Bpifa1 Cas9-KO Strategy

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Project Overview

Project Name	***Bpifa1***
Project type	**Cas9-KO**
Strain background	**C57BL/6JGpt**

Knockout strategy

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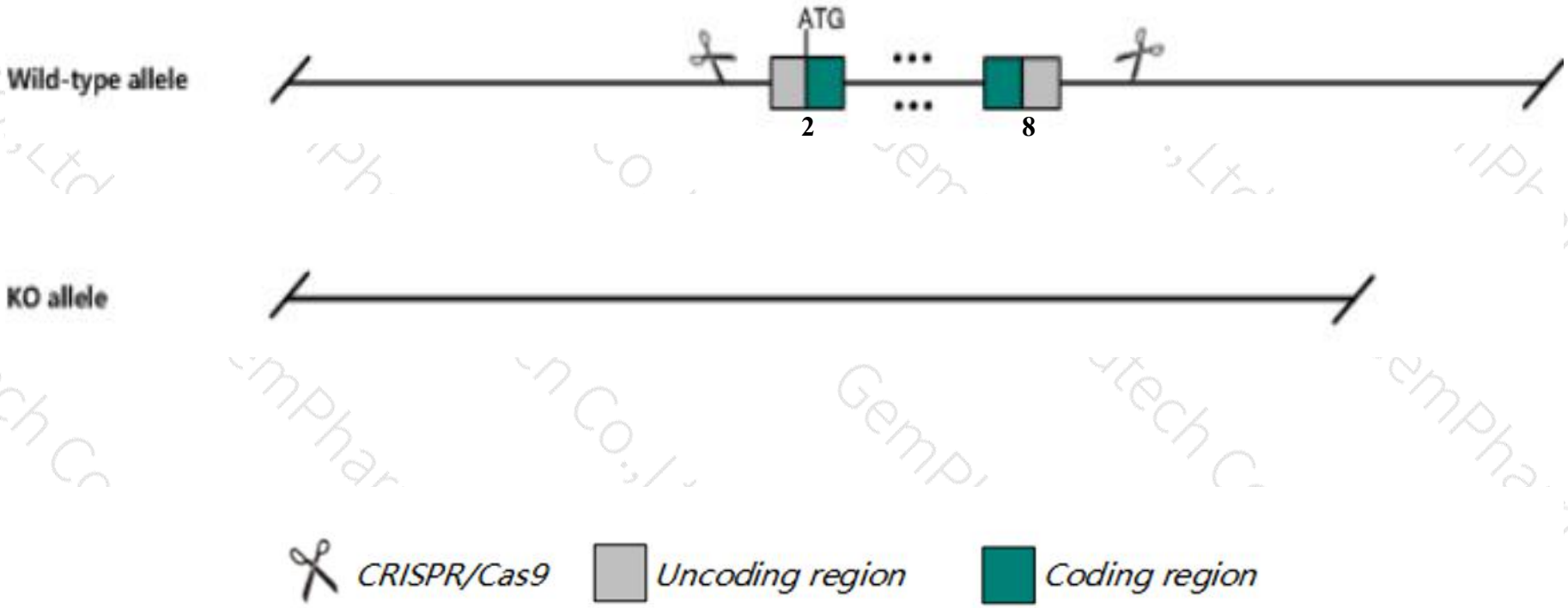
This model will use CRISPR/Cas9 technology to edit the *Bpifa1* gene. The schematic diagram is as follows:



Technical routes

➢ The *Bpifa1* gene has 3 transcripts. According to the structure of *Bpifa1* gene, exon2-exon8 of *Bpifa1-201*(ENSMUST00000028985.7) transcript is recommended as the knockout region.The region contains all of the coding sequence.Knock out the region will result in disruption of protein function.

➢ In this project we use CRISPR/Cas9 technology to modify *Bpifa1* 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.

Notice

➢ According to the existing MGI data,mice homozygous for a knock-out or ENU-induced allele exhibit increased susceptiblity to Mycoplasma pneumoniae infection. Club cell-specific conditional or constitutive homozygous KO also increases susceptibility to Influenza A virus infection.

➢ The *Bpifa1* 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）

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Bpifa1 BPI fold containing family A, member 1 [Mus musculus (house mouse)]

Gene ID: 18843, updated on 13-Mar-2020

Summary

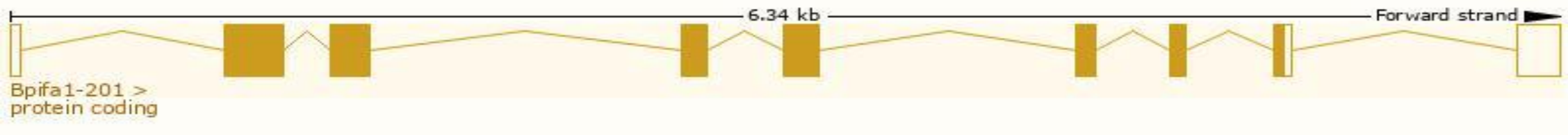
Official Symbol	Bpifa1 provided by MGI
Official Full Name	BPI fold containing family A, member 1 provided by MGI
Primary source	MGI:MGI:1338036
See related	Ensembl:ENSMUSG00000027483
Gene type	protein coding
RefSeq status	VALIDATED
Organism	Mus musculus
Lineage	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Myomorpha; Muroidea; Muridae; Murinae; Mus; Mus
Also known as	LUNX, NASG, Plunc, SPLUNC1, SPURT
Expression	Biased expression in lung adult (RPKM 182.2) and heart adult (RPKM 116.8)See more
Orthologs	human all

Transcript information（Ensembl）

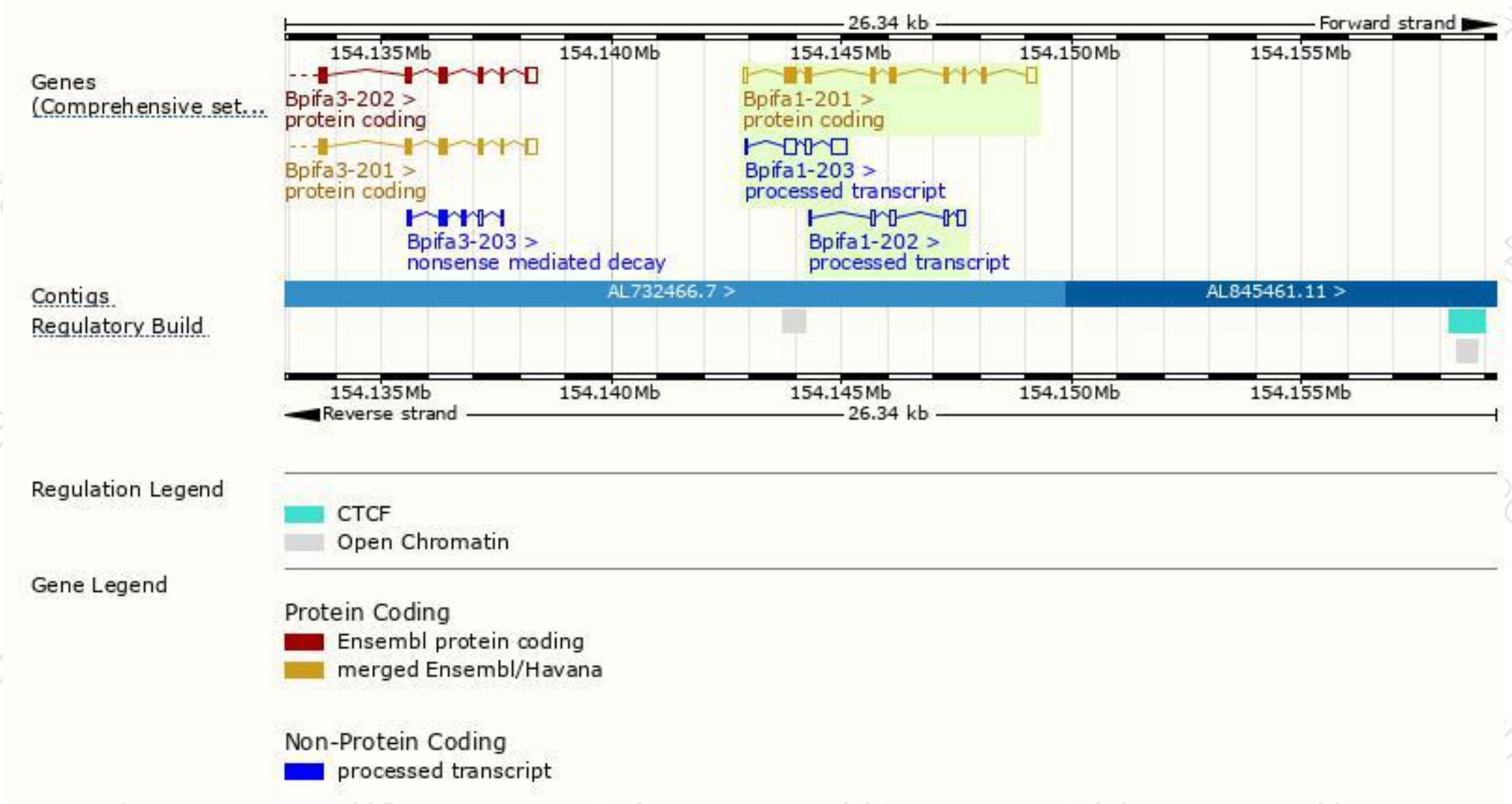
The gene has 3 transcripts,all transcripts are shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Bpifa1-201	ENSMUST00000028985.7	1106	278aa	Protein coding	CCDS16925	P97361	TSL:1 GENCODE basic APPRIS is a system to annotate alternatively spliced transcripts based on a range of computational methods to identify the most functionally important transcript(s) of a gene. APPRIS P1
Bpifa1-203	ENSMUST00000144665.1	765	No protein	Processed transcript	-	-	TSL:5
Bpifa1-202	ENSMUST00000140006.1	559	No protein	Processed transcript	-	-	TSL:3

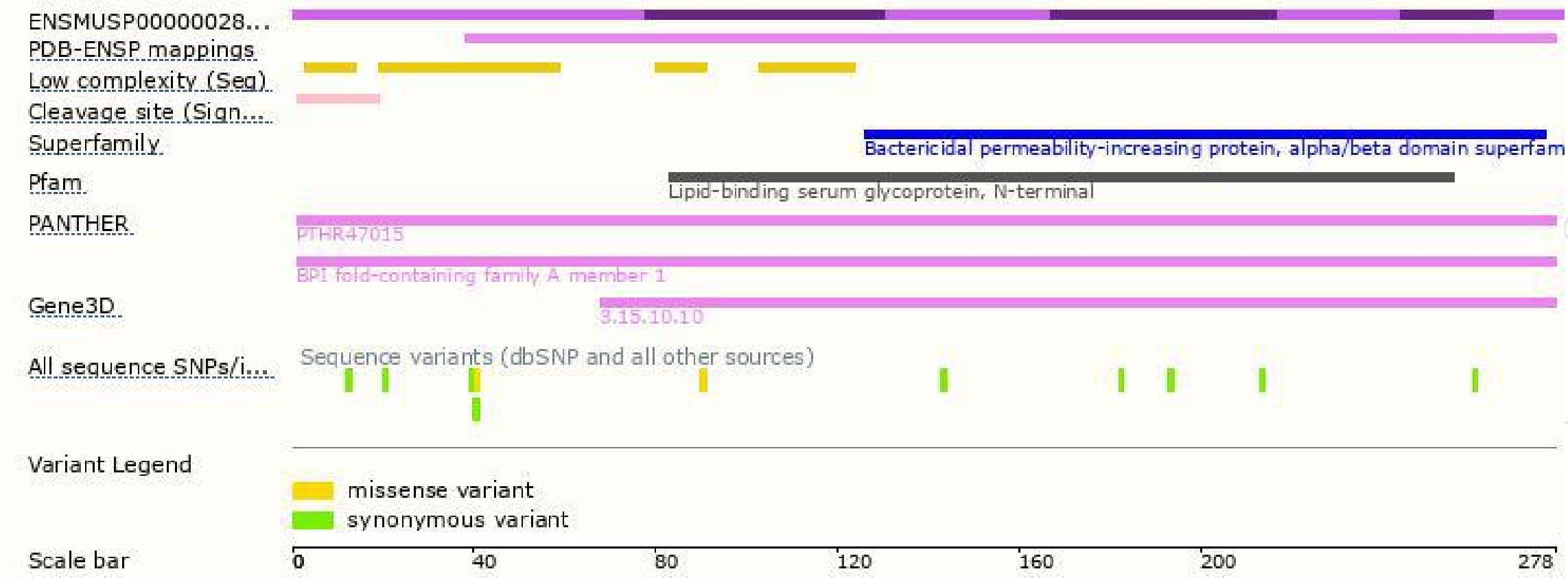
The strategy is based on the design of *Bpifa1-201* transcript,the transcription is shown below:



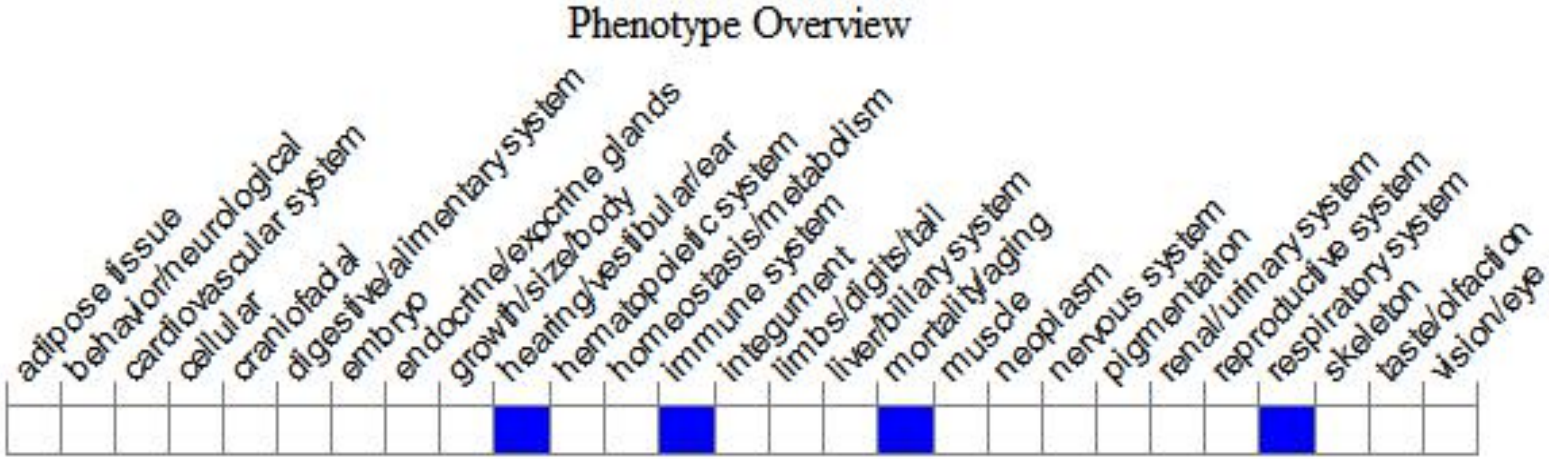
Genomic location distribution



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,mice homozygous for a knock-out or ENU-induced allele exhibit increased susceptiblity to Mycoplasma pneumoniae infection. Club cell-specific conditional or constitutive homozygous KO also increases susceptibility to Influenza A virus infection.

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

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