

Prss8 Cas9-KO Strategy

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Project Overview

Project Name

Prss8

Project type

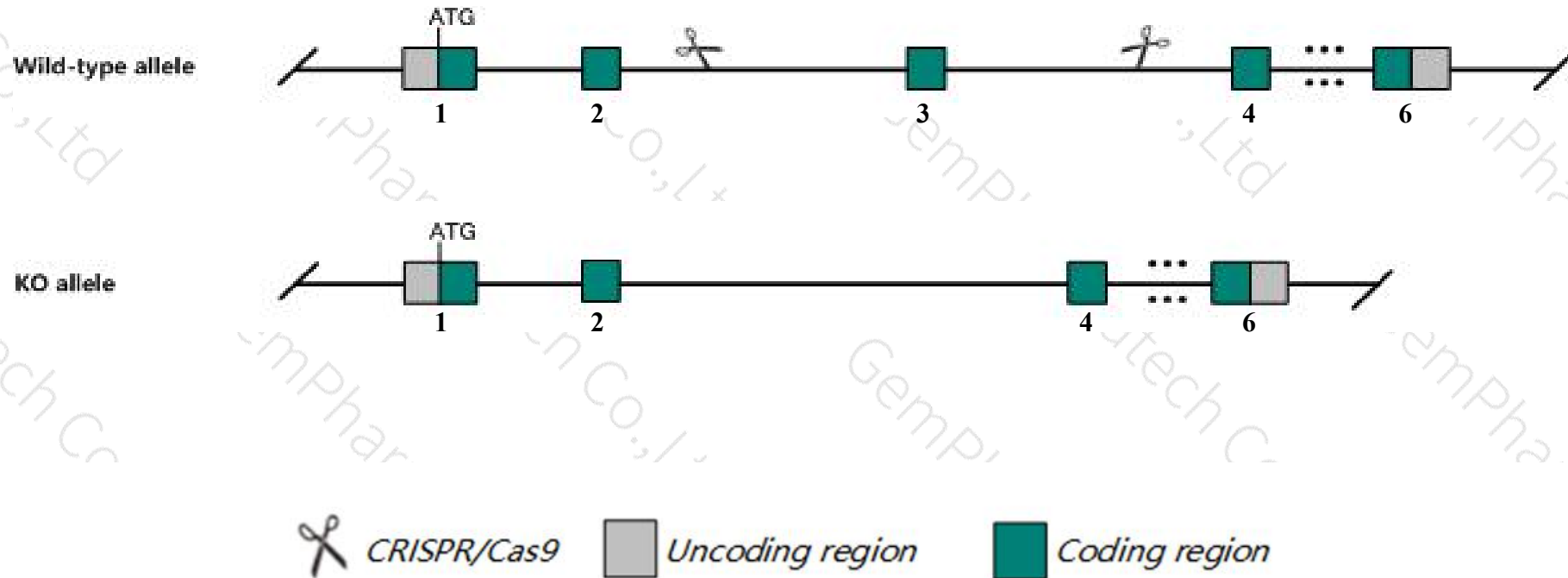
Cas9-KO

Strain background

C57BL/6JGpt

Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *Prss8* gene. The schematic diagram is as follows:



- The *Prss8* gene has 3 transcripts. According to the structure of *Prss8* gene, exon3 of *Prss8-201* (ENSMUST00000032988.9) transcript is recommended as the knockout region. The region contains 163bp coding sequence. Knock out the region will result in disruption of protein function.
- In this project we use CRISPR/Cas9 technology to modify *Prss8* gene. The brief process is as follows: CRISPR/Cas9 system

- According to the existing MGI data, nullizygous mutations result in impaired skin barrier function, dehydration, and postnatal lethality.
- *Kat8* gene is about 2.0kb away from *Prss8* exon3. This strategy may affect the 3-terminal regulation function of *Kat8* gene.
- The *Prss8* gene is located on the Chr7. 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)

Prss8 protease, serine 8 (prostasin) [*Mus musculus* (house mouse)]

Gene ID: 76560, updated on 12-Aug-2019

Summary



Official Symbol Prss8 provided by [MGI](#)

Official Full Name protease, serine 8 (prostasin) provided by [MGI](#)

Primary source [MGI:MGI:1923810](#)

See related [Ensembl:ENSMUSG00000030800](#)

Gene type protein coding

RefSeq status VALIDATED

Organism [Mus musculus](#)

Lineage Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Myomorpha; Muroidea; Muridae; Murinae; Mus; Mus

Also known as fr; CAP1; mCAP1; C79772; AI313909; 2410039E18Rik

Expression Biased expression in kidney adult (RPKM 285.2), placenta adult (RPKM 115.0) and 10 other tissues [See more](#)

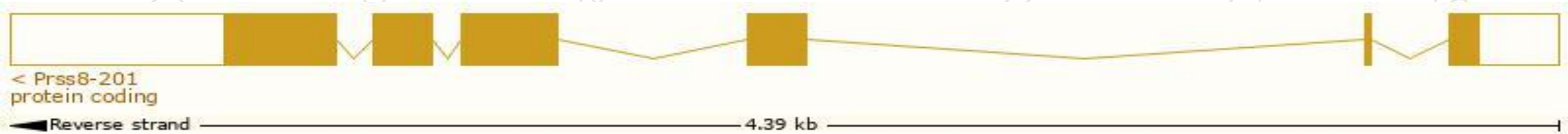
Orthologs [human](#) [all](#)

Transcript information (Ensembl)

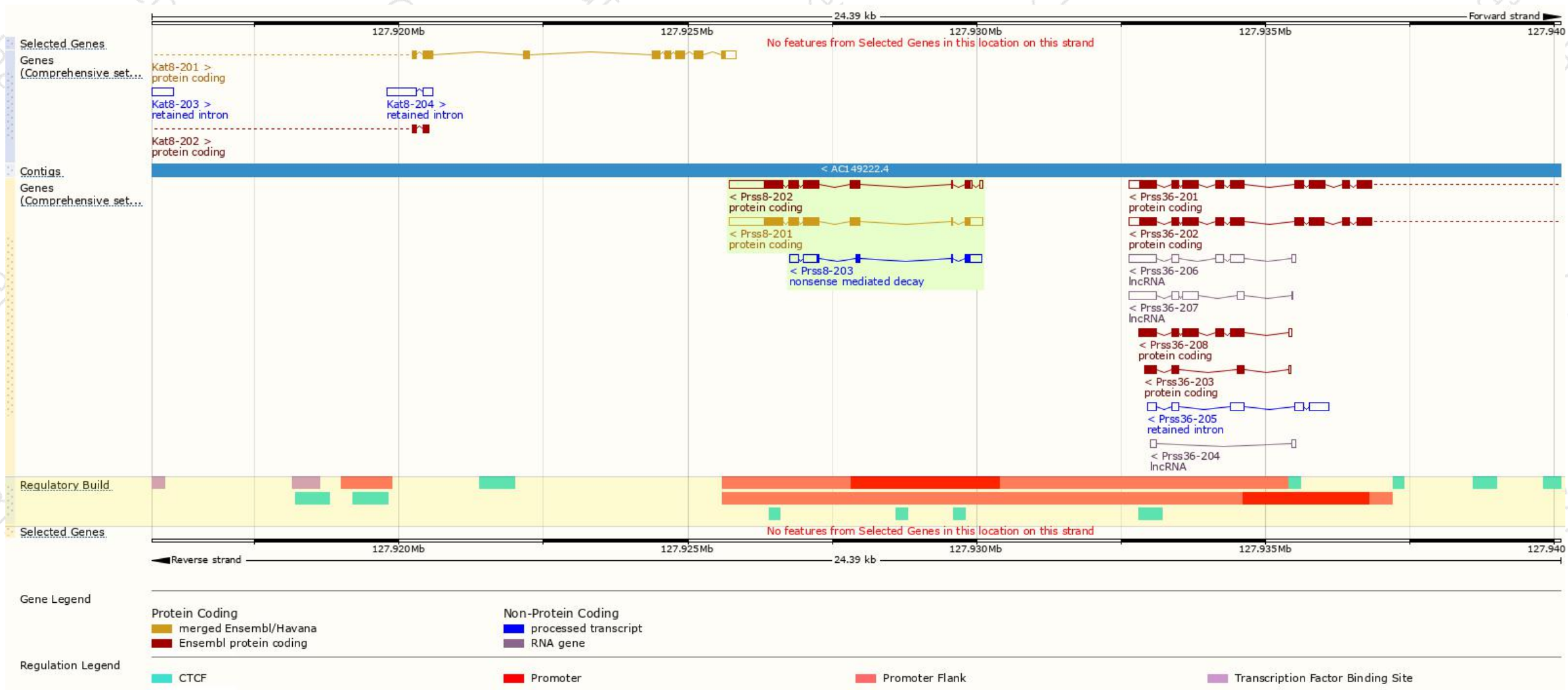
The gene has 3 transcripts,all transcripts are shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Prss8-201	ENSMUST00000032988.9	1852	339aa	Protein coding	CCDS40147	Q99L44	TSL:1 GENCODE basic APPRIS P1
Prss8-202	ENSMUST00000206124.1	1709	339aa	Protein coding	CCDS40147	Q99L44	TSL:1 GENCODE basic APPRIS P1
Prss8-203	ENSMUST00000206568.1	795	62aa	Nonsense mediated decay	-	A0A0U1RQA6	TSL:3

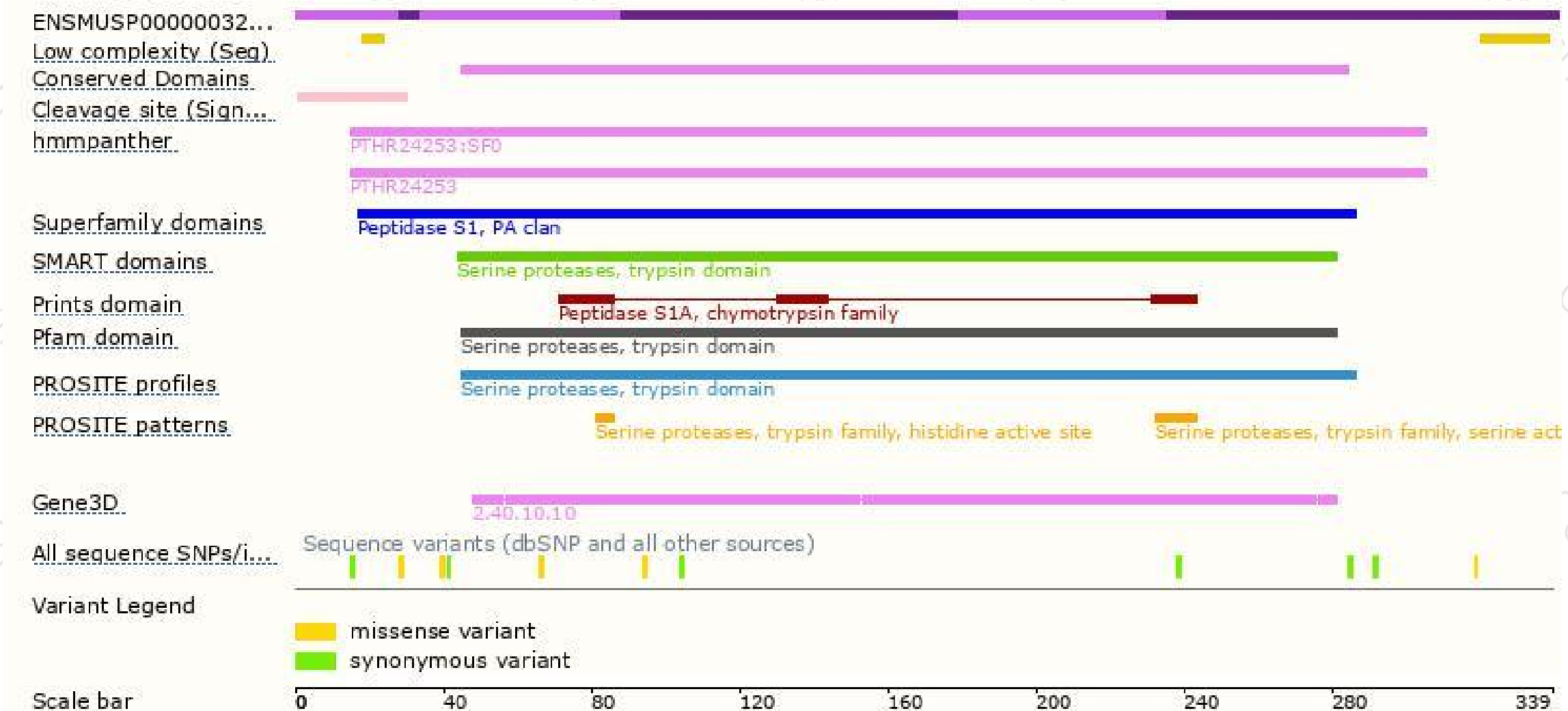
The strategy is based on the design of *Prss8-201* transcript,The transcription is shown below



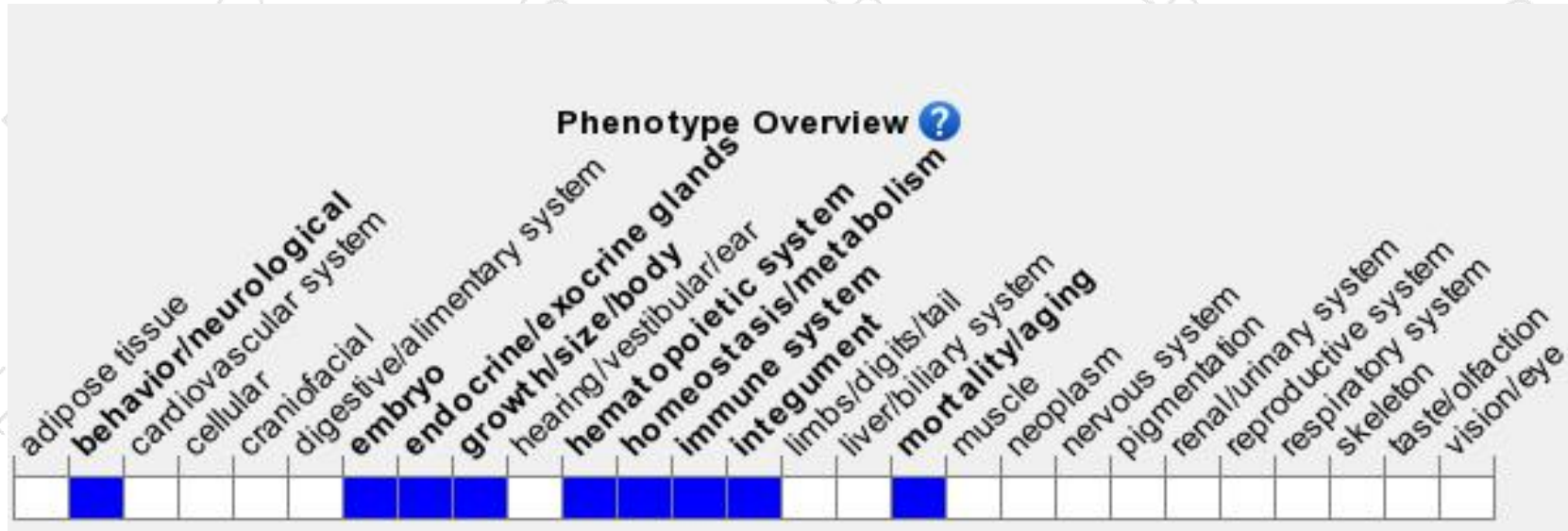
Genomic location distribution



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, Nullizygous mutations result in impaired skin barrier function, dehydration, and postnatal lethality.

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

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