

# *Krt19* Cas9-KO Strategy

**Designer:**

**Yanhua Shen**

**Reviewer:**

**Xueting Zhang**

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# Project Overview

**Project Name**

***Krt19***

**Project type**

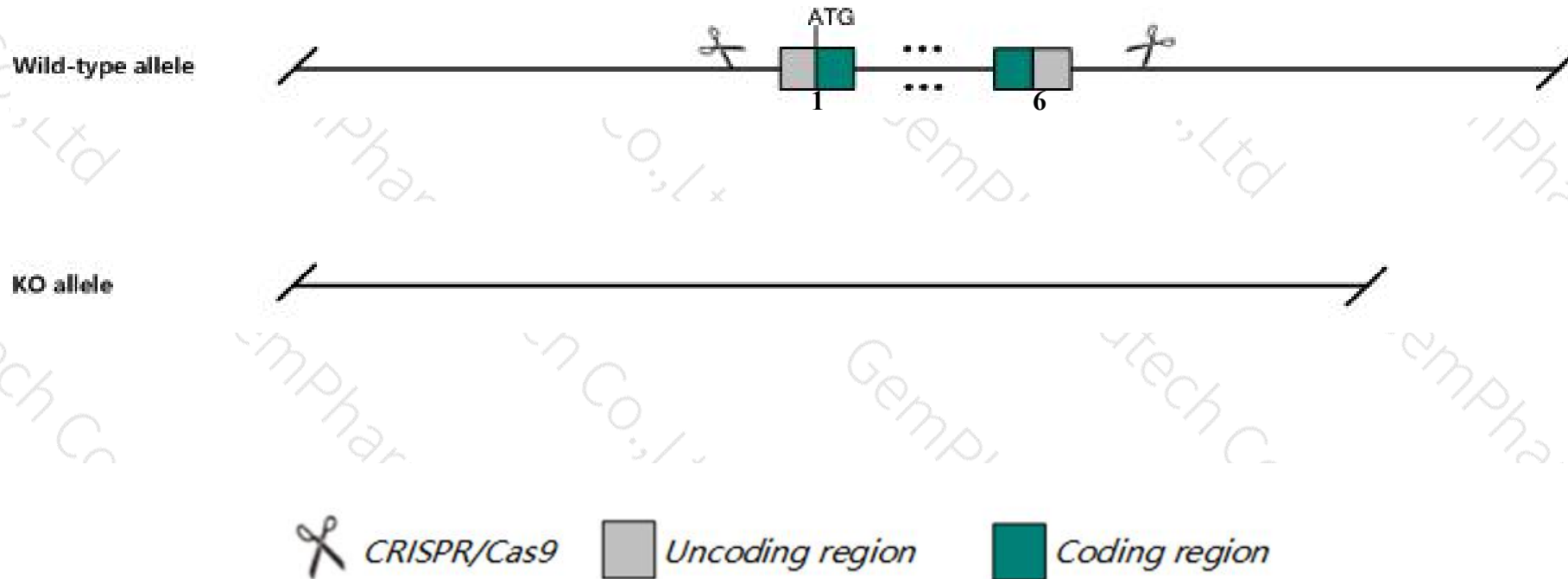
**Cas9-KO**

**Strain background**

**C57BL/6JGpt**

# Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *Krt19* gene. The schematic diagram is as follows:



- The *Krt19* gene has 3 transcripts. According to the structure of *Krt19* gene, exon1-exon6 of *Krt19-201* (ENSMUST00000007317.7) transcript is recommended as the knockout region. The region contains all 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 *Krt19* gene. The brief process is as follows: CRISPR/Cas9 system

- According to the existing MGI data, Mice homozygous for a knock-in allele are viable. Mice homozygous for a reporter allele show partial and strain-dependent preweaning lethality but no anatomical or behavioral defects. Mice that are either homozygous or heterozygous for a targeted insertion into intron 6 exhibit sperm tail defects.
- The *Krt19* 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)

## Krt19 keratin 19 [ *Mus musculus* (house mouse) ]

Gene ID: 16669, updated on 14-Jan-2020

### Summary

Official Symbol	Krt19 provided by MGI
Official Full Name	keratin 19 provided by MGI
Primary source	<a href="#">MGI:MGI:96693</a>
See related	<a href="#">Ensembl:ENSMUSG00000020911</a>
Gene type	protein coding
RefSeq status	REVIEWED
Organism	<a href="#">Mus musculus</a>
Lineage	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Myomorpha; Muroidea; Muridae; Murinae; Mus; Mus
Also known as	K19; CK-19; EndoC; Krt1-19; AI663979; Krt-1.19
Summary	The protein encoded by this gene is a member of the keratin family. The keratins are intermediate filament proteins responsible for the structural integrity of epithelial cells and are subdivided into cytokeratins and hair keratins. The type I cytokeratins consist of acidic proteins which are arranged in pairs of heterotypic keratin chains. Unlike its related family members, this smallest known acidic cytokeratin is not paired with a basic cytokeratin in epithelial cells. It is specifically expressed in the periderm, the transiently superficial layer that envelopes the developing epidermis. Two transcript variants encoding different isoforms have been found for this gene. [provided by RefSeq, Sep 2015]
Expression	Biased expression in colon adult (RPKM 2054.0), stomach adult (RPKM 1224.1) and 8 other tissues <a href="#">See more</a>
Orthologs	<a href="#">human</a> <a href="#">all</a>

### Genomic context

Location: 11 D; 11 63.42 cM

Exon count: 7

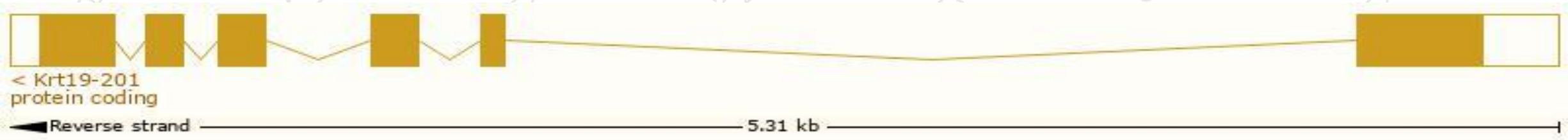
See Krt19 in [Genome Data Viewer](#)

# Transcript information (Ensembl)

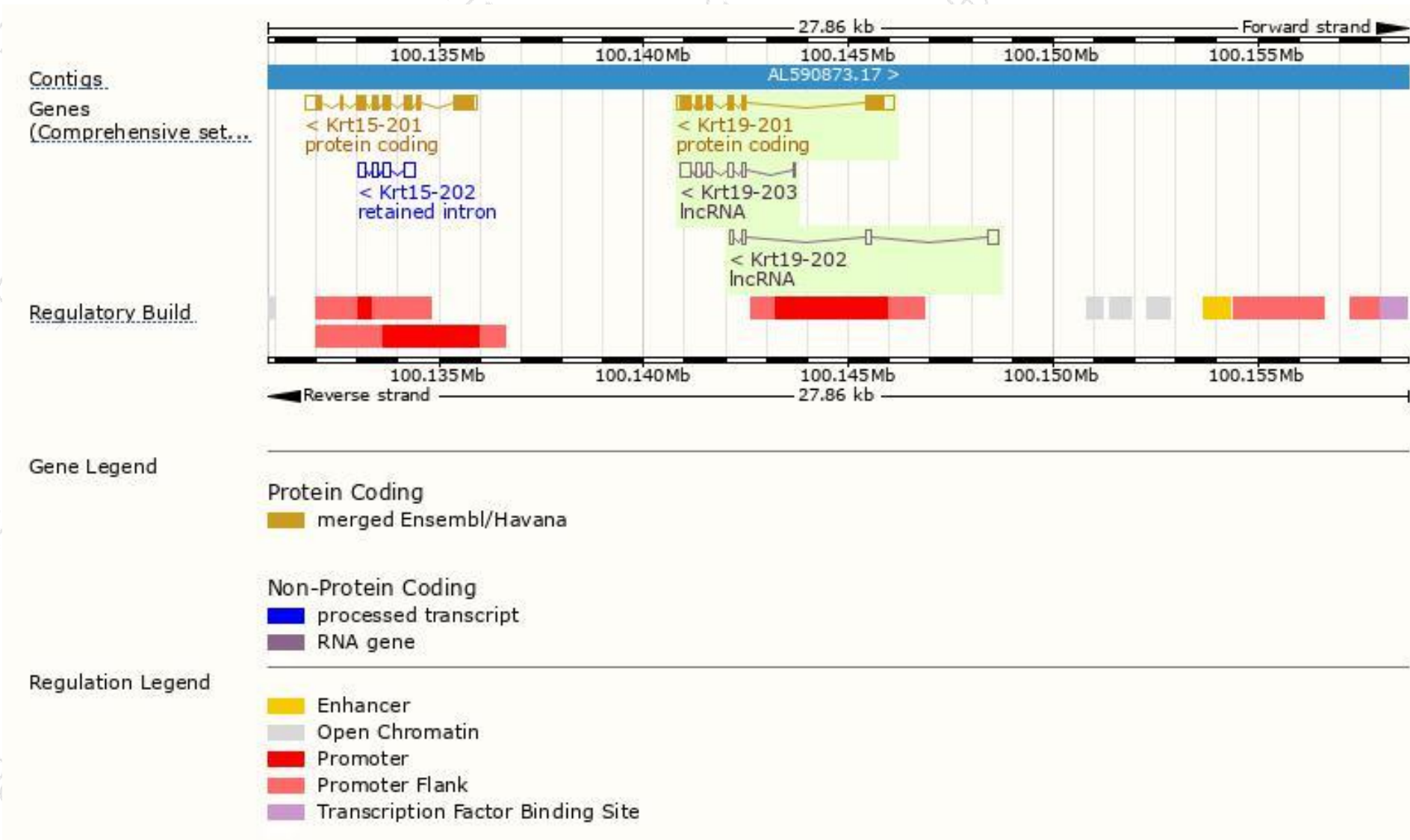
The gene has 3 transcripts,all transcripts are shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Krt19-201	<a href="#">ENSMUST00000007317.7</a>	1576	<a href="#">403aa</a>	Protein coding	<a href="#">CCDS25411</a>	<a href="#">B1AQ78 P19001</a>	TSL:1 GENCODE basic APPRIS P1
Krt19-203	<a href="#">ENSMUST00000126460.7</a>	823	No protein	lncRNA	-	-	TSL:3
Krt19-202	<a href="#">ENSMUST00000125888.1</a>	546	No protein	lncRNA	-	-	TSL:5

The strategy is based on the design of *Krt19-201* transcript,The transcription is shown below

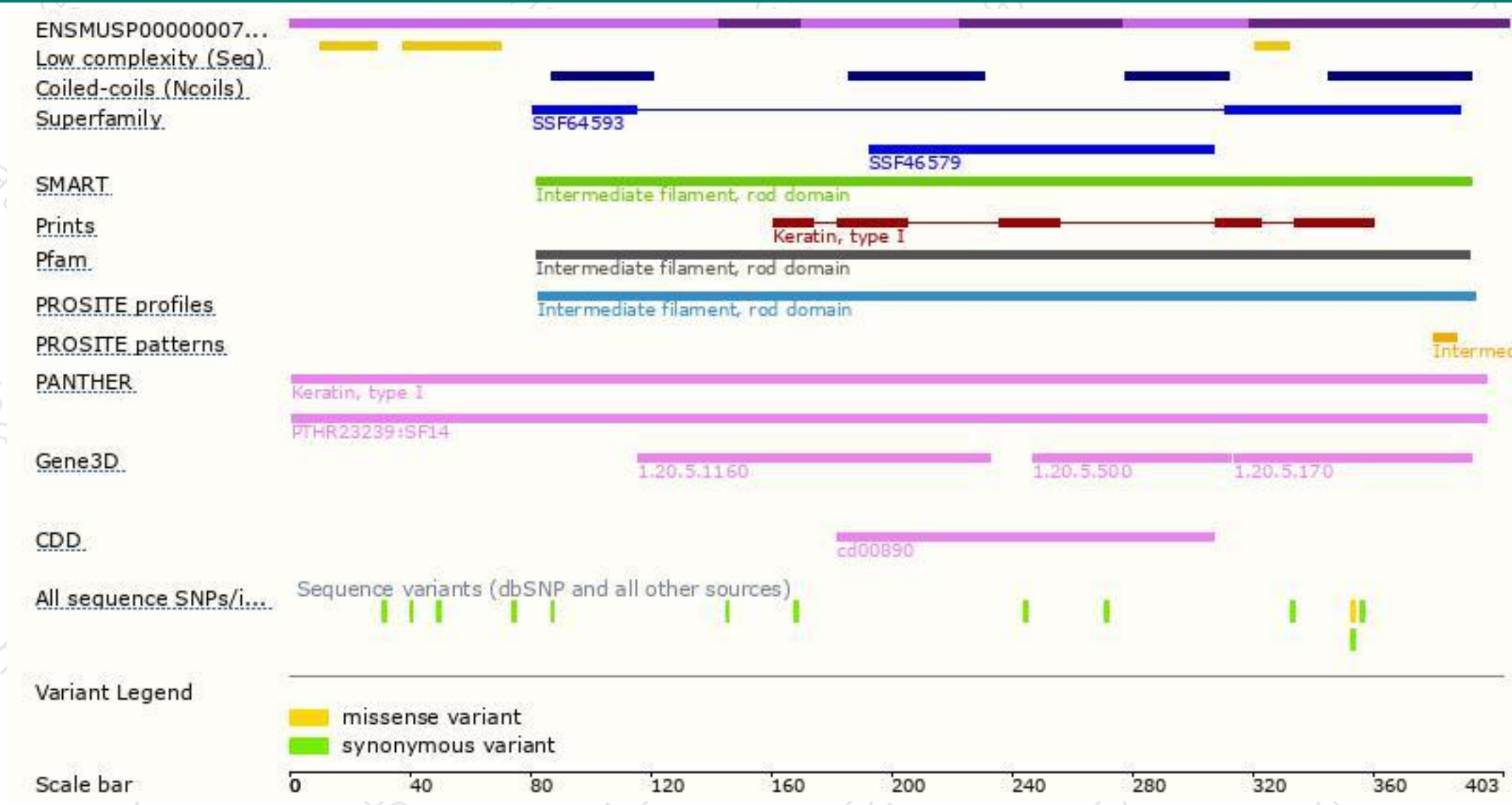


# Genomic location distribution

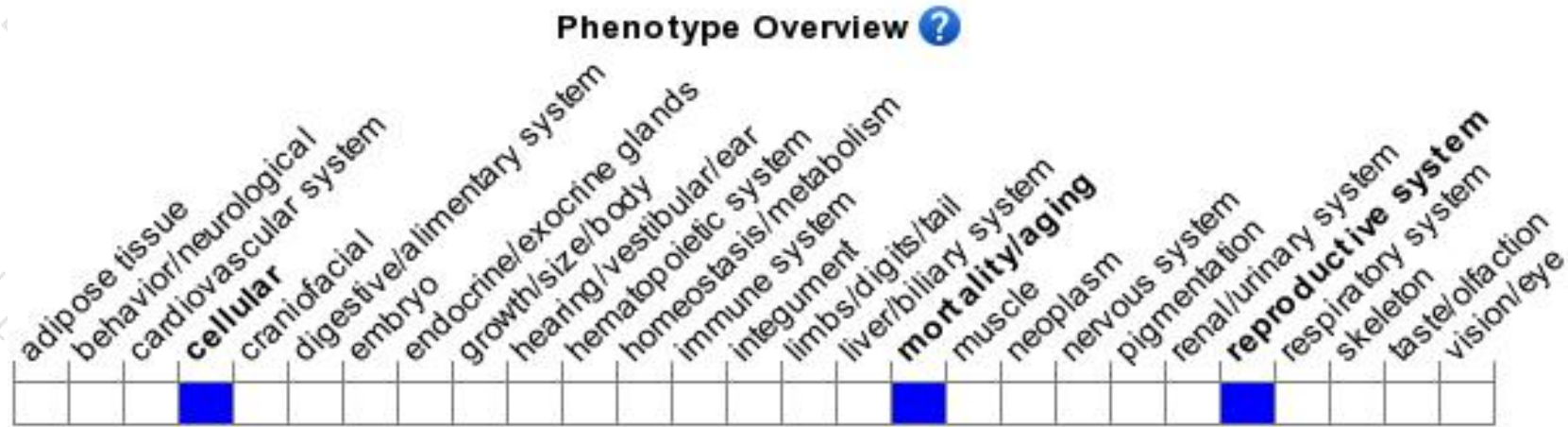




# Protein domain



# 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, Mice homozygous for a knock-in allele are viable. Mice homozygous for a reporter allele show partial and strain-dependent preweaning lethality but no anatomical or behavioral defects. Mice that are either homozygous or heterozygous for a targeted insertion into intron 6 exhibit sperm tail defects.

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

Tel: 400-9660890

