#### Cellular, Tissue, and Gene Therapies Advisory Committee Meeting

Individuals using assistive technology may not be able to fully access the information contained in this file. For assistance, please send an e-mail to: <a href="mailto:ocod@fda.hhs.gov">ocod@fda.hhs.gov</a> and include 508 Accommodation and the title of the document in the subject line of your e-mail.

## beti-cel & eli-cel Advisory Committee Meeting: Introduction – June 9, 2022, Afternoon Lentiviral Vector Safety

#### Anne-Virginie Eggimann, MSc

Chief Regulatory Officer bluebird bio, Inc.



#### Lenti-D LVV



elivaldogene autotemcel (eli-cel) for early active cerebral adrenoleukodystrophy (CALD) BLA 125755

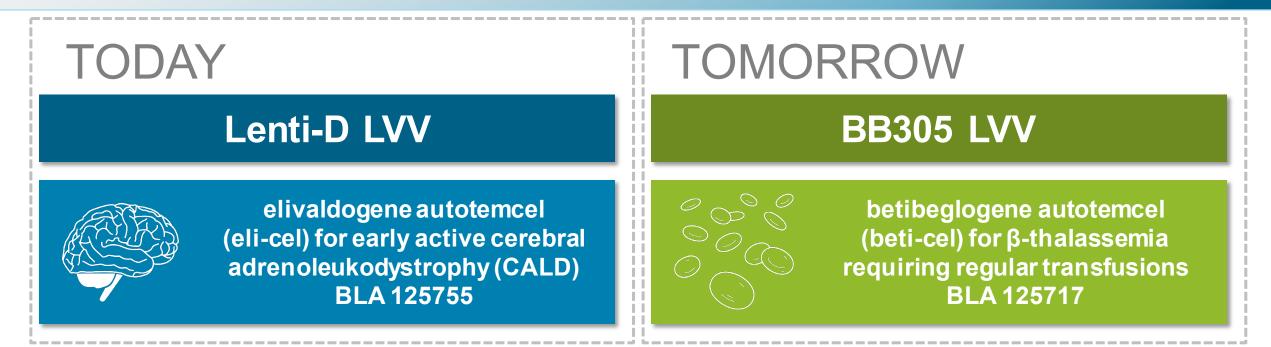
#### Lenti-D LVV

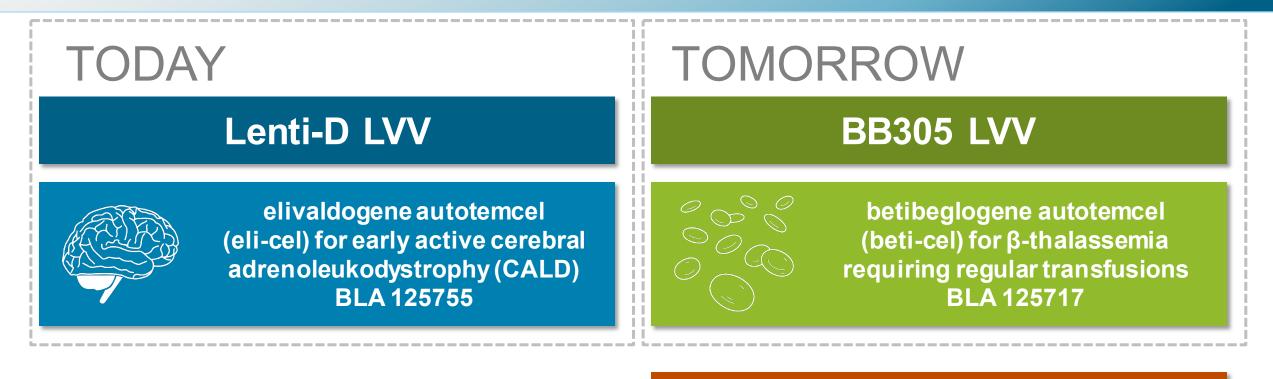
#### BB305 LVV



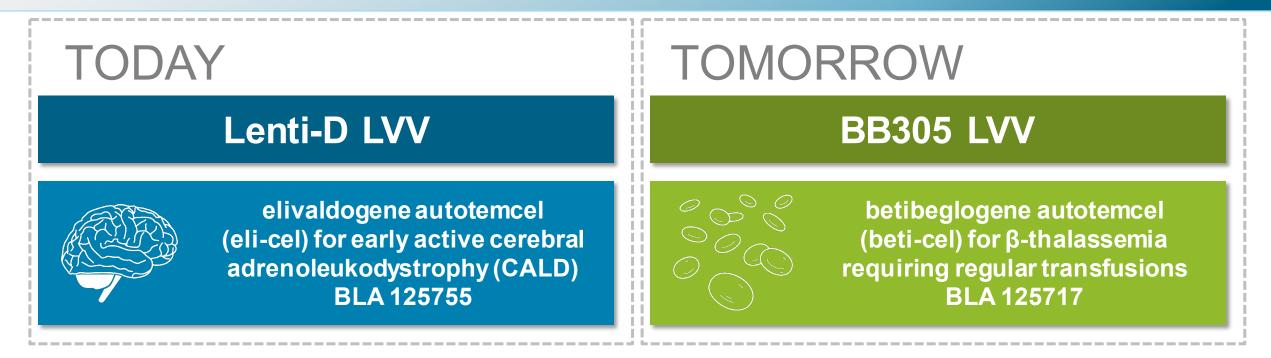
elivaldogene autotemcel (eli-cel) for early active cerebral adrenoleukodystrophy (CALD) BLA 125755

betibeglogene autotemcel (beti-cel) for β-thalassemia requiring regular transfusions BLA 125717





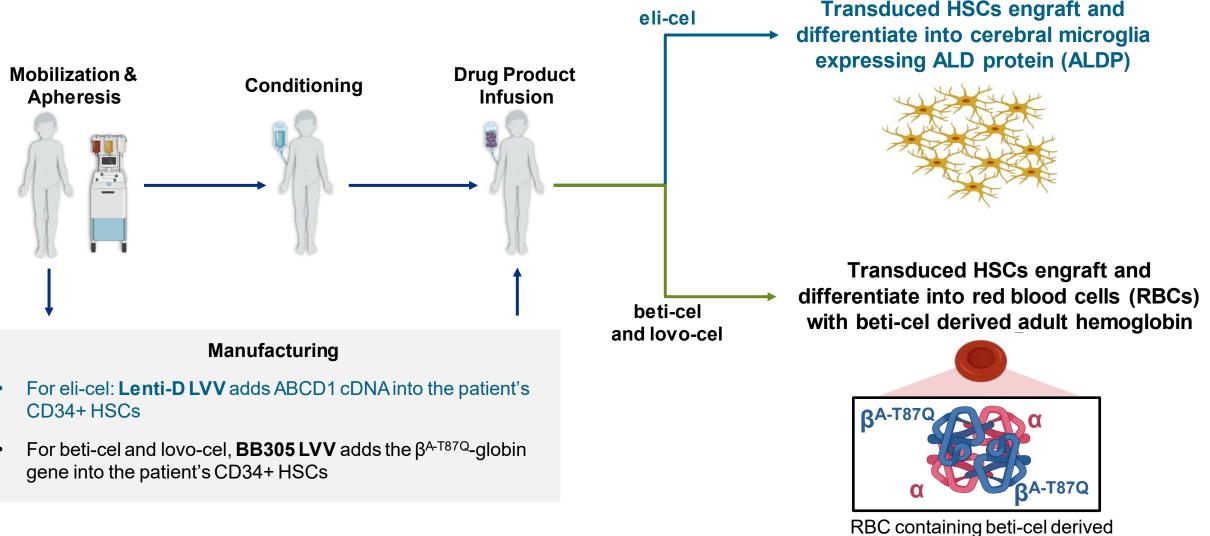
lovotibeglogene autotemcel (lovo-cel) for sickle cell disease in Phase 3 clinical development



lovotibeglogene autotemcel (lovo-cel) for sickle cell disease in Phase 3 clinical development

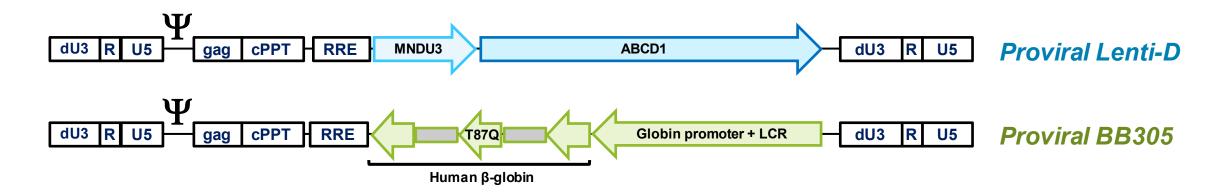
Each LVV is custom-designed for a specific mechanism of action, and each LVV has a distinct safety profile

# Each Lentiviral Vector is Custom Designed to Express a Specific Protein in a Specific Cell Type



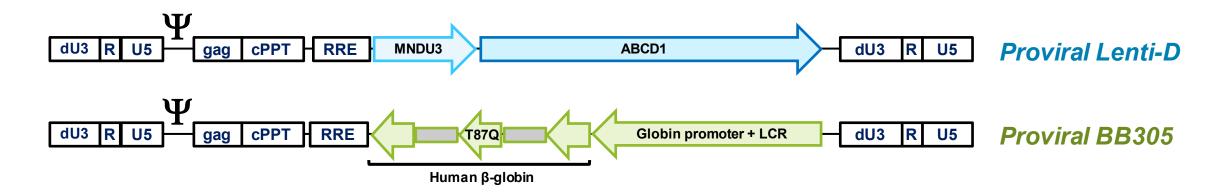
adult Hb, referred to as **HbA<sup>T87Q</sup>** 

#### Lenti-D and BB305 LVV Have Several Different Key Features, Including a Different Promoter



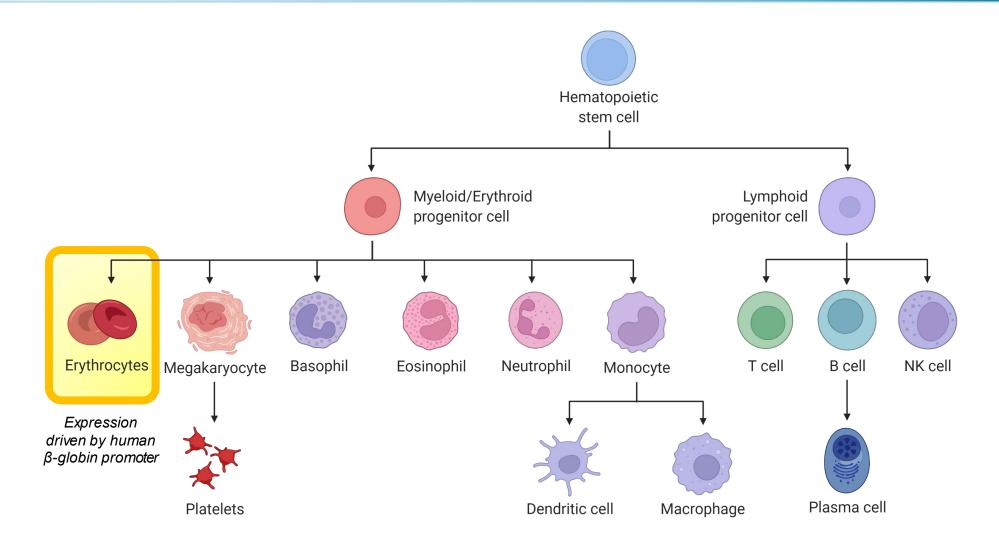
Feature	Lenti-D LVV	BB305 LVV
Transgene	ABCD1	β <sup>Α-T87Q</sup> globin
Transcriptional control	modified viral MNDU3 promoter	human β-globin promoter and locus control region
Gene structure	cDNA	natural exon/intron
Cell type	ubiquitous; all hematopoietic lineages	specific; erythrocytes / red blood cells
Splicing	no transgene splicing	transgene undergoes splicing
PolyA signal	3'LTR	human β-globin

#### Lenti-D and BB305 LVV Have Several Different Key Features, Including a Different Promoter

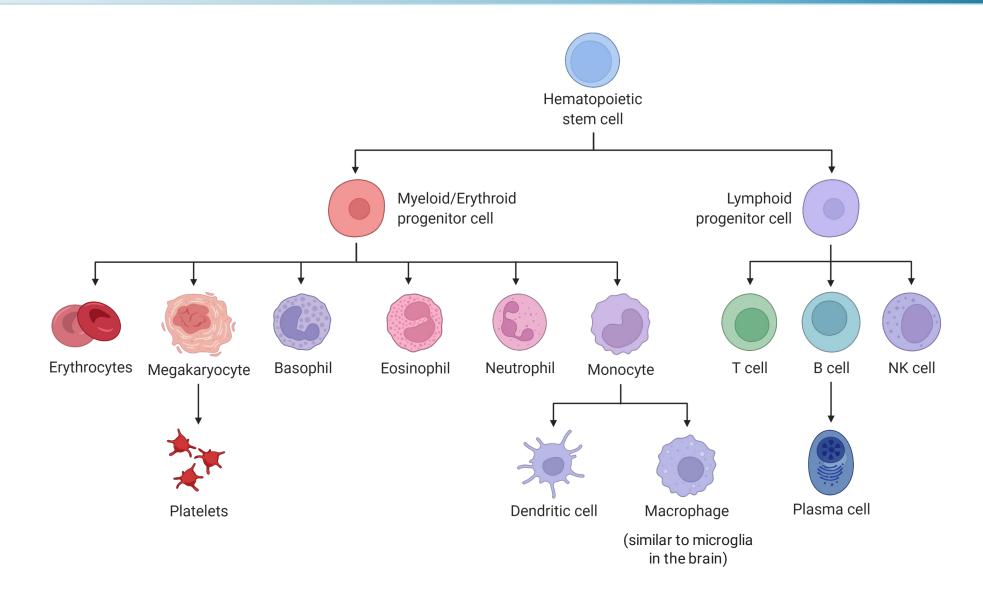


Feature	Lenti-D LVV	BB305 LVV
Transgene	ABCD1	β <sup>Α-Τ87Q</sup> globin
Transcriptional control	modified viral MNDU3 promoter	human β-globin promoter and locus control region
Gene structure	cDNA	natural exon/intron
Cell type	ubiquitous; all hematopoietic lineages	specific; erythrocytes / red blood cells
Splicing	no transgene splicing	transgene undergoes splicing
PolyA signal	3'LTR	human β-globin

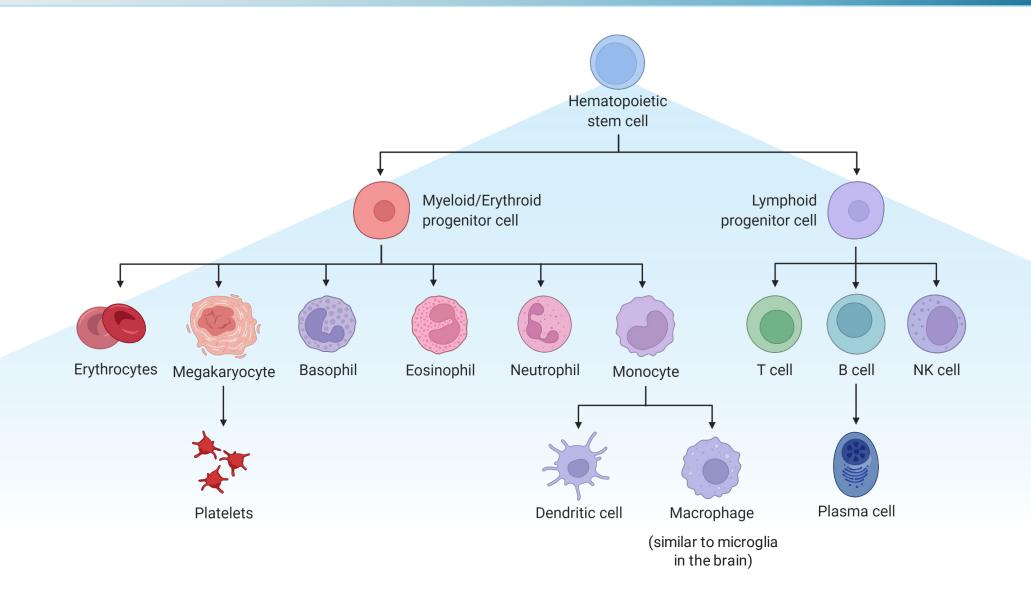
## BB305 LVV uses Human β-globin Promoter which Drives High Gene Expression only in **Erythroid Lineage**



## Lenti-D LVV Uses a Modified Viral MNDU3 Promoter which Drives High Levels of Gene Expression in **All Lineages**



## Lenti-D LVV Uses a Modified Viral MNDU3 Promoter which Drives High Levels of Gene Expression in **All Lineages**



## Each LVV is Designed for a Specific Purpose and Has a Unique Safety Profile

LVV safety, along with the inherent risks of the treatment process, must be weighed against:



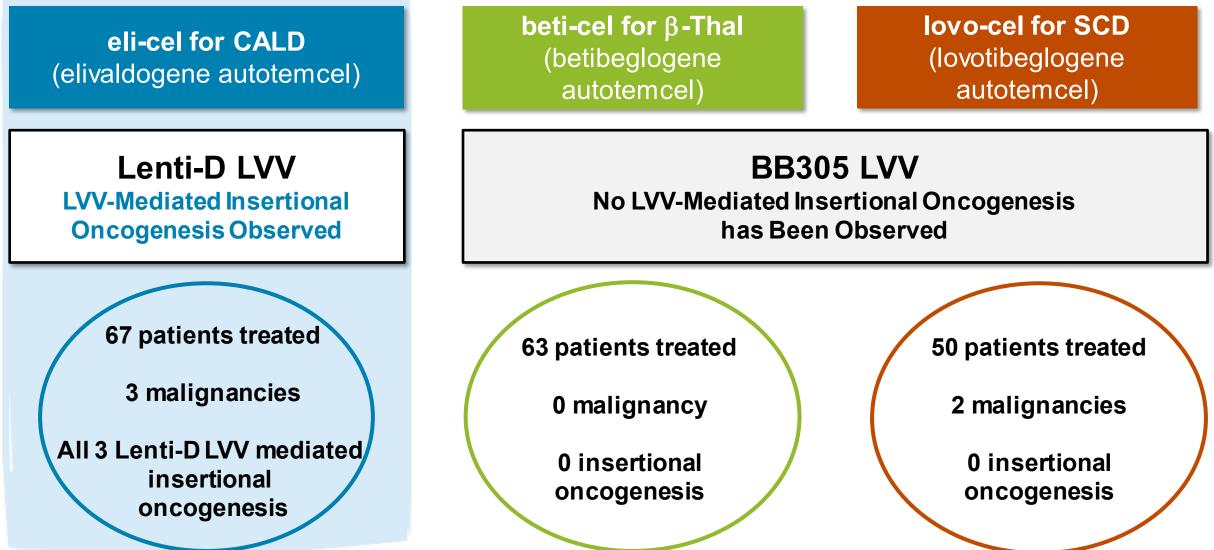
## beti-cel & eli-cel Advisory Committee Meeting: Lentiviral Vector Safety

#### Melissa Bonner, Ph.D.

Senior Vice President, Head of Research bluebird bio, Inc.



#### **Vector-Related Safety Profiles Differ**



CALD: cerebral adrenoleukodystrophy; β-thal: β-thalassemia; SCD: sickle cell disease; LVV: lentiviral vector

## Agenda

#### Background on retroviral vectors

- Safety events warranted development of safer vector designs
- Current LVVs designed to lower risk of insertional oncogenesis
- Benefits and risks of LVV
- LVV traceability and Integration Site Analysis

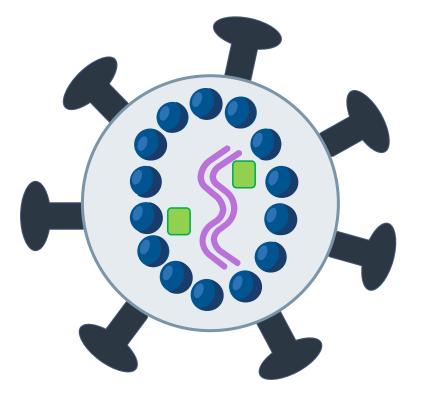
#### Lenti-D LVV used for manufacture of eli-cel

- Mechanism of action necessitates ubiquitous transgene promoter
- LVV mediated safety events

- Mechanism of action necessitates erythroid specific promoter
- No LVV mediated safety events

### Retroviruses are a Family of RNA Viruses

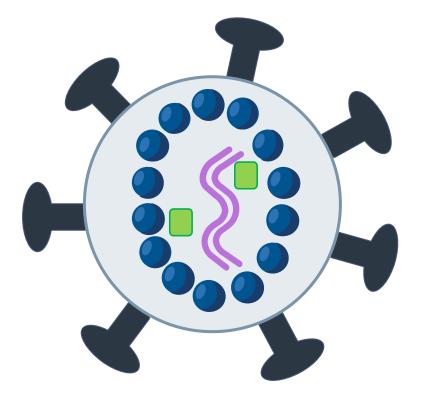
 Gammaretroviral vectors (GRVs) and lentiviral vectors (LVVs) are 2 distinct classes of retroviral vectors used for hematopoietic stem cell gene therapies with different clinical safety profiles



- **Pol** (reverse transcriptase/integrase/protease)
- **Gag** (Capsid/Matrix/Nucleocapsid)
- T Envelope

## Retroviruses are a Family of RNA Viruses

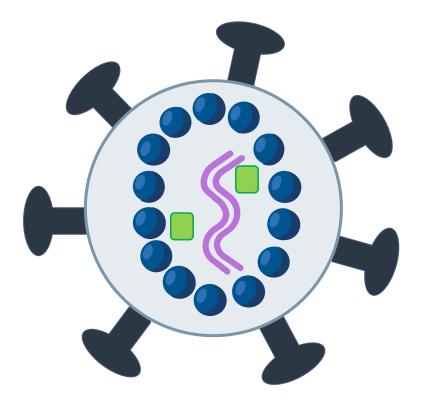
- Gammaretroviral vectors (GRVs) and lentiviral vectors (LVVs) are 2 distinct classes of retroviral vectors used for hematopoietic stem cell gene therapies with different clinical safety profiles
- Retroviruses are RNA viruses that reverse transcribe viral RNA into DNA which can be integrated into genomic DNA of target cells



- **Pol** (reverse transcriptase/integrase/protease)
- **Gag** (Capsid/Matrix/Nucleocapsid)
- T Envelope

## Retroviruses are a Family of RNA Viruses

- Gammaretroviral vectors (GRVs) and lentiviral vectors (LVVs) are 2 distinct classes of retroviral vectors used for hematopoietic stem cell gene therapies with different clinical safety profiles
- Retroviruses are RNA viruses that reverse transcribe viral RNA into DNA which can be integrated into genomic DNA of target cells
- Retroviral vectors are modified retroviruses
  - Viral genes are replaced with a therapeutic transgene which can be delivered to target cells via a process called transduction
  - Absence of intact viral genes that encode proteins renders these vectors replication incompetent



- Pol (reverse transcriptase/integrase/protease)
- **Gag** (Capsid/Matrix/Nucleocapsid)
- T Envelope

## GRVs Led to Insertional Oncogenesis in Some Gene Therapy Patients

- Insertional oncogenesis refers to a malignancy that has directly resulted from the integration of a provirus
- GRVs used across a number of different diseases led to outcomes of insertional oncogenesis (occurrence 2-90%)<sup>1</sup>
  - 6 cases of T-cell acute lymphoblastic leukemia out of 25 X-SCID patients treated
  - 5 cases of myeloblastic syndromes out of 15 CGD patients treated
  - 9 cases of acute leukemia out of 10 WAS patients treated
  - 1 case of lymphoid T-cell leukemia out of 68 ADA-SCID patients treated
  - 84% of insertional oncogenesis cases occurred within 5 years of treatment<sup>1</sup>

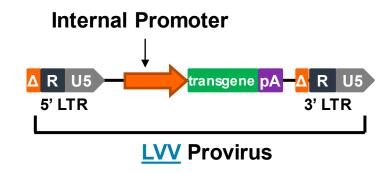
GRV: gammaretroviral vector; X-SCID: X-linked severe combined immunodeficiency; CGD: chronic granulomatous disease; WAS: Wiskott-Aldrich syndrome; ADA-SCID: adenosine deaminase-severe combined immunodeficiency **LV-21** <sup>1</sup>Tucci et al., *Nat Commun.* 2022;13(1):13

## GRVs Led to Insertional Oncogenesis in Some Gene Therapy Patients

- Insertional oncogenesis refers to a malignancy that has directly resulted from the integration of a provirus
- GRVs used across a number of different diseases led to outcomes of insertional oncogenesis (occurrence 2-90%)<sup>1</sup>
  - 6 cases of T-cell acute lymphoblastic leukemia out of 25 X-SCID patients treated
  - 5 cases of myeloblastic syndromes out of 15 CGD patients treated
  - 9 cases of acute leukemia out of 10 WAS patients treated
  - 1 case of lymphoid T-cell leukemia out of 68 ADA-SCID patients treated
  - 84% of insertional oncogenesis cases occurred within 5 years of treatment<sup>1</sup>
- These clinical trials demonstrated strong efficacy, but the serious adverse events necessitated development of a safer vector design

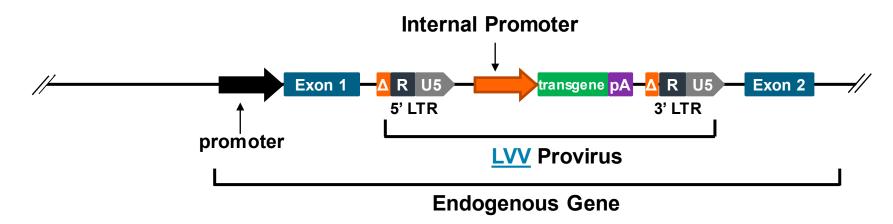
GRV: gammaretroviral vector; X-SCID: X-linked severe combined immunodeficiency; CGD: chronic granulomatous disease; WAS: Wiskott-Aldrich syndrome; ADA-SCID: adenosine deaminase-severe combined immunodeficiency LV-22 <sup>1</sup>Tucci et al., *Nat Commun.* 2022;13(1):13

# Current LVVs are Designed to Lower Risk of Insertional Oncogenesis



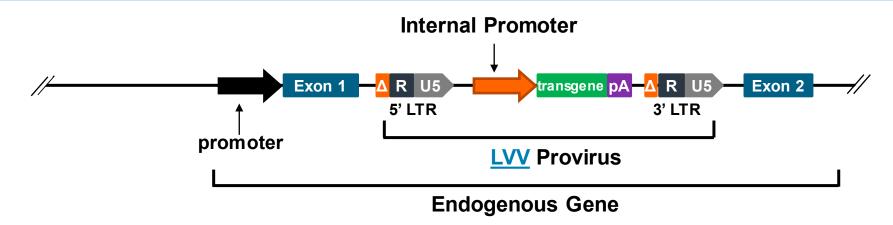
- Designed to be SIN by deleting the viral promoter and enhancer from the LTRs
  - Diminished potential for influencing the expression of nearby genes
- Expression of the therapeutic transgene is controlled by an internal promoter which can allow for expression in the appropriate cell type

## Current LVVs are Designed to Lower Risk of Insertional Oncogenesis



- Designed to be SIN by deleting the viral promoter and enhancer from the LTRs
  - Diminished potential for influencing the expression of nearby genes
- Expression of the therapeutic transgene is controlled by an internal promoter which can allow for expression in the appropriate cell type
- LVVs disfavor the promoter region in favor of the body of gene resulting in integrations primarily within introns

## Current LVVs are Designed to Lower Risk of Insertional Oncogenesis



- Designed to be SIN by deleting the viral promoter and enhancer from the LTRs
  - Diminished potential for influencing the expression of nearby genes
- Expression of the therapeutic transgene is controlled by an internal promoter which can allow for expression in the appropriate cell type
- LVVs disfavor the promoter region in favor of the body of gene resulting in integrations primarily within introns
- Contains no intact viral genes
  - <25% of HIV-1 genome in provirus</p>

## LVVs have Features that are Ideal for One-Time Therapies...

#### **Benefit**

- Therapeutic vector is stably integrated into host cell genome
  - LVV integrate into dividing and nondividing cells
  - Transgene is carried to all daughter cells
  - Important for hematopoietic stem cell-based gene therapy
- Therapeutic vector is durable
  - Therapeutic benefit expected to be life-long
- Integrations are traceable
  - Integration site analysis is a robust, sensitive tool

## ...but are Not Without Some Potential Risks

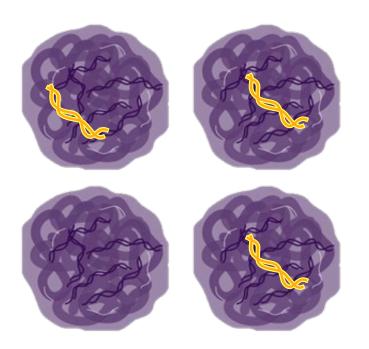
#### **Benefit**

- Therapeutic vector is stably integrated into host cell genome
  - LVV integrate into dividing and nondividing cells
  - Transgene is carried to all daughter cells
  - Important for hematopoietic stem cell-based gene therapy
- Therapeutic vector is durable
  - Therapeutic benefit expected to be life-long
- Integrations are traceable
  - Integration site analysis is a robust, sensitive tool

#### **Risk**

- All insertions are mutations
- Mutations may impact an endogenous gene
  - No effect
  - Impaired gene function/knock-out
  - Altered splicing
  - Increased gene activity
- Integration into the genome could lead to *insertional oncogenesis*

## LVV Integration Creates a Unique and Traceable Genetic Barcode



Semi-random LVV integration creates unique mappable insertion sites

Unique locations of integrated provirus in the genome can be mapped by sequencing genomic DNA

This high throughput way of identifying vector insertion sites is called **Integration Site Analysis (ISA)** 

## Integration Site Analysis (ISA) is an Important Tool for Tracking Transduced Cells

**Representation of ISA Data** 

100

50

**Relative Frequency, %** 

Identifies a population of unique mappable insertion sites<sup>1</sup>

Allows tracking of clonal populations

All other IS ISA enables further investigation to help determine the potential role of a specific vector insertion in gene dysregulation and oncogenesis<sup>1,2</sup>

## Top 10 insertion sites are usually the focus of ISA and indicated by colored bars

ISA: integration site analysis; IS: insertion site

1. Biasco L et al., *Mol Ther Methods Clin Dev.* 2018; 8: 21–30. 2017; 2. Biasco L., *Hum Gene Ther.* 2017;28:1122-1129.

**Top 10 IS** 

#### What ISA Can (and Cannot) Do

#### ISA <u>Can</u>

Track clonal dynamics over time

Nominate individual clones for further characterization

Suggest whether >1 insertions are likely present in a single clone

Identify oligoclonality for regulatory reporting, communications to treating physicians

#### **ISA** Cannot

Predict which (if any) clones will become predominant

Predict whether oligoclonality will decrease/increase over time

Predict clinical outcomes or disease onset

Detect oligoclonality in untransduced cells

ISA is a useful tool that allows for traceability of clonal populations, but it is not predictive

## What ISA Can (and Cannot) Do

ISA <u>Can</u>

Track clonal dynamics over time

Nominate individual clones for further characterization

Suggest whether >1 insertions are likely present in a single clone

Identify oligoclonality for regulatory reporting, communications to treating physicians

#### **ISA** Cannot

Predict which (if any) clones will become predominant

Predict whether oligoclonality will decrease/increase over time

Predict clinical outcomes or disease onset

Detect oligoclonality in untransduced cells

ISA is a useful tool that allows for traceability of clonal populations, but it is not predictive

### What ISA Can (and Cannot) Do

#### ISA <u>Can</u>

Track clonal dynamics over time

Nominate individual clones for further characterization

Suggest whether >1 insertions are likely present in a single clone

Identify oligoclonality for regulatory reporting, communications to treating physicians

#### ISA Cannot

Predict which (if any) clones will become predominant

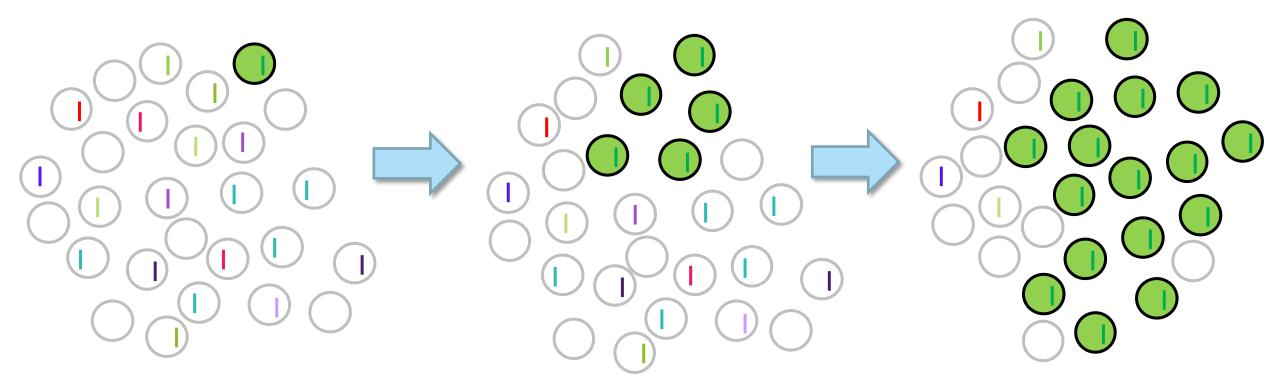
Predict whether oligoclonality will decrease/increase over time

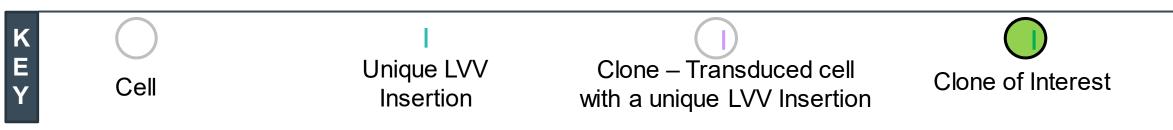
Predict clinical outcomes or disease onset

Detect oligoclonality in untransduced cells

ISA is a useful tool that allows for traceability of clonal populations, but it is not predictive

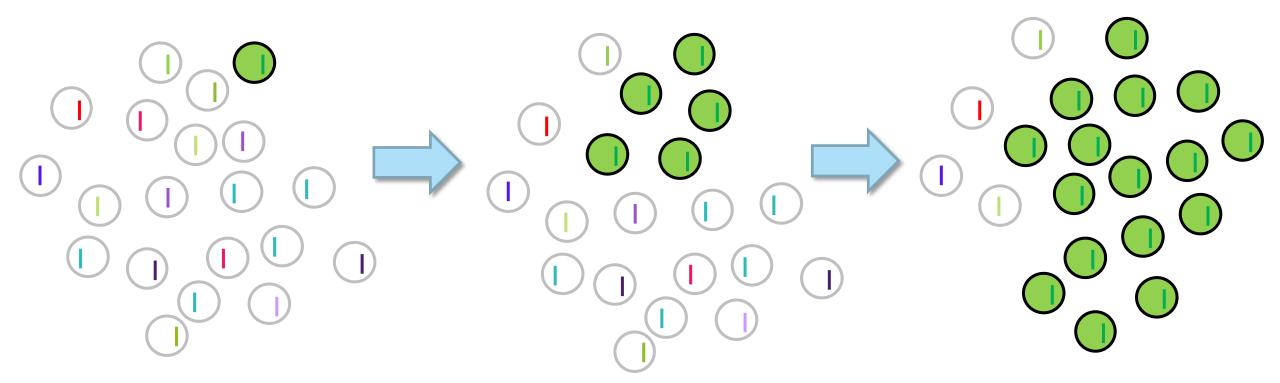
#### Illustrative Example ISA Tracking Over Time





ISA: integration site analysis; LVV: lentiviral vector; IS: insertion site

## Illustrative Example ISA Tracking Over Time ISA Only Detects Transduced Cells



 K
 I

 E
 I

 Y
 Cell

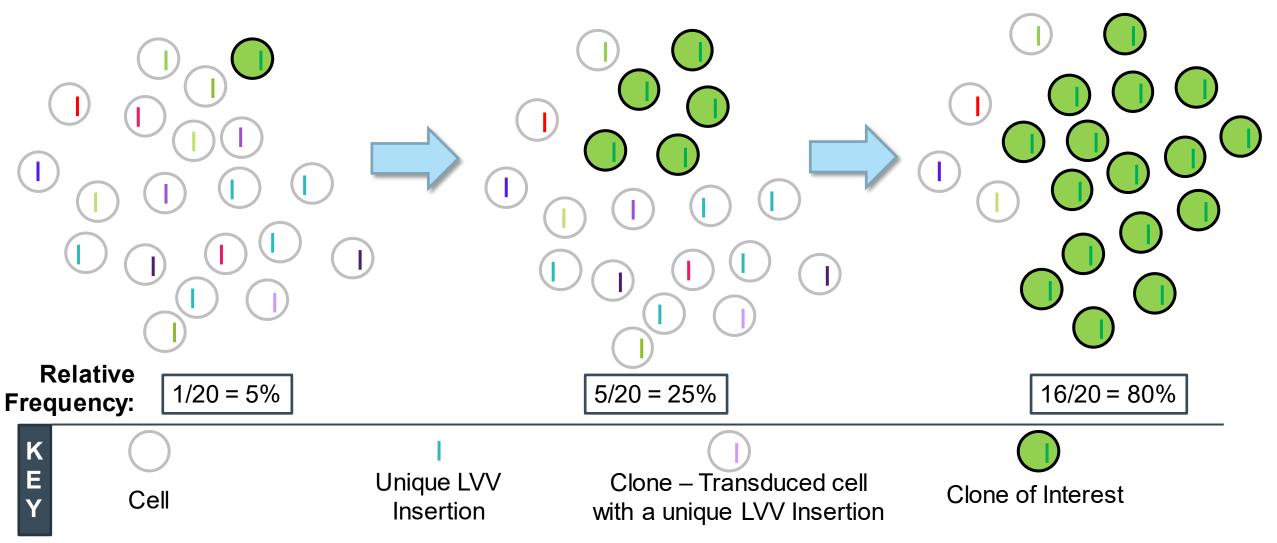
 I
 Clone – Transduced cell

 Y
 Clone of Interest

 Y
 Clone of Interest

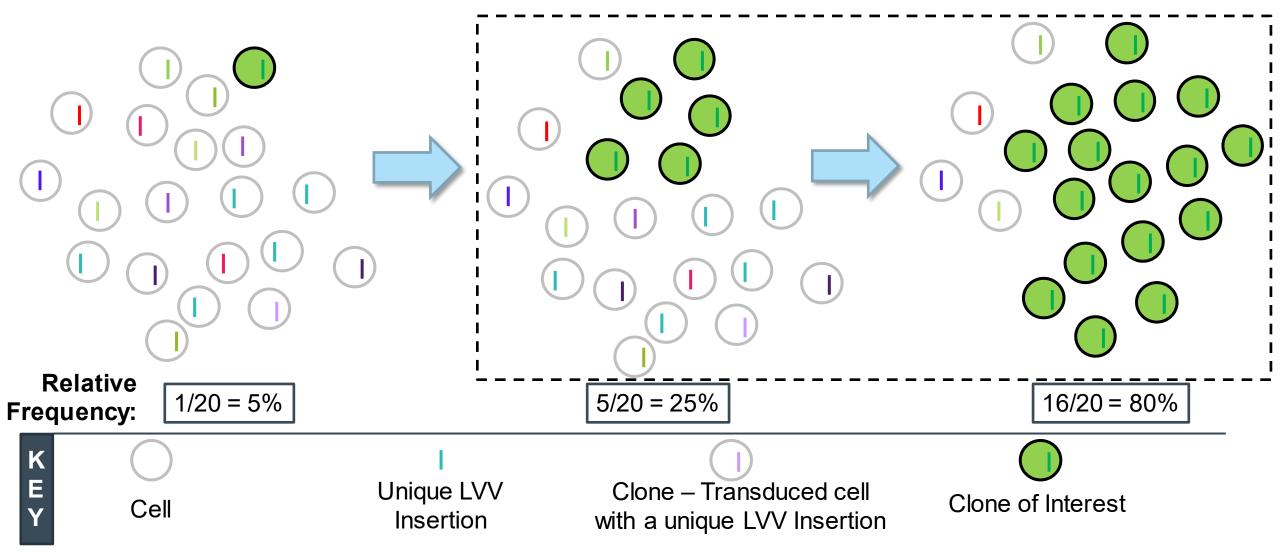
ISA: integration site analysis; LVV: lentiviral vector; IS: insertion site

## Illustrative Example ISA Tracking Over Time ISA Only Detects Transduced Cells



ISA: integration site analysis; LVV: lentiviral vector; IS: insertion site

# Illustrative Example ISA Tracking Over Time ISA Only Detects Transduced Cells



## What Does 'Oligoclonality' Mean?

#### **Oligoclonality** <u>Can</u>

Suggest clonal hematopoiesis

Occur in the absence of a hematological abnormality

Satisfy regulatory guidance for post-treatment monitoring in clinical setting

Trigger follow-up testing (i.e., CBC) out of abundance of caution

#### **Oligoclonality** <u>Cannot</u>

**Diagnose malignancy** 

Predict development of malignancy

Determine contribution of a clone to heterogeneous population containing untransduced cells

#### Oligoclonality does <u>not</u> equal malignancy

ISA: integration site analysis; CBC: complete blood count

## What Does 'Oligoclonality' Mean?

#### **Oligoclonality** <u>Can</u>

Suggest clonal hematopoiesis

Occur in the absence of a hematological abnormality

Satisfy regulatory guidance for post-treatment monitoring in clinical setting

Trigger follow-up testing (i.e., CBC) out of abundance of caution

#### **Oligoclonality** <u>Cannot</u>

**Diagnose malignancy** 

Predict development of malignancy

Determine contribution of a clone to heterogeneous population containing untransduced cells

#### **Oligoclonality does** <u>not</u> equal malignancy

ISA: integration site analysis; CBC: complete blood count

## What Does 'Oligoclonality' Mean?

#### **Oligoclonality** <u>Can</u>

Suggest clonal hematopoiesis

Occur in the absence of a hematological abnormality

Satisfy regulatory guidance for post-treatment monitoring in clinical setting

Trigger follow-up testing (i.e., CBC) out of abundance of caution

#### **Oligoclonality** <u>Cannot</u>

#### **Diagnose malignancy**

Predict development of malignancy

Determine contribution of a clone to heterogeneous population containing untransduced cells

#### **Oligoclonality does <u>not</u> equal malignancy**

ISA: integration site analysis; CBC: complete blood count

eli-cel for CALD	beti-cel for β-Thal	lovo-cel for SCD n=49
***	***	<u> </u>
	****	****
00000000000000	****	<u> </u>
***	****	* * * * * * * * * * * *
***	<u> </u>	00000000000

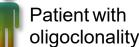
#### Treated patient

K E Y

Data as of 29Apr2022 for all patients, except for 2 patients indicated by an asterisk, which included late breaking data. n defined as treated patients with available ISA data at time of data cut. Persistent oligoclonality: 2 or more consecutive oligoclonality for any insertion site; Current oligoclonality: last visit was first oligoclonal result; ISA: integration site analysis; IS: insertion site; PB: peripheral blood; VCN: vector copy number; c/dg: copies per diploid genome

eli-cel for CALD	beti-cel for β-Thal	lovo-cel for SCD n=49
<b>• • • • • • • • • •</b> •	<b>.</b>	<b>.</b>
		00000000000000
0 0 0 0 0 0 0 0 0 0 0 0	$\dot{0} \dot{0} \mathbf{$	<u> </u>
***	***	<u> </u>
***	0 0 0 0 0 0 0 0 0 0 0 0	$\hat{0}$
***	***	

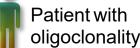
Treated patient



Data as of 29Apr2022 for all patients, except for 2 patients indicated by an asterisk, which included late breaking data. n defined as treated patients with available ISA data at time of data cut. Persistent oligoclonality: 2 or more consecutive oligoclonality for any insertion site; Current oligoclonality: last visit was first oligoclonal result; ISA: integration site analysis; IS: insertion site; PB: LV-41 peripheral blood; VCN: vector copy number; c/dg: copies per diploid genome

	e	eli-	се	<b>l fc</b> n=		CA	LD	)			b	eti	-Ce	<b>el f</b> ( n=		β <b>-</b>	Γha	al				ov	0-0		<b>fo</b> 49	r S	C	
Ì	İ	Ì	Ì	Ì	Ì	Ì	Ŷ	Ŷ	Ŷ	Ť	İ	•	Ì	Ŷ	Ŷ	Ŷ	Ŷ	Ŷ	Ŷ	İ	<b>n</b> *	Ŷ	Ŷ	Ŷ	Ŷ	Ì	Ŷ	Î
	Ũ	Ũ	Ì	Ŷ	Î	Ŷ	Ŷ	Ŷ	Ŷ	Ĥ	Ũ	Ì	Û	Ŷ	Ì			Õ	Ì	Ì	Û	Ŷ	Ŷ	Ŷ	Ŷ	Ì	Ŷ	
	Ì	Ĩ	Ŷ	Ŷ	Ì	Ŷ	Ì	Ŷ	Ì	Ŷ	Ì	Ì		Ŷ	Ŷ	Ĩ	Ŷ	Ŷ		Ì	Ŷ	Ŷ	Ŷ	Ĩ	Ŷ	Ŷ	Ì	
Ì	Ì	Ì		Ŵ	Ũ	Ŷ		Ŷ	Ì	Ŷ	Ì	Ì	Û	Ì	Ì	Ì	Ì	Ì	Ì	Î	Ŷ	Ũ	Ŷ	Ŷ	Û	ì	Ì	
	Ũ	Ŷ	Ì	Ũ	Ŷ	Ŷ	Ì	Ŷ	Ŷ	Ŷ	Ũ	Î	Û	Ŷ	Ì	Î		Õ	Î	Ì	Ũ	Ŷ	Ŷ	Ŷ	Ŷ	Ŷ	Ĩ	
þ	Ì	Ŷ	Ŷ	Ŷ	Ŷ	Ì	Ŷ	Ŷ	Ũ		Ŷ	Û	Ĩ	Ì	Ì	Û	Û	Ŷ	Î									
	Ì	Î								Ĥ	Ŷ	Ŷ																

Treated patient



Data as of 29Apr2022 for all patients, except for 2 patients indicated by an asterisk, which included late breaking data. n defined as treated patients with available ISA data at time of data cut. Persistent oligoclonality: 2 or more consecutive oligoclonality for any insertion site; Current oligoclonality: last visit was first oligoclonal result; ISA: integration site analysis; IS: insertion site; PB: peripheral blood; VCN: vector copy number; c/dg: copies per diploid genome

		eli-	ce	<b>l fc</b> n=		CA	LD				b	eti	-Ce	<b>el f</b> n=		β-	Γha	al				ov	0-0		<b>fo</b> 49	r S	C	)	
İ	ŕ	Ì	İ	ŕ	İ	İ	Ŷ	Ŷ	Ŷ	Ì	İ		Ì		Ì	Ì	Ŷ	Ŷ	Ŷ	İ	<b>n</b> *	Ŷ	Ŷ	Î	Ŷ	Ì	Ì	Ŷ	ĺ
Ì	Ũ		Ì	Ŷ	Ŷ	Ŷ	Ì	Ŷ	Ũ	Ŷ	Ũ	Ì	Ũ	Ũ	Ì	Î	Û	Ŷ	Ì	Ì	Û	Ŷ		Ũ	Ũ		Ŷ	Ŷ	
Ì	Ũ	Î	Ì	Ŷ	Ì	Ŷ	Ì	Ŷ	Ŷ	Ŷ	Ŷ	Ŷ	Ì	Ì		Ì	Û	Ŷ	Î	Ì	Ì	Ì	Ũ	Ì	Ì		Ŷ	Ì	
	Ŷ	Ŷ	Û	Ŷ	Ĩ	Ŷ	Ì	Ŷ	Ŷ	Ŷ	Ì	Ì	Ũ	Ì	Ŷ	Ŷ	Û	Ĩ	Ŷ	Ì	Ŷ	Ũ	Ŷ	Ì	Ŷ	Ũ	Ì		(
	Ì	Ŷ		Ũ	Ŷ	Û		Ŷ	Ŷ	Ŷ	Ì	Ì	Ũ	Ũ	Ì	Û	Û	Ŷ	Î	Ì	Ũ	Ŷ	Ŷ	Ŷ	Ŷ	Ŷ	Ĩ	Ì	
	Ì		Ì	Û	Ŷ	Ì	Ì	Ŷ	Ũ	Ŷ	Ŷ	Ŷ	Ì	Ì		Ì	Û	Ŷ	Ĩ										
	Ì	Ŷ	Ì							Ŷ	Ũ	Ŷ																	

Diagnosed with MDS and no longer followed for ISA

Data as of 29Apr2022 for all patients, except for 2 patients indicated by an asterisk, which included late breaking data. n defined as treated patients with available ISA data at time of data cut. Persistent oligoclonality: 2 or more consecutive oligoclonality for any insertion site; Current oligoclonality: last visit was first oligoclonal result; ISA: integration site analysis; IS: insertion site; PB: LV-43 peripheral blood; VCN: vector copy number; c/dg: copies per diploid genome

Patient with

oligoclonality

K E Y

**Treated** patient

eli-cel for CALD	beti-cel for β-Thal	lovo-cel for SCD n=49
<b>† † † † † † †</b> ů ů ů	<b>.</b>	<b>n n</b> n n n n n n n n
000000000000		<u> </u>
<u> </u>		<u> </u>
		<u> </u>
***		

Treated patient

K E

Patient with oligoclonality

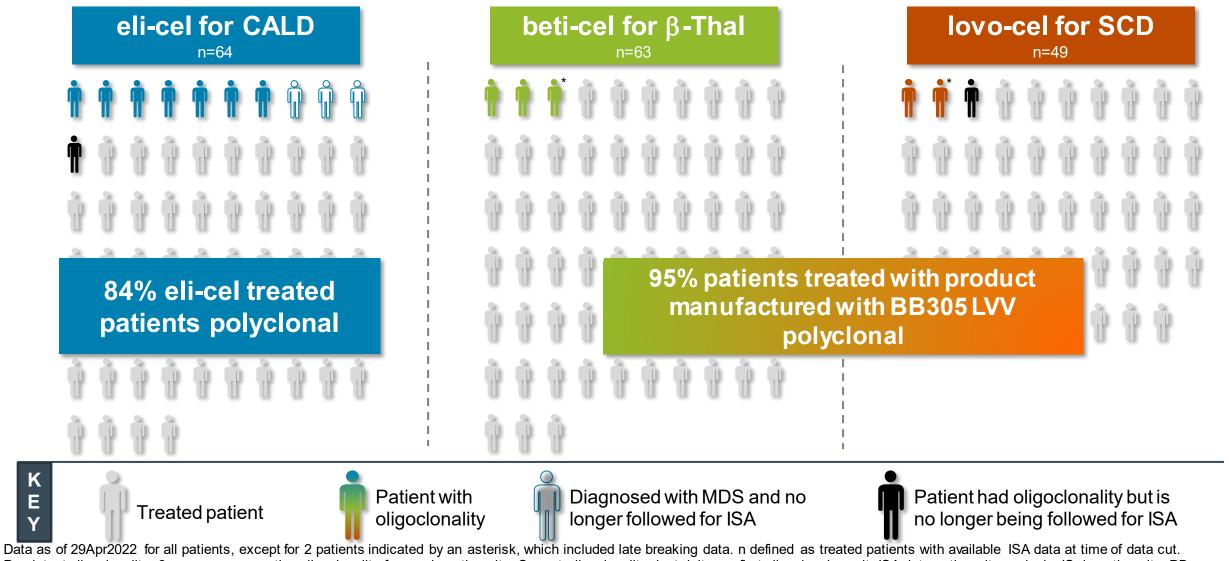
Diagnosed with MDS and no longer followed for ISA



Patient had oligoclonality but is no longer being followed for ISA

Data as of 29Apr2022 for all patients, except for 2 patients indicated by an asterisk, which included late breaking data. n defined as treated patients with available ISA data at time of data cut. Persistent oligoclonality: 2 or more consecutive oligoclonality for any insertion site; Current oligoclonality: last visit was first oligoclonal result; ISA: integration site analysis; IS: insertion site; PB: peripheral blood; VCN: vector copy number; c/dg: copies per diploid genome

# >90% of Patients Currently Have Polyclonal ISA Profiles



Data as of 29Apr2022 for all patients, except for 2 patients indicated by an asterisk, which included late breaking data. n defined as treated patients with available ISA data at time of data cut. Persistent oligoclonality: 2 or more consecutive oligoclonality for any insertion site; Current oligoclonality: last visit was first oligoclonal result; ISA: integration site analysis; IS: insertion site; PB: peripheral blood; VCN: vector copy number; c/dg: copies per diploid genome

# Agenda

#### Background on retroviral vectors

- Safety events warranted development of safer vector designs
- Current LVVs designed to lower risk of insertional oncogenesis
- Benefits and risks of LVV
- LVV traceability and Integration Site Analysis

#### Lenti-D LVV used for manufacture of eli-cel

- Mechanism of action necessitates ubiquitous transgene promoter
- LVV mediated safety events

#### BB305 LVV used for manufacture of beti-cel and lovo-cel

- Mechanism of action necessitates erythroid specific promoter
- No LVV mediated safety events

# Lenti-D Lentiviral Vector Was Designed to Treat Patients with CALD

The Lenti-D LVV is designed to deliver intact copies of *ABCD1* to autologous HSCs to enable production of functional copies of ALDP<sup>1</sup>

- The ubiquitous MNDU3 promoter determined to be an appropriate promoter for use in Lenti-D LVV for expression of functional ALDP in engrafted hematopoietic-derived cells in the central nervous system to stabilize disease progression
- Suitability of MNDU3 promoter for gene therapy for CALD was first demonstrated by Cartier et al, 2009<sup>2</sup>
- Nonclinical assessments using Lenti-D LVV-transduced CD34+ HSPCs have not identified oncogenesis (tumorigenicity) as a quantifiable hazard



1. Eichler F, et al. *N Engl J Med.* 2017;377(17):1630-8.2. Cartier N, et al. *Science* 2009;326(5954):818-23. CALD: cerebral adrenoleukodystrophy; HSPC: hematopoietic stem and progenitor cell; LTR: long terminal repeat; ALDP: adrenoleukodystrophy protein

		<b>104-1</b> 8 <sup>1</sup>	<b>104-0</b> 8 <sup>1</sup>	102-03 <sup>2</sup>
	Finding	Thrombocytopenia	Pancytopenia/Thrombocytopenia	Thrombocytopenia
CBC Finding	First Seen	Persistently post-infusion; PE >D100	Persistently post-infusion; PE >D100	At MDS diagnosis, Month 92
Persistent	First Met Criterion	Month 12	Month 12	Month 92*
Oligoclonality	Insertion Sites	MECOM, SLC6A16	<b>MECOM</b> , ACTR3, RAP2C-AS1, ST3GAL6-AS1	<b>PRDM16</b> , GAB3, CAMK2A, TYK2, SNX12, MIR106A
	Morphology	Megakaryoc	yte dy splasia	Multiline age dy splasia
Bone marrow	Blasts	<5	5%	15-20%
evaluation at diagnosis	Karyotype	46XY, Chr. 14 aberration, germline	46XY, normal	46XY, normal
-	NGS	<i>CDKN2A</i> c.168C>G, germline**	None Detected	<i>KRAS</i> c.35G>C, 14% VAF <i>NRAS</i> c.35G>C, 3% VAF
Diagnosis		MDS-SLD	MDS-SLD	MDS-EB-2
Time of Diagno	osis	Month 14	Month 26	Month 92
Insertional On	cogenesis	Likely Insertional Oncogenesis	Likely Insertional Oncogenesis	Likely Insertional Oncogenesis

PE >D100, platelet engraftment after relative day 100; MDS-SLD, myelodysplastic syndrome with single lineage dysplasia; MDS-EB-2, myelodysplastic syndrome with excess blasts 2;

VAF, variant allele frequency; 1. Data as of Aug 2021; 2. Data as of Nov 2021; ongoing studies with an open database

\*Month 60 was prior visit, between Month 60 and Month 92 patient had virtual visits due to COVID-19 pandemic

		104-18 <sup>1</sup>	<b>104-0</b> 8 <sup>1</sup>	102-03 <sup>2</sup>
	Finding	Thrombocytopenia	Pancytopenia/Thrombocytopenia	Thrombocytopenia
CBC Finding	First Seen	Persistently post-infusion; PE >D100	Persistently post-infusion; PE >D100	At MDS diagnosis, Month 92
Persistent	First Met Criterion	Month 12	Month 12	Month 92*
Oligoclonality	Insertion Sites	MECOM, SLC6A16	<b>MECOM</b> , ACTR3, RAP2C-AS1, ST3GAL6-AS1	<b>PRDM16</b> , GAB3, CAMK2A, TYK2, SNX12, MIR106A
	Morphology	Megakaryoc	yte dy splasia	Multiline age dy splasia
Bone marrow	Blasts	<{	5%	15-20%
evaluation at diagnosis	Karyotype	46XY, Chr. 14 aberration, germline	46XY, normal	46XY, normal
	NGS	CDKN2A c.168C>G, germline**	None Detected	<i>KRAS</i> c.35G>C, 14% VAF <i>NRAS</i> c.35G>C, 3% VAF
Diagnosis		MDS-SLD	MDS-SLD	MDS-EB-2
Time of Diagno	osis	Month 14	Month 26	Month 92
Insertional On	cogenesis	Likely Insertional Oncogenesis	Likely Insertional Oncogenesis	Likely Insertional Oncogenesis

PE >D100, platelet engraftment after relative day 100; MDS-SLD, myelodysplastic syndrome with single lineage dysplasia; MDS-EB-2, myelodysplastic syndrome with excess blasts 2;

VAF, variant allele frequency; 1. Data as of Aug 2021; 2. Data as of Nov 2021; ongoing studies with an open database

\*Month 60 was prior visit, between Month 60 and Month 92 patient had virtual visits due to COVID-19 pandemic

		104-18 <sup>1</sup>	<b>104-0</b> 8 <sup>1</sup>	102-03 <sup>2</sup>
	Finding	Thrombocytopenia	Pancytopenia/Thrombocytopenia	Thrombocytopenia
CBC Finding	First Seen	Persistently post-infusion; PE >D100	Persistently post-infusion; PE >D100	At MDS diagnosis, Month 92
Persistent	First Met Criterion	Month 12	Month 12	Month 92*
Oligoclonality	Insertion Sites	MECOM, SLC6A16	<b>MECOM</b> , ACTR3, RAP2C-AS1, ST3GAL6-AS1	<b>PRDM16</b> , GAB3, CAMK2A, TYK2, SNX12, MIR106A
	Morphology	Megakaryoc	yte dy splasia	Multiline age dy splasia
Bone marrow	Blasts	<{	5%	15-20%
evaluation at diagnosis	Karyotype	46XY, Chr. 14 aberration, germline	46XY, normal	46XY, normal
	NGS	CDKN2A c.168C>G, germline**	None Detected	<i>KRAS</i> c.35G>C, 14% VAF <i>NRAS</i> c.35G>C, 3% VAF
Diagnosis		MDS-SLD	MDS-SLD	MDS-EB-2
Time of Diagno	osis	Month 14	Month 26	Month 92
Insertional On	cogenesis	Likely Insertional Oncogenesis	Likely Insertional Oncogenesis	Likely Insertional Oncogenesis

PE >D100, platelet engraftment after relative day 100; MDS-SLD, myelodysplastic syndrome with single lineage dysplasia; MDS-EB-2, myelodysplastic syndrome with excess blasts 2;

VAF, variant allele frequency; 1. Data as of Aug 2021; 2. Data as of Nov 2021; ongoing studies with an open database

\*Month 60 was prior visit, between Month 60 and Month 92 patient had virtual visits due to COVID-19 pandemic

		104-18 <sup>1</sup>	104-08 <sup>1</sup>	102-03 <sup>2</sup>
	Finding	Thrombocytopenia	Pancytopenia/Thrombocytopenia	Thrombocytopenia
CBC Finding	First Seen	Persistently post-infusion; PE >D100	Persistently post-infusion; PE >D100	At MDS diagnosis, Month 92
Persistent	First Met Criterion	Month 12	Month 12	Month 92*
Oligoclonality	Insertion Sites	MECOM, SLC6A16	<b>MECOM</b> , ACTR3, RAP2C-AS1, ST3GAL6-AS1	<b>PRDM16</b> , GAB3, CAMK2A, TYK2, SNX12, MIR106A
	Morphology	Megakaryoc	yte dysplasia	Multiline age dy splasia
Bone marrow	Blasts	<5	5%	15-20%
evaluation at diagnosis	Karyotype	46XY, Chr. 14 aberration, germline	46XY, normal	46XY, normal
	NGS	CDKN2A c.168C>G, germline**	None Detected	<i>KRAS</i> c.35G>C, 14% VAF <i>NRAS</i> c.35G>C, 3% VAF
Diagnosis		MDS-SLD	MDS-SLD	MDS-EB-2
Time of Diagno	osis	Month 14	Month 26	Month 92
Insertional Oncogenesis		Likely Insertional Oncogenesis	Likely Insertional Oncogenesis	Likely Insertional Oncogenesis

PE >D100, platelet engraftment after relative day 100; MDS-SLD, myelodysplastic syndrome with single lineage dysplasia; MDS-EB-2, myelodysplastic syndrome with excess blasts 2;

VAF, variant allele frequency; 1. Data as of Aug 2021; 2. Data as of Nov 2021; ongoing studies with an open database

\*Month 60 was prior visit, between Month 60 and Month 92 patient had virtual visits due to COVID-19 pandemic

		104-18 <sup>1</sup>	<b>104-0</b> 8 <sup>1</sup>	102-03 <sup>2</sup>				
	Finding	Thrombocytopenia	Pancytopenia/Thrombocytopenia	Thrombocytopenia				
CBC Finding	First Seen	Persistently post-infusion; PE >D100	Persistently post-infusion; PE >D100	At MDS diagnosis, Month 92				
Persistent	First Met Criterion	Month 12	Month 12	Month 92*				
Oligoclonality	Insertion Sites	MECOM, SLC6A16	<b>MECOM</b> , ACTR3, RAP2C-AS1, ST3GAL6-AS1	<b>PRDM16</b> , GAB3, CAMK2A, TYK2, SNX12, MIR106A				
	Morphology	Megakaryoc	yte dy splasia	Multiline age dy splasia				
Bone marrow	Blasts	<{	<5%					
evaluation at diagnosis	Karyotype	46XY, Chr. 14 aberration, germline	46XY, normal	46XY, normal				
	NGS	CDKN2A c.168C>G, germline**	None Detected	<i>KRAS</i> c.35G>C, 14% VAF <i>NRAS</i> c.35G>C, 3% VAF				
Diagnosis		MDS-SLD	MDS-SLD	MDS-EB-2				
Time of Diagno	osis	Month 14	Month 26	Month 92				
Insertional Oncogenesis		Likely Insertional Oncogenesis	Likely Insertional Oncogenesis	Likely Insertional Oncogenesis				

PE >D100, platelet engraftment after relative day 100; MDS-SLD, myelodysplastic syndrome with single lineage dysplasia; MDS-EB-2, myelodysplastic syndrome with excess blasts 2;

VAF, variant allele frequency; 1. Data as of Aug 2021; 2. Data as of Nov 2021; ongoing studies with an open database

\*Month 60 was prior visit, between Month 60 and Month 92 patient had virtual visits due to COVID-19 pandemic

		104-18 <sup>1</sup>	<b>104-08</b> <sup>1</sup>	102-03 <sup>2</sup>				
	Finding	Thrombocytopenia	Pancytopenia/Thrombocytopenia	Thrombocytopenia				
CBC Finding	First Seen	Persistently post-infusion; PE >D100	Persistently post-infusion; PE >D100	At MDS diagnosis, Month 92				
Persistent	First Met Criterion	Month 12	Month 12	Month 92*				
Oligoclonality	Insertion Sites	MECOM, SLC6A16	<b>MECOM</b> , ACTR3, RAP2C-AS1, ST3GAL6-AS1	<b>PRDM16</b> , GAB3, CAMK2A, TYK2, SNX12, MIR106A				
	Morphology	Megakaryoc	yte dy splasia	Multiline age dy splasia				
Bone marrow	Blasts	<5	<5%					
evaluation at diagnosis	Karyotype	46XY, Chr. 14 aberration, germline	46XY, normal	46XY, normal				
	NGS	CDKN2A c.168C>G, germline**	None Detected	KRAS c.35G>C, 14% VAF NRAS c.35G>C, 3% VAF				
Diagnosis		MDS-SLD	MDS-SLD	MDS-EB-2				
Time of Diagno	osis	Month 14	Month 26	Month 92				
Insertional Oncogenesis		Likely Insertional Oncogenesis	Likely Insertional Oncogenesis	Likely Insertional Oncogenesis				

PE >D100, platelet engraftment after relative day 100; MDS-SLD, myelodysplastic syndrome with single lineage dysplasia; MDS-EB-2, myelodysplastic syndrome with excess blasts 2;

VAF, variant allele frequency; 1. Data as of Aug 2021; 2. Data as of Nov 2021; ongoing studies with an open database

\*Month 60 was prior visit, between Month 60 and Month 92 patient had virtual visits due to COVID-19 pandemic

#### **LVV Exoneration Criteria**

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

#### **LVV Exoneration Criteria**

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

#### **Criteria Met?**

 $(\mathbf{X})$ 

?

#### **Findings**

No classic MDS/AML driver mutations identified (2/3 patients)

No definitive known MDS/AML driver alterations

#### **LVV Exoneration Criteria**

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

#### **Criteria Met?**

 $(\mathbf{X})$ 

?

 $(\mathbf{X})$ 

#### **Findings**

- No classic MDS/AML driver mutations identified (2/3 patients)
- No definitive known MDS/AML driver alterations

MECOM and PRDM16 known proto-oncogenes

#### **LVV Exoneration Criteria**

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

#### **Criteria Met?**

 $(\mathbf{X})$ 

?

 $(\mathbf{X})$ 

#### **Findings**

- No classic MDS/AML driver mutations identified (2/3 patients)
- No definitive known MDS/AML driver alterations
- MECOM and PRDM16 known proto-oncogenes
  - Insertion sites do not disrupt mapped genomic features
- MECOM and PRDM16 are common insertion sites

#### **LVV Exoneration Criteria**

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

#### **Criteria Met?**

#### **Findings**

No classic MDS/AML driver mutations identified  $(\mathbf{X})$ (2/3 patients) ? No definitive known MDS/AML driver alterations  $(\mathbf{X})$ MECOM and PRDM16 known proto-oncogenes Insertion sites do not disrupt mapped genomic features MECOM and PRDM16 are common insertion sites **(X**) Aberrant gene expression found in all 3 patients ? No blasts in 2 patients; aberrant gene expression in all 3

# Lenti-D LVV-Mediated Insertional Oncogenesis Likely Multifactorial

- Gene expression signature changes seen in all genes analyzed, including known proto-oncogenes, in 3 eli-cel patients diagnosed with MDS
  - Clones all contain between 2 and 6 insertion sites
- No clear alternative driver MDS/AML mutations in 2 patients

- The presence of vector insertion sites in proto-oncogenes are common, and the vast majority of clones do not expand
  - In a non-bluebird clinical trial for ADA-SCID using an MND-containing retrovirus MECOM was the most common insertion sites and there were no clonal expansions and no malignancy<sup>1, 2</sup>

LVV, lentiviral vector; MDS, myelodysplastic syndrome; AML, acute myeloid leukemia; ADA-SCID, adenosine deaminase-deficient severe combined immunodeficiency; *MECOM*: MDS1 and EVI1 Complex Locus;

1. Cooper et al., *Blood* 2017; 129(19):2624-2635.; 2. Reinhardt et al., *Blood* 2021; 138(15):1304-1316.

# Agenda

#### Background on retroviral vectors

- Safety events warranted development of safer vector designs
- Current LVVs designed to lower risk of insertional oncogenesis
- Benefits and risks of LVV
- LVV traceability and Integration Site Analysis

#### Lenti-D LVV used for manufacture of eli-cel

- Mechanism of action necessitates ubiquitous transgene promoter
- LVV mediated safety events

#### BB305 LVV used for manufacture of beti-cel and lovo-cel

- Mechanism of action necessitates erythroid specific promoter
- No LVV mediated safety events

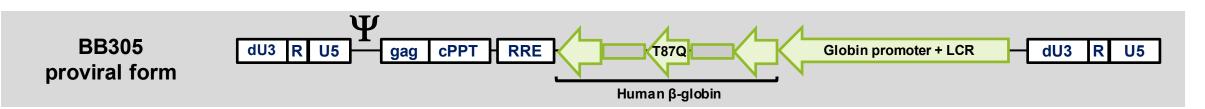
# beti-cel: No Cases of Malignancy or Insertional Oncogenesis

No malignancy, no insertional oncogenesis

# beti-cel: No Cases of Malignancy or Insertional Oncogenesis

#### No malignancy, no insertional oncogenesis

- β-globin promoter selected for appropriate and optimized expression transgenic β<sup>A-T87Q</sup> in erythroid lineage cells
  - SIN LVV design with internal cell-type specific (erythroid) promoter limits potential for aberrant enhancer activity affecting expression of nearby genes
- Nonclinical assessments using BB305 LVV-transduced CD34+ HSPCs have not identified oncogenesis (tumorigenicity) as a quantifiable hazard
- No evidence of baseline increased risk of hematologic malignancy in patients with βthalassemia in literature



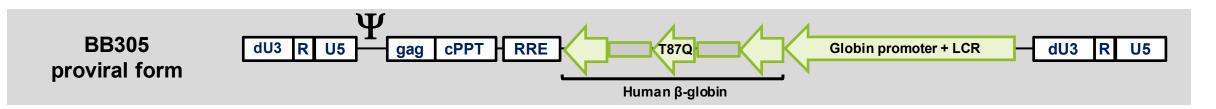
# Iovo-cel for sickle cell disease: 2 Malignancies; No Insertional Oncogenesis

2 malignancies, no insertional oncogenesis

# Iovo-cel for sickle cell disease: 2 Malignancies; No Insertional Oncogenesis

#### 2 malignancies, no insertional oncogenesis

- β-globin promoter selected for appropriate and optimized expression transgenic βA-T87Q in erythroid lineage cells
  - SIN LVV design with internal cell-type specific (erythroid) promoter limits potential for aberrant enhancer activity affecting expression of nearby genes
- Nonclinical assessments using BB305 LVV-transduced CD34+ HSPCs have not identified oncogenesis (tumorigenicity) as a quantifiable hazard
- Evidence of baseline increased risk of hematologic malignancy in patients with SCD in literature



# Malignancy, but NOT Insertional Oncogenesis, Observed in 2 Group A lovo-cel Patients

		206-A-2	206-A-1		
CPC Finding	Finding	Abnormal CBC and Peripheral Blasts (3%)	Abnormal CBC and Peripheral Blasts (9%)		
CBC Finding	First Seen	Month 36	Month 66		
Persistent	First Met Criterion	N/A	Month 60		
Oligoclonality <sup>1</sup>	Insertion Sites	N/A	VAMP4		
	Blasts	10%	22 – 50%		
Bone Marrow Evaluation at Diagnosis	Karyotype & Molecular Diagnostics	<ul> <li>Monosomy 7</li> <li>Abnormal 19p</li> <li><i>RUNX1</i> (NP_001745.2:p.Asp198Gly),</li> <li><i>PTPN11</i> (NP_002825.3:p.Phe71Leu),</li> <li><i>KRAS</i> NP_203524.1:p.Gly12Ala</li> </ul>	<ul> <li>Monosomy 7</li> <li>Partial loss of 11p</li> <li><i>RUNX1</i> Exon 5 stop gained p.A149*fs</li> <li><i>PTPN11</i> Exon 3 missense: p.A72V</li> </ul>		
Diagnosis		MDS/AML	AML		
Insertional Oncogenesis		<b>No</b> – no LVV	<b>No</b> – VAMP4 insertion exonerated		

# Malignancy, but NOT Insertional Oncogenesis, Observed in 2 Group A lovo-cel Patients

		206-A-2	206-A-1
CBC Finding	Finding	Abnormal CBC and Peripheral Blasts (3%)	Abnormal CBC and Peripheral Blasts (9%)
	First Seen	Month 36	Month 66
Persistent Oligoclonality <sup>1</sup>	First Met Criterion	N/A	Month 60
	Insertion Sites	N/A	VAMP4
Bone Marrow Evaluation at Diagnosis	Blasts	10%	22 – 50%
	Karyotype & Molecular Diagnostics	<ul> <li>Monosomy 7</li> <li>Abnormal 19p</li> <li><i>RUNX1</i> (NP_001745.2:p.Asp198Gly),</li> <li><i>PTPN11</i> (NP_002825.3:p.Phe71Leu),</li> <li><i>KRAS</i> NP_203524.1:p.Gly12Ala</li> </ul>	<ul> <li>Monosomy 7</li> <li>Partial loss of 11p</li> <li><i>RUNX1</i> Exon 5 stop gained p.A149*fs</li> <li><i>PTPN11</i> Exon 3 missense: p.A72V</li> </ul>
Diagnosis		MDS/AML	AML
Insertional Oncogenesis		<b>No</b> – no LVV	<b>No</b> – <i>VAMP4</i> insertion exonerated

# Malignancy, but NOT Insertional Oncogenesis, Observed in 2 Group A lovo-cel Patients

		206-A-2	206-A-1
CBC Finding	Finding	Abnormal CBC and Peripheral Blasts (3%)	Abnormal CBC and Peripheral Blasts (9%)
	First Seen	Month 36	Month 66
Persistent Oligoclonality <sup>1</sup>	First Met Criterion	N/A	Month 60
	Insertion Sites	N/A	VAMP4
Bone Marrow Evaluation at Diagnosis	Blasts	10%	22 – 50%
	Karyotype & Molecular Diagnostics	<ul> <li>Monosomy 7</li> <li>Abnormal 19p</li> <li><i>RUNX1</i> (NP_001745.2:p.Asp198Gly),</li> <li><i>PTPN11</i> (NP_002825.3:p.Phe71Leu),</li> <li><i>KRAS</i> NP_203524.1:p.Gly12Ala</li> </ul>	<ul> <li>Monosomy 7</li> <li>Partial loss of 11p</li> <li><i>RUNX1</i> Exon 5 stop gained p.A149*fs</li> <li><i>PTPN11</i> Exon 3 missense: p.A72V</li> </ul>
Diagnosis		MDS/AML	AML
Insertional Oncogenesis		<b>No</b> – no LVV	<b>No</b> – VAMP4 insertion exonerated

# HGB-206 Group A 2021 AML Case: Not Insertional Oncogenesis

#### **LVV Exoneration Criteria**

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

#### Findings

Monosomy 7, partial loss of 11p, *RUNX1, PTPN11* 



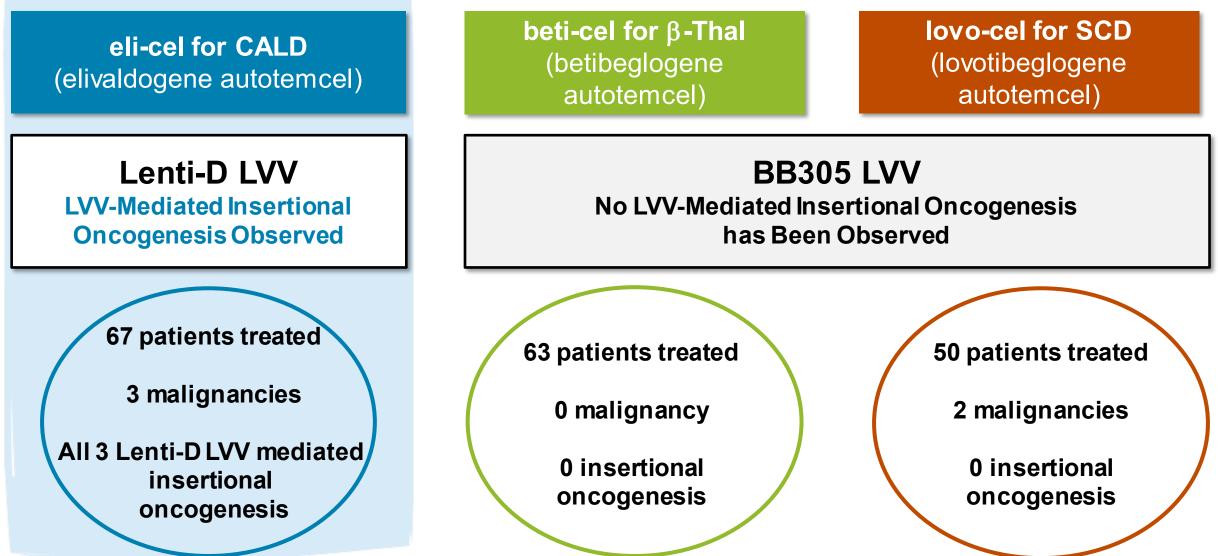
- RNAseq data consistent with monosomy 7 and contains *PTPN11* and *RUNX1* mutations
- VAMP4 has no known association with cellular proliferation or oncogenesis



- *VAMP4* insertion does not disrupt mapped genomic features
- VAMP4 IS common and this patient is the only one with VAMP4 IS >0.05% at any point
- No remarkable expression changes in 10 MB region around *VAMP4* IS
- Very low level HBB detected in CD34+ cells

MDS, myelodysplastic syndrome; AML, acute myeloid leukemia; VAMP4, Vesicle-Associated Membrane Protein 4; IS, insertion site; HBB, Hemoglobin Subunit Beta; RUNX1, RUNX Family Transcription Factor 1; PTPN11, Protein Tyrosine Phosphatase Non-Receptor Type 11. Goyal, S et al. N Engl J Med. 2022; 386:138-147.

## **Vector-Related Safety Profiles Differ**



 $\beta$ -thal:  $\beta$ -thalassemia; SCD: sickle cell disease; CALD: cerebral adrenoleukodystrophy; LVV: lentiviral vector

# Summary of LVV Safety and Insertional Oncogenesis

 LVVs used for gene therapy have both inherent (insertion biases) and engineered (SIN and replication incompetent) properties to limit risk of insertional mutagenesis leading to endogenous gene dysregulation

# Summary of LVV Safety and Insertional Oncogenesis

- LVVs used for gene therapy have both inherent (insertion biases) and engineered (SIN and replication incompetent) properties to limit risk of insertional mutagenesis leading to endogenous gene dysregulation
- ISA is a useful tool that allows for traceability of clonal populations, but it is not predictive
- Regular CBC analyses for all patients treated with novel, one-time therapies is recommended

# Summary of LVV Safety and Insertional Oncogenesis

- LVVs used for gene therapy have both inherent (insertion biases) and engineered (SIN and replication incompetent) properties to limit risk of insertional mutagenesis leading to endogenous gene dysregulation
- ISA is a useful tool that allows for traceability of clonal populations, but it is not predictive
- Regular CBC analyses for all patients treated with novel, one-time therapies is recommended
- Different severe genetic diseases have unique disease-specific and treatment-related risks of malignancy
  - eli-cel: malignancy, likely mediated by Lenti-D LVV insertion and considered to be insertional oncogenesis
  - beti-cel: to-date no malignancy, no insertional oncogenesis

# Vector Related Safety Profiles Differ

# TODAY

#### Lenti-D LVV



used for manufacture of elivaldogene autotemcel (eli-cel) for cerebral adrenoleukodystrophy (CALD)

LVV-Mediated Insertional Oncogenesis Observed

67 patients treated 3 malignancies 3 insertional oncogenesis

# Vector Related Safety Profiles Differ

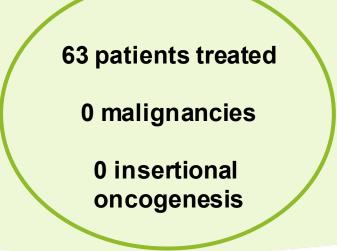
TODAY	TOMORROW
<b>CALD</b>	BB305 LVV used for manufacture of betibeglogene autotemcel (beti-cel) for β-thalassemia requiring regular transfusions
LVV-Mediated Insertional	No LVV-Mediated Insertional
Oncogenesis Observed	Oncogenesis Observed
67 patients treated	63 patients treated
3 malignancies	0 malignancies
3 insertional oncogenesis	0 insertional oncogenesis

# beti-cel Benefit/Risk Positive

**beti-cel for** β**-Thal** (betibeglogene autotemcel)

#### **BB305 LVV**

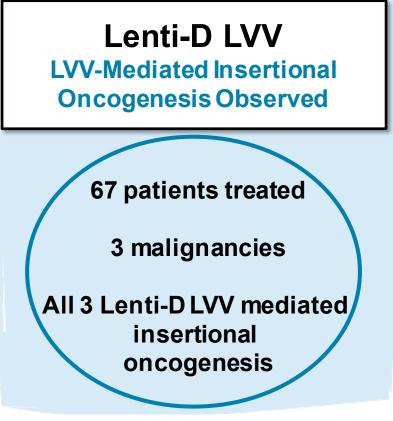
No LVV-Mediated Insertional Oncogenesis has Been Observed



- In β-thalassemia patients treated with beti-cel, the great majority of patients achieved transfusion independence, across all phases of clinical studies, all ages, and all genotypes
- Durable transfusion independence up to 7 years post-treatment
- The safety profile largely reflects known side effects of mobilization and conditioning agents

# eli-cel Benefit/Risk Positive Despite Insertional Oncogenesis





- eli-cel is an essential life-saving therapy for patients with mismatched donors, and a meaningful option for those with a MUD
- Treatment with eli-cel allows for the possibility that a fatal neurodegenerative disease can be stabilized, with preservation of physical and intellectual function in the majority of patients
- eli-cel treated patients are more likely to achieve both overall and event free survival than allo-HSCT patients treated with an NMSD graft

Each LVV gene therapy safety profile, along with the inherent risk of autologous transplant, must be weighed against :

