

Sall3 Cas9-CKO Strategy

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Project Overview

Project Name

Sall3

Project type

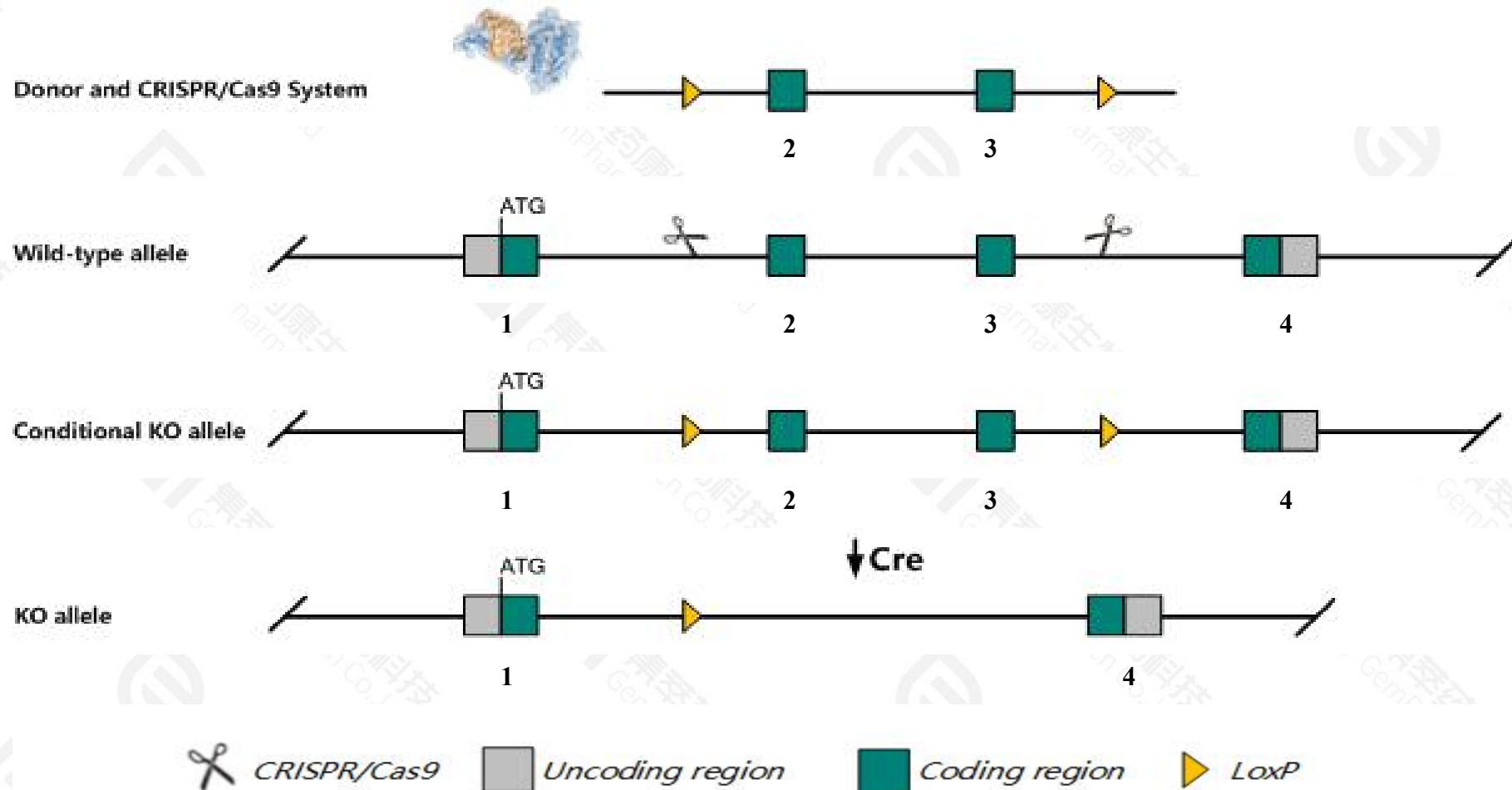
Cas9-CKO

Strain background

C57BL/6JGpt

Conditional Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *Sall3* gene. The schematic diagram is as follows:



- The *Sall3* gene has 3 transcripts. According to the structure of *Sall3* gene, exon2-exon3 of *Sall3*-201(ENSMUST00000057950.9) transcript is recommended as the knockout region. The region contains 3233bp coding sequence. Knock out the region will result in disruption of protein function.
- In this project we use CRISPR/Cas9 technology to modify *Sall3* 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.

- According to the existing MGI data, homozygous null mice display neonatal lethality with an impaired suckling ability, truncated soft palate, small epiglottis, and abnormal cranial nerve morphology.
- The *Sall3* gene is located on the Chr18. 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)

Sall3 spalt like transcription factor 3 [Mus musculus (house mouse)]

Gene ID: 20689, updated on 17-Nov-2020

Summary



Official Symbol Sall3 provided by [MGI](#)

Official Full Name spalt like transcription factor 3 provided by [MGI](#)

Primary source [MGI:MGI:109295](#)

See related [Ensembl:ENSMUSG00000024565](#)

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 B130022O04Rik, M, Msa, Msal, Msal-1, S, Sal, Salt, Spalt

Expression Biased expression in whole brain E14.5 (RPKM 3.6), frontal lobe adult (RPKM 3.4) and 7 other tissues [See more](#)

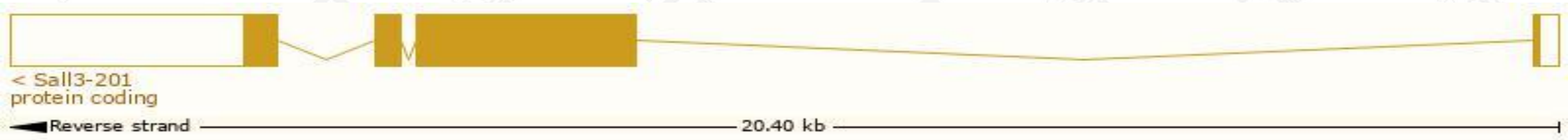
Orthologs [human](#) [all](#)

Transcript information (Ensembl)

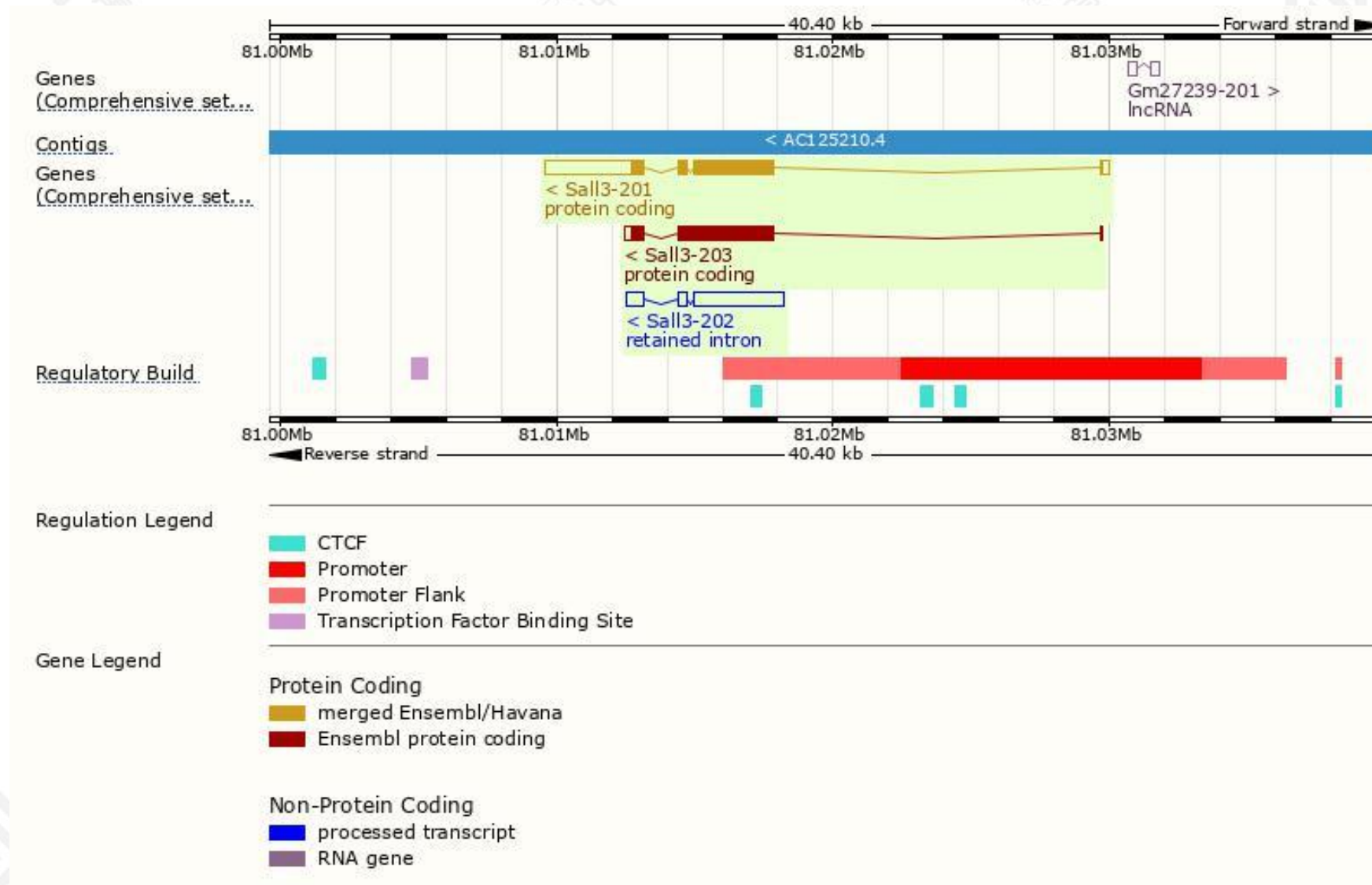
The gene has 3 transcripts,all transcripts are shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Sall3-201	ENSMUST00000057950.9	7079	1248aa	Protein coding	CCDS29371		TSL:1 , GENCODE basic ,
Sall3-203	ENSMUST00000238808.2	4214	1320aa	Protein coding	-		GENCODE basic , APPRIS P1 ,
Sall3-202	ENSMUST00000235746.2	4254	No protein	Retained intron	-		

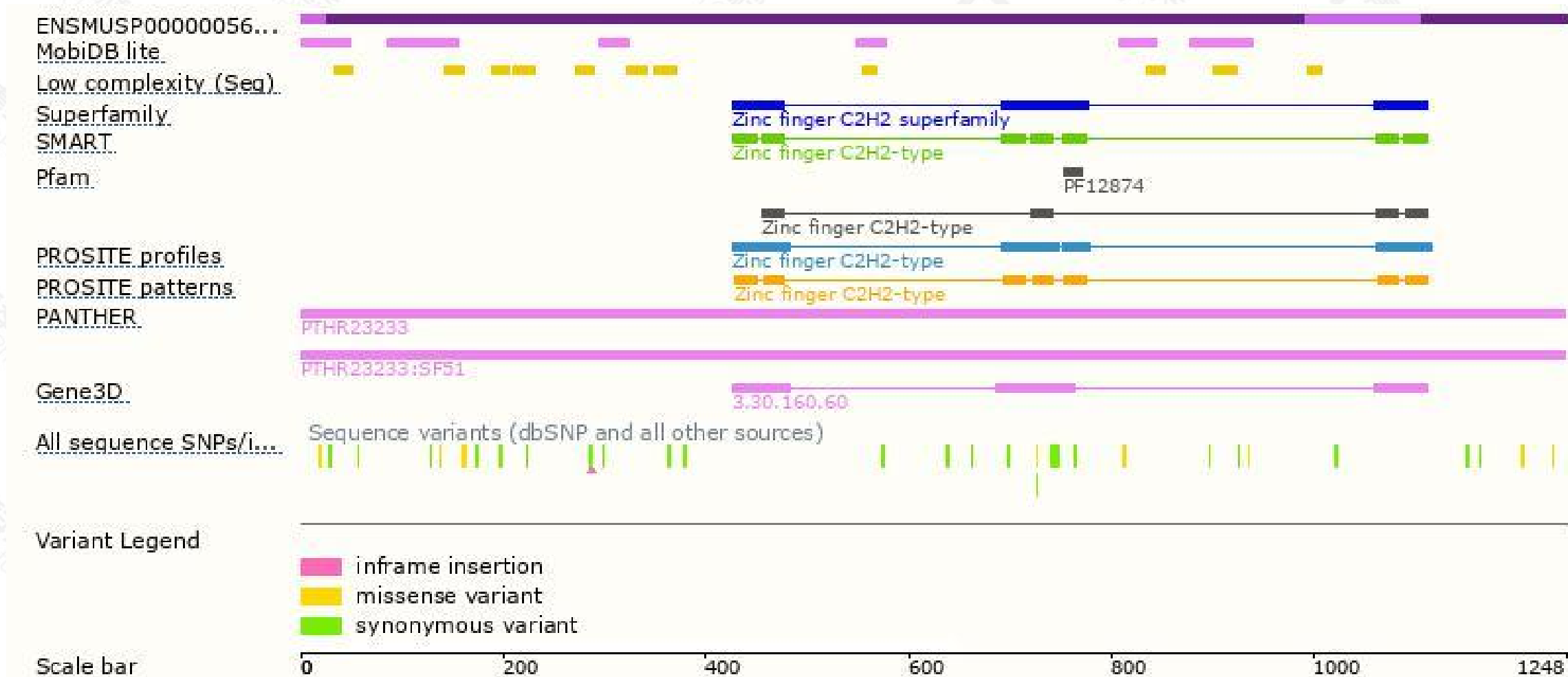
The strategy is based on the design of *Sall3-201* transcript,the transcription is shown below:



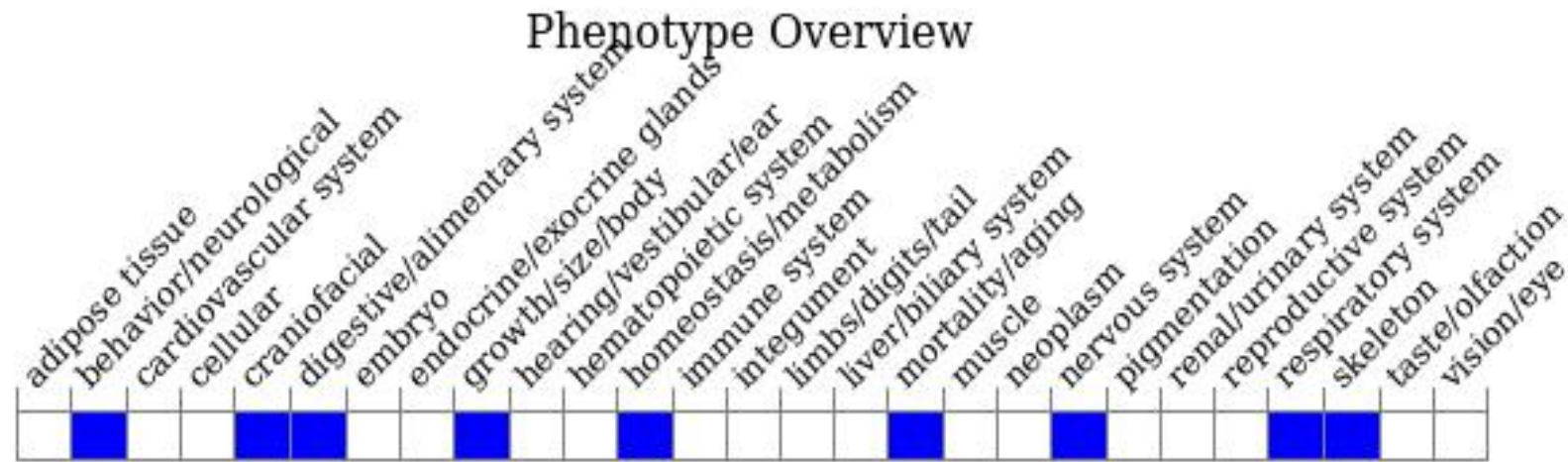
Genomic location distribution



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, homozygous null mice display neonatal lethality with an impaired suckling ability, truncated soft palate, small epiglottis, and abnormal cranial nerve morphology.

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