

# ***Zfp422* Cas9-KO Strategy**

Designer: Ruirui Zhang

# Project Overview

**Project Name**

***Zfp422***

**Project type**

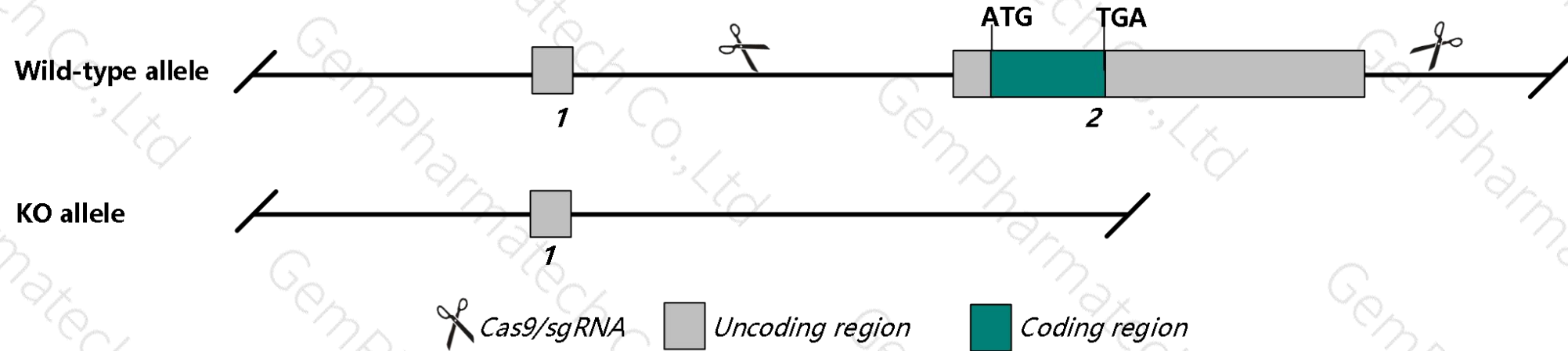
**Cas9-KO**

**Strain background**

**C57BL/6J**

# Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *Zfp422* gene. The schematic diagram is as follows:



- The *Zfp422* gene has 4 transcripts. According to the structure of *Zfp422* gene, exon2 of *Zfp422-202* (ENSMUST00000079749.5) transcript is recommended as the knockout region. The region contains all the coding sequence. Knock out the region will result in disruption of protein function.
- In this project we use CRISPR/Cas9 technology to modify *Zfp422* gene. The brief process is as follows: sgRNA was transcribed in vitro. Cas9 and sgRNA were microinjected into the fertilized eggs of C57BL/6J mice. Fertilized eggs were transplanted to obtain positive F0 mice which were confirmed by PCR and sequencing. A stable F1 generation mouse model was obtained by mating positive F0 generation mice with C57BL/6J mice.

- The *Zfp422* 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 gene transcription and translation processes, all risks cannot be predicted under existing information.



# Gene information (NCBI)

## Zfp422 zinc finger protein 422 [Mus musculus (house mouse)]

Gene ID: 67255, updated on 31-Jan-2019

### Summary



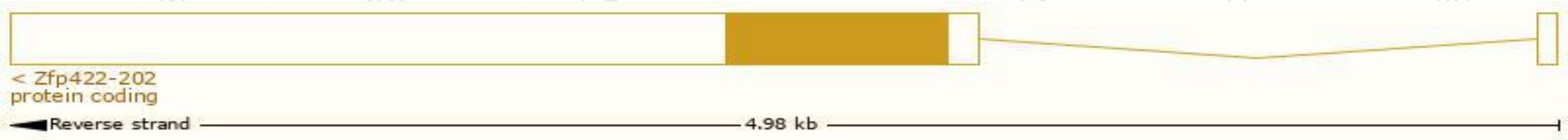
<b>Official Symbol</b>	Zfp422 provided by <a href="#">MGI</a>
<b>Official Full Name</b>	zinc finger protein 422 provided by <a href="#">MGI</a>
<b>Primary source</b>	<a href="#">MGI:MGI:1914505</a>
<b>See related</b>	<a href="#">Ensembl:ENSMUSG00000059878</a>
<b>Gene type</b>	protein coding
<b>RefSeq status</b>	REVIEWED
<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>	2900028O21Rik, AU041373, KOX15, Krox-25-2, Krox-26, Krox25, Krox26, Znf22
<b>Summary</b>	This gene encodes a putative C2H2 zinc finger transcription factor that may play a role in tooth development. A pseudogene related to this gene is located on chromosome 17. Alternative splicing results in multiple transcript variants. [provided by RefSeq, Oct 2014]
<b>Expression</b>	Broad expression in CNS E11.5 (RPKM 40.6), CNS E14 (RPKM 29.8) and 21 other tissues <a href="#">See more</a>
<b>Orthologs</b>	<a href="#">human</a> <a href="#">all</a>

# Transcript information (Ensembl)

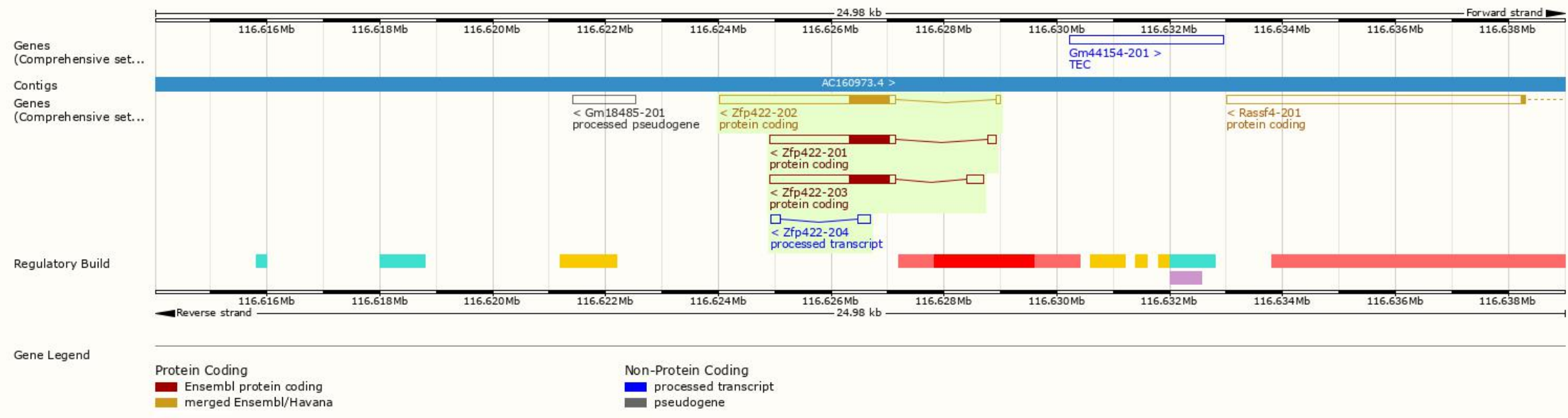
The gene has 4 transcripts,all transcripts are shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Zfp422-202	<a href="#">ENSMUST00000079749.5</a>	3187	<a href="#">237aa</a>	Protein coding	<a href="#">CCDS20459</a>	<a href="#">Q9ERU3</a>	TSL:1 GENCODE basic APPRIS P1
Zfp422-203	<a href="#">ENSMUST00000112880.7</a>	2523	<a href="#">237aa</a>	Protein coding	<a href="#">CCDS20459</a>	<a href="#">Q9ERU3</a>	TSL:1 GENCODE basic APPRIS P1
Zfp422-201	<a href="#">ENSMUST00000057540.5</a>	2375	<a href="#">237aa</a>	Protein coding	<a href="#">CCDS20459</a>	<a href="#">Q9ERU3</a>	TSL:1 GENCODE basic APPRIS P1
Zfp422-204	<a href="#">ENSMUST00000204557.1</a>	398	No protein	Processed transcript	-	-	TSL:2

The strategy is based on the design of *Zfp422-202* transcript,The transcription is shown below



# Genomic location distribution

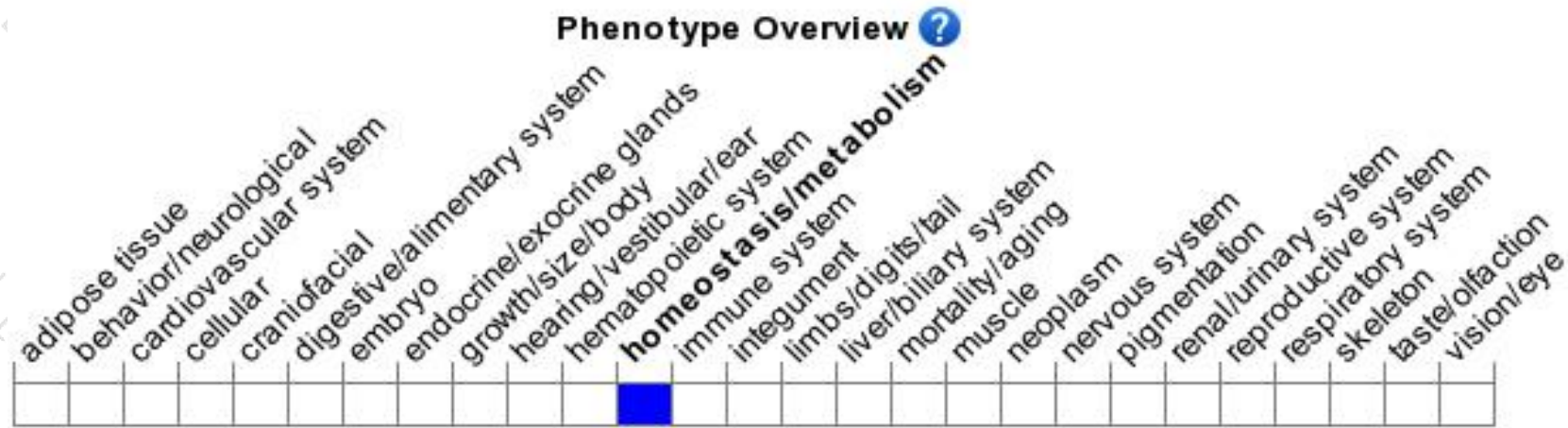




# Protein domain



# Mouse phenotype description(MGI )



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

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

Tel: 025-5864 1534

