

Siah1a Cas9-CKO Strategy

Designer: Wenjing Li

Reviewer: Jiayuan Yao

Design Date: 2020/10/22

Project Overview

Project Name

Siah1a

Project type

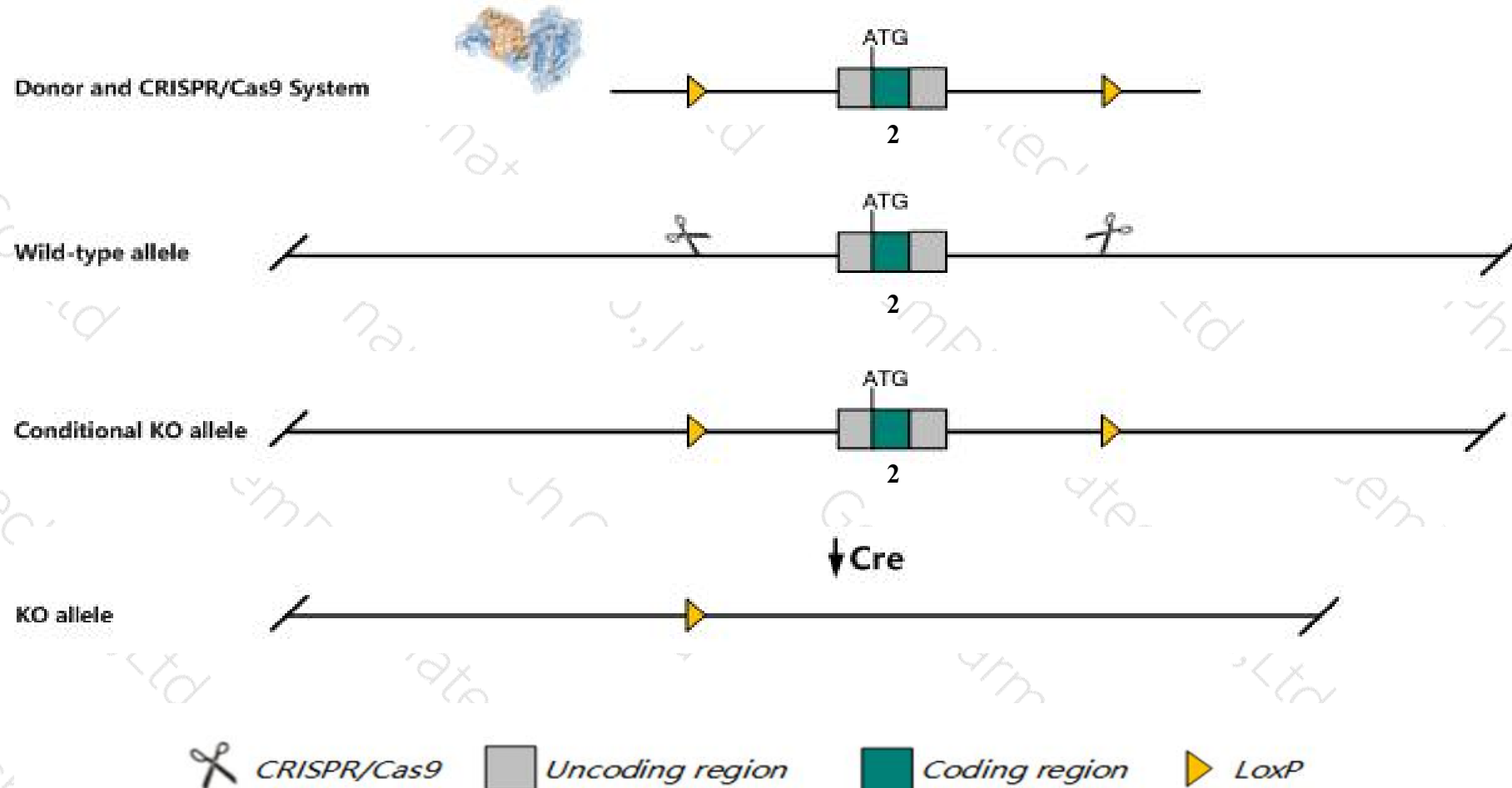
Cas9-CKO

Strain background

C57BL/6JGpt

Conditional Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *Siah1a* gene. The schematic diagram is as follows:



Technical routes

- The *Siah1a* gene has 1 transcript. According to the structure of *Siah1a* gene, exon2 of *Siah1a-201*(ENSMUST00000045296.5) 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 *Siah1a* 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.

- The KO region may contain region of the *Lonp2* gene. Knockout the region may affect the function of *Lonp2* gene.
- According to the existing MGI data, homozygotes for a targeted null mutation exhibit retarded postnatal growth, and high preweaning and postweaning mortality. Surviving females are subfertile, having few, if any, offspring, while males are sterile due to a block at meiotic metaphase I.
- The *Siah1a* gene is located on the Chr8. 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)

Siah1a siah E3 ubiquitin protein ligase 1A [Mus musculus (house mouse)]

Gene ID: 20437, updated on 13-Mar-2020

Summary



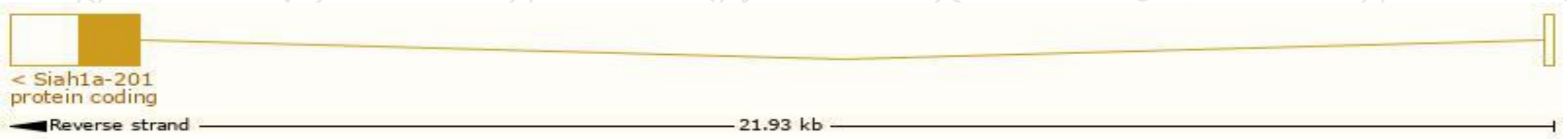
Official Symbol	Siah1a provided by MGI
Official Full Name	siah E3 ubiquitin protein ligase 1A provided by MGI
Primary source	MGI:MGI:108064
See related	Ensembl:ENSMUSG00000036840
Gene type	protein coding
RefSeq status	VALIDATED
Organism	Mus musculus
Lineage	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Myomorpha; Muroidea; Muridae; Murinae; Mus; Mus
Also known as	AA982064, AI853500, Sinh1a
Expression	Ubiquitous expression in whole brain E14.5 (RPKM 8.3), CNS E14 (RPKM 8.0) and 28 other tissues See more
Orthologs	human all

Transcript information (Ensembl)

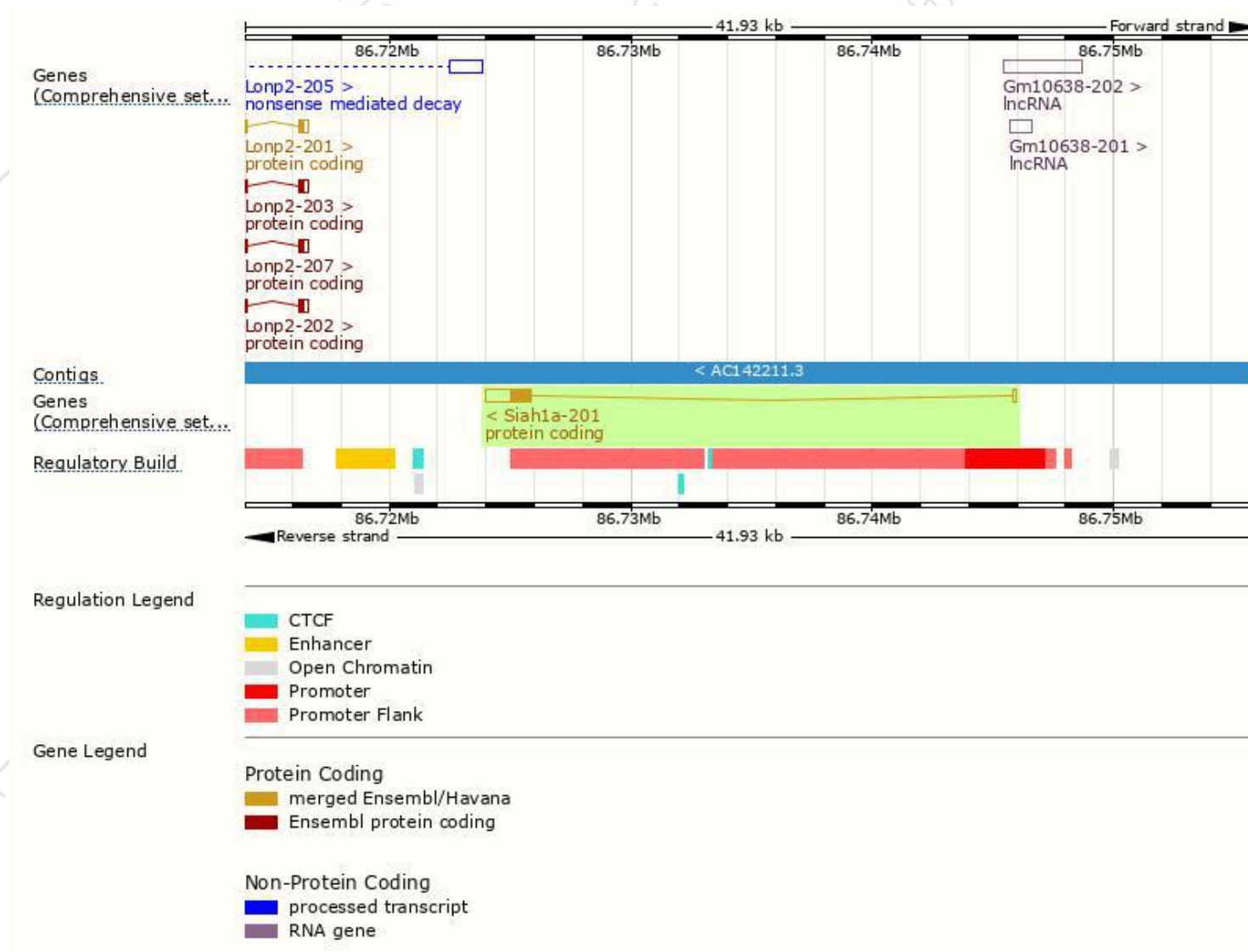
The gene has 1 transcript, and the transcript is shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Siah1a-201	ENSMUST00000045296.5	1968	282aa	Protein coding	CCDS22504	P61092	TSL:1 GENCODE basic APPRIS P1

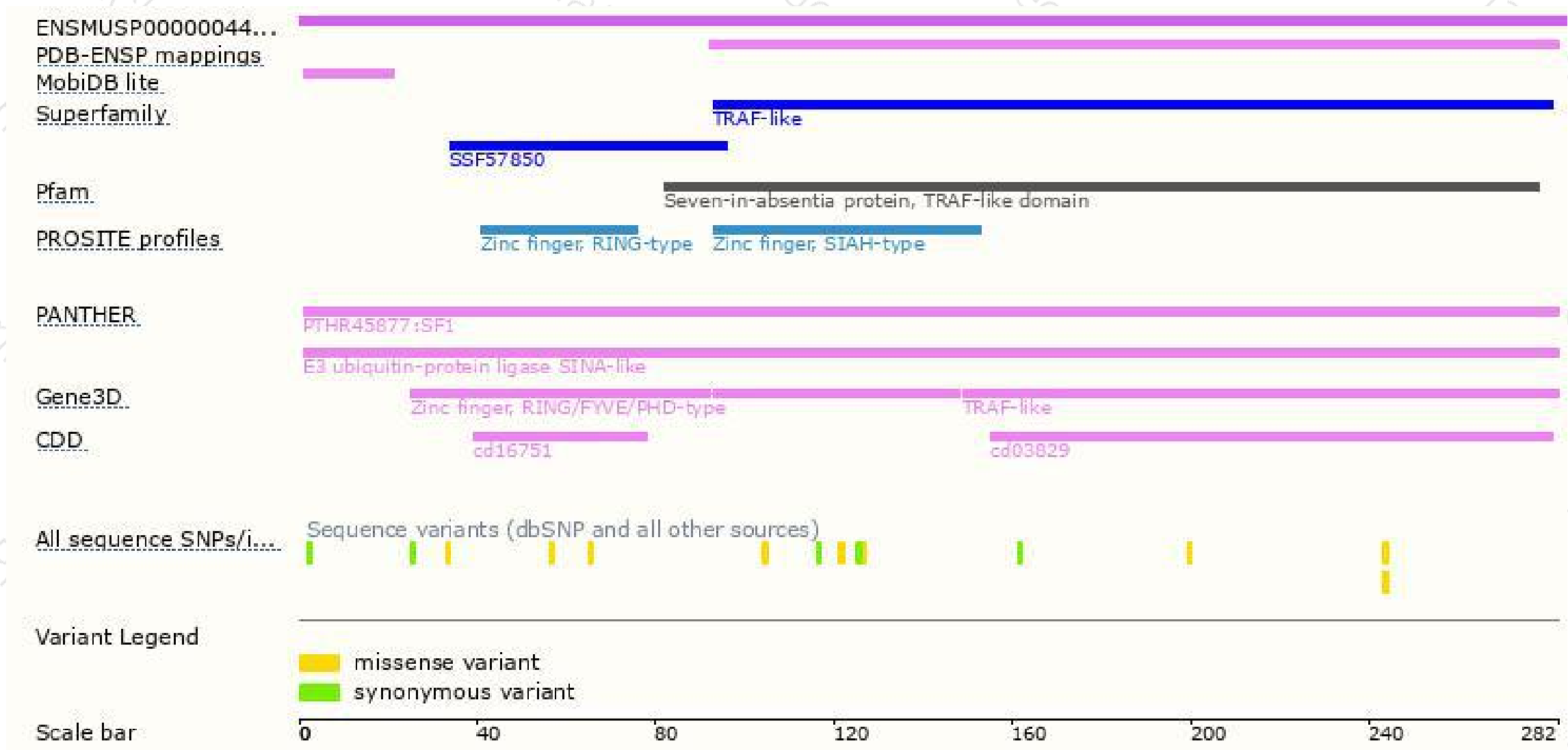
The strategy is based on the design of *Siah1a-201* transcript, the transcription is shown below:



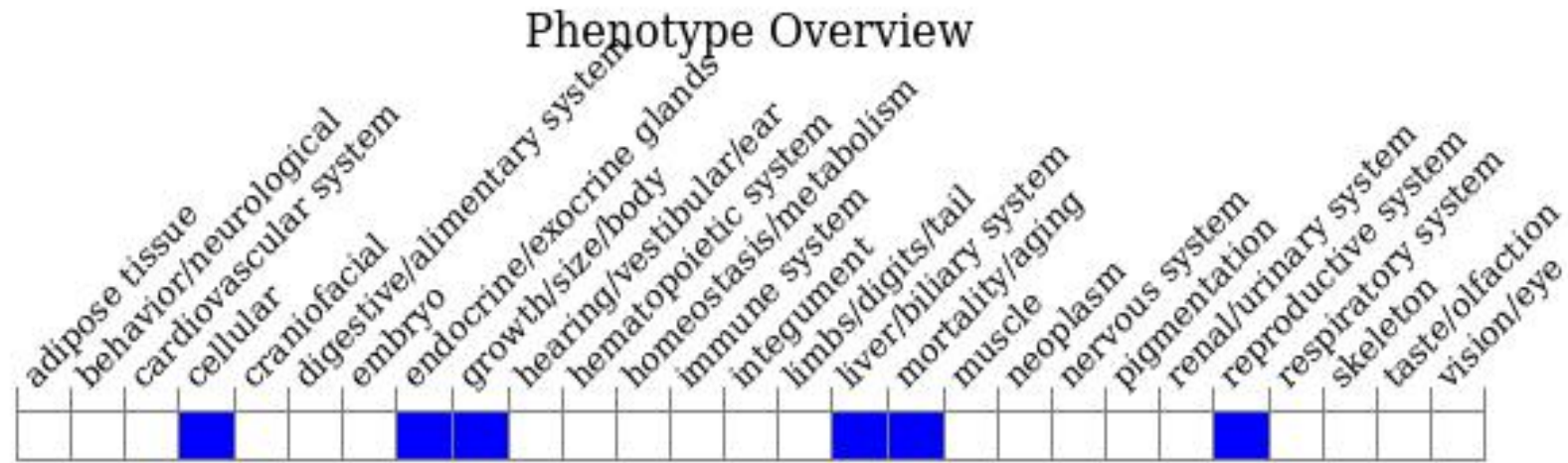
Genomic location distribution



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, homozygotes for a targeted null mutation exhibit retarded postnatal growth, and high preweaning and postweaning mortality. Surviving females are subfertile, having few, if any, offspring, while males are sterile due to a block at meiotic metaphase I.

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

Tel: 400-9660890

