

Arrb1 Cas9-CKO Strategy

Designer:

Daohua Xu

Reviewer:

Huimin Su

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Project Overview

Project Name

Arrb1

Project type

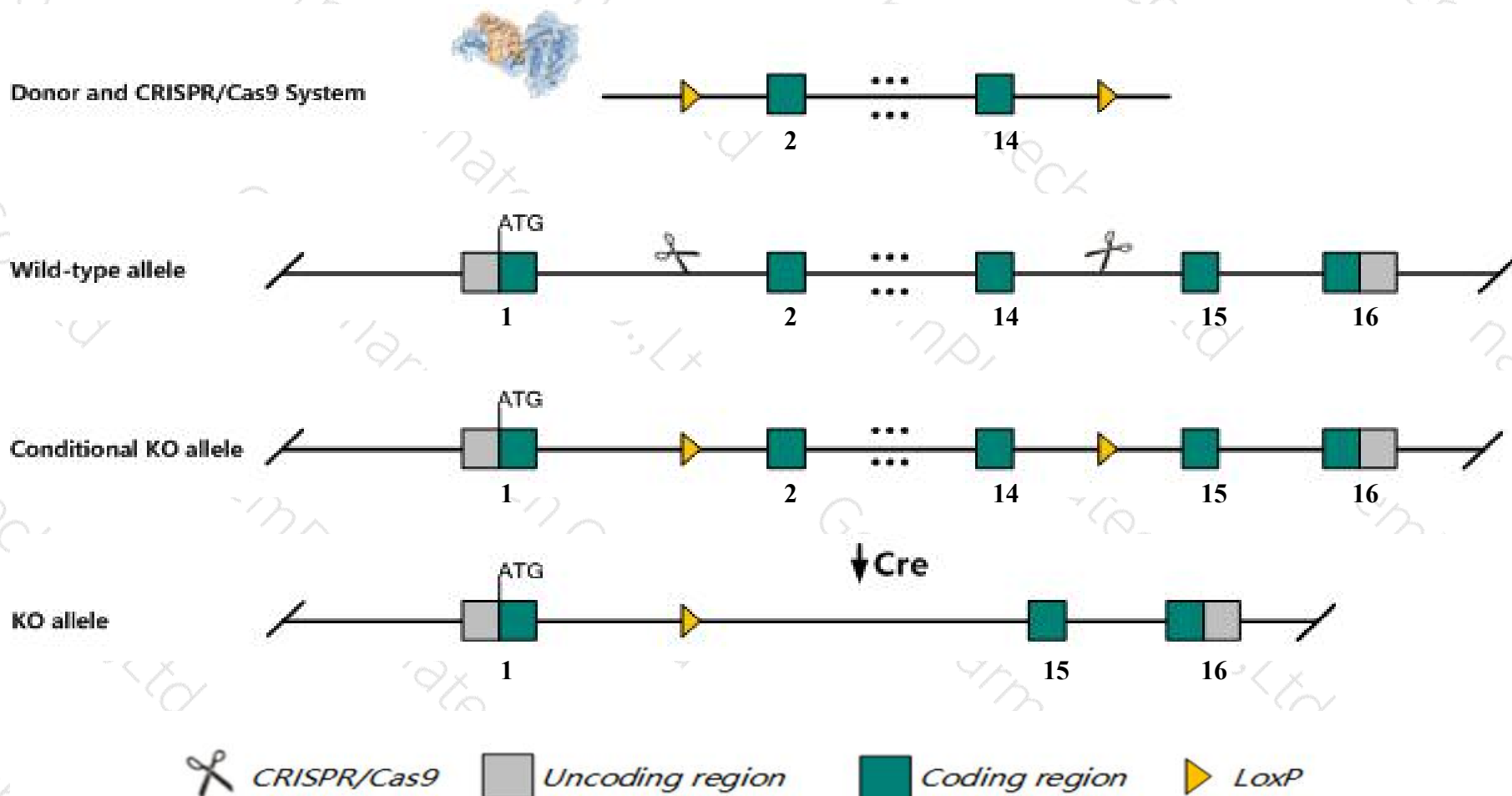
Cas9-CKO

Strain background

C57BL/6JGpt

Conditional Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *Arrb1* gene. The schematic diagram is as follows:



Technical routes

- The *Arrb1* gene has 10 transcripts. According to the structure of *Arrb1* gene, exon2-exon14 of *Arrb1*-202 (ENSMUST00000098266.8) transcript is recommended as the knockout region. The region contains 1073bp coding sequence. Knock out the region will result in disruption of protein function.
- In this project we use CRISPR/Cas9 technology to modify *Arrb1* 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.

- According to the existing MGI data, Homozygotes for targeted null mutations exhibit impaired quenching of rod photocurrent flash responses and greater sensitivity to beta-receptor agonist-stimulated ventricular ejection fraction.
- The *Arrb1* gene is located on the Chr7. 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)

Arrb1 arrestin, beta 1 [Mus musculus (house mouse)]

Gene ID: 109689, updated on 5-Mar-2019

Summary



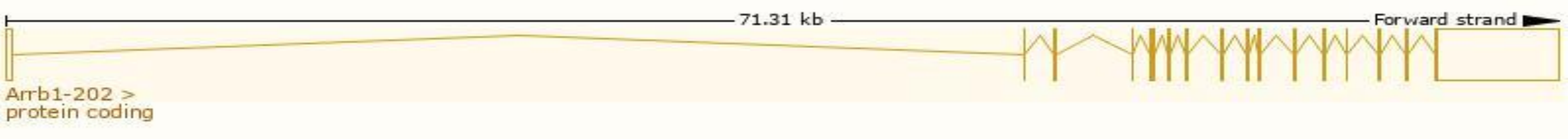
Official Symbol	Arrb1 provided by MGI
Official Full Name	arrestin, beta 1 provided by MGI
Primary source	MGI:MGI:99473
See related	Ensembl:ENSMUSG00000018909
Gene type	protein coding
RefSeq status	VALIDATED
Organism	Mus musculus
Lineage	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Myomorpha; Muroidea; Muridae; Murinae; Mus; Mus
Also known as	1200006I17Rik, AW208571, G430100A01Rik
Expression	Ubiquitous expression in liver E14.5 (RPKM 46.5), liver E14 (RPKM 43.8) and 27 other tissues See more
Orthologs	human all

Transcript information (Ensembl)

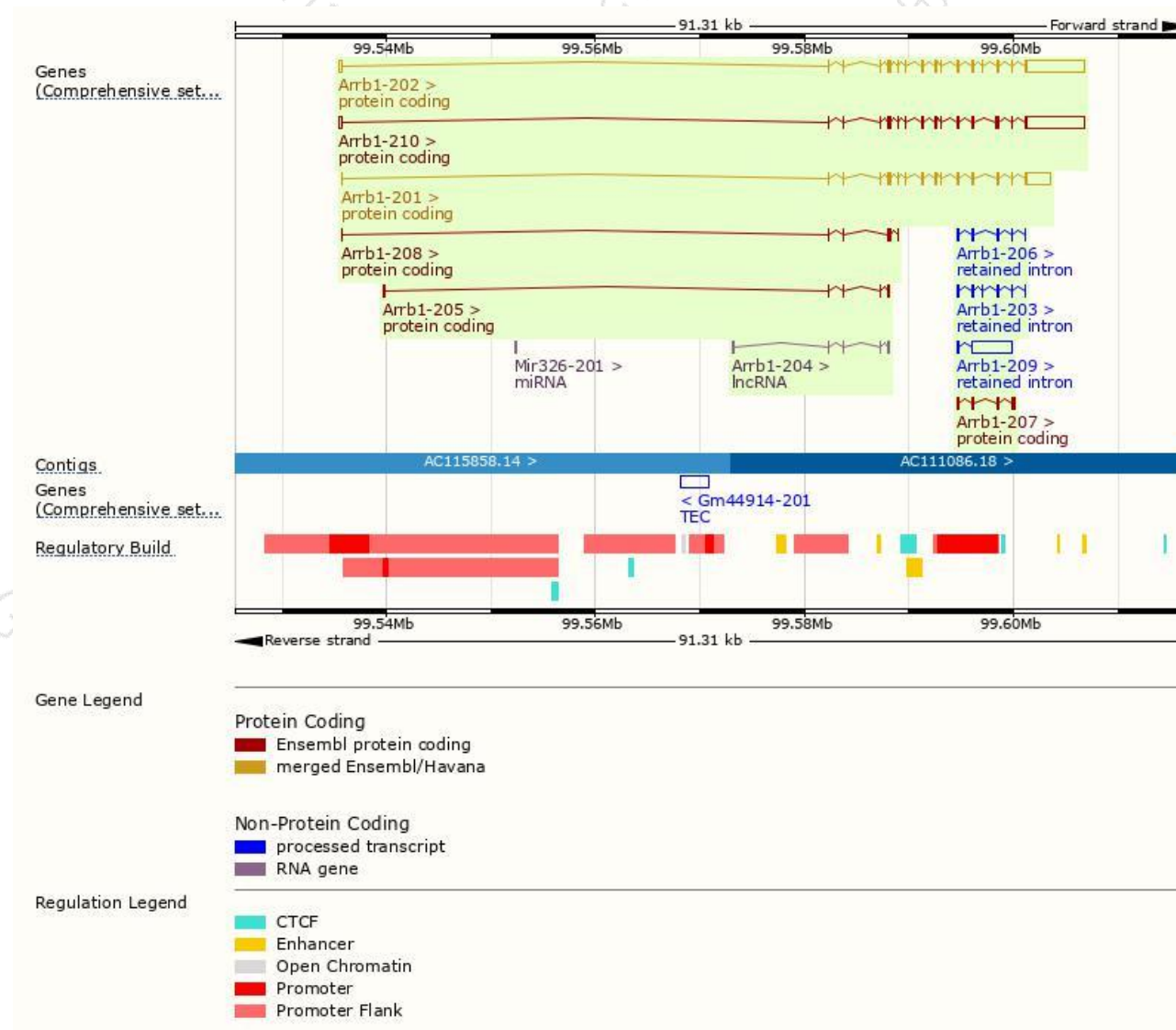
The gene has 10 transcripts,all transcripts are shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Arrb1-202	ENSMUST00000098266.8	7132	418aa	Protein coding	CCDS40032	Q8BWG8	TSL:1 GENCODE basic APPRIS ALT 1
Arrb1-201	ENSMUST00000032995.14	3715	410aa	Protein coding	CCDS21484	Q8BWG8	TSL:1 GENCODE basic APPRIS P3
Arrb1-210	ENSMUST00000179755.7	7135	419aa	Protein coding	-	J3QNU6	TSL:5 GENCODE basic
Arrb1-205	ENSMUST00000161525.1	487	135aa	Protein coding	-	E0CY53	CDS 3' incomplete TSL:2
Arrb1-208	ENSMUST00000162404.7	431	118aa	Protein coding	-	E0CYB1	CDS 3' incomplete TSL:3
Arrb1-207	ENSMUST00000162290.1	421	121aa	Protein coding	-	F7DF62	CDS 5' incomplete TSL:2
Arrb1-209	ENSMUST00000162933.1	3917	No protein	Retained intron	-	-	TSL:1
Arrb1-203	ENSMUST00000159642.1	434	No protein	Retained intron	-	-	TSL:2
Arrb1-206	ENSMUST00000162043.7	417	No protein	Retained intron	-	-	TSL:1
Arrb1-204	ENSMUST00000161268.1	395	No protein	lncRNA	-	-	TSL:2

The strategy is based on the design of *Arrb1-202* transcript,The transcription is shown below



Genomic location distribution



Protein domain

ENSMUSP00000095...

[MobiDB lite](#)

[Low complexity \(Seq\)](#)

[Superfamily](#)

[SMART](#)

[Prints](#)

[Pfam](#)

[PROSITE patterns](#)

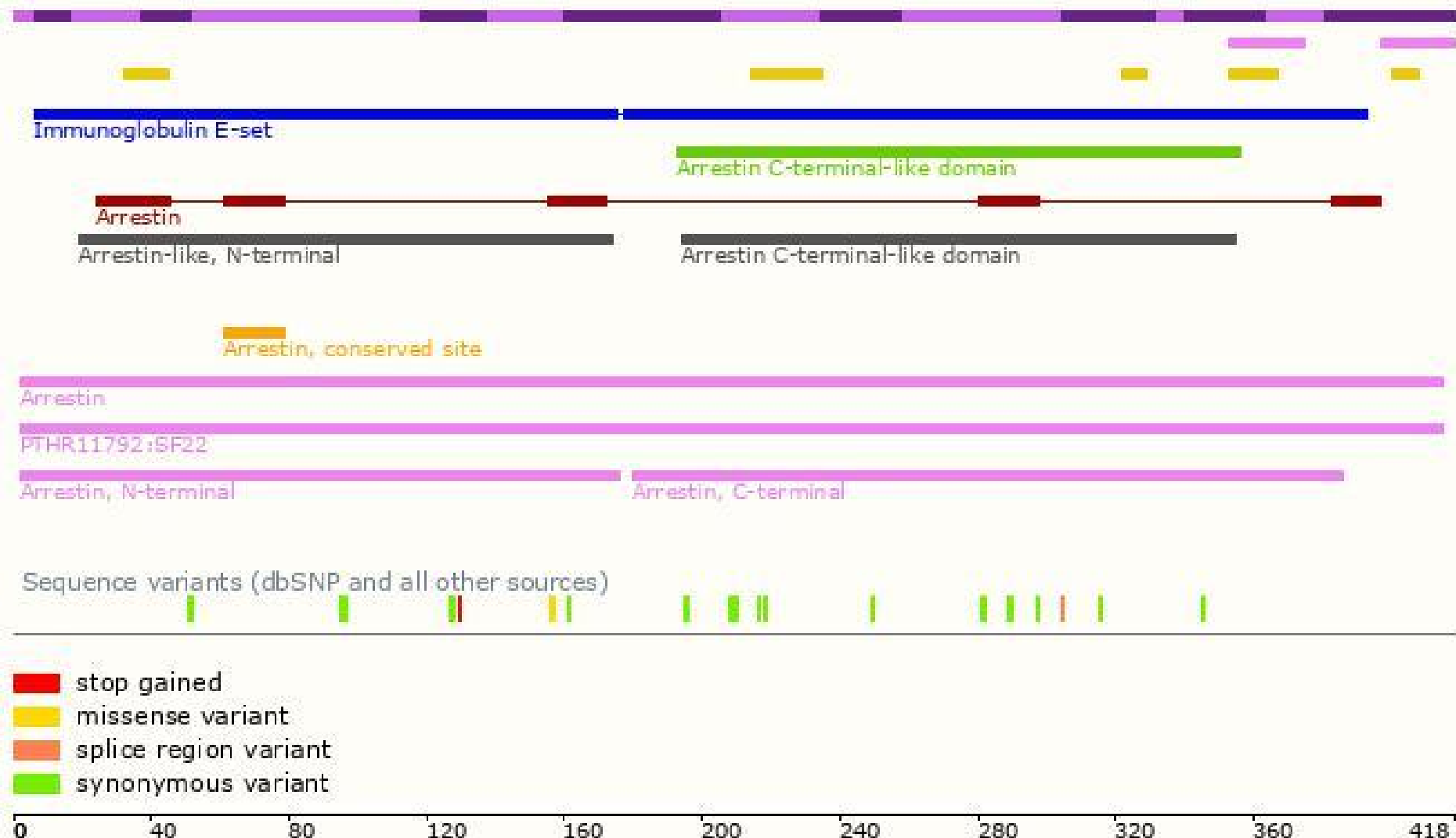
[PANTHER](#)

[Gene3D](#)

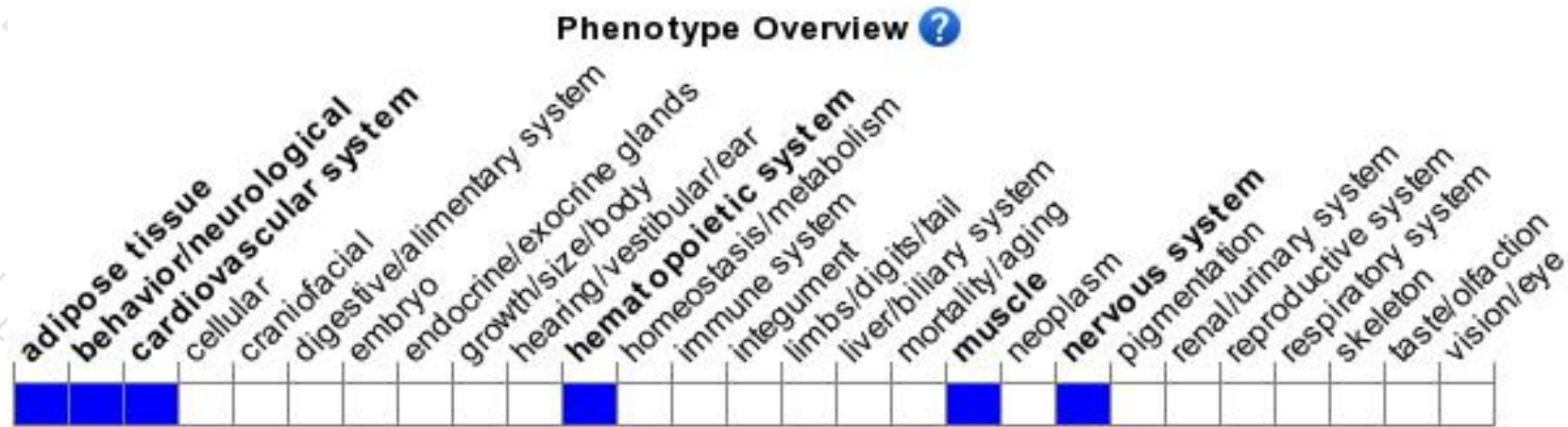
[All sequence SNPs/i...](#)

[Variant Legend](#)

[Scale bar](#)



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 mutations exhibit impaired quenching of rod photocurrent flash responses and greater sensitivity to beta-receptor agonist-stimulated ventricular ejection fraction.

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

Tel: 400-9660890

