Cautionary note regarding forward-looking statements

This presentation contains forward-looking statements within the meaning of the Private Securities Litigation Reform Act of 1995. Such forward-looking statements include statements regarding: the initiation, timing, progress and results of preclinical studies and research and development programs, including the initiation and progress of clinical trials, including our BEACON trial and our BEAM-201 trial; the advancement of our pipeline, including the advancement of BEAM-101, BEAM-201, BEAM-301, BEAM-302, and additional CAR-T and liver programs in multiple preclinical studies; our current expectations and anticipated results of operations, including our expected use of capital; the potential activities and benefits under license and collaboration agreements and the formation of new collaborations; and the therapeutic applications and potential of our technology, including our potential to develop life-long, curative, precision genetic medicines for patients through base editing, including potential safety advantages, all of which are subject to known and unknown important risks, uncertainties and other factors that may cause our actual results, performance or achievements, market trends, or industry results to differ materially from those expressed or implied by such forward-looking statements. Therefore, any statements contained herein that are not statements of historical fact may be forward-looking statements and should be evaluated as such. Without limiting the foregoing, the words "anticipate," "expect," "suggest," "plan," "vision," "believe," "intend," "project," "forecast," "estimates," "targets," "projections," "potential," "should," "could," "would," "may," "might," "will," and the negative thereof and similar words and expressions are intended to identify forward-looking statements.

Each forward-looking statement is subject to important risks and uncertainties that could cause actual results to differ materially from those expressed or implied in such statement, including, without limitation, risks and uncertainties related to: our ability to develop, obtain regulatory approval for, and commercialize our product candidates, which may take longer or cost more than planned; our ability to raise additional funding, which may not be available; our ability to obtain, maintain and enforce patent and other intellectual property protection for our product candidates; the potential impact of the COVID-19 pandemic; that preclinical testing of our product candidates and preliminary or interim data from preclinical studies and clinical trials may not be predictive of the results or success of ongoing or later clinical trials; that initiation and enrollment of our clinical trials may take longer than expected; that our product candidates may experience manufacturing or supply interruptions or failures; risks related to competitive products; and the other risks and uncertainties identified under the headings "Risk Factors Summary" and "Risk Factors" and elsewhere in our annual report on Form 10-K for the year ended December 31, 2022, our Quarterly Report on Form 10-Q for the quarter ended March 31, 2023, our Quarterly Report on Form 10-Q for the quarter ended June 30, 2023, and in any subsequent filings with the Securities and Exchange Commission (the "SEC") which are available on the SEC’s website at www.sec.gov. Additional information will be made available by our annual and quarterly reports and other filings that we make from time to time with the SEC. These forward-looking statements speak only as of the date of this presentation. Factors or events that could cause our actual results to differ may emerge from time to time, and it is not possible for us to predict all of them. We undertake no obligation to update any forward-looking statement, whether as a result of new information, future developments or otherwise, except as may be required by applicable law.
Our vision is to provide life-long cures for patients suffering from serious diseases

- Potential for one-time, curative therapies
- Gene editing for rare and common diseases
- Platform for rapidly-programmable precision medicines
Base editing is a differentiated, potentially best-in-class gene editing technology

<table>
<thead>
<tr>
<th></th>
<th>Nuclease</th>
<th>Base editing</th>
</tr>
</thead>
<tbody>
<tr>
<td><strong>Precise targeting?</strong></td>
<td>Yes (guide RNA or ZF/TALE)</td>
<td>Yes (guide RNA)</td>
</tr>
<tr>
<td><strong>Durability of edit?</strong></td>
<td>Permanent</td>
<td>Permanent</td>
</tr>
<tr>
<td><strong>Double strand breaks?</strong></td>
<td>Yes</td>
<td>No</td>
</tr>
<tr>
<td><strong>Applications?</strong></td>
<td>Primarily knockout</td>
<td>Correct, modify, activate, multiplex</td>
</tr>
<tr>
<td><strong>Editing predictability</strong></td>
<td>Random insertions and deletions 100s of uncharacterized edits</td>
<td>Single base edits All edits fully characterized</td>
</tr>
<tr>
<td><strong>Efficiency of precise edit?</strong></td>
<td>Low – dividing cells only</td>
<td>High – any cell type</td>
</tr>
</tbody>
</table>
A precise gene editing technology with highly versatile applications

1. Activate expression (eg, BEAM-101)
2. Knock out proteins (eg, BEAM-201)
3. Correct proteins (eg, BEAM-301, BEAM-302)
4. Modify proteins (eg, ESCAPE)
5. Multiplex simultaneous edits (eg, four gRNAs in BEAM-201)

...And many other applications possible
We are establishing a leading platform for precision genetic medicine

Suite of gene editing technologies
- Base editing
  - ABE: A-to-G (or T-to-C) editors
  - CBE: C-to-T (or G-to-A) editors
  - Additional kinds of base editors
- Nuclease editing
- RNA editing
- Prime editing

Suite of delivery technologies
- Autologous cell therapy
- Allogeneic cell therapy
- mRNA
- LNP vectors
- Viral vectors

Internal manufacturing capability
- 100,000 square foot cGMP clinical/commercial facility in NC, phased build, anticipated to be cGMP operational in late 2023
Advancing a diversified pipeline into the clinic

<table>
<thead>
<tr>
<th>DELIVERY</th>
<th>PROGRAM / DISEASE</th>
<th>EDITING APPROACH</th>
<th>RESEARCH</th>
<th>LEAD OPTIMIZATION</th>
<th>IND ENABLING</th>
<th>PHASE I/II</th>
<th>PIVOTAL</th>
</tr>
</thead>
<tbody>
<tr>
<td>Ex vivo HSCs</td>
<td>BEAM-101 Sickle Cell Disease Beta Thalassemia</td>
<td>Activation of fetal hemoglobin</td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>Ex vivo T cells</td>
<td>ESCAPE Sickle Cell Disease Beta Thalassemia</td>
<td>Multiplex CD117 edit-antibody pair</td>
<td></td>
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</tr>
<tr>
<td>Ex vivo T cells</td>
<td>BEAM-201 T-ALL / T-LL CD7+ AML</td>
<td>Multiplex silenced CD7 CAR-T</td>
<td></td>
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<td></td>
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</tr>
<tr>
<td>In vivo LNP</td>
<td>BEAM-302 Alpha-1 Antitrypsin Deficiency</td>
<td>Correction of E342K mutation</td>
<td></td>
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</tr>
<tr>
<td>In vivo LNP</td>
<td>BEAM-301 Glycogen Storage Disease Ia</td>
<td>Correction of R83C mutation</td>
<td></td>
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<td></td>
<td></td>
</tr>
<tr>
<td>In vivo LNP</td>
<td>Glycogen Storage Disease Ia</td>
<td>Correction of Q347X mutation</td>
<td></td>
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<tr>
<td>In vivo LNP</td>
<td>Hepatitis B Virus</td>
<td>Multiplex silencing</td>
<td></td>
<td></td>
<td></td>
<td></td>
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</tr>
<tr>
<td>In vivo LNP</td>
<td>Complement Pathway (Apellis)</td>
<td>Undisclosed</td>
<td></td>
<td></td>
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<tr>
<td>In vivo LNP</td>
<td>3 undisclosed targets (Pfizer)</td>
<td>Undisclosed</td>
<td></td>
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</tr>
</tbody>
</table>

LNP = Lipid Nanoparticle; HSC = Hematopoietic Stem Cell; T-ALL / TLL = T-Cell Acute Lymphoblastic Leukemia / T-Cell Lymphoblastic Lymphoma; AML = Acute Myeloid Leukemia; ESCAPE: Engineered Stem Cell Antibody Paired Evasion
Beam is developing medicines across three franchises, each with near- and long-term potential.

**Near term:**
- **HEMATOLOGY**
  - BEAM-101
  - ESCAPE for conditioning
  - In vivo HSC delivery

**Future platforms:**
- **IMMUNOLOGY-ONCOLOGY**
  - BEAM-201
  - Next-generation allogeneic platform (4-6+ edits)

- **GENETIC DISEASES**
  - BEAM-301, BEAM-302
  - Multiple new liver targets
  - Barcoded LNP beyond liver

- **Lead Programs:** Potentially de-risk technology (higher probability of technical success, faster path), generate revenue, and benefit patients with high unmet need.

- **Future platforms:** Expand addressable patient populations to create highly valuable, differentiated franchises through further innovation in editing and delivery.
# Key progress and anticipated milestones

<table>
<thead>
<tr>
<th>Hematology</th>
<th>2022 Achievements</th>
<th>2023 Achievements and Upcoming Milestones</th>
</tr>
</thead>
<tbody>
<tr>
<td>✓</td>
<td>First subject enrolled for <strong>BEAM-101</strong></td>
<td>✓ Complete <strong>BEACON</strong> sentinel cohort enrollment and initiate enrollment of expansion cohort in 2023</td>
</tr>
<tr>
<td>✓</td>
<td>Refocused on new technology: ESCAPE &amp; LNP</td>
<td>☐ Data presentation on multiple patients from <strong>BEACON</strong> in 2024</td>
</tr>
</tbody>
</table>

<table>
<thead>
<tr>
<th>Immunology - Oncology</th>
<th>2022 Achievements</th>
<th>2023 Achievements and Upcoming Milestones</th>
</tr>
</thead>
<tbody>
<tr>
<td>✓</td>
<td>Submit IND for <strong>BEAM-201</strong> and respond to hold</td>
<td>✓ Dose first <strong>BEAM-201</strong> patient by mid 2023</td>
</tr>
<tr>
<td>✓</td>
<td>Refocused on next gen allogeneic strategies</td>
<td>☐ Regulatory filing for <strong>BEAM-302</strong> in Q1 2024</td>
</tr>
</tbody>
</table>

<table>
<thead>
<tr>
<th>Genetic disease</th>
<th>2022 Achievements</th>
<th>2023 Achievements and Upcoming Milestones</th>
</tr>
</thead>
<tbody>
<tr>
<td>✓</td>
<td>Initiate IND-enabling studies for <strong>BEAM-301</strong></td>
<td>☐ Regulatory filing for <strong>BEAM-301</strong> in 1H 2024</td>
</tr>
<tr>
<td>✓</td>
<td>Nominated <strong>BEAM-302</strong> development candidate</td>
<td>☐</td>
</tr>
</tbody>
</table>
BEAM-101: Designed to treat sickle cell disease with a potentially one-time, direct, non-cutting activation of HbF

**Sickle Cell Disease:** 100,000 patients in the US; severe pain crises, multi-organ damage, early mortality

**Designed for best-in-class profile:**
- One-time therapy with potential for highest fetal hemoglobin (HbF) induction
- Direct editing of HbF genes to turn them on
- Potential for greatest reduction of disease-causing HbS due to hemoglobin switching
- Non-viral: No detectable random insertion
- Non-cutting: Lower risk for genotoxic stress and chromosomal abnormalities

**Investment in patient delivery to differentiate:**
- Wholly owned manufacturing: control over quality and connection to patient services
- Investment in patient services: optimizing patient experience

Duplicated fetal hemoglobin (HbF) genes

- HBG2
- HBG1

Sickle hemoglobin (HbS) gene

A single base editor + gRNA edits regulatory element of both fetal hemoglobin genes, without cutting DNA

HPFH = Hereditary Persistence of Fetal Hemoglobin
Potentially best-in-class attributes of BEAM-101 product

Edited human CD34+ cells followed by 16 week engraftment in mice

Base editing at HBG1/2 promoters

- >90% Base Editing (%)

HbF protein levels

- 65% γ-globin/Total β-like globins (%)

HbS protein levels

- <40% βs-globin/Total β-like globins (%)

Potential for highest HbF induction and lowest residual HbS levels versus other approaches in the field

Building capabilities for potential best-in-class patient delivery including internal manufacturing

Preclinical data presented at ASGCT 2020; Edited human HSPCs analyzed 16 weeks after infusion in NBSGW mice (Mean±SEM, n=4-6); 1. Sorted human Lineage-CD34+ bulk bone marrow; 2. Sorted erythroid cells (GlyA+)
BEAM-101 is the first clinical base editing program in the U.S., accelerating path to patients and the market.

**BEACON-101 Phase 1/2 Study Design**

Select inclusion criteria:
- Patients with sickle cell disease (SCD) with severe vaso-occlusive crises despite hydroxyurea or other supportive measures
- Age ≥18 to ≤35 years for initial cohort

Select safety endpoints:
- Proportion of patients with successful neutrophil engraftment by day 42
- Safety and tolerability assessments

Select efficacy endpoints:
- Severe vaso-occlusive crises
- Transfusion requirements
- Hemoglobin F levels
- Quality of life and ability to function
- Red blood cell function and organ damage

Transfusion & Mobilization
Manufacturing
Conditioning & Transplant
Engraftment

Follow-up

6 months (+/-)

Patient 1
Patient 2
Patient 3

Patients 4-45
Well positioned to deliver potentially best-in-class regimens for SCD patients, now and in the future

Wave 1
Base Editing + HSC Transplant

Precise gene editing (non-cutting, non-viral)
Busulfan conditioning

---------
BEAM-101 (HbF)

Wave 2
Improved Conditioning

Less toxic conditioning selects for edited cells – potential to expand to younger and broader patient population

---------
ESCAPE-1 (HbF+CD117)
ESCAPE-2 (Makassar+CD117)

Wave 3
In vivo Delivery

In vivo editing after infusion of HSC-targeted LNPs (no transplant)

---------
HbF or Makassar could be utilized

* ESCAPE: Engineered Stem Cell Antibody Paired Evasion
ESCAPE* designed for selective depletion of diseased cells, which may enable non-genotoxic conditioning

- Stem cell factor (SCF) signaling via CD117 is required for HSC survival and proliferation
- A single base edit changes an epitope on the CD117 receptor and is designed not to impact HSC biology
- Customized conditioning antibody depletes diseased unedited cells, but enables CD117-edited cells to “ESCAPE” and grow normally

*ESCAPE: Engineered Stem Cell Antibody Paired Evasion
BEAM-201: Base edited allogeneic cell therapy candidate with an opportunity to treat aggressive CD7+ leukemias

T-Cell Acute Leukemia: 15% of ALL, not treated by B-cell CARTs, few options for relapsed/refractory patients

- Multiplex base editing: Unlike nuclease editors, no detected chromosomal rearrangements, normal cell expansion, and no detected DNA damage response in preclinical studies.
- Clinical-scale process: 96-99% editing, >90% quad edited\(^1\)
- BEAM-201 first patient dosed in August 2023

Preclinical data presented at SITC 2020; 1. Simultaneous base editing at four target loci using clinical-scale process as measured by NGS.
BEAM-201: Significant advantages of multiplex base editing without double strand breaks

**Chromosomal rearrangements**

Percent of cells with translocations

<table>
<thead>
<tr>
<th>Base editing</th>
<th>Nuclease</th>
</tr>
</thead>
<tbody>
<tr>
<td>0%</td>
<td>22%</td>
</tr>
</tbody>
</table>

4 edits: TRAC, CD52, PD1, CD7

**Impact on cell expansion**

Percent yield after editing

Base editing: 100%
Nuclease: <40%

3 edits: TRAC, B2M, PD1

▸ Multiplex editing more efficient with base editing which translates to better cell product
▸ Optimization of platform ongoing with focus on generating next generation “true allogeneic” products

Preclinical data presented at SITC 2020; 1. Base editing versus nuclease editing with the same four guide RNAs measured via G-banded karyotypes from 100 cells; updated analysis shows <0.1% translocations using first generation CBE (data unpublished) 2. Extensive guide screen across three targets, with BE4 and spCas9 sgRNAs selected for high editing efficiency and expansion in single-plex test, final cell yields compared between 3 edits, normalized to electroporation only control
BTX-ALO-001: Multiplex edited BEAM-201 enables evaluation in aggressive T-cell cancers using optimized lymphodepletion (LD)

Select inclusion criteria
- ≥18 to ≤50 yrs for dose exploration
- ≥1 yrs for peds after FDA review
- T-ALL or T-LL with one of following:
  - Relapsed after 2nd CR
  - Relapse after HSCT
  - Primary refractory or R/R
- Eligible for allo HSCT (donor available)

Select safety endpoints
- Incidence and severity of treatment emergent adverse events (TEAE) and treatment-related AEs, including serious AEs (SAEs) and DLTs

Select efficacy endpoints
- Proportion of T-ALL pts with CR or CRi or T-LL pts with CR or PR any time post BEAM-201
- Proportion of pts eligible for HSCT based on response to BEAM-201
- Proportion achieving MRD-negative status
- Duration of response, OS, etc

Phase 1 dose exploration (≤36 pts)
- LD with alemtuzumab (Up to 3 CAR-T dose levels)
- LD without alemtuzumab (Up to 3 CAR-T dose levels)

Phase 1 dose expansion (≤18 pts)
- Expansion Cohort 1
- Expansion Cohort 2
- Pediatric cohort (gated initiation of enrollment)

Phase 2 (~48 pts)
- Recommended phase 2 dose and lymphodepletion regimen

T-ALL = T cell acute lymphoblastic leukemia; T-LL = T cell lymphoblastic lymphoma; CR = Complete response; CRi = CR with incomplete count recovery; PR = Partial response; OS = Overall survival; HSCT = Hematopoietic stem cell transplant; DLT = Dose limiting toxicity; MRD = Minimal residual disease
### Alpha-1 Anti-trypsin Deficiency (AATD): 60,000 ZZ patients in US; severe progressive lung & liver disease

<table>
<thead>
<tr>
<th></th>
<th>Genetics</th>
<th>Liver</th>
<th>Respiratory</th>
</tr>
</thead>
<tbody>
<tr>
<td><strong>Normal AAT Function</strong></td>
<td><img src="image" alt="Wild type SERPINA1 gene" /></td>
<td><img src="image" alt="AAT protein is secreted, protecting lungs" /></td>
<td><img src="image" alt="Low functional AAT and presence of Z-AAT aggregates in circulation causes lung damage, emphysema, etc." /></td>
</tr>
<tr>
<td><strong>AAT Deficiency</strong></td>
<td><img src="image" alt="E342K* (PiZ) mutation" /></td>
<td><img src="image" alt="AAT aggregates and causes liver damage/failure" /></td>
<td></td>
</tr>
</tbody>
</table>

* Also referred to as E366K (includes the signal peptide subject to post-translational cleavage)

** Aggregates also referred to as polymers
In vivo correction of the causative AATD “PiZ” point mutation in mice with BEAM-302

Liver editing
Numbers = % corrected alleles out of total alleles

Corrected alleles include WT correction and WT correction plus D341G bystander edit – both proteins observed to function and secrete normally
Correction of PiZ mutation in mice with BEAM-302* decreased liver aggregates

Reduction in toxic liver aggregates

Control

Correction

* Research grade BEAM-302
AATD mice dosed with BEAM-302 had decreased serum PiZ AAT and increased corrected AAT.

Measured secreted AAT in blood 1-week post-dose.
Increased serum AAT in mice after BEAM-302 dosing corresponded to increased functional AAT.

Collect serum from dosed NSG-PiZ mice.

Incubate with neutrophil elastase.

Measure inhibition of elastase activity as Functional AAT.

**Functional AAT**

![Functional AAT graph](image)

- **Pre-dose**
- **Post-dose**

<table>
<thead>
<tr>
<th>Concentration</th>
<th>Functional AAT (μg/ml)</th>
</tr>
</thead>
<tbody>
<tr>
<td>Vehicle</td>
<td>2500</td>
</tr>
<tr>
<td>0.05mpk</td>
<td>2500</td>
</tr>
<tr>
<td>0.1mpk</td>
<td>2500</td>
</tr>
<tr>
<td>0.25mpk</td>
<td>2500</td>
</tr>
<tr>
<td>0.5mpk</td>
<td>2500</td>
</tr>
<tr>
<td>0.75mpk</td>
<td>7500</td>
</tr>
<tr>
<td>1mpk</td>
<td>9750</td>
</tr>
</tbody>
</table>

* P<0.05, **P<0.005, ***P<0.0005

One-way ANOVA with Sidak's Multiple Comparison test.
BEAM-301 program aims to restore impaired glycogen metabolism which otherwise causes significant morbidity

Glycogen Storage Disease la: 900 US R83C patients; severe hypoglycemia, liver & kidney dysfunction

GSD1a unmet need:
► Low G6PC activity can result in severe drop in blood glucose levels within 1-3 hrs
► Hypoglycemia may result in seizures or can be lethal
► Multiple organ dysfunction (e.g. renal and liver)

BEAM-301 potential:
► Near-normal serum metabolites, G6PC activity, hepatic morphology, increased survival in mice
► Animal studies suggest 11% editing sufficient for restoring fasting glucose\(^1\)

Key points:
► Beam’s first \textit{in vivo} DC
► First DC in industry with \textit{in vivo} direct correction gene editing\(^2\)
► Regulatory filing expected in 1H 2024

2. Based on publicly announced development candidates
BEAM-301 program aims to restore impaired glycogen metabolism which otherwise causes significant morbidity.

- ABE correction of GSDIa R83C mutation associated with improved survival of R83C mice
- Near-normal serum metabolites, G6PC activity, hepatic morphology and lipid deposition

Preclinical data presented at ESGCT 2021. Homozygous huG6PC-R83C mice untreated or treated with LNP via temporal vein shortly after birth, and untreated mice survived less than 3 days with glucose therapy.
Multiplex base editing of hepatitis B virus genome reduced viral markers and prevented rebound

**Hepatitis B**: 850,000 US patients living with chronic hepatitis B; nearly 300 million worldwide

- Current antivirals do not eliminate the HBV genome, leading to viral rebound and preventing cure
- Multiplex base editing has potential to silence covalently closed circular DNA (cccDNA)
- Base editing also has potential to silence HBV integrated in human genome, without fear of chromosomal rearrangements caused by double-stranded DNA breaks

Base editing caused durable inhibition of HBV infection, unlike standard of care antiviral

Presented at International HBV Meeting 2023; Data shown from primary hepatocyte co-cultures
Beam is developing medicines across three franchises, each with near- and long-term potential

- **Lead Programs:** Potentially de-risk technology (higher probability of technical success, faster path), generate revenue, and benefit patients with high unmet need
- **Future platforms:** Expand addressable patient populations to create highly valuable, differentiated franchises through further innovation in editing and delivery

**HEMATOLOGY**
- Near term: BEAM-101
- Future platforms: ESCAPE for conditioning, In vivo delivery

**IMMUNOLOGY-ONCOLOGY**
- Near term: BEAM-201
- Future platforms: Next-generation allogeneic platform (4-6+ edits)

**GENETIC DISEASES**
- Future platforms: BEAM-301, BEAM-302
- Multiple new liver targets, Barcoded LNP beyond liver

**ESCAPE:** Engineered Stem Cell Antibody Paired Evasion
Additional strategic and innovator deals potentially unlock base editing value and broaden therapeutic impact

**Strategic deals**
- **Pfizer**
  - $300M upfront, $1B+ in potential milestones
  - 3 gene targets using Beam’s editing and delivery to target liver, muscle, CNS
  - **Beam option at end of P1/2 for 35% WW cost/net profit split on one program**

- **Apellis**
  - $75M in upfront payments for base editing for complement mediated diseases
  - **Beam opt-in to 50% of US rights after Phase 1 on one program**

- **Sana Biotechnology**
  - $50M upfront for license to Cas12b nuclease for certain engineered cell therapies
  - **Non-exclusive license – Beam retains ability to use or repartner Cas12b**

**Innovator deals**
- **Verve Therapeutics**
  - License to Beam’s base editing technology for the prevention of cardiovascular disease
  - 3 targets: PCSK9 (VERVE-101 and VERVE-102), ANGPTL3 (VERVE 201), Undisclosed #3
  - **Beam opt-in after P1: 50% US (PCSK9 and ANGPTL3) or 35% of WW (Target 3) cost/profit**

- **Prime Medicine**
  - Prime editing (PE) is a novel gene editing technology, complementary to base editing
  - Beam provides delivery and CRISPR technology/know-how
  - **Beam has exclusive rights to PE: SCD transversion edit, any transitions (30% of mutations)**

- **Orbital Therapeutics**
  - Next-gen RNA and delivery; Beam provides interim leadership and RNA/LNP capabilities
  - **Beam has meaningful equity stake in Orbital**
  - **Beam access to Orbital IP for gene editing (exclusive) and certain fields (non-exclusive)**
Meet the Beam Team

John Evans  
Chief Executive Officer

Giuseppe Ciaramella, PhD  
President, Chief Scientific Officer

Terry-Ann Burrell  
Chief Financial Officer

Amy Simon, MD  
Chief Medical Officer

Christine Bellon  
PhD, JD  
Chief Legal Officer

Susan O'Connor  
Chief Human Resources Officer

Brian Riley  
Chief Manufacturing Officer

Manmohan Singh, PhD  
Chief Technology Officer

John Lo, PhD  
Chief Commercial Officer

Gopi Shanker, PhD  
Chief Scientific Officer

Significant team track record in discovery, development, approval of first-in-class medicines
Thank you