

# ***Zfp287* Cas9-KO Strategy**

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**Reviewer:Shilei Zhu**

**Design Date:**

# Project Overview

**Project Name**

***Zfp287***

**Project type**

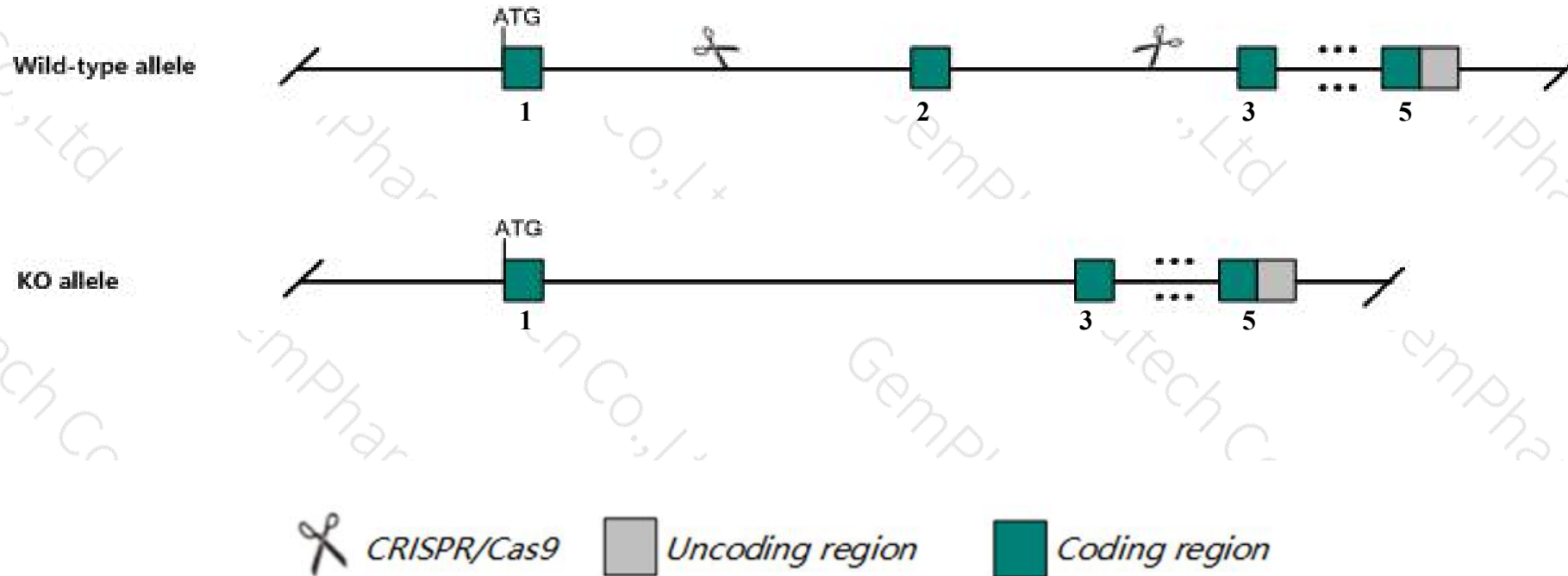
**Cas9-KO**

**Strain background**

**C57BL/6JGpt**

# Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *Zfp287* gene. The schematic diagram is as follows:



- The *Zfp287* gene has 6 transcripts. According to the structure of *Zfp287* gene, exon2 of *Zfp287-206* (ENSMUST00000185656.6) transcript is recommended as the knockout region. The region contains 104bp coding sequence. Knock out the region will result in disruption of protein function.
- In this project we use CRISPR/Cas9 technology to modify *Zfp287* gene. The brief process is as follows: CRISPR/Cas9 system

- The *Zfp287* 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 the gene knockout on gene transcription, RNA splicing and protein translation cannot be predicted at the existing technology level.



# Gene information (NCBI)

## Zfp287 zinc finger protein 287 [Mus musculus (house mouse)]

Gene ID: 170740, updated on 31-Jan-2019

### Summary



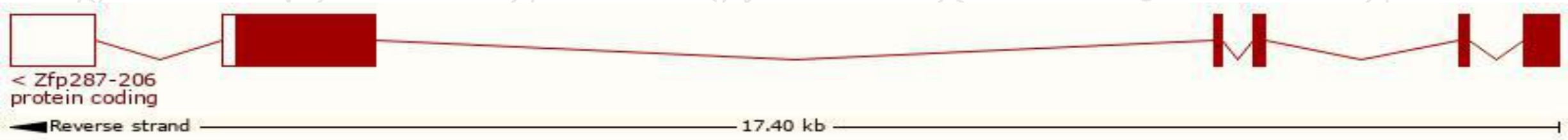
<b>Official Symbol</b>	Zfp287 provided by <a href="#">MGI</a>
<b>Official Full Name</b>	zinc finger protein 287 provided by <a href="#">MGI</a>
<b>Primary source</b>	<a href="#">MGI:MGI:2176561</a>
<b>See related</b>	<a href="#">Ensembl:ENSMUSG00000005267</a>
<b>Gene type</b>	protein coding
<b>RefSeq 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>	B230333C16Rik, SKAT-2, Skat2, Znf287, mszf16, mszf74, zfp-287
<b>Expression</b>	Broad expression in CNS E18 (RPKM 1.9), CNS E14 (RPKM 1.8) and 21 other tissues <a href="#">See more</a>
<b>Orthologs</b>	<a href="#">human</a> <a href="#">all</a>

# Transcript information (Ensembl)

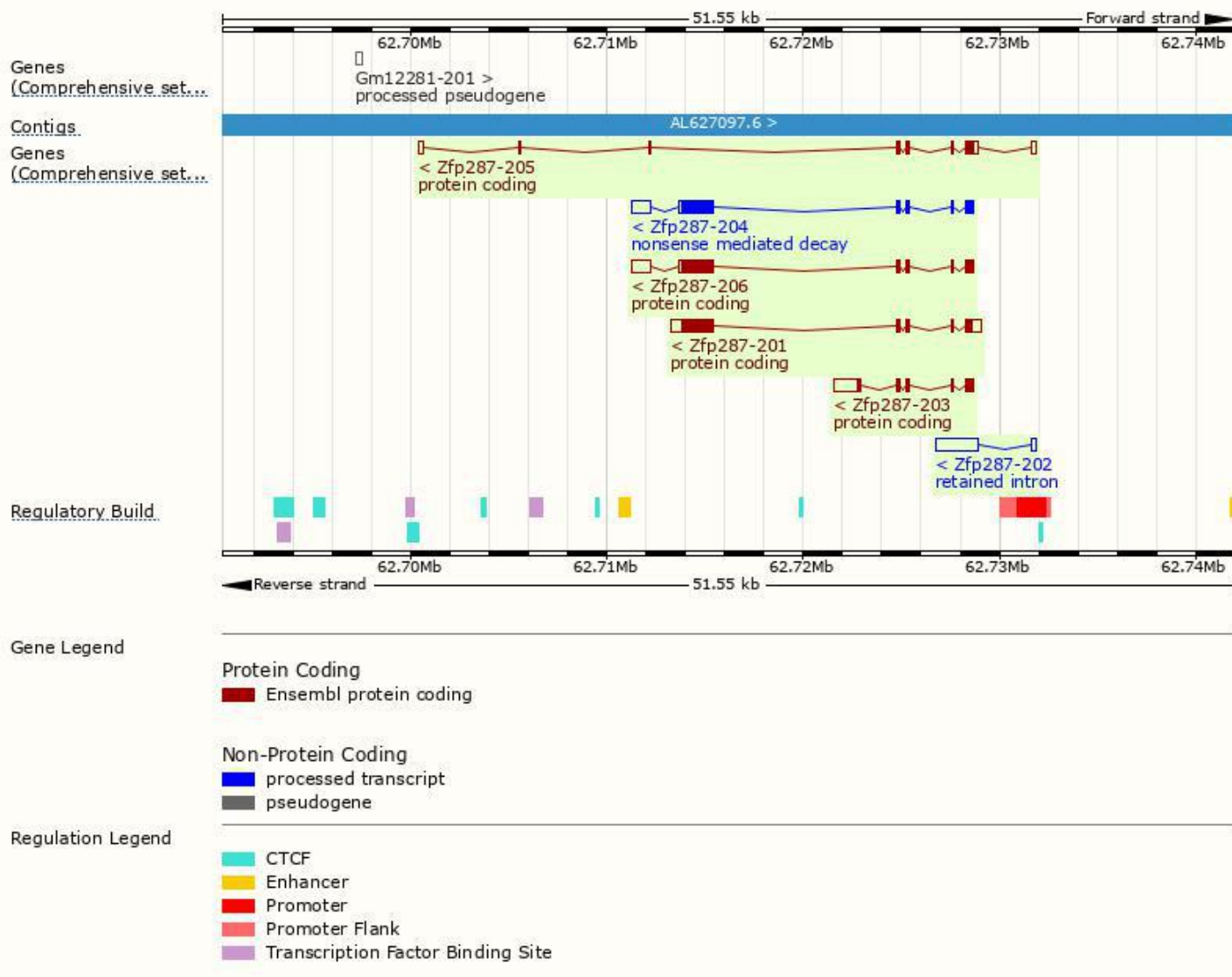
The gene has 6 transcripts,all transcripts are shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Zfp287-206	<a href="#">ENSMUST00000185656.6</a>	3370	<a href="#">759aa</a>	Protein coding	<a href="#">CCDS24830</a>	<a href="#">Q9EQB9</a>	TSL:1 GENCODE basic APPRIS P2
Zfp287-201	<a href="#">ENSMUST00000005399.9</a>	3220	<a href="#">748aa</a>	Protein coding	-	<a href="#">Q5SVS9</a>	TSL:1 GENCODE basic APPRIS ALT2
Zfp287-203	<a href="#">ENSMUST00000128370.1</a>	2062	<a href="#">274aa</a>	Protein coding	-	<a href="#">B7ZC81</a>	TSL:1 GENCODE basic
Zfp287-205	<a href="#">ENSMUST00000150336.7</a>	1605	<a href="#">297aa</a>	Protein coding	-	<a href="#">Q3UZW0</a>	TSL:1 GENCODE basic
Zfp287-204	<a href="#">ENSMUST00000149228.7</a>	3391	<a href="#">759aa</a>	Nonsense mediated decay	<a href="#">CCDS24830</a>	<a href="#">Q9EQB9</a>	TSL:1
Zfp287-202	<a href="#">ENSMUST00000127732.1</a>	2403	No protein	Retained intron	-	-	TSL:1

The strategy is based on the design of *Zfp287-206* transcript,The transcription is shown below



# Genomic location distribution

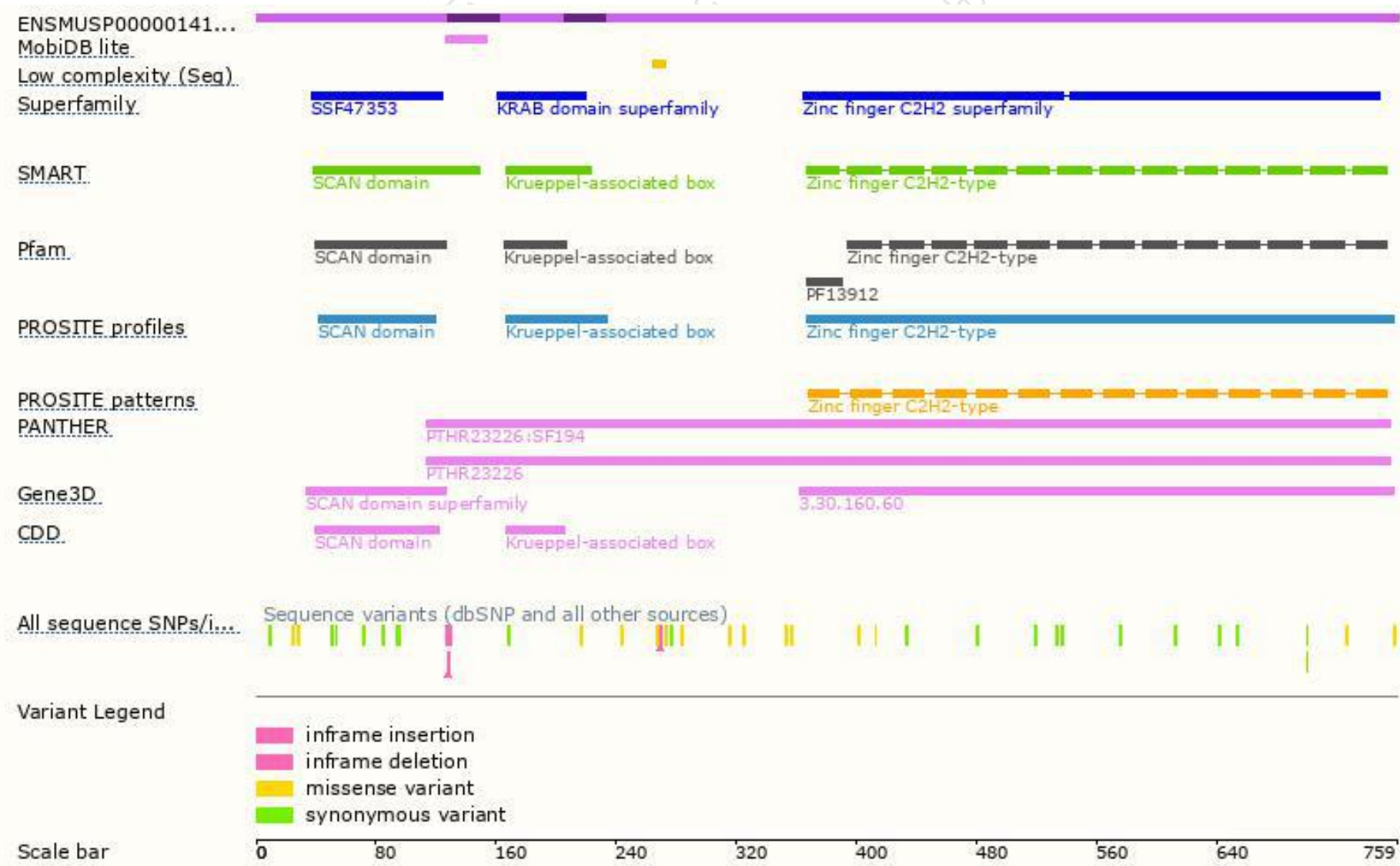




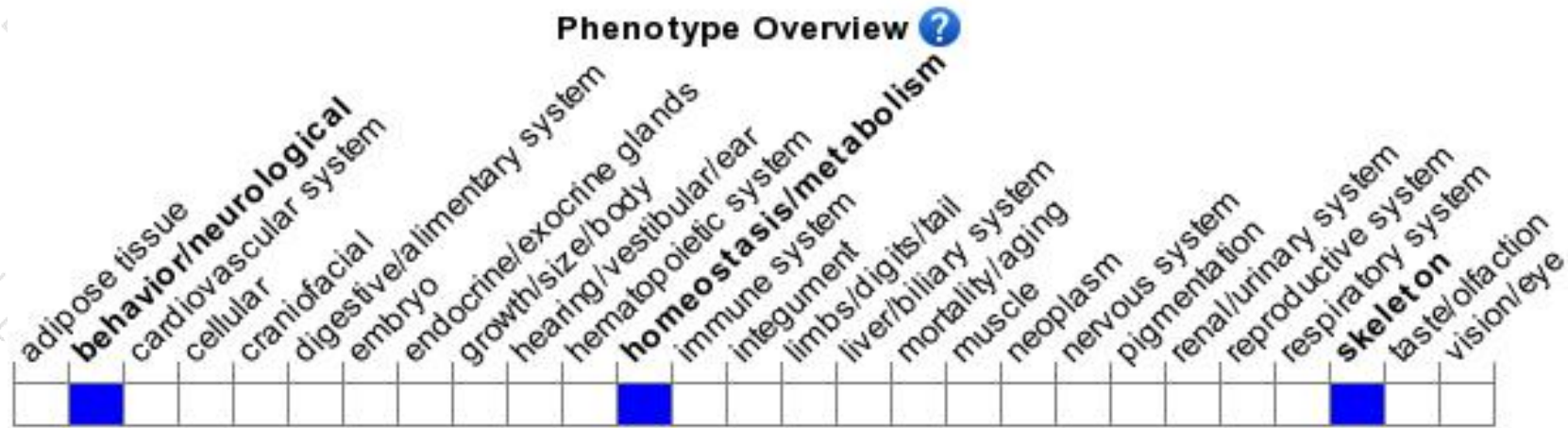
# Protein domain



集萃药康  
GemPharmatech



# 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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