

Updated Results from HGB-206 LentiGlobin for Sickle Cell Disease Gene Therapy Study: Group C Data and Group A AML Case Investigation

John F Tisdale, Alexis A Thompson, Janet L Kwiatkowski, Markus Y Mapara, Lakshmanan Krishnamurti, Banu Aygun, Kimberly A Kasow, Stacey Rifkin-Zenenberg, Manfred Schmidt, Alex Miller, Xinyan Zhang, Dennis Kim, Dustin Whitney, Hans Bitter, Phillip D Gregory, Melissa Bonner, Sunita Goyal, Jennifer J Jaroscak, Julie Kanter, Mark C Walters

Disclosure

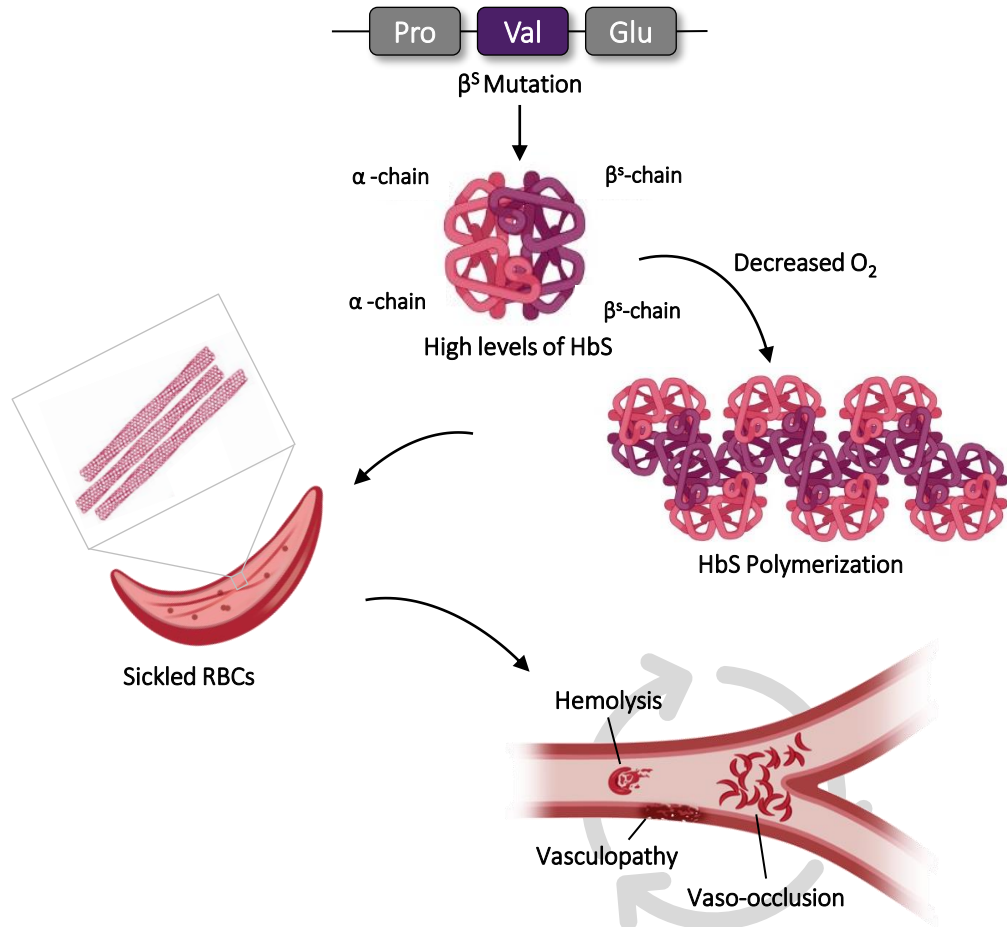
John F Tisdale

Nothing to Disclose

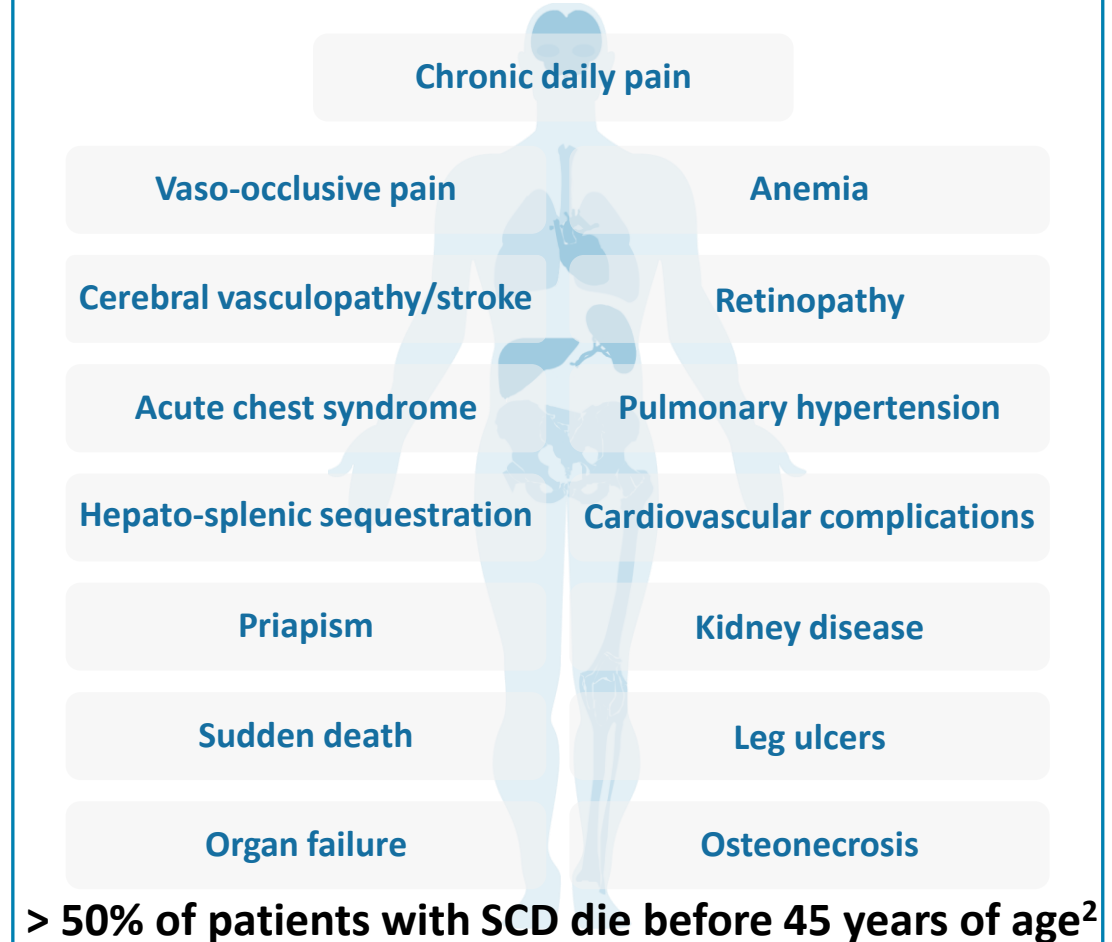
SCD is characterized by high morbidity and early mortality

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Pathophysiology of SCD¹



Complications^{2,3}



HGB-206: Study design

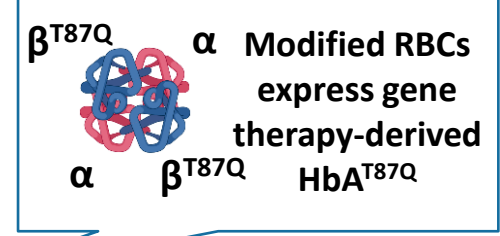
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HSC collection
Bone marrow harvest or mobilization with plerixafor & apheresis

Busulfan myeloablative conditioning

DP infusion

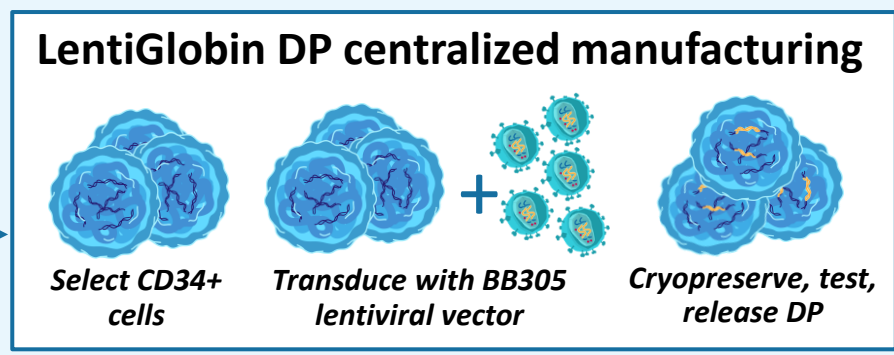
Transduced HSCs engraft and contribute to reconstitution of functional RBCs



2-yr follow-up

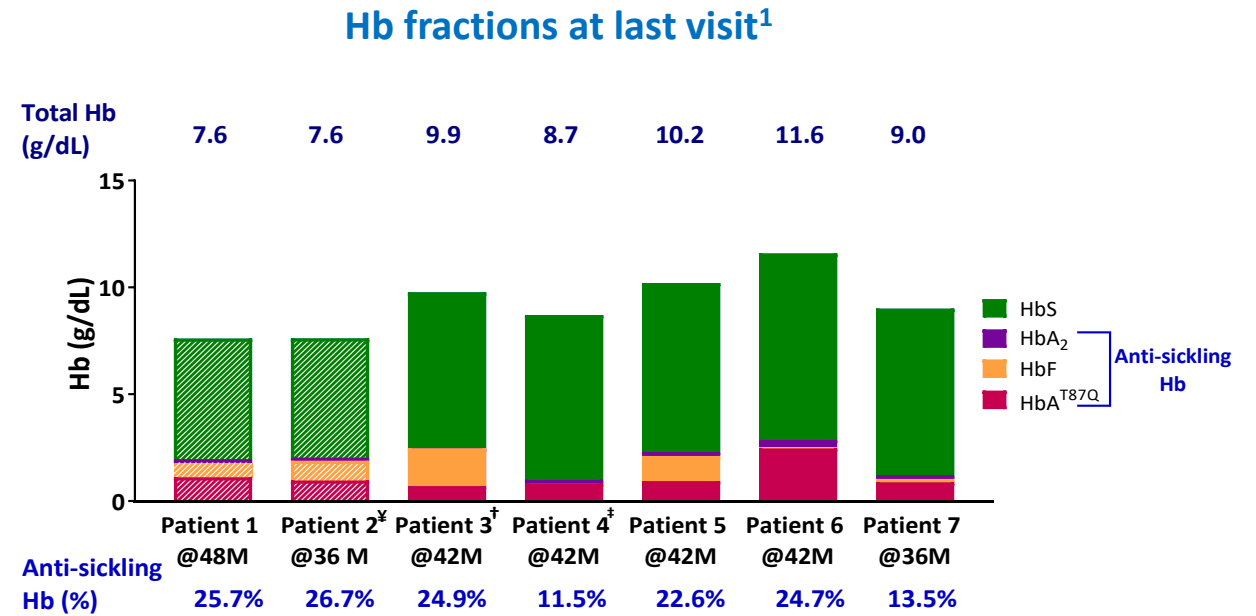
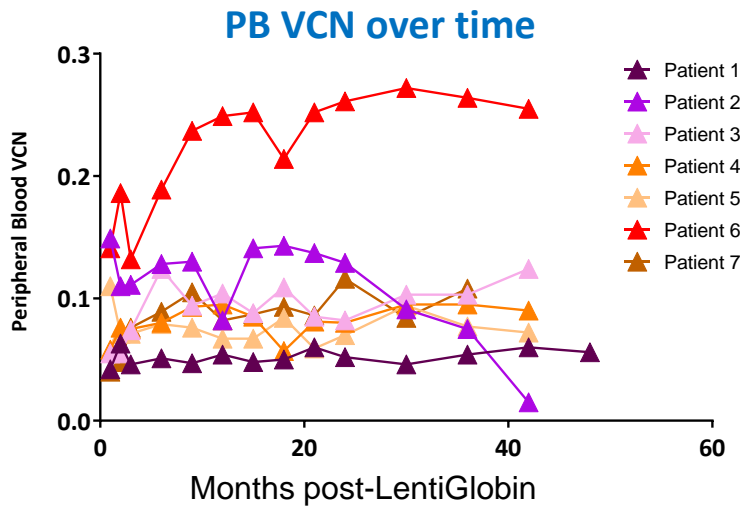
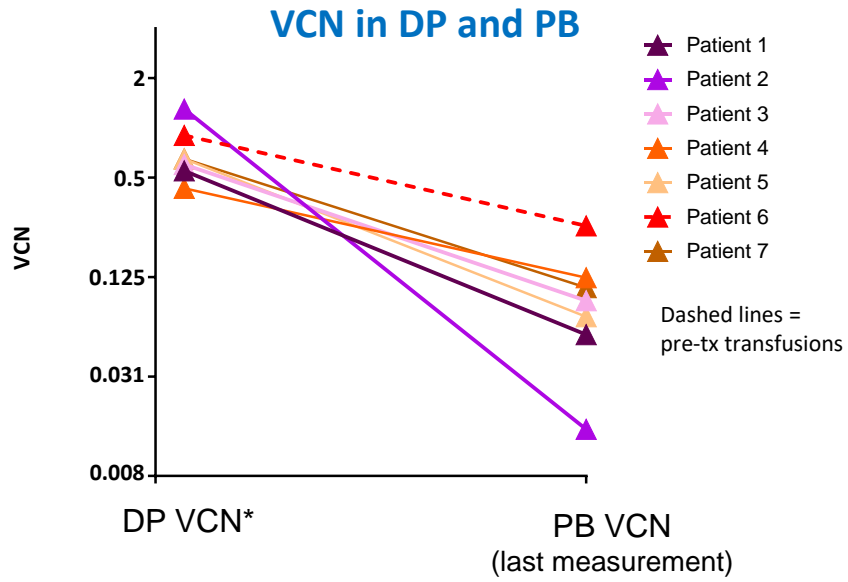
Long-Term Follow-Up Study

	Group A	Group B	Group C
Pre-collection transfusion regimen	Optional	Required	Required
HSC source	Bone marrow	Bone marrow	Mobilized PB
Manufacturing process	Original	Orig → Refined	Refined



HGB-206 Group A: Decline in PB VCN after product infusion resulted in low HbA^{T87Q} production

For video

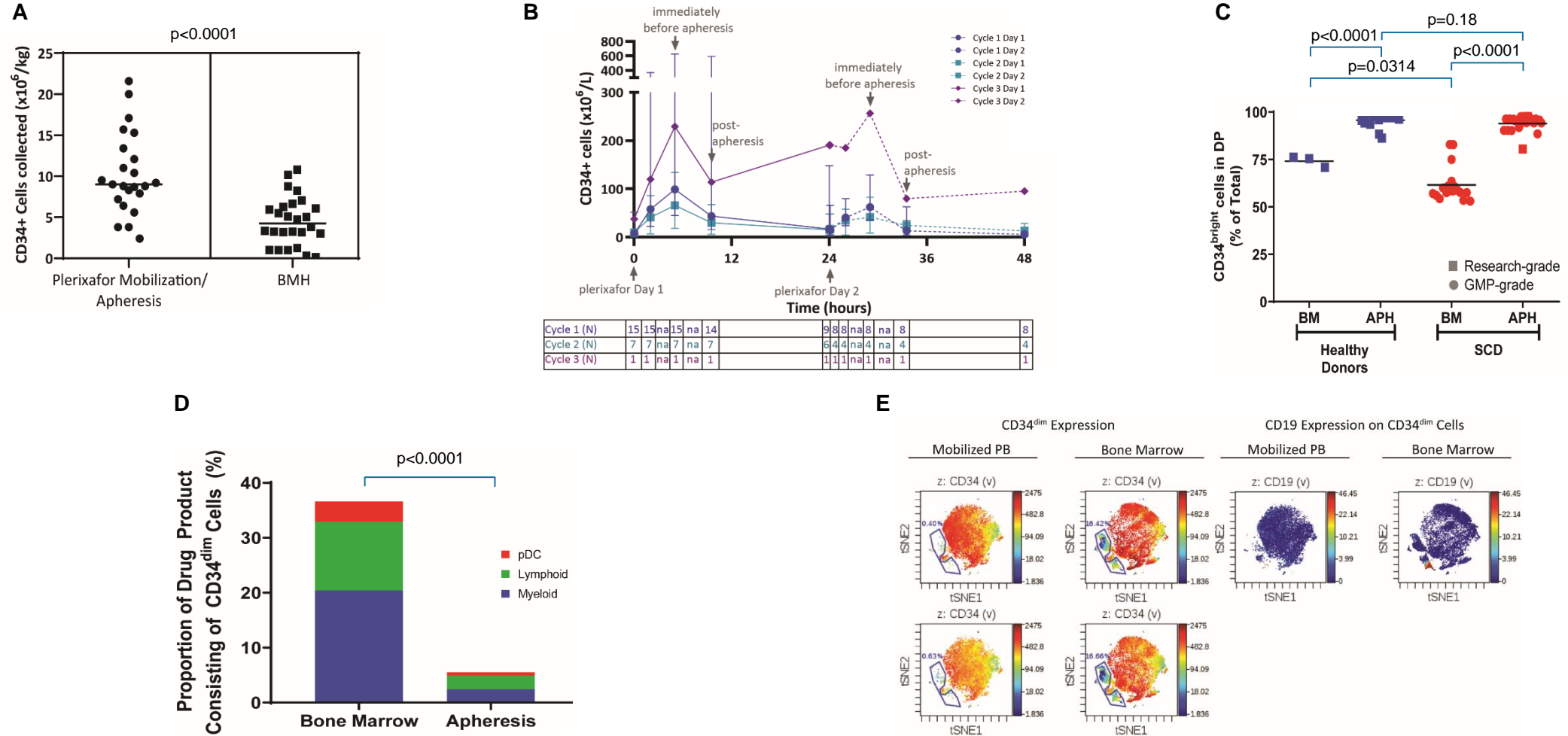


Hatched bars show patients on regular transfusions and HU post-engraftment

*Mean DP VCNs used for patients with >1 DP lot; †Given confounding effect of myelodysplastic syndrome and subsequent chemotherapy on the Hb fractions data, these laboratory values were censored from the start of chemotherapy administered after MDS diagnosis; ‡HbA₂ levels are pending; †Group A pt 4 had 2 transfusions post-engraftment. PB, peripheral blood; Hb, hemoglobin; MDS, myelodysplastic syndrome; pt, patient.
1. Walters M et al. Presented at ASH; December 7–10, 2019; Orlando, FL.

HGB-206: Plerixafor mobilization improves HSC collection compared with BMH

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Protocol evolution in the open-label, phase 1/2 HGB-206 study of LentiGlobin GT (bb1111) in severe SCD

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HSC Source Shift

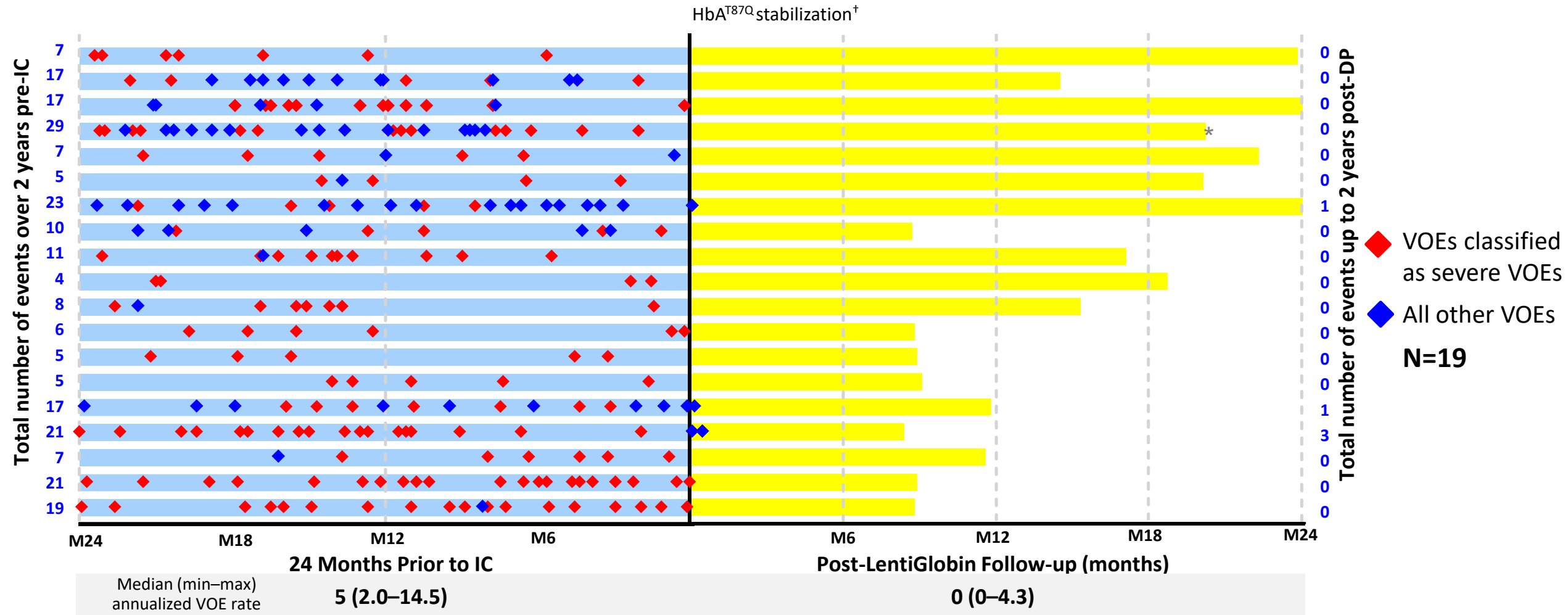
	Group A ¹⁻⁶	Group B ¹⁻⁶	Group C ¹⁻⁶
Pre-collection transfusion regimen	Optional	Required	Required
HSC Source	Bone marrow	Bone marrow	Plerixafor-mobilization and apheresis
Conditioning AUC Target, $\mu\text{M}^*\text{min}$ per dose^a	4,000 (Median AUC: 4747)	4,500 (median AUC: 5136)	5,000 (median AUC: 4843)
Manufacturing Process	Original	Original → Refined	Refined
Total Cell Dose, $\times 10^6$ cells/kg (Median total CD34+, CD34hi/+ HSCs)	Low (2.1, 1.6)	Medium (2.7, NA)	High ^b (6.9, 5.8)
Transduction Efficiency (Median DP VCN, Median % Transduced)	Low (0.6, 25.0%)	High (3.1, 78.4%)	High (3.8, 80.2%)

^aFor a once daily dosing regimen^{5,6}

^bFollowing transduction of isolated CD34+ HSCs with BB305 lentiviral vector, the bb1111 cell dose will be $\geq 3.0 \times 10^6$ CD34+ cells/kg for each subject³

HGB-206 Group C: Complete resolution of VOsE ≥ 6 months post-LentiGlobin treatment

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Protocol VOsEs are shown; Patients with ≥ 4 sVOEs at baseline before IC and with ≥ 6 months of follow-up post-DP infusion are included. A VOE includes episodes of acute pain with no medically determined cause other than a vaso-occlusion, lasting more than 2 hours and severe enough to require care at a medical facility, a VOE includes acute episodes of pain, acute chest syndrome, acute hepatic sequestration, and acute splenic sequestration; [†]HbA^{T87Q} expression stabilizes within 6 months; *One death, unlikely related to LentiGlobin, > 18 months post treatment in a patient with significant baseline SCD-related cardiopulmonary disease.

Note: In the last dataset, one patient had a non-serious VOC at Day 107. The event is recorded as an investigator reported VOE but does not meet the definition of a protocol VOE.

HGB-206 Group C: Safety profile

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Treatment-emergent ≥ Grade 3 AEs	N=32
<i>Reported in ≥ 2 patients*</i>	<i>n (%)</i>
Stomatitis	21 (65.6)
Febrile neutropenia	14 (43.8)
Increased ALT	4 (12.5)
Increased AST	4 (12.5)
Increased GGT	4 (12.5)
Nausea	4 (12.5)
Increased blood bilirubin	2 (6.3)
Premature menopause	2 (6.3)
Upper abdominal pain	2 (6.3)
Serious treatment-emergent AEs	
<i>Reported in ≥ 2 patients</i>	
Abdominal pain	2 (6.3)
Nausea	2 (6.3)
Drug withdrawal syndrome	2 (6.3)
Vomiting	2 (6.3)

- 1 patient with a nonserious Grade 2 DP-related neutropenic fever (resolved)
- No cases of veno-occlusive liver disease, graft failure
- No vector-mediated RCL and no insertional oncogenesis
- One death, attributed to cardiopulmonary disease and unlikely related to LentiGlobin, > 18 months post treatment in a patient with significant baseline SCD burden

*Hematologic AEs commonly observed post-transplantation have been excluded.

HGB-206 clinical trial hold following two suspected unexpected serious adverse reactions (SUSARs)

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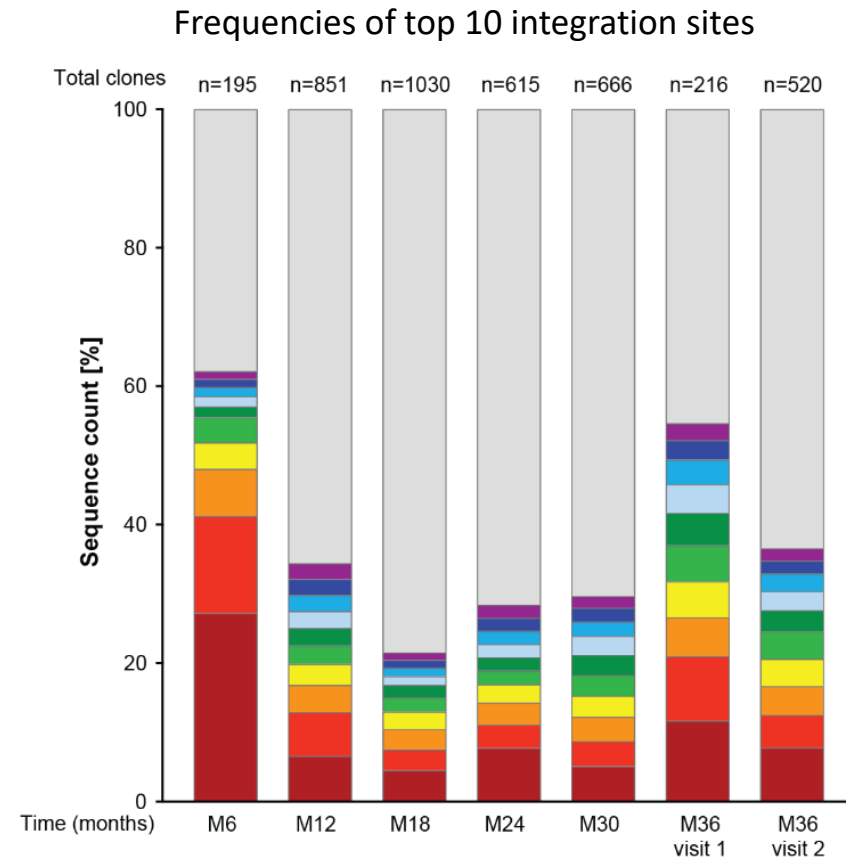
- Beyond the 20 Aug 2020 data cut, two SUSARs were reported and as of February 2021, HGB-206 is on a clinical hold
 - **Group C: Initially reported MDS diagnosis revised to transfusion-dependent anemia**
 - A patient had persistent anemia 6 months after transplant and was found to have trisomy 8 in 6% of cells scored on a 6-month BM aspirate but no blasts or dysplastic cells
 - Investigator assessed as serious, Grade 3, ongoing, and possibly related to LentiGlobin for SCD
 - A follow-up BM aspirate revealed no genetic or chromosomal abnormalities and no evidence of myeloid neoplasm, and the diagnosis was changed to transfusion-dependent anemia with investigations ongoing
 - **Group A: Patient diagnosed with AML > 5 years post-LentiGlobin treatment.**
 - Investigator assessed as serious, Grade 4, ongoing, and possibly related to LentiGlobin for SCD

HGB-206 Group A: 2018 MDS/AML case unrelated to vector

For video

- At ~36 months post LentiGlobin GT, a patient was diagnosed with MDS in 2018
- BM biopsy showed 15% myeloblasts and dysplasia
- Cytogenetics showed monosomy 7 and abnormal chromosome 19p in 8 of 20 metaphases
- Blast cells (CD34+) had low VCN consistent with the absence of LVV integration
- The patient passed away due to relapsed AML in 2020

No evidence of clonal predominance by ISA



HGB-206 Group A: Two cases of AML

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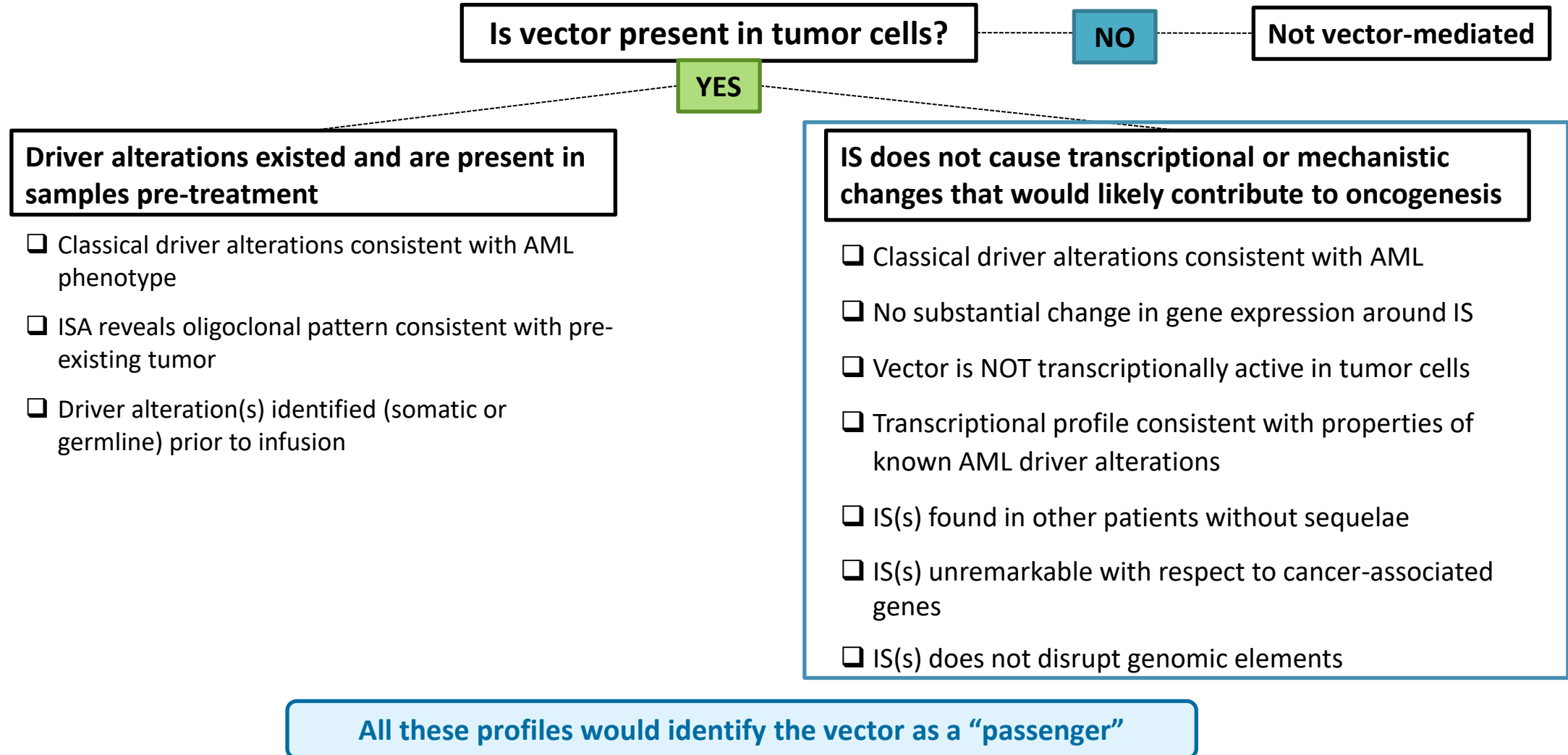
	2018 MDS/AML case ¹	2021 AML case
Mutations at baseline	No mutations or cytogenetic abnormalities (microarray, NGS)	No mutations or cytogenetic abnormalities (microarray, NGS)
Mutations post-treatment prior to AML diagnosis	NA*	No mutations M3, M6, M18, M24 (microarray, NGS)
Mutations at AML diagnosis	<ul style="list-style-type: none"> • Monosomy 7 • Abnormal 19p • <i>RUNX1</i> (NP_001745.2:p.Asp198Gly), • <i>PTPN11</i> (NP_002825.3:p.Phe71Leu), • <i>KRAS</i> NP_203524.1:p.Gly12Ala 	<ul style="list-style-type: none"> • Monosomy 7 • Partial loss of 11p • <i>RUNX1</i> Exon 5 stop gained p.A149*fs • <i>PTPN11</i> Exon 3 missense: p.A72V
Vector in blasts?	No	Yes; insertion in 4 th intron of <i>VAMP4</i>

*Only baseline mutations available. AML, acute myeloid leukemia; NGS, next generation sequencing; NA, not available.

1. Hsieh MM et al. *Blood Adv.* 2020; 4: 2058–2063

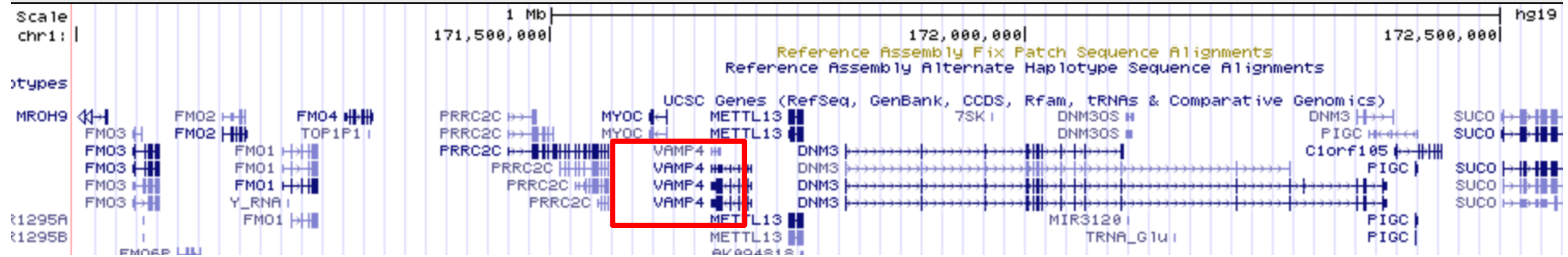
HGB-206 Group A 2021 AML case: Is the vector a “passenger” or “driver” of oncogenesis?

For video



HGB-206 Group A 2021 AML case: What role does *VAMP4* play?

For video



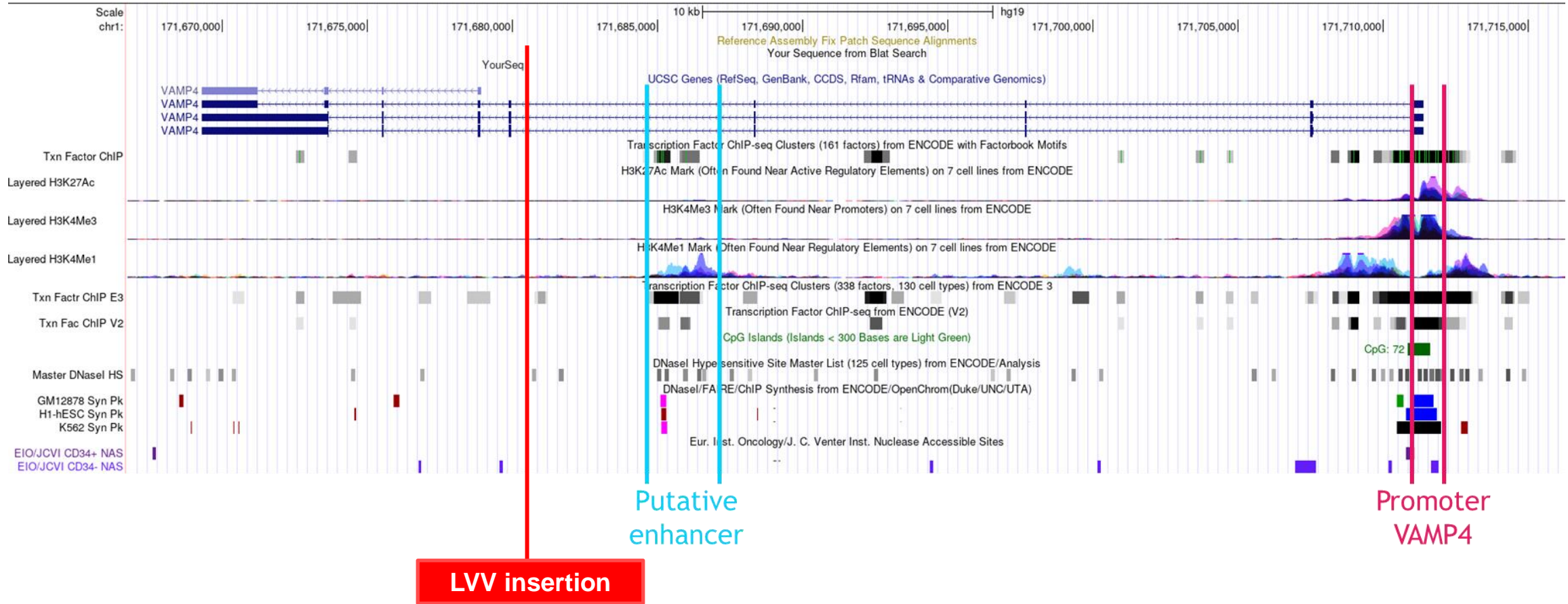
What role does *VAMP4* play?

- Located on chromosome 1q
- Implicated in Golgi ribbon formation, transport from the Golgi to the membrane, and neurotransmission^{1,2}
- No role in cellular proliferation or survival based on analysis of gene databases (COSMIC, cBioPortal, DepMap, and CCGD)

***VAMP4* has no reported role in cellular proliferation or oncogenesis**

HGB-206 Group A 2021 AML case: Did the *VAMP4* IS disrupt any genomic features?

For video



IS mapped to the non-coding region of *VAMP4* in a location with no annotated genomic features*

*Evaluated genomic features included enhancer elements, promoters, boundary elements (eg, CTCF binding sites), areas of chromatin accessibility (incl. ATAC-seq), and regions of chromosomal looping (Hi-C contact matrix)

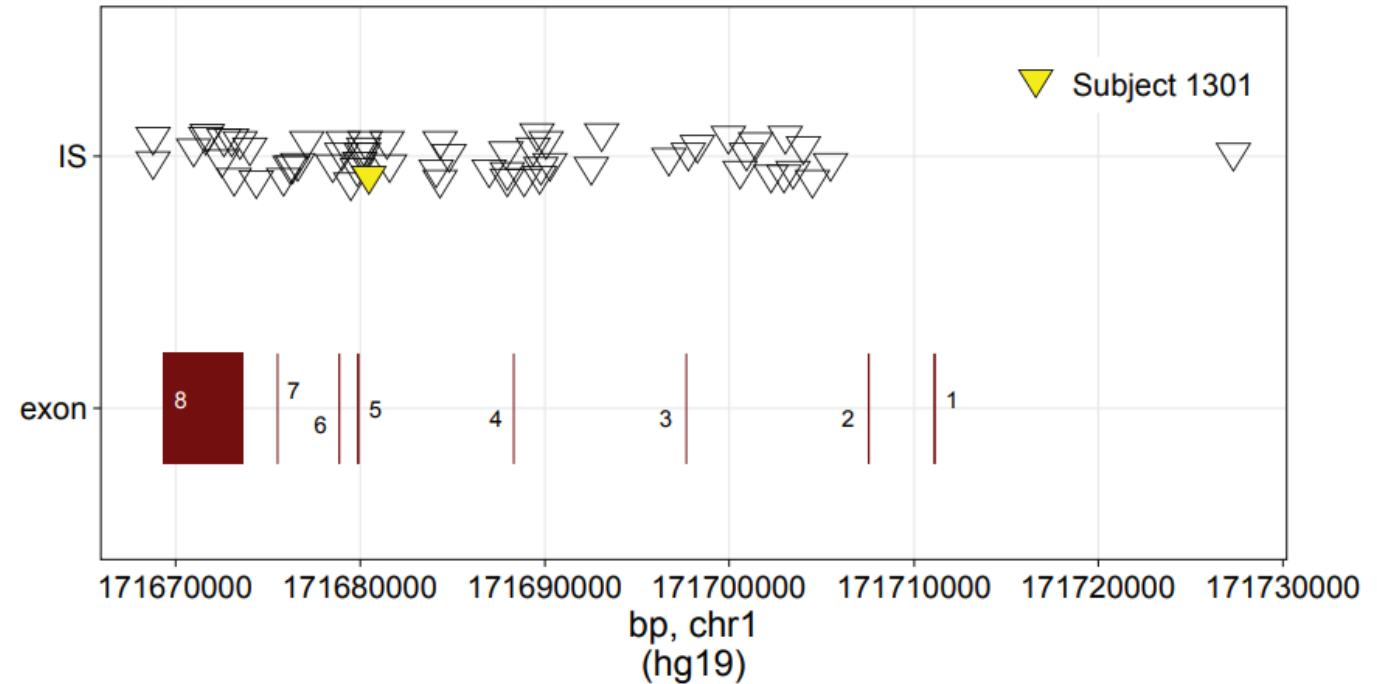
AML, acute myeloid leukemia; IS, integration site; LVV, lentiviral vector; *VAMP4*, vesicle-associated membrane protein 4.

HGB-206 Group A 2021 AML case: Is *VAMP4* IS associated with clonal predominance in other patients with SCD?

For video

Frequency and location of *VAMP4* insertions

- Of 35 patients with SCD with ISA data, 25 had IS in *VAMP4*
- 60 unique IS were mapped
- 14 unique IS in intron between exons 4 and 5
- Only the patient diagnosed with AML had *VAMP4* IS >0.05% at any time point



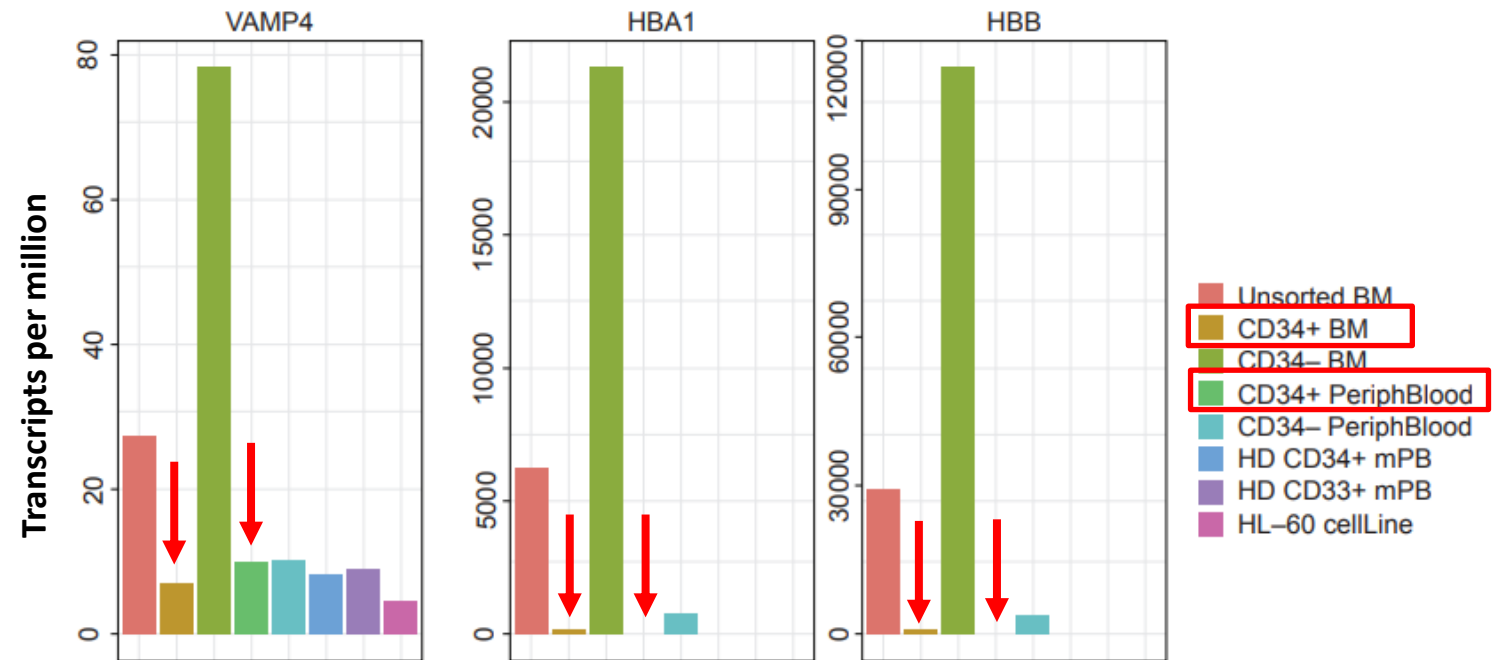
***VAMP4* IS was present in the majority (71%) of patients in HGB-206 without sequelae in any other patient**

HGB-206 Group A 2021 AML case: Is the vector transcriptionally active in tumor cells?

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- Highest expression levels of *HBA1* and *HBB* were in unsorted and CD34- BM samples that include erythroid progenitors
- *HBB* expression in CD34+ BM is 0.6% of the CD34- BM expression
 - Of those, the majority (60%) were endogenous β^S transcripts and 40% were from the β^{T87Q} transgene

Gene expression analysis*



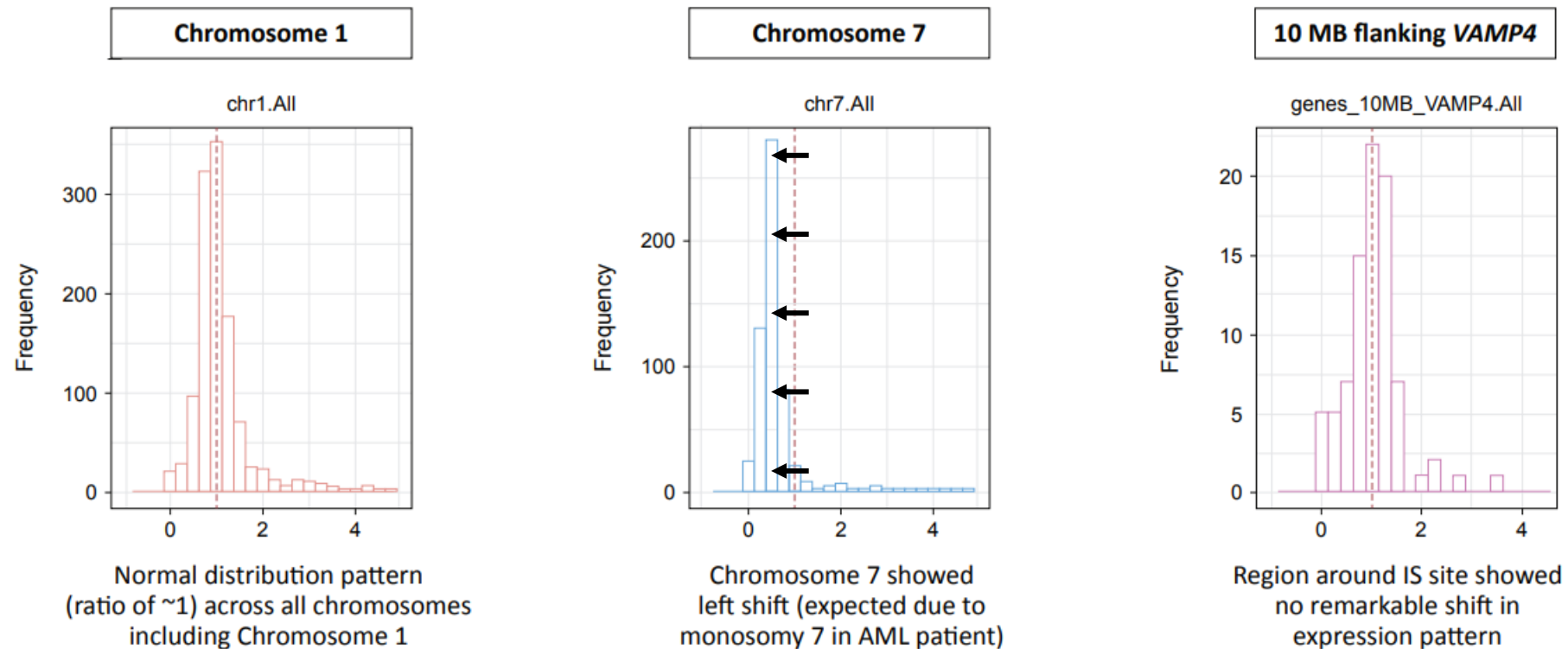
Vector is minimally transcriptionally active in tumor cells and does not significantly affect *VAMP4* expression

*Blast cells indicated by red arrows and boxes in figure and legend.

HGB-206 Group A 2021 AML case: Did *VAMP4* IS impact expression of nearby genes or chromosome-wide expression?

For video

Gene expression ratios in AML vs healthy donor CD34+ BM cells



***VAMP4* IS did not impact gene expression proximal to the vector insertion
Normal pattern of distribution (ratio of ~1) was detected across all chromosomes**

HGB-206 Group A 2021 AML case: Unlikely related to vector-mediated insertional oncogenesis

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Criteria

1. Classical driver alterations consistent with AML
2. No substantial change in gene expression around IS
3. Vector is NOT transcriptionally active in tumor cells
4. Transcriptional profile consistent with properties of known AML driver alterations
5. IS(s) found in other patients without sequelae
6. IS(s) unremarkable with respect to cancer-associated genes
7. IS(s) does not disrupt genomic elements

Findings

- ✓ Monosomy 7, partial loss of 11p, *RUNX1*, *PTPN11*
- ✓ No remarkable expression changes in 10 MB region around *VAMP4* IS
- ✓ Very low level *HBB* detected in CD34+ cells
- ✓ RNAseq data consistent with monosomy 7 and contains *PTPN11* and *RUNX1* mutations
- ✓ *VAMP4* IS common and this patient is the only one with *VAMP4* IS >0.05% at any point
- ✓ *VAMP4* has no known association with cellular proliferation or oncogenesis
- ✓ *VAMP4* IS does not disrupt mapped genomic features

HGB-206 Group A 2021 AML case: What may have contributed to the development of AML?

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- **Patients with SCD have a higher rate of hematological malignancies compared with the general population^{1,2}** and age, gender, race, and ethnicity matched non-SCD patients³
- There may be **higher risk for the development of malignancy following graft rejection/failure⁴⁻⁷**
- In SCD patients with unsuccessful or partly successful transplantation, hematopoietic stress from continued disease and proliferative stress from initial reconstitution of the BM by engrafting HSPCs may also contribute to risk of hematologic malignancies^{4,5,7}
- The **underlying increased risk of hematologic malignancies in SCD, combined with the transplant procedure and associated proliferative stress, as well as continued hematopoietic stress due to minimal clinical benefit** in these two Group A patients (DP manufactured using stem cells collected via BMH and using a previous manufacturing process which has since been discontinued) may have contributed to the development of AML

Elevated risk of hematological malignancies in patients with SCD and following transplant, particularly suboptimal transplant

AML, acute myeloid leukaemia; MDS, myelodysplastic syndrome SCD, sickle cell disease; BM, bone marrow; HSPC, hematopoietic stem and progenitor cells; DP, drug product; BMH, bone marrow harvest.

1. Brunson A, et al. *Blood*. 2017;130:1597-9; 2. Seminog OO et al. *J R Soc Med*. 2016;109:303-9; 3. Jain S et al. *Blood*. 132; 1087; 4. Eapen M et al. *Lancet Hematol*. 2019; 6:e585-e596; 5. Ghannam JY et al. *Blood*. 2020;135:1185-1188; 6. Janakiram M et al. *Leuk Lymphoma*. 2018;59:241-244; 7. Fitzhugh et al. *Blood Adv*. 2017;1:652-661.

MDS/AML documented in patients following transplantation with different conditioning regimens and with different donor sources in SCD

For video

	Matched 0170	Matched 0077	Matched (Chicago,Riyadh)	Haplo 0225	Haplo 0069	Eapen CIBMTR	Gene Therapy with BB305 LVV Busulfan	
	TBI/Campath	TBI/Campath Pentostatin/Cy	TBI/Campath	TBI/Campath -/+ Cy	TBI/Campath/Cy Pentostatin/Cy	Many types	LentiGlobin for SCD [‡]	Beti-cel [§] for TDT
N in study	58	26	64	21	19	910	49 Median follow up (min –max) months 23.1 (0.8–74.9)	63 Median follow up (min –max) months 29.54 (0.9–76.4)
MDS, AML	2 (3.5%)	1 (3.8%)	1 (1.6%)	3 (14%)*	0	6+ (1.0%)	2 (4.3%)	0
	1 graft failure (MDS)	1 low engraft (AML)	1 graft failure (MDS)	2 graft failure MDS, AML		Details not available	2 in Group A ^{1,2}	

*Two patients with preexisting TP53 mutations; †overlap with NIH reporting in n=2; ‡as of 17 Feb 2021; §as of 30 Nov 2020.

- MDS/AML more common in patients with graft failure
- Improved engraftment in NIH haplo trial appears to have improved risk of MDS/AML
- Median follow up not sufficient to be conclusive

AML, acute myeloid leukaemia; MDS, myelodysplastic syndrome; SCD, sickle cell disease; TDT, transfusion-dependent β-thalassemia; TBI, total body irradiation; CY, cyclophosphamide.

Data from NIH Intramural Program; 1. Hsieh MM et al. *Blood Adv.* 2020; 4: 2058–2063; 2. Kwiatkowski J et al. Presented at ASPHO. April 20–23, 2021. Virtual. 3. Eapen M et al. *Lancet Hematol.* 2019; 6:e585-e596; 4. Ghannam JY et al *Blood.* 2020;135:1185-1188

- The ongoing Phase 1/2 HGB-206 study is the largest clinical trial of GT in SCD to date with longest follow up > 5 years
- Data in the initial 7 patients (Group A) showed low PB VCN and HbA^{T87Q} expression, prompting protocol improvements (eg, HSC mobilization with plerixafor and improved transduction efficiency) for Group C patients who demonstrated positive outcomes:
 - Complete resolution of severe VOs, median total Hb was consistently ≥ 11 g/dL, median anti-sickling HbA^{T87Q} $\geq 40\%$
- Investigation into 2 AML cases in Group A indicates they were unlikely related to vector-mediated insertional oncogenesis
 - We demonstrated the absence of vector integration in the blast cells of an MDS/AML case in 2018¹
 - In the 2021 case, we report the IS was in *VAMP4*, a gene with no reported role in oncogenesis, and had no significant effects on regional or global gene expression, indicating that vector insertion was a passenger to AML development and not a driver of oncogenesis
- The underlying increased risk of hematologic malignancies in SCD, combined with the transplant procedure and associated proliferative stress, as well as continued hematopoietic stress due to minimal clinical benefit in these two Group A patients may have contributed to the development of AML
- The benefit-risk balance of LentiGlobin for SCD remains positive, and the safety profile post-LentiGlobin for SCD remains generally consistent with the risks of autologous stem cell transplant, myeloablative single-agent busulfan conditioning, and underlying SCD

Thank you to all for their important contributions to the AML case investigation

For video

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