Wave Life Sciences

Corporate Presentation

March 6, 2024

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

AATD (RNA editing), DMD (splicing), and HD (antisense) clinical programs advancing

INHBE program for obesity (siRNA) designed for fat loss, muscle sparing, improved metabolic profile

Multi-modal drug discovery and development platform; therapeutic candidates that optimally address disease biology

Leader in RNA editing with best-in-class oligonucleotide chemistry

In-house GMP manufacturing; Strong and broad IP portfolio

Strategic collaborations to expand and advance pipeline

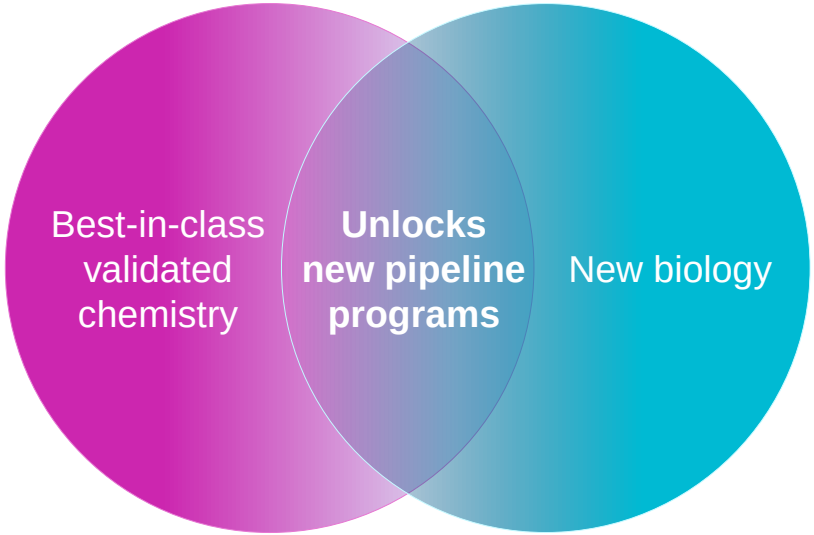
Well-capitalized with cash runway into 4Q 2025*

Anticipated Upcoming Milestones

- Proof-of-mechanism data from RestorAATion clinical program of WVE-006 for AATD in 2024
- Initiate clinical trial of INHBE candidate for obesity in 1Q 2025
- Data from FORWARD-53 clinical trial of WVE-N531 for DMD in 3Q 2024
- Data from SELECT-HD clinical trial of WVE-003 for HD in 2Q 2024

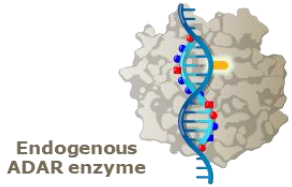
*Cash runway does not include potential future milestones or opt-in payments under GSK and Takeda collaborations

Combining best-in-class chemistry with novel biology and genetic insights: Opportunities for new high-impact medicines

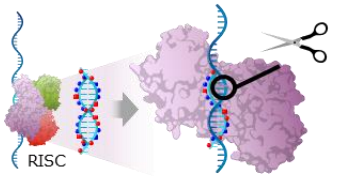


- Accessing new endogenous enzymes for novel modalities (RNA editing)
- Opening up new targets, including prevalent diseases

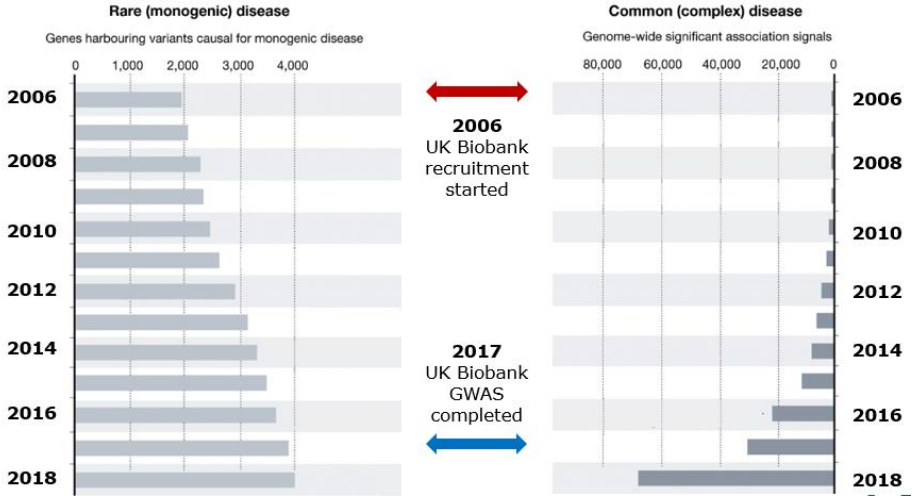
Wave's versatile RNA medicines platform ideal for capitalizing on new genetic insights in rare and common diseases

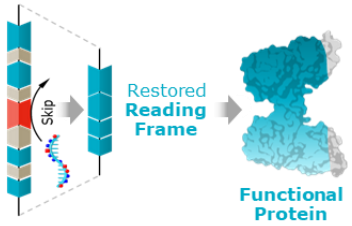


editing

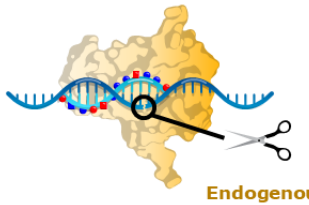


siRNA silencing





splicing



antisense silencing

Accessing UK Biobank and building proprietary machine learning models to generate unique genetic insights

Claussnitzer, et al. Nature (2020) 577, 179; King et al. PLoS Genet (2019) 15, e1008489

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

Program	Discovery / Preclinical	IND / CTA Enabling Studies	Clinical	Rights	Patient population (US & Europe)
RNA EDITING					
WVE-006 SERPINA1 (AATD)	RestorAATion Clinical Program			GSK exclusive global license	200K
Multiple undisclosed Correction				100% global	>20K (multiple)
Multiple undisclosed Upregulation				100% global	>3M (multiple)
SILENCING: siRNA					
INHBE lead clinical candidate (Obesity and other metabolic disorders)				100% global	47M
SPLICING					
WVE-N531 Exon 53 (DMD)	FORWARD-53 Trial (Phase 2)			100% global	2.3K
Other exons (DMD)				100% global	Up to 18K
SILENCING: ANTISENSE					
WVE-003 mHTT (HD)	SELECT-HD Trial (Phase 1b/2a)			Takeda 50:50 Option	25K Manifest (SNP3) 60K Pre-Manifest (SNP3)

Editing for correction Editing for upregulation

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AATD: Alpha-1 antitrypsin deficiency; DMD: Duchenne muscular dystrophy; HD: Huntington's disease

Strategic collaboration with GSK to develop transformative RNA medicines

Collaboration Highlights

- $170 million upfront[1]
- Additional research funding
- Potential for up to $3.3 billion in milestones[2]
- Leverage GSK's expertise in genetics and genomics

	Maximize global potential for WVE-006 for AATD	Advance up to eight GSK collaboration programs	Expand Wave's pipeline
	Up to $505 million in additional milestones and **tiered royalties on net sales**	**Up to $2.8 billion** in total milestones and **tiered royalties on net sales**	Wave to advance up to **three wholly owned collaboration programs** (or more with GSK's consent)[3]
Recent Highlights	✓ **$20 million milestone** achieved with first individual dosing in 4Q 2023	✓ Advancing work on **multiple targets spanning multiple modalities** beyond RNA editing, including siRNA	✓ **INHBE is Wave's first wholly owned program** emerging from GSK collaboration

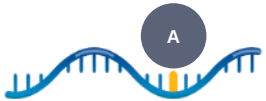
1. $120 million in cash and $50 million equity investment received in January 2023, 2. Initiation, development, launch, and commercialization milestones for WVE-006 and programs progressed during initial 4-year research term (8 GSK collaboration programs), 3. GSK eligible to receive tiered royalty payments and commercial milestones from Wave

WVE-006 (RNA editing)

AATD

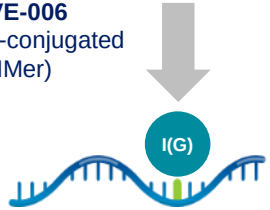
WVE-006: Designed to correct mutant SERPINA1 transcript to address both liver and lung manifestations of AATD

WVE-006 for AATD



SERPINA1 Z allele mRNA encodes Z-AAT protein with E342K mutation

WVE-006
(GalNAc-conjugated AIMer)



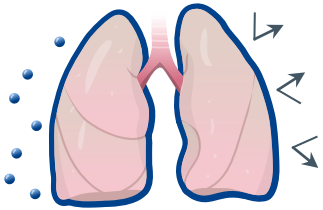
Edited *SERPINA1* mRNA enables wild-type M-AAT protein production

WVE-006 ADAR editing approach to address key goals of AATD treatment:

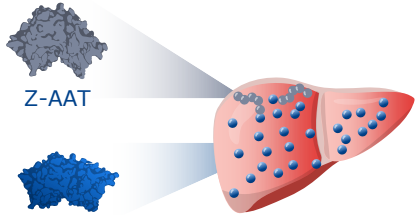
1) Restore circulating, functional wild-type M-AAT

2) Reduce Z-AAT protein aggregation in liver

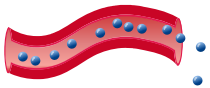
3) Retain M-AAT physiological regulation



M-AAT reaches lungs to protect from proteases



RNA correction replaces mutant Z-AAT protein with wild-type M-AAT protein



M-AAT secretion into bloodstream

200,000 Pi*ZZ patients in US and Europe

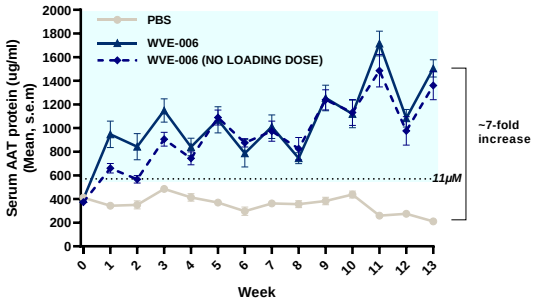
AAT: Alpha-1 antitrypsin Strnad et al., 2020 N Engl J Med 382:1443-55; Blanco et al., 2017 Int J Chron Obstruct Pulmon Dis 12:561-69; Remih et al., 2021 Curr Opin Pharmacol 59:149-56.

WVE-006 in AATD: First-in-class RNA editing clinical candidate

Potentially comprehensive approach to address both lung and liver manifestations of AATD

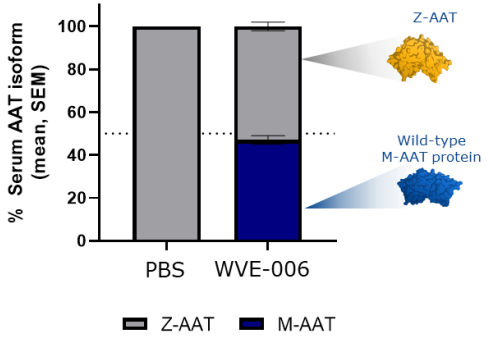
Increased AAT protein in NSG-PiZ mice

WVE-006 treatment results in serum AAT protein levels of up to 30 uM in NSG-PiZ mice



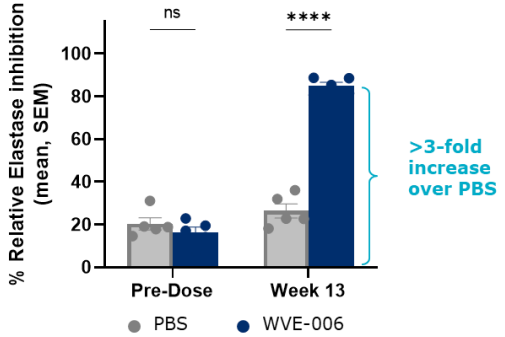
Confirmed restored wild-type M-AAT protein

Overall percentages of serum AAT protein isoforms in NSG-PiZ mice (Week 13)



Demonstrated functionality of M-AAT protein

Serum neutrophil elastase inhibition activity in NSG-PiZ mice



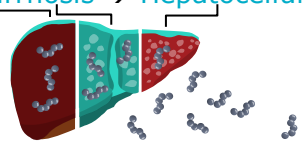
≥50% editing supports restoration of MZ phenotype

AATD: Alpha-1 antitrypsin deficiency; M-AAT protein: wild-type AAT protein; WVE-006 administered subcutaneously (10 mg/kg bi-weekly) in 7-week old NSG-PiZ mice (n=5 per group); Loading dose: 3 x 10 mg/kg at Day 0. Left: Liver biopsies collected at wk 13 (1 wk after last dose) and SERPINA1 editing quantified by Sanger sequencing; Right: Total serum AAT protein quantified by ELISA; Stats: Two-Way ANOVA with adjustment for multiple comparisons (Tukey)

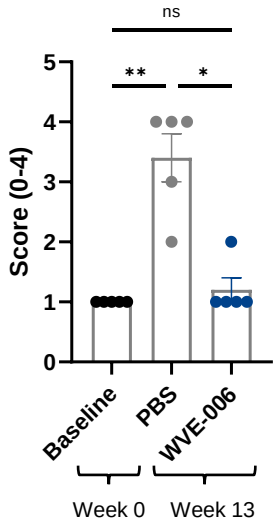
WVE-006 decreases lobular inflammation and PAS-D globule size, prevents increase in hepatocyte turnover

Correction of gain-of-function liver phenotypes

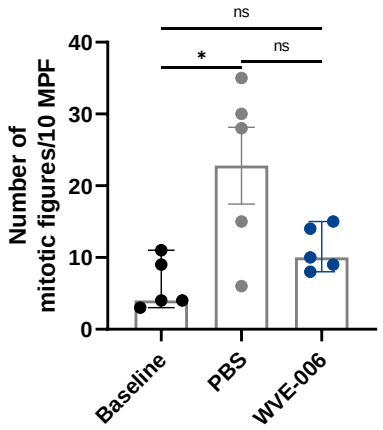
Fibrosis → Cirrhosis → Hepatocellular Carcinoma



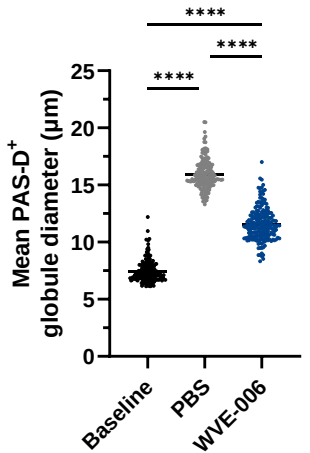
Lobular inflammation
(NSG PiZ mice, week 13)



Mitoses
(NSG PiZ mice, week 13)



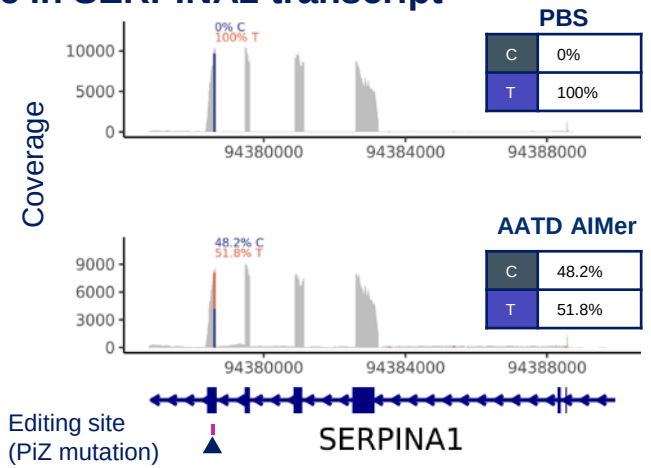
PAS-D-positive globule size
(NSG PiZ mice, week 13)



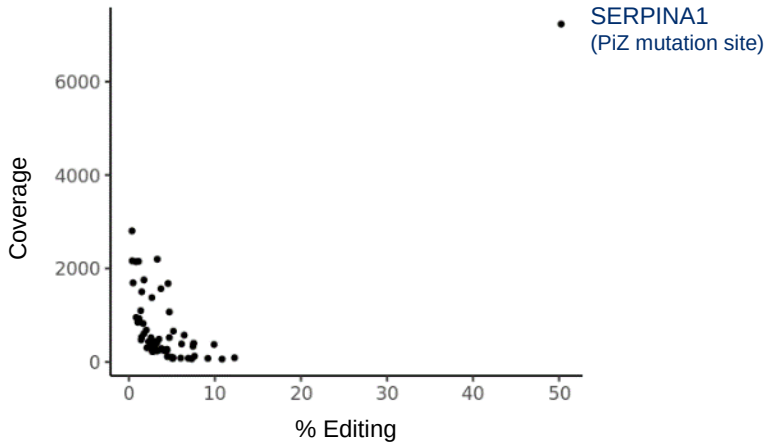
Left (Lobular inflammation) and Middle (Mitoses): Scatter plot showing inflammation grade or mitoses score. Each circle represents an individual mouse, (Mean ± SEM); Right (PAS-D Globule Size): 40 largest globules in each of 5 mice were measured. Each circle represents a single PAS-D globule, (Mean ± SEM). Baseline: week 0 (7 weeks old); Treated week 13 (20 weeks old); Stats: Kruskal-Wallis followed by Dunn's test

AIMer-directed editing is highly specific in mice

RNA editing only detected at PiZ mutation site in SERPINA1 transcript



RNA editing across transcriptome



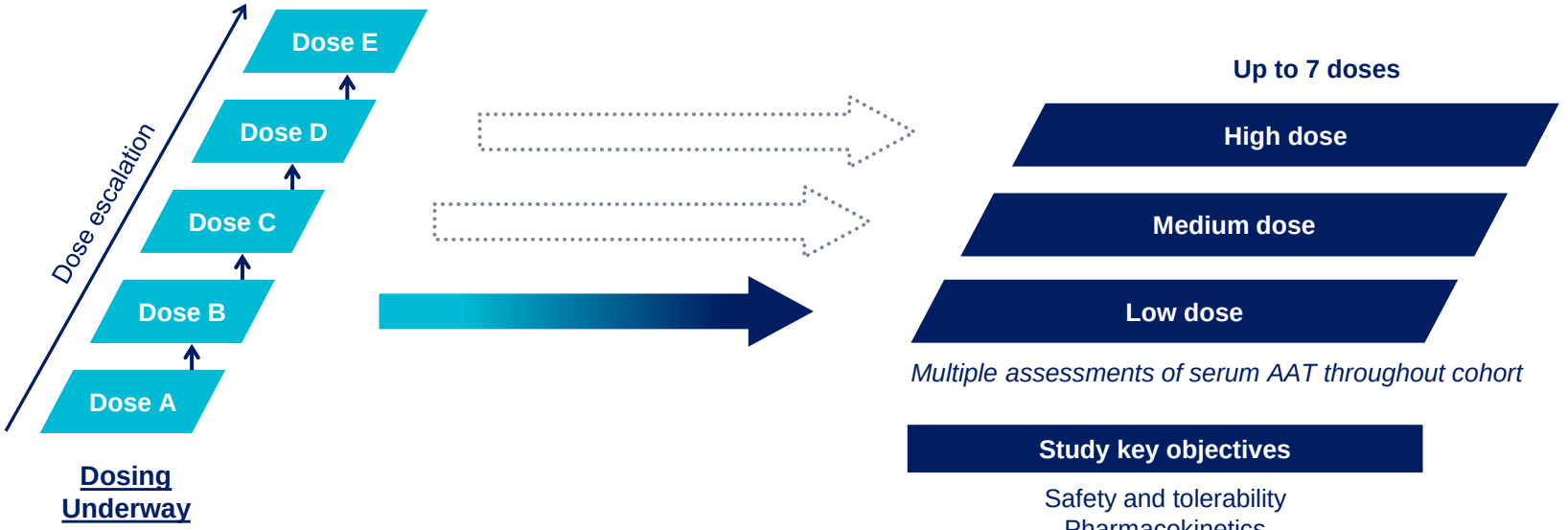
No bystander editing observed on SERPINA1 transcript

Dose 3x10 mg/kg (days 0, 2, 4) SC with AATD AIMer (SA1 – 4). Liver biopsies day 7. RNA-seq to quantify on-target SERPINA1 editing, to quantify off-target editing reads mapped to entire mouse genome; plotted circles represent sites with LOD>3 (N=4), SERPINA1 edit site is indicated

Proof-of-mechanism data from RestorAATion-2 expected in 2024

RestorAATion-1: Healthy Volunteers → Informs dose & dose frequency → **RestorAATion-2: AATD Patients**

SAD → MAD cohorts



HV: healthy volunteer; SAD: single-ascending dose; MAD: multi-ascending dose

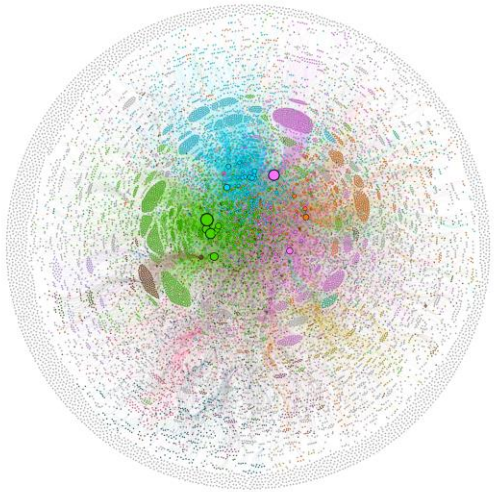
AIMers

RNA editing capability

The AIMer-targetable ‘Edit-Verse’ is substantial

- **The Edit-verse is the editable gene-disease universe, including upregulation**
- **>13,000 genes** with a high-probability[1] of being amenable to transcriptional regulation with A-to-G editing
- Model development ongoing to expand access to **more protein-coding genes** and expand the Edit-verse
- AIMers are expected to be able to target ~50% of the transcriptome

Gene-Disease Network



[1](score >95th p-tile)

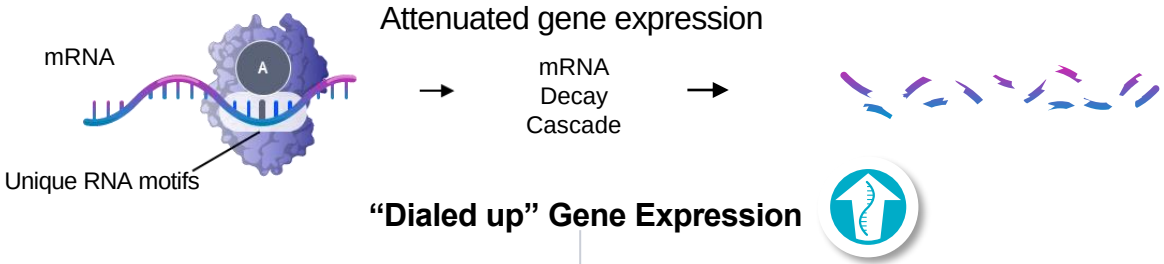
Innovating on applications of ADAR beyond restoring protein function

Restore or correct protein function

- Correct G-to-A driver mutations with AIMers

WVE-006
(GalNAc-AIMer)
AATD

Upregulate expression to increase endogenous protein activity



Multiple RNA editing opportunities to build high-value pipeline beyond WVE-006

Potential to advance any combination of targets into preclinical development

	Hepatic (GalNAc-AIMers)				Extra-Hepatic (AIMers)	
	Target A	**Target B**	**Target X**	**Target E**	**Target F**	**Target G**
Approach	Upregulation	Upregulation	Upregulation	Correction	Upregulation	Correction
Tissue	Liver	Liver	Liver	Liver	Kidney	Lung
Therapeutic Area	Metabolic	Metabolic	Renal	Rare	Renal	Rare
Estimated Patients (US and Europe)	~90M	~3M	~170K	~17K	~85K	~5K

- The Edit-verse is substantial and still expanding
- Advancing work for a diverse set of undisclosed targets addressing areas of high unmet need, including both rare and prevalent diseases

INHBE program (siRNA silencing)

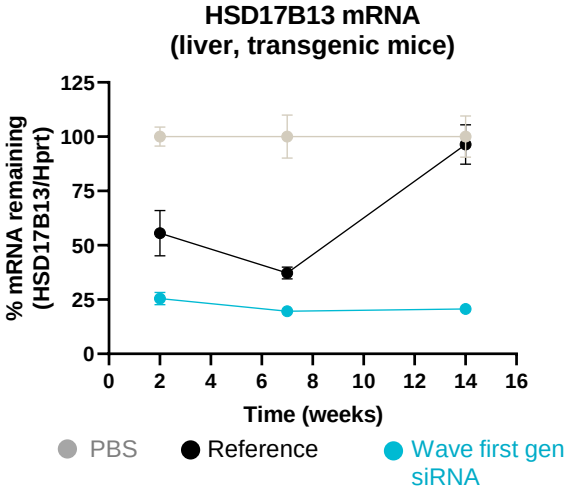
Obesity and other metabolic disorders

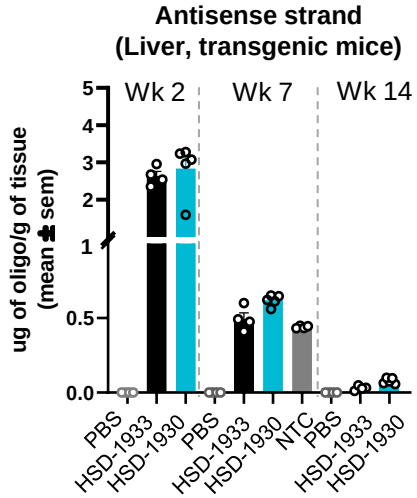
Potential for best-in-class siRNA enabled by Wave's PRISM platform

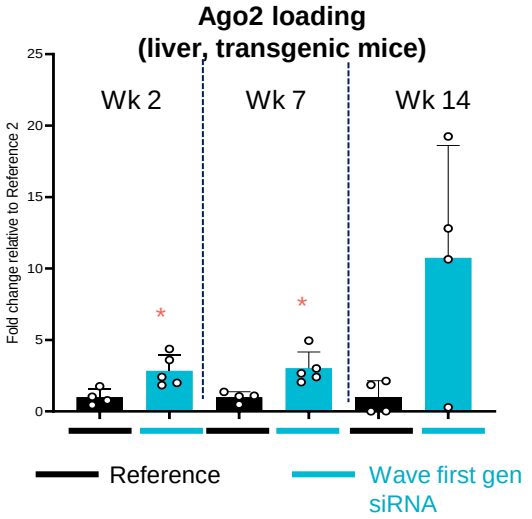
Nucleic Acids Research

Impact of stereopure chimeric backbone chemistries on the potency and durability of gene silencing by RNA interference

- Unprecedented Ago2 loading increases potency and durability of silencing following administration of single subcutaneous dose







siRNA silencing is one of multiple Wave modalities being advanced in strategic research collaboration with GSK

Left, Middle, and right: Mice expressing human HSD17B13 transgene treated with siRNA (3 mg/kg) or PBS, liver mRNA, guide strand concentration, Ago2 loading quantified. Stats: Two-way ANOVA with post-hoc test * P<0.05, ****P<0.0001. Liu et al., 2023 Nuc Acids Res doi: 10.1093/nar/gkad268;

Driven by clinical genetics, Wave's first RNAi program addresses high unmet need in obesity

INHBE program (GalNAc-siRNA) is Wave's first wholly owned program to emerge from GSK collaboration

GLP-1 receptor agonists have several reported limitations

- × Lead to weight loss at the expense of muscle mass[1]
- × Associated with poor tolerability profile[4] with 68% drop-off after 1 year[3]
- × Discontinuation of therapy leads to rapid weight regain
- × Suppress general reward system[4]

Wave's INHBE siRNA program may address these limitations and / or work synergistically with GLP-1s

INHBE silencing expected to induce fat loss, while maintaining muscle mass

- siRNA to silence INHBE gene is expected to recapitulate the healthy metabolic profile of INHBE loss of function (LoF) heterozygous human carriers, including:[1,2,3]
  - ✓ Reduced waist-to-hip ratio
  - ✓ Reduced odds ratio of type 2 diabetes and coronary artery disease by >25%
  - ✓ Reduced serum triglycerides
  - ✓ Elevated HDL-c
- INHBE expressed primarily in liver and gene product (activin E) acts on its receptor in adipose tissue[4]
- Lowering of INHBE mRNA or blocking of its receptor promotes fat burning (lipolysis) and decreases fat accumulation (adiposity)[5,6]

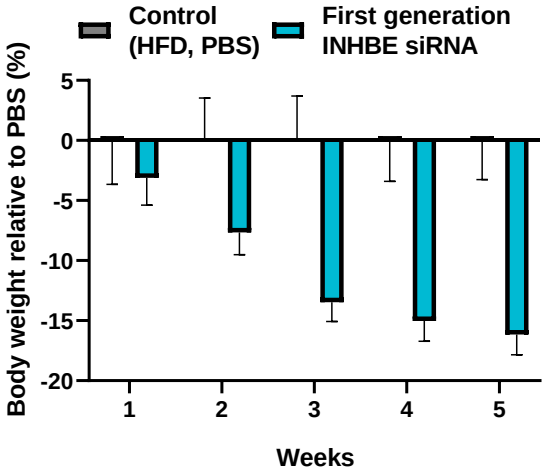
≥50% reduction of INHBE in patients expected to restore and maintain a healthy metabolic profile

1. Sargeant, et al. 2019 Endocrinol Metab (Seoul) 34(3):247-262; 2. Prime Therapeutics Claims Analysis, July 2023; 3. Müller, et al. 2019 Molecular Metabolism 30: 72-130.

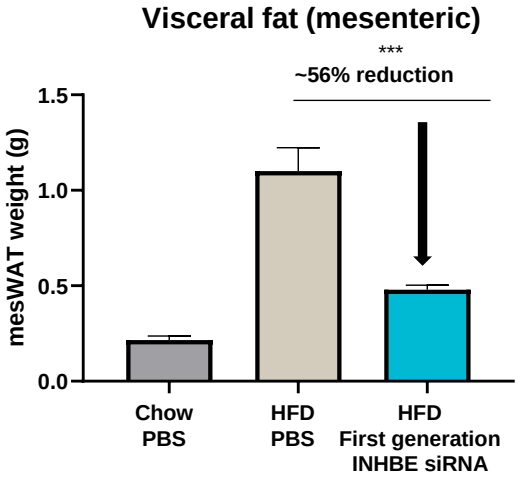
1. Nat Commun 2022. https://doi.org/10.1038/s41467-022-32398-7; 2. Nat Commun 2022. https://doi.org/10.1038/s41467-022-31757-8; 3. PLOS ONE 2018. https://doi.org/10.1371/journal.pone.0194798; 4. Adam, RC. et.al. Proc Natl Acad Sci USA. 2023, 120(32): e2309967120. 5. Yogosawa et al. 2013 https://www.ncbi.nlm.nih.gov/pmc/articles/PMC3526038/ 6. Zhao et al. 2023 https://pubmed.ncbi.nlm.nih.gov/36626233/

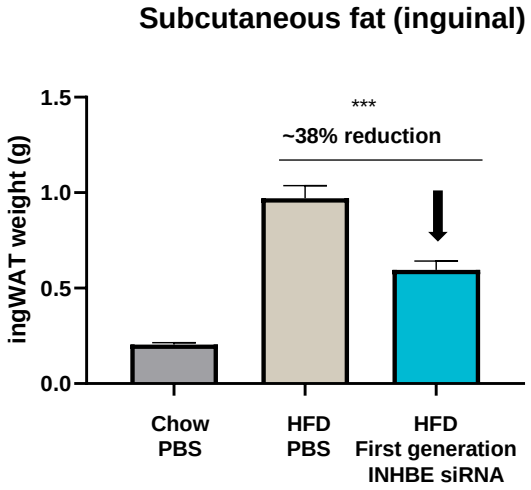
First generation INHBE GalNAc-siRNA led to lower body weight and significant decrease in visceral fat in DIO mouse model

Lower body weight as compared to control



Reduction in fat mass across multiple types of white adipose tissue, with preferential effect on visceral fat reduction



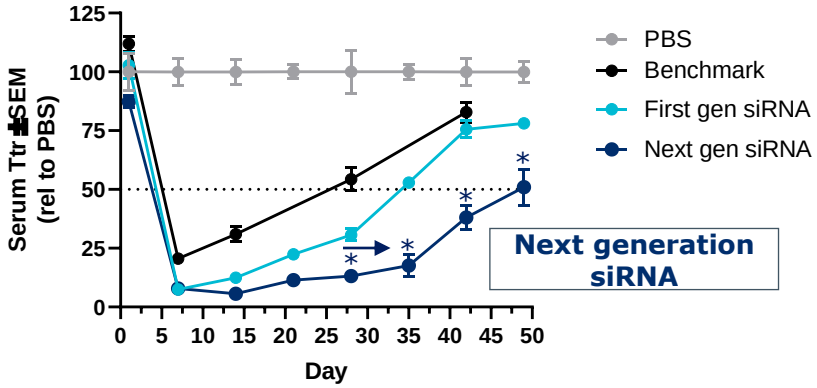


Results of *in vivo* preclinical study are consistent with UK Biobank human data on loss-of-function carriers

Right: Reduction in fat mass at Week 5

INHBE lead clinical candidate has Wave's next generation siRNA format and best-in-class profile

Next generation siRNA results in more potent and durable target knockdown



INHBE program: Data from DIO mouse model supports best-in-class profile

- ✓ Highly potent silencing (ED50 < 1mg/kg)
- ✓ Durable silencing following one, low-single-digit dose, supporting every-six-month or annual dosing
- ✓ Weight loss with no loss of muscle mass
- ✓ Reduction in fat mass, with preferential effect to the visceral fat

Expect to initiate clinical trial for INHBE candidate in 1Q 2025

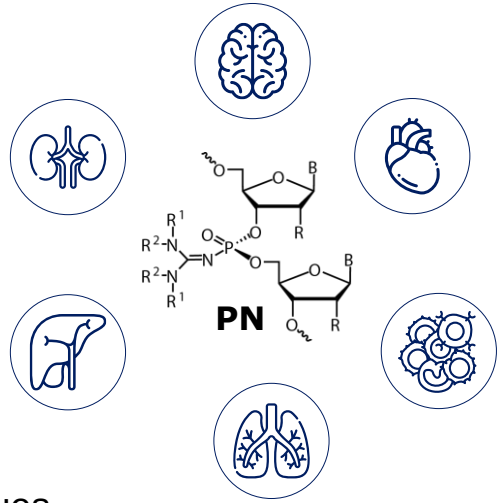
WAVE LIFE SCIENCES

Foster, DJ. et.al. Mol Ther. 2018, 26(3), 708. B6 mice administered PBS or 0.5 mg/kg of siRNA (subcutaneous). Benchmark: Stats: Mixed Two-way ANOVA followed by post hoc test comparing siRNA vs. Next gen siRNA per day derived from linear mixed effects model * P < 0.0001

Wave's platform chemistry enables siRNA extra-hepatic delivery

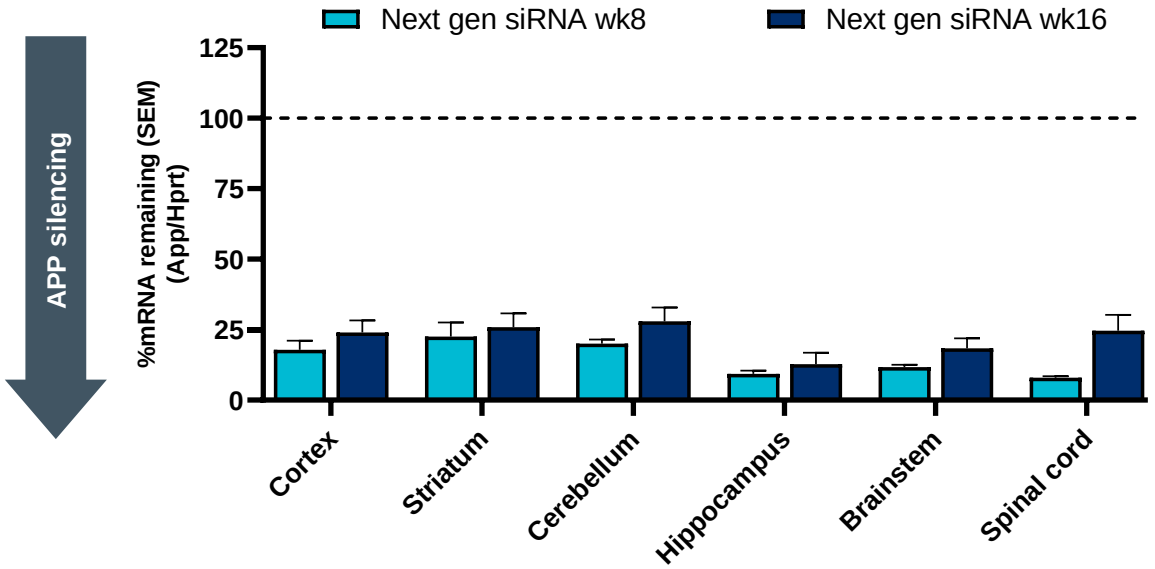
- Chemical impact
  - Introduction of neutral backbone
  - Unique structural feature of PN, specifically guanidine
  - Increased lipophilicity
  - Stereochemistry

- Extra-hepatic delivery
  - Titrating siRNA lipophilicity tunable PNs (PN variants)
  - Maintaining high Ago2 loading and intracellular trafficking
  - Titrating plasma protein binding
  - Altered delivery, enhanced potency and durability in various tissues

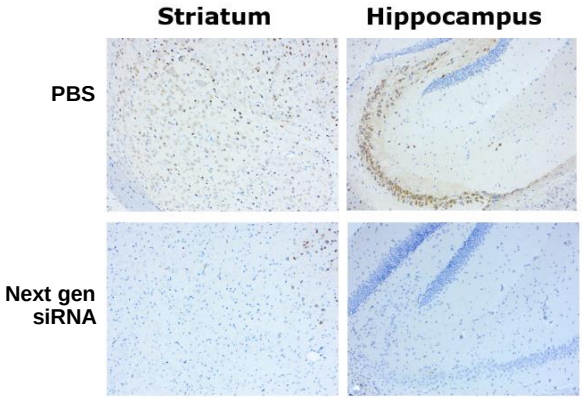


PN can tune extra-hepatic delivery of siRNA using rational design, including placement, number of modifications and PN variants

Single dose of next generation siRNA delivers broad, potent and durable CNS target engagement



Robust target engagement translates to substantial App protein reduction across brain regions 8-weeks post single dose



Sustained APP knockdown of at least 75% throughout the 16-week study *in vivo* in mice

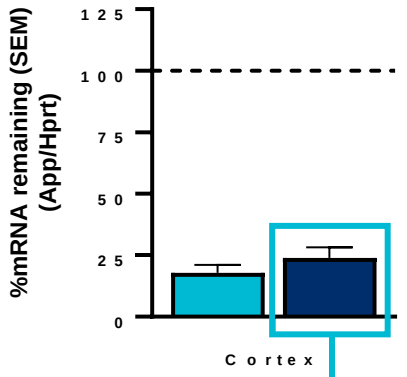
PBS (dotted line) or 100 µg of App siRNA administered ICV (n=7). PCR assays for RNA PD, relative fold changes of *App* to *Hprt* mRNA normalized to % of PBS; Stats: Three-way ANOVA followed by Bonferroni-adjusted post hoc test comparing condition to PBS (data not shown), Next gen siRNA significantly lower than PBS at both time points for all tissues at P < 0.0001 level; Immunohistochemical analysis of FFPE Mouse Brain tissue labeling App protein (Color Brown) with CS#19389 followed by a ready to use Polymer-HRP 2nd Detection antibody. Nuclei were counterstained with Hematoxylin (Color Blue). Single 100 ug ICV injection

Wave siRNA demonstrates more potent and durable silencing as compared to published state-of-the-art

Wave (APP – Cortex)

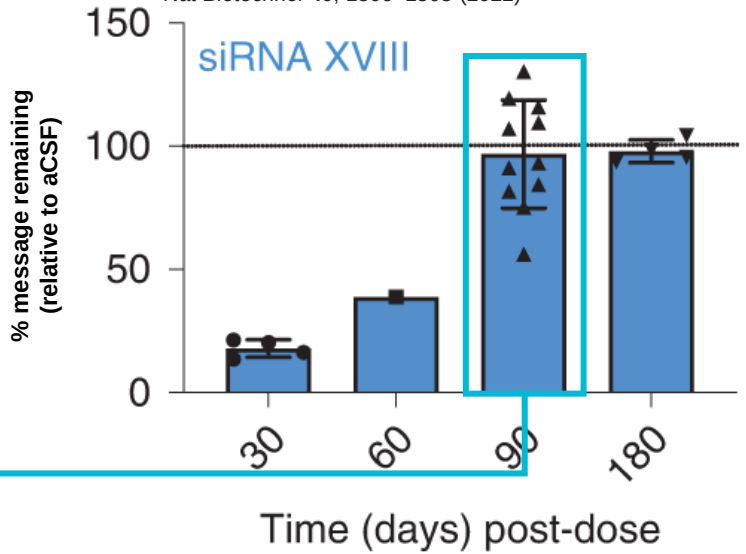
Single dose 100 µg by ICV

Knockdown > 112 days post-dose



Alnylam (APP – Cortex)

Nat Biotechnol **40**, 1500–1508 (2022)



Single dose 120 µg by ICV

Knockdown < 90 days post-dose

Wave next generation siRNA Week 8 (Day 56)

Wave next generation siRNA Week 16 (Day 112)

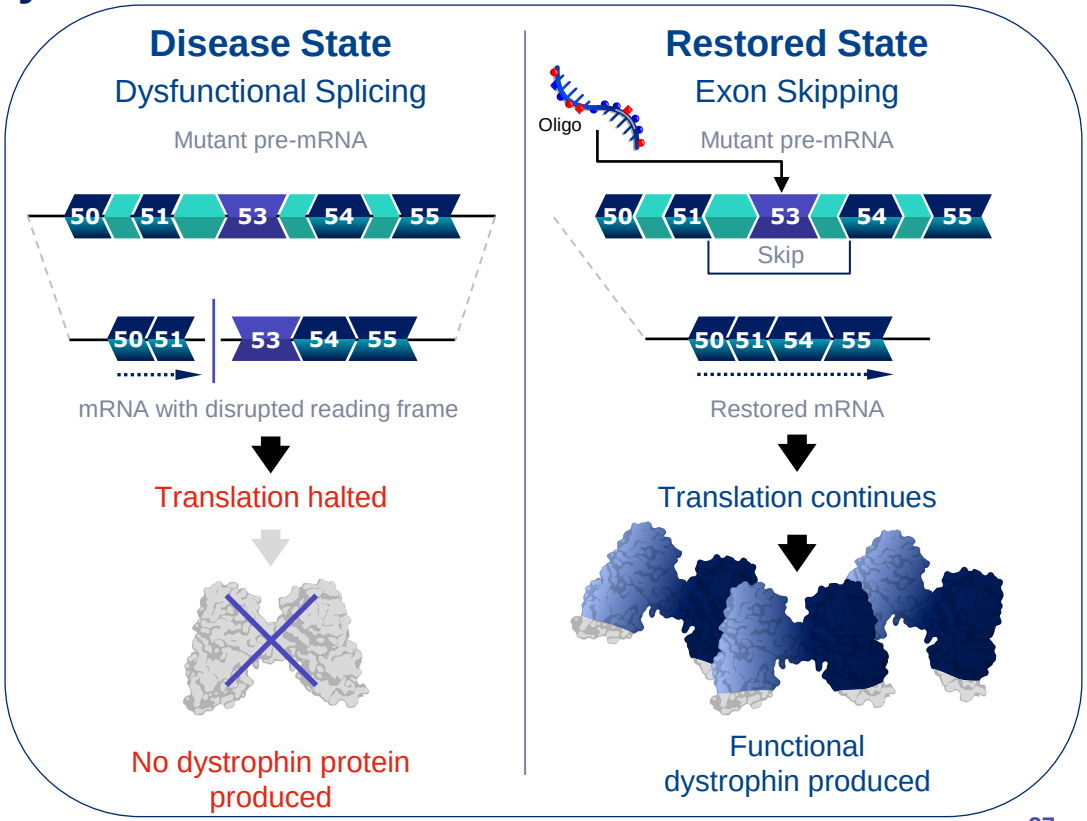
PBS (dotted line) or 100 µg of App siRNA administered ICV (n=7). PCR assays for RNA PD, relative fold changes of App to Hprt mRNA normalized to % of PBS; Stats: Three-way ANOVA followed by Bonferroni-adjusted post hoc test comparing condition to PBS (data not shown), Next gen siRNA significantly lower than PBS at both time points for all tissues at P < 0.0001 level. Source: Brown, K.M., Nair, J.K., Janas, M.M. et al. Expanding RNAi therapeutics to extrahepatic tissues with lipophilic conjugates. Nat Biotechnol 40, 1500–1508 (2022).

WVE-N531 (splicing)

Duchenne muscular dystrophy

Duchenne muscular dystrophy

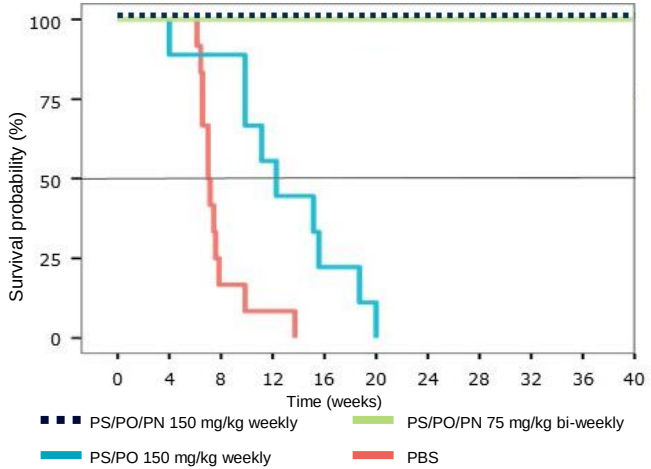
- **Genetic mutation in dystrophin gene prevents the production of dystrophin protein**, a critical component of healthy muscle function
- **Impacts approx. 1 in every 5,000 newborn boys each year**; approx. 20,000 new cases annually worldwide
  - Approx. 8-10% are amenable to exon 53 skipping
- **Dystrophin protein established by FDA as surrogate endpoint** reasonably likely to predict benefit in boys[1] for accelerated approval in DMD
- Increasing amount of functional dystrophin expression over minimal amount shown with approved therapies is expected to result in greater benefit for boys with DMD



[1]Vyondys: www.fda.gov; viltepso; www.fda.gov; Exondys; www.fda.gov; Amondys: www.fda.gov

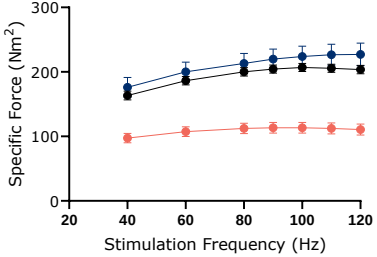
Extended survival in dKO preclinical model supports potential of Wave's PN-modified exon-skipping therapeutics for DMD

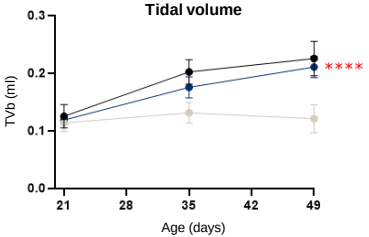
100% survival at time of study termination

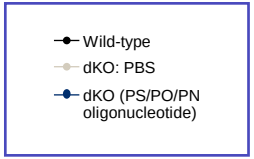


Note: Untreated, age-matched mdx mice had 100% survival at study termination [not shown]

Restored muscle and respiratory function to wild-type levels





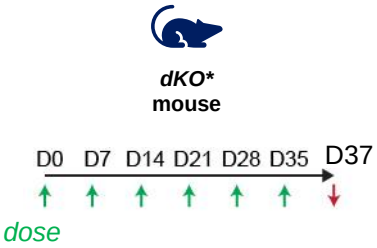


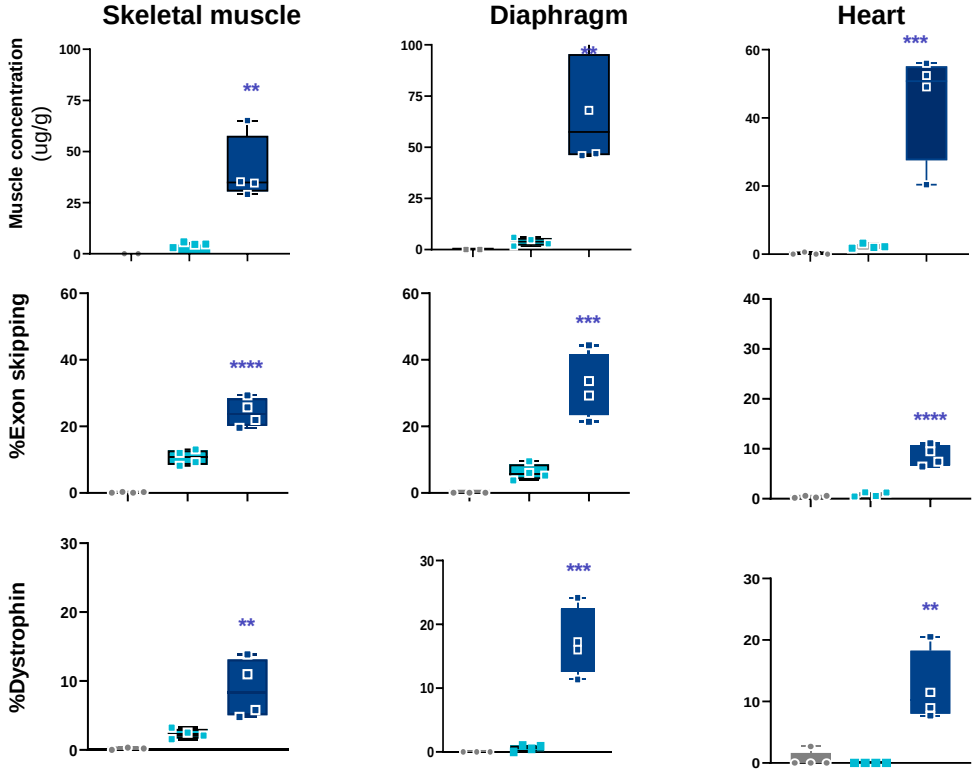
PN chemistry improved function and survival in dKO mice

Kandasamy et al., 2022; doi: 10.1093/nar/gkac018
dKO: double knock-out

Wave's PN chemistry yields excellent muscle exposure, exon skipping and dystrophin protein expression in *dKO* mouse model

- PBS
- PS/PO modified oligonucleotides for mouse exon 23
- PS/PO/PN modified oligonucleotides for mouse exon 23

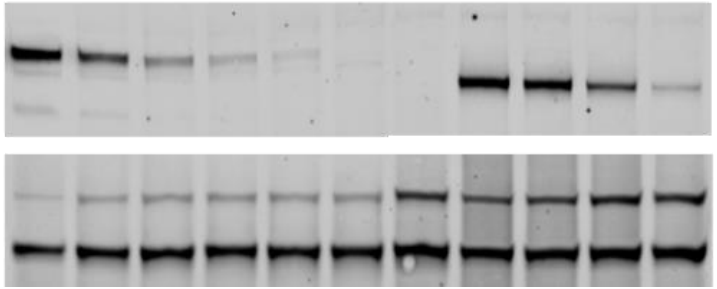




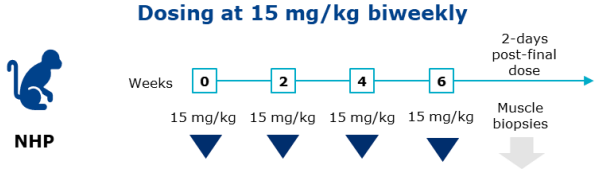
Preclinical data supported advancing WVE-N531 to clinical development

WVE-N531: Dystrophin restoration of up to 71% *in vitro* in patient-derived myoblasts

Standard Curve (% WT lysate in D45-52 lysate)						D45-52 Cells				
						Mock	WVE-N531			
						0	10	3.3	1.1	0.3
100%	50%	25%	12%	6%	0%	0%	71%	65%	37%	9.5%



WVE-N531 reached high concentrations in heart and diaphragm in NHP



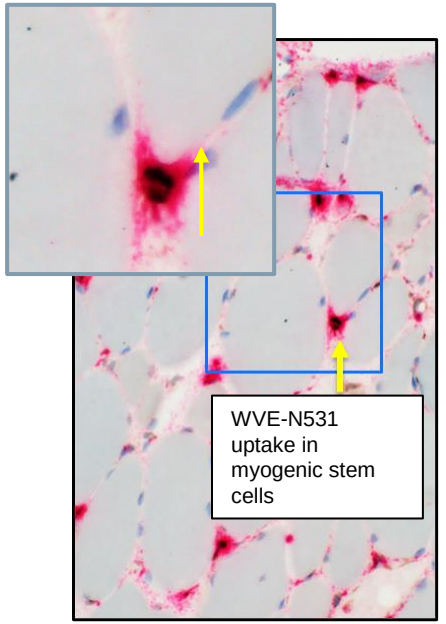
	Mean Tissue Concentration		
	Skeletal muscle	Diaphragm	Heart
15 mg/kg* IV dose	2.17 ug/g	10.8 ug/g	57.2 ug/g

*approximately equivalent to 10 mg/kg in patients based on plasma AUC values

Clinical data from WVE-N531 Part A: High exon-skipping & muscle concentrations after three doses every other week

	suvodirsen	WVE-N531
Mean muscle concentration	0.7 µg/g (700 ng/g)	**42 µg/g (42,000 ng/g)[1]**
Mean exon skipping	Not detectable	**53%**
Half-life in plasma	18 hours	**25 days**
Dose	22 weekly doses of 5 mg/kg	**3 doses of 10 mg/kg every other week**

WVE-N531 uptake in myocyte stem cells



Important for potential muscle regeneration

1: 42 µg/g = 6.1 µM (6,100 nM), WVE-N531 data presented March 22, 2023 at Muscular Dystrophy Association Clinical and Scientific Conference; WVE-N531 biopsies collected ~2 weeks post-last dose (3 biweekly doses of 10 mg/kg); Suvodirsen biopsies collected post-last dose (weekly doses of 5 mg/kg) on week 22; Half-life as indicated by PK analysis; suvodirsen: discontinued first-generation non-PN chemistry compound; Right: Dual staining utilizing in-situ hybridization for WVE-N531 and PAX7 immunohistochemistry for stem cells. Suvodirsen N= 8; WVE-N531 N=3 boys

Dosing underway in FORWARD-53, a potentially registrational Phase 2 clinical trial of WVE-N531 in DMD (Exon 53)

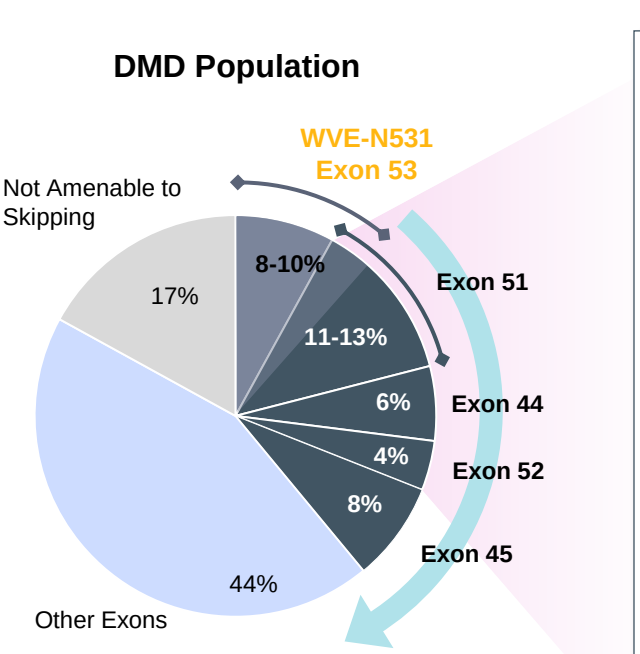
- Design of FORWARD-53: Phase 2, open-label, 10 mg/kg every other week
- Endpoints: Dystrophin (powered for >5% of normal), safety/tolerability, pharmacokinetics, digital and functional assessments (incl. NSAA and others)
- Muscle biopsies to assess dystrophin expression
- Fully enrolled (n=11) and dosing underway

FORWARD-53

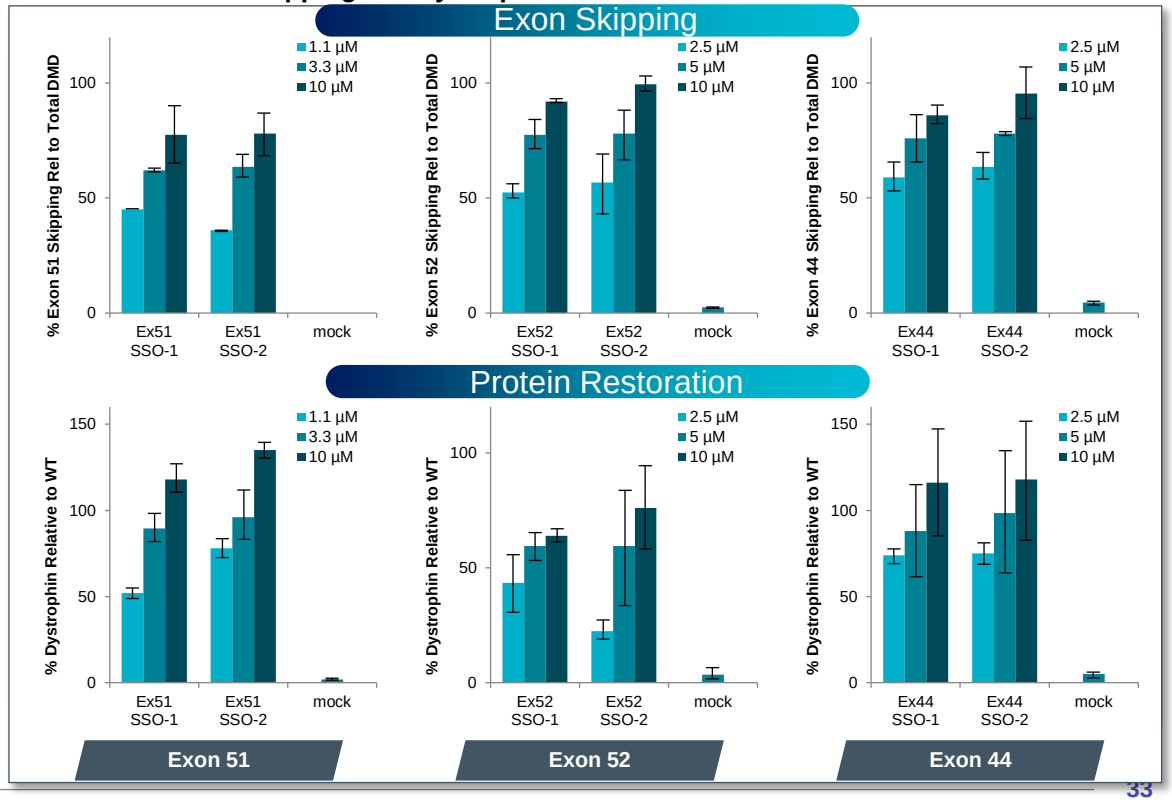
Potentially registrational 24-week dystrophin expression data are expected in 3Q 2024

IV: intravenous; NSAA: North star ambulatory assessment

Potential for Wave to address up to 40% of DMD population



Exon skipping and dystrophin restoration demonstrated *in vitro*



Left: Aartsma-Rus, et al. 2009 Hum Mutat 30, 293.

WVE-003 (antisense silencing)

Huntington’s Disease

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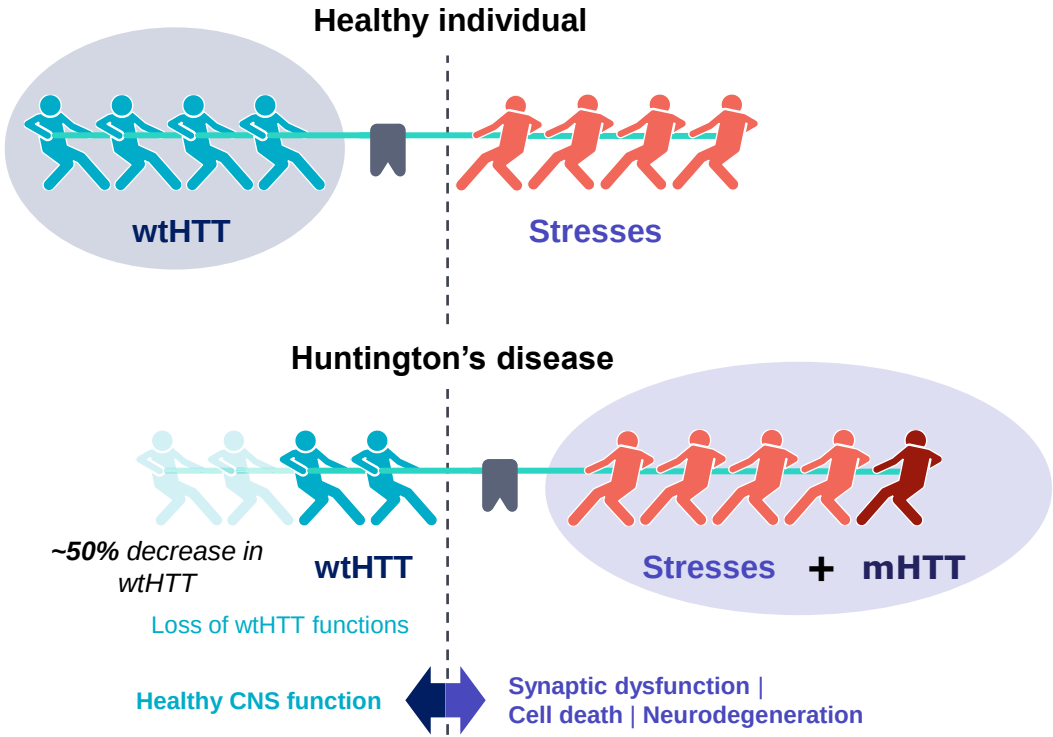
mHTT toxic effects lead to neurodegeneration; loss of wtHTT functions may also contribute to HD

Huntington's disease (HD)

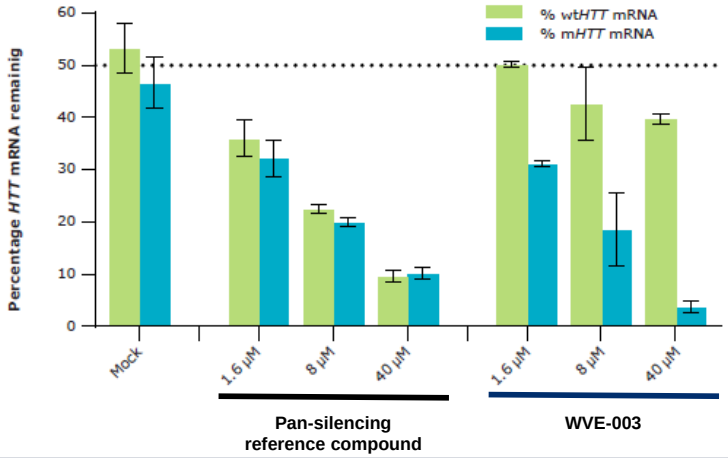
- Wild-type HTT (wtHTT) is critical for normal neuronal function[1]
- Expanded CAG triplet repeat in HTT gene results in production of mutant huntingtin protein (mHTT)
- HD is a monogenic autosomal dominant genetic disease; fully penetrant and affects entire brain
- Fatal disease characterized by cognitive decline, psychiatric illness, and chorea
- 30,000 people with HD in the US and more than 200,000 at risk of developing HD



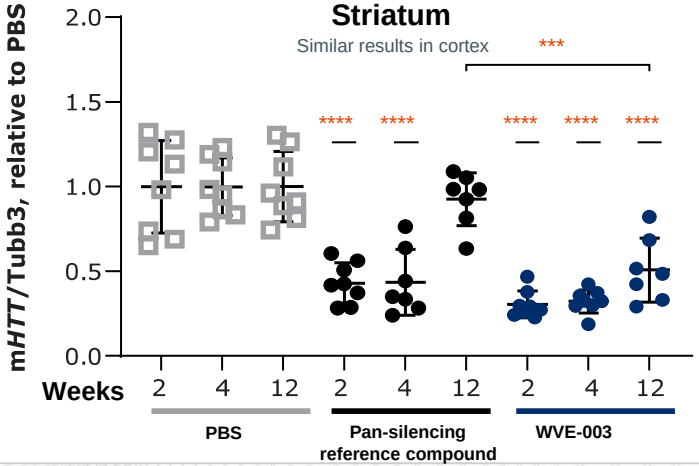
1 – Sources on wtHTT: 1. Leavitt 2006 2. Cattaneo 2005 3. Kumar 2016 4. Franco-Iborra 2020 5. Hamilton 2015 6. Ochaba 2014 7. Wong 2014 8. Rui 2015 9. Caviston 2007 10. Twelvetrees 2010 11. Strehlow 2007 12. Milnerwood 2010 13. Smith-Dijak 2019 14. Tousley 2019 15. Zhang 2018 16. McAdam 2020 17. Altar 1997 18. Zuccato 2001 19. Gauthier 2004 20. Ferrer 2000 21. Baquet 2004 22. Liu 2011 23. Karam 2015

WVE-003 (SNP3) demonstrates selective, potent, and durable reduction of mHTT in preclinical models

Selectively reduces mHTT mRNA in HD iPSC neurons in vitro



Durable striatal mHTT knockdown for 12 weeks in BACHD mouse model

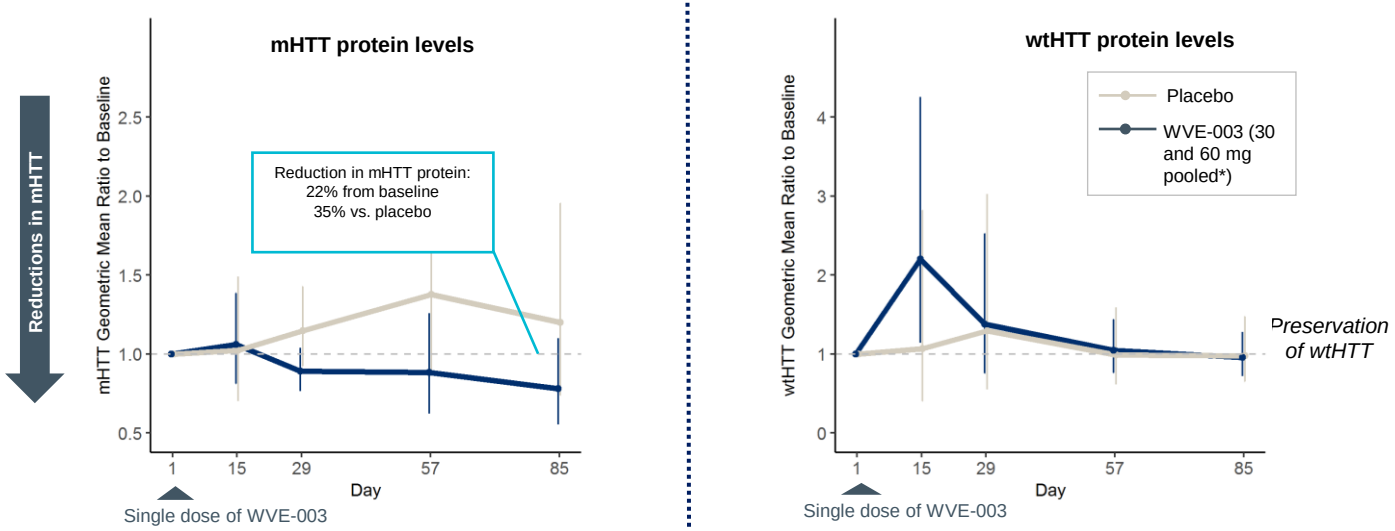


NHP study demonstrating significant tissue exposure levels of WVE-003 in deep brain regions resulted in $7 million milestone payment from Takeda in 4Q 2023

Results from ND50036 iPSC-derived medium spiny neurons. Total HTT knockdown quantified by qPCR and normalized to HPRT1. Oligonucleotide or PBS [100 µg ICV injections through cannula on days 1, 3, 5] delivered to BACHD transgenic. Mean ± SD (n=8, *P<0.0332, ***P<0.0002, ****P<0.0001 versus PBS unless otherwise noted). HPRT1, hypoxanthine-guanine phosphoribosyl transferase; iPSC, induced pluripotent stem cell; ICV, intracerebroventricular; PBS, phosphate-buffered saline

WVE-003: First-in-class allele-selective candidate for HD

Reductions in mean CSF mHTT and preservation of wtHTT observed in pooled analysis of single-dose cohorts in SELECT-HD clinical study

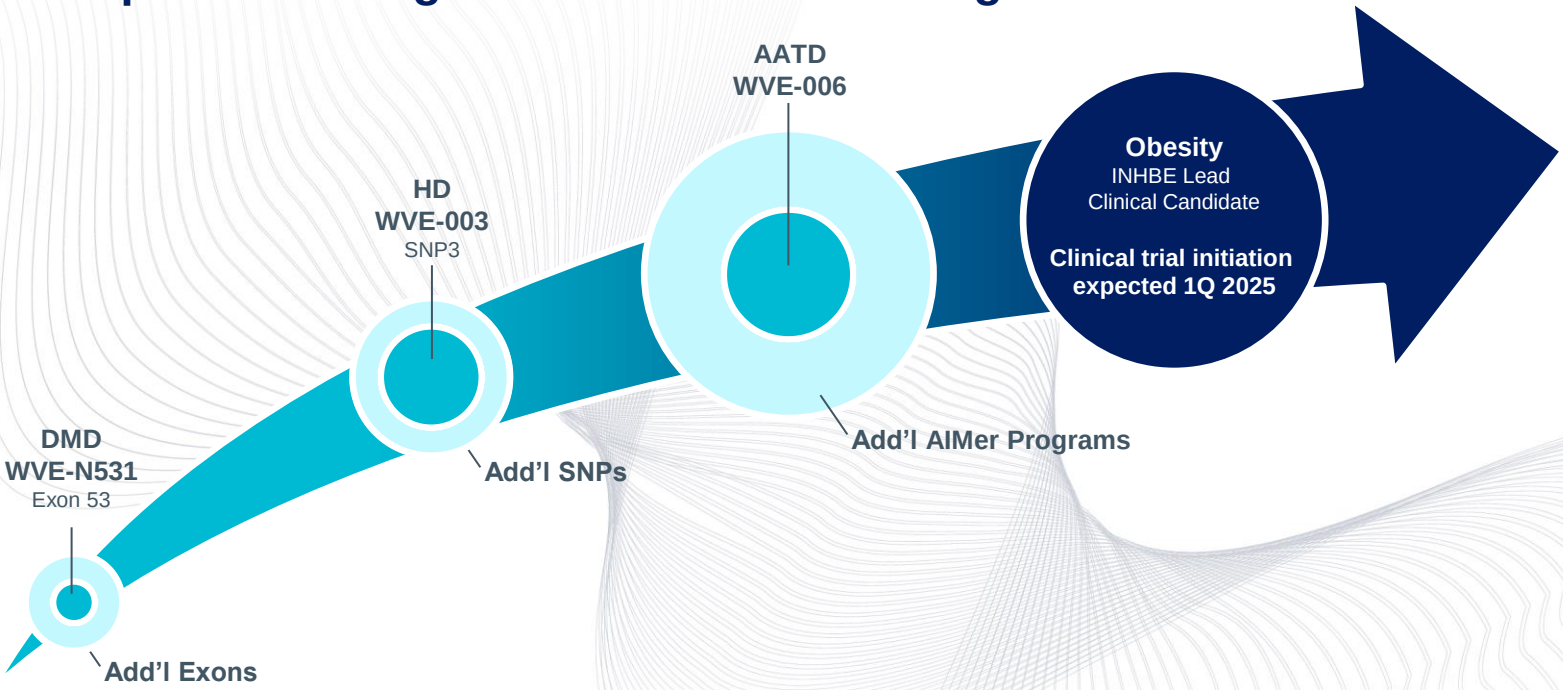


Data from 30 mg multi-dose cohort with extended follow-up, along with all single-dose data, expected 2Q 2024

mHTT: mutant huntingtin protein; wtHTT: wild-type huntingtin protein
*Pooled considering no apparent dose response between 2 single-dose cohorts; Data cut-off: August 29, 2022

Anticipated upcoming milestones

Wave is poised for significant and sustained growth



Clinical data in 2024 and advancement of INHBE candidate unlock potential to address > 50M patients in US and Europe

Note: Bubble size illustrative of size of total addressable US market (assuming 100% share of addressable patients)

Anticipated milestones in 2024 and beyond

WVE-006 (AATD) *Most advanced RNA editing candidate & potential best-in-class approach for AATD*	**2024:** Deliver proof-of-mechanism data from RestorAATion clinical program
INHBE lead clinical candidate (Obesity) *Driven by protective LoF variants in human genetics, potential next-gen therapeutic for obesity*	✓ Selected INHBE lead clinical candidate, with clinical trial application (CTA) expected as early as year-end 2024 **1Q 2025:** Initiate clinical trial for INHBE candidate
WVE-N531 (DMD) *Potential best-in-class approach with highest exon skipping reported*	**3Q 2024:** Deliver potentially registrational 24-week dystrophin expression data from FORWARD-53
WVE-003 (HD) *First-in-class mHTT lowering, wtHTT-sparing approach*	**2Q 2024:** Deliver data from 30 mg multi-dose cohort with extended follow up, along with all single-dose data

Potential for significant cash inflows in 2024 from collaboration milestones from GSK and Takeda

AATD: Alpha-1 antitrypsin deficiency; DMD: Duchenne muscular dystrophy; HD: Huntington's disease; mHTT: Mutant huntingtin; wtHTT: Wild-type huntingtin

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