Kcnab2 Cas9-CKO Strategy

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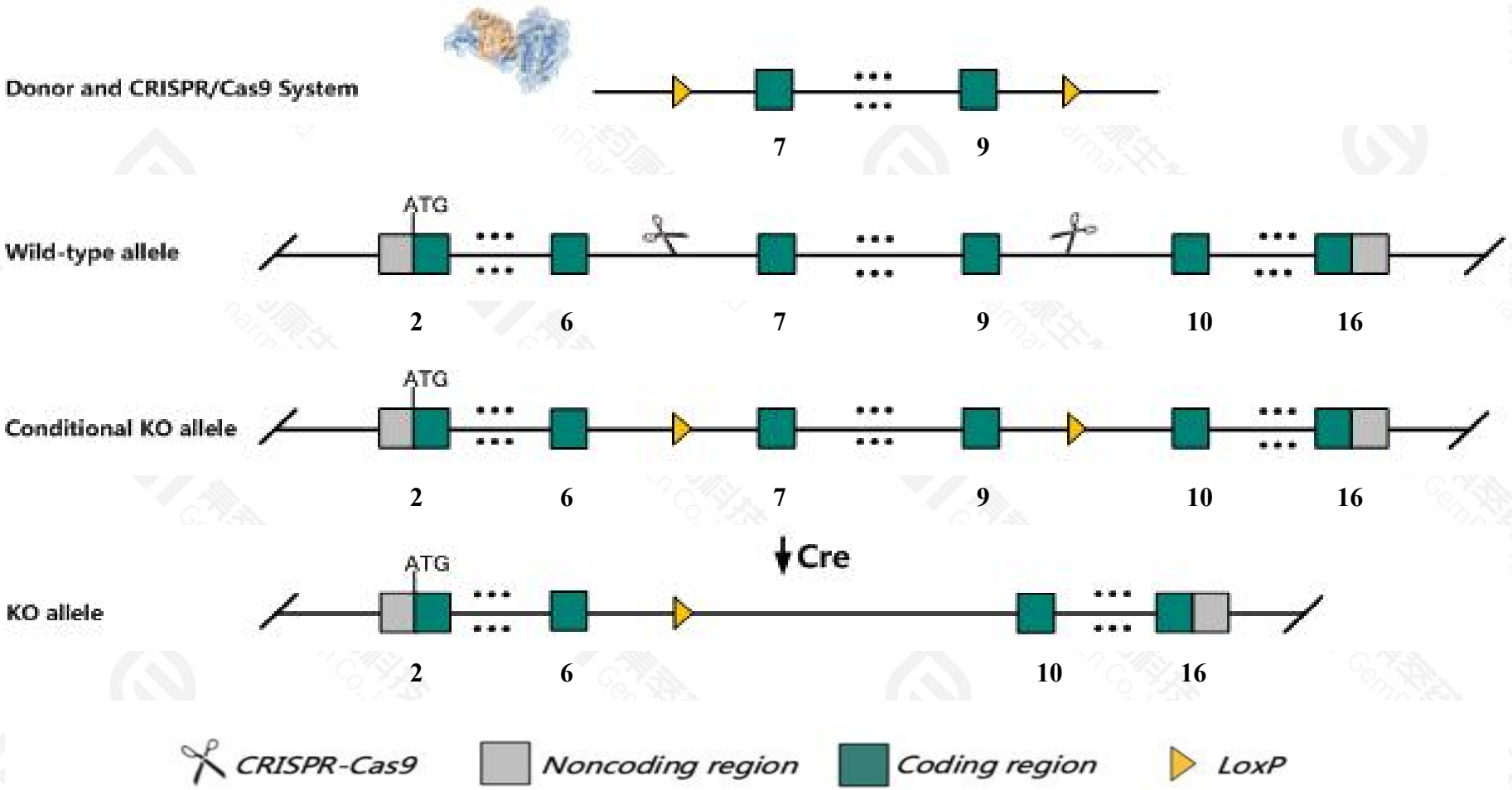
Project Overview

Project Name	***Kcnab2***
Project type	**Cas9-CKO**
Strain background	**C57BL/6JGpt**

Conditional Knockout strategy

This model will use CRISPR-Cas9 technology to edit the *Kcnab2* gene. The schematic diagram is as follows:



Technical routes

➢ The *Kcnab2* gene has 18 transcripts. According to the structure of *Kcnab2* gene, exon 7-exon 9 of *Kcnab2-208*(ENSMUST00000160884.9) transcript is recommended as the knockout region.The region contains 134 bp coding sequence. Knock out the region will result in disruption of protein function.

➢ In this project we use CRISPR-Cas9 technology to modify *Kcnab2* 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, homozygous null mice show strain-specific changes in survival, body weight, thermoregulation and cold-swim induced tremors, impaired associative learning and memory, sporadic seizures and amygala hyperexcitability. Mice homozygous for a knock-in mutationshow no deficits in associative learning.
- The effect on transcripts 205, 211,212, 213, 214,215 is unknown.
- The flox region contain the *Gm16333* gene, which may delet it after Cre.
- The *Kcnab2* gene is located on the Chr 4. 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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Kcnab2 potassium voltage-gated channel, shaker-related subfamily, beta member 2 [*Mus musculus* (house mouse)]

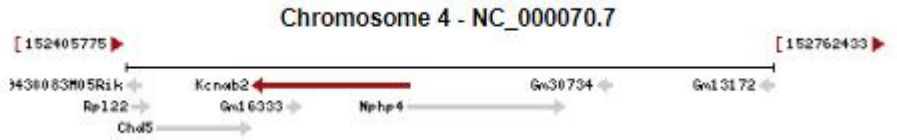
Gene ID: 16498, updated on 18-Jul-2022

Download Datasets

Summary

Official Symbol	Kcnab2 provided by MGI
Official Full Name	potassium voltage-gated channel, shaker-related subfamily, beta member 2 provided by MGI
Primary source	MGI:MGI:109239
See related	Ensembl:ENSMUSG00000028931 AllianceGenome:MGI:109239
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	F5; I2rf5; Kcnb3; kv-beta-2
Summary	Predicted to enable aldo-keto reductase (NADP) activity; potassium channel regulator activity; and transmembrane transporter binding activity. Involved in neuromuscular process. Acts upstream of or within hematopoietic progenitor cell differentiation. Located in axon and postsynaptic density. Is expressed in several structures, including central nervous system; genitourinary system; hemolymphoid system; intestine; and sensory organ. Used to study chromosome 1p36 deletion syndrome. Orthologous to human KCNAB2 (potassium voltage-gated channel subfamily A regulatory beta subunit 2). [provided by Alliance of Genome Resources, Apr 2022]
Expression	Biased expression in cortex adult (RPKM 40.8), frontal lobe adult (RPKM 32.0) and 9 other tissues See more
Orthologs	human all

NEW Try the new Gene table
Try the new Transcript table

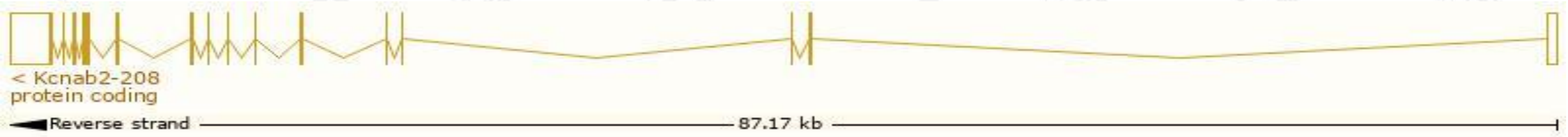


Transcript information（Ensembl）

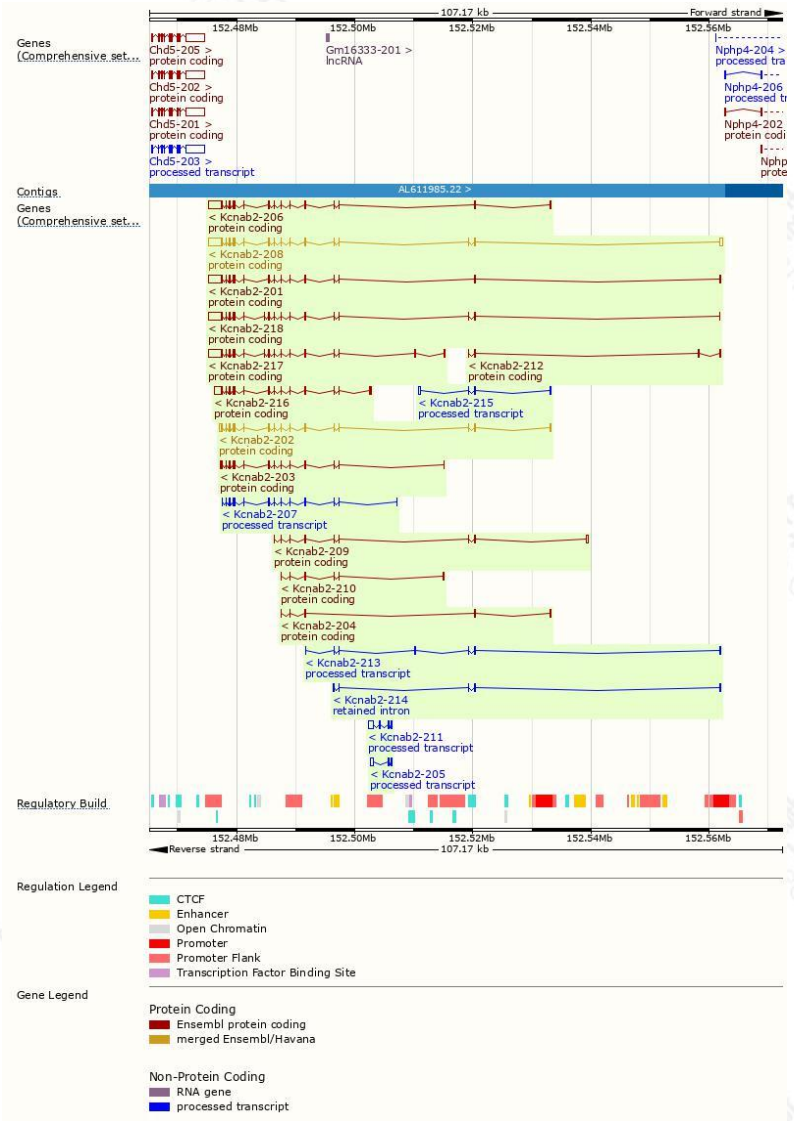
The gene has 18 transcripts,all transcripts are shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Kcnab2-208	ENSMUST00000160884.9	3961	367aa	Protein coding	CCDS19000		TSL:1 , GENCODE basic , APPRIS P1 ,
Kcnab2-201	ENSMUST00000030768.10	3597	353aa	Protein coding	CCDS57316		TSL:1 , GENCODE basic ,
Kcnab2-206	ENSMUST00000159840.8	3574	353aa	Protein coding	CCDS57316		TSL:1 , GENCODE basic ,
Kcnab2-202	ENSMUST00000105648.10	1799	367aa	Protein coding	CCDS19000		TSL:1 , GENCODE basic , APPRIS P1 ,
Kcnab2-217	ENSMUST00000238715.2	3803	415aa	Protein coding	-		GENCODE basic ,
Kcnab2-218	ENSMUST00000238738.2	3533	382aa	Protein coding	-		GENCODE basic ,
Kcnab2-216	ENSMUST00000238252.2	2674	398aa	Protein coding	-		GENCODE basic ,
Kcnab2-203	ENSMUST00000159186.9	1325	300aa	Protein coding	-		TSL:5 , GENCODE basic ,
Kcnab2-209	ENSMUST00000161236.8	668	134aa	Protein coding	-		CDS 3' incomplete , TSL:3 ,
Kcnab2-210	ENSMUST00000161496.9	484	56aa	Protein coding	-		CDS 3' incomplete , TSL:5 ,
Kcnab2-212	ENSMUST00000162017.3	406	38aa	Protein coding	-		CDS 3' incomplete , TSL:5 ,
Kcnab2-204	ENSMUST00000159435.8	365	51aa	Protein coding	-		CDS 3' incomplete , TSL:3 ,
Kcnab2-211	ENSMUST00000161844.3	1332	No protein	Processed transcript	-		TSL:3 ,
Kcnab2-207	ENSMUST00000159844.9	1004	No protein	Processed transcript	-		TSL:5 ,
Kcnab2-205	ENSMUST00000159488.2	694	No protein	Processed transcript	-		TSL:3 ,
Kcnab2-213	ENSMUST00000162165.3	638	No protein	Processed transcript	-		TSL:3 ,
Kcnab2-215	ENSMUST00000162518.2	491	No protein	Processed transcript	-		TSL:3 ,
Kcnab2-214	ENSMUST00000162200.8	543	No protein	Retained intron	-		TSL:2 ,

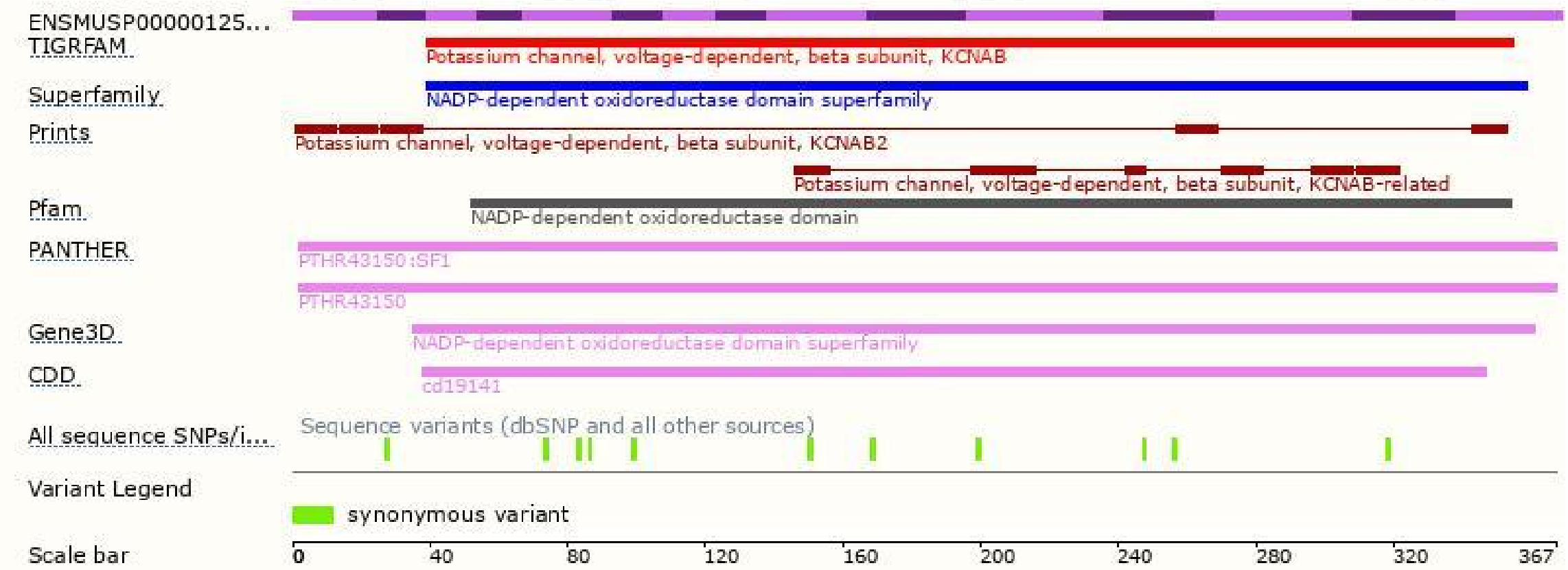
The strategy is based on the design of *Kcnab2-208* transcript,the transcription is shown below:



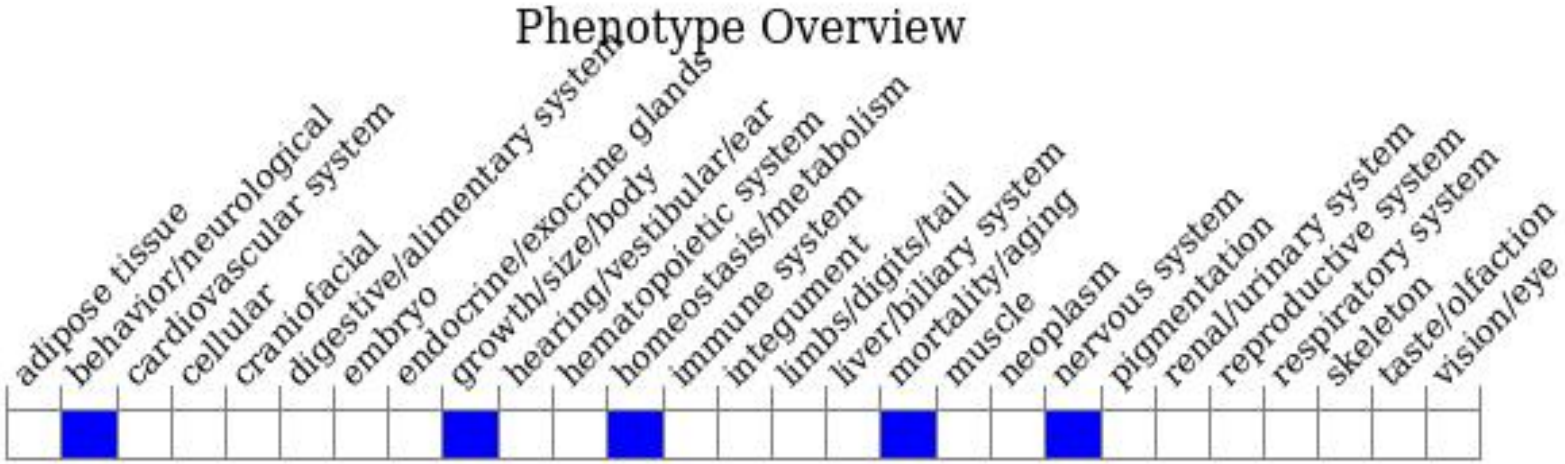
Genomic location distribution



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 show strain-specific changes in survival, body weight, thermoregulation and cold-swim induced tremors, impaired associative learning and memory, sporadic seizures and amygala hyperexcitability. Mice homozygous for a knock-in mutationshow no deficits in associative learning.

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