

Pharmacokinetics and pharmacodynamics of EDIT-401(mu), *in vivo* gene-editing therapy for lowering LDL-C in mice

Jimit Raghav, Parth Amin, Meetu Seth, Morgan Thompson, Salvatore Iovino, James Bochicchio, Eugenio Marco, Salu Rizal, Paul Wrighton, Shreya Prajapat, Ameya Apte, Wei Zhen, Ruhong Dong, Yosif Yaqub, Stephen Pietrasiewicz, Linda Burkly, Jenny Xie, Anshul Gupta

Editas Medicine, Inc., Cambridge, MA, United States

Poster #3423

Introduction

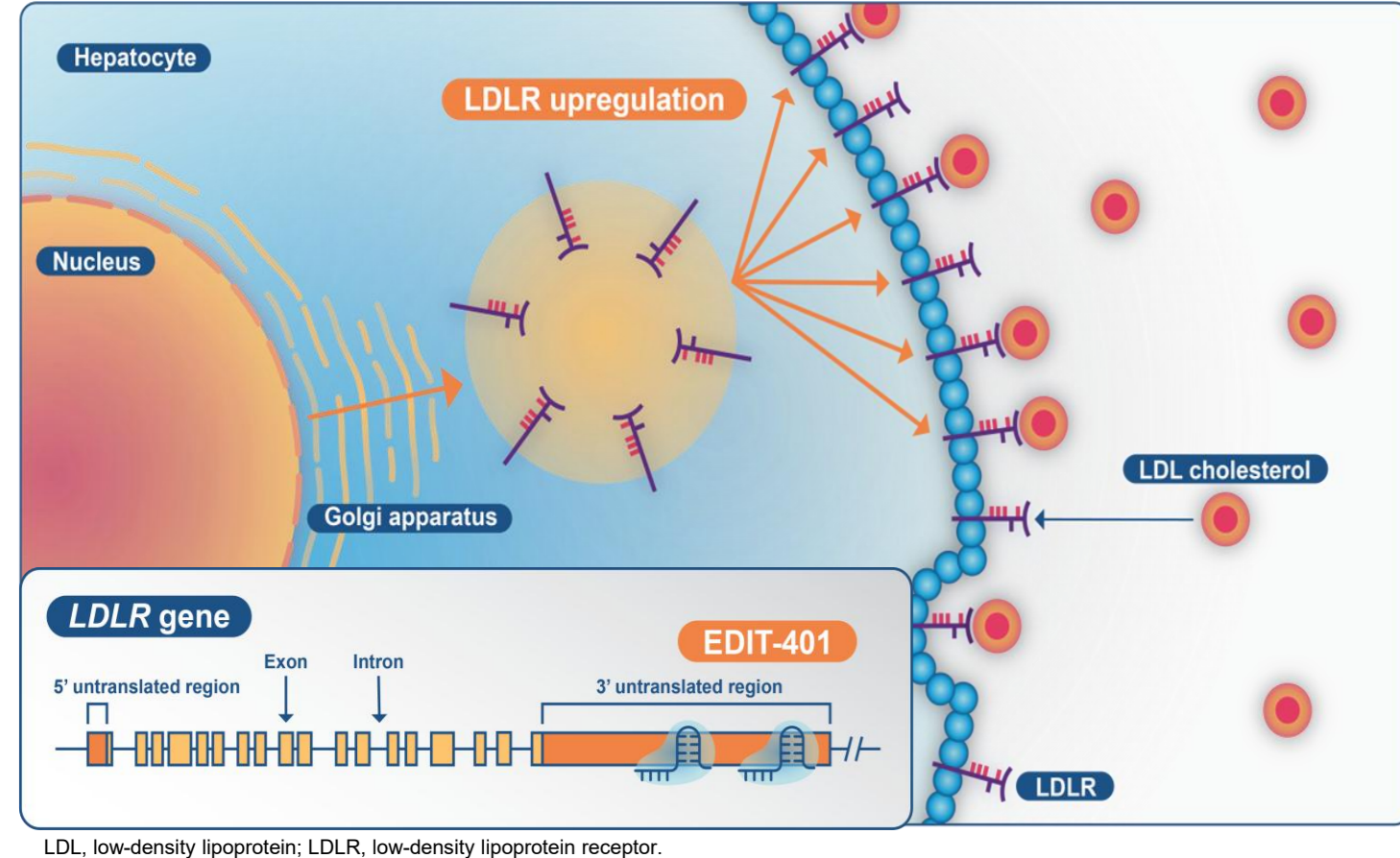
- Heterozygous familial hypercholesterolemia (HeFH) is a genetic disease caused primarily by autosomal dominant, loss-of-function mutations in the low-density lipoprotein receptor (*LDLR*) gene, leading to severely elevated low-density lipoprotein cholesterol (LDL-C) levels and increased risk of atherosclerotic cardiovascular disease.
- Despite maximally tolerated standard of care treatment, patients with HeFH often fail to achieve target LDL-C levels, warranting development of a transformative LDL-C-lowering therapy.
- EDIT-401, a single-dose, experimental, *in vivo*, clustered regularly interspaced short palindromic repeats (CRISPR)-based gene-editing medicine, currently in preclinical development, edits the *LDLR* gene to increase LDLR protein expression on hepatocyte cell surface and consequently reduces serum LDL-C levels.
- The nonclinical studies were designed to evaluate pharmacokinetics (PK) and pharmacodynamics (PD) of EDIT-401(mu), EDIT-401 containing murine surrogate guide RNAs (gRNAs), in wild-type (WT) C57BL/6J and heterozygous murine low-density lipoprotein receptor (*Ldlr*) knockout (*Ldlr*^{-/-}) C57BL/6J mice. *Ldlr*^{-/-} knockout mice harbor a loss-of-function mutation in a single *Ldlr* allele, modelling patients with HeFH, and have an elevated level of LDL-C compared with WT mice. This study enables us to evaluate whether human dose predicted based on non-human primate (NHP) data, needs to be adjusted for patients with HeFH.

Methods

EDIT-401 is an N-acetylgalactosamine (GalNAc)-based liver-targeting lipid nanoparticle (LNP) (licensed from Genevieve Sciences) carrying CRISPR-associated protein 9 (Cas9) mRNA and two gRNAs targeting the 3' untranslated region of *LDLR* gene. PK and PD of EDIT-401(mu) were evaluated in WT and *Ldlr*^{-/-} mice following a single intravenous bolus administration across multiple dose levels. Both WT and *Ldlr*^{-/-} mice (n=4 per dose group) received single dose ranging from 0.05 to 1 mg/kg. Following EDIT-401(mu) dosing, sparse plasma samples were collected for PK analysis, with Cas9 mRNA measured as a proxy for EDIT-401(mu) by reverse transcription droplet digital polymerase chain reaction (RT-ddPCR). Liver samples were also collected up to 14 days post-dose to assess Cas9 mRNA exposure, editing, and LDLR protein upregulation. Serum samples were collected up to 14 days post-dose to measure LDL-C levels by high-performance liquid chromatography (HPLC). LDLR protein was measured by enzyme-linked immunosorbent assay (ELISA). PK parameters were derived using non-compartmental analysis (NCA) with Phoenix WinNonlin software and are reported as mean values for all the tested doses of EDIT-401(mu). LDL-C reduction and LDLR fold-upregulation were analyzed using non-linear fit with GraphPad Prism (V10.4.0).

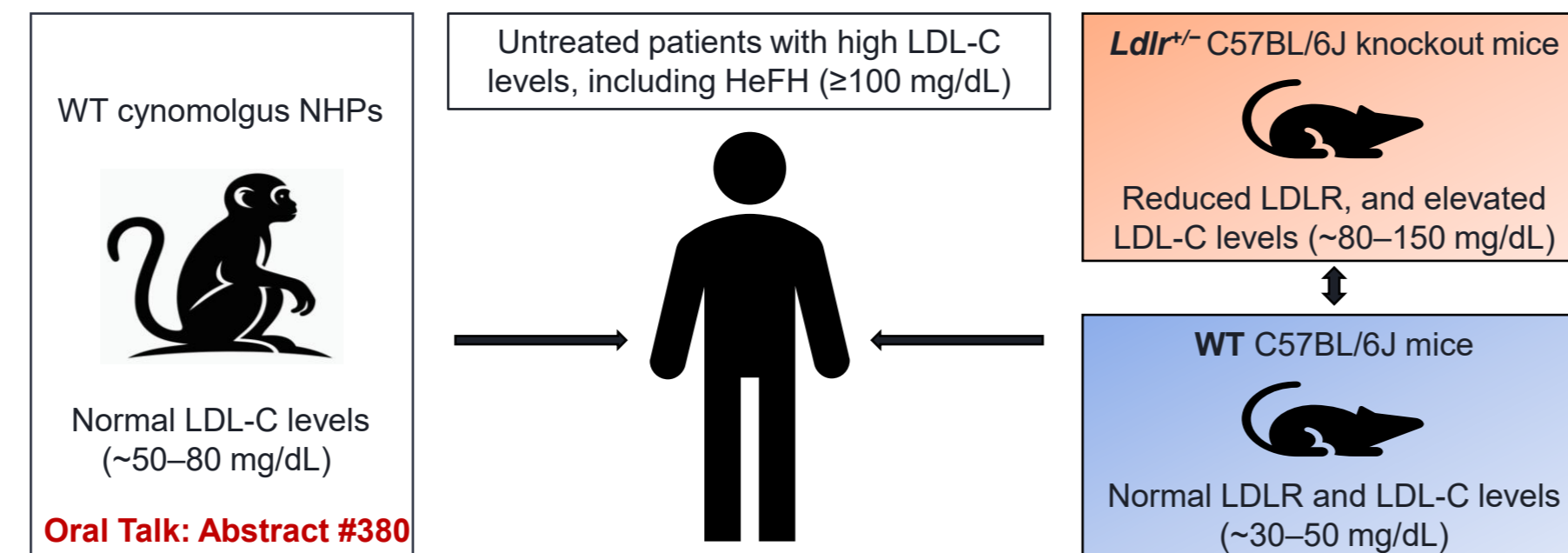
EDIT-401 uses a differentiated mechanism of action to reduce LDL-C

EDIT-401 therapeutic strategy for LDLR upregulation



- CRISPR/Cas9 nuclease and dual gRNAs disrupt negative regulatory elements of the *LDLR* gene, increasing mRNA stability, enabling LDLR protein upregulation.
- This amplification approach enables ≥90% mean reduction in serum LDL-C in NHP and mouse models.

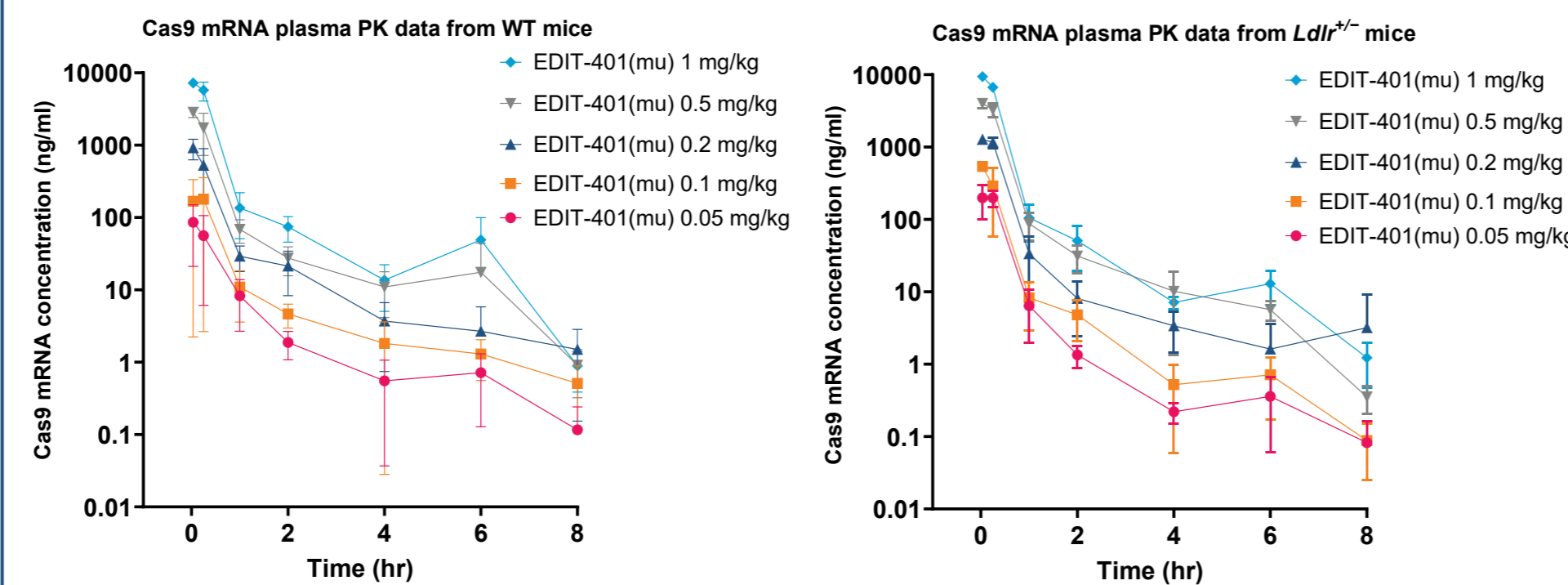
Figure 1: Elevated levels of LDL-C observed in heterozygous loss-of-function (*Ldlr*^{+/-}) mice modeling HeFH



Reference for *Ldlr*^{-/-} homozygous mice: <https://www.jax.org/strain/002207>. HeFH, heterozygous familial hypercholesterolemia; LDL-C, low-density lipoprotein cholesterol; LDLR, low-density lipoprotein receptor; *Ldlr*, murine low-density lipoprotein receptor; NHP, non-human primate; WT, wild-type.

Ldlr^{+/-} C57BL/6J mice were generated by inserting a neomycin resistance cassette at exon 4 leading to the disruption of *Ldlr* coding DNA sequence. *Ldlr*^{+/-} C57BL/6J mice have one intact *Ldlr* allele and one mutated *Ldlr* allele, generated by crossing WT mice with *Ldlr*^{-/-} mice. The basal levels of LDL-C in *Ldlr*^{+/-} mice is higher compared with control WT C57BL/6J mice.

Figure 2: EDIT-401(mu) exposure in systemic circulation is transient and increases with dose in both *Ldlr*^{+/-} mice and WT mice



PK parameters	0.05 mg/kg	0.1 mg/kg	0.2 mg/kg	0.5 mg/kg	1 mg/kg
C _{max} (ng/mL)	85.8	179	919	2850	7260
AUC ₀₋₈ (hr*ng/mL)	45.8	110	380	1120	3060

PK parameters	0.05 mg/kg	0.1 mg/kg	0.2 mg/kg	0.5 mg/kg	1 mg/kg
C _{max} (ng/mL)	199	537	1270	4030	9430
AUC ₀₋₈ (hr*ng/mL)	98.2	178	597	1710	3410

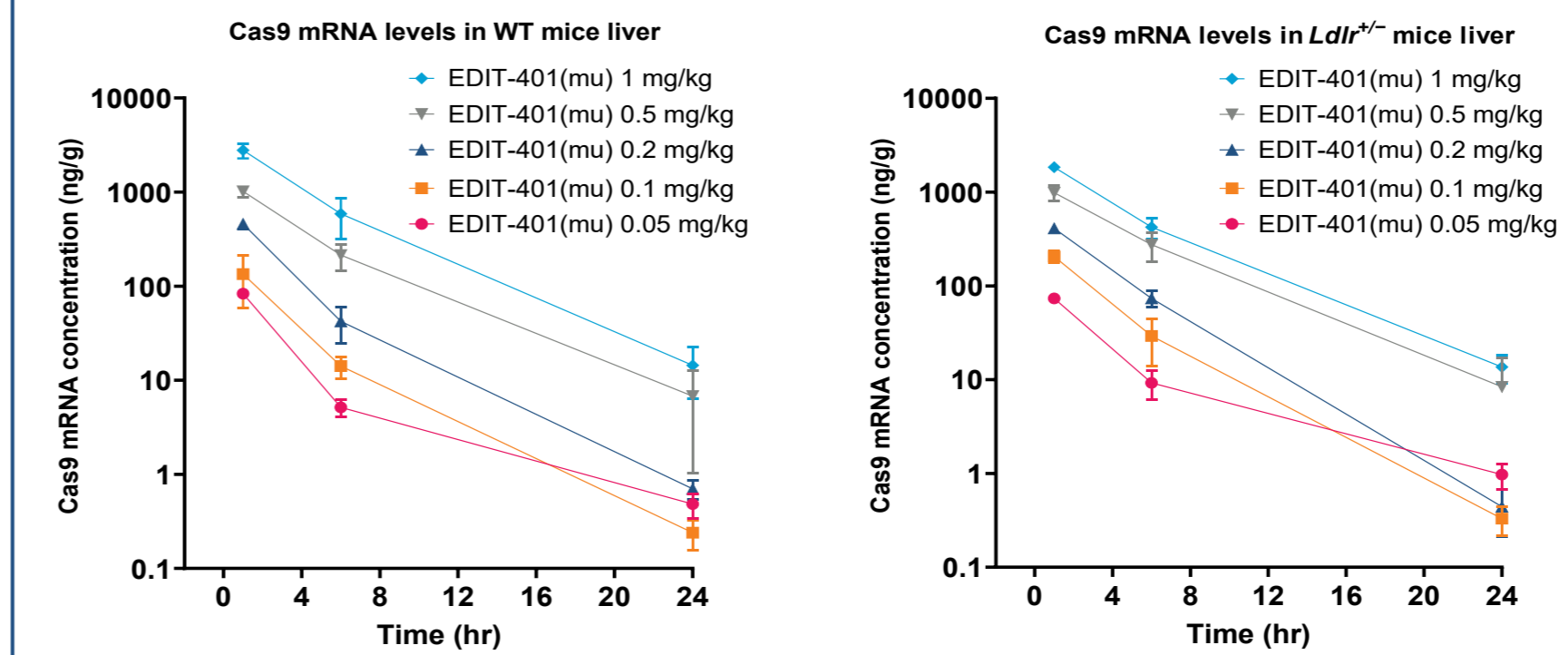
AUC, area under the curve; Cas9, CRISPR-associated protein 9; CRISPR, clustered regularly interspaced short palindromic repeats; C_{max}, maximum concentration; hr, hour; *Ldlr*, murine low-density lipoprotein receptor; PK, pharmacokinetic; WT, wild-type.

Total RNA was extracted from the collected sparse plasma samples and the levels of Cas9 mRNA were quantified by RT-ddPCR. Cas9 mRNA data was used to perform NCA using Phoenix WinNonlin.

Conclusions

- Preclinical PK findings demonstrate rapid uptake of EDIT-401(mu) from the systemic circulation into the liver in both WT and *Ldlr*^{+/-} mice.
- Comparable and dose-dependent increase in total editing observed in both WT and *Ldlr*^{+/-} mice.
- Rapid and robust decrease in LDL-C levels with similar reductions observed between WT and *Ldlr*^{+/-} mice.
- Mouse PK/PD data demonstrate that EDIT-401 dose adjustments (estimated based on WT NHP data) may not be needed in patients with HeFH.

Figure 3: Comparable dose-dependent liver exposure of EDIT-401(mu) observed between WT and *Ldlr*^{+/-} mice



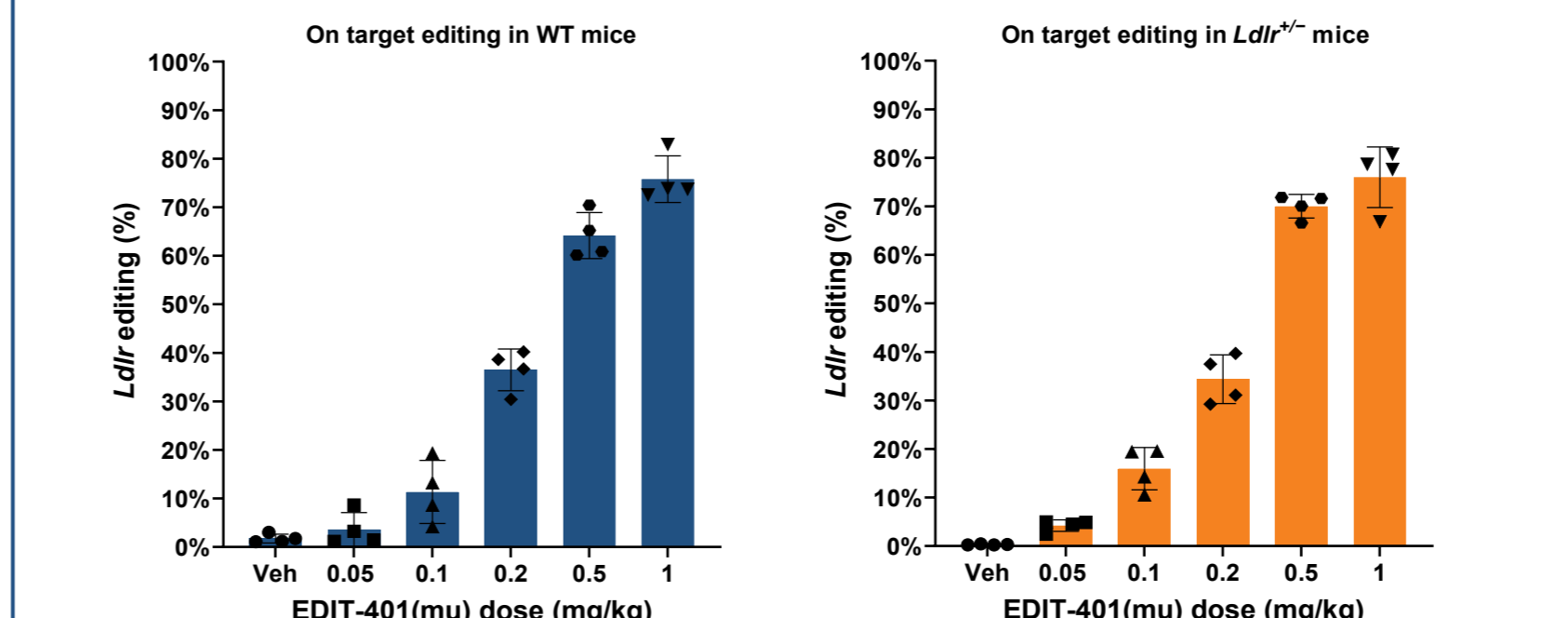
PK parameters	0.05 mg/kg	0.1 mg/kg	0.2 mg/kg	0.5 mg/kg	1 mg/kg
C _{max} (ng/g)	83.4	134	459	1020	2780
AUC ₀₋₂₄ (hr*ng/g)	290	497	1650	4890	13200
t _{1/2} (hr)	3.48	2.61	2.60	3.28	3.11

PK parameters	0.05 mg/kg	0.1 mg/kg	0.2 mg/kg	0.5 mg/kg	1 mg/kg
C _{max} (ng/g)	73.7	206	410	989	1840
AUC ₀₋₂₄ (hr*ng/g)	318	819	1730	5330	10700
t _{1/2} (hr)	4.05	2.50	2.36	3.40	3.34

AUC, area under the curve; Cas9, CRISPR-associated protein 9; C_{max}, maximum concentration; CRISPR, clustered regularly interspaced short palindromic repeats; hr, hour; *Ldlr*, murine low-density lipoprotein receptor; PK, pharmacokinetic; t_{1/2}, half-life; WT, wild-type.

Total RNA was extracted from liver samples collected at 1, 6, 24, 168, and 336 hours and the levels of Cas9 mRNA were quantified by RT-ddPCR. Cas9 mRNA levels were below limit of quantification at 168 and 336 hours post-dosing. Cas9 mRNA data was used to perform NCA using Phoenix WinNonlin.

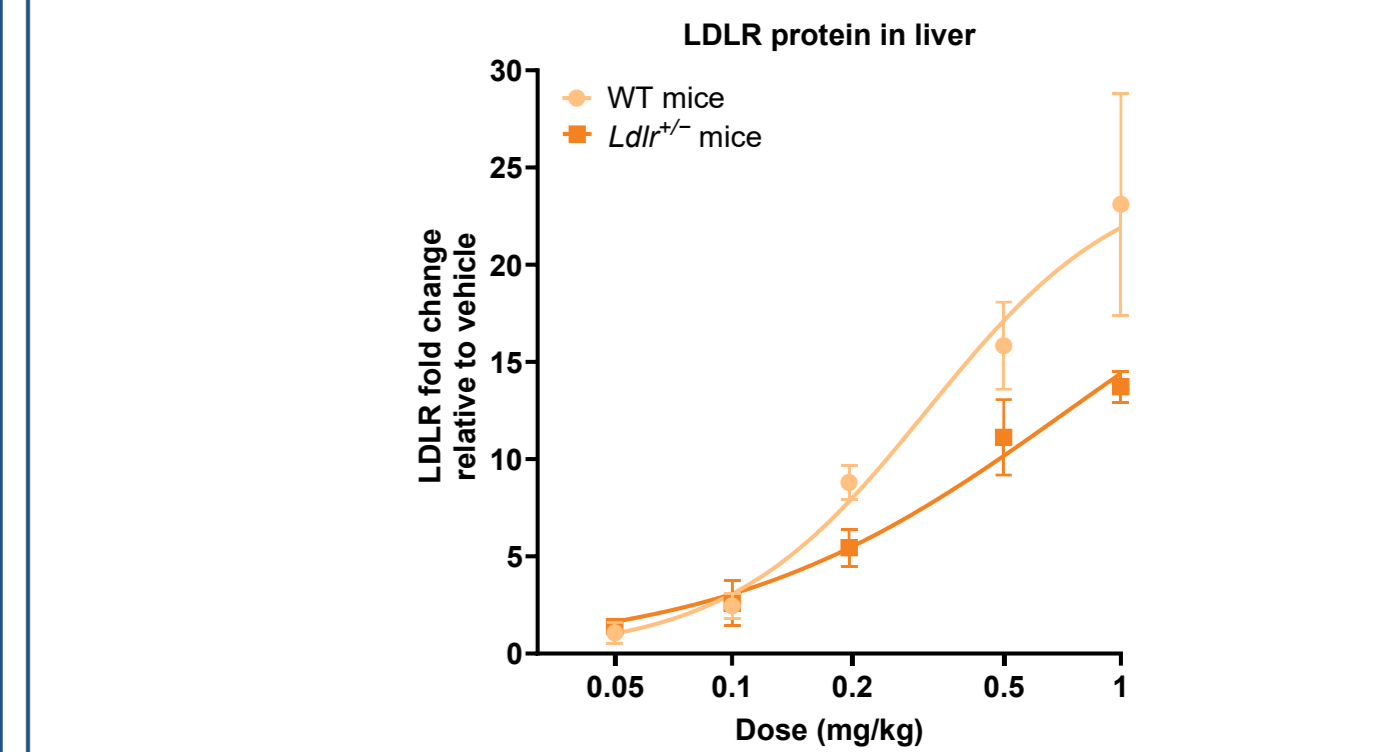
Figure 4: Comparable total editing observed between WT and *Ldlr*^{+/-} mice



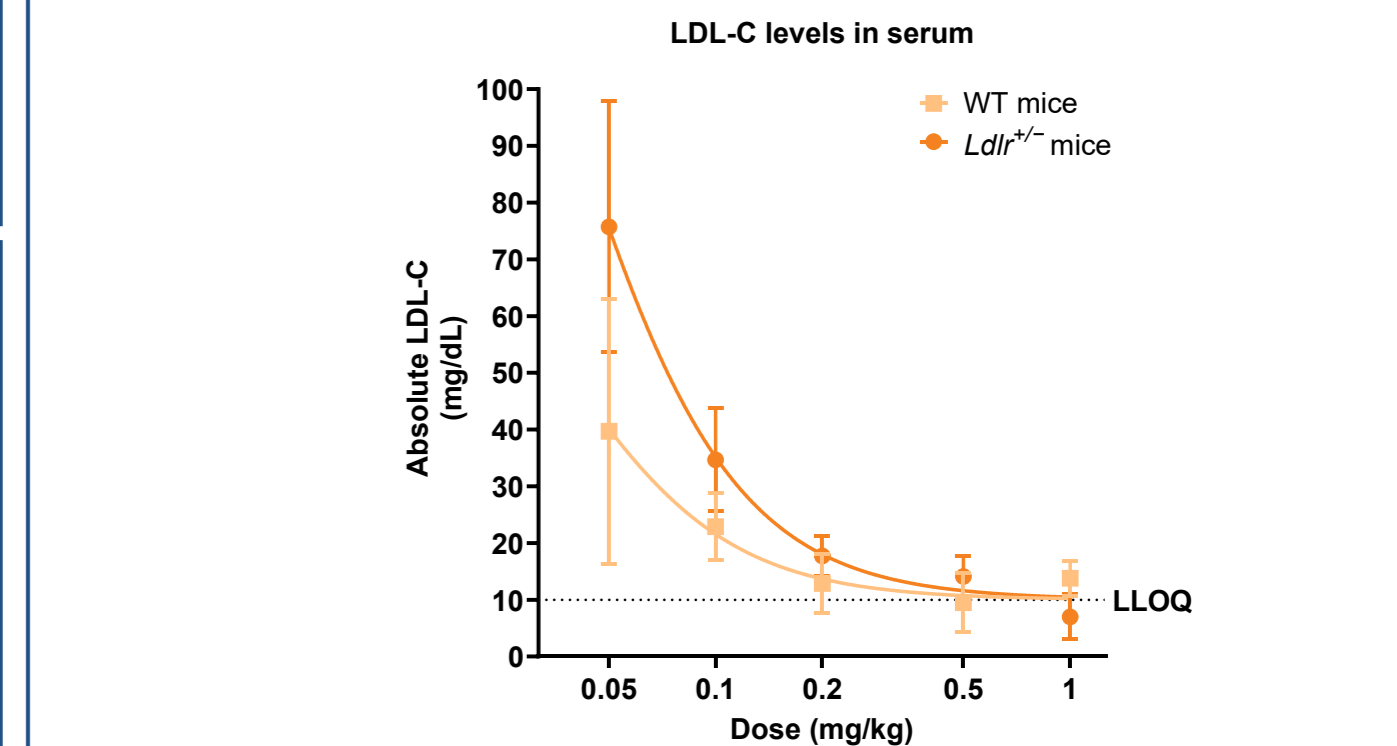
Reference for UDiTaS: 10.1186/s12864-018-4561-9. *Ldlr*, murine low-density lipoprotein receptor; UDiTaS, Uni-Directional Targeted Sequencing; Veh, vehicle; WT, wild-type.

Genomic DNA was extracted from liver samples collected at 336 hours post-dose. Percentage of total editing at the *Ldlr*^{+/-} locus was then assessed by Uni-Directional Targeted Sequencing (UDiTaS).

Figure 5: Comparable LDL-C reduction between WT and *Ldlr*^{+/-} mice with dose-dependent upregulation of LDLR



Mice strain	E _{max} LDLR fold change mean (± SD)	ED ₅₀ mg/kg mean (95% CI)
WT mice	23.1 (4.95)	0.31 (0.26–0.39)
<i>Ldlr</i> ^{+/-} mice	13.7 (0.71)	0.27 (0.23–0.31)



Mice strain	ED ₅₀ mg/kg
WT mice	0.04281
<i>Ldlr</i> ^{+/-} mice	0.03445

The slope of the two DRC curves were compared using extra sum-of-squares F test, and the difference in ED₅₀ was not statistically significant, with a *P*-value of 0.848. The bottom of the curve was constrained to 10 mg/dL and shared Hill slope was applied across datasets. CI, confidence interval; DRC, dose response curve; ED₅₀, median effective dose; E_{max}, maximum effect; LDL-C, low-density lipoprotein cholesterol; LDLR, low-density lipoprotein receptor; *Ldlr*, murine low-density lipoprotein receptor; LLOQ, lower limit of quantification; SD, standard deviation; WT, wild-type.

At 336 hours post-dose, levels of LDLR protein were analyzed from liver samples by ELISA, and LDL-C levels were analyzed in serum samples using HPLC.

Acknowledgments and disclosures

We would like to thank our Editas Medicine colleagues and collaborators who provided support in sequencing, RNA and LNP manufacturing, animal studies, and scientific discourse. All authors are current or former employees and shareholders of Editas Medicine, Inc. The authors have filed a patent application on the data presented here. We also thank our Genevieve Sciences Corporation collaborators for licensure of LNPs. Editorial assistance was provided by Porterhouse Medical US and funded by Editas Medicine, Inc. according to Good Publication Practice (GPP) guidelines.