Lbp Cas9-CKO Strategy

Designer: Huan Fan

Reviewer: Huan Wang

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Project Overview

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

Conditional Knockout strategy

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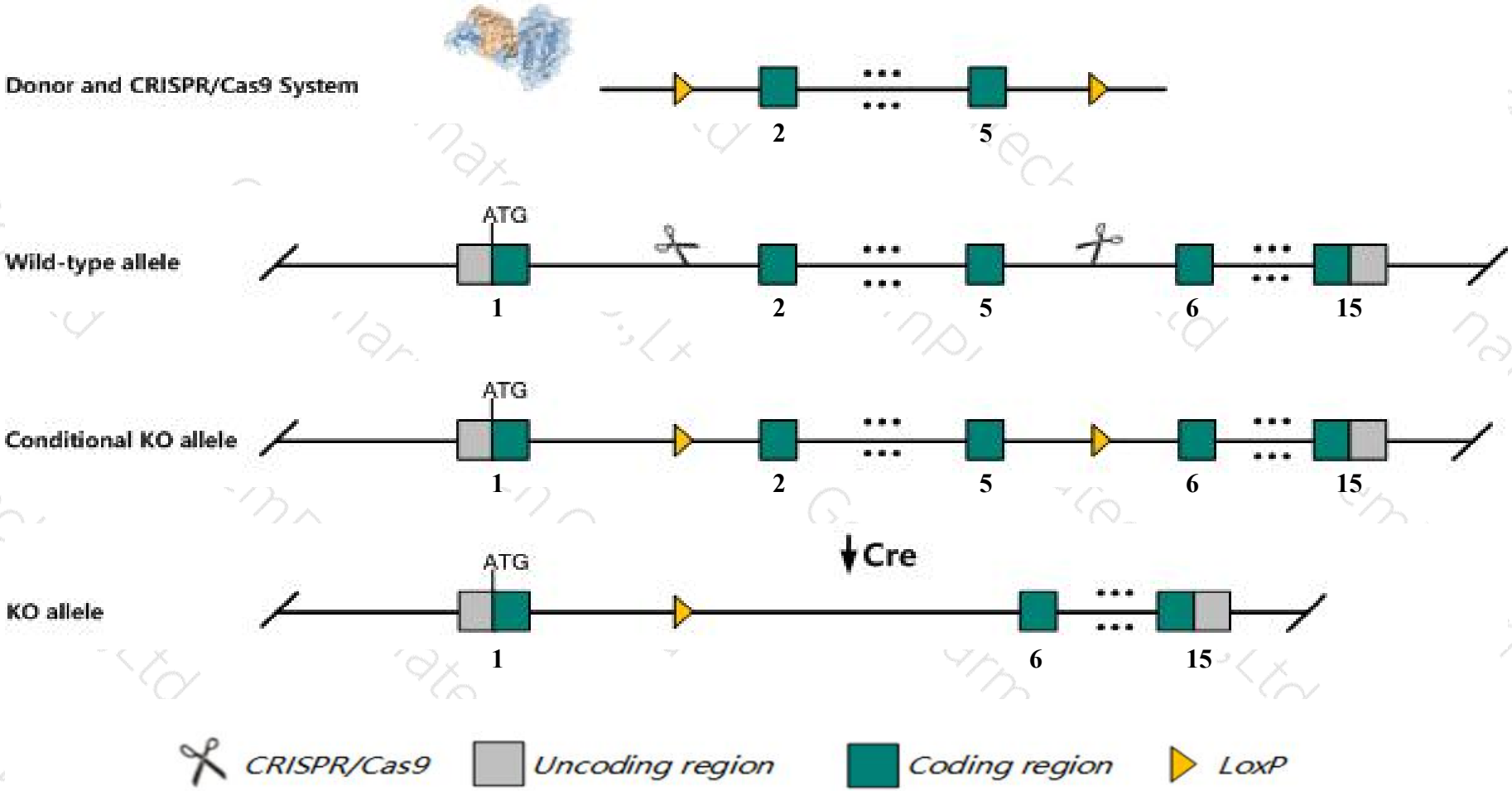
This model will use CRISPR/Cas9 technology to edit the *Lbp* gene. The schematic diagram is as follows:



Technical routes

- The *Lbp* gene has 5 transcripts. According to the structure of *Lbp* gene, exon2-exon5 of *Lbp-201* (ENSMUST00000016168.8) transcript is recommended as the knockout region.The region contains 464bp coding sequence. Knock out the region will result in disruption of protein function.

- In this project we use CRISPR/Cas9 technology to modify *Lbp* 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 mice have a generally normal phenotype but have an increased sensitivity to infection by gram negative bacteria.

- The *Lbp* 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 loxp insertion on gene transcription, RNA splicing and protein translation cannot be predicted at existing technological level.

Gene information （NCBI）

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Lbp lipopolysaccharide binding protein [Mus musculus (house mouse)]

Gene ID: 16803, updated on 31-Jan-2019

Summary

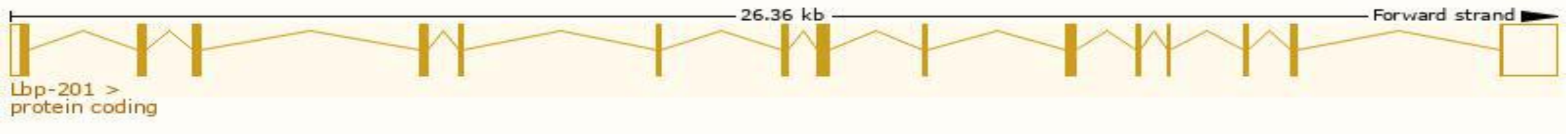
Official Symbol	Lbp provided by MGI
Official Full Name	lipopolysaccharide binding protein provided by MGI
Primary source	MGI:MGI:1098776
See related	Ensembl:ENSMUSG00000016024
Gene type	protein coding
RefSeq status	VALIDATED
Organism	Mus musculus
Lineage	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Myomorpha; Muroidea; Muridae; Murinae; Mus; Mus
Also known as	Bpifd2, Ly88
Expression	Biased expression in subcutaneous fat pad adult (RPKM 102.2), genital fat pad adult (RPKM 70.3) and 10 other tissues See more
Orthologs	human all

Transcript information（Ensembl）

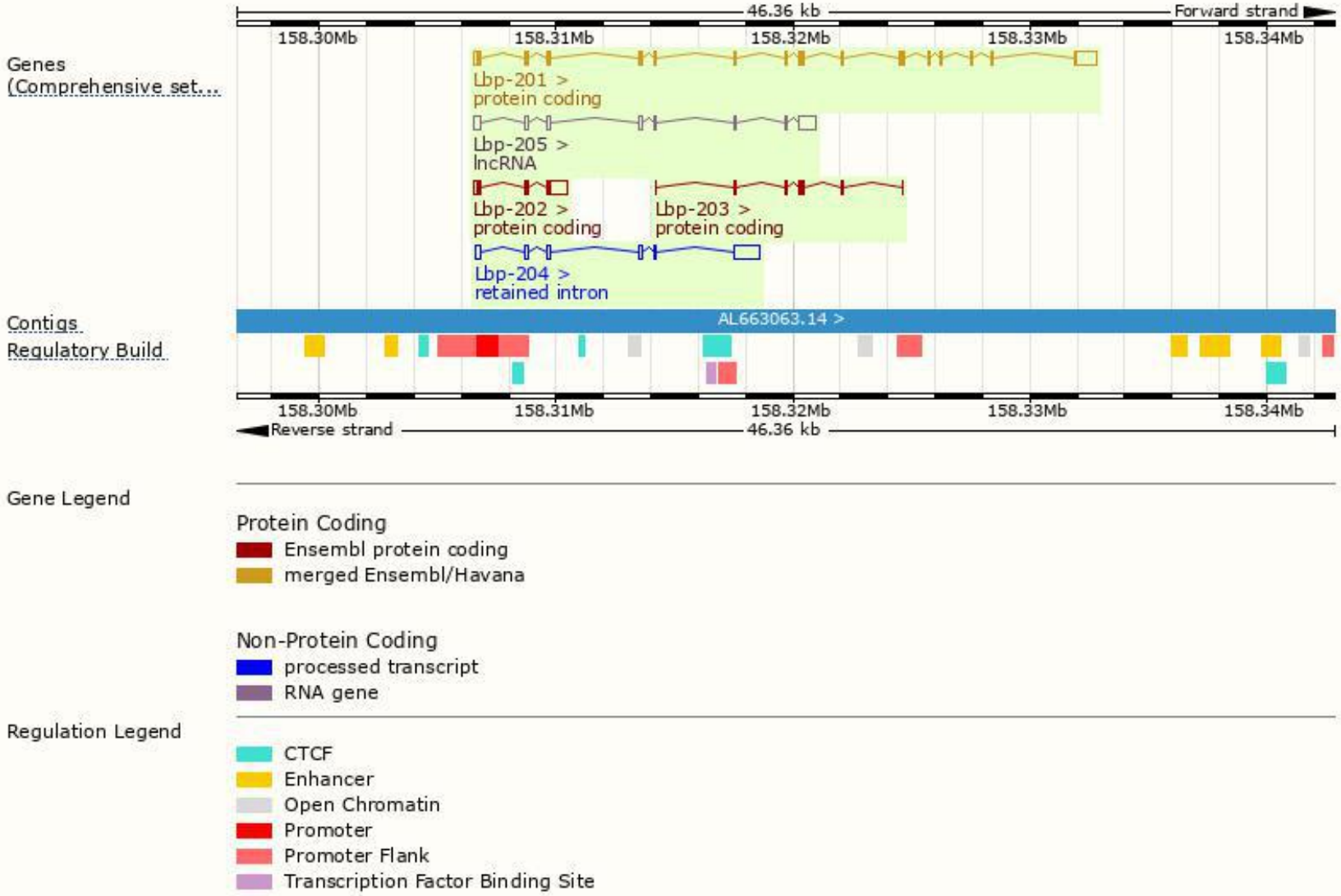
The gene has 5 transcripts,all transcripts are shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Lbp-201	ENSMUST00000016168.8	2525	481aa	Protein coding	CCDS16988	Q61805	TSL:1 GENCODE basic APPRIS P1
Lbp-202	ENSMUST00000109491.7	1322	123aa	Protein coding	-	A2AC65	TSL:2 GENCODE basic
Lbp-203	ENSMUST00000129811.1	436	145aa	Protein coding	-	F6XKX9	5' and 3' truncations in transcript evidence prevent annotation of the start and the end of the CDS. CDS 5' and 3' incomplete TSL:5
Lbp-204	ENSMUST00000146600.1	1723	No protein	Retained intron	-	-	TSL:1
Lbp-205	ENSMUST00000152541.7	1614	No protein	lncRNA	-	-	TSL:1

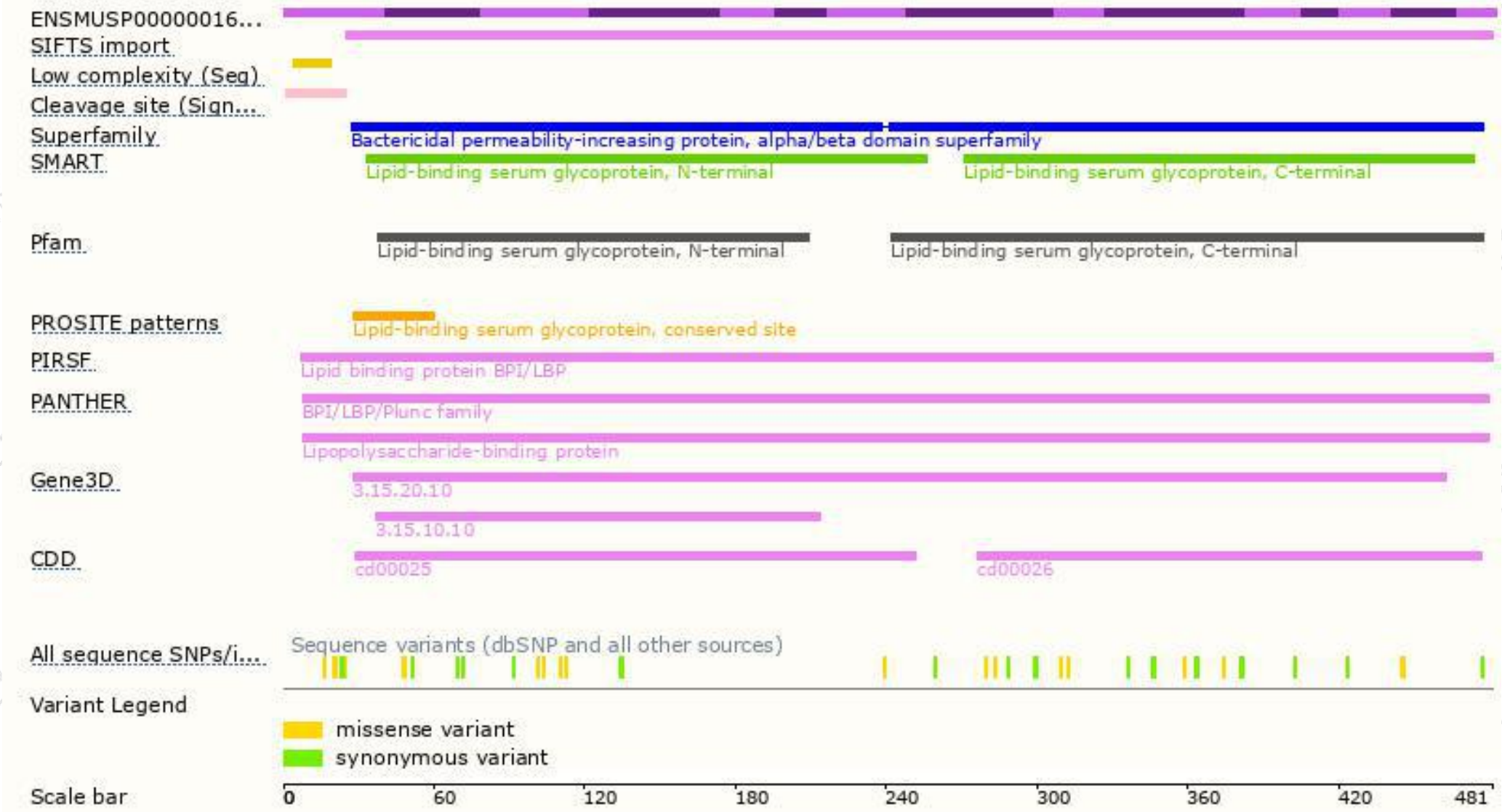
The strategy is based on the design of *Lbp-201* transcript,The transcription is shown below



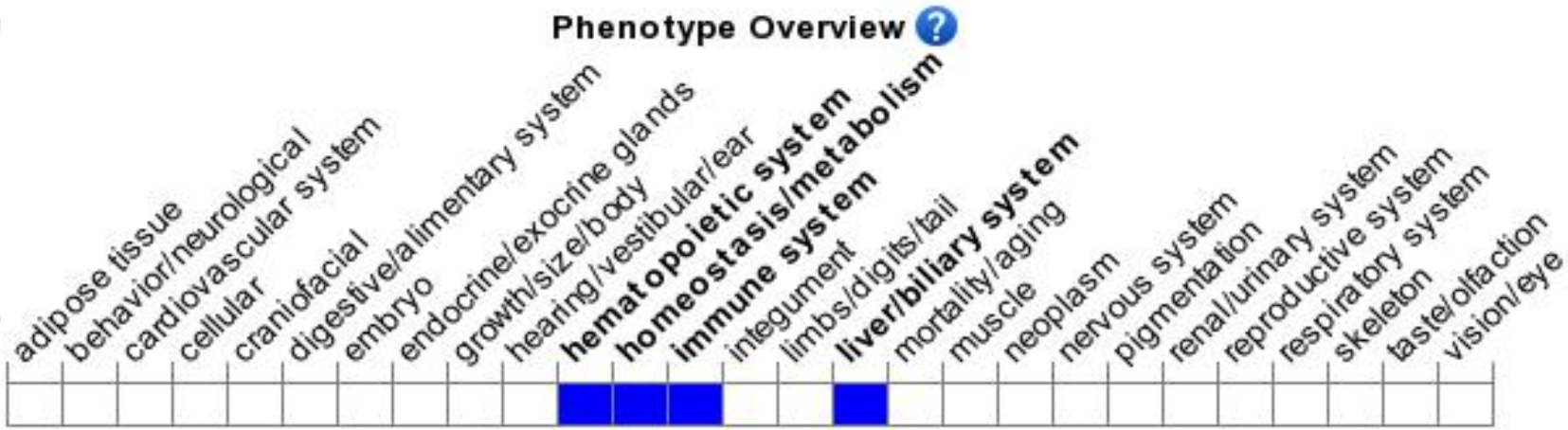
Genomic location distribution



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,Homozygous mice have a generally normal phenotype but have an increased sensitivity to infection by gram negative bacteria.

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

Tel: 400-9660890

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GemPharmatech Co.,Ltd