

# *Helz2* Cas9-KO Strategy

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**Reviewer:**

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# Project Overview

**Project Name**

*Helz2*

**Project type**

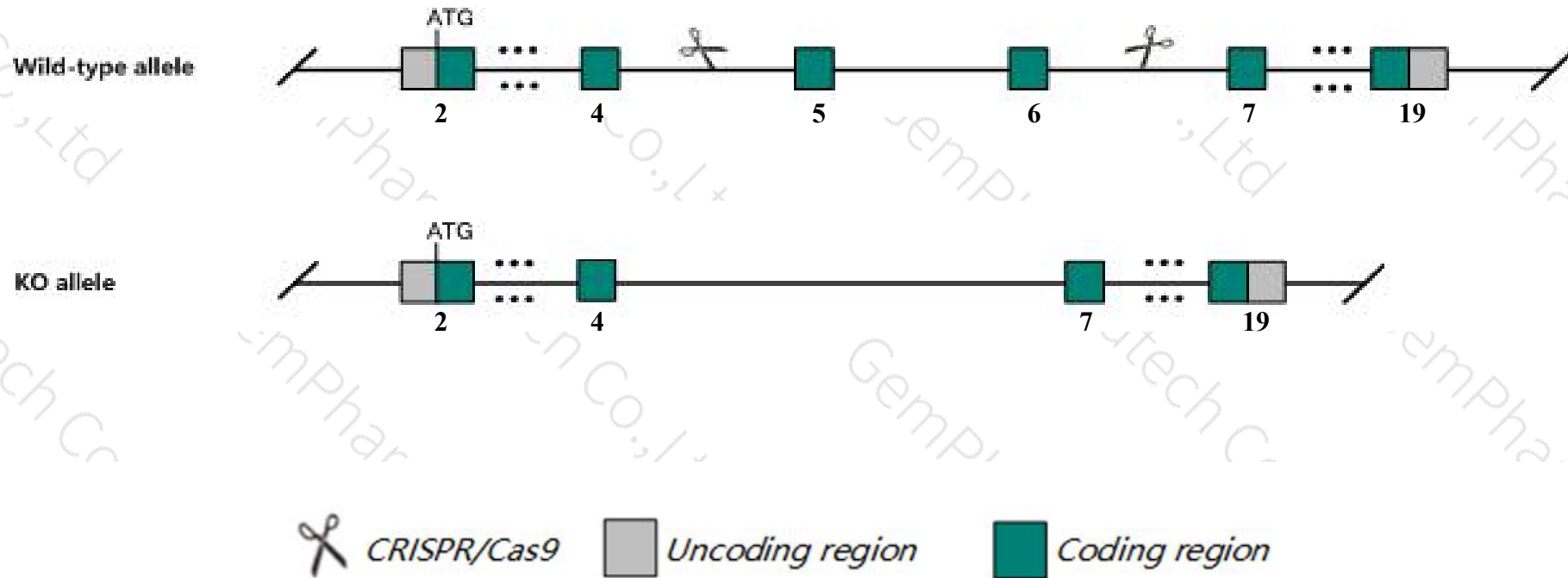
**Cas9-KO**

**Strain background**

**C57BL/6JGpt**

# Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *Helz2* gene. The schematic diagram is as follows:



- The *Helz2* gene has 5 transcripts. According to the structure of *Helz2* gene, exon5-exon6 of *Helz2-202* (ENSMUST00000108831.7) transcript is recommended as the knockout region. The region contains 1160bp coding sequence. Knock out the region will result in disruption of protein function.
- In this project we use CRISPR/Cas9 technology to modify *Helz2* gene. The brief process is as follows: CRISPR/Cas9 system

- According to the existing MGI data, Mice homozygous for a knock-out allele exhibit slower weight gain, hyperleptinemia, increased oxygen consumption, decreased respiratory quotient, decreased liver triglyceride level and ameliorated hyperlipidemia and hepatosteatosis when fed a high-fat diet.
- The *Helz2* gene is located on the Chr2. If the knockout mice are crossed with other mice strains to obtain double gene positive homozygous mouse offspring, please avoid the two genes on the same chromosome.
- This Strategy is designed based on genetic information in existing databases. Due to the complexity of biological processes, all risk of the gene knockout on gene transcription, RNA splicing and protein translation cannot be predicted at the existing technology level.



# Gene information (NCBI)

## Helz2 helicase with zinc finger 2, transcriptional coactivator [ *Mus musculus* (house mouse) ]

Gene ID: 229003, updated on 12-Aug-2019

### Summary

<b>Official Symbol</b>	Helz2 provided by <a href="#">MGI</a>
<b>Official Full Name</b>	helicase with zinc finger 2, transcriptional coactivator provided by <a href="#">MGI</a>
<b>Primary source</b>	<a href="#">MGI:MGI:2385169</a>
<b>See related</b>	<a href="#">Ensembl:ENSMUSG00000027580</a>
<b>Gene type</b>	protein coding
<b>RefSeq status</b>	VALIDATED
<b>Organism</b>	<a href="#">Mus musculus</a>
<b>Lineage</b>	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Myomorpha; Muroidea; Muridae; Murinae; Mus; Mus
<b>Also known as</b>	PDIP1; mPDIP1; Pric285; mKIAA1769
<b>Expression</b>	Broad expression in spleen adult (RPKM 53.3), thymus adult (RPKM 35.0) and 18 other tissues <a href="#">See more</a>
<b>Orthologs</b>	<a href="#">human</a> <a href="#">all</a>

# Transcript information (Ensembl)

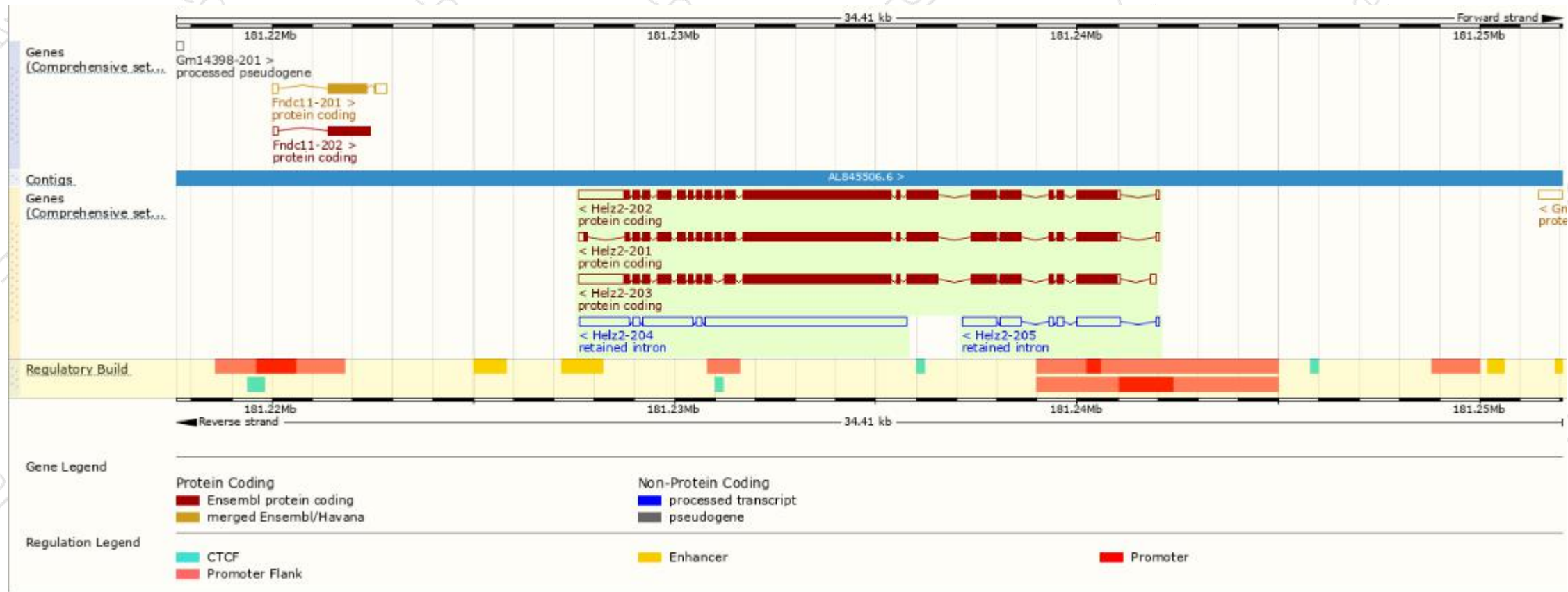
The gene has 5 transcripts,all transcripts are shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Helz2-202	<a href="#">ENSMUST00000108831.7</a>	10109	<a href="#">2947aa</a>	Protein coding	<a href="#">CCDS38380</a>	<a href="#">E9QAM5</a>	TSL:5 GENCODE basic APPRIS P2
Helz2-203	<a href="#">ENSMUST00000121484.1</a>	10063	<a href="#">2903aa</a>	Protein coding	-	<a href="#">A2AS05</a>	TSL:5 GENCODE basic
Helz2-201	<a href="#">ENSMUST00000094203.10</a>	9162	<a href="#">2970aa</a>	Protein coding	-	<a href="#">A2AS03</a>	TSL:5 GENCODE basic APPRIS ALT2
Helz2-204	<a href="#">ENSMUST00000149417.1</a>	7787	No protein	Retained intron	-	-	TSL:1
Helz2-205	<a href="#">ENSMUST00000155049.1</a>	2800	No protein	Retained intron	-	-	TSL:1

The strategy is based on the design of *Helz2-202* transcript,The transcription is shown below

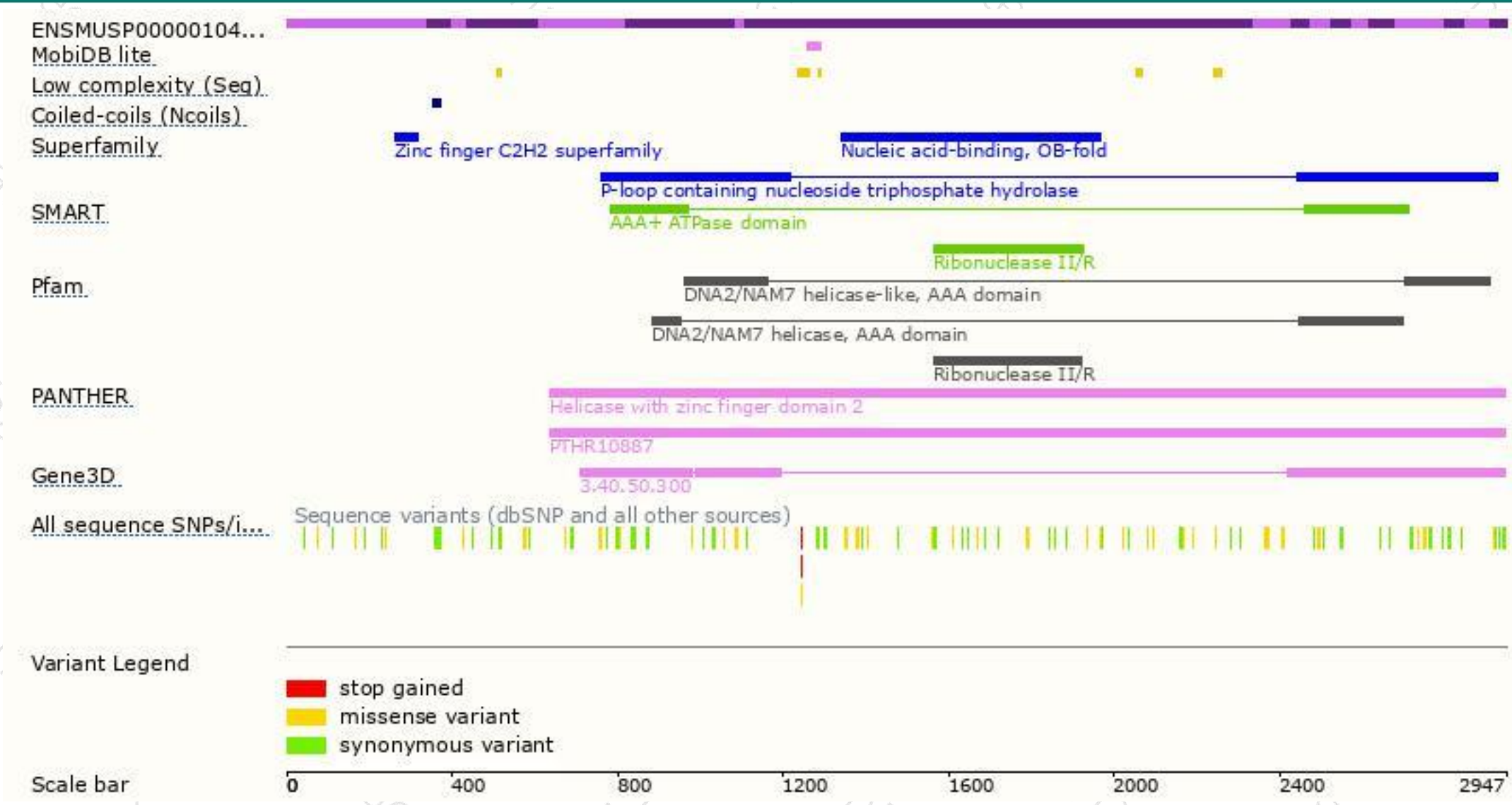


# Genomic location distribution

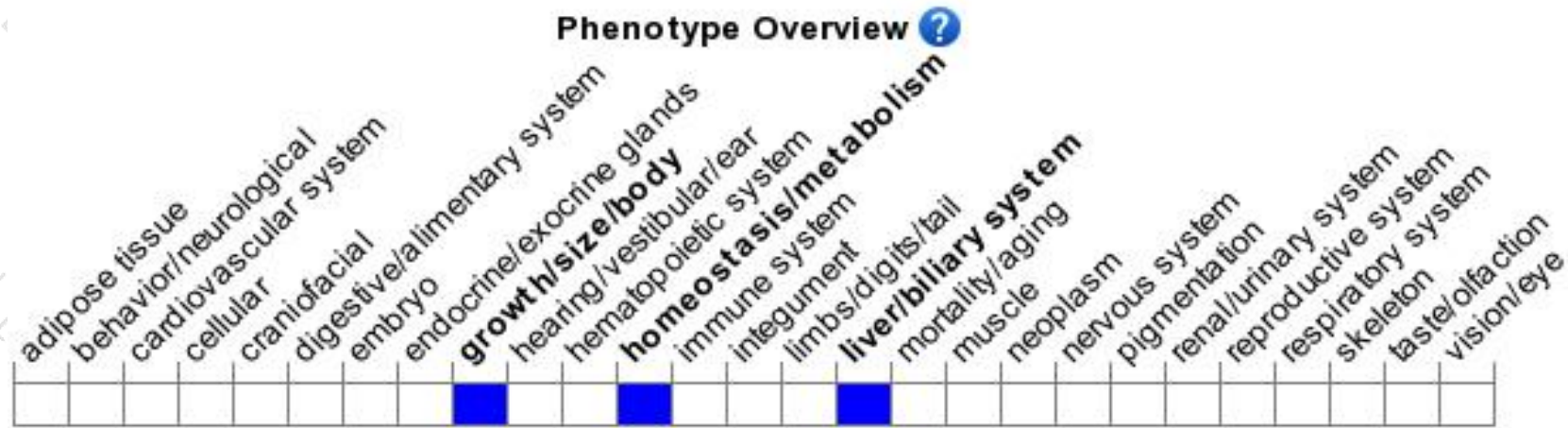




# Protein domain



# Mouse phenotype description(MGI )



*Phenotypes affected by the gene are marked in blue. Data quoted from MGI database(<http://www.informatics.jax.org/>).*

According to the existing MGI data, Mice homozygous for a knock-out allele exhibit slower weight gain, hyperleptinemia, increased oxygen consumption, decreased respiratory quotient, decreased liver triglyceride level and ameliorated hyperlipidemia and hepatosteatosis when fed a high-fat diet.

If you have any questions, you are welcome to inquire.

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