

Smc3 Cas9-KO Strategy

Designer: Rui Xiong

Reviewer: Longyun Hu

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Project Overview

Project Name

Smc3

Project type

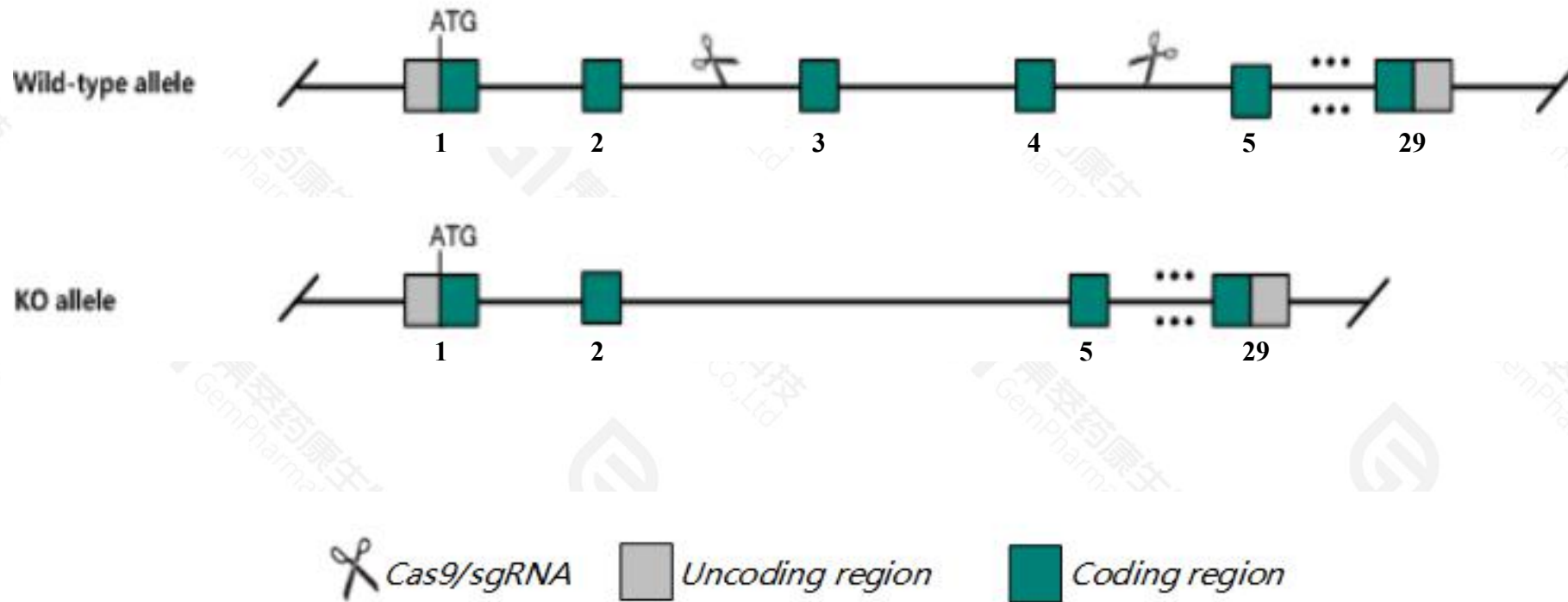
Cas9-KO

Strain background

C57BL/6JGpt

Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *Smc3* gene. The schematic diagram is as follows:



- The *Smc3* gene has 3 transcripts. According to the structure of *Smc3* gene, exon3-exon4 of *Smc3-201*(ENSMUST00000025930.10) transcript is recommended as the knockout region. The region contains 107bp coding sequence. Knock out the region will result in disruption of protein function.
- In this project we use CRISPR/Cas9 technology to modify *Smc3* gene. The brief process is as follows: sgRNA was transcribed in vitro. Cas9 and sgRNA 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.

- According to the existing MGI data, mice homozygous for a knock-out allele exhibit complete embryonic lethality. Mice heterozygous for this allele exhibit partial postnatal lethality, decreased body weight, abnormal craniofacial morphology, and increased T cell number.
- The *Smc3* gene is located on the Chr19. 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.

Smc3 structural maintenance of chromosomes 3 [Mus musculus (house mouse)]

Gene ID: 13006, updated on 9-Mar-2021

Summary



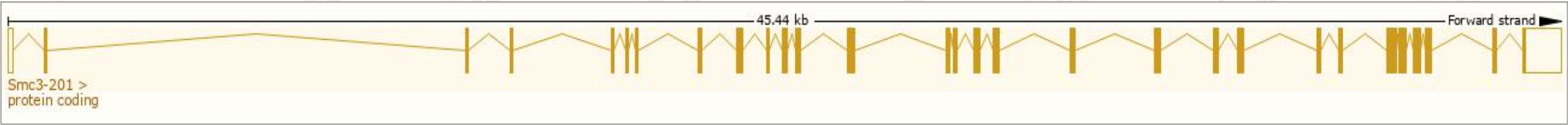
Official Symbol	Smc3 provided by MGI
Official Full Name	structural maintenance of chromosomes 3 provided by MGI
Primary source	MGI:MGI:1339795
See related	Ensembl:ENSMUSG00000024974
Gene type	protein coding
RefSeq status	VALIDATED
Organism	Mus musculus
Lineage	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Myomorpha; Muroidea; Muridae; Murinae; Mus; Mus
Also known as	Bam, Bamacan, Csp, Cspg6, HCAP, Mmi, Mmip1, SMC-3, Smc, SmcD
Expression	Broad expression in CNS E11.5 (RPKM 31.0), liver E14 (RPKM 18.2) and 17 other tissues See more
Orthologs	human all

Transcript information (Ensembl)

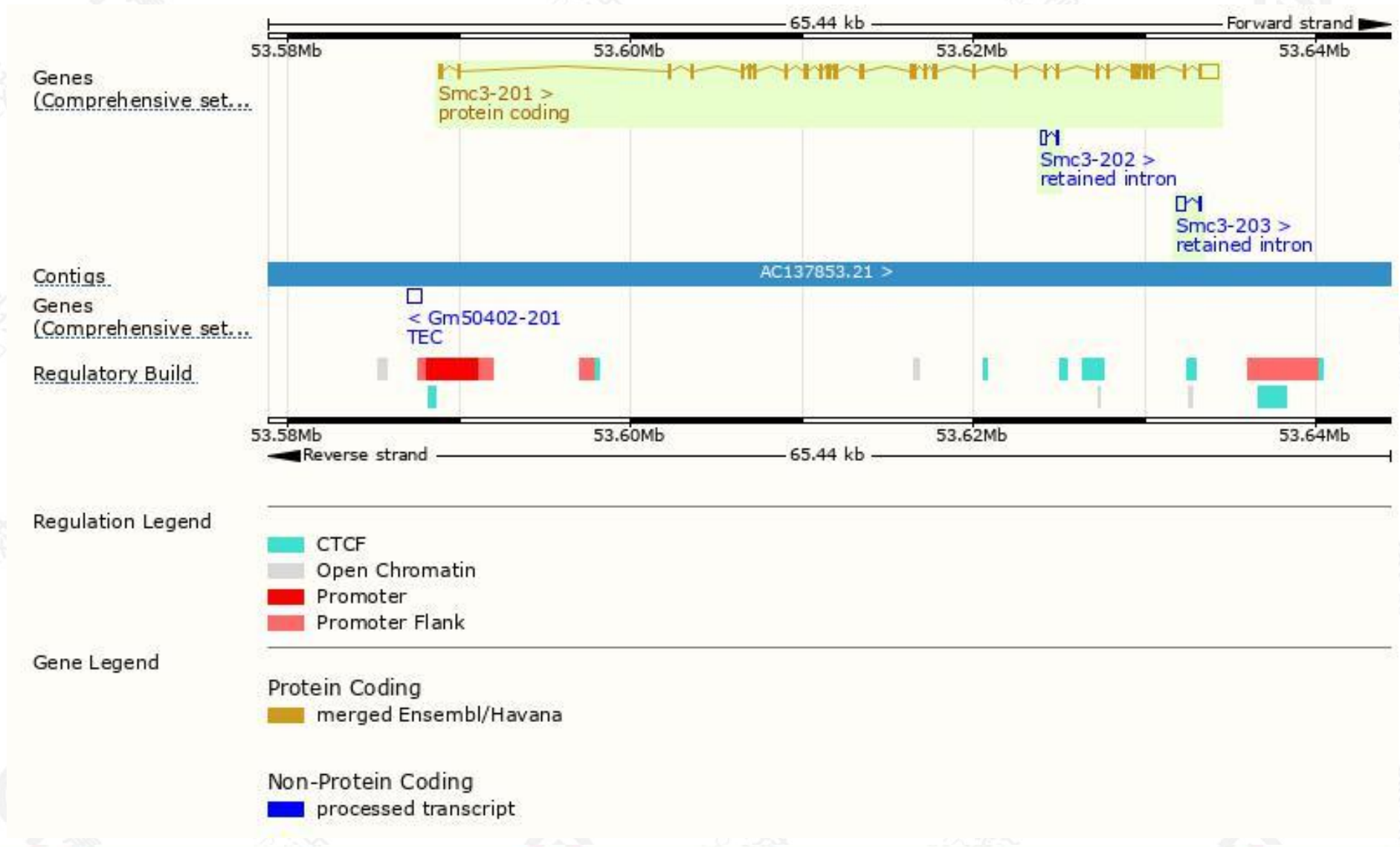
The gene has 3 transcripts,all transcripts are shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Smc3-201	ENSMUST00000025930.10	4851	1217aa	Protein coding	CCDS38025		TSL:1 , GENCODE basic , APPRIS P1 ,
Smc3-203	ENSMUST00000171083.2	695	No protein	Retained intron	-		TSL:2 ,
Smc3-202	ENSMUST00000157053.2	471	No protein	Retained intron	-		TSL:2 ,

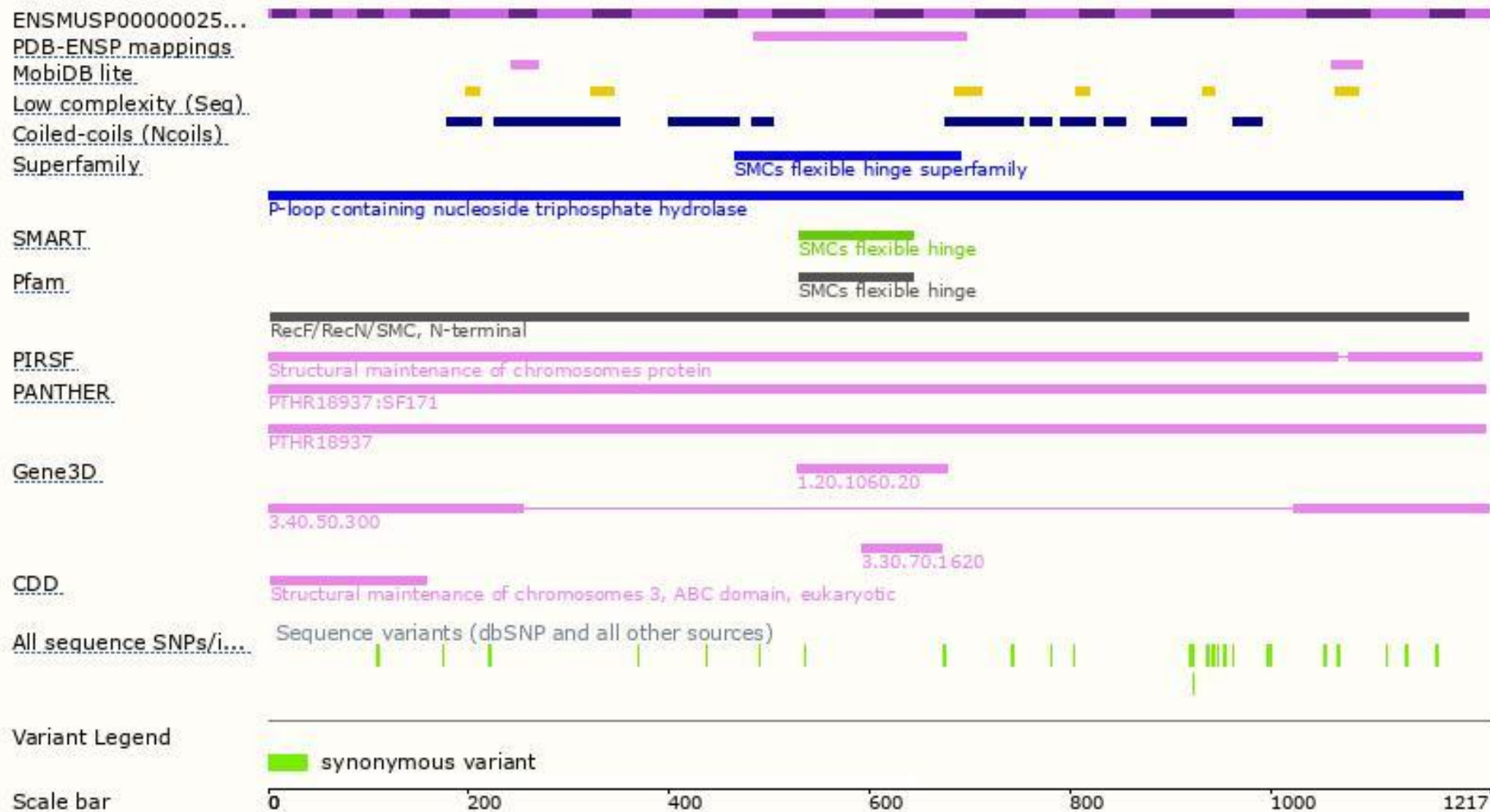
The strategy is based on the design of *Smc3-201* transcript,the transcription is shown below:



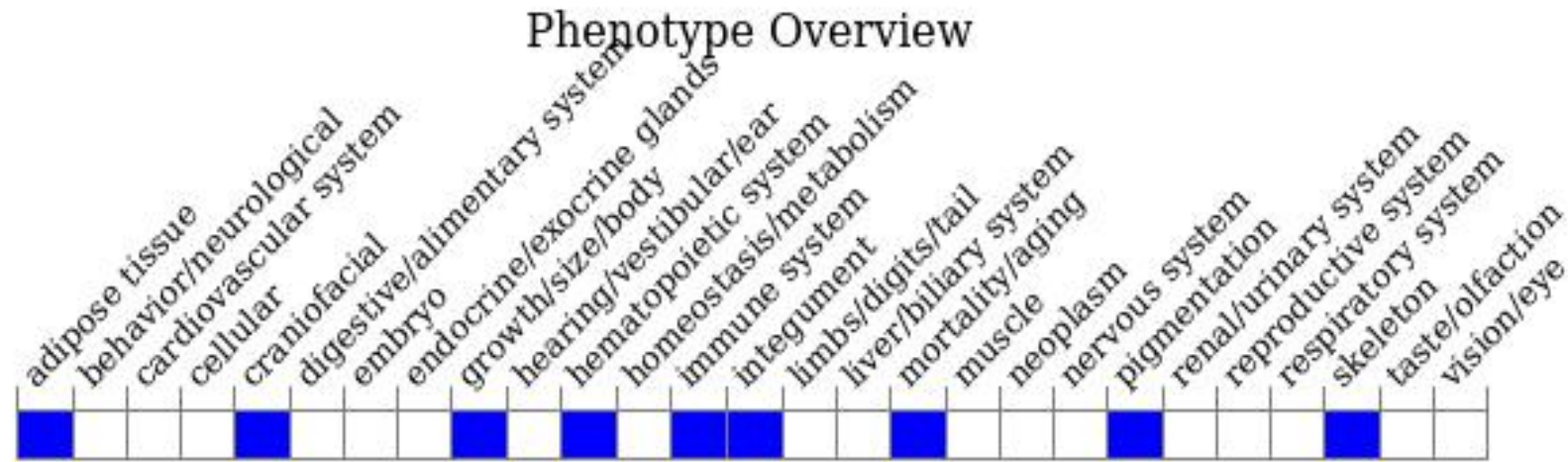
Genomic location distribution



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 a knock-out allele exhibit complete embryonic lethality.

Mice heterozygous for this allele exhibit partial postnatal lethality, decreased body weight, abnormal craniofacial morphology, and increased T cell number.

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

Tel: 025-5864 1534

