

Nlrp3 Cas9-KO Strategy

Designer:

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Design Date:

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Project Overview

Project Name

Nlrp3

Project type

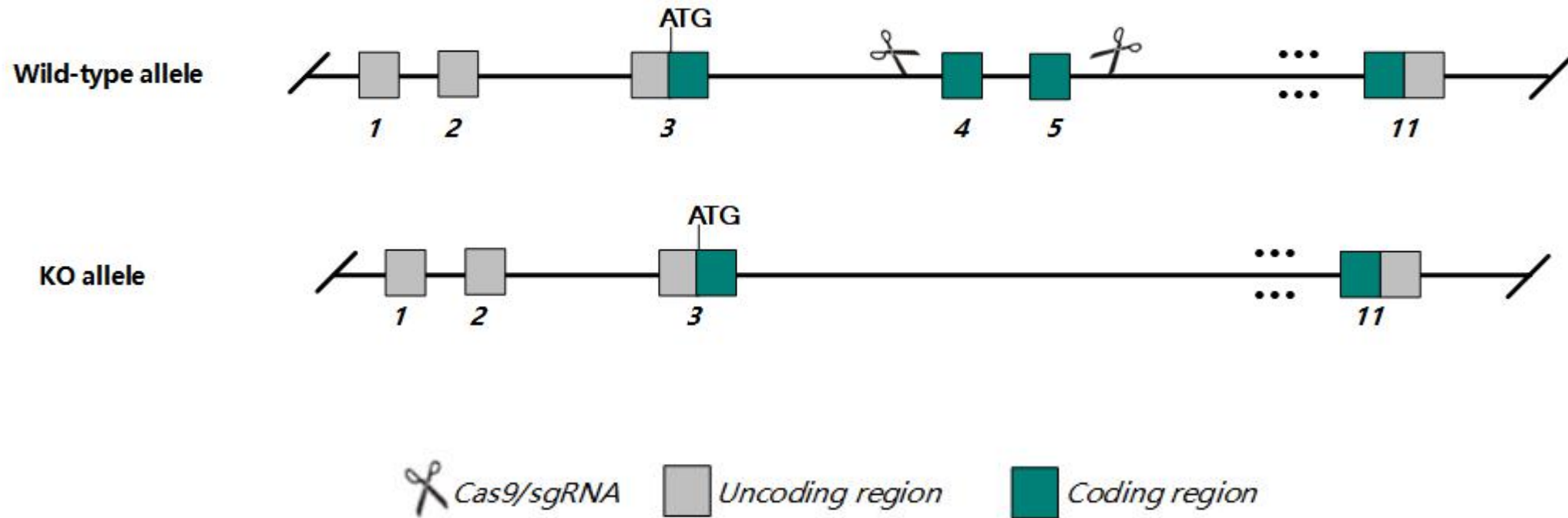
Cas9-KO

Strain background

C57BL/6J

Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *Nlrp3* gene. The schematic diagram is as follows:



- The *Nlrp3* gene has 3 transcripts. According to the structure of *Nlrp3* gene, exon4-exon5 of *Nlrp3-201* (ENSMUST00000079476.9) transcript is recommended as the knockout region. The region contains 1870bp coding sequence. Knock out the region will result in disruption of protein function.
- In this project we use CRISPR/Cas9 technology to modify *Nlrp3* 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.

- According to the existing MGI data, Mice homozygous for null mutations exhibit attenuated inflammatory responses related to decrease secretion of IL-1 β and IL-18. Mice heterozygous for activating mutations suffer from autoinflammatory attacks that lead to organ failure and death before weaning.
- The *Nlrp3* 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)

Nlrp3 NLR family, pyrin domain containing 3 [Mus musculus (house mouse)]

Gene ID: 216799, updated on 9-Apr-2019

Summary



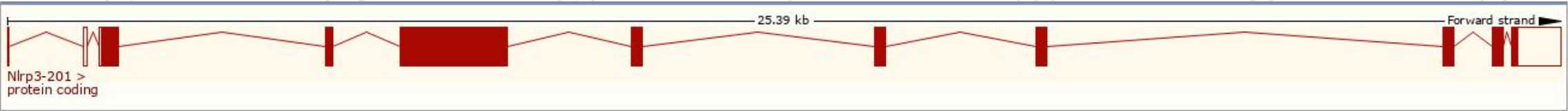
Official Symbol	Nlrp3 provided by MGI
Official Full Name	NLR family, pyrin domain containing 3 provided by MGI
Primary source	MGI:MGI:2653833
See related	Ensembl:ENSMUSG00000032691
Gene type	protein coding
RefSeq status	VALIDATED
Organism	Mus musculus
Lineage	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Myomorpha; Muroidea; Muridae; Murinae; Mus; Mus
Also known as	AGTAVPRL, Ail/AVP, Cias1, FCAS, FCU, MWS, Mmig1, NALP3, Pypaf1
Expression	Broad expression in spleen adult (RPKM 1.1), lung adult (RPKM 0.8) and 25 other tissues See more
Orthologs	human all

Transcript information (Ensembl)

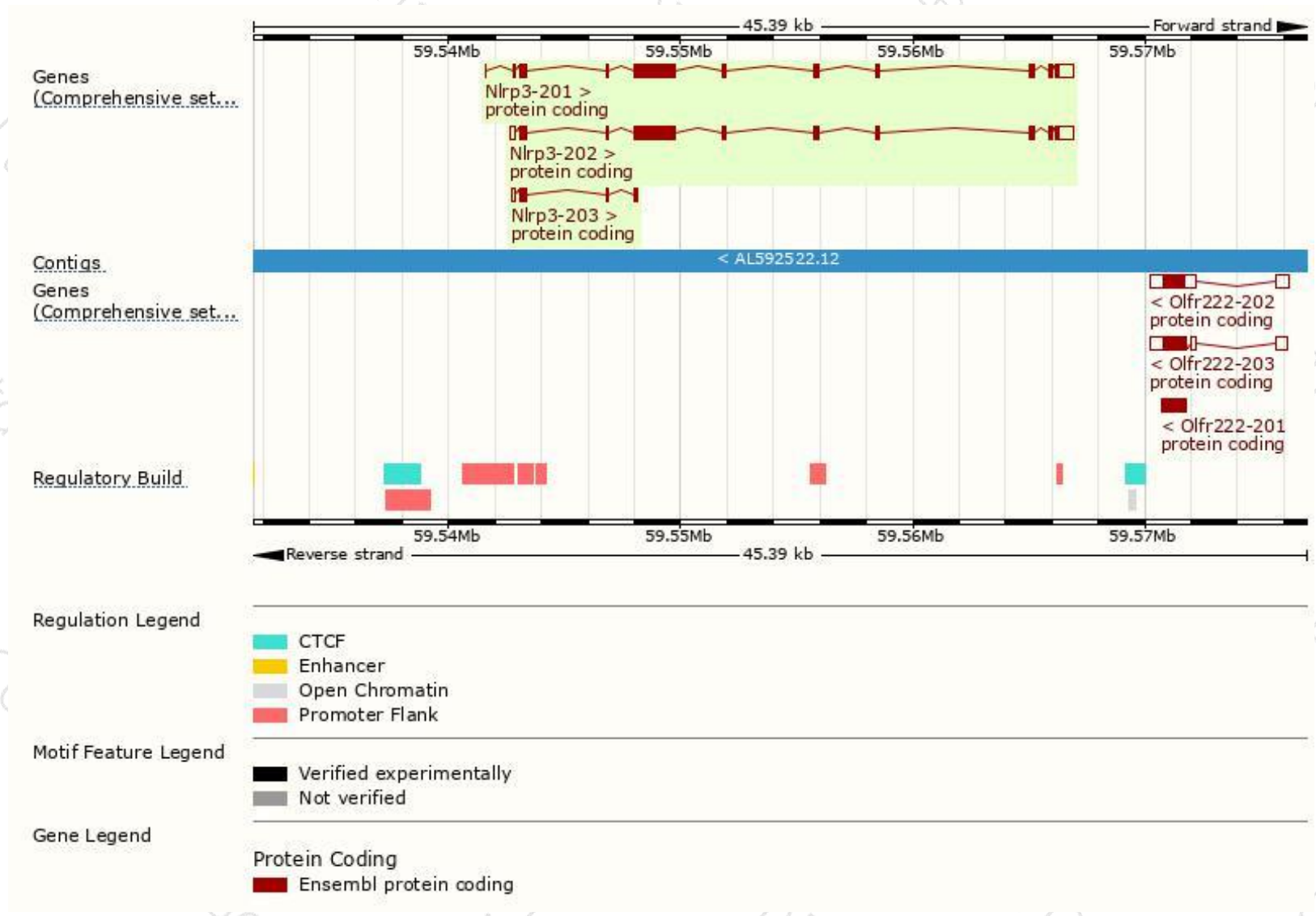
The gene has 3 transcripts,all transcripts are shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Nlrp3-202	ENSMUST00000101148.8	4021	1033aa	Protein coding	CCDS24771	Q8R4B8	TSL:1 GENCODE basic APPRIS P1
Nlrp3-201	ENSMUST00000079476.9	3933	1033aa	Protein coding	CCDS24771	Q8R4B8	TSL:1 GENCODE basic APPRIS P1
Nlrp3-203	ENSMUST00000149126.1	676	173aa	Protein coding	-	Q5SXI6	CDS 3' incomplete TSL:2

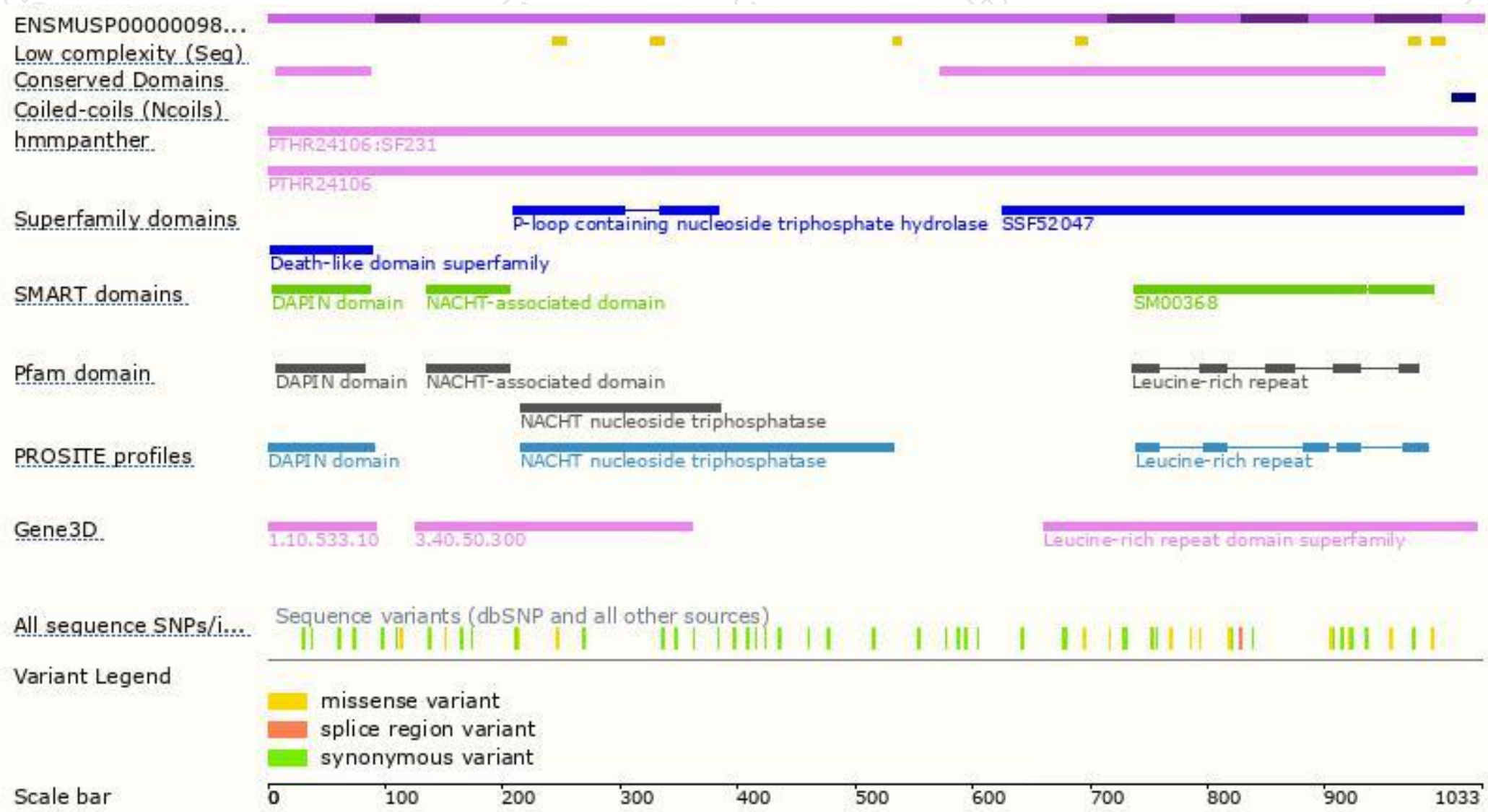
The strategy is based on the design of *Nlrp3-201*transcript,The transcription is shown below



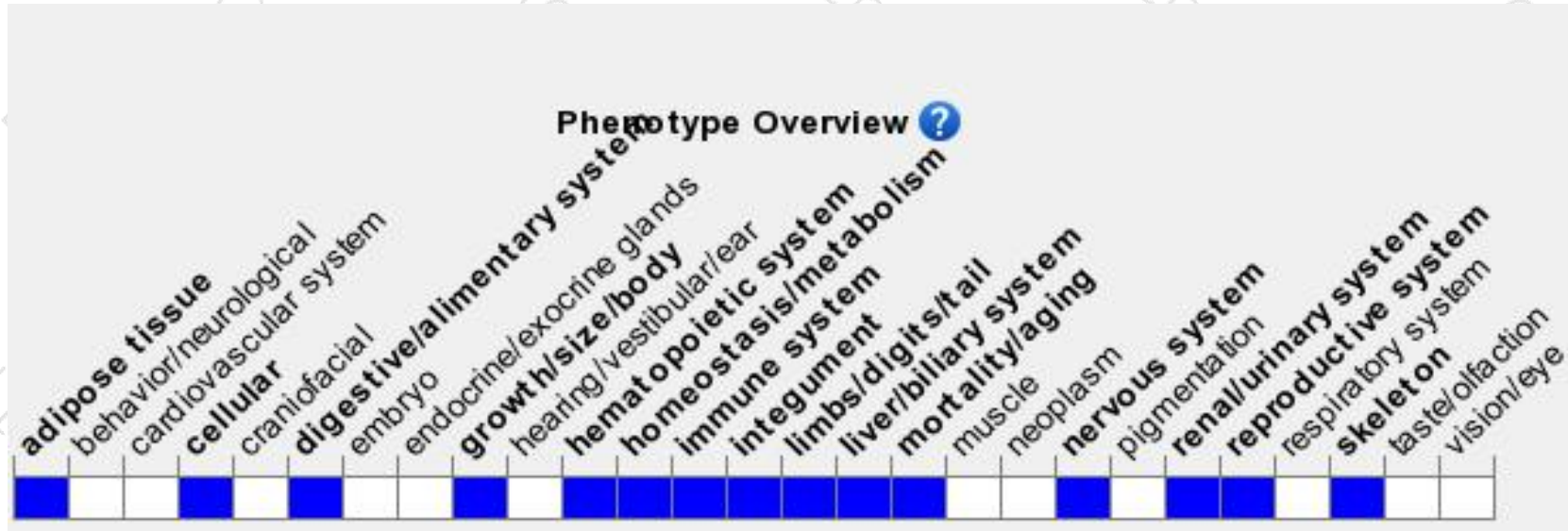
Genomic location distribution



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 null mutations exhibit attenuated inflammatory responses related to decrease secretion of IL-1 β and IL-18. Mice heterozygous for activating mutations suffer from autoinflammatory attacks that lead to organ failure and death before weaning.

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

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