

Gene Therapy for Sickle Cell Disease

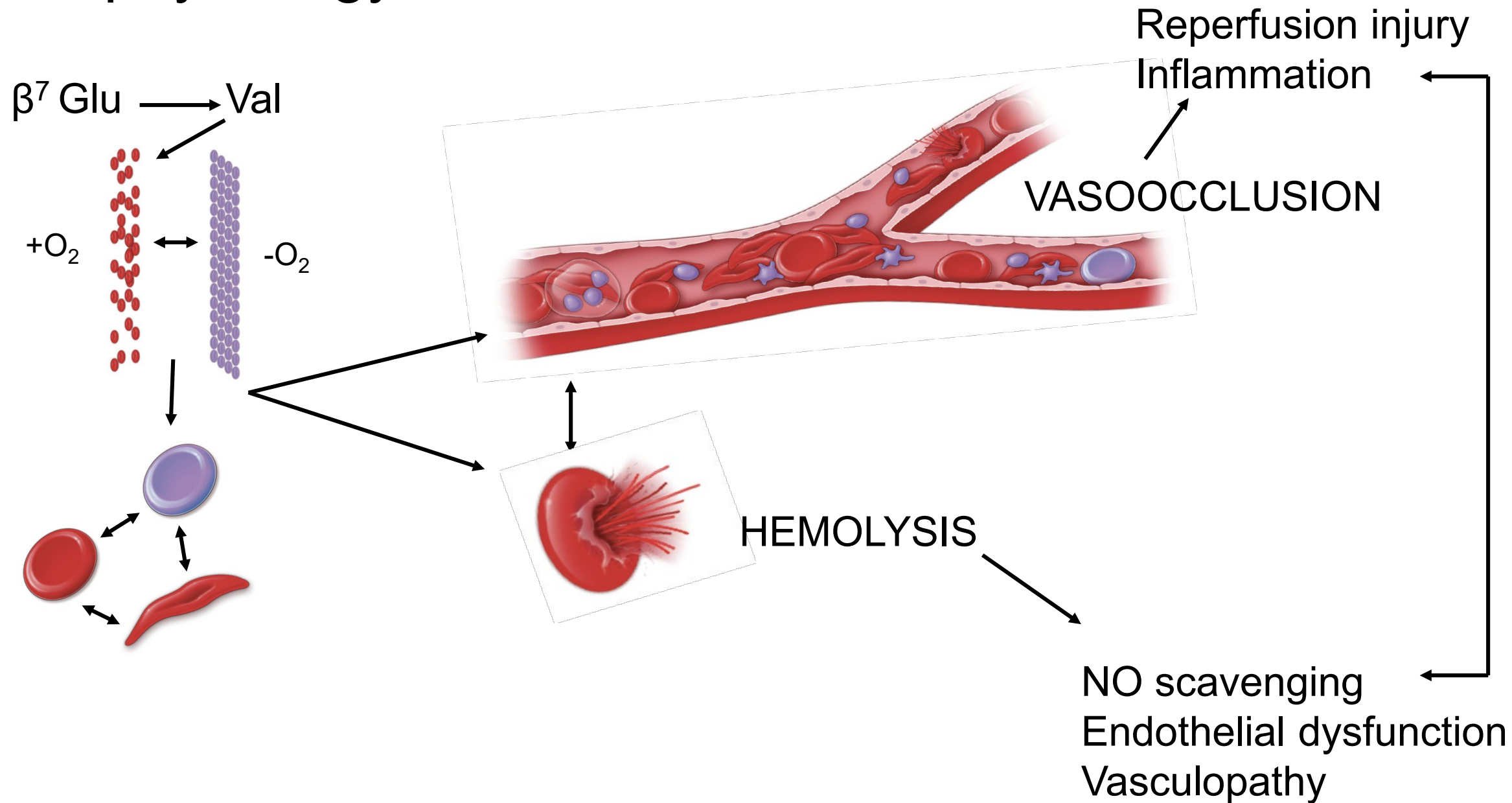
—Targeting HbS Polymerization —

Martin H Steinberg

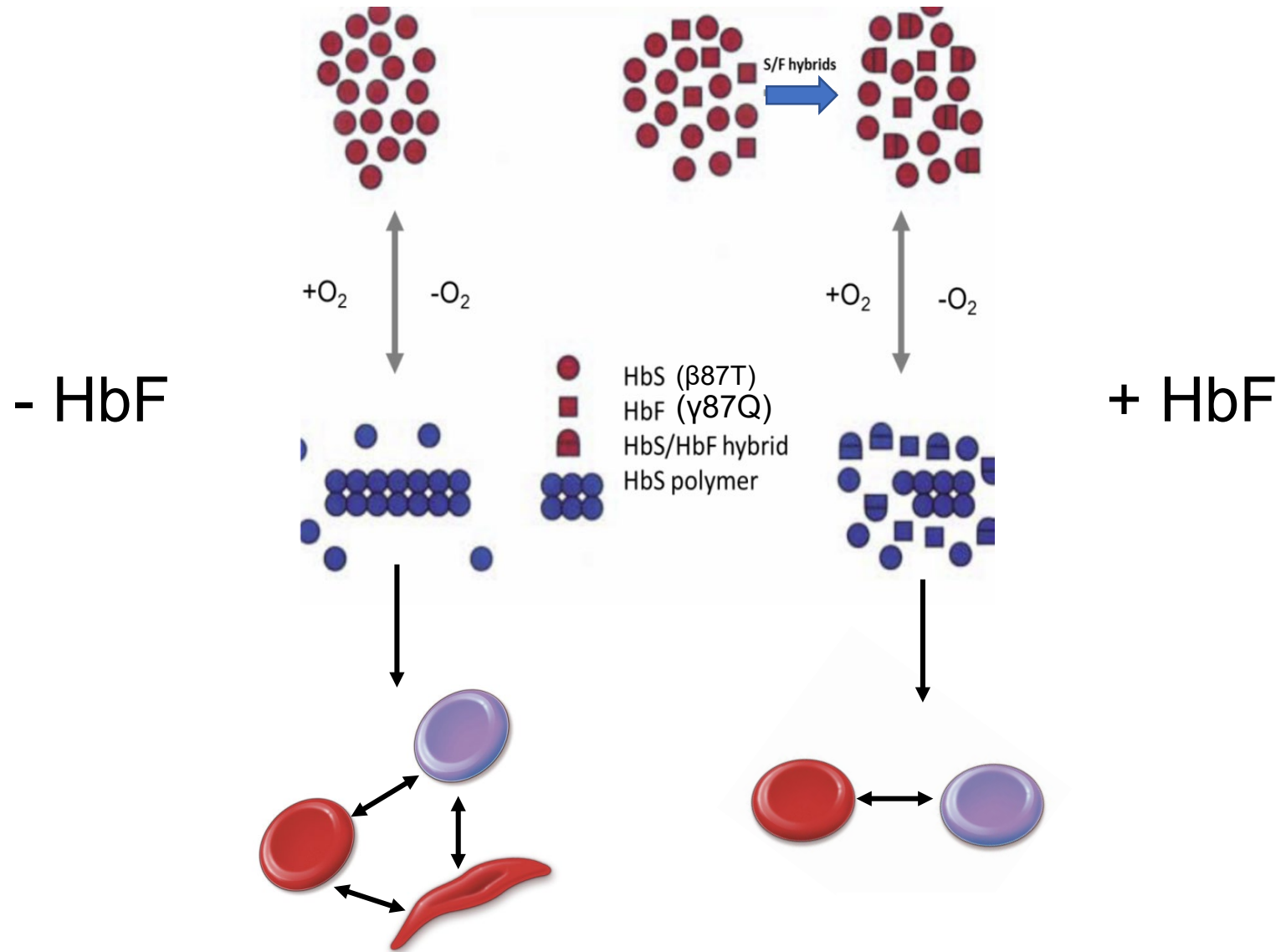
Department of Medicine, Boston University School of
Medicine, Boston, MA



Pathophysiology of Sickle Cell Disease



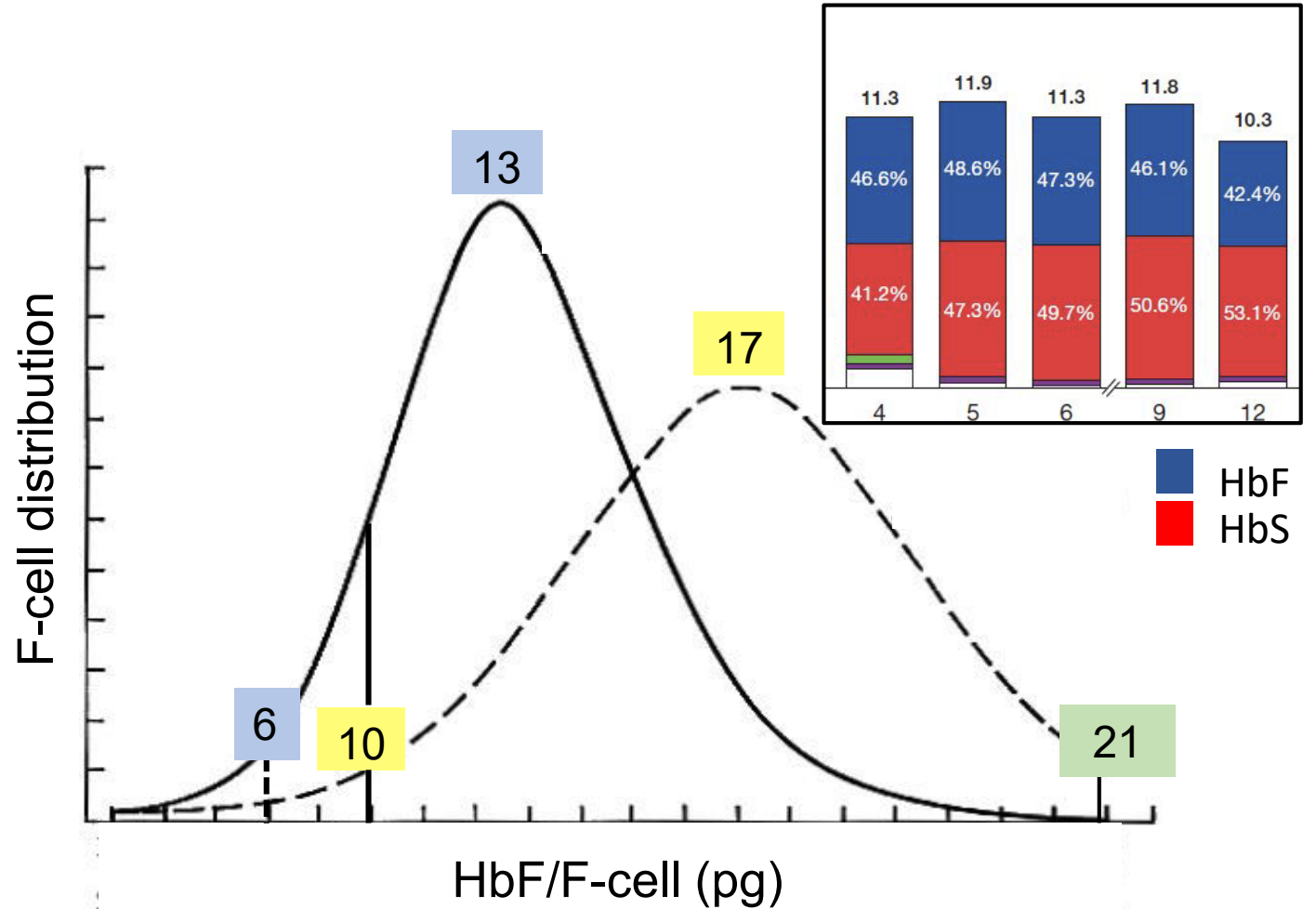
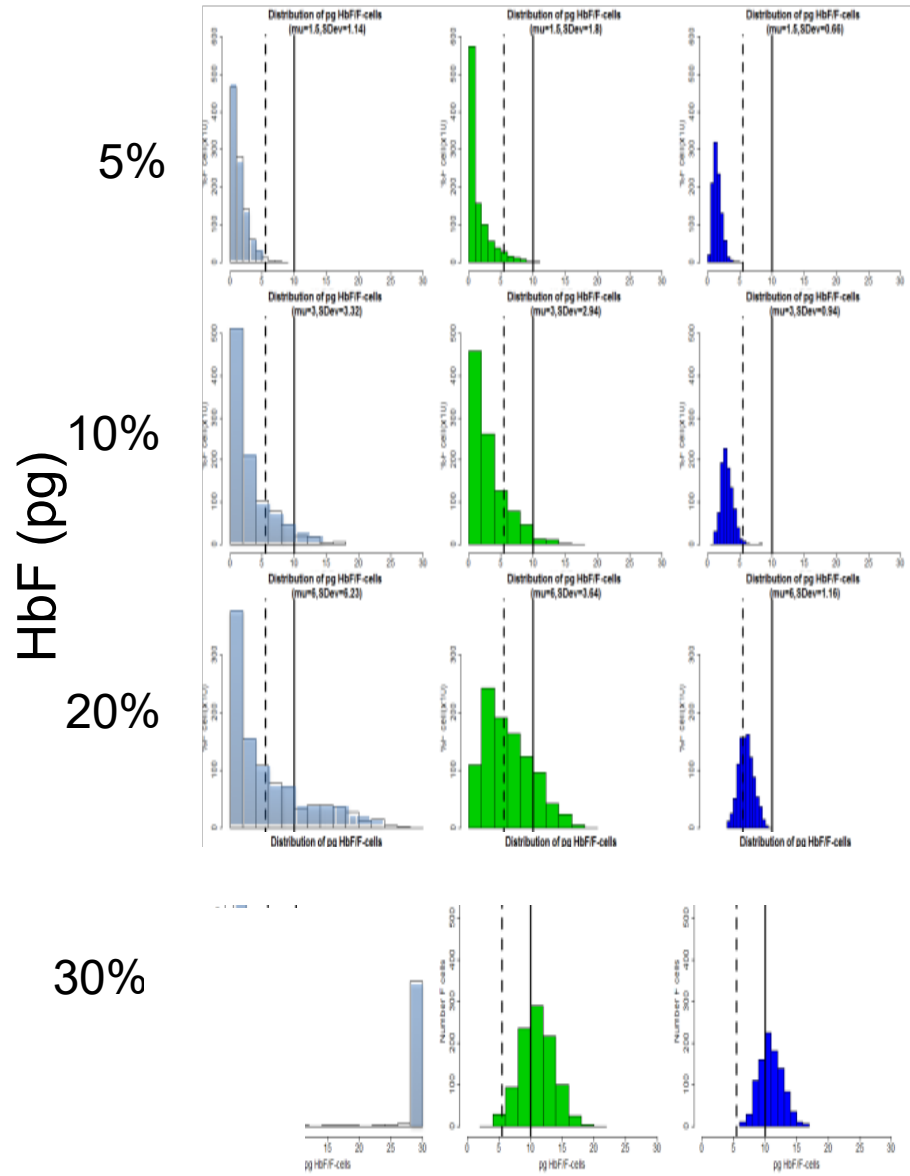
HbF interferes with deoxyHbS polymerization



HbF

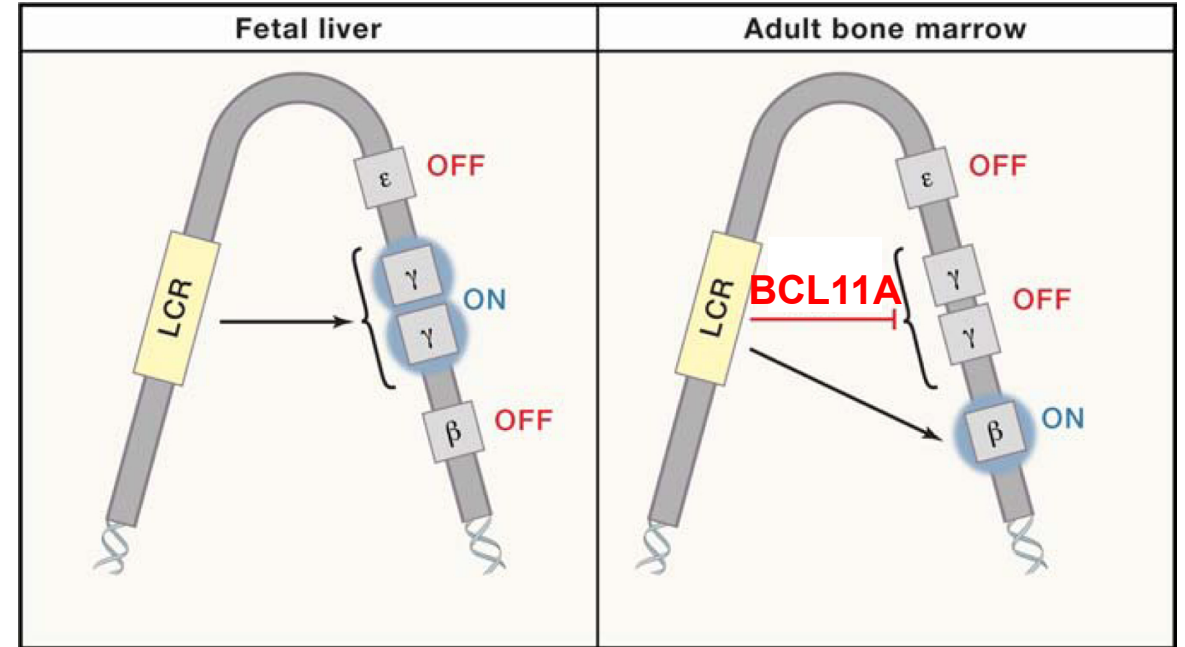
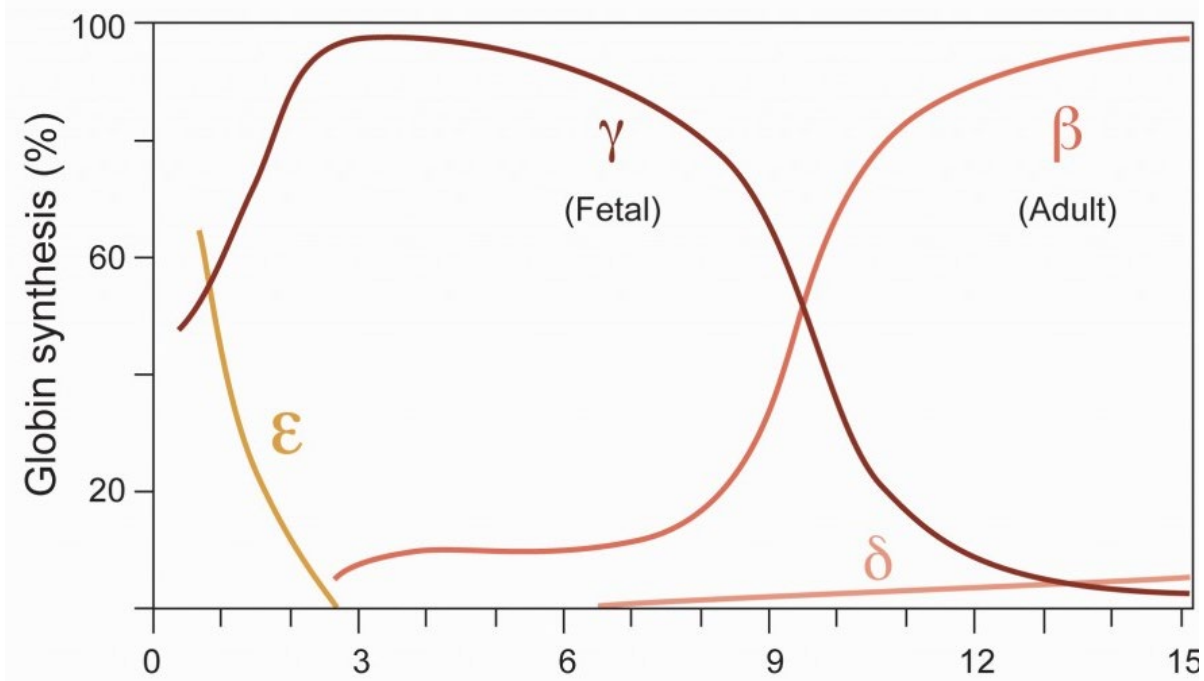
- HbF $\alpha_2\gamma_2$ (HbA $\alpha_2\beta_2$; HbS $\alpha_2\beta^s_2$)
 γ - differs from β -globin in 39 or 40 amino acids
- ~80% HbF in newborns
<1% by 12 months in people without hemoglobinopathies
- In SCD, HbF levels fall with time, but remain elevated
4-10% HbF in most patients of African descent
16-23% HbF in many patients of Arab and Indian descent
- F-cells are RBCs with FACS-detectable HbF
4-6 pg. HbF/cell is needed for detection
- HbF is heterogeneously distributed amongst F-cells

HbF in F-cells

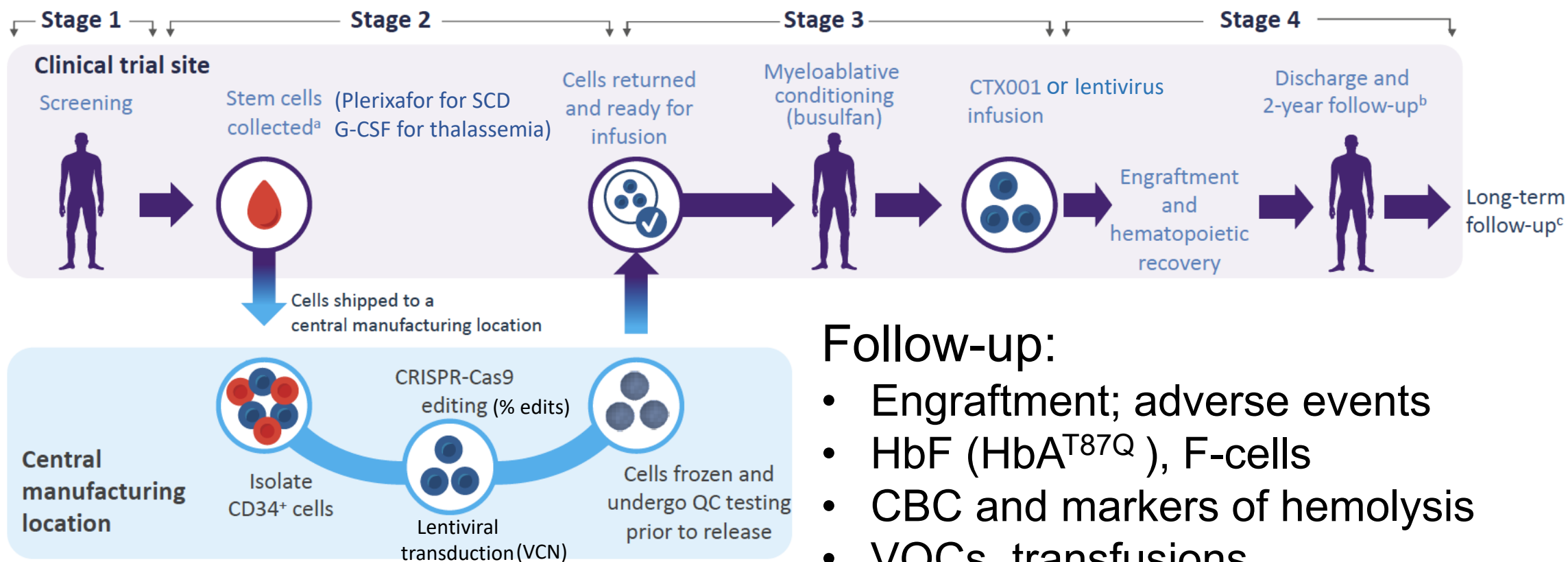


— Lower limit of HbF “total” protection
 - - - Lower limit of HbF detection

Hemoglobin switching



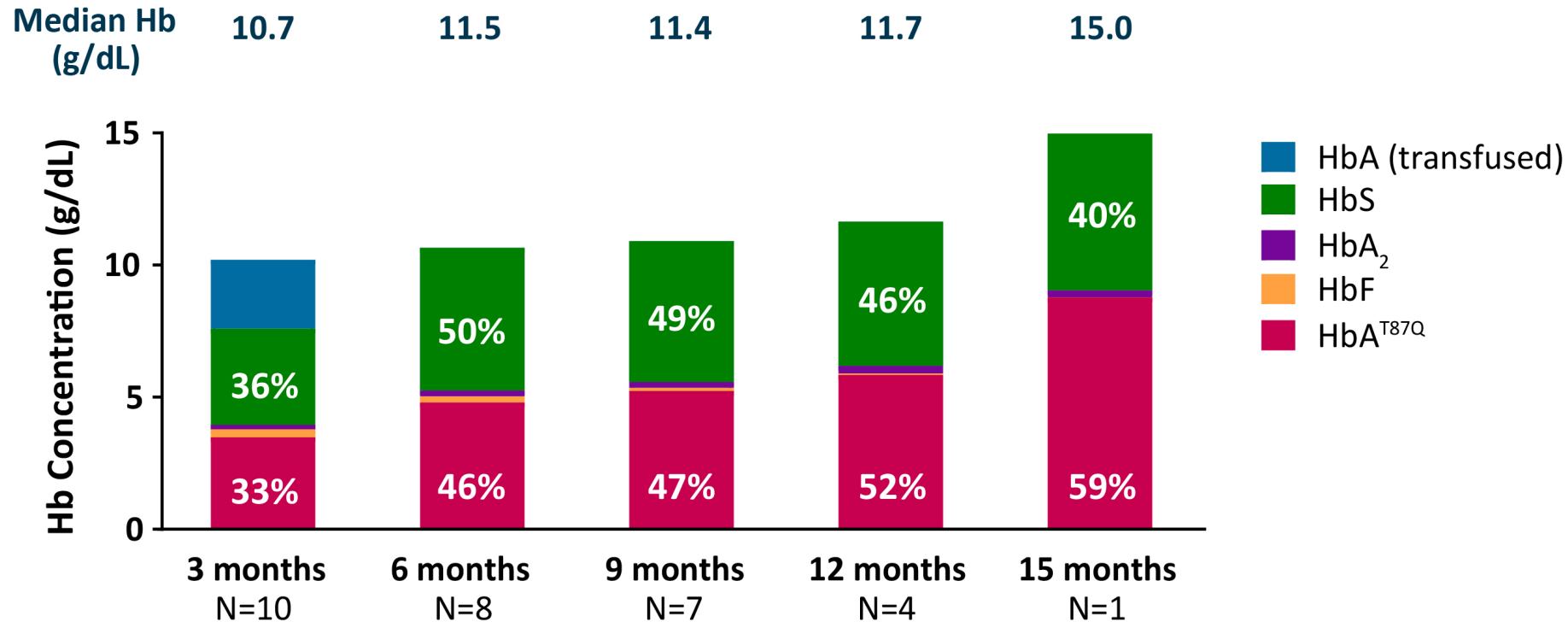
Approaches to gene therapy using CD34⁺ HSPCs



Follow-up:

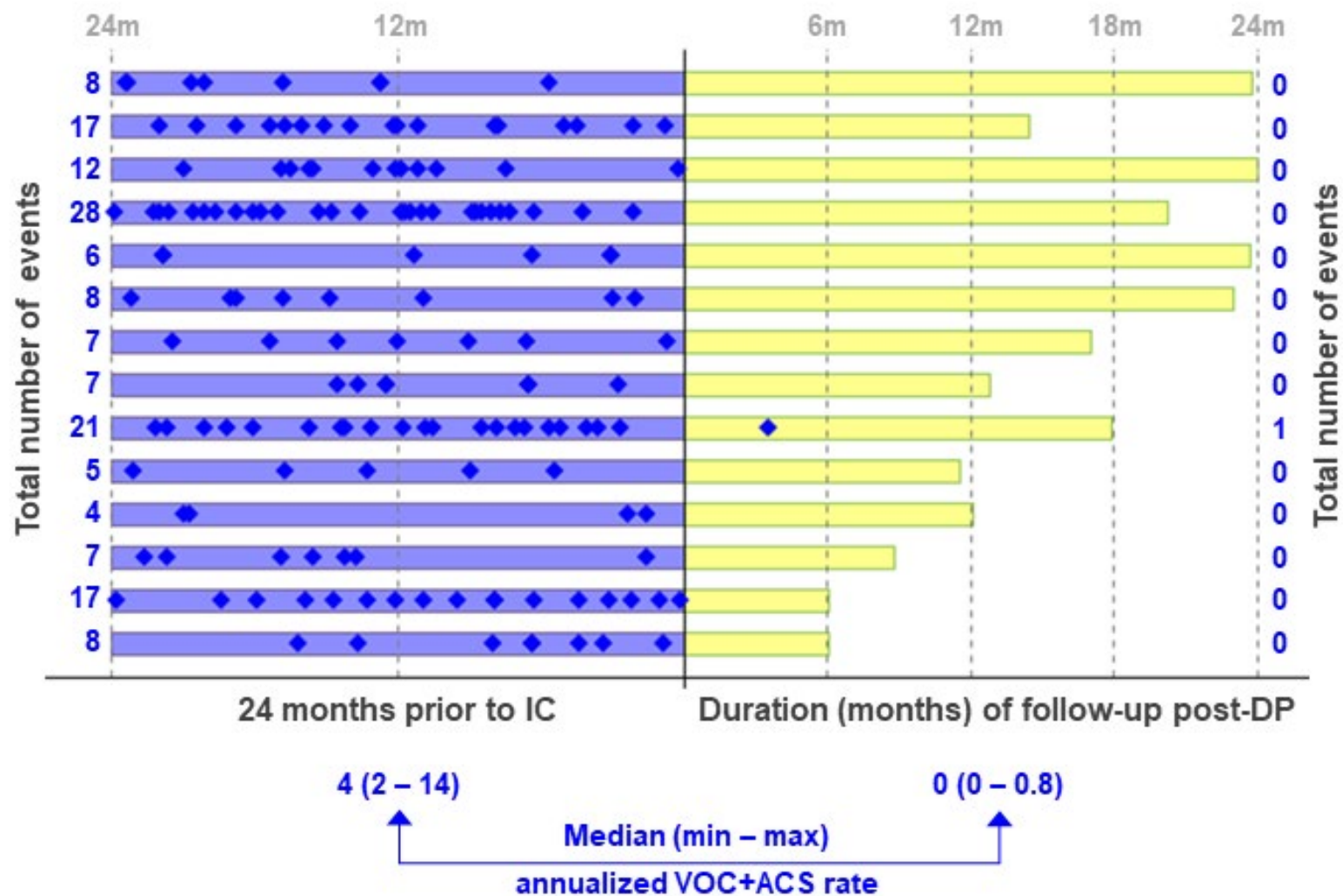
- Engraftment; adverse events
- HbF (HbA^{T87Q}), F-cells
- CBC and markers of hemolysis
- VOCs, transfusions
- Allelic editing; VCN
- Off-target edits

Lentivirus-mediated (β^{T87Q}) gene therapy: SCD

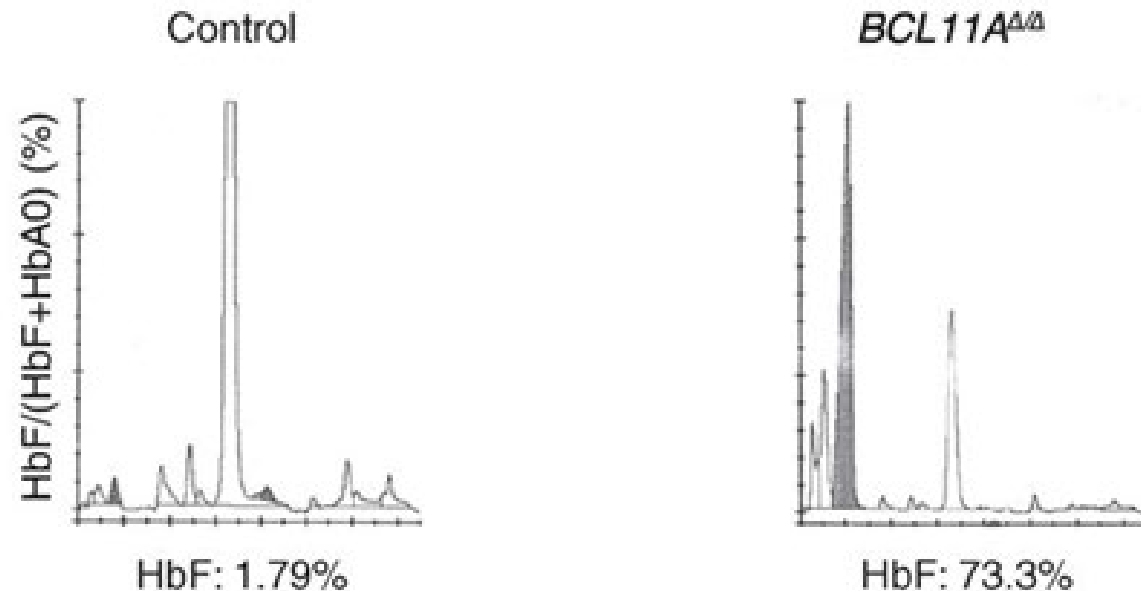
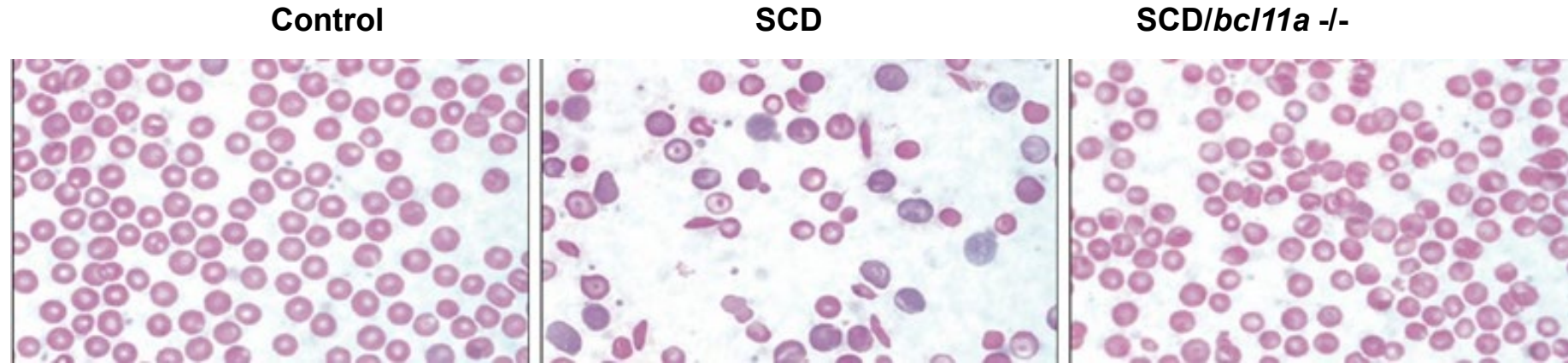


- LDH 225.0 (130.0–337.0) U/L; Reticulocytes 150.0 (42.1–283.0) 109/L; bilirubin 1.3 (0.2–2.0) mg/dL
- No VOC or ACS
- *MDS, AML reported 2/16/21*

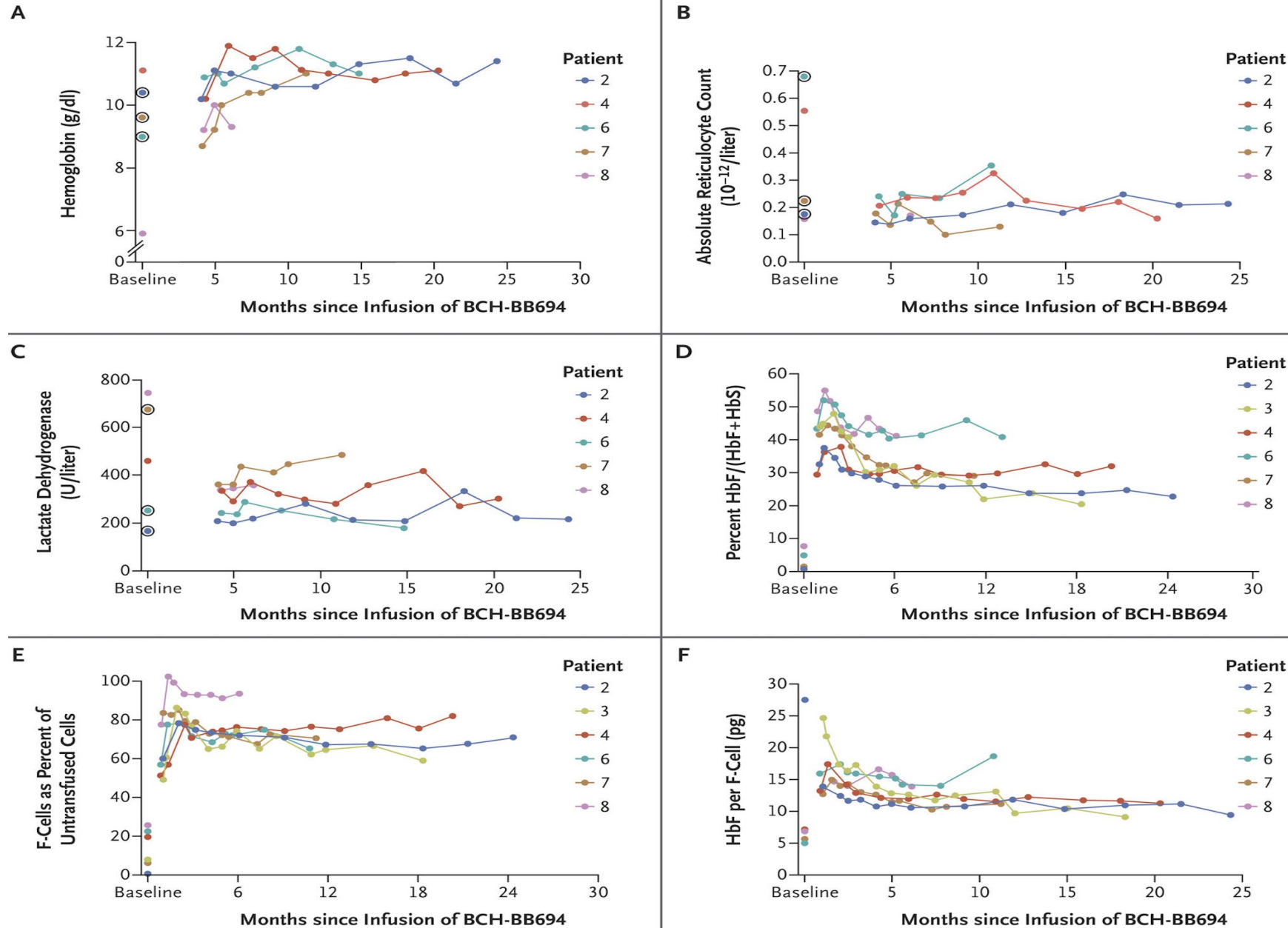
Sickle vasoocclusion following gene therapy with LentiGlobin



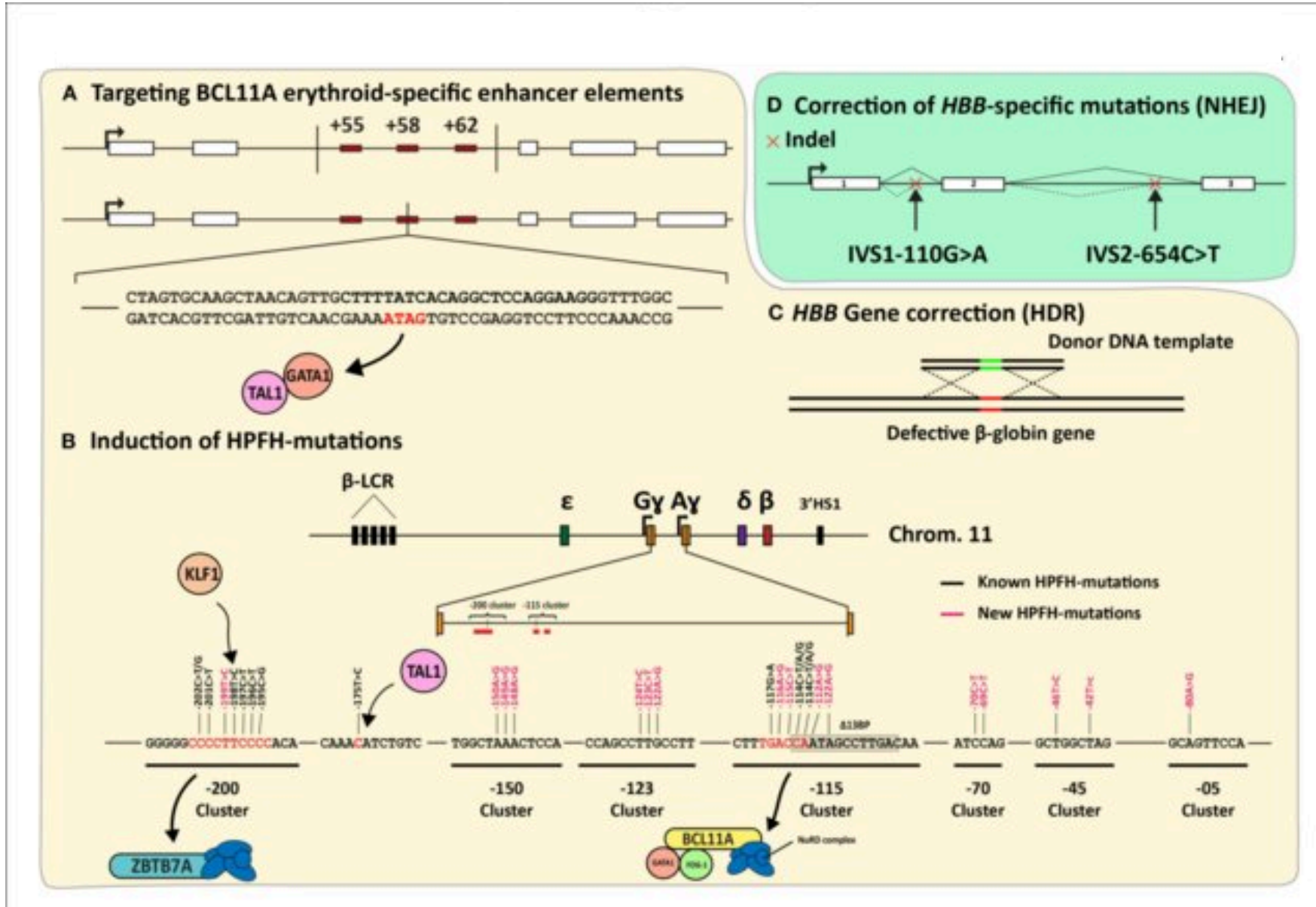
Trans-acting regulation of *HBG* expression: *bcl11a* represses *HBG2/1* in transgenic mice and HUDEP2 cells



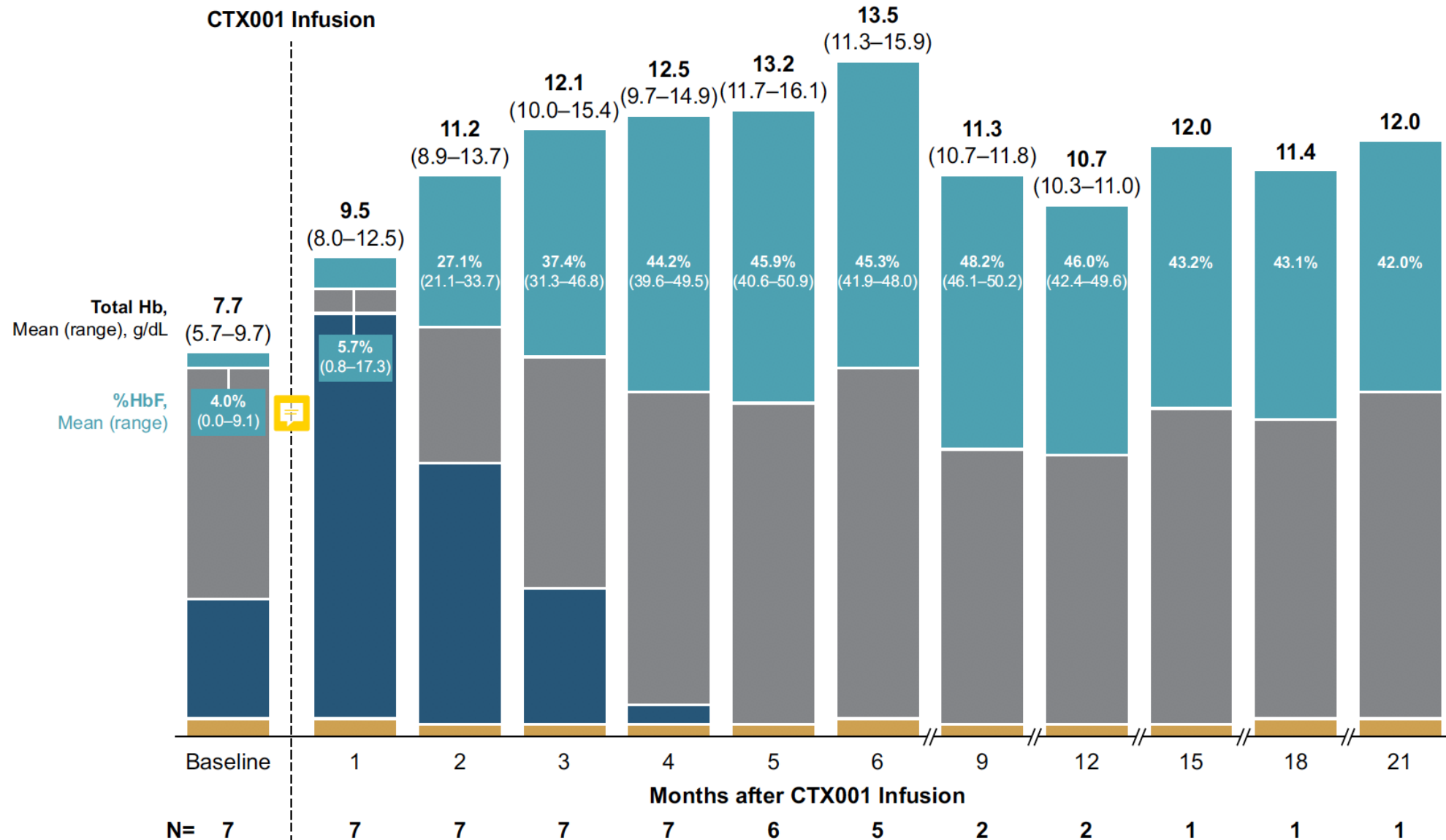
shmRNA directed to the erythroid enhancer of *BCL11A* increases HbF



Genome editing to “cure” β hemoglobinopathies



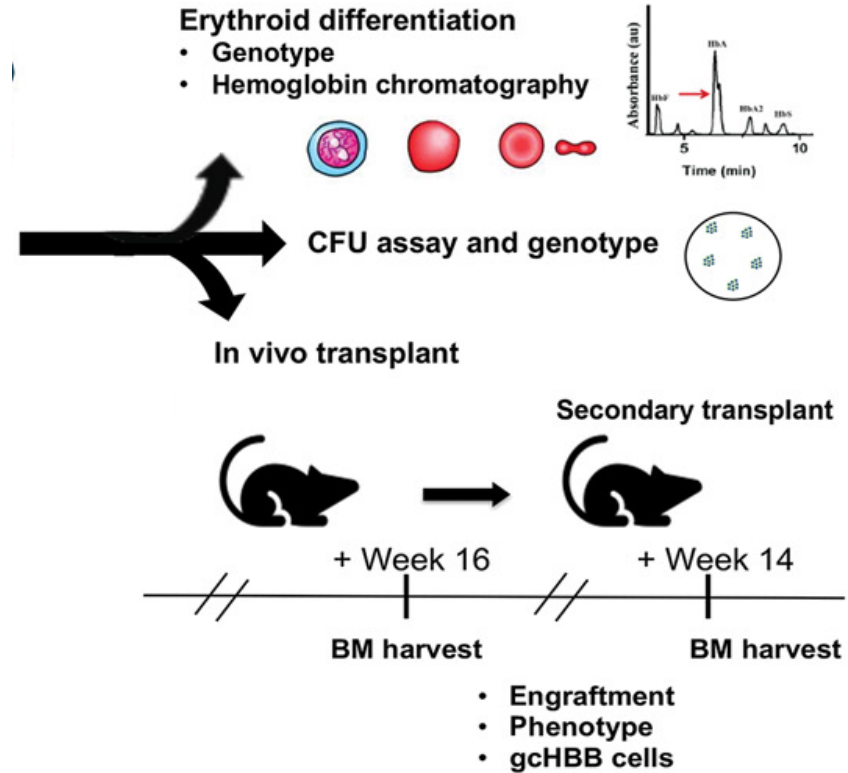
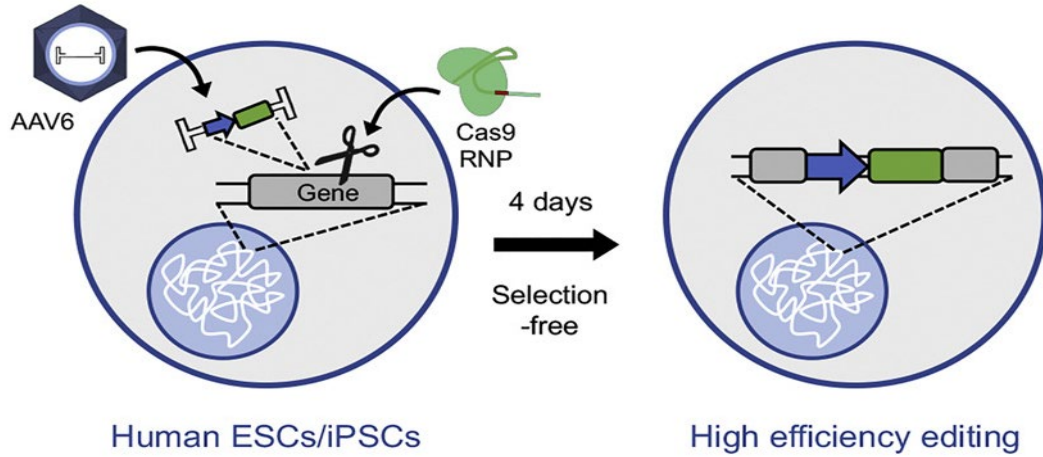
Hemoglobin fractions after *BCL11A* enhancer disruption in sickle HPSCs



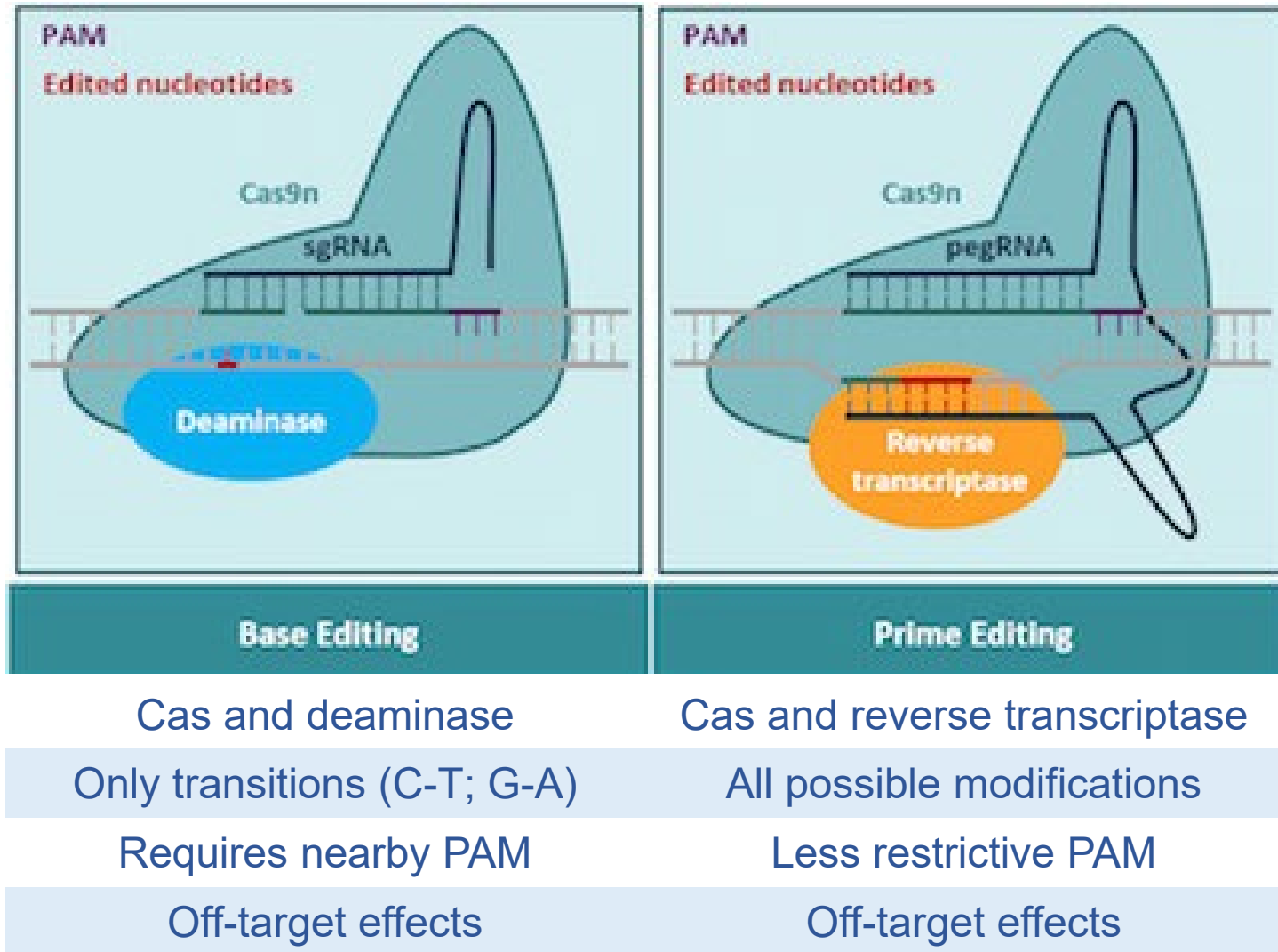
An efficient approach to HDR; correcting the HbS gene

Repair template

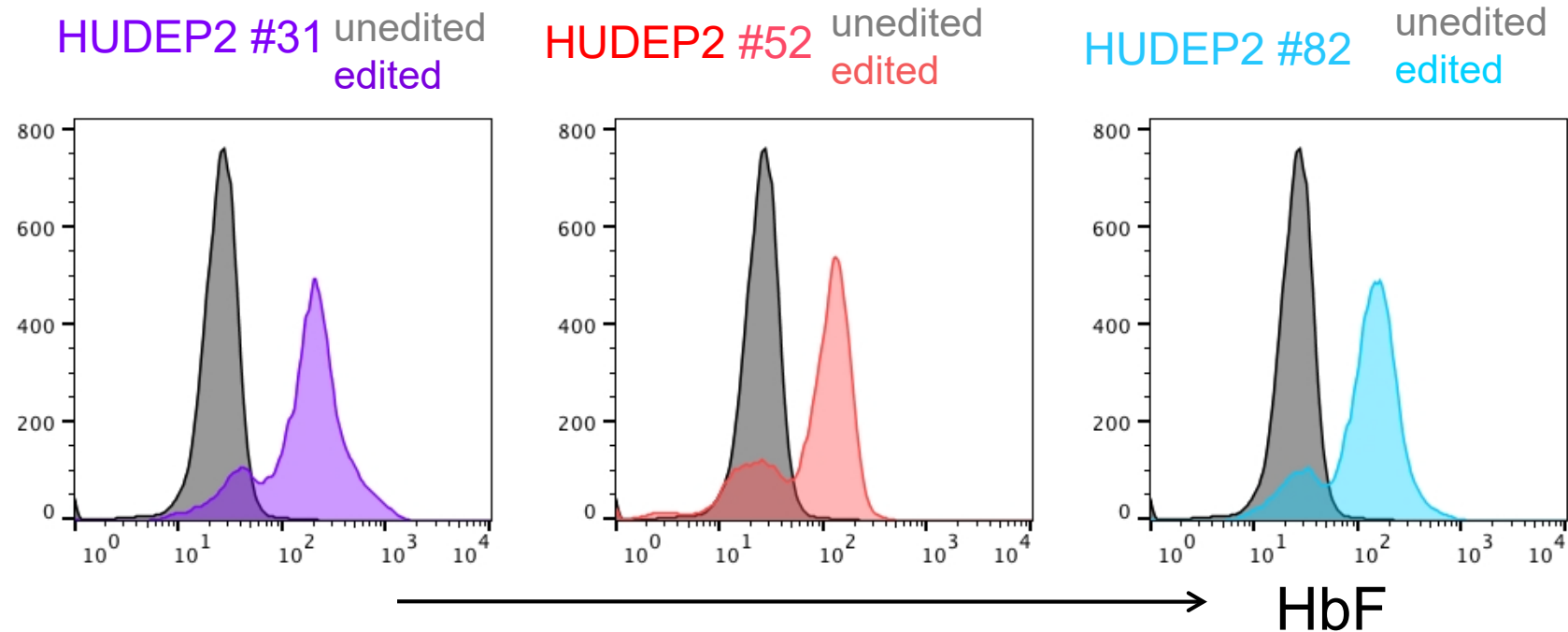
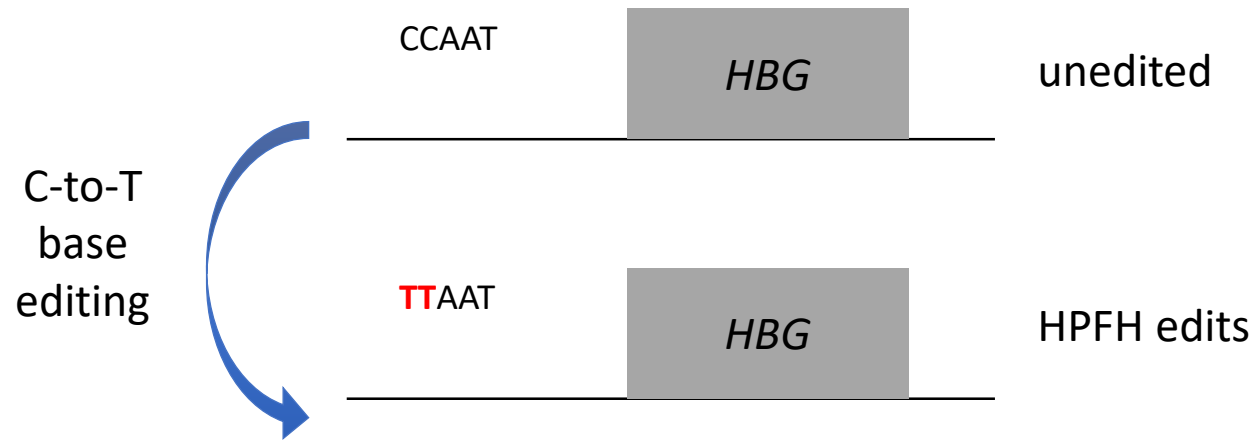
Nuclease



Other gene editing technologies

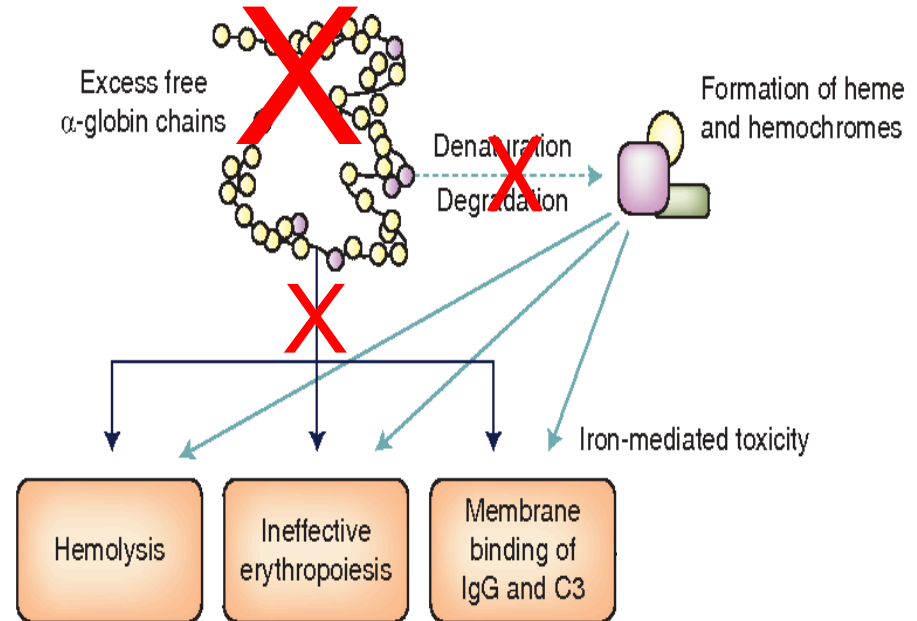
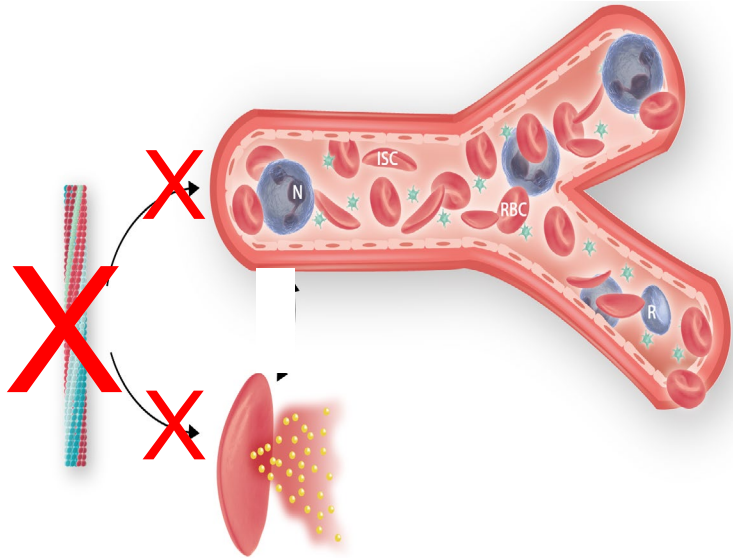


BCL11A binding motif base-editing increases HbF



Summary

cellular therapeutics → induce ~50% HbF
→ correct (replace) HbS (β thalassemia) gene



- Benefits depend on amount of HbF induced and HbF distribution amongst F-cells
- With ~50% HbF β hemoglobinopathies are “cured”

Can too much HbF be harmful?

- Fetal development is normal
- Homozygotes for deletion HPFH have 100% HbF and:
 - low P_{50}
 - mild erythrocytosis
 - low MCV
 - α/γ biosynthesis ratio ~ 1.5 , $\approx \beta$ thalassemia trait
- HbF $>70\%$ has been associated with IUGR
- Pregnant patients with HbSS had fewer complications when HbF $>15\%$
- In HbS-HPFH (30% HbF), P_{50} is nearly normal as the predominant tetramer is $\alpha_2\beta^S\gamma$, not $\alpha_2\gamma_2$

Issues

- Genotoxic conditioning regimens
 - single dose melphalan vs. busulfan?
 - non-genotoxic antibody-based regimens
- MDS, AML
 - complication of SCD ?
 - complication of conditioning?
 - complication of random vector insertion?
 - complication of lentiviral vectors?
- Off-target editing effects
 - depends on editing approach?
 - induces thalassemia?

Future of gene-based therapy

- Non-myeloablative, non-genotoxic conditioning
- Improved methods of stem cell collection
- Use of iPSC-derived HPSCs
- In vivo delivery of “editors” to HPSCs
- Small, orally available molecules that induce high concentrations of pancellularly distributed HbF