

Socs3 Cas9-KO Strategy

Designer:

Daohua Xu

Reviewer:

Huimin Su

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Project Overview

Project Name

Socs3

Project type

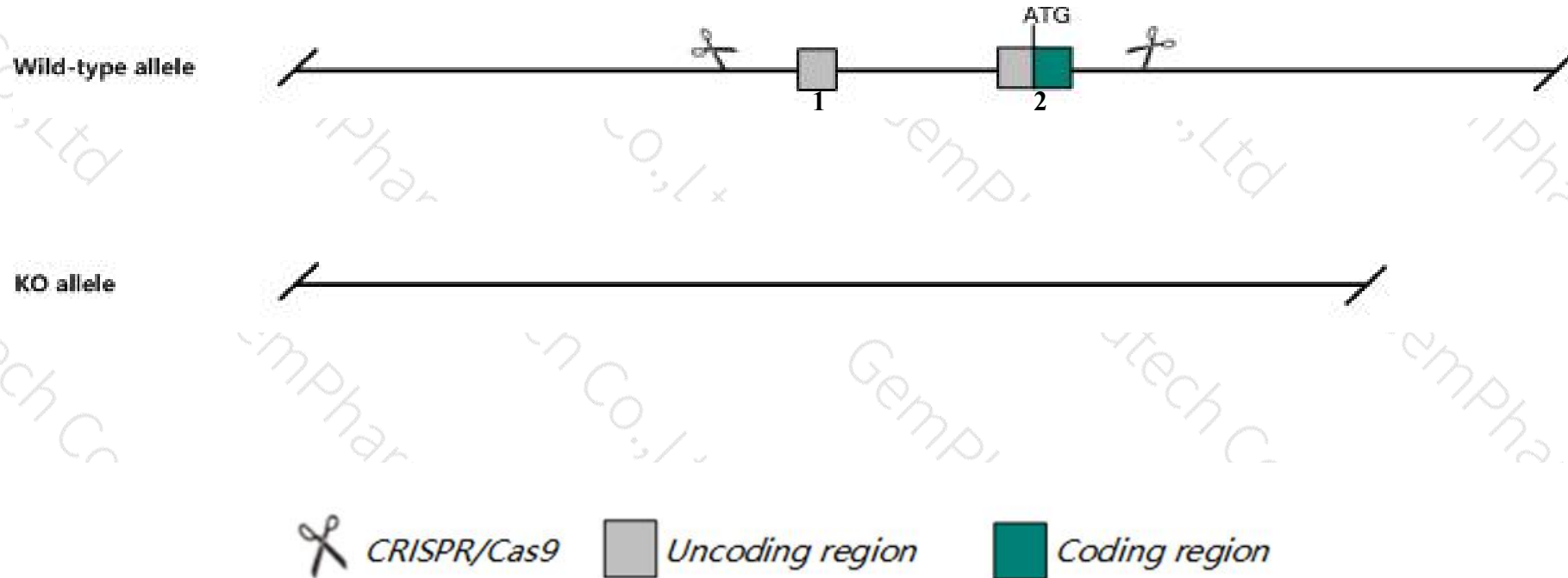
Cas9-KO

Strain background

C57BL/6JGpt

Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *Socs3* gene. The schematic diagram is as follows:



- The *Socs3* gene has 3 transcripts. According to the structure of *Socs3* gene, exon1-exon2 of *Socs3-201* (ENSMUST00000054002.3) 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 *Socs3* gene. The brief process is as follows: CRISPR/Cas9 system

- According to the existing MGI data, Mice homozygous for mutations cause impairment if gene expression show immunological and hematopoietic abnormalities. Complete gene disruption causes lethality.
- The *Socs3* 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)

Socs3 suppressor of cytokine signaling 3 [Mus musculus (house mouse)]

Gene ID: 12702, updated on 2-Apr-2019

Summary



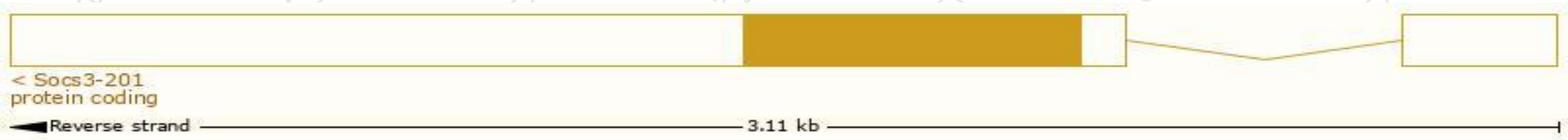
Official Symbol	Socs3 provided by MGI
Official Full Name	suppressor of cytokine signaling 3 provided by MGI
Primary source	MGI:MGI:1201791
See related	Ensembl:ENSMUSG00000053113
Gene type	protein coding
RefSeq status	VALIDATED
Organism	Mus musculus
Lineage	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Myomorpha; Muroidea; Muridae; Murinae; Mus; Mus
Also known as	Cis3, Cish3, EF-10, Ef10, SSI-3, Ssi3
Expression	Broad expression in large intestine adult (RPKM 19.8), duodenum adult (RPKM 16.3) and 25 other tissues See more
Orthologs	human all

Transcript information (Ensembl)

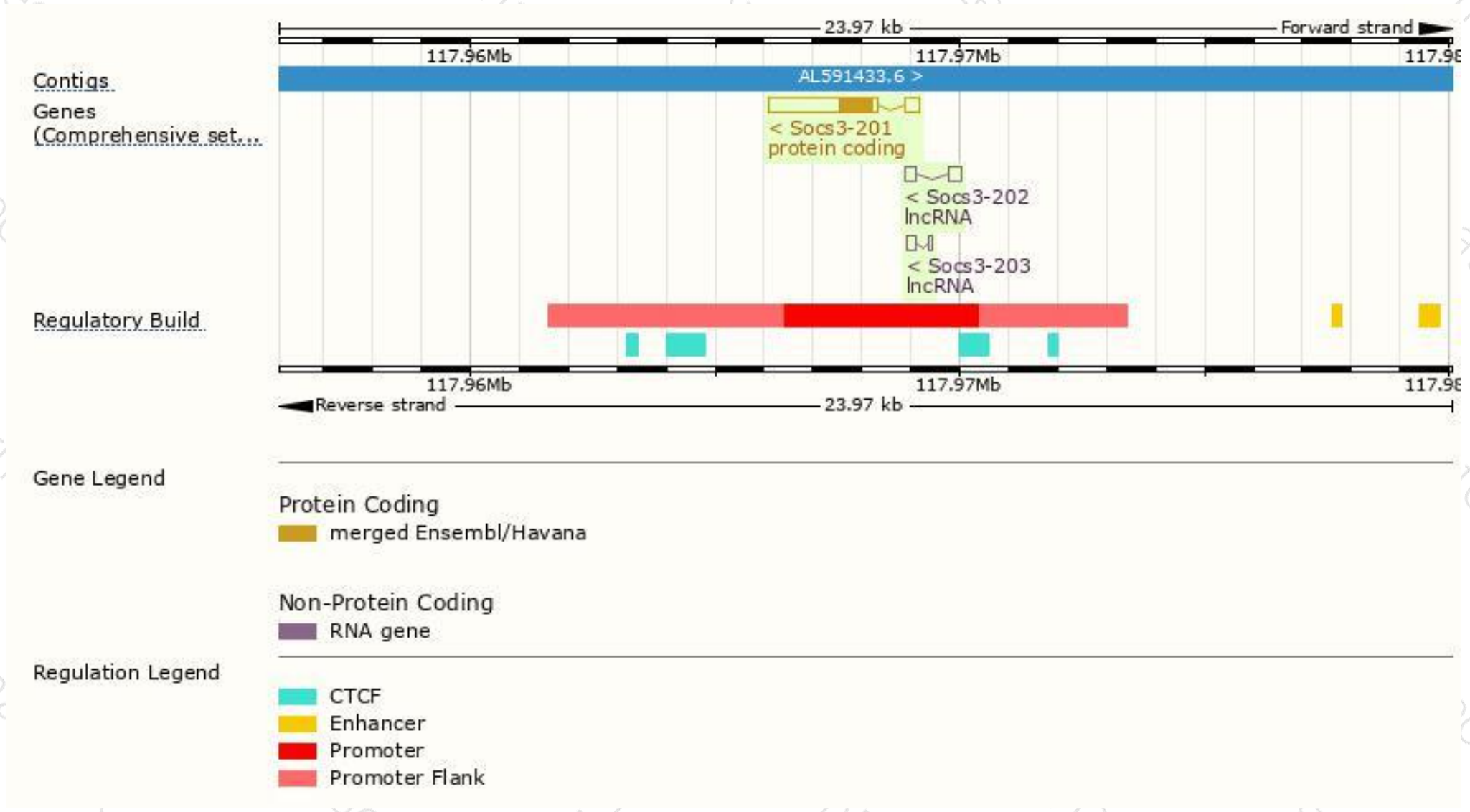
The gene has 3 transcripts,all transcripts are shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Socs3-201	ENSMUST00000054002.3	2552	225aa	Protein coding	CCDS25697	Q35718	TSL:1 GENCODE basic APPRIS P1
Socs3-202	ENSMUST00000123255.1	490	No protein	lncRNA	-	-	TSL:3
Socs3-203	ENSMUST00000132295.1	246	No protein	lncRNA	-	-	TSL:5

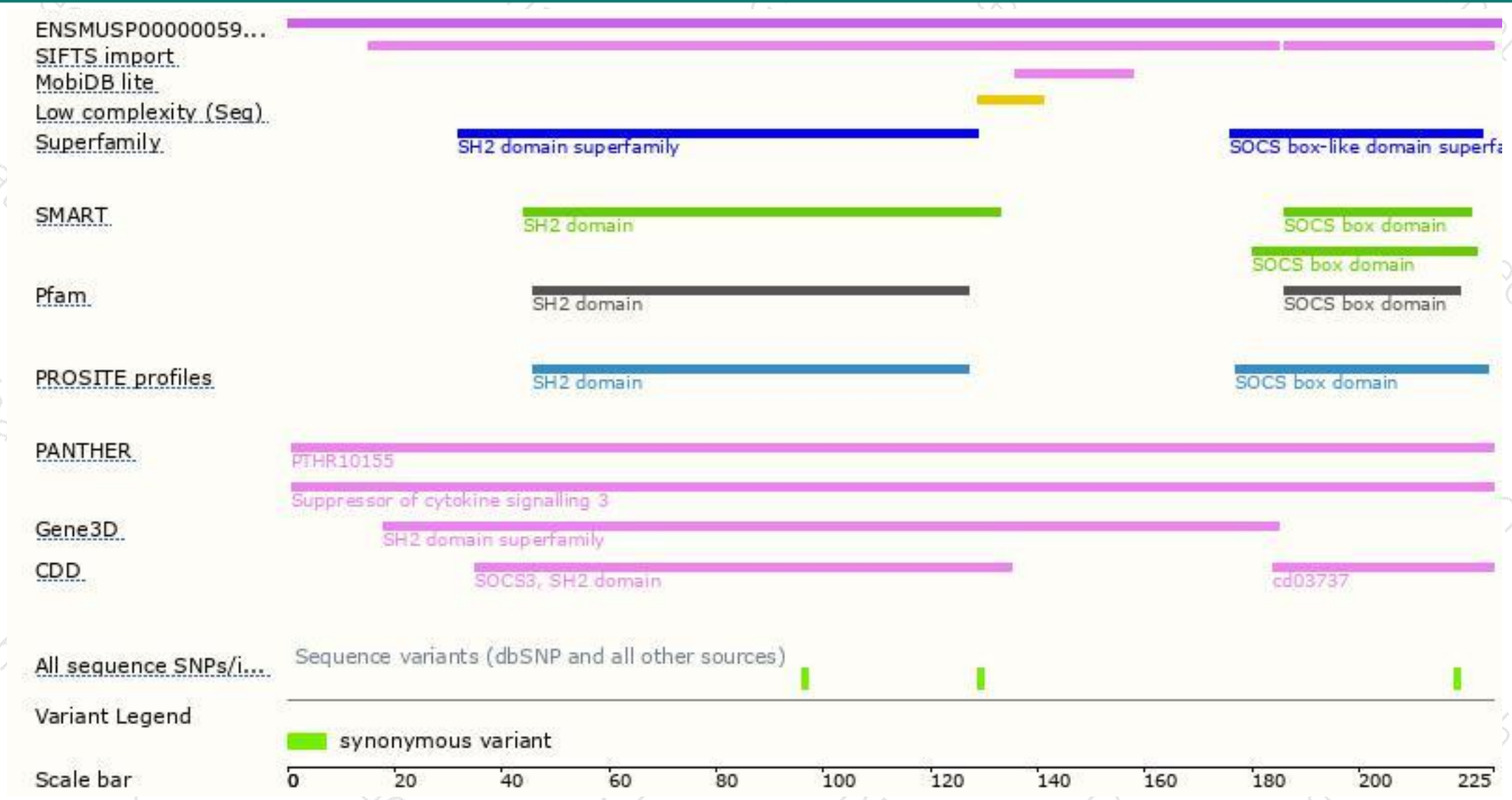
The strategy is based on the design of *Socs3-201* transcript,The transcription is shown below



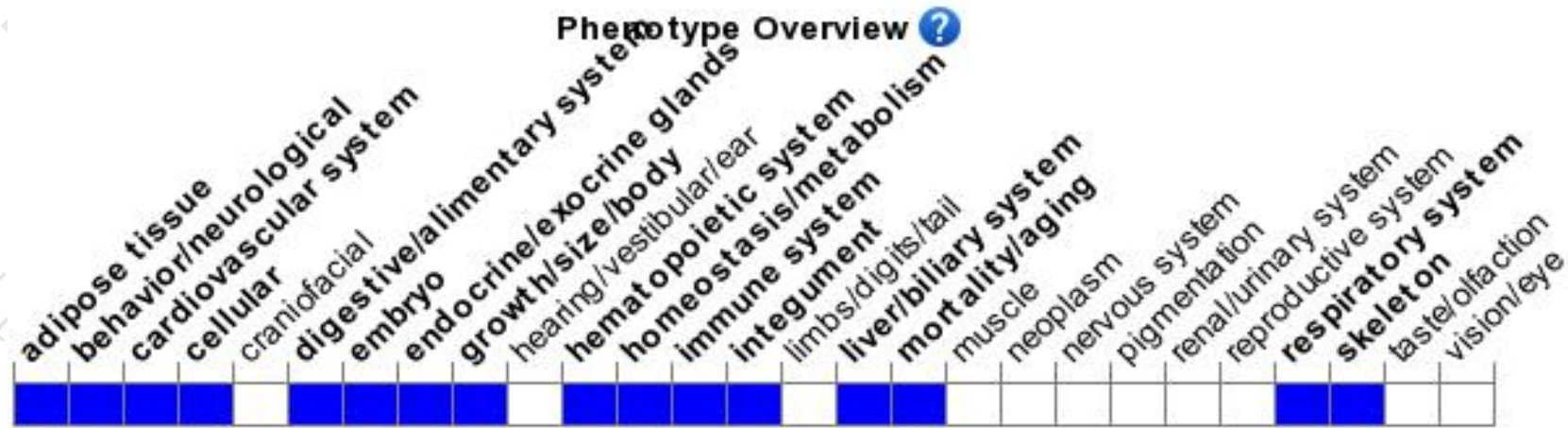
Genomic location distribution



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 mutations cause impairment if gene expression show immunologic and hematopoietic abnormalities. Complete gene disruption causes lethality.

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

Tel: 400-9660890

