

***Stat1* Cas9-KO Strategy**

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Project Overview

Project Name

Stat1

Project type

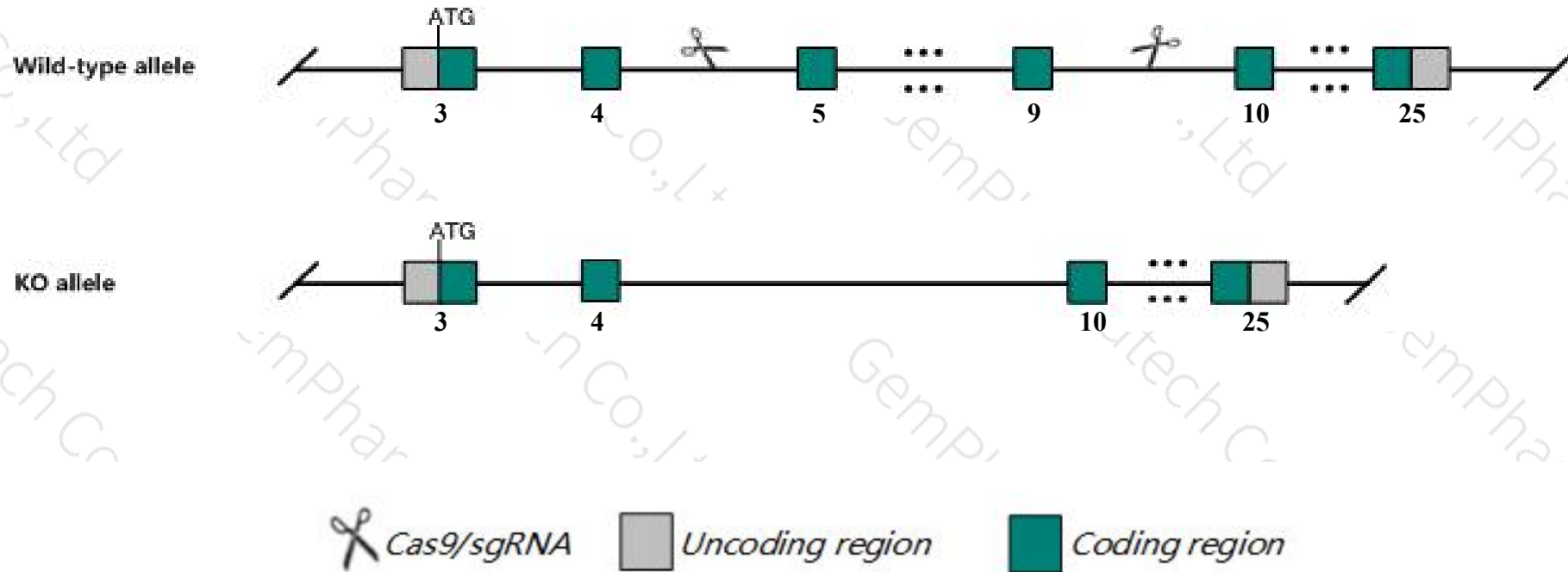
Cas9-KO

Strain background

C57BL/6J

Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *Stat1* gene. The schematic diagram is as follows:



- The *Stat1* gene has 12 transcripts. According to the structure of *Stat1* gene, exon5-exon9 of *Stat1*-203 (ENSMUST00000186057.6) transcript is recommended as the knockout region. The region contains 512bp coding sequence. Knock out the region will result in disruption of protein function.
- In this project we use CRISPR/Cas9 technology to modify *Stat1* 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, homozygotes for targeted null mutations are largely unresponsive to interferon, fail to thrive, are susceptible to viral diseases and cutaneous leishmaniasis, and show excess osteoclastogenesis leading to increased bone mass.
- **Homozygous mice are viable and fertile when maintained under specific pathogen-free (SPF) conditions.**
In conventional health status vivaria (non-SPF), homozygotes tend to be runted and die within 48 hours of weaning due to hepatic necrosis due to viral infection.
- The *Stat1* gene is located on the Chr1. 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)

Stat1 signal transducer and activator of transcription 1 [Mus musculus (house mouse)]

Gene ID: 20846, updated on 9-Apr-2019

Summary

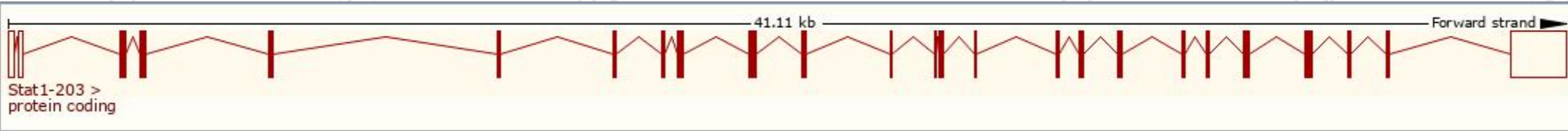
Official Symbol	Stat1 provided by MGI
Official Full Name	signal transducer and activator of transcription 1 provided by MGI
Primary source	MGI:MGI:103063
See related	Ensembl:ENSMUSG00000026104
Gene type	protein coding
RefSeq status	VALIDATED
Organism	Mus musculus
Lineage	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Myomorpha; Muroidea; Muridae; Murinae; Mus; Mus
Also known as	2010005J02Rik, AA408197
Expression	Ubiquitous expression in thymus adult (RPKM 23.3), spleen adult (RPKM 19.5) and 28 other tissues See more
Orthologs	human all

Transcript information (Ensembl)

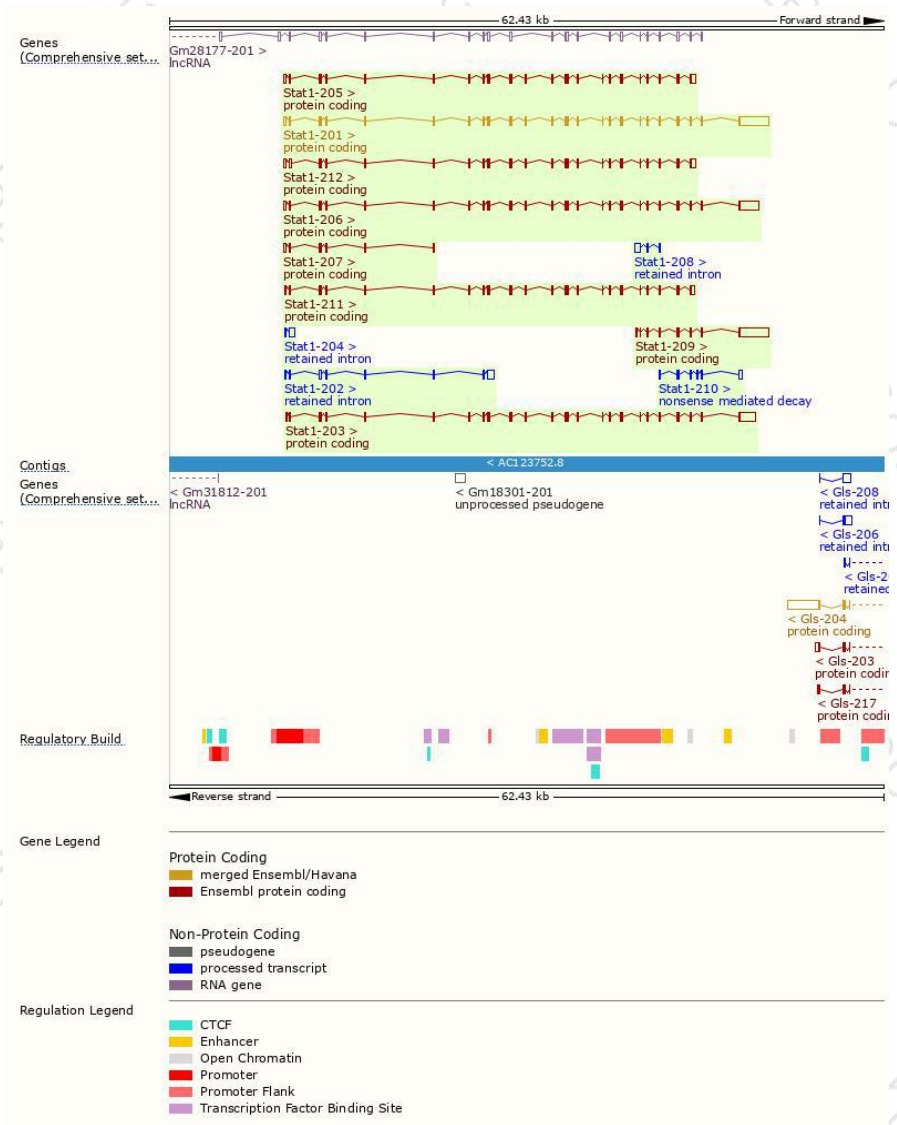
The gene has 12 transcripts,all transcripts are shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Stat1-201	ENSMUST00000070968.13	5151	749aa	Protein coding	CCDS56628	Q8C3V4	TSL:1 GENCODE basic APPRIS P1
Stat1-206	ENSMUST00000186857.6	4241	749aa	Protein coding	CCDS56628	Q8C3V4	TSL:1 GENCODE basic APPRIS P1
Stat1-203	ENSMUST00000186057.6	3998	755aa	Protein coding	CCDS78581	A0A087WSP5	TSL:1 GENCODE basic
Stat1-209	ENSMUST00000189244.6	3298	243aa	Protein coding	-	Q8CFQ1	CDS 5' incomplete TSL:1
Stat1-205	ENSMUST00000186574.6	2834	712aa	Protein coding	-	Q99K94	TSL:1 GENCODE basic
Stat1-212	ENSMUST00000191435.6	2803	712aa	Protein coding	-	Q99K94	TSL:5 GENCODE basic
Stat1-211	ENSMUST00000189347.6	2588	712aa	Protein coding	-	Q99K94	TSL:5 GENCODE basic
Stat1-207	ENSMUST00000188681.6	715	154aa	Protein coding	-	A0A087WSQ5	CDS 3' incomplete TSL:2
Stat1-210	ENSMUST00000189336.1	886	131aa	Nonsense mediated decay	-	A0A087WRI1	CDS 5' incomplete TSL:3
Stat1-202	ENSMUST00000185743.1	1344	No protein	Retained intron	-	-	TSL:1
Stat1-208	ENSMUST00000189075.1	827	No protein	Retained intron	-	-	TSL:2
Stat1-204	ENSMUST00000186186.1	548	No protein	Retained intron	-	-	TSL:2

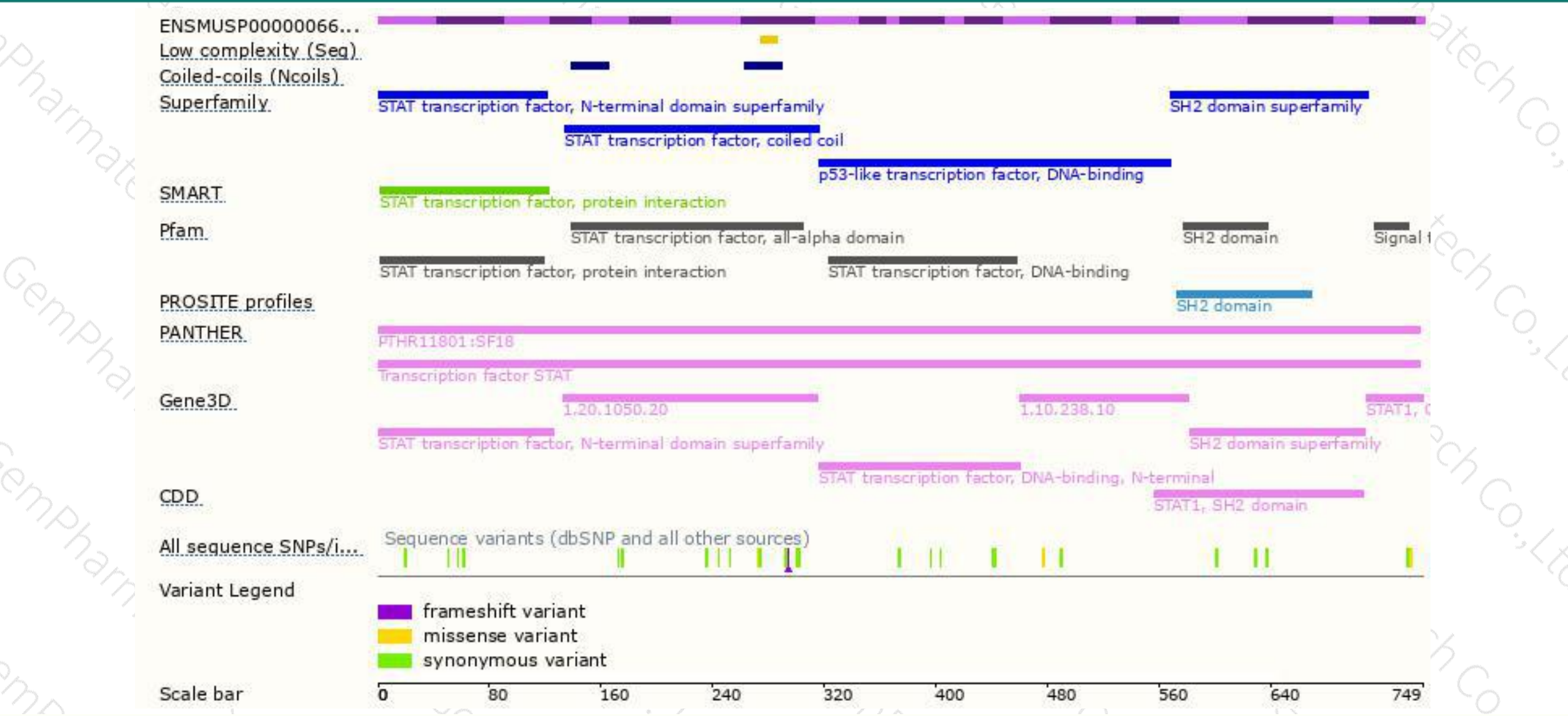
The strategy is based on the design of *Stat1-203* transcript,The transcription is shown below



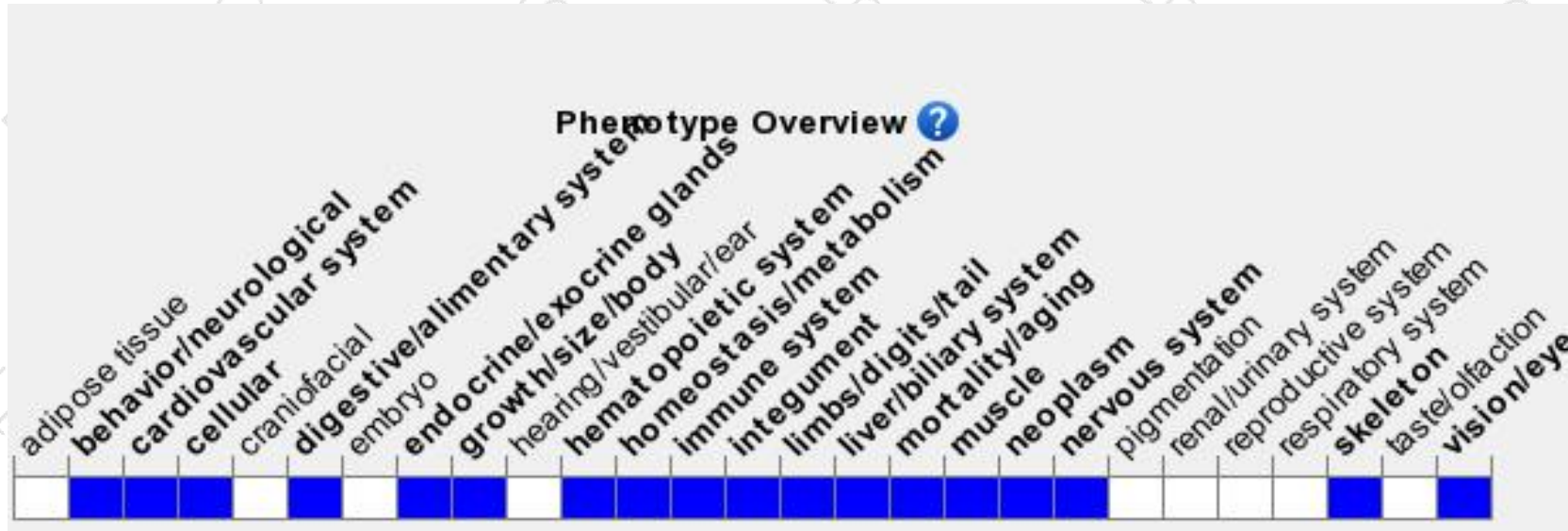
Genomic location distribution



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/>).

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

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