

Nacc2 Cas9-KO Strategy

Designer: Zihe Cui

Reviewer: Yanhua Shen

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Project Overview

Project Name

Nacc2

Project type

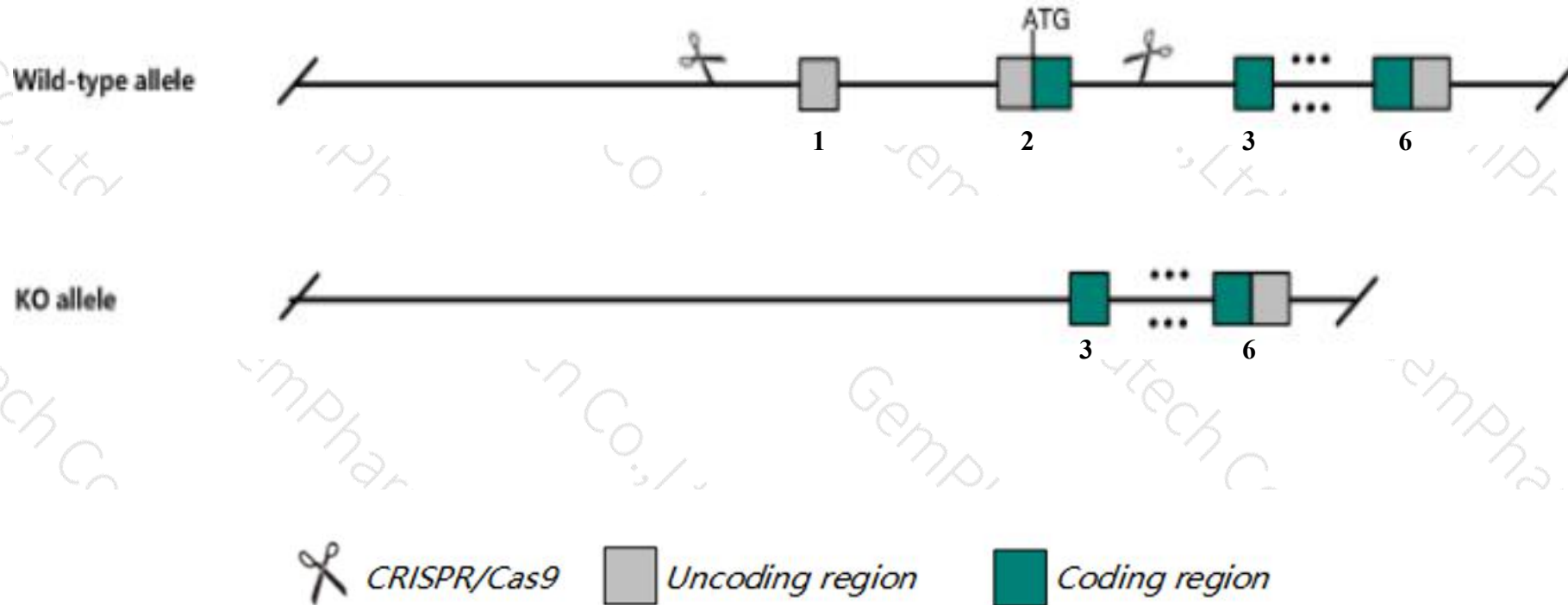
Cas9-KO

Strain background

C57BL/6JGpt

Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *Nacc2* gene. The schematic diagram is as follows:



Technical routes

➤ The *Nacc2* gene has 8 transcripts. According to the structure of *Nacc2* gene, exon1-exon2 of *Nacc2*-202(ENSMUST00000114159.8) transcript is recommended as the knockout region. The region contains start codon ATG.

Knock out the region will result in disruption of protein function.

➤ In this project we use CRISPR/Cas9 technology to modify *Nacc2* gene. The brief process is as follows: CRISPR/Cas9 system 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.

- Transcript *Nacc2*-203 may not be affected.
- The KO region contains start codon ATG, new protein may be formed.
- The *Nacc2* gene is located on the Chr2. 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.

Gene information (NCBI)

Nacc2 nucleus accumbens associated 2, BEN and BTB (POZ) domain containing [*Mus musculus* (house mouse)]

Gene ID: 67991, updated on 25-Sep-2020

Summary



Official Symbol Nacc2 provided by [MGI](#)

Official Full Name nucleus accumbens associated 2, BEN and BTB (POZ) domain containing provided by [MGI](#)

Primary source [MGI:MGI:1915241](#)

See related [Ensembl:ENSMUSG00000026932](#)

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 Btbd14; Btbd14a; AI448087; 0610020I02Rik; C030048H19Rik

Expression Ubiquitous expression in cerebellum adult (RPKM 26.3), bladder adult (RPKM 17.2) and 25 other tissues [See more](#)

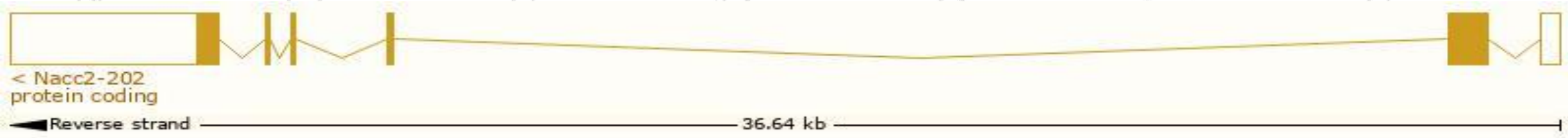
Orthologs [human](#) [all](#)

Transcript information (Ensembl)

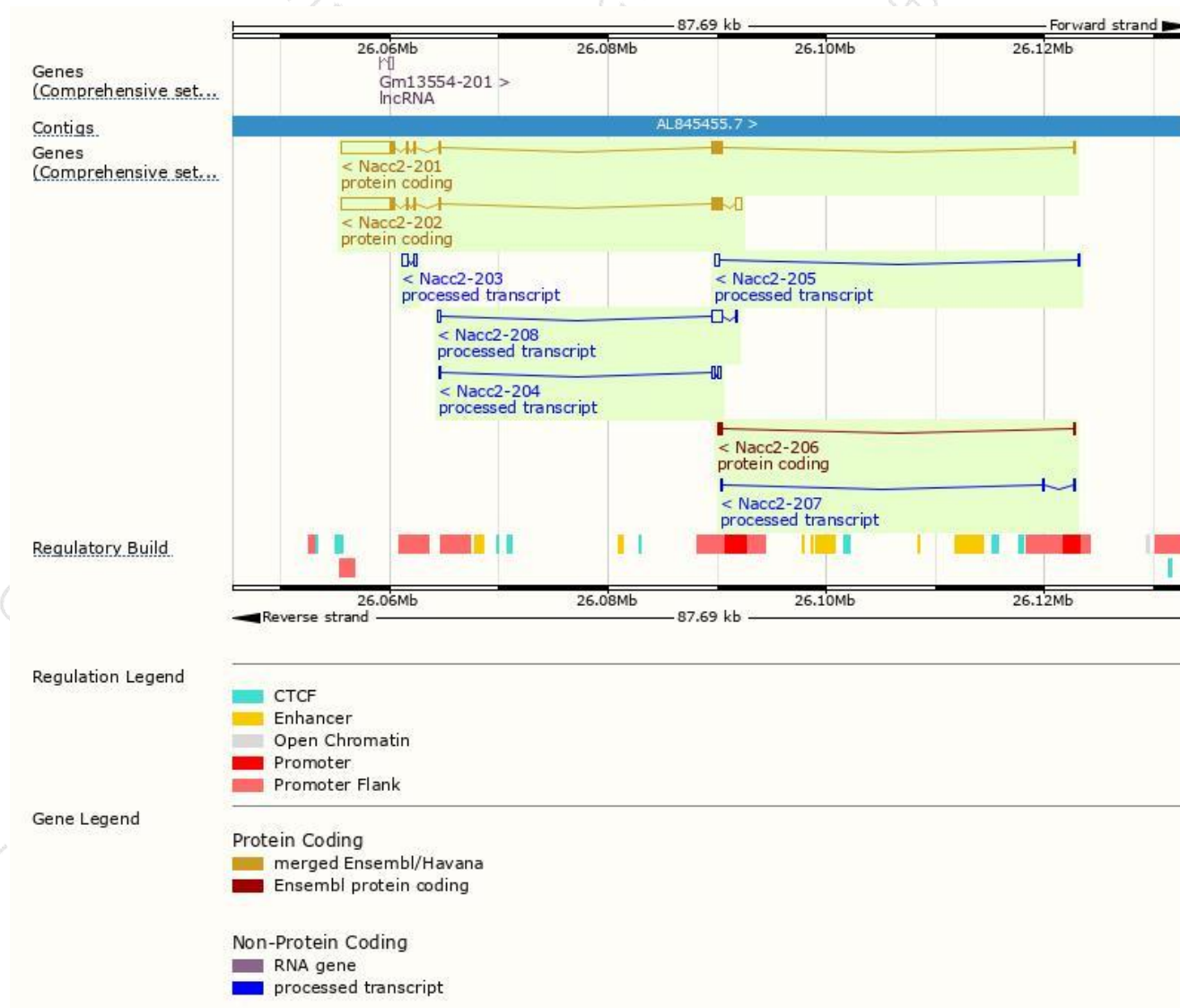
The gene has 8 transcripts,all transcripts are shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Nacc2-202	ENSMUST00000114159.8	6675	586aa	Protein coding	CCDS15796	Q9DCM7	TSL:1 GENCODE basic APPRIS P1
Nacc2-201	ENSMUST00000028300.5	6378	586aa	Protein coding	CCDS15796	Q9DCM7	TSL:1 GENCODE basic APPRIS P1
Nacc2-206	ENSMUST00000140993.1	411	85aa	Protein coding	-	A2ARL3	CDS 3' incomplete TSL:2
Nacc2-208	ENSMUST00000152133.1	1258	No protein	Processed transcript	-	-	TSL:1
Nacc2-203	ENSMUST00000126921.1	906	No protein	Processed transcript	-	-	TSL:5
Nacc2-204	ENSMUST00000128674.1	628	No protein	Processed transcript	-	-	TSL:5
Nacc2-205	ENSMUST00000133212.1	482	No protein	Processed transcript	-	-	TSL:3
Nacc2-207	ENSMUST00000149408.1	351	No protein	Processed transcript	-	-	TSL:3

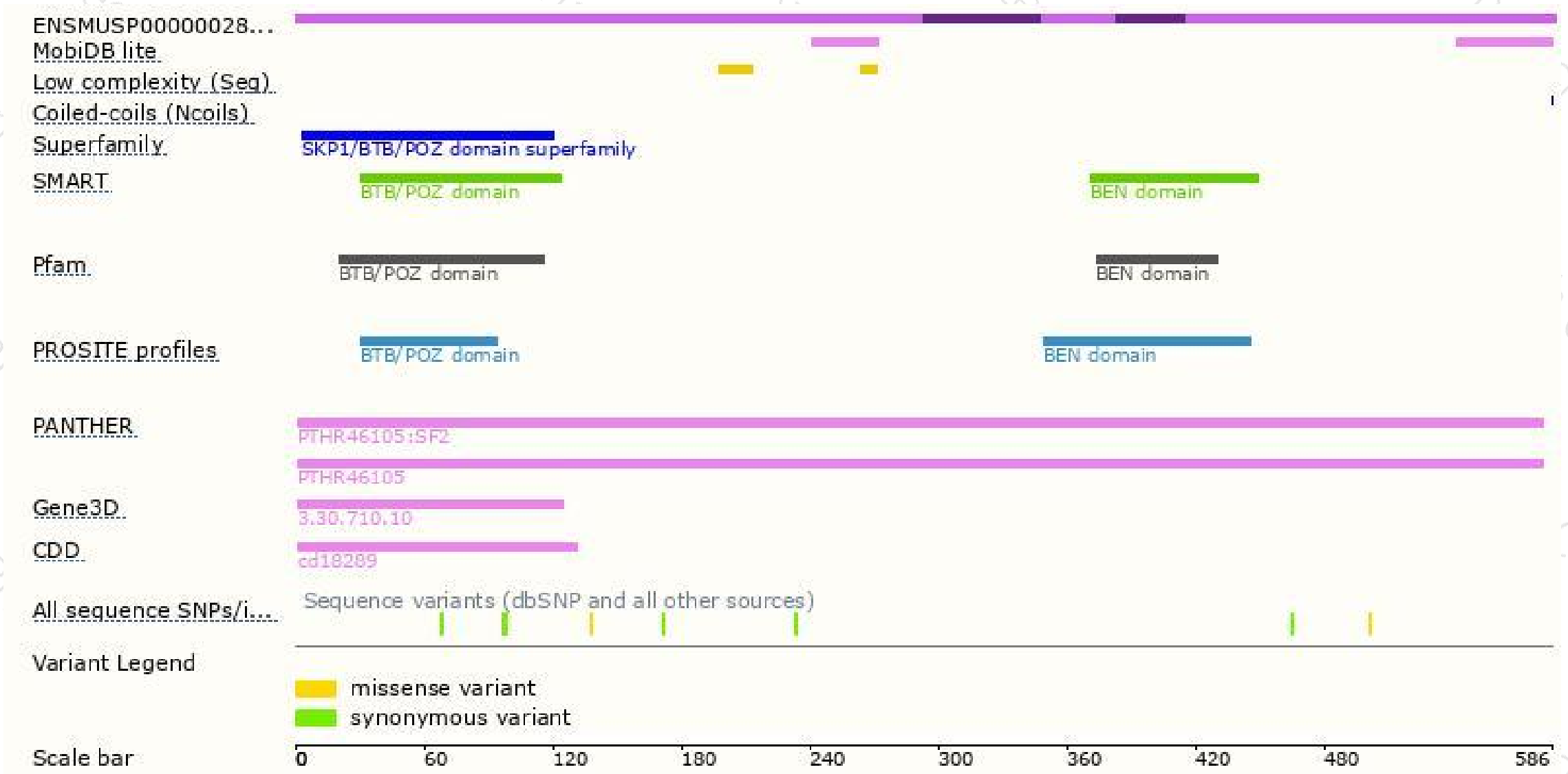
The strategy is based on the design of *Nacc2-202* transcript,the transcription is shown below:



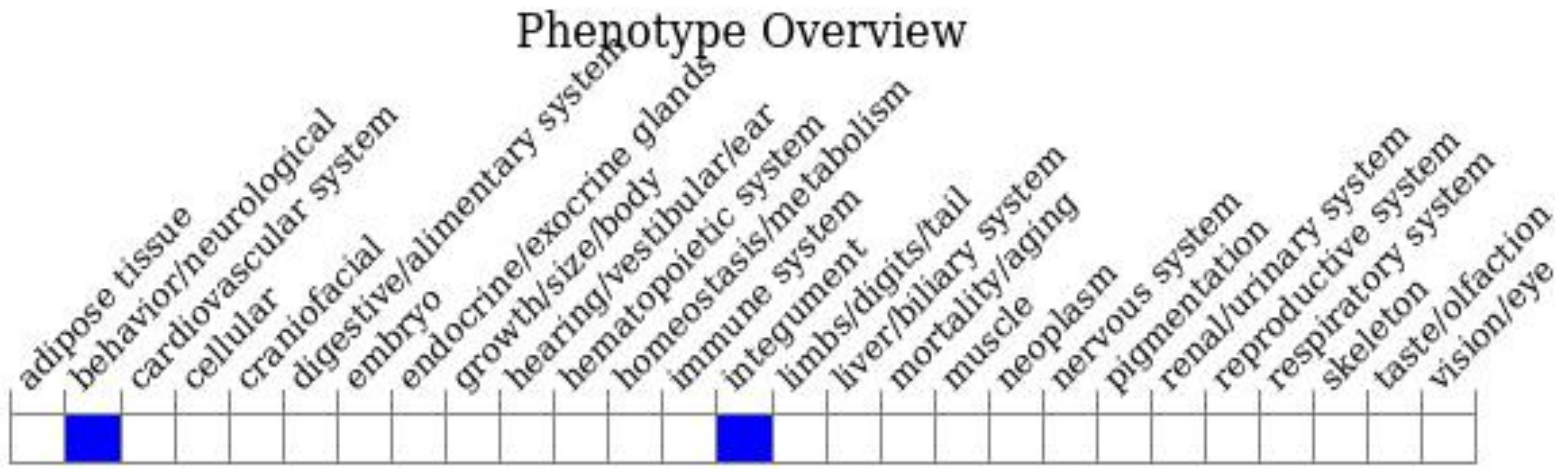
Genomic location distribution



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/>).

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

Tel: 400-9660890

