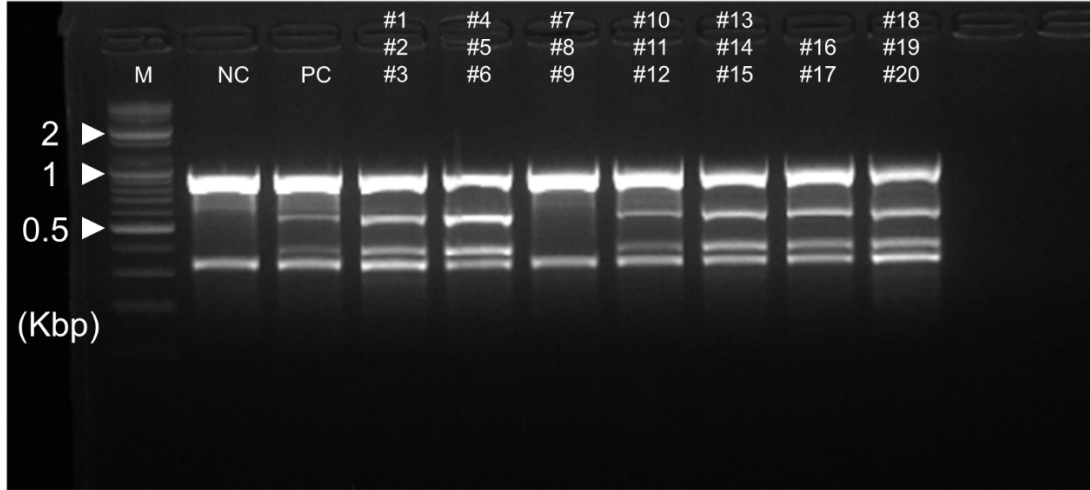


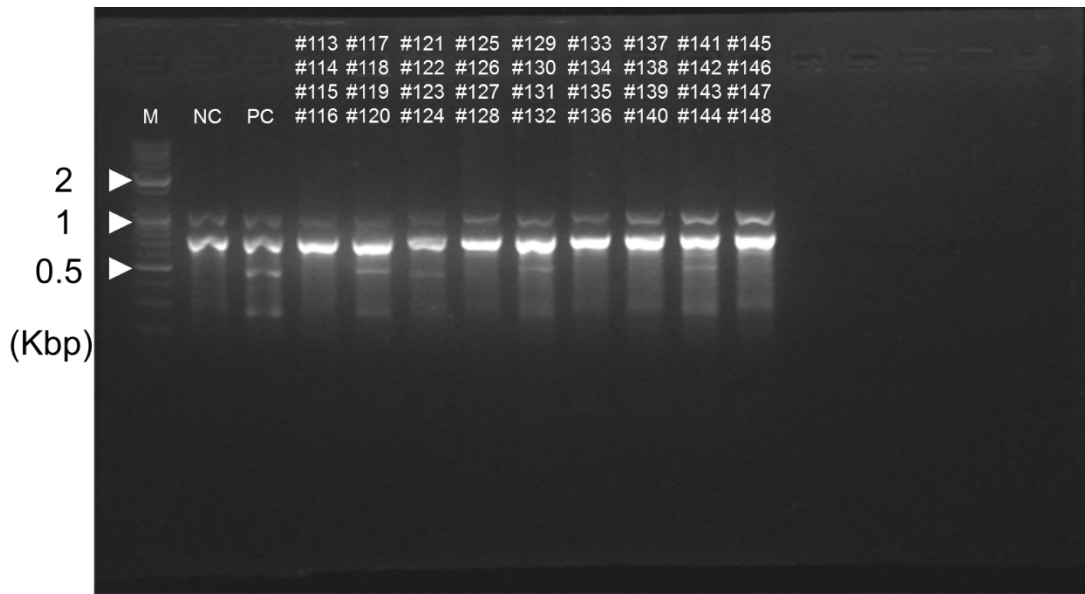
Exon 4
(RHD_E4_TALENs)





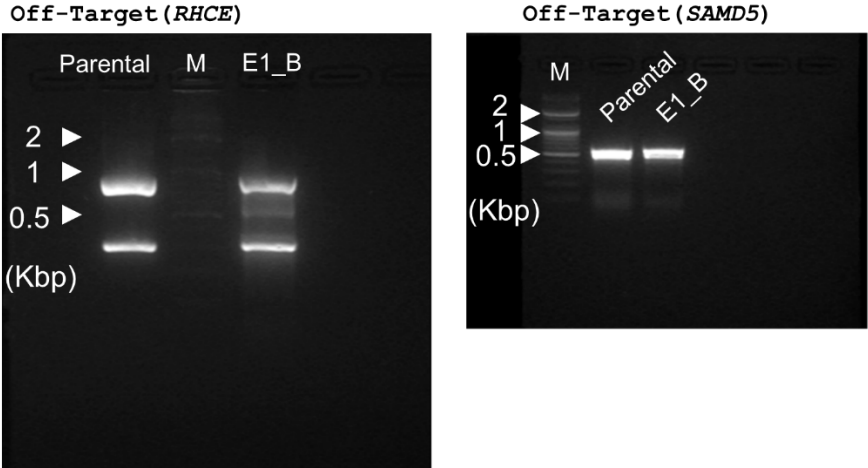
Supplementary Figure 13. Uncropped images of gels shown in Supplementary Fig 3.



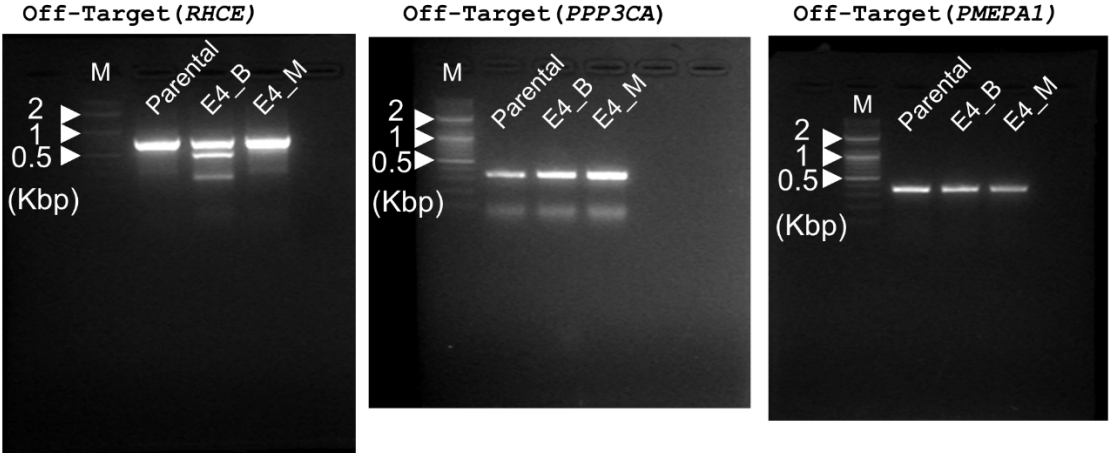


Supplementary Figure 14. Uncropped images of gels shown in Supplementary Fig. 6a (a) and 6c (b).

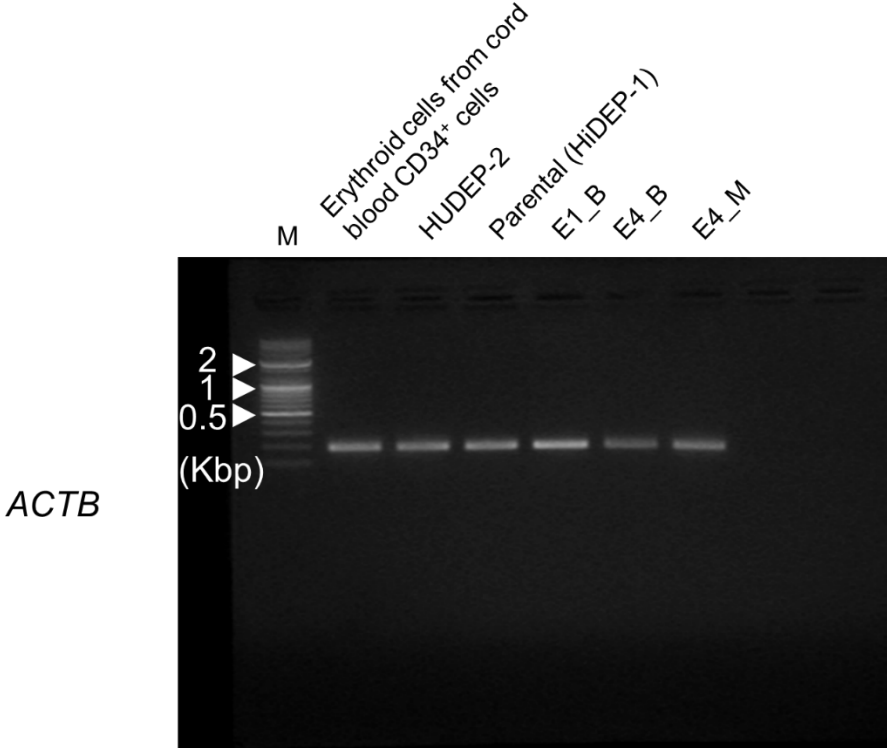
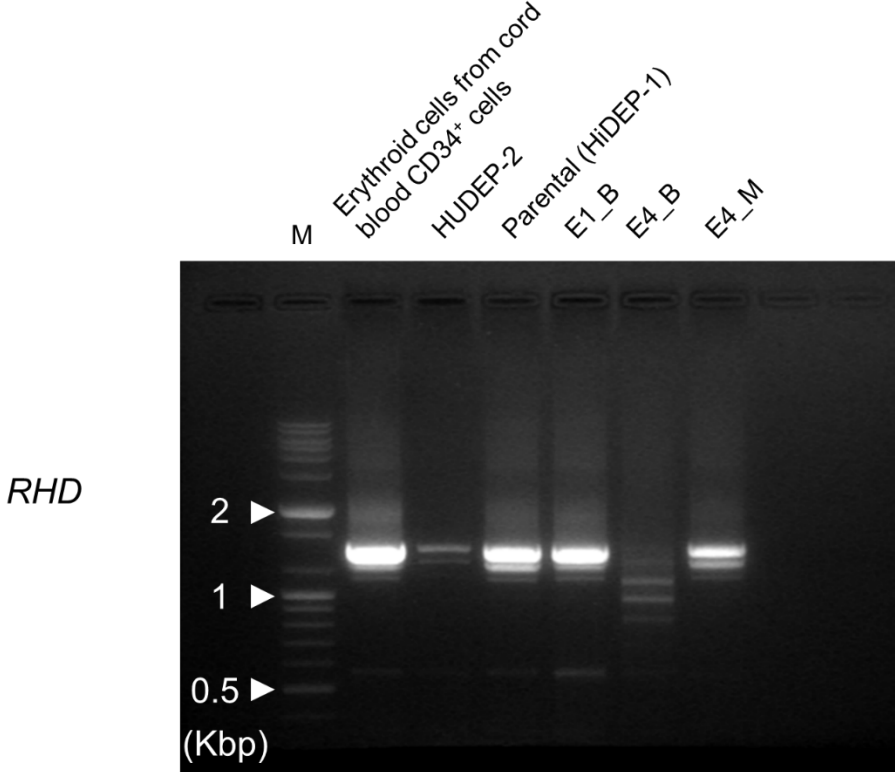
a



b



Supplementary Figure 15. Uncropped images of gels shown in Fig. 4a.

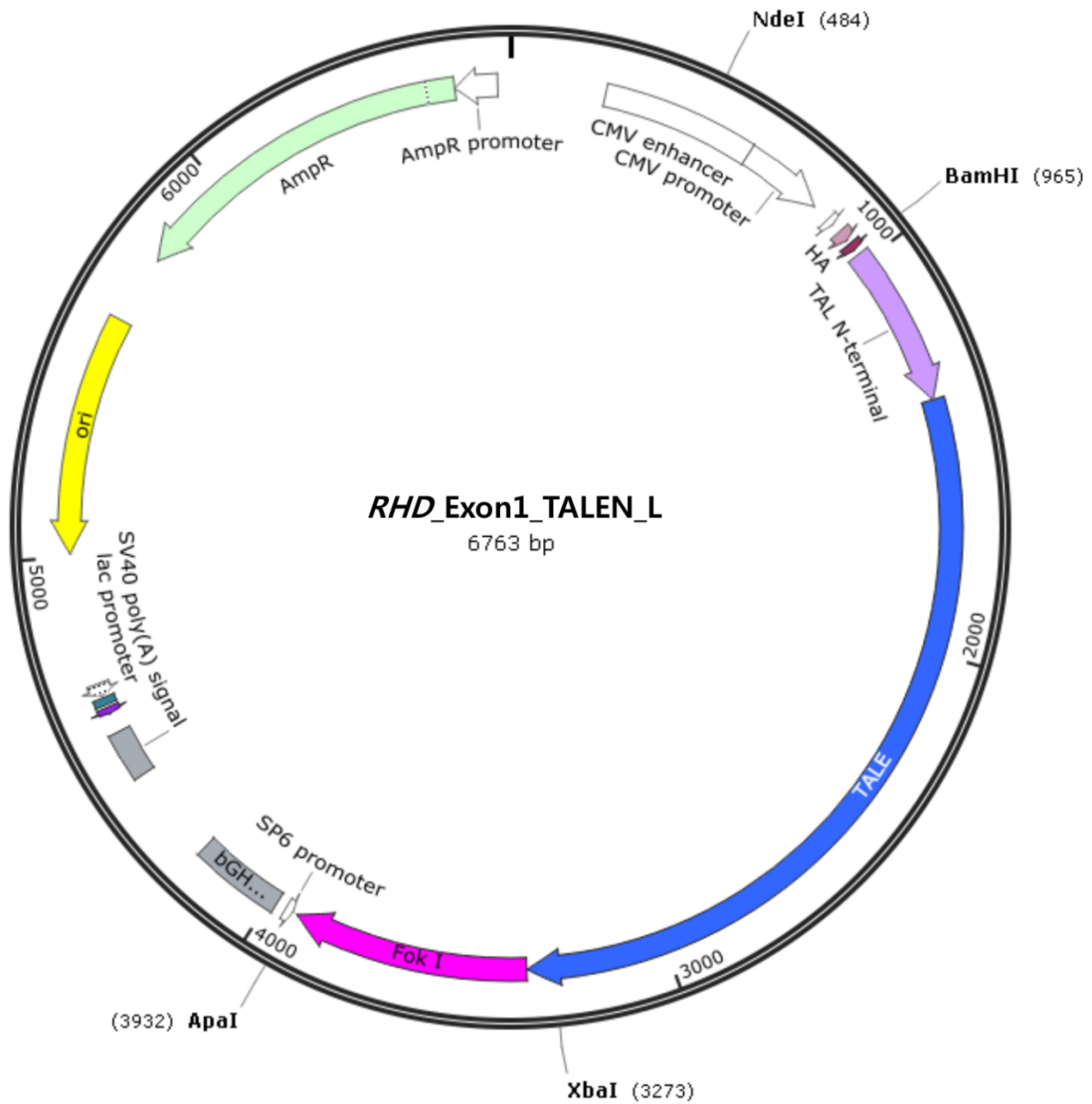


Supplementary Table 1. The sequences of primers used in this study.

primer	sequence (5'-3')
<i>RHD</i> _exon1_1st_forward	ATG GGA GCA CAG GGG AAG TT
<i>RHD</i> _exon1_1st_reverse	AAA AAT TAG CCA GGC ATG GT
<i>RHD</i> _exon1_2nd_forward	TTA AGA GCT CAC TGG GTG CC
<i>RHD</i> _exon1_2nd_reverse	GGG GAA GCA GAG AAG CAG AG
<i>RHD</i> _exon4_1st_forward	GGT CAA AAG CAT ATA AGA GCT ACT G
<i>RHD</i> _exon4_1st_reverse	ACT CCC CGT TAA GCA CTT TAC AT
<i>RHD</i> _exon4_2nd_forward	GCA GTG GCT CAT GCC TGT AAT
<i>RHD</i> _exon4_2nd_reverse	CCT GCT CTG TGA AGT GCT TAA TTC
sequencing_T7 primer	TAA TAC GAC TCA CTA TAG GG
RT-PCR_ <i>RHD</i> _forward	ACA CAG GAT GAG CTC TAA GT
RT-PCR_ <i>RHD</i> _reverse	GTG GCA GAG AAA GGA TTC AAC TCC
off-target_ <i>RHCE</i> _exon1_1st_forward	GGA TGG GAG CAC AGT TCC GG
off-target_ <i>RHCE</i> _exon1_1st_reverse	AAT TTA GCC AGG CAT GGT GGT G
off-target_ <i>RHCE</i> _exon1_2nd_forward	TTA AGA GCT CAC TGG GTG CC
off-target_ <i>RHCE</i> _exon1_2nd_reverse	GGG GAA GCA GAG AAG CAG AG
off-target_ <i>RHCE</i> _exon4_1st_forward	CTT TCT CCA GTA GCC CAC TAA A
off-target_ <i>RHCE</i> _exon4_1st_reverse	TCA CTT GTC CGT TTC CCT CC
off-target_ <i>RHCE</i> _exon4_2nd_forward	CAC AGT GGC TCA TGC CTG TA
off-target_ <i>RHCE</i> _exon4_2nd_reverse	GGT CCC TAA AAG GAA GTG CTT
off-target_ <i>SAMD5</i> _forward	CAA TGA GTT CCA GGC TAC CAG AAG
off-target_ <i>SAMD5</i> _reverse	GCC ATT TAT TGA GGT TTT CCC CCC
off-target_ <i>PMEPA1</i> _forward	GGG CTT TTT CTC TGA TGA GTG CTG
off-target_ <i>PMEPA1</i> _reverse	AAA AGA ACA CTC CAA GTA CCC CCG
off-target_ <i>PPP3CA</i> _forward	CTT TTG ATA TCC CTG GGG GAT TGG
off-target_ <i>PPP3CA</i> _reverse	GTG CTT GCA CTC CTA TGA GAG TC

Supplementary Note 1. Map and sequences of the TALEN-encoding plasmids used in this study.

RHD_Exon1_TALEN_L



CMV promoter

T7 Promoter

Star codon-HA tag-NLS

TAL N-terminal domain

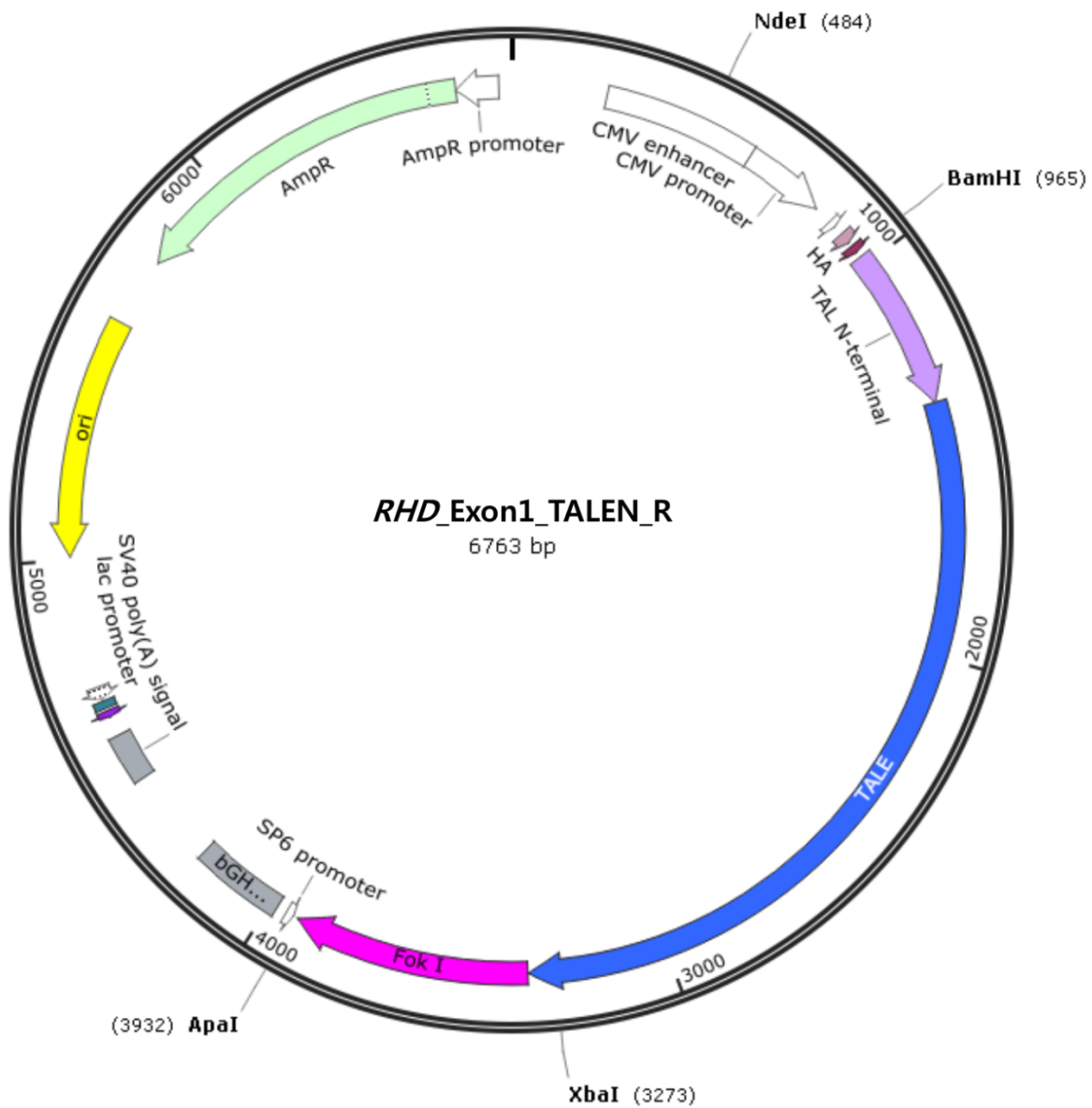
Target Specific TALE array

Fok I (DAS(Left)/RR(Right) - heterodimer-specific FokI variant)

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RHD_Exon1_TALEN_R



CMV promoter

T7 Promoter

Star codon-HA tag-NLS

TAL N-terminal domain

Target Specific TALE array

Fok I (DAS(Left)/RR(Right) - heterodimer-specific Fok I variant)

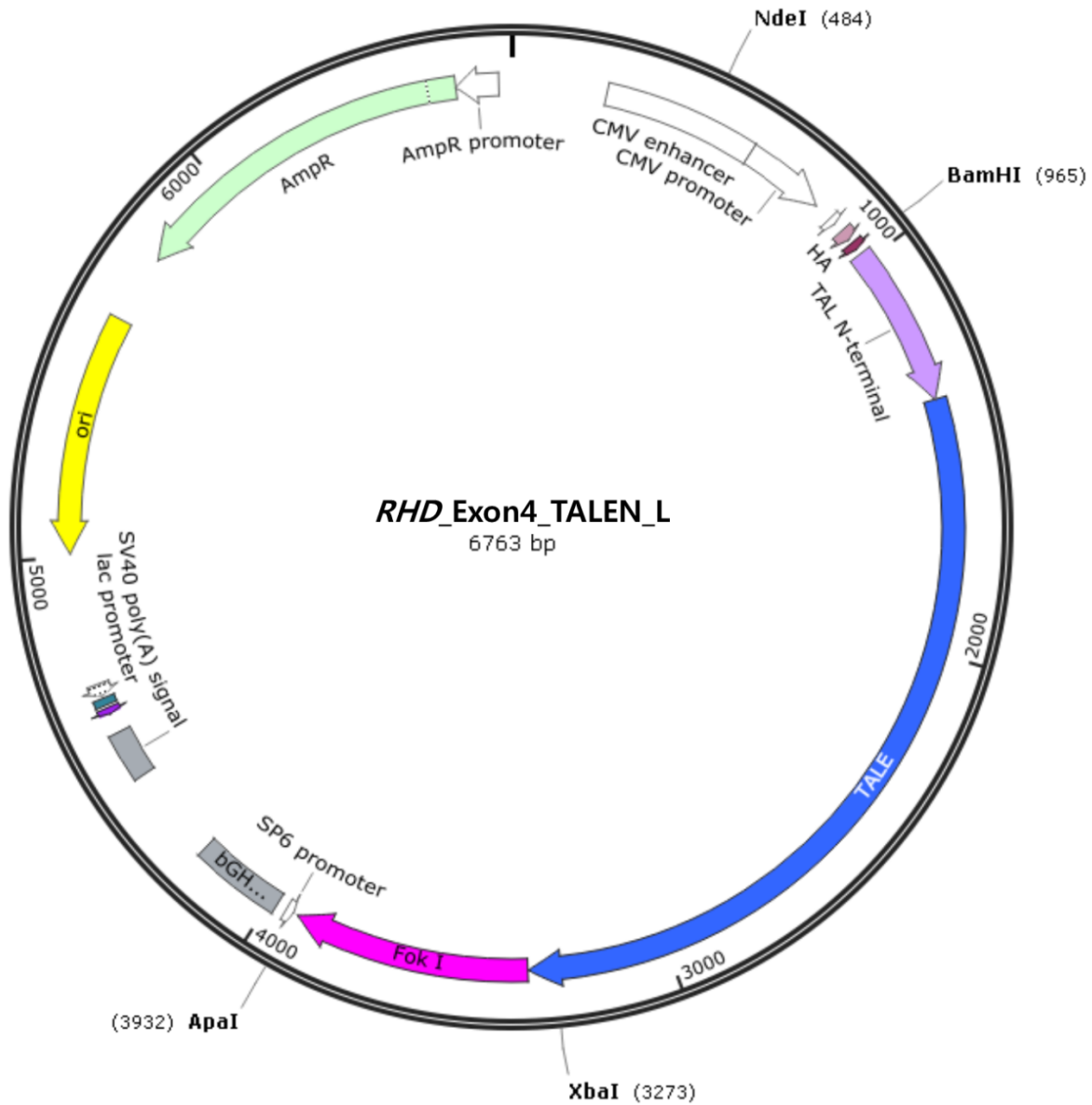
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RHD_Exon4_TALEN_L



CMV promoter

T7 Promoter

Star codon-HA tag-NLS

TAL N-terminal domain

Target Specific TALE array

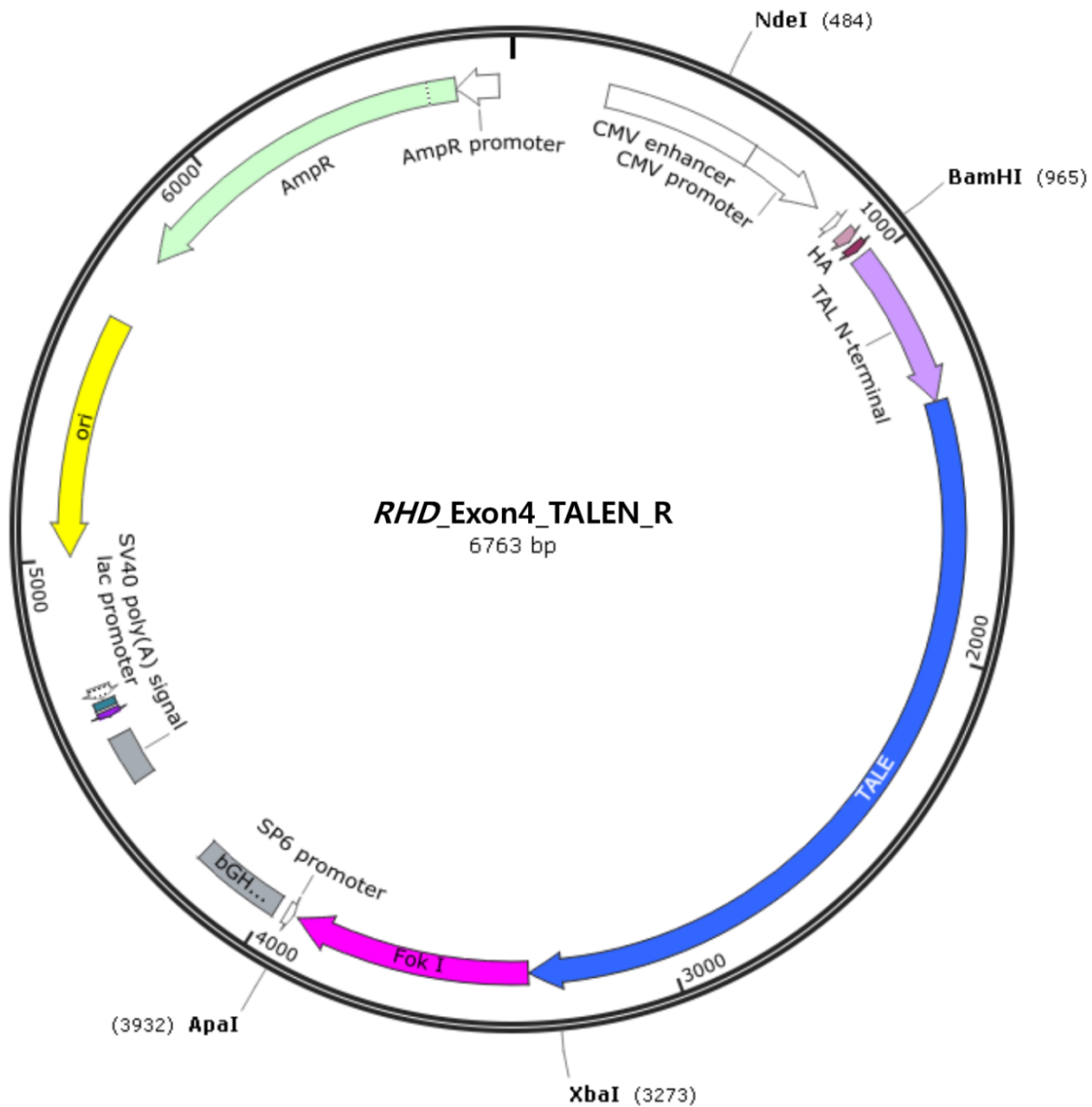
Fok I (DAS(Left)/RR(Right) - heterodimer-specific FokI variant)

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RHD_Exon4_TALEN_R



CMV promoter

T7 Promoter

Star codon-HA tag-NLS

TAL N-terminal domain

Target Specific TALE array

Fok I (DAS(Left)/RR(Right) - heterodimer-specific FokI variant)

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Supplementary Reference

47. Flegel, W.A. et al. In-frame triplet deletions in RHD alter the D antigen phenotype. *Transfusion* **46**, 2156–2161 (2006).