

# *Dspp* Cas9-CKO Strategy

**Designer:**

**Daohua Xu**

**Reviewer:**

**Huimin Su**

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# Project Overview

**Project Name**

*Dspp*

**Project type**

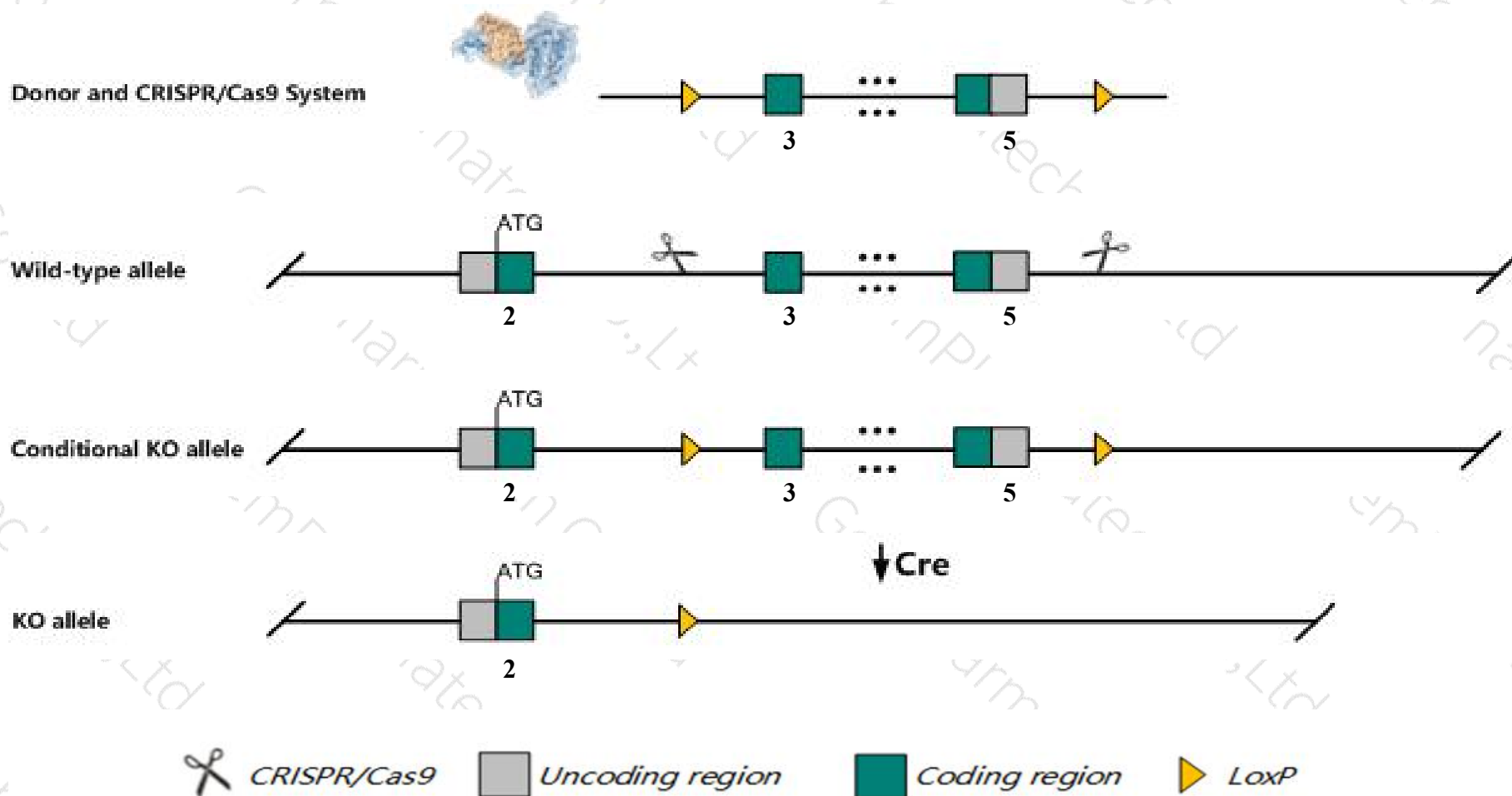
**Cas9-CKO**

**Strain background**

**C57BL/6JGpt**

# Conditional Knockout strategy

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



- The *Dspp* gene has 1 transcript. According to the structure of *Dspp* gene, exon3-exon5 of *Dspp-201* (ENSMUST00000112771.1) 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 *Dspp* gene. The brief process is as follows: CRISPR/Cas9 system and Donor were microinjected into the fertilized eggs of C57BL/6JGpt 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/6JGpt mice.
- The flox mice will be knocked out after mating with mice expressing Cre recombinase, resulting in the loss of function of the target gene in specific tissues and cell types.

- According to the existing MGI data, Aging mice homozygous for a reporter/null allele display tooth abnormalities, including enlarged pulp cavities, a widened predentin zone, dentin hypomineralization, pulp exposure, and occasional brittle incisors.
- The *Dspp* gene is located on the Chr5. 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 loxp insertion on gene transcription, RNA splicing and protein translation cannot be predicted at existing technological level.



# Gene information (NCBI)

## Dspp dentin sialophosphoprotein [Mus musculus (house mouse)]

Gene ID: 666279, updated on 31-Jan-2019

### Summary



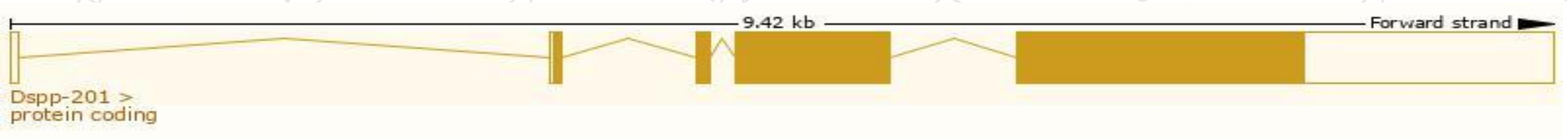
<b>Official Symbol</b>	Dspp provided by <a href="#">MGI</a>
<b>Official Full Name</b>	dentin sialophosphoprotein provided by <a href="#">MGI</a>
<b>Primary source</b>	<a href="#">MGI:MGI:109172</a>
<b>See related</b>	<a href="#">Ensembl:ENSMUSG000000053268</a>
<b>Gene type</b>	protein coding
<b>RefSeq 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>	Dmp2, Dmp3, Dpp, Dsp
<b>Summary</b>	This gene encodes a member of the small integrin-binding ligand N-linked glycoprotein (SIBLING) family of proteins. The encoded preproprotein is secreted by odontoblasts and proteolytically processed to generate two principal proteins of the dentin extracellular matrix of the tooth, dentin sialoprotein and dentin phosphoprotein. These two protein products may play distinct but related roles in dentin mineralization. Mice lacking the encoded protein exhibit hypomineralization defects in dentin, similar to human dentinogenesis imperfecta. [provided by RefSeq, Feb 2016]
<b>Expression</b>	Low expression observed in reference dataset <a href="#">See more</a>
<b>Orthologs</b>	<a href="#">human</a> <a href="#">all</a>

# Transcript information (Ensembl)

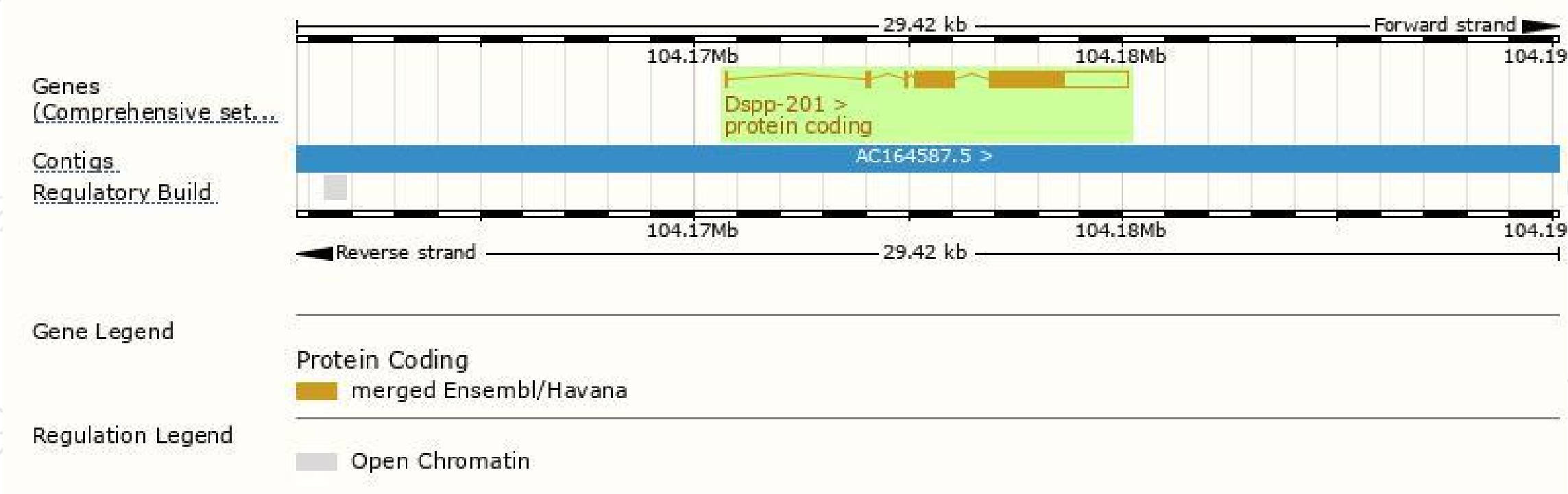
The gene has 1 transcript, and the transcript is shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Dspp-201	<a href="#">ENSMUST00000112771.1</a>	4431	<a href="#">945aa</a>	Protein coding	<a href="#">CCDS39190</a>	<a href="#">E9Q9Z9</a>	TSL:1 GENCODE basic APPRIS P1

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

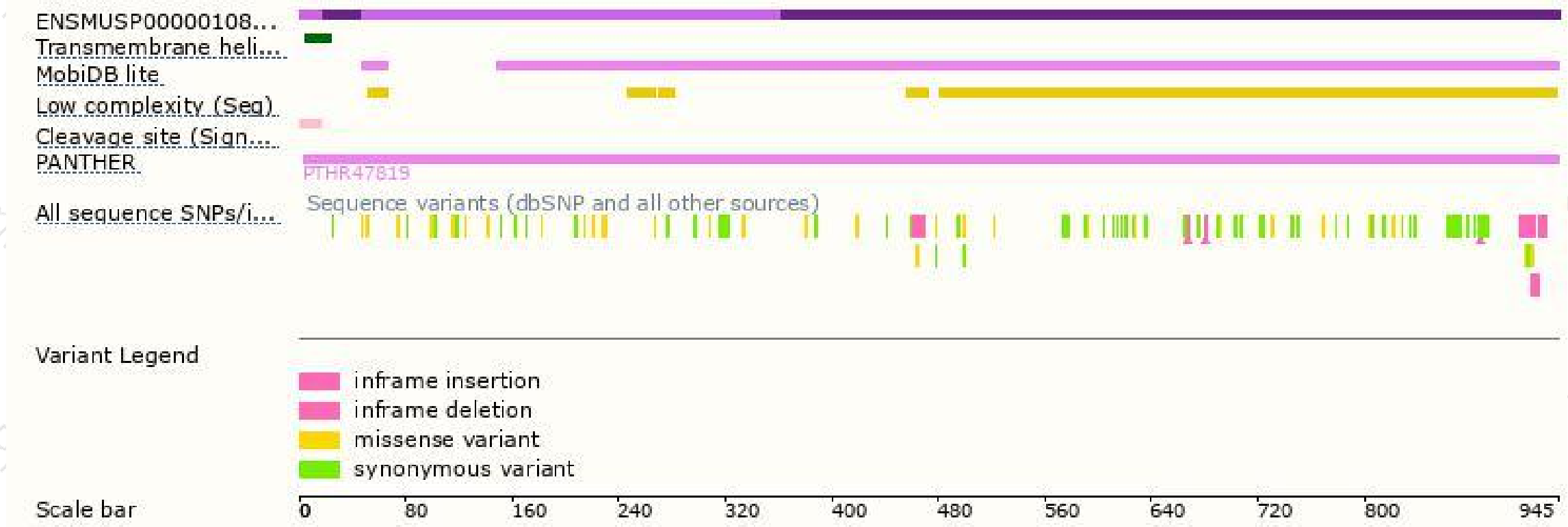


# Genomic location distribution

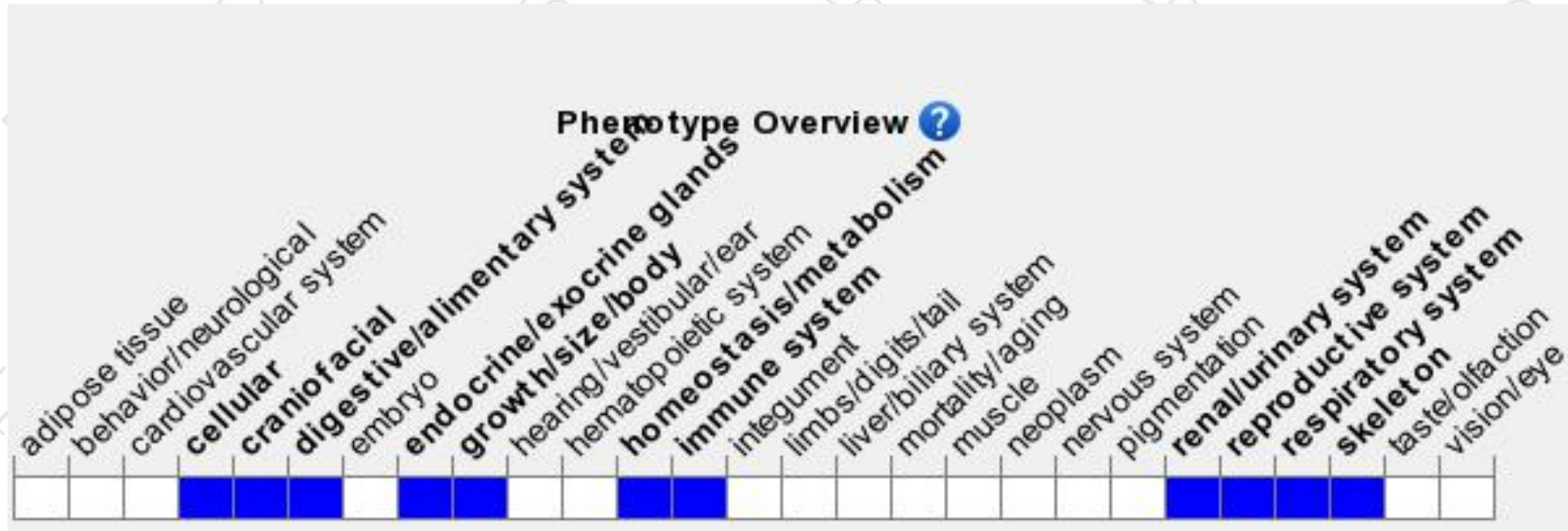




# Protein domain



# Mouse phenotype description(MGI)



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

According to the existing MGI data, Aging mice homozygous for a reporter/null allele display tooth abnormalities, including enlarged pulp cavities, a widened predentin zone, dentin hypomineralization, pulp exposure, and occasional brittle incisors.

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

Tel: 400-9660890

