Socs2 Cas9-CKO Strategy

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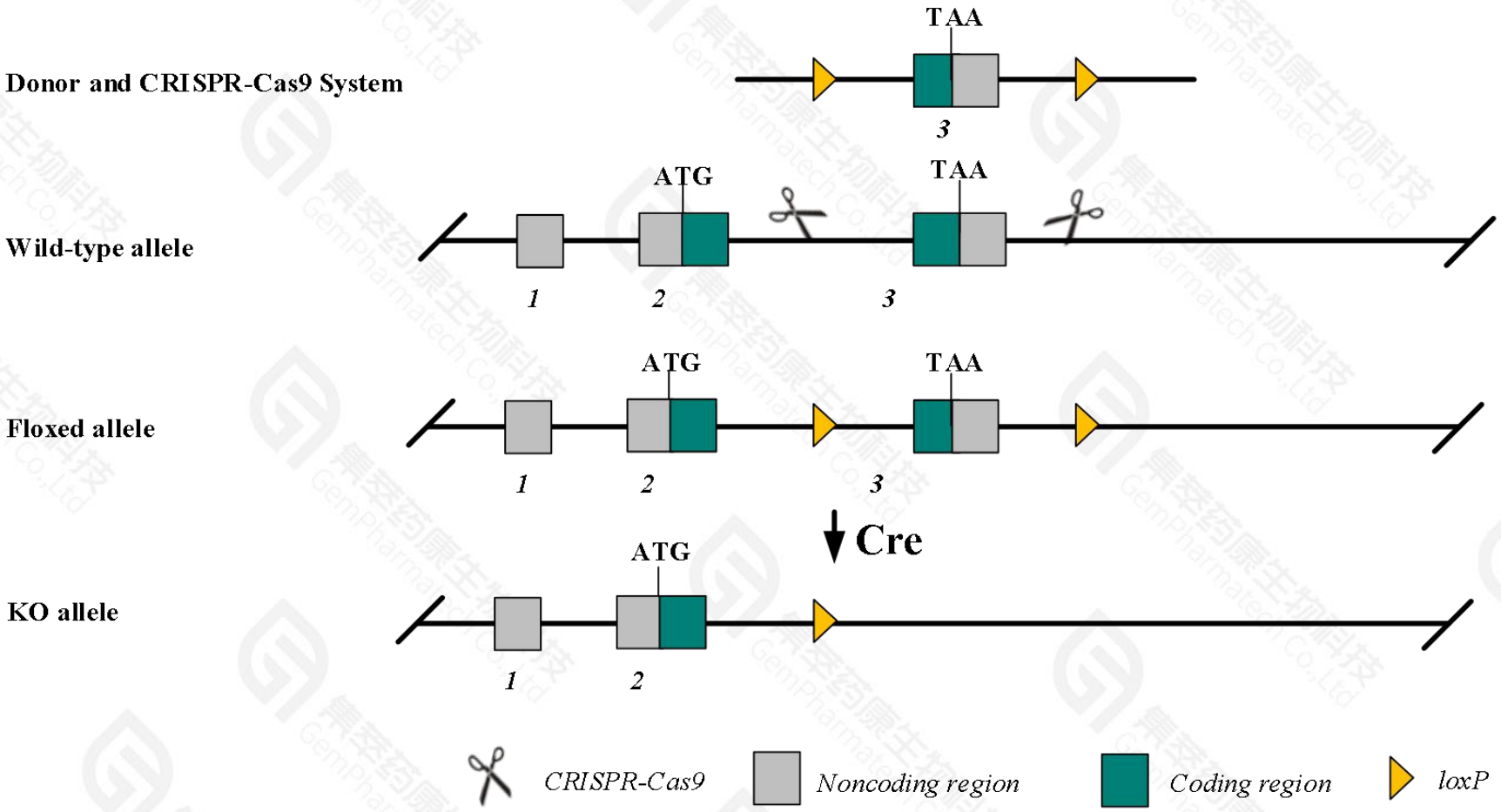
Project Overview

Project Name	***Socs2***
Project type	**Cas9-CKO**
Strain background	**C57BL/6JGpt**

Conditional Knockout strategy

This model will use CRISPR-Cas9 technology to edit the *Socs2* gene. The schematic diagram is as follows:



Technical routes

➢ The *Socs2* gene has 14 transcripts. According to the structure of *Socs2* gene, exon3 of *Socs2-201*(ENSMUST00000020215.16) transcript is recommended as the knockout region.The region contains most of coding sequence. Knock out the region will result in disruption of protein function.

➢ In this project we use CRISPR-Cas9 technology to modify *Socs2* gene. The brief process is as follows: CRISPR-Cas9 system and Donor were microinjected into the fertilized eggs of C57BL/6JGpt 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/6JGpt mice.

➢ The flox mice will be knocked out after mating with mice expressing Cre recombinase, resulting in the loss of function of the target gene in specific tissues and cell types.

Notice

➢ According to the existing MGI data,mutations in this gene cause accelerated postnatal growth. Homozygotes for a targeted mutation also show increased bone growth, enlargement of most organs, collagen deposition in the skin and some ducts and vessels, lower major urinary protein levels, and elevated IGF-I mRNA levels in some tissues.

➢ The KO region near to the *5730420D15Rik* gene. Knockout the region may affect the function of *5730420D15Rik* gene.

➢ The *Socs2* gene is located on the Chr10. 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 loxp insertion on gene transcription, RNA splicing and protein translation cannot be predicted at existing technological level.

Gene information（NCBI）

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Socs2 suppressor of cytokine signaling 2 [*Mus musculus* (house mouse)]

Download Datasets

Gene ID: 216233, updated on 7-Mar-2022

Summary

Official Symbol	Socs2 provided by MGI
Official Full Name	suppressor of cytokine signaling 2 provided by MGI
Primary source	MGI:MGI:1201787
See related	Ensembl:ENSMUSG00000020027 AllianceGenome:MGI:1201787
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	hg; JAB; CIS2; Cish2; SSI-2; SOCS-2; AI527257; AW108012; 8030460M17; D130043N08Rik
Summary	Enables growth hormone receptor binding activity. Acts upstream of or within several processes, including mammary gland development; negative regulation of receptor signaling pathway via JAK-STAT; and positive regulation of neuron differentiation. Predicted to be located in cytoplasm. Predicted to be part of phosphatidylinositol 3-kinase complex. Is expressed in several structures, including lung; primary sex cord; retina; and ureteric tip. Human ortholog(s) of this gene implicated in endometrial cancer and ovarian carcinoma. Orthologous to human SOCS2 (suppressor of cytokine signaling 2). [provided by Alliance of Genome Resources, Nov 2021]
Expression	Ubiquitous expression in ovary adult (RPKM 9.8), lung adult (RPKM 5.2) and 24 other tissues See more
Orthologs	human all

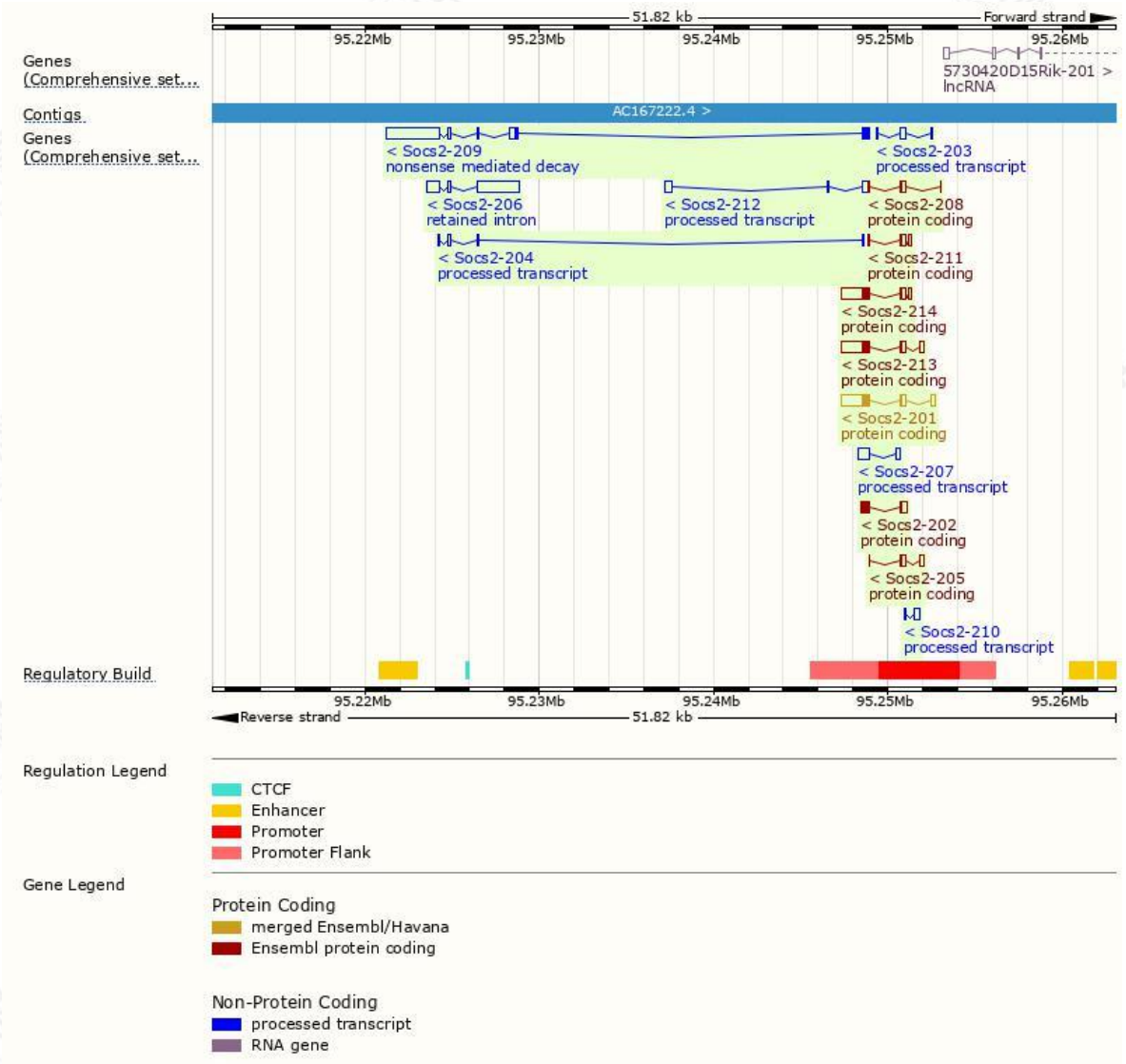
Transcript information（Ensembl）

The gene has 14 transcripts,all transcripts are shown below:

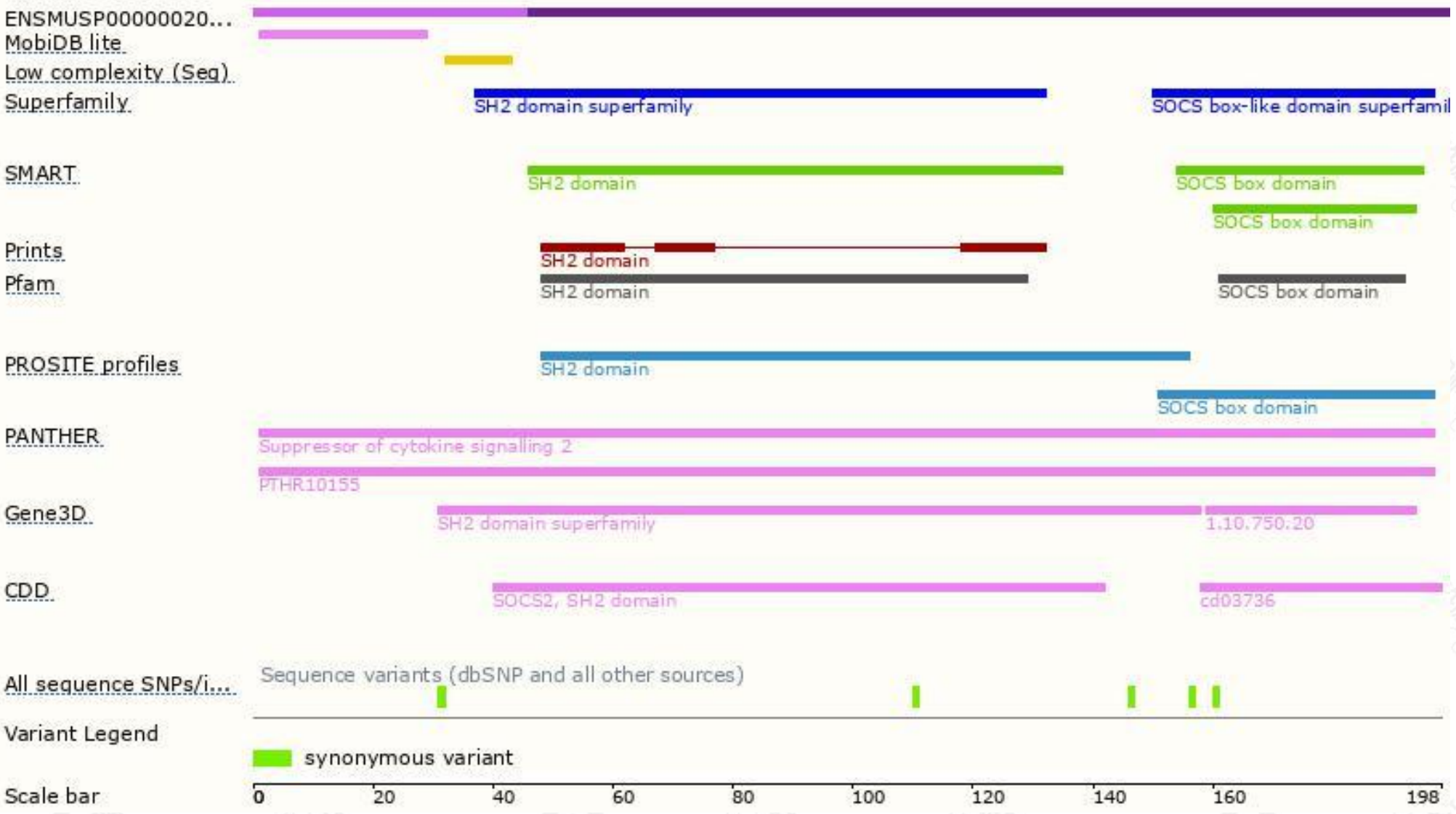
Transcript ID	Name	bp	Protein	Biotype	CCDS	UniProt Match	Flags
ENSMUST00000020215.16	Socs2-201	2222	198aa	Protein coding	CCDS24136	O35717 Q548Q7	Ensembl Canonical GENCODE basic APPRIS P1 TSL:1
ENSMUST00000170690.8	Socs2-213	2195	198aa	Protein coding	CCDS24136	O35717 Q548Q7	GENCODE basic APPRIS P1 TSL:3
ENSMUST00000172070.8	Socs2-214	2153	198aa	Protein coding	CCDS24136	O35717 Q548Q7	GENCODE basic APPRIS P1 TSL:2
ENSMUST00000119917.2	Socs2-202	948	198aa	Protein coding	CCDS24136	O35717 Q548Q7	GENCODE basic APPRIS P1 TSL:1
ENSMUST00000129942.2	Socs2-205	623	62aa	Protein coding	-	D3Z441	TSL:3 CDS 3' incomplete
ENSMUST00000150432.8	Socs2-211	605	70aa	Protein coding	-	D3Z355	TSL:2 CDS 3' incomplete
ENSMUST00000135822.8	Socs2-208	497	80aa	Protein coding	-	D3YZ26	TSL:3 CDS 3' incomplete
ENSMUST00000139210.8	Socs2-209	4242	201aa	Nonsense mediated decay	-	F6RVG2	TSL:1 CDS 5' incomplete
ENSMUST00000155148.2	Socs2-212	893	No protein	Processed transcript	-	-	TSL:3
ENSMUST00000134918.2	Socs2-207	874	No protein	Processed transcript	-	-	TSL:3
ENSMUST00000128363.2	Socs2-203	502	No protein	Processed transcript	-	-	TSL:5
ENSMUST00000145847.2	Socs2-210	479	No protein	Processed transcript	-	-	TSL:3
ENSMUST00000128854.2	Socs2-204	352	No protein	Processed transcript	-	-	TSL:3
ENSMUST00000130784.8	Socs2-206	3285	No protein	Retained intron	-	-	TSL:1

The strategy is based on the design of *Socs2-201* transcript,the transcription is shown below:

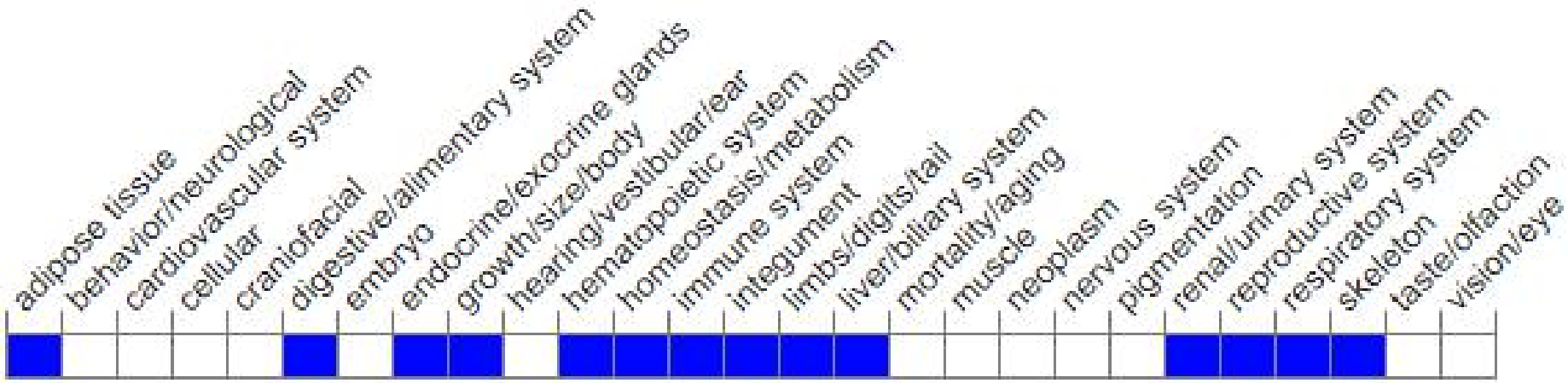
Genomic location distribution



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/).

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