

***Znhit6* Cas9-KO Strategy**

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Reviewer:

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Project Overview

Project Name

Znhit6

Project type

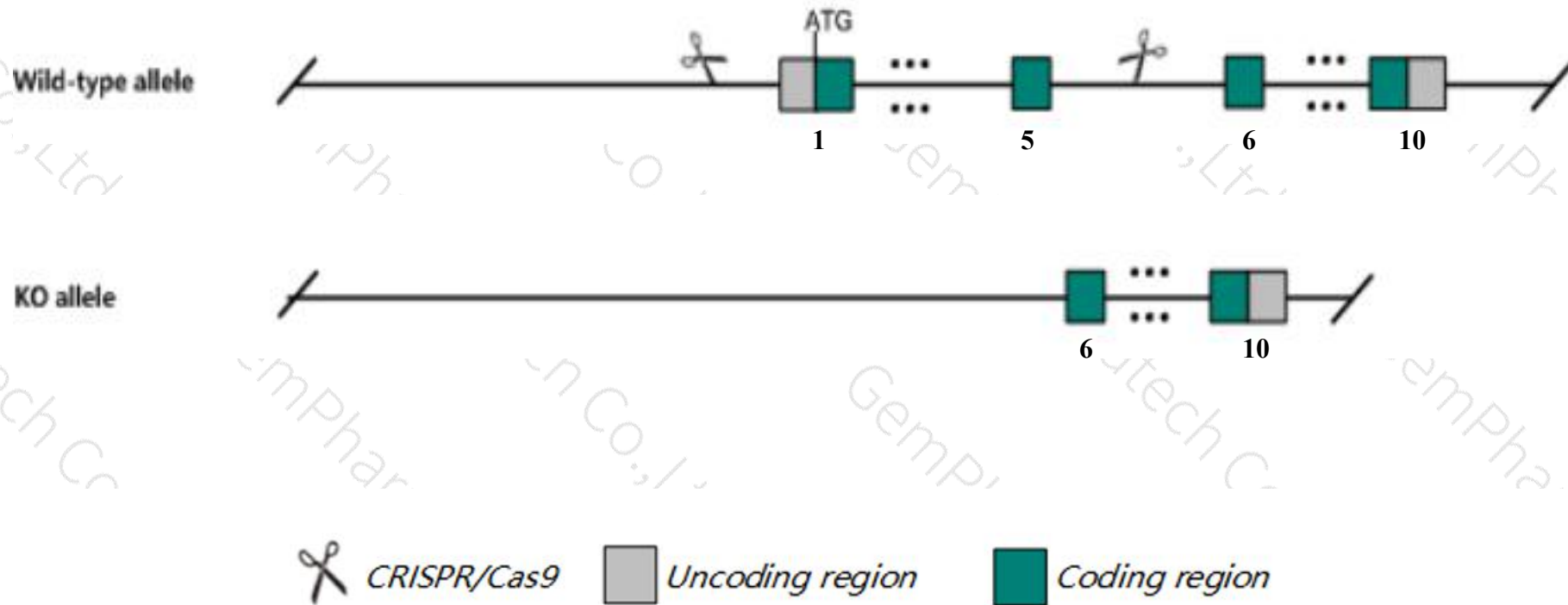
Cas9-KO

Strain background

C57BL/6JGpt

Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *Znhit6* gene. The schematic diagram is as follows:



- The *Znhit6* gene has 7 transcripts. According to the structure of *Znhit6* gene, exon1-exon5 of *Znhit6-201* (ENSMUST00000098534.8) transcript is recommended as the knockout region. The region contains start codon ATG. Knock out the region will result in disruption of protein function.
- In this project we use CRISPR/Cas9 technology to modify *Znhit6* gene. The brief process is as follows: CRISPR/Cas9 system

- The *Znhit6* gene is located on the Chr3. 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)

Znhit6 zinc finger, HIT type 6 [Mus musculus (house mouse)]

Gene ID: 229937, updated on 13-Mar-2020

Summary



Official Symbol	Znhit6 provided by MGI
Official Full Name	zinc finger, HIT type 6 provided by MGI
Primary source	MGI:MGI:1916996
See related	Ensembl:ENSMUSG00000074182
Gene type	protein coding
RefSeq status	VALIDATED
Organism	Mus musculus
Lineage	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Myomorpha; Muroidea; Muridae; Murinae; Mus; Mus
Also known as	2410019A14Rik
Expression	Broad expression in CNS E11.5 (RPKM 7.2), CNS E14 (RPKM 4.5) and 18 other tissues See more
Orthologs	human all

Transcript information（Ensembl）

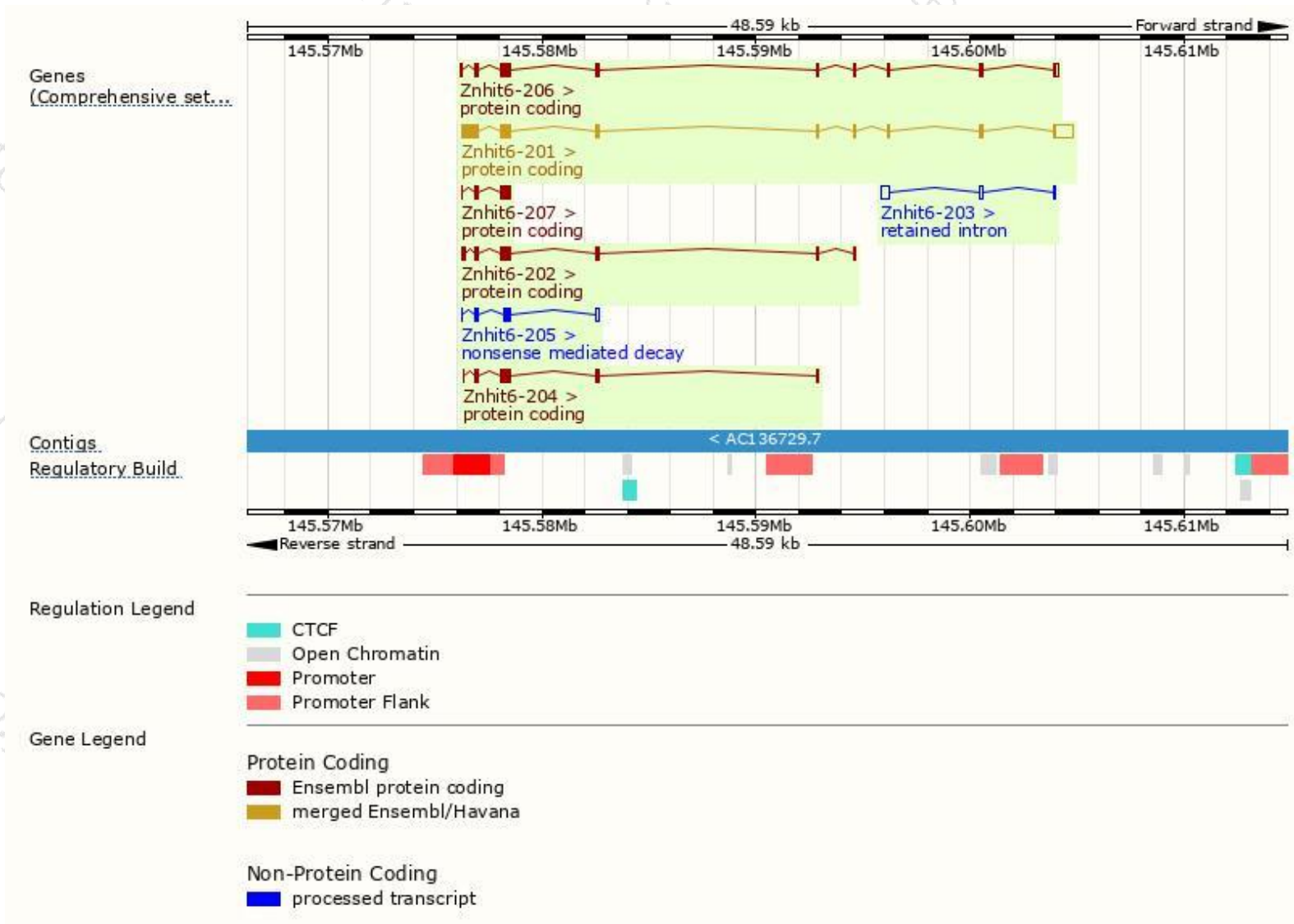
The gene has 7 transcripts,all transcripts are shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Znhit6-201	ENSMUST00000098534.8	2339	460aa	Protein coding	CCDS38662	Q3UFB2	TSL:1 GENCODE basic APPRIS is a system to annotate alternatively spliced transcripts based on a range of computational methods to identify the most functionally important transcript(s) of a gene. APPRIS P3
Znhit6-206	ENSMUST00000199033.4	1127	292aa	Protein coding	CCDS84683	Q3UFB2	TSL:1 GENCODE basic APPRIS is a system to annotate alternatively spliced transcripts based on a range of computational methods to identify the most functionally important transcript(s) of a gene. APPRIS ALT2
Znhit6-202	ENSMUST00000196413.4	805	231aa	Protein coding	-	A0A0G2JG05	CDS 3' incomplete TSL:5
Znhit6-204	ENSMUST00000197604.2	602	185aa	Protein coding	-	A0A0G2JGA1	CDS 3' incomplete TSL:5
Znhit6-207	ENSMUST00000200574.4	443	128aa	Protein coding	-	A0A0G2JFP8	CDS 3' incomplete TSL:3
Znhit6-205	ENSMUST00000197940.4	498	61aa	Nonsense mediated decay	-	A0A0G2JE59	TSL:5
Znhit6-203	ENSMUST00000197474.1	534	No protein	Retained intron	-	-	TSL:2

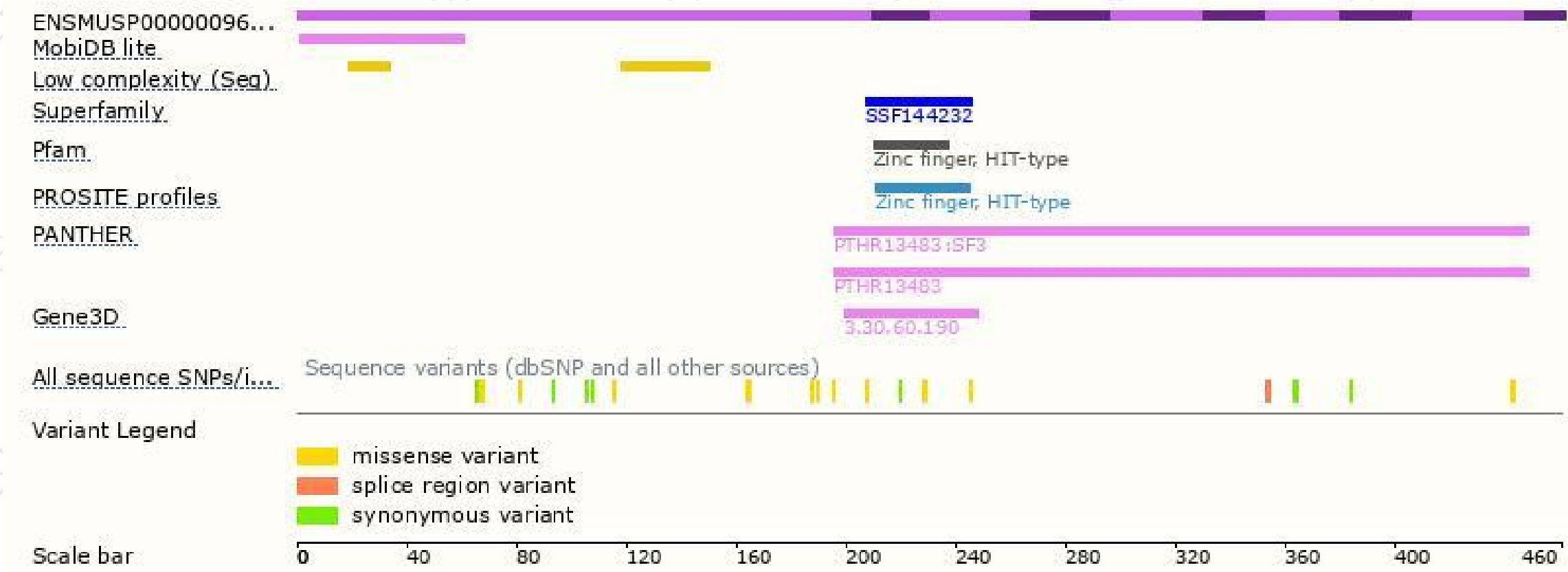
The strategy is based on the design of *Znhit6-201* transcript,The transcription is shown below



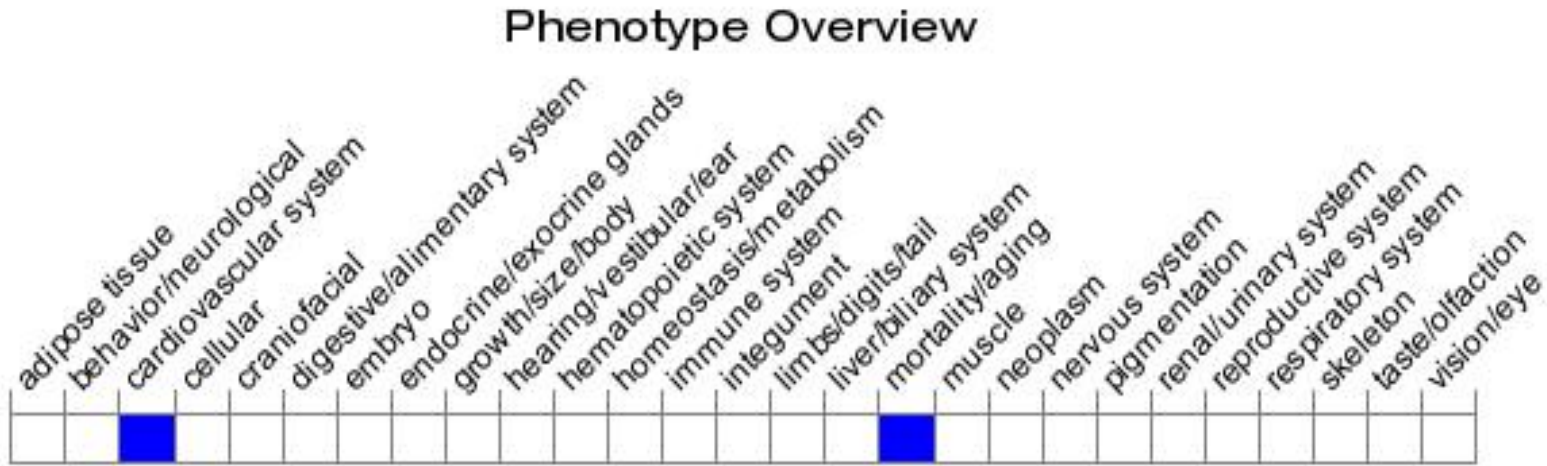
Genomic location distribution



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/>).

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

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