Slc19a2 Cas9-CKO Strategy

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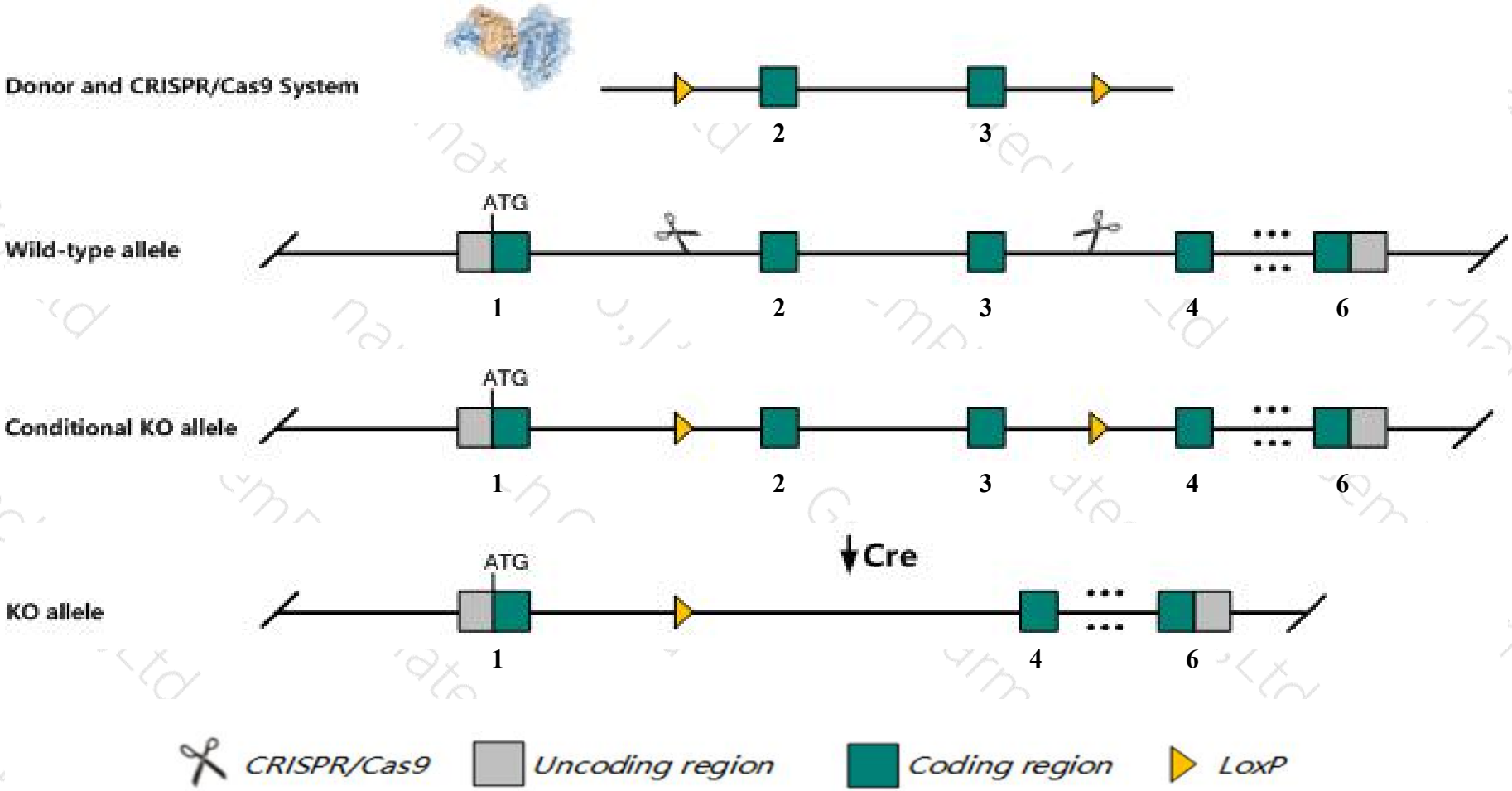
Project Overview

Project Name	***Slc19a2***
Project type	**Cas9-CKO**
Strain background	**C57BL/6JGpt**

Conditional Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *Slc19a2* gene. The schematic diagram is as follows:



Technical routes

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- The *Slc19a2* gene has 4 transcripts. According to the structure of *Slc19a2* gene, exon2-exon3 of *Slc19a2-201* (ENSMUST00000044021.11) transcript is recommended as the knockout region.The region contains 829bp coding sequence. Knock out the region will result in disruption of protein function.

- In this project we use CRISPR/Cas9 technology to modify *Slc19a2* 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,homozygotes for targeted null alleles exhibit a grossly normal phenotype except for reduced testis size and male infertility. on a low-thiamine diet, mutants show premature death and sensorineural deafness, while homozygotes for one targeted allele also display diabetes mellitus and megaloblastosis.
- The *Slc19a2* gene is located on the Chr1. 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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Slc19a2 solute carrier family 19 (thiamine transporter), member 2 [Mus musculus (house mouse)]

Gene ID: 116914, updated on 13-Mar-2020

Summary

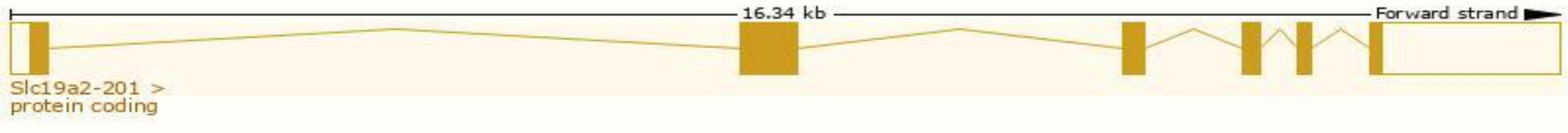
Official Symbol	Slc19a2 provided by MGI
Official Full Name	solute carrier family 19 (thiamine transporter), member 2 provided byMGI
Primary source	MGI:MGI:1928761
See related	Ensembl:ENSMUSG00000040918
Gene type	protein coding
RefSeq status	VALIDATED
Organism	Mus musculus
Lineage	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Myomorpha; Muroidea; Muridae; Murinae; Mus; Mus
Also known as	AV276020, AW322295, DDA1, THTR1, TRMA, ThTr-1
Expression	Broad expression in liver adult (RPKM 32.8), liver E18 (RPKM 17.1) and 27 other tissuesSee more
Orthologs	human all

Transcript information（Ensembl）

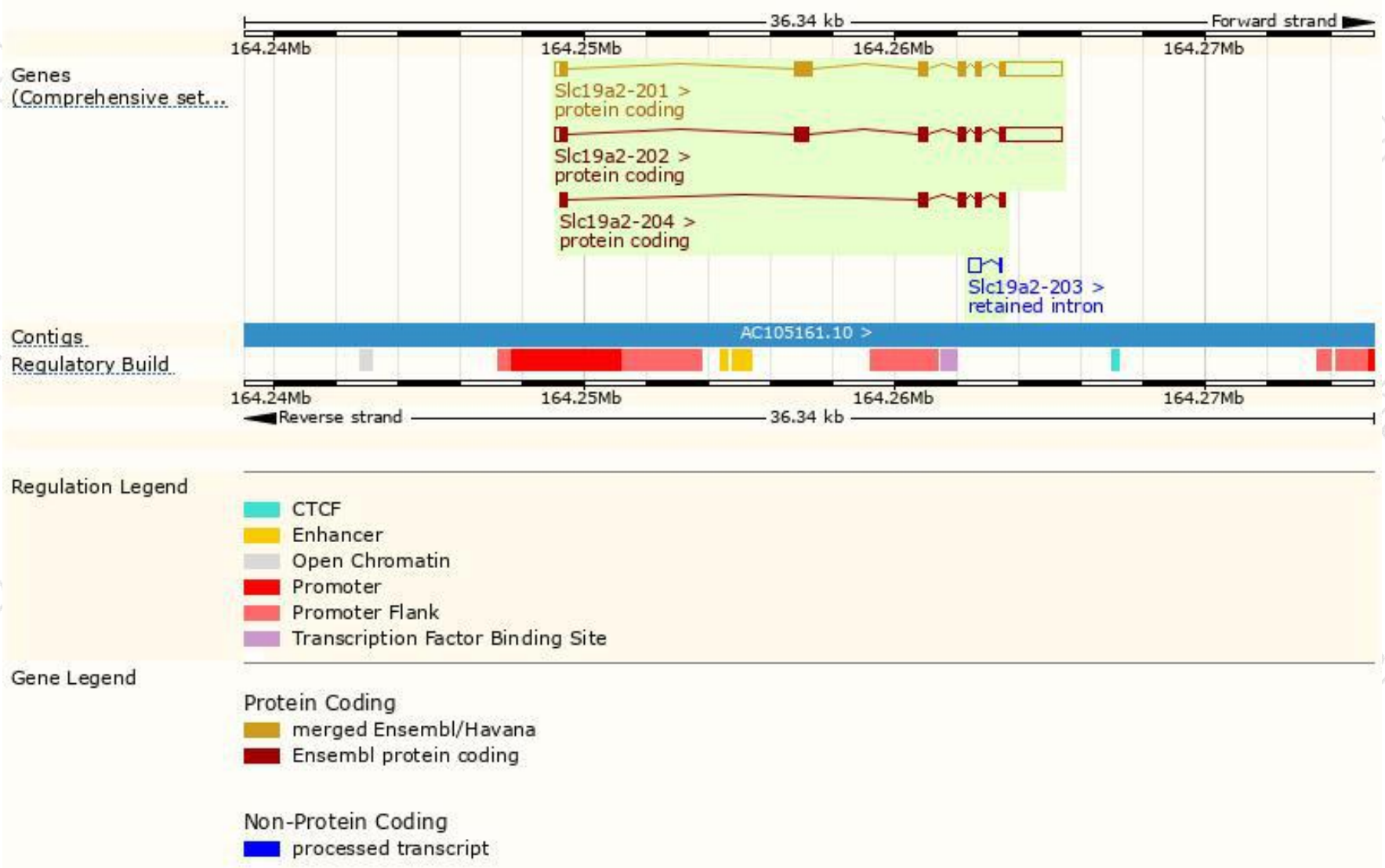
The gene has 4 transcripts,all transcripts are shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Slc19a2-201	ENSMUST00000044021.11	3571	498aa	Protein coding	CCDS15433	Q9EQN9	TSL:1 GENCODE basic APPRIS P1
Slc19a2-202	ENSMUST00000159230.7	3432	460aa	Protein coding	CCDS69968	Q9EQN9	TSL:1 GENCODE basic
Slc19a2-204	ENSMUST00000169394.1	894	297aa	Protein coding	-	E9Q2R3	TSL:5 GENCODE basic
Slc19a2-203	ENSMUST00000160773.1	471	No protein	Retained intron	-	-	TSL:1

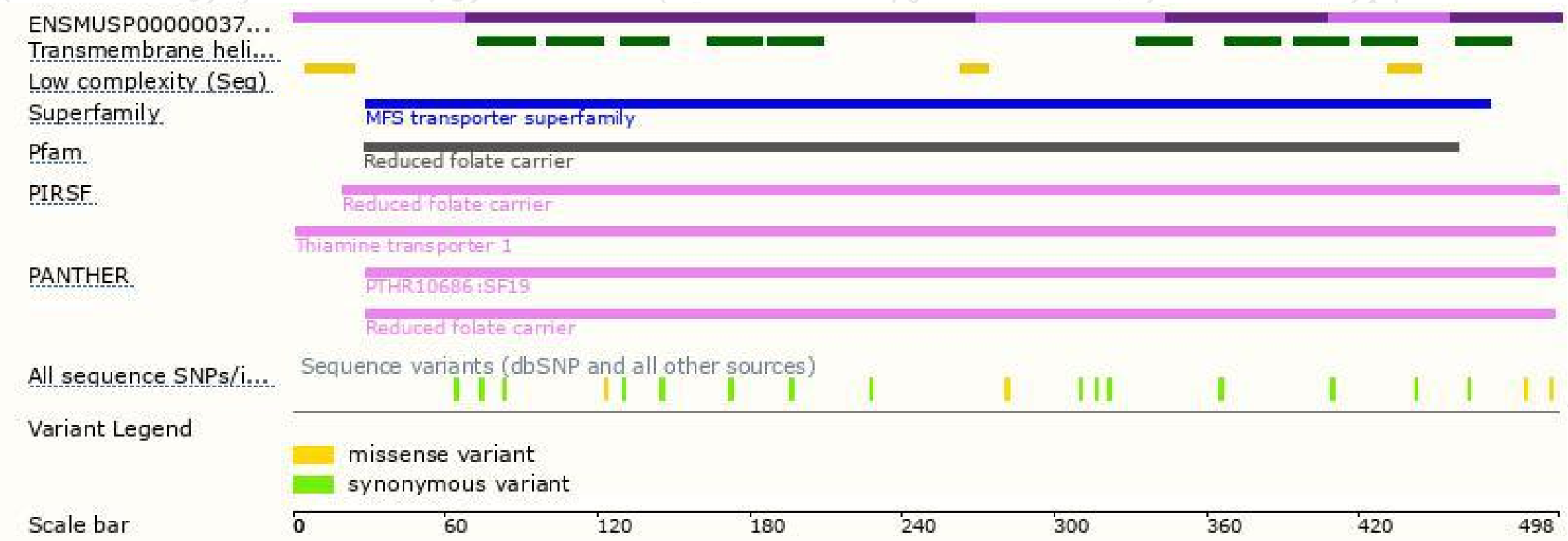
The strategy is based on the design of *Slc19a2-201* transcript,the transcription is shown below:



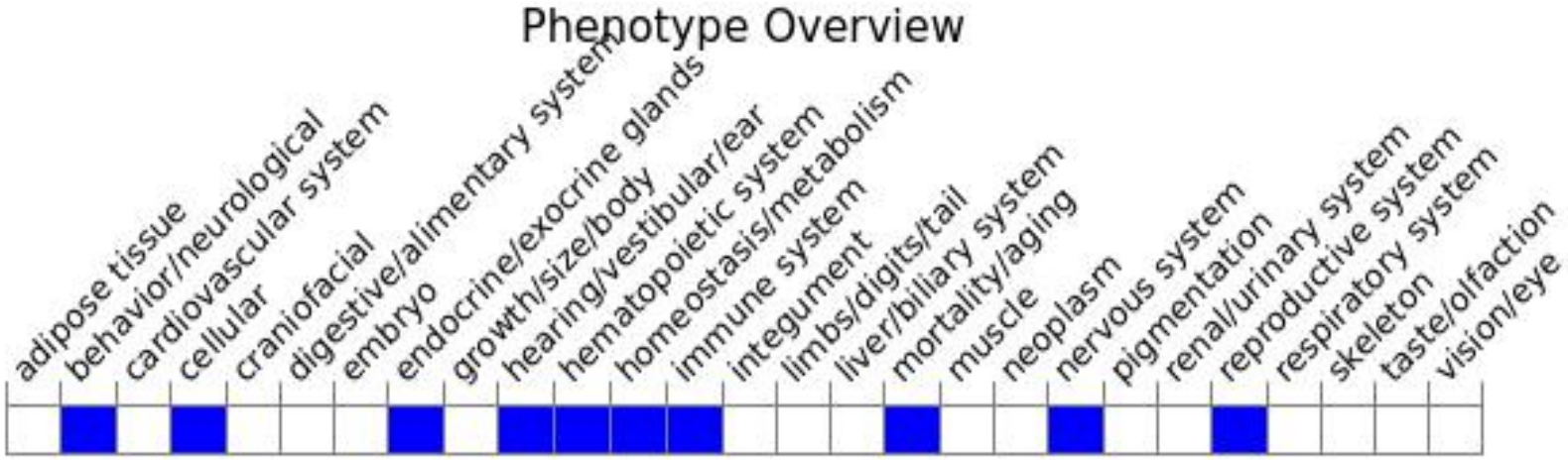
Genomic location distribution



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 targeted null alleles exhibit a grossly normal phenotype except for reduced testis size and male infertility. On a low-thiamine diet, mutants show premature death and sensorineural deafness, while homozygotes for one targeted allele also display diabetes mellitus and megaloblastosis.

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

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