

Plekha7 Cas9-CKO Strategy

Designer:

JiaYu

Reviewer:

Xiaojing Li

Design Date:

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Project Overview

Project Name

Plekha7

Project type

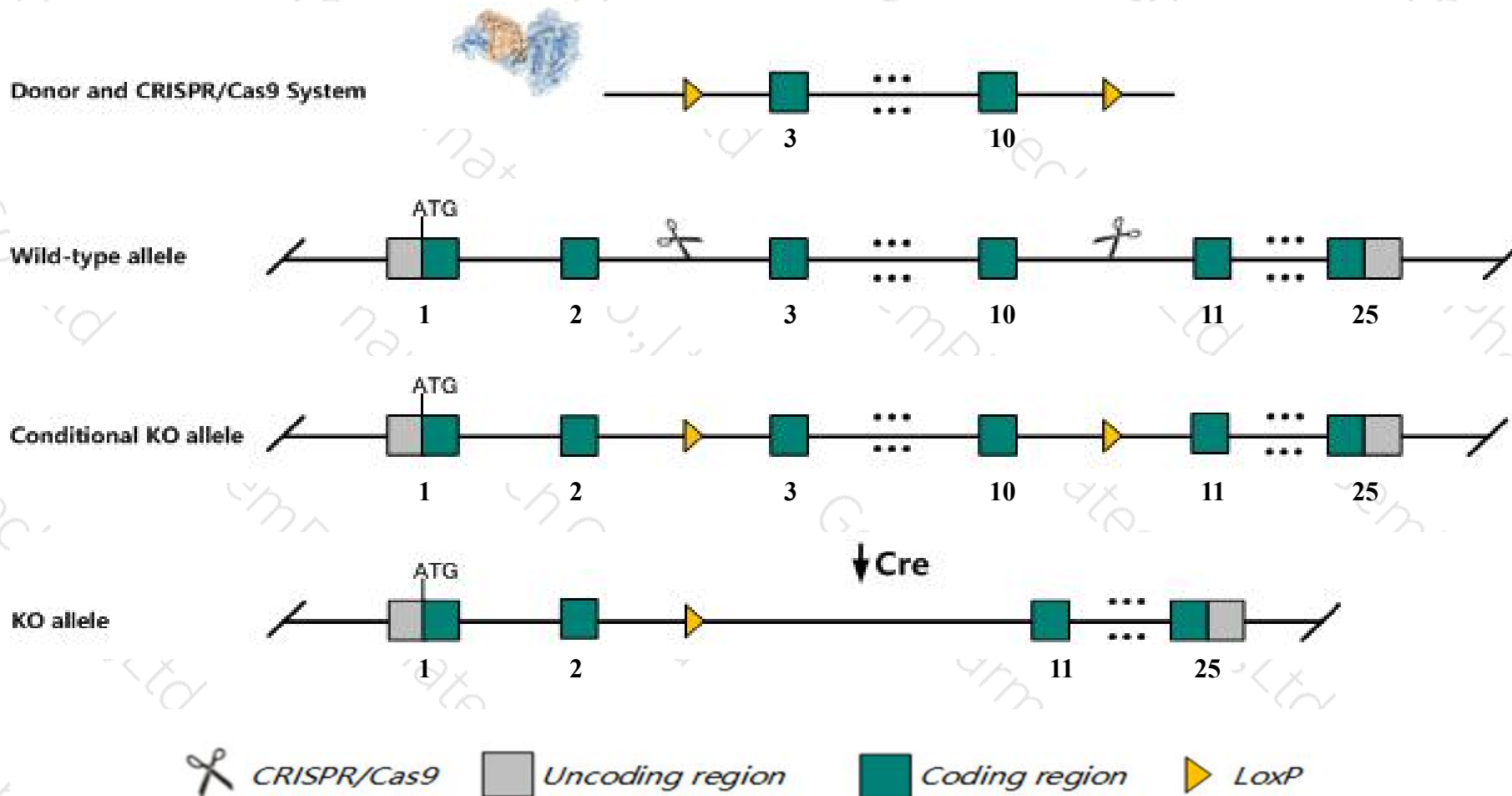
Cas9-CKO

Strain background

C57BL/6JGpt

Conditional Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *Plekha7* gene. The schematic diagram is as follows:



Technical routes

- The *Plekha7* gene has 20 transcripts. According to the structure of *Plekha7* gene, exon3-exon10 of *Plekha7*-210 (ENSMUST00000182834.7) transcript is recommended as the knockout region. The region contains 1642bp coding sequence. Knock out the region will result in disruption of protein function.
- In this project we use CRISPR/Cas9 technology to modify *Plekha7* 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, Mice homozygous for a null allele show decreased susceptibility to bacterial infection.
- The *Plekha7* 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)

Plekha7 pleckstrin homology domain containing, family A member 7 [Mus musculus (house mouse)]

Gene ID: 233765, updated on 31-Jan-2019

Summary



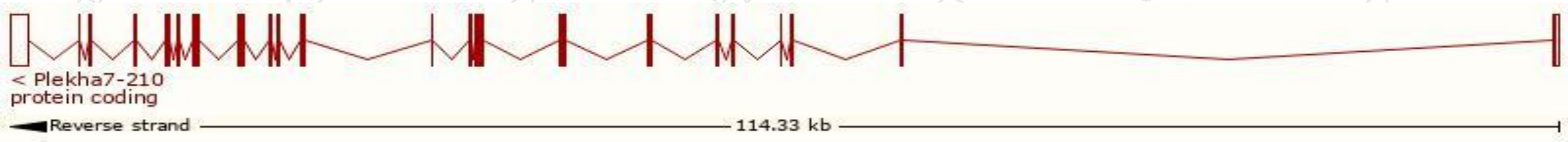
Official Symbol	Plekha7 provided by MGI
Official Full Name	pleckstrin homology domain containing, family A member 7 provided by MGI
Primary source	MGI:MGI:2445094
See related	Ensembl:ENSMUSG00000045659
Gene type	protein coding
RefSeq status	VALIDATED
Organism	Mus musculus
Lineage	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Myomorpha; Muroidea; Muridae; Murinae; Mus; Mus
Also known as	A430081P20Rik, AI414265
Expression	Ubiquitous expression in colon adult (RPKM 7.5), small intestine adult (RPKM 5.2) and 28 other tissues See more

Transcript information (Ensembl)

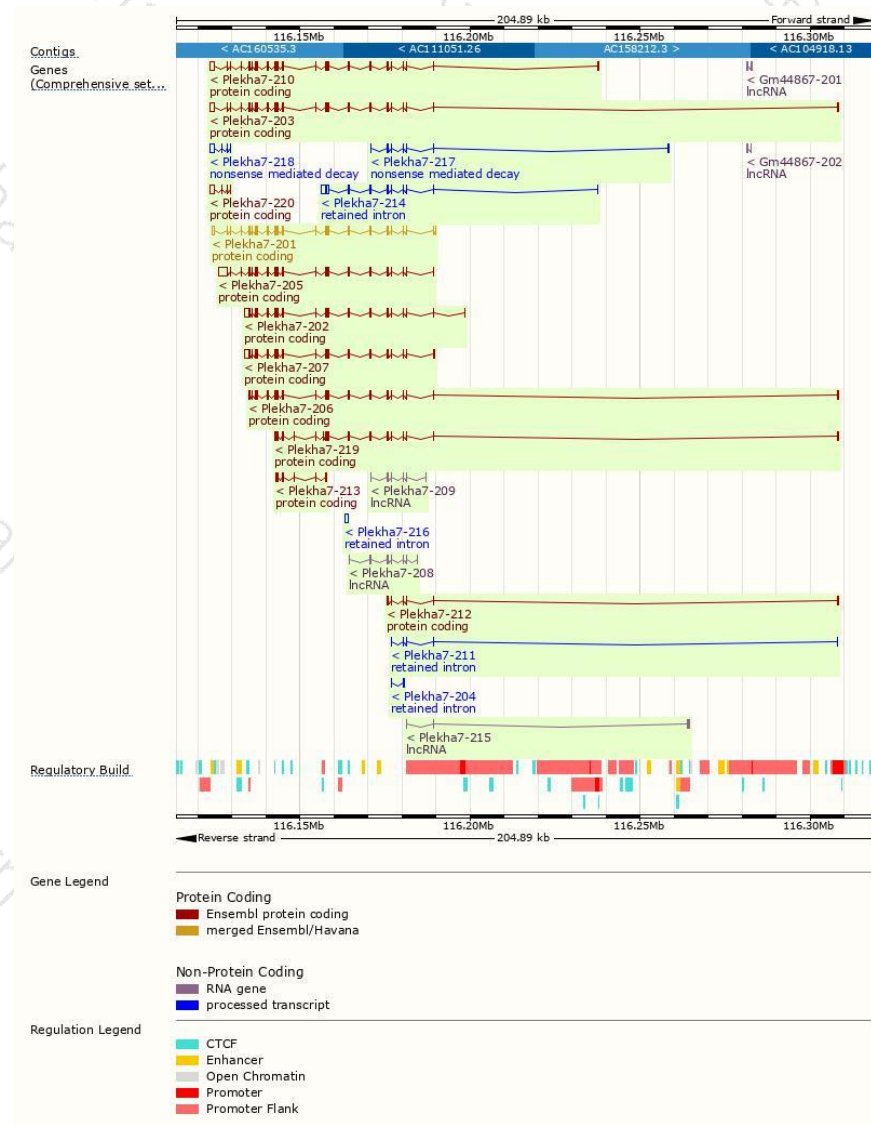
The gene has 20 transcripts,all transcripts are shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Plekha7-210	ENSMUST00000182834.7	5257	1220aa	Protein coding	CCDS85396	Q3UIL6	TSL:1 GENCODE basic
Plekha7-203	ENSMUST00000181998.7	5149	1266aa	Protein coding	CCDS85397	Q3UIL6	TSL:1 GENCODE basic APPRIS P2
Plekha7-202	ENSMUST00000181981.7	4633	1013aa	Protein coding	CCDS80791	Q3UIL6	TSL:1 GENCODE basic
Plekha7-207	ENSMUST00000182511.7	4502	1056aa	Protein coding	CCDS85395	Q3UIL6	TSL:2 GENCODE basic
Plekha7-201	ENSMUST00000084664.10	4312	1030aa	Protein coding	CCDS40099	Q3UIL6	TSL:1 GENCODE basic
Plekha7-205	ENSMUST00000182443.7	6059	1212aa	Protein coding	-	A0A0U1RPA0	CDS 5' incomplete TSL:1
Plekha7-206	ENSMUST00000182487.7	3476	1118aa	Protein coding	-	Q3UIL6	TSL:5 GENCODE basic APPRIS ALT2
Plekha7-219	ENSMUST00000216517.1	2601	867aa	Protein coding	-	A0A1L1SQ79	CDS 3' incomplete TSL:5
Plekha7-220	ENSMUST00000217046.1	1713	124aa	Protein coding	-	A0A1L1SU82	CDS 5' incomplete TSL:5
Plekha7-212	ENSMUST00000183057.1	685	176aa	Protein coding	-	S4R243	CDS 3' incomplete TSL:3
Plekha7-213	ENSMUST00000183281.1	623	207aa	Protein coding	-	S4R190	5' and 3' truncations in transcript evidence prevent annotation of the start and the end of the CDS. CDS 5' and 3' incomplete TSL:3
Plekha7-218	ENSMUST00000214700.1	1708	98aa	Nonsense mediated decay	-	A0A1L1SV63	CDS 5' incomplete TSL:5
Plekha7-217	ENSMUST00000206662.1	768	64aa	Nonsense mediated decay	-	A0A0U1RP25	CDS 5' incomplete TSL:5
Plekha7-214	ENSMUST00000183308.7	3354	No protein	Retained intron	-	-	TSL:2
Plekha7-216	ENSMUST00000206097.1	936	No protein	Retained intron	-	-	TSL:NA
Plekha7-211	ENSMUST00000182890.2	482	No protein	Retained intron	-	-	TSL:3
Plekha7-204	ENSMUST00000182312.1	292	No protein	Retained intron	-	-	TSL:5
Plekha7-208	ENSMUST00000182549.7	630	No protein	lncRNA	-	-	TSL:5
Plekha7-209	ENSMUST00000182693.7	462	No protein	lncRNA	-	-	TSL:5
Plekha7-215	ENSMUST00000205446.1	363	No protein	lncRNA	-	-	TSL:5

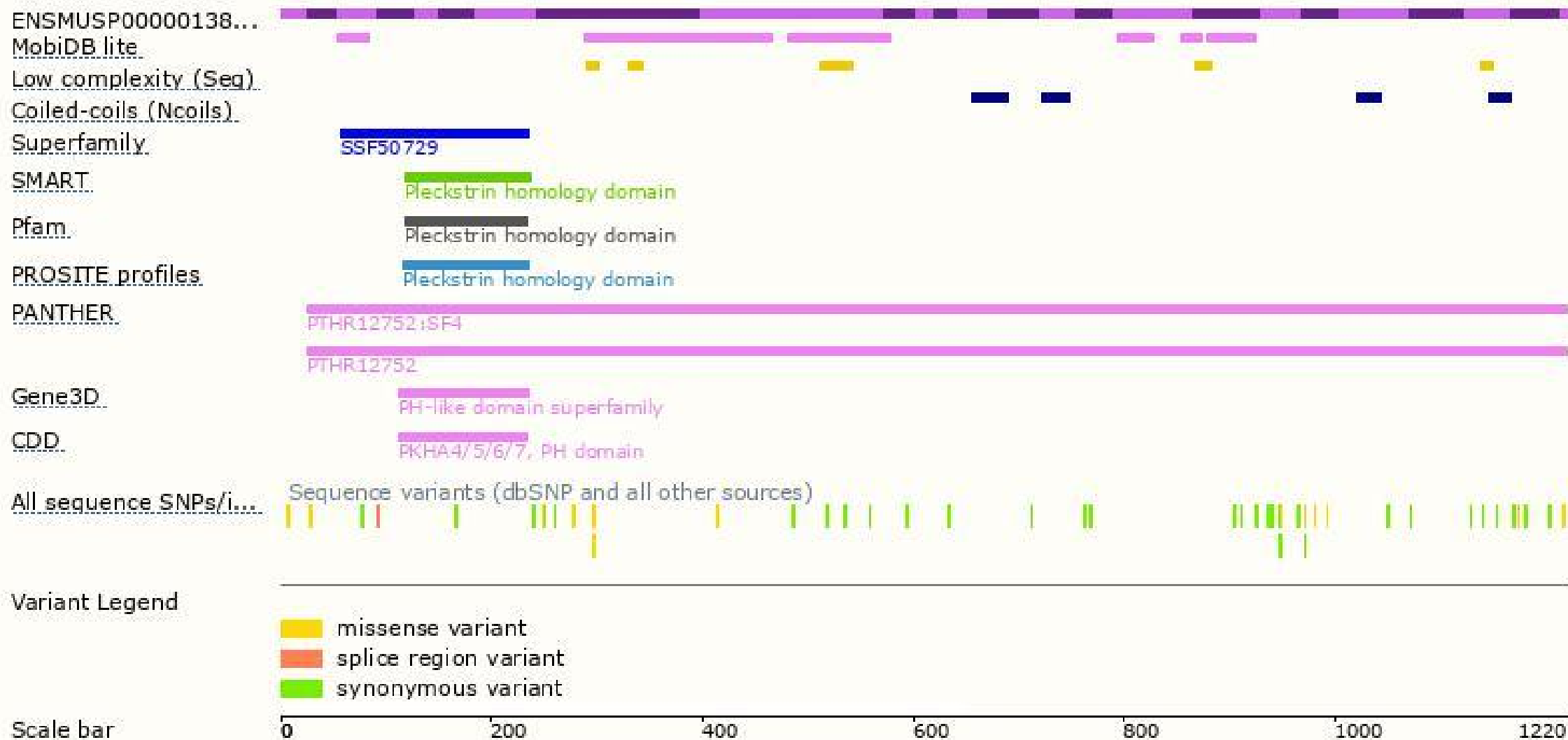
The strategy is based on the design of *Plekha7-210* transcript,The transcription is shown below



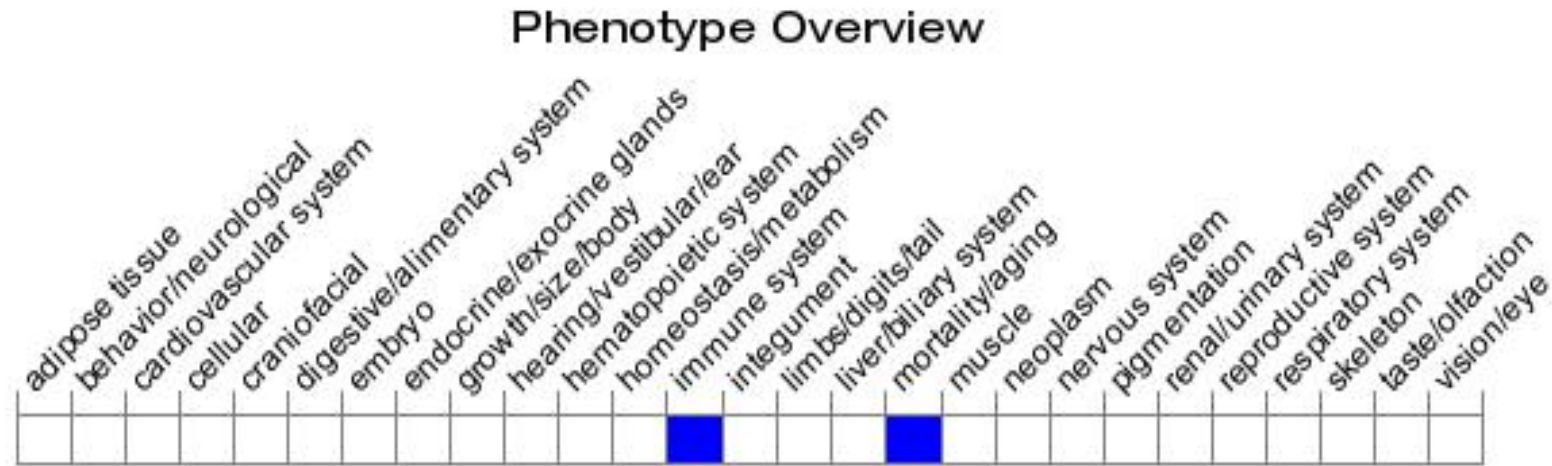
Genomic location distribution



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, Mice homozygous for a null allele show decreased susceptibility to bacterial infection.

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

Tel: 400-9660890

