Zmiz2 Cas9-KO Strategy

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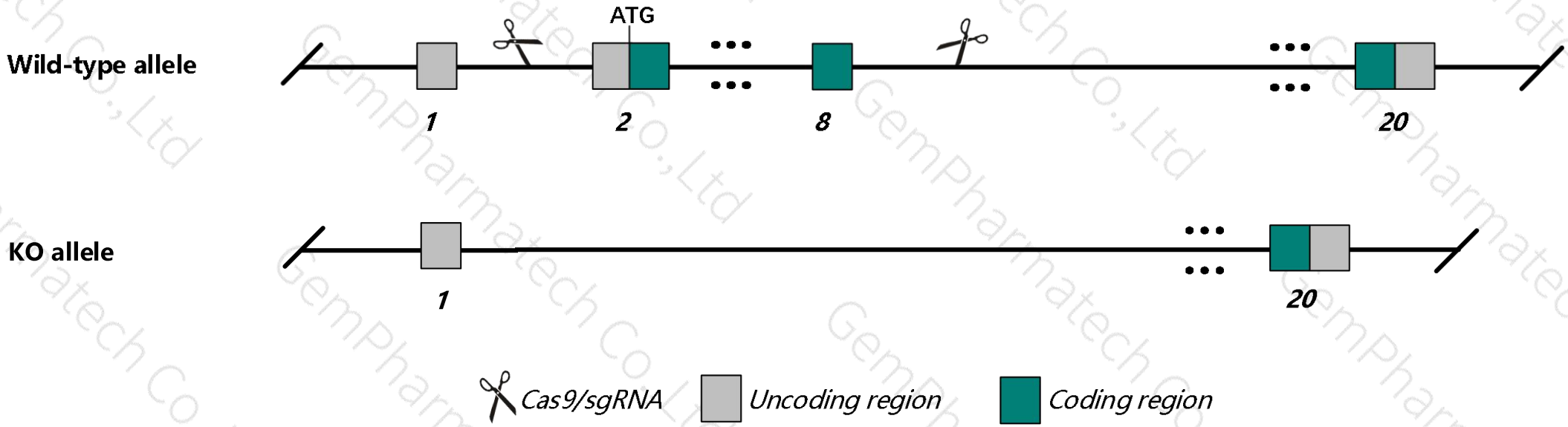
Project Overview

Project Name	***Zmiz2***
Project type	**Cas9-KO**
Strain background	**C57BL/6JGpt**

Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *Zmiz2* gene. The schematic diagram is as follows:



Technical routes

➢ The *Zmiz2* gene has 6 transcripts. According to the structure of *Zmiz2* gene, exon2-exon8 of *Zmiz2-201* (ENSMUST00000012612.10) 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 *Zmiz2* gene. The brief process is as follows:CRISPR/Cas9 system tra

Notice

➢ The *Zmiz2* gene is located on the Chr11. 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 gene knockout on gene transcription, RNA splicing and protein translation cannot be predicted at existing technological level.

Gene information （NCBI）

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Zmiz2 zinc finger, MIZ-type containing 2 [Mus musculus (house mouse)]

Gene ID: 52915, updated on 31-Jan-2019

Summary

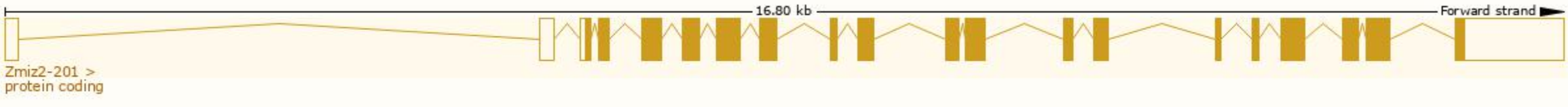
Official Symbol	Zmiz2 provided by MGI
Official Full Name	zinc finger, MIZ-type containing 2 provided by MGI
Primary source	MGI:MGI:106374
See related	Ensembl:ENSMUSG00000041164
Gene type	protein coding
RefSeq status	VALIDATED
Organism	Mus musculus
Lineage	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Myomorpha; Muroidea; Muridae; Murinae; Mus; Mus
Also known as	Zimp7
Expression	Ubiquitous expression in testis adult (RPKM 50.9), spleen adult (RPKM 44.1) and 27 other tissues See more
Orthologs	human all

Transcript information（Ensembl）

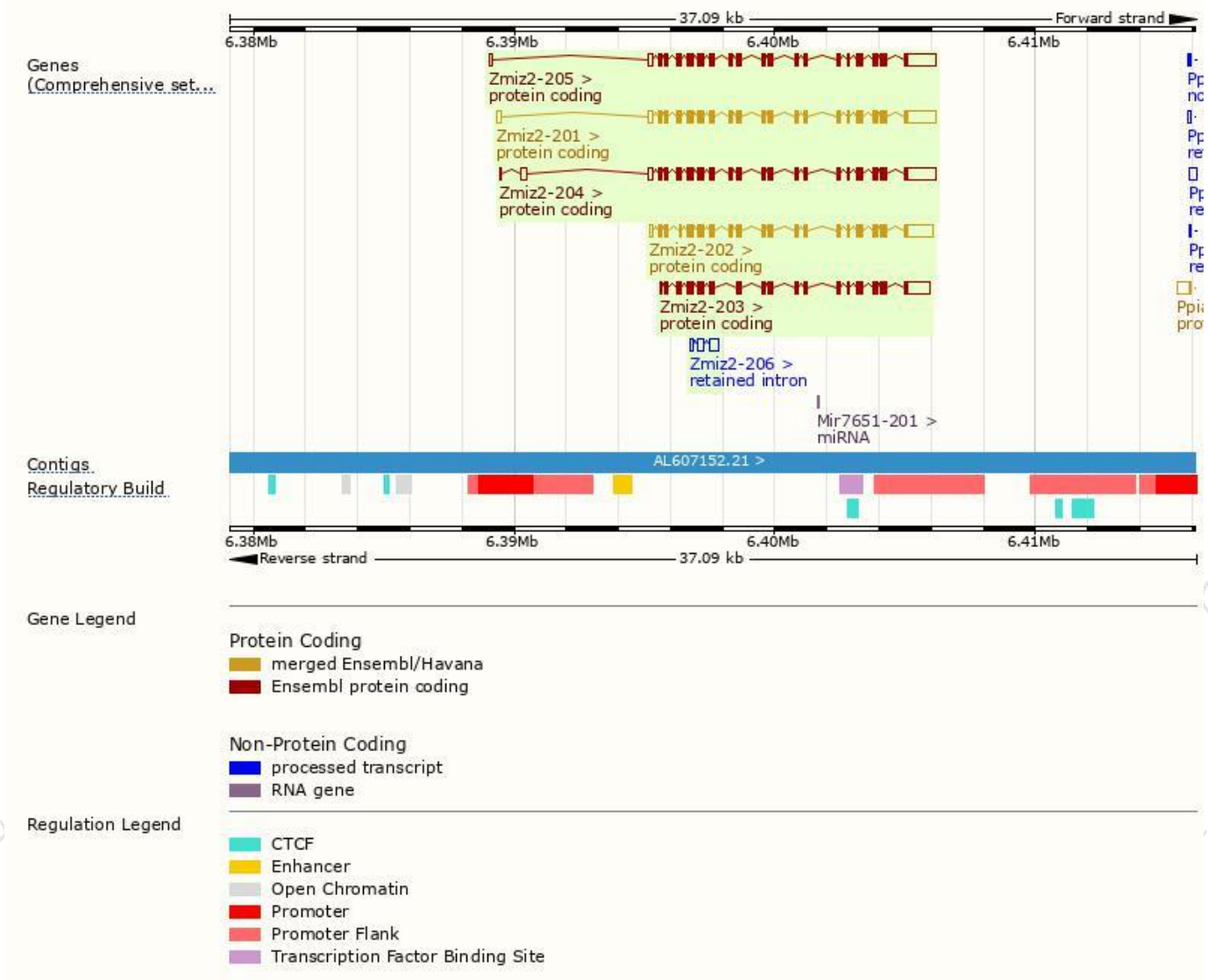
The gene has 6 transcripts,all transcripts are shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Zmiz2-204	ENSMUST00000109786.7	4319	920aa	Protein coding	CCDS24418	Q8CIE2	TSL:5 GENCODE basic APPRIS P4
Zmiz2-201	ENSMUST00000012612.10	4199	920aa	Protein coding	CCDS24418	Q8CIE2	TSL:5 GENCODE basic APPRIS P4
Zmiz2-205	ENSMUST00000109787.7	4116	920aa	Protein coding	CCDS24418	Q8CIE2	TSL:5 GENCODE basic APPRIS P4
Zmiz2-202	ENSMUST00000102914.9	3806	888aa	Protein coding	CCDS24417	Q8CIE2	TSL:1 GENCODE basic APPRIS ALT2
Zmiz2-203	ENSMUST00000109785.1	3542	894aa	Protein coding	-	Q8CIE2	TSL:5 GENCODE basic APPRIS ALT2
Zmiz2-206	ENSMUST00000124588.1	723	No protein	Retained intron	-	-	TSL:2

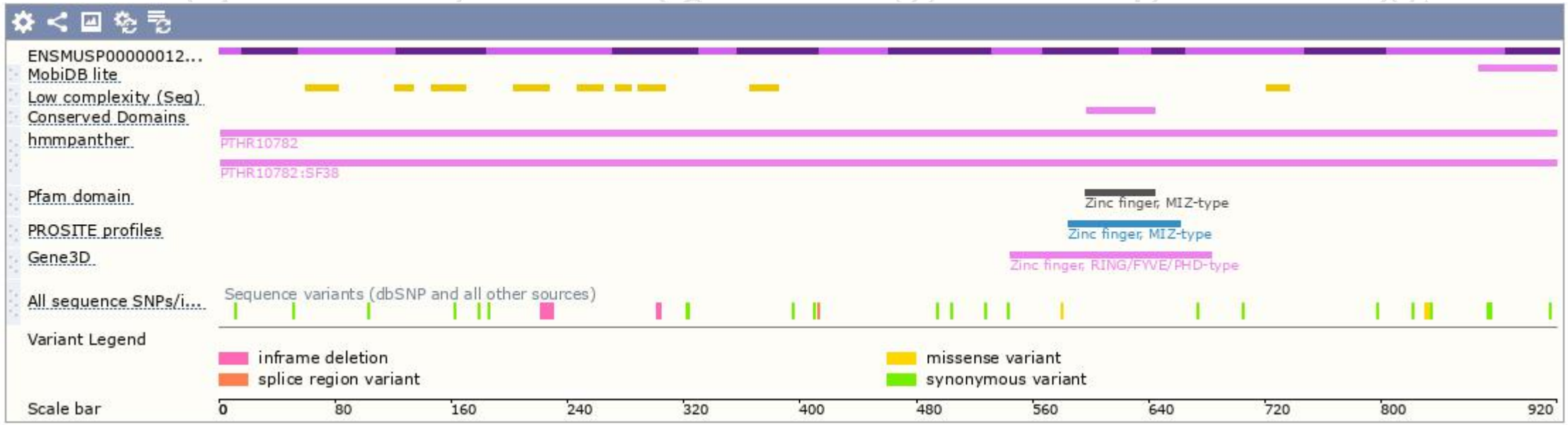
The strategy is based on the design of *Zmiz2-201* transcript,The transcription is shown below



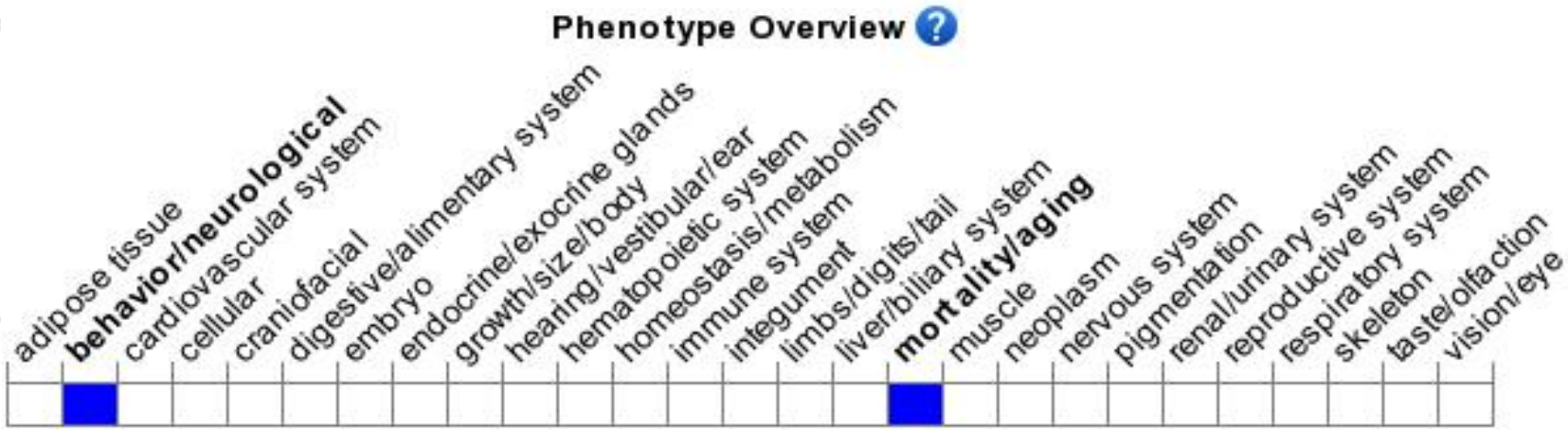
Genomic location distribution



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/).

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

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