

# *Zfp637* Cas9-KO Strategy

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**Reviewer:**

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# Project Overview

**Project Name**

***Zfp637***

**Project type**

**Cas9-KO**

**Strain background**

**C57BL/6JGpt**

# Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *Zfp637* gene. The schematic diagram is as follows:



- The *Zfp637* gene has 11 transcripts. According to the structure of *Zfp637* gene, exon3 of *Zfp637-203* (ENSMUST00000112860.1) transcript is recommended as the knockout region. The region contains most of the coding sequence. Knock out the region will result in disruption of protein function.
- In this project we use CRISPR/Cas9 technology to modify *Zfp637* gene. The brief process is as follows: CRISPR/Cas9 system

- The *Zfp637* gene is located on the Chr6. 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)

## Zfp637 zinc finger protein 637 [Mus musculus (house mouse)]

Gene ID: 232337, updated on 31-Jan-2019

### Summary



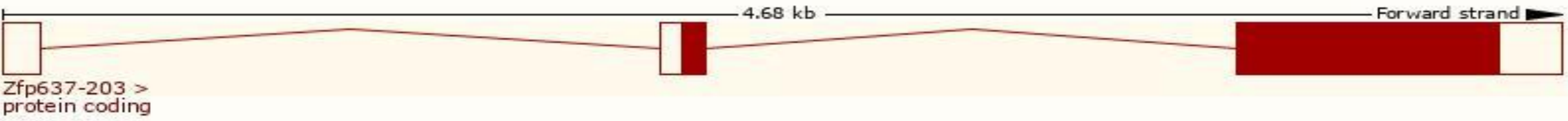
<b>Official Symbol</b>	Zfp637 provided by <a href="#">MGI</a>
<b>Official Full Name</b>	zinc finger protein 637 provided by <a href="#">MGI</a>
<b>Primary source</b>	<a href="#">MGI:MGI:2448537</a>
<b>See related</b>	<a href="#">Ensembl:ENSMUSG00000059689</a>
<b>Gene type</b>	protein coding
<b>RefSeq 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>	Al646709, BC021601, Znf32
<b>Expression</b>	Ubiquitous expression in CNS E18 (RPKM 16.4), CNS E14 (RPKM 16.1) and 28 other tissues <a href="#">See more</a>
<b>Orthologs</b>	<a href="#">human</a> <a href="#">all</a>

# Transcript information (Ensembl)

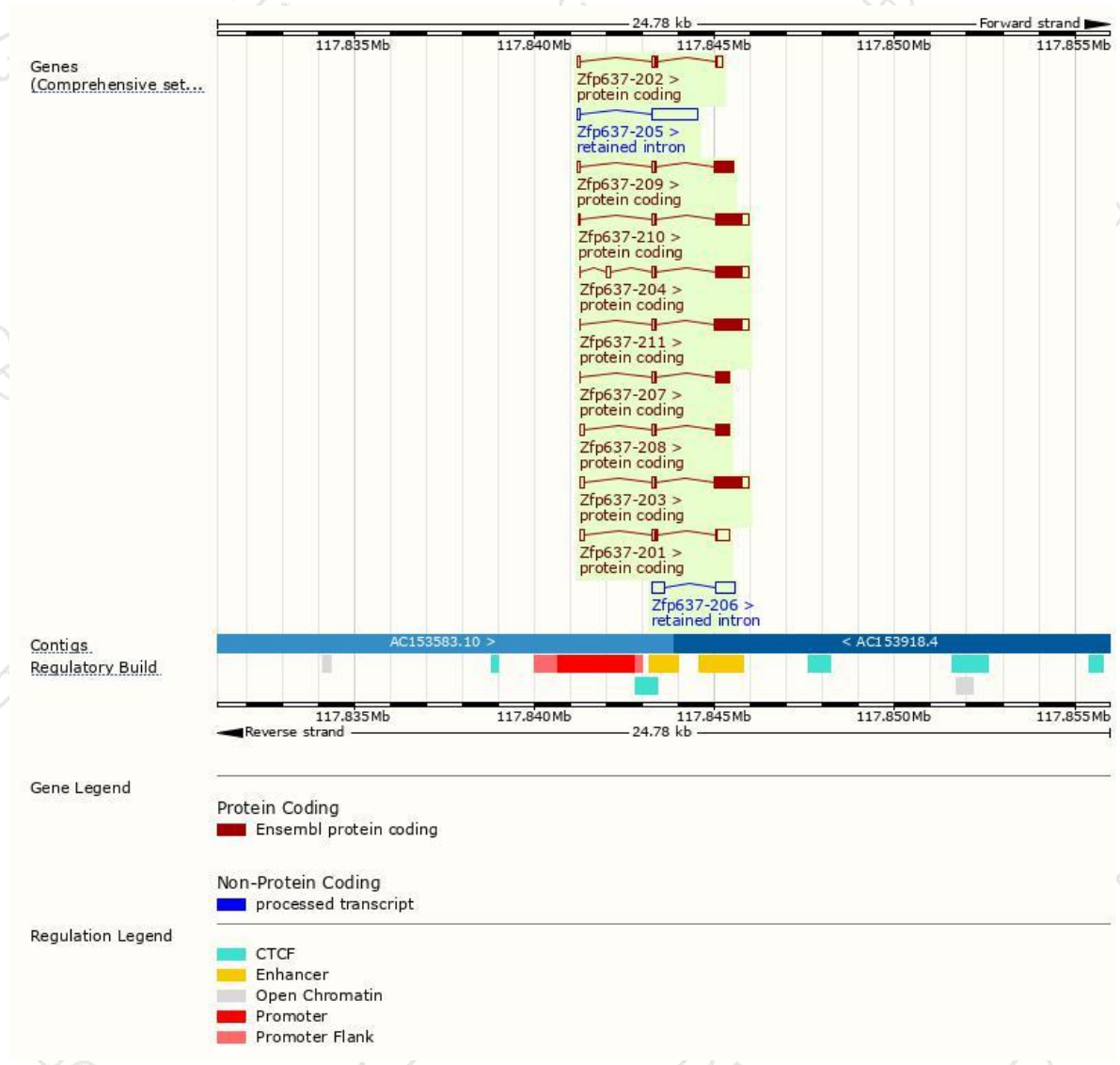
The gene has 11 transcripts,all transcripts are shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Zfp637-203	<a href="#">ENSMUST00000112860.1</a>	1231	<a href="#">286aa</a>	Protein coding	<a href="#">CCDS85139</a>	<a href="#">Q80V23</a>	TSL:1 GENCODE basic
Zfp637-204	<a href="#">ENSMUST00000112861.7</a>	1202	<a href="#">272aa</a>	Protein coding	<a href="#">CCDS39607</a>	<a href="#">Q80V23</a>	TSL:2 GENCODE basic APPRIS P1
Zfp637-211	<a href="#">ENSMUST00000223041.1</a>	1128	<a href="#">286aa</a>	Protein coding	<a href="#">CCDS85139</a>	<a href="#">Q80V23</a>	TSL:1 GENCODE basic
Zfp637-210	<a href="#">ENSMUST00000164472.7</a>	1098	<a href="#">272aa</a>	Protein coding	<a href="#">CCDS39607</a>	<a href="#">Q80V23</a>	TSL:1 GENCODE basic APPRIS P1
Zfp637-209	<a href="#">ENSMUST00000137224.7</a>	765	<a href="#">202aa</a>	Protein coding	-	<a href="#">D3Z0E5</a>	CDS 3' incomplete TSL:1
Zfp637-208	<a href="#">ENSMUST00000136889.7</a>	659	<a href="#">153aa</a>	Protein coding	-	<a href="#">D3YYX3</a>	CDS 3' incomplete TSL:3
Zfp637-201	<a href="#">ENSMUST00000112858.7</a>	650	<a href="#">33aa</a>	Protein coding	-	<a href="#">D3Z3T2</a>	TSL:2 GENCODE basic
Zfp637-207	<a href="#">ENSMUST00000134526.7</a>	543	<a href="#">153aa</a>	Protein coding	-	<a href="#">D3YYX3</a>	CDS 3' incomplete TSL:5
Zfp637-202	<a href="#">ENSMUST00000112859.7</a>	421	<a href="#">33aa</a>	Protein coding	-	<a href="#">D3Z3T2</a>	TSL:2 GENCODE basic
Zfp637-205	<a href="#">ENSMUST00000127593.7</a>	1355	No protein	Retained intron	-	-	TSL:1
Zfp637-206	<a href="#">ENSMUST00000132644.1</a>	905	No protein	Retained intron	-	-	TSL:3

The strategy is based on the design of *Zfp637-203* transcript,The transcription is shown below

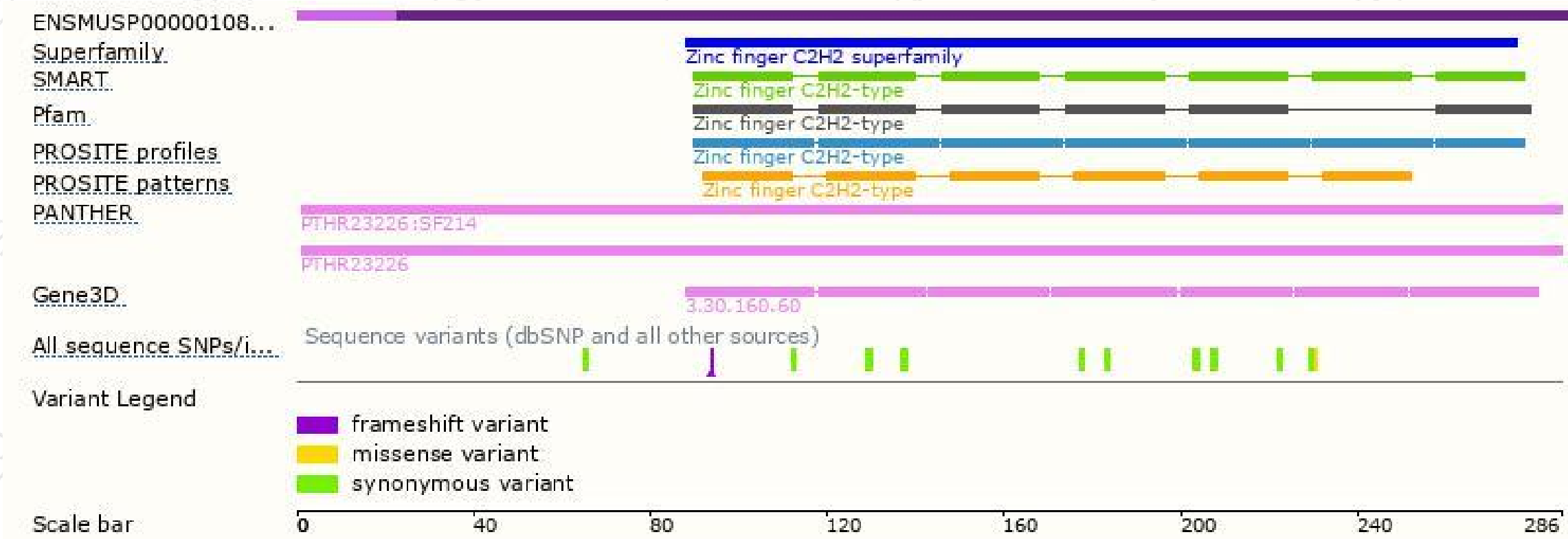


# Genomic location distribution





# Protein domain



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

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