



Wave Life Sciences

Corporate Presentation

November 20, 2024

WAVE[™]
LIFE SCIENCES

Forward-looking statements

This document contains forward-looking statements. All statements other than statements of historical facts contained in this document, including statements regarding possible or assumed future results of operations, preclinical and clinical studies, business strategies, research and development plans, collaborations and partnerships, regulatory activities and timing thereof, competitive position, potential growth opportunities, use of proceeds and the effects of competition are forward-looking statements. These statements involve known and unknown risks, uncertainties and other important factors that may cause the actual results, performance or achievements of Wave Life Sciences Ltd. (the “Company”) to be materially different from any future results, performance or achievements expressed or implied by the forward-looking statements. In some cases, you can identify forward-looking statements by terms such as “may,” “will,” “should,” “expect,” “plan,” “aim,” “anticipate,” “could,” “intend,” “target,” “project,” “contemplate,” “believe,” “estimate,” “predict,” “potential” or “continue” or the negative of these terms or other similar expressions. The forward-looking statements in this presentation are only predictions. The Company has based these forward-looking statements largely on its current expectations and projections about future events and financial trends that it believes may affect the Company’s business, financial condition and results of operations. These forward-looking statements speak only as of the date of this presentation and are subject to a number of risks, uncertainties and assumptions, including those listed under Risk Factors in the Company’s Form 10-K and other filings with the SEC, some of which cannot be predicted or quantified and some of which are beyond the Company’s control. The events and circumstances reflected in the Company’s forward-looking statements may not be achieved or occur, and actual results could differ materially from those projected in the forward-looking statements. Moreover, the Company operates in a dynamic industry and economy. New risk factors and uncertainties may emerge from time to time, and it is not possible for management to predict all risk factors and uncertainties that the Company may face. Except as required by applicable law, the Company does not plan to publicly update or revise any forward-looking statements contained herein, whether as a result of any new information, future events, changed circumstances or otherwise.

Building a leading RNA medicines company

Novel RNA medicines platform (PRISM®)



- Multi-modal: RNA editing, RNAi, splicing, allele-selective silencing
- Best-in-class, clinically-validated oligonucleotide chemistry (PN, stereochemistry)

Differentiated RNA medicines pipeline

WVE-006 in AATD



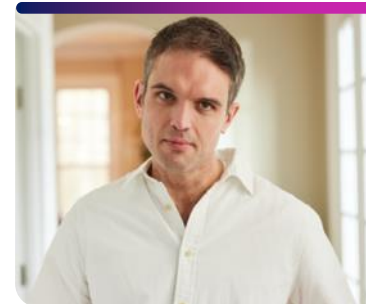
WVE-007 in Obesity



WVE-N531 in DMD



WVE-003 in HD



Strong and broad IP

In-house GMP manufacturing

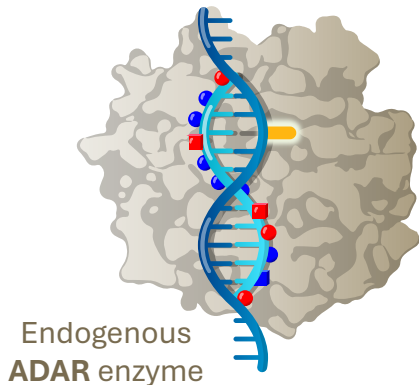
**Well-capitalized with cash
runway into 2027***

Wave's best-in-class multi-modal platform

Clinically-validated oligonucleotide chemistry (including PN, stereochemistry)

Editing

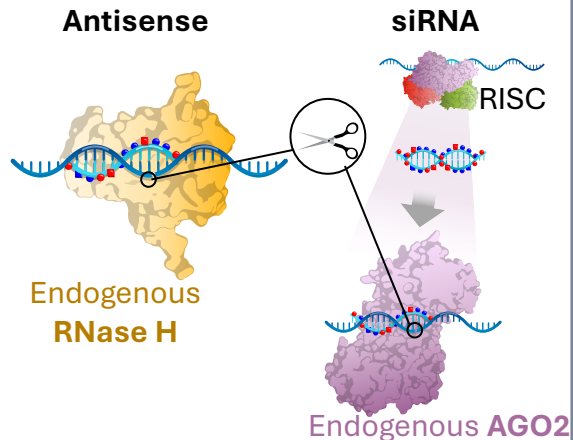
Efficient editing of RNA bases to **restore or modulate** protein production



WVE-006 (AATD)
PNPLA3 (Liver disease), LDLR, APOB (HeFH)

Silencing

Degradation of RNA transcripts to **turn off** protein production

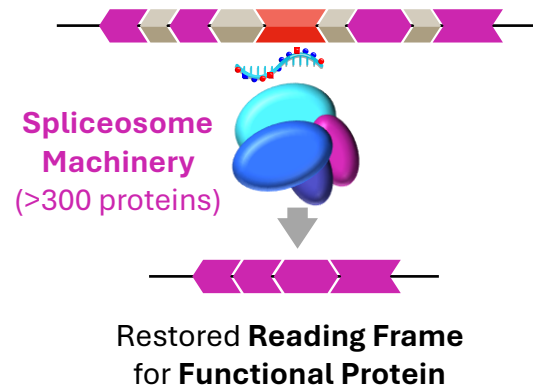


WVE-003 (HD)

WVE-007 (obesity)

Splicing

Restore RNA transcripts and **turn on** protein production



WVE-N531 (DMD)

Wave has driven foundational advances in nucleic acid chemistry to expand platform technologies and develop next generation of RNA therapeutics

Further information can be found in recent platform publications

Silencing (RNase H and Ago2)

Splicing

Editing



NAR Breakthrough Article

Impact of guanidine-containing backbone linkages on stereore antise oligonucleotides in the CNS

Pachamuthu Kandasamy, Yueshan Liu, Vincent Adams, Sandeep Aggar, Rowshan Alam, Eric Anderson, David Bradley, Kelly Brennan, Mitchell Burns, Matteo Camorani, David Chan, Li Di, Dip Seng, Sarah L. Huxford, Ian Marks, Fakhri Mirza, Mark Pridmore, Kelly Reid, Kevin Rieckhoff, David Schneider, Shouping Song, Chris Spill, Daniel S. Taylor, David J. Teague, Daniel E. W. Thomas, and James Watson

Preclinical evaluation of stereore antise oligonucleotides for allele-selective lowering of mutant *HTT*

Nandi Inamati, Yang Zhang, Mattia Franzini, Akhila Nagaraja, Yi-Chen Yang, Robin Tabbot, Neeraj Kulkarni, Alex Adams, Karthikeyan, Ishu Datta, Nathan Lovett, Yueshan Liu, Yi-Hsueh Chen, Jie Chen, Prathima Kandasamy, Feng Liu, Ken Long, Richard Lloyd, Momoji, Yifei Miao, John P. Quinn, Eric Percec, Prathima Kandasamy, Prathima Shiva Prakash, Jayashankar Kumarasamy, Arjun Lakshminarayanan, Arvind Chinnaiyil, David Chen, David C. Deshpande, Hanxin Huang, Huifang Jiang, Yueshan Liu, Anshu Rao, Prathima Shiva Prakash, Mike Stone, Isaac D. Taylor, J. Teague, and Chandu Vagstad

Stereore antise oligonucleotides in vivo mRNA expression atlas

Abstract: Stereore antise (SSA) is a naturalized derivative developed for the expression of specific exons present in CNS targets in order to deplete HTT protein levels. The modified HTT gene strands (HTT SSA) (HTT SSA) are highly sequence specific for the target and function of the target exon. We have generated an atlas of SSA (SSA) sequences for testing and research. We have tested SSA (SSA) sequences in vivo to assess the efficacy of SSA (SSA) in lowering the levels of HTT protein in the CNS. We have found that SSA (SSA) is a promising approach for allele-selective lowering of mutant HTT protein in the CNS. We have also found that SSA (SSA) is a promising approach for allele-selective lowering of mutant HTT protein in the CNS. We have also found that SSA (SSA) is a promising approach for allele-selective lowering of mutant HTT protein in the CNS.



Control of backbone chemistry and chirality boost oligonucleotide splice switching activity

Pachamuthu Kandasamy¹, Graham McCleary¹, Mamoru Shimizu², Nayantara Kothari¹, Bhawesh Akani¹, Naoki Inamati¹, Jayashankar Kumarasamy¹, Gopal B. Bommeneni¹, Adam Beizhan¹, Onamung Chivatarn¹, David C. D. Butler¹, Michael Byrne¹, Katarzyna Chwaliszka¹, Kay E. Davies¹, Roger Deas¹, Jull D. Sheikh¹, An F. Durtin¹, Ruth Eremangul¹, Ben Edwards¹, Jack Godfrey¹, Andrew Hesse¹, Fangjun Liu¹, Kenneth Longo¹, Gerrit Liu¹, Subramanian Maraganan¹, Jacopo Oleari¹, H. Hyon Park¹, Erin Percec Estabrook¹, Chikiko Shiwakita¹, Maave Tashbiri¹, Tomomi Kawasumi¹, Carlo Rinaldi^{1,3}, Joana Rajko-Saravaj¹, Snehalata Topisetti¹, Hailin Yan¹, Yuan Yin¹, Xianxi Zhou¹, Cong Zhou¹, Jason Zhang¹, Luciano Apponi¹, Matthew J. A. Wood^{2,4} and Chandu Vargese^{1,5*}

Impact of stereore chimeric backbone chemistry on the potency and durability of gene silencing by RNA interference

Wei Liu¹, Nandi Inamati¹, Subramanian Maraganan¹, Khari Liu, Snehalata Topisetti, Erin Percec Estabrook, Juli Dilli Sheikh, Himani Shah, Anthony Lamattina, Qiandui P. Brett Schmidt, Frank Favazza, Meghna Bedekar, Arundhan Chatterjee, Jagar Desai¹, Tomomi Kawasumi, Gerrit Liu, Lisa Mettelwerk, Mitolika Kanasawone, Prayana Shiva Prakash, Hailin Yan, Yuan Yin, Xu, Paloma N. G. Gungor, Michael Byrne, Pachamuthu Kandasamy and Chandu Vargese¹

Abstract: Second generation approaches of splice-switching oligonucleotides (SSOs) for the treatment of human genetic disease such as Spina Muscular Dystrophy has been an advance for the improvement of quality of life. However, second generation SSOs have limited clinical benefit due to poor pharmacokinetics. To overcome limitations of existing technologies, we have designed chimeric backbone SSOs containing phosphonate (PN) and phosphorothioate (PT) backbones. We demonstrate that these chimeric SSOs demonstrate improved pharmacokinetics and efficacy compared to PN-modified oligonucleotides, preventing premature death and improving median survival of 88 days by at least 30% in a genetic mouse model with an aggressive phenotype. These chimeric SSOs also demonstrated improved pharmacokinetics and efficacy compared to PN-modified oligonucleotides. We demonstrate that these chimeric SSOs demonstrate improved pharmacokinetics and efficacy compared to PN-modified oligonucleotides.



Endogenous ADAR-mediated RNA editing in non-human primates using stereore chemically modified oligonucleotides

Prashant Mani¹, Chikiko Shiwakita¹, Gerrit Liu¹, Mamoru Shimizu², David Bradley¹, Jayashankar Kumarasamy¹, Michael Byrne¹, Arvind Chinnaiyil, Daniel Chen, David C. Deshpande, Frank Favazza¹, Jack Godfrey¹, Andrew Hesse¹, Naoki Inamati¹, Tomomi Kawasumi¹, Jayashankar Kumarasamy¹, Anthony Lakshminarayanan, Arundhan Chatterjee, Fangjun Liu, Richard Lloyd, Subramanian Maraganan, Jake Mettelwerk, Bonnielle Murphy¹, Jeff Rossi¹, Tom Pui, Bijay Bhattarai¹, Stephany Stanbury, Snehalata Prakash, Hailin Yan, Yuan Yin, Hui-Yi, Ian Harding, Straine Biem, Luciano H. Ai

Rational design of base, sugar and backbone modifications improves ADAR-mediated RNA editing

Gerrit Liu¹, Chikiko Shiwakita¹, Prashant Mani¹, Hui-Yi, Ian Harding, Straine Biem, Michael Byrne, Alys Farame, Stephen Fred, Olivia Huth, Naoki Inamati, Tomomi Kawasumi, Jayashankar Kumarasamy, Anthony Lakshminarayanan, Kenneth Longo, Leah McCarty, Andrew McKay, Allison Mohi, Qianli Pan, Tom Pui, Erin Percec Estabrook, Jeff Rossi, Stephany Stanbury, Carina Thomas, Alexandra Walen, Hailin Yan, Pachamuthu Kandasamy¹ and Chandu Vargese^{1,2*}

Abstract: RNA editing by ADARs is a naturalized derivative developed for the expression of specific exons present in CNS targets in order to deplete HTT protein levels. We have generated an atlas of SSA (SSA) sequences for testing and research. We have tested SSA (SSA) sequences in vivo to assess the efficacy of SSA (SSA) in lowering the levels of HTT protein in the CNS. We have found that SSA (SSA) is a promising approach for allele-selective lowering of mutant HTT protein in the CNS. We have also found that SSA (SSA) is a promising approach for allele-selective lowering of mutant HTT protein in the CNS.



Full list of Wave publications: <https://ir.wavelifesciences.com/events-publications/publications>




Three clinical updates in 2024 demonstrate continued platform translation

Proprietary PRISM platform





Stereopure oligonucleotides

Novel backbone modifications
(including PN chemistry)

Novel base and sugar
chemistry modifications

Therapeutic modalities	Preclinical publication	Clinical translation	Clinical trial results
Splicing (WVE-N531 for DMD)	✓	✓ 53% exon skipping, 42 µg/g muscle tissue concentrations in 6 weeks	✓ 9.0% mean muscle-adjusted dystrophin; safe and tolerable (interim analysis) 
Allele-selective silencing (WVE-003 for HD)	✓	✓ 35% allele-selective mHTT silencing with single dose	✓ 46% allele-selective mHTT silencing; correlation with slowing of caudate atrophy 
GalNAc-RNA editing (WVE-006 for AATD)	✓	✓ First ever RNA editing achieved; 11 µM total AAT protein, >60% (6.9 µM) M-AAT with single dose	Multidose data expected in 2025 
GalNAc-RNAi (WVE-007 for obesity)	✓	Clinical trial initiation expected 1Q 2025	

Robust, diversified RNA medicines pipeline including first-in-class RNA editing programs

Program	Discovery	IND / CTA Enabling Studies	Clinical	Rights	Patient population (US & Europe)
RNA EDITING					
WVE-006 SERPINA1 (AATD)		RestorAATion Clinical Program		GSK exclusive global license	200K
GalNAc-AIMer PNPLA3 (liver disease)				100% global	9M
GalNAc-AIMer LDLR (HeFH)				100% global	900K (30M expansion)
GalNAc-AIMer APOB (HeFH)				100% global	70K
RNAi					
WVE-007 (GalNAc) INHBE (Obesity and other metabolic disorders)				100% global	47M
GalNAc-siRNA Undisclosed				100% global	--
SPLICING					
WVE-N531 Exon 53 (DMD)			FORWARD-53 Trial (Phase 2)	100% global	2.3K
Other exons (DMD)				100% global	Up to 18K
ALLELE-SELECTIVE SILENCING					
WVE-003 mHTT (HD)			SELECT-HD Trial (Phase 1b/2a) - Trial Completed	100% global	25K Symptomatic (SNP3) 60K Pre-Symptomatic (SNP3)



Editing for correction



Editing for upregulation

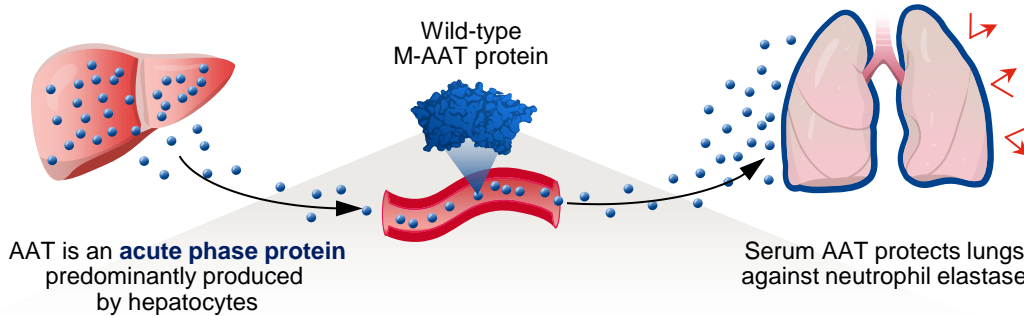
WVE-006

RNA editing (AIMers)

Alpha-1 antitrypsin deficiency (AATD)

WVE-006: GalNAc-conjugated Aimer designed to correct mutant SERPINA1 transcript to address both liver and lung manifestations of AATD

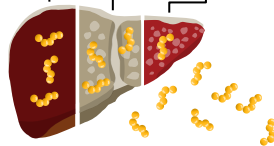
Healthy



AATD

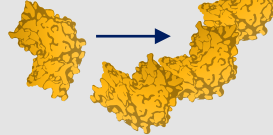
Gain of Function: Liver Disease

Fibrosis → Cirrhosis → Hepatocellular Carcinoma



Z protein causes AAT proteotoxic stress, leading to progressive liver disease

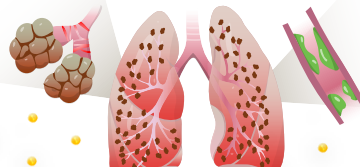
Misfolded Z-AAT protein with E342K mutation



Polymerization

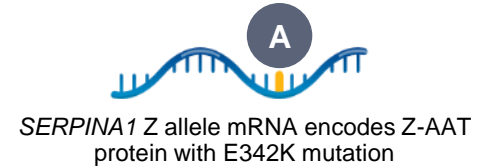
Loss of Function: Lung Disease

Emphysema Bronchiectasis



Low serum AAT leads to lung disease

WVE-006 for AATD



Edited *SERPINA1* mRNA enables wild-type M-AAT protein production



✓ Subcutaneous injection (GalNAc)



✓ Infrequent dosing



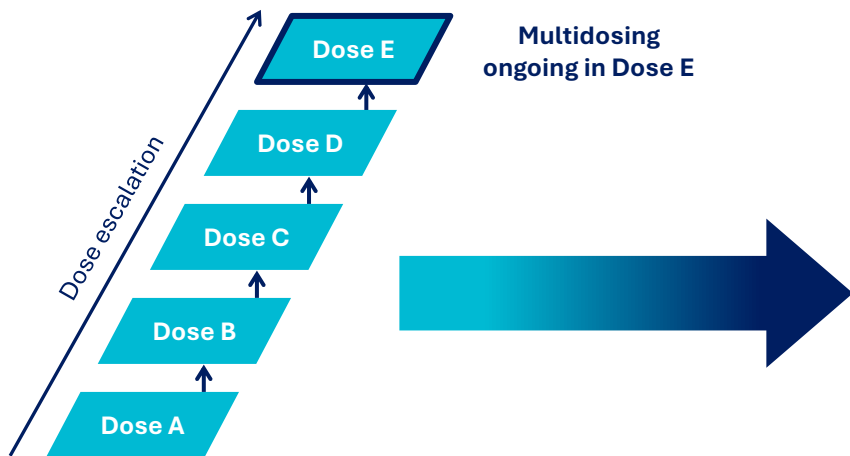
✓ Highly specific (No bystanders)

RestorAATion-1 and RestorAATion-2 ongoing

RestorAATion-1: Healthy Volunteers

RestorAATion-2: AATD Patients

Single ascending dose (SAD) → Multiple-ascending dose (MAD) cohorts



Multidosing
ongoing in Dose E



Up to 7 doses

Cohort 3

Cohort 2

Cohort 1
200 mg

Study key objectives

Safety and tolerability
Pharmacokinetics
Serum M-AAT levels

Achieved proof-of-mechanism for Wave's RNA editing platform

Proof-of-mechanism after a single dose in RestorAATion-2

- **Circulating wild-type M-AAT protein in plasma:** Mean of 6.9 μM at day 15; more than 60% of total AAT
- **Increases in neutrophil elastase inhibition from baseline:** Consistent with production of functional M-AAT
- **Mean total AAT protein:** Increased from below level of quantification at baseline to 10.8 μM at day 15
 - Meets level that has been the basis for regulatory approval for AAT augmentation therapies
- **Increases in total AAT from baseline and M-AAT protein:** Observed as early as day 3 and through day 57
- WVE-006 well tolerated with a favorable safety profile; all AEs mild-to-moderate, no SAEs

Wave expects to share multidose data from RestorAATion-2 in 2025

Strategic collaboration with GSK to develop transformative RNA medicines

Collaboration Highlights

- \$170 million upfront¹
- Additional research funding
- Potential for up to \$3.3 billion in milestones²
- Leverage GSK's expertise in genetics and genomics

Maximize global potential for WVE-006 for AATD

Up to \$525 million in total milestones and tiered royalties on net sales

✓
\$20 million milestone with first individual dosing
RestorAATion-2 trial underway (AATD patients)

Advance up to eight GSK collaboration programs

Up to \$2.8 billion in total milestones and tiered royalties on net sales

✓
\$12 million aggregate initiation payment for GSK's selection of two programs to advance

Expand Wave's pipeline

Wave to advance up to **three wholly owned collaboration programs** (or more with GSK's consent)³

✓
INHBE is Wave's first wholly owned program emerging from GSK collaboration

Recent Highlights

Wholly owned GalNAc-AIMer programs

New targets meet key criteria, expected to improve probability of success:

- ✓ Strongly supported by human genetics
- ✓ Leverage unique platform capabilities; GalNAc-AIMers building on learnings of WVE-006
- ✓ Completely novel ways of treating diseases with high unmet need
- ✓ Readily accessible biomarkers and approaches to assess PD, defined regulatory paths

Correction of PNPLA3
Genetically defined liver disease



Upregulation of LDLR
Familial hypercholesterolemia



Correction of APOB
Familial hypercholesterolemia



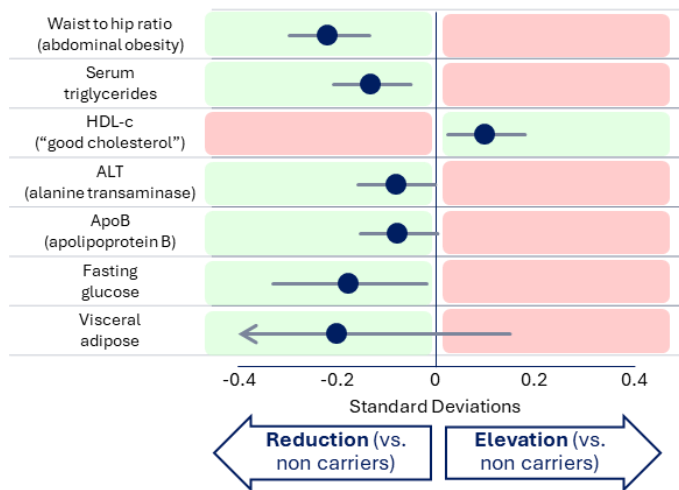
PNPLA3, LDLR, APOB clinical candidates expected in 2025

WVE-007 (INHBE program)
GalNAc-siRNA silencing

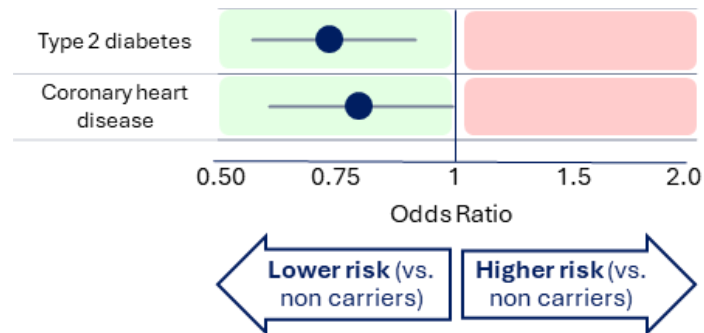
Obesity and other metabolic disorders

Human genetic data demonstrate that INHBE heterozygous carriers have a healthy metabolic profile

Heterozygous INHBE LoF carriers have favorable traits: lower abdominal obesity, lower triglycerides, higher HDL-c



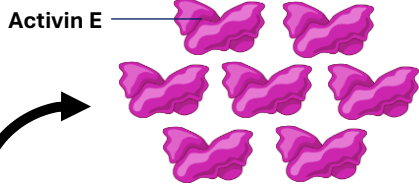
Heterozygous INHBE LoF carriers have lower risk of Type 2 diabetes and CHD



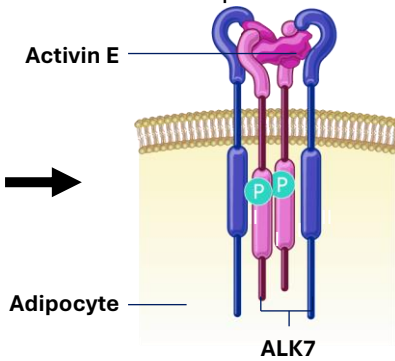
Silencing INHBE mRNA by $\geq 50\%$ is expected to recapitulate the healthy metabolic profile of heterozygous INHBE loss of function (LoF) carriers

INHBE GalNAc-RNA expected to address health issues associated with pathogenesis of obesity, associated metabolic disease

Release of **dimerized** INHBE subunits creates hepatokine **Activin E**



Binds to and **activates** **ACVR1C (ALK7)** receptor in adipose tissue

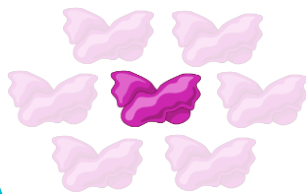


Block adipose lipolysis

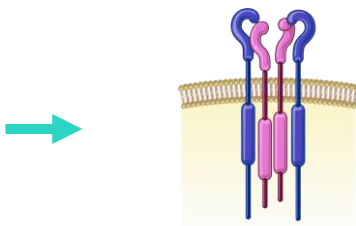


Increased abdominal adiposity leads to **obesity, CVD and T2D**

Reduced release of hepatokine **Activin E**



Diminished activation of **ACVR1C (ALK7)** receptor in adipose tissue



Increased adipose lipolysis and shrink adipocytes



Decreased abdominal adiposity leads to **weight loss and reduced risk for CVD and T2D**

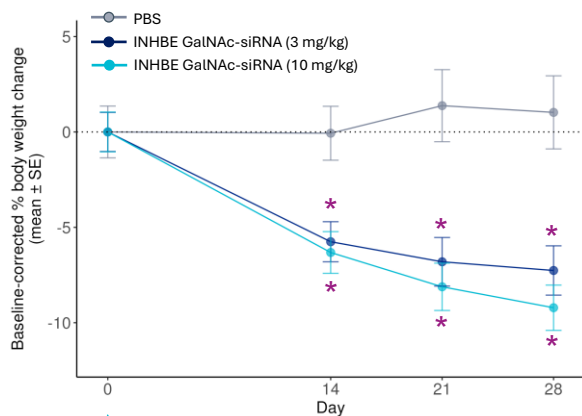
GalNAc-siRNA

Single doses of INHBE GalNAc-siRNA result in dose-dependent weight loss and reduction of visceral fat, without affecting muscle mass

✓ Reduction in body weight

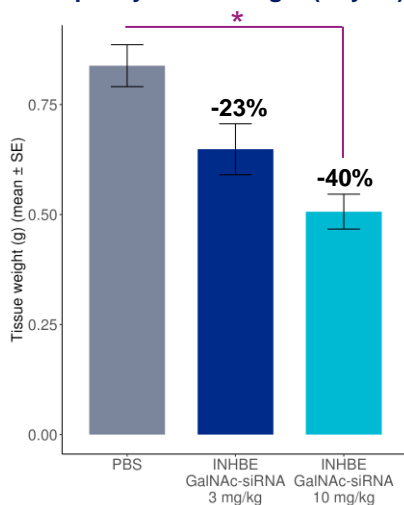
✓ Reduction in visceral fat

✓ No muscle loss

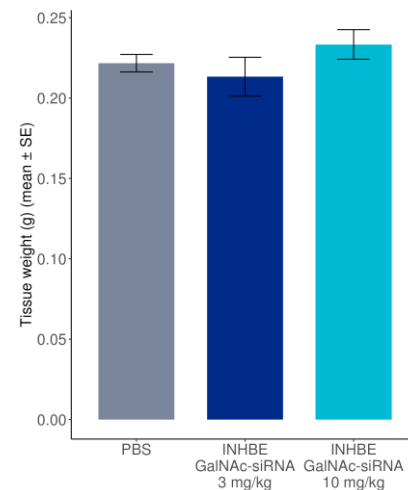


Single dose INHBE GalNAc-siRNA

Epididymal fat weight (Day 28)



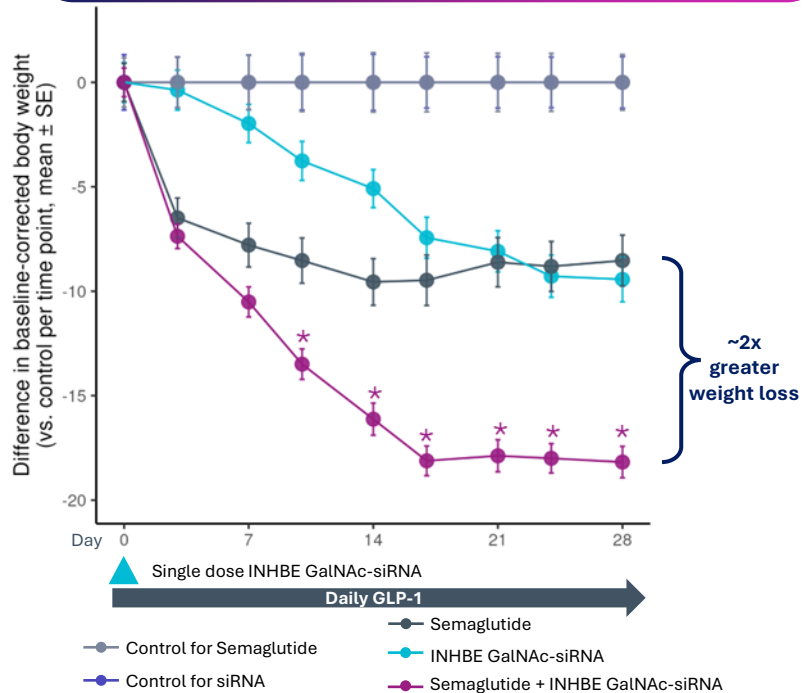
Quadriceps weight (Day 28)



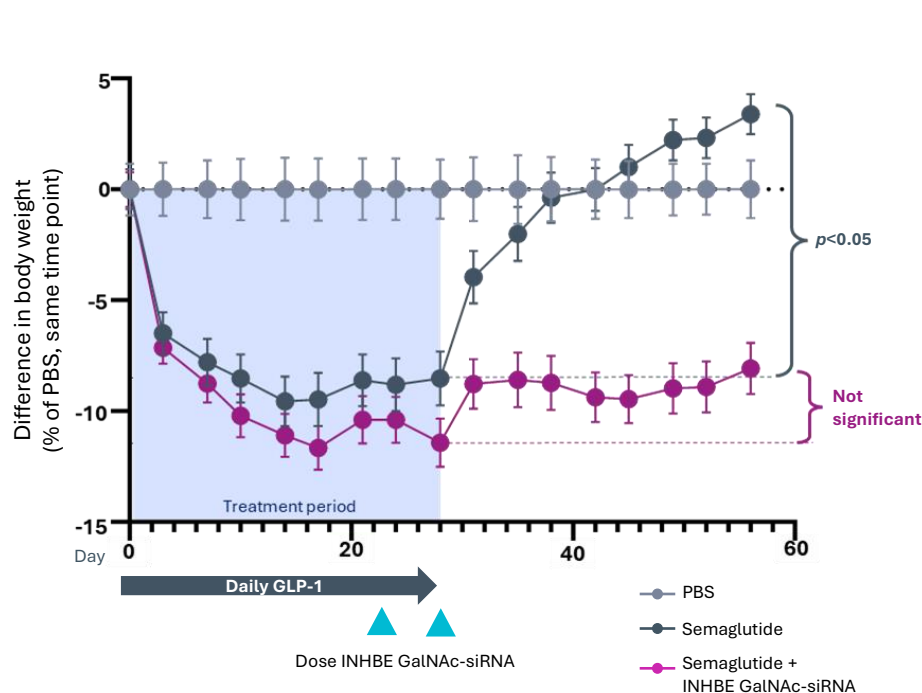
INHBE GalNAc-siRNA has potential as monotherapy weight loss therapeutic

INHBE GalNAc-siRNA can be used synergistically with GLP-1s or to prevent weight regain after the cessation of treatment with GLP-1s

✓ ~2x greater overall weight loss when added to GLP-1s



✓ Prevents weight regain after the cessation of GLP-1s



Preclinical data support best-in-class profile and potential to use WVE-007 across multiple treatment settings with 1-2x a year dosing

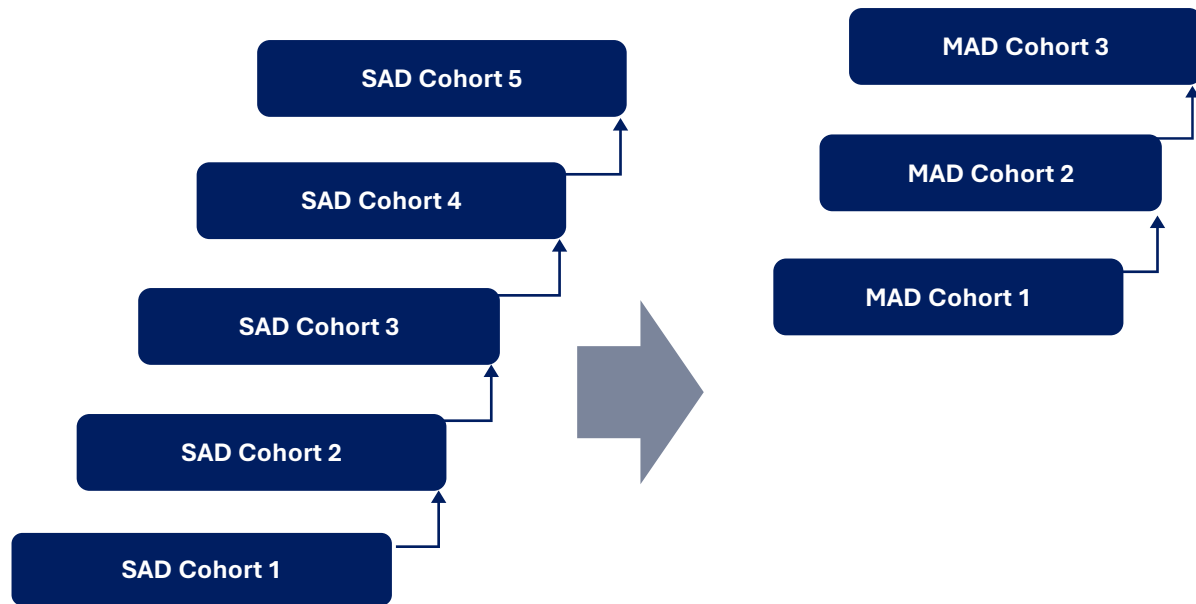
- ✓ **Monotherapy: as a single agent.** Weight loss similar to semaglutide with no loss of muscle mass and a reduction in fat mass with preferential effect to the visceral fat, and without suppressing food intake
- ✓ **Add-on to GLP-1s: WVE-007 in addition to GLP-1 therapy.** When administered as an add-on with semaglutide, a single dose of Wave's INHBE GalNAc-siRNA doubled the weight loss observed with semaglutide alone
- ✓ **Maintenance: for patients who stop treatment with GLP-1 therapy.** Curtailed rebound weight gain upon cessation of semaglutide and prevention of weight cycling, which worsens the outcomes of various metabolic diseases

CTA expected before year-end for Phase 1 trial of WVE-007 in adults living with overweight or obesity, otherwise healthy

Randomized, double-blind, placebo-controlled study of ascending doses of WVE-007

Trial Design

- **Objective:** Assess dose safety, tolerability, PK and PD
- **Key measurements**
 - **Primary:** Safety and Tolerability
 - **Secondary:** PK, Activin E
 - **Exploratory PD:**
 - Body Weight
 - Body compositions
 - Metabolic health
 - Biochemical markers



Expect to initiate clinical trial for WVE-007 in 1Q 2025

WVE-N531

Splicing

Duchenne muscular dystrophy

Urgent need for improved therapeutic options for the treatment of DMD

Duchenne is a devastating and fatal disease

- Genetic mutation in dystrophin gene prevents the production of dystrophin protein, a critical component of healthy muscle function
- Impacts ~1 / 5,000 newborn boys annually; ~20,000 new cases annually worldwide
 - ~8–10% are amenable to exon 53 skipping
 - Potential for Wave to address up to 40% of DMD with additional exon skipping therapeutics

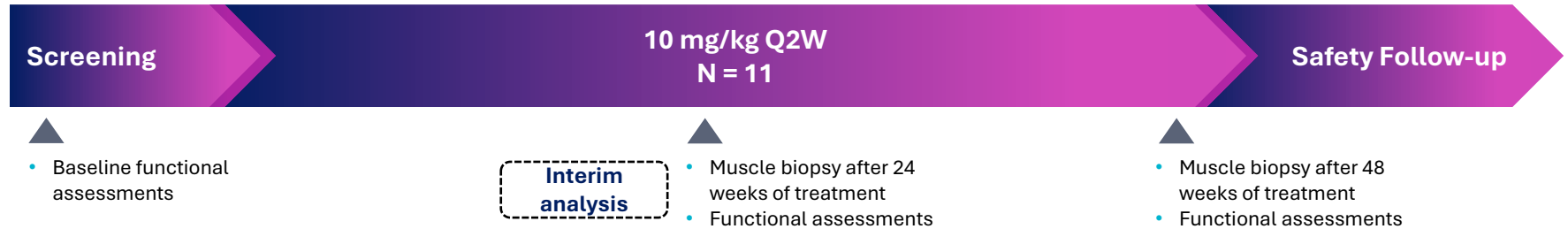
Multiple urgent unmet needs

- Need for therapies delivering **more consistent dystrophin expression**, as few patients today achieve dystrophin >5% of normal
- **Opportunity to extend dosing intervals** beyond weekly standard of care to alleviate burden for patients and caregivers
- **Need to reach stem cells and distribute broadly to muscle tissues** to potentially enable muscle regeneration and impact respiratory and cardiac function



Boy living with DMD

FORWARD-53: An ongoing potentially registrational open-label Phase 2 clinical trial of WVE-N531 in boys with DMD amenable to exon 53 skipping



Key Assessments:

- Safety and tolerability
- Muscle biopsies after 24 and 48 weeks of treatment
 - PK: Drug tissue concentrations
 - PD: Exon-skipping, Dystrophin level (% of normal) as assessed by Western Blot
- Functional outcome measures
- 11 participants enrolled, including two from prior Part A clinical trial
 - Pre-specified analyses in ambulatory patients

Results of interim analysis: WVE-N531 has potential to be the best-in-class therapeutic for exon 53 DMD



Highly consistent dystrophin expression across patients

- 9.0% muscle-content adjusted dystrophin (5.5% unadjusted), quantified from two isoforms that are consistent with Becker patients who display milder disease
- 89% of patients over 5% of normal (muscle-content adjusted)



Muscle delivery and extended dosing intervals

- Skeletal muscle tissue concentrations of WVE-N531: ~41,000 ng/g
- WVE-N531 tissue half-life of 61 days supports monthly dosing
- Preclinical data suggests WVE-N531 is translating in heart and diaphragm



Evidence supporting improved muscle health

- Improvement in serum biomarkers for muscle health
- Localization of WVE-N531 in myogenic stem cells
- Improvement in myofiber regeneration



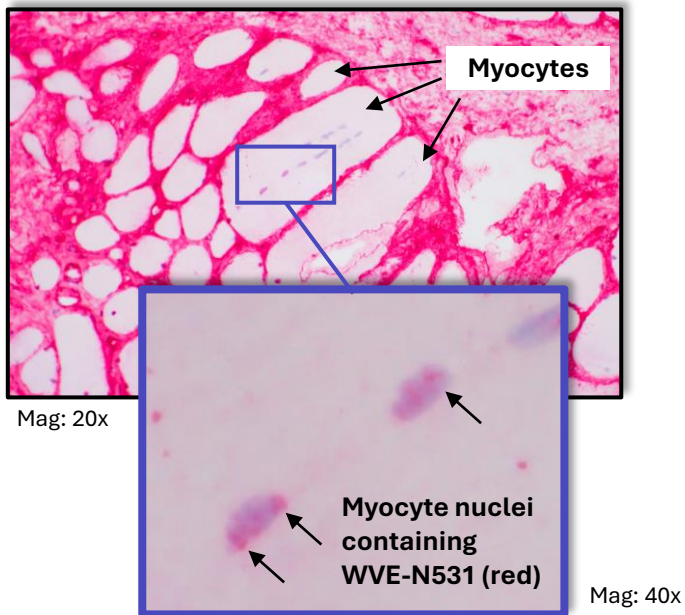
Safe and well tolerated

- No SAEs
- No discontinuations
- No oligonucleotide class effects

Expect to receive feedback from regulators on pathway to accelerated approval and deliver 48-week FORWARD-53 data in 1Q 2025

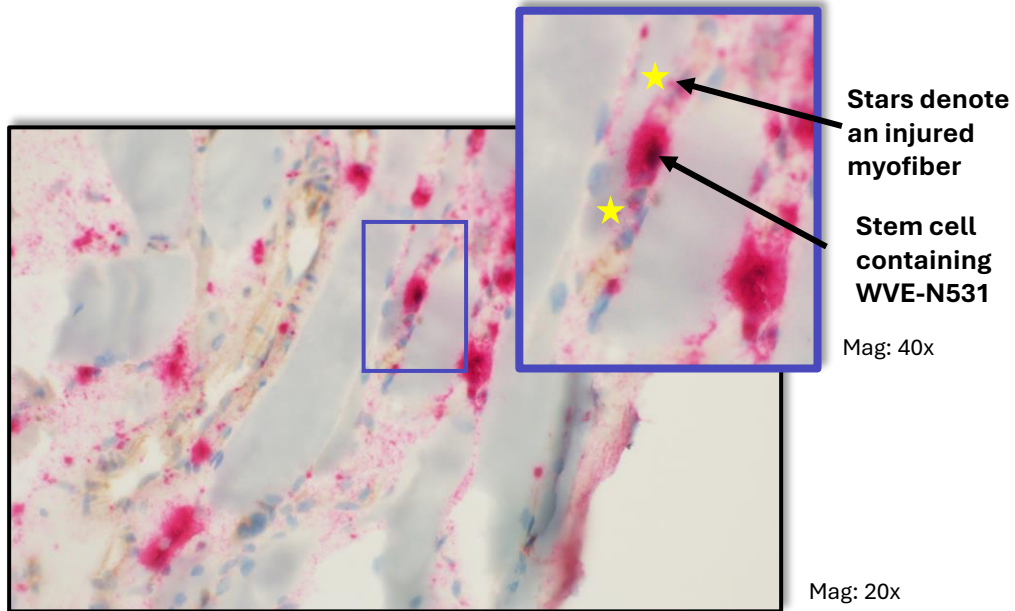
WVE-N531 was localized in myofiber nuclei and myogenic stem cells

WVE-N531 uptake in myofiber nuclei



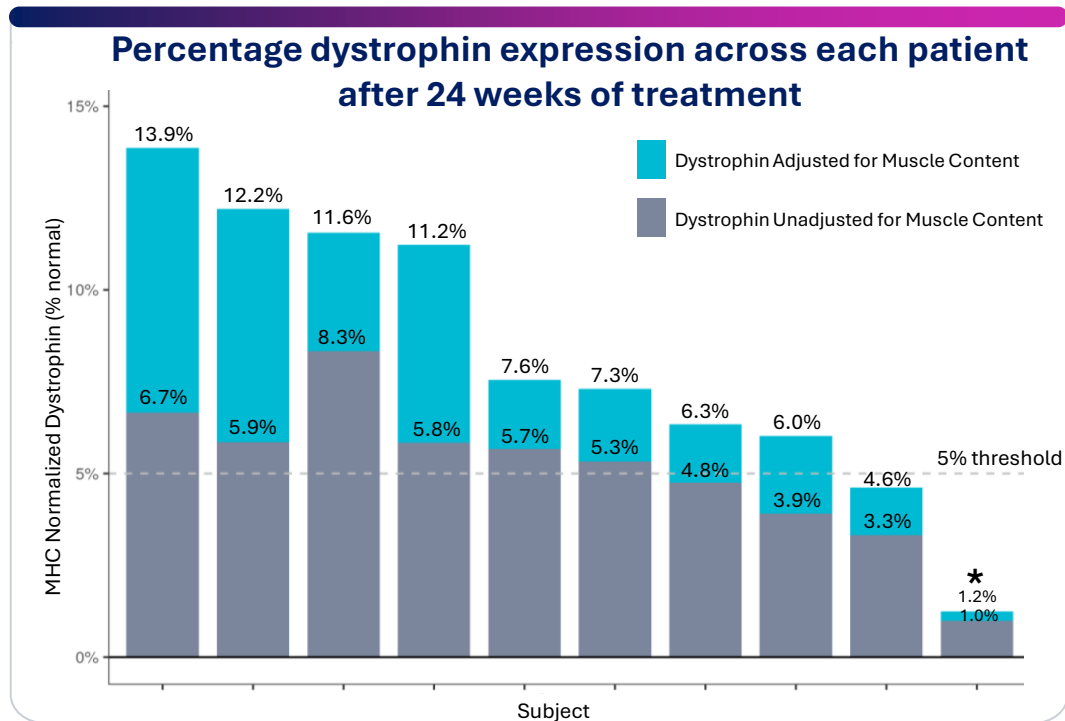
In-situ hybridization for WVE-N531

WVE-N531 uptake in myogenic stem cells



Dual staining utilizing in-situ hybridization for WVE-N531 and PAX7 immunohistochemistry for stem cells

Dystrophin expression of up to ~14% with high consistency across participants

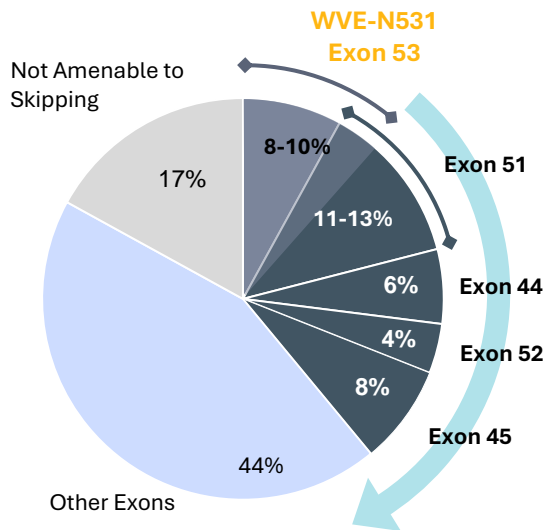


- Mean 9.0% absolute muscle content adjusted dystrophin
- Mean 5.5% absolute unadjusted dystrophin
- Dystrophin expression was quantified from two isoforms consistent with those observed in Becker patients who display milder disease

89% of ambulatory participants achieve muscle content-adjusted dystrophin levels of at least 5%

Unlocking Wave's best-in-class exon skipping portfolio

DMD Population



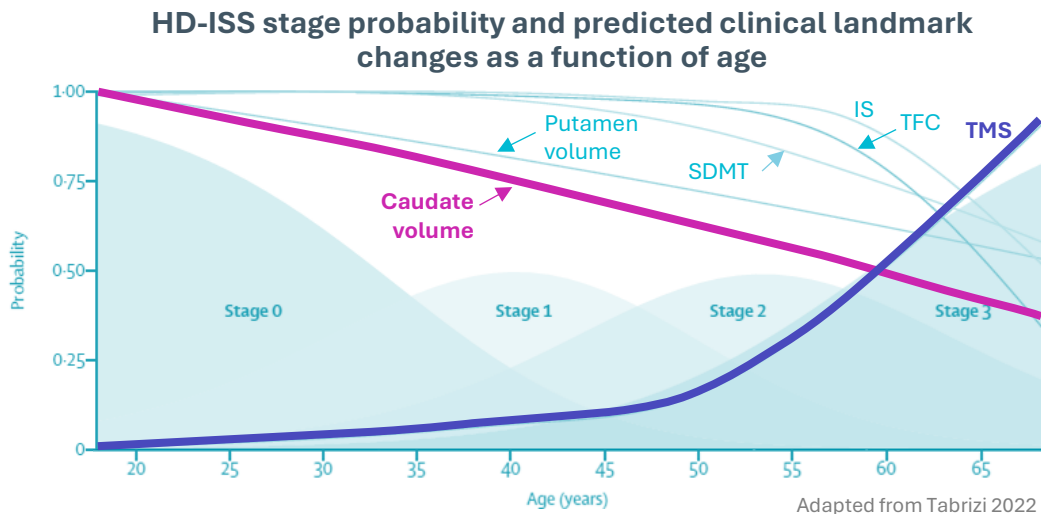
- Data for exons 51, 44, 52, 45 demonstrate potential for even greater dystrophin expression
- Opportunity to address up to 40% of population
- Expect to engage regulators on a platform trial design that incorporates multiple exons

WVE-003
Allele-selective silencing

Huntington's Disease

Huntington's disease is a devastating neurological disorder caused by a toxic gain of function and concurrent loss of function

- HD is a monogenic autosomal dominant genetic disease; fully penetrant and affects entire brain
- No current disease modifying therapies for HD
- Characterized by cognitive decline, psychiatric illness, and chorea; ultimately fatal
- Expanded CAG triplet repeat in *HTT* gene results in production of mutant huntingtin protein (mHTT) and loss of function in wild-type huntingtin protein (wtHTT)



>200,000 patients with HD across all disease states

Pre-Symptomatic HD

(~160K in US and Europe)

Symptomatic HD

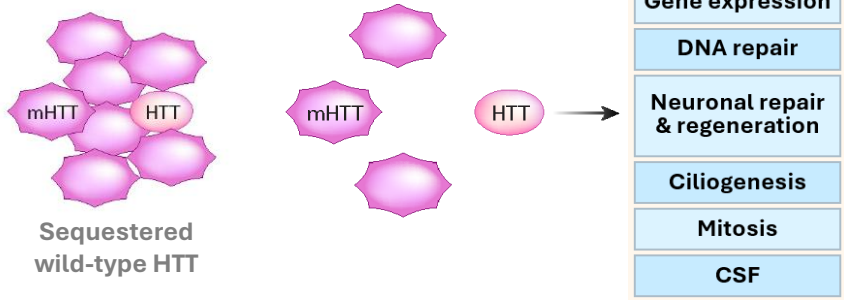
(~65K in US and Europe)

An allele-selective, wtHTT-sparing approach is uniquely suited to address HD across all stages of disease

Wild-type HTT (wtHTT) is critical for normal neuronal function and loss of wtHTT contributes to cellular dysfunction

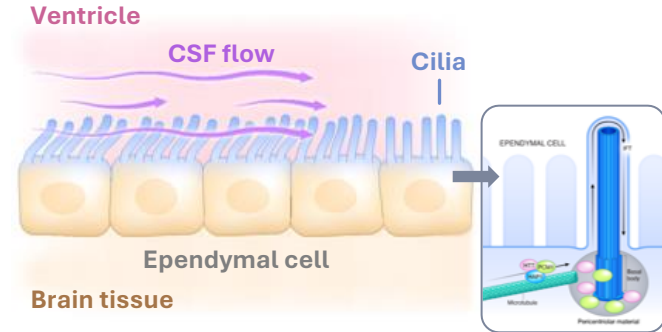
Mutant HTT has a detrimental effect on wild-type HTT function

- Lowering mHTT is expected to restore physiological control over HTT gene expression and relieve its detrimental effect on wtHTT function



Wild-type HTT is crucial for cilia health

- In the absence of wtHTT, ciliogenesis fails, disrupting CSF flow, causing hydrocephalus

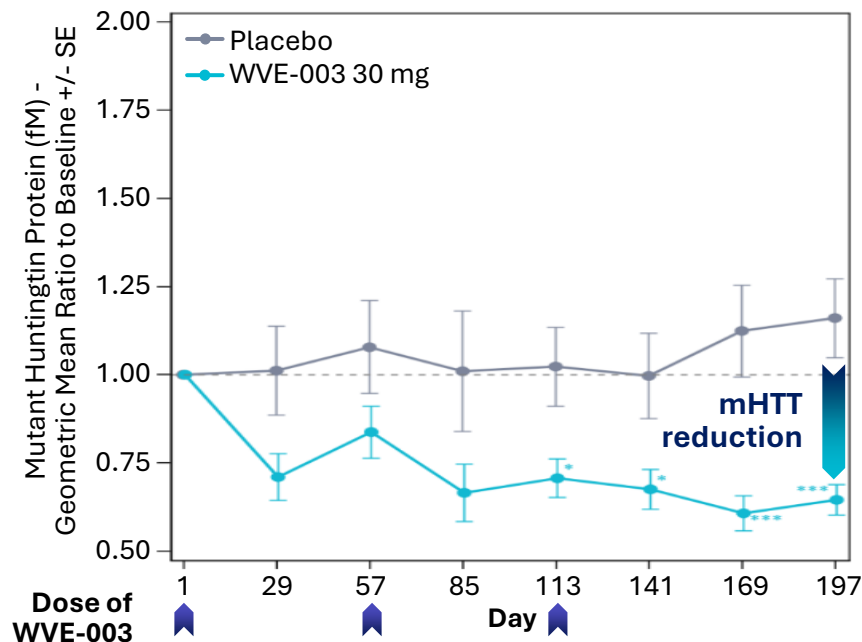


Only an allele-selective approach can ameliorate both loss-of-function and gain-of-function disruptions driven by mHTT

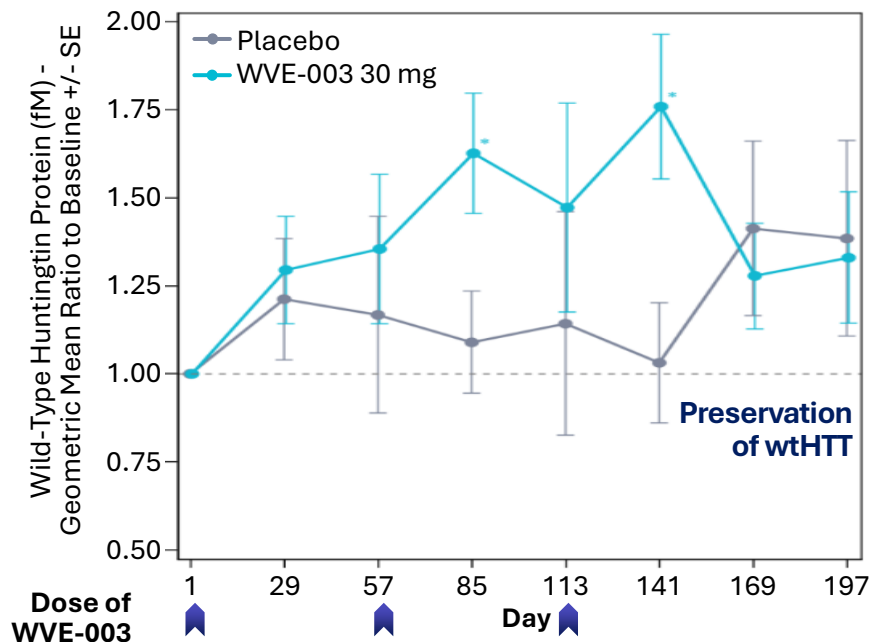
Allele-selective lowering of mutant HTT protein of up to 46% with three doses of WVE-003 and preservation of wild-type HTT

Durability of mHTT reductions supports potential for quarterly dosing intervals

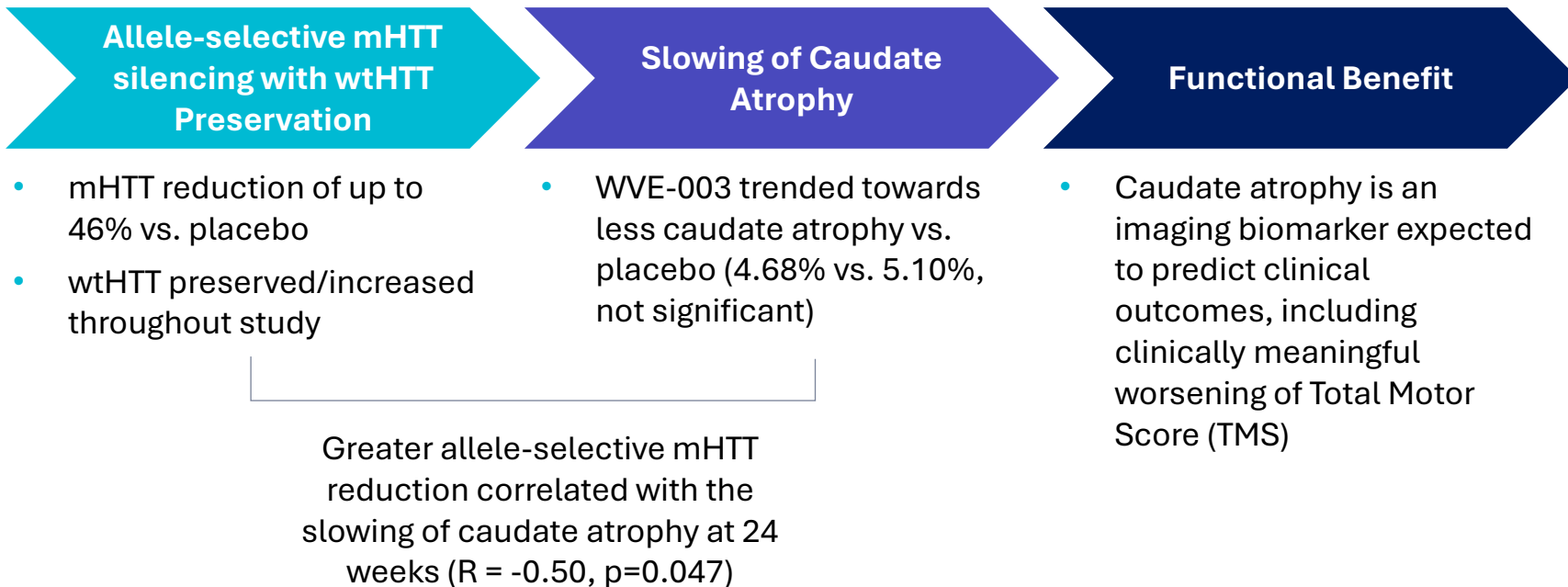
Mutant HTT protein levels



Wild-type HTT protein levels

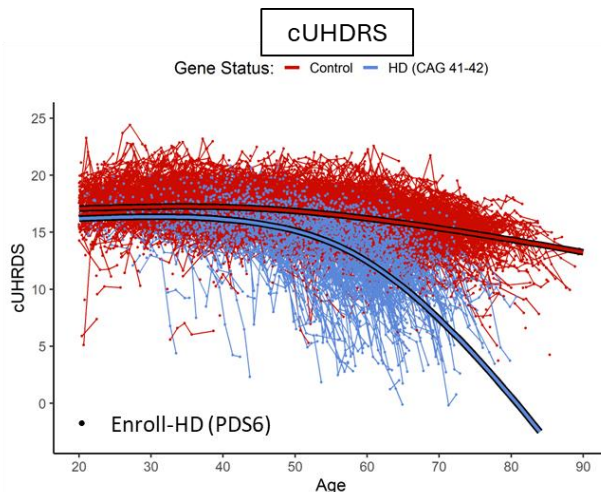
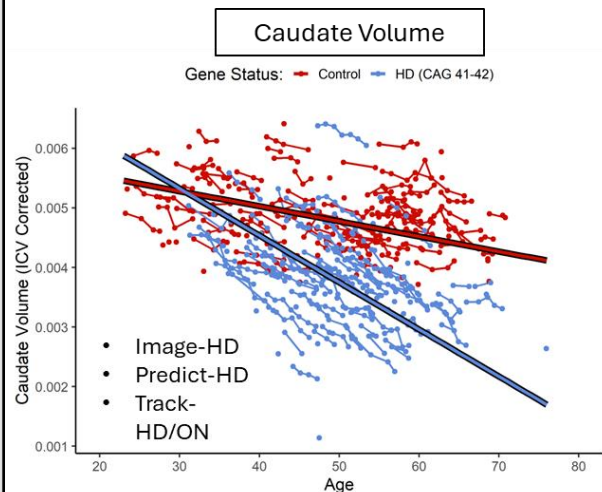


WVE-003 leads to allele-selective mHTT reduction, correlating with slowing of caudate atrophy



Regularity of caudate change makes it an ideal biomarker for more efficient clinical development in HD

• HD-ISS Stage 2



- Caudate volume has a more regular, linear change at individual level versus variability in individual trajectories with cUHDRS
- Wave analysis¹ of PREDICT and TRACK-HD reinforces the relationship between caudate volume loss and clinical outcomes
 - Difference of 1% reduction in rate of caudate atrophy results in ≥6-year delay in loss of function (i.e. reduction from TFC 13)
- Using caudate volume as a primary endpoint will enable smaller, faster and more efficient clinical trials

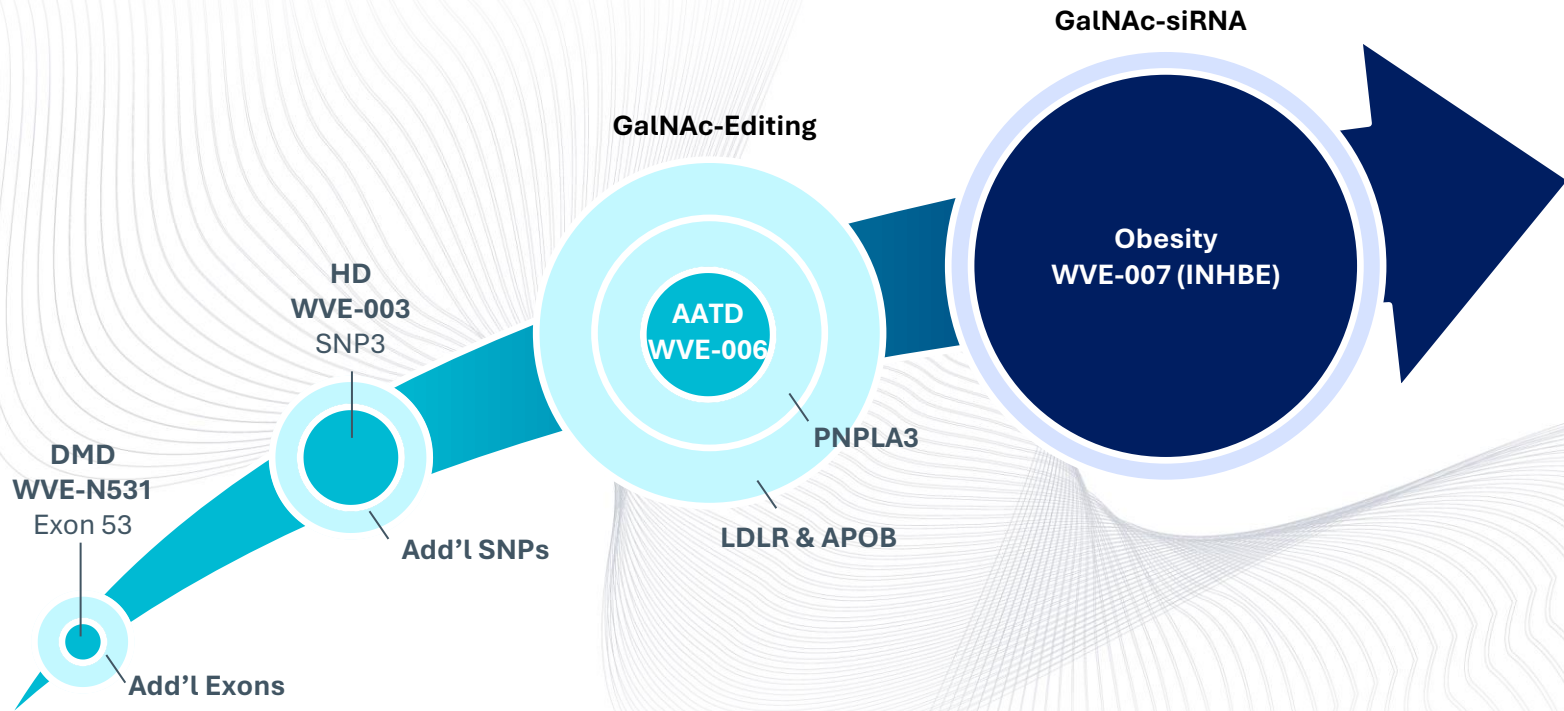
Preservation of caudate volume offers an efficient pathway for potential accelerated approval for HD

- Received supportive initial feedback from FDA:
 - Recognize the severity of HD
 - Receptive to and engaged with Wave regarding a potential pathway to accelerated approval
 - Open to Wave's plan to evaluate biomarkers, including vMRI for caudate atrophy, as an endpoint to assess HD progression with the potential to predict clinical outcome
- Planning is underway for a global, potentially registrational Phase 2/3 study in adults with SNP3 and HD, including finalization of key aspects of design

Wave expects to submit an IND for WVE-003 in 2H 2025

Reimagining RNA medicines

Poised for significant and sustained growth driven by editing and siRNA



Wave's platform is translating in the clinic and has potential to treat >90M patients in the US and Europe

Anticipated upcoming milestones

<i>GalNAc-RNA editing</i>		<i>GalNAc-siRNA</i>	<i>Splicing</i>	<i>Allele-selective silencing</i>
WVE-006 AATD	PNPLA3 - Liver disease LDLR, APOB - HeFH	WVE-007 (INHBE) Obesity	WVE-N531 (Exon 53) DMD	WVE-003 (SNP3) HD
2025: Deliver multidose data from RestorAATion-2	2025: Select clinical candidates	Year-end 2024: Submit CTA 1Q 2025: Initiate clinical trial	1Q 2025: Deliver 48-week FORWARD-53 data & receive feedback from regulators on pathway to accelerated approval	2H 2025: Submit an Investigational New Drug (“IND”) application

Well-capitalized with cash runway into 2027

WAVETM
LIFE SCIENCES

Reimagine possible.

For questions contact:
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