Baz1b Cas9-CKO Strategy

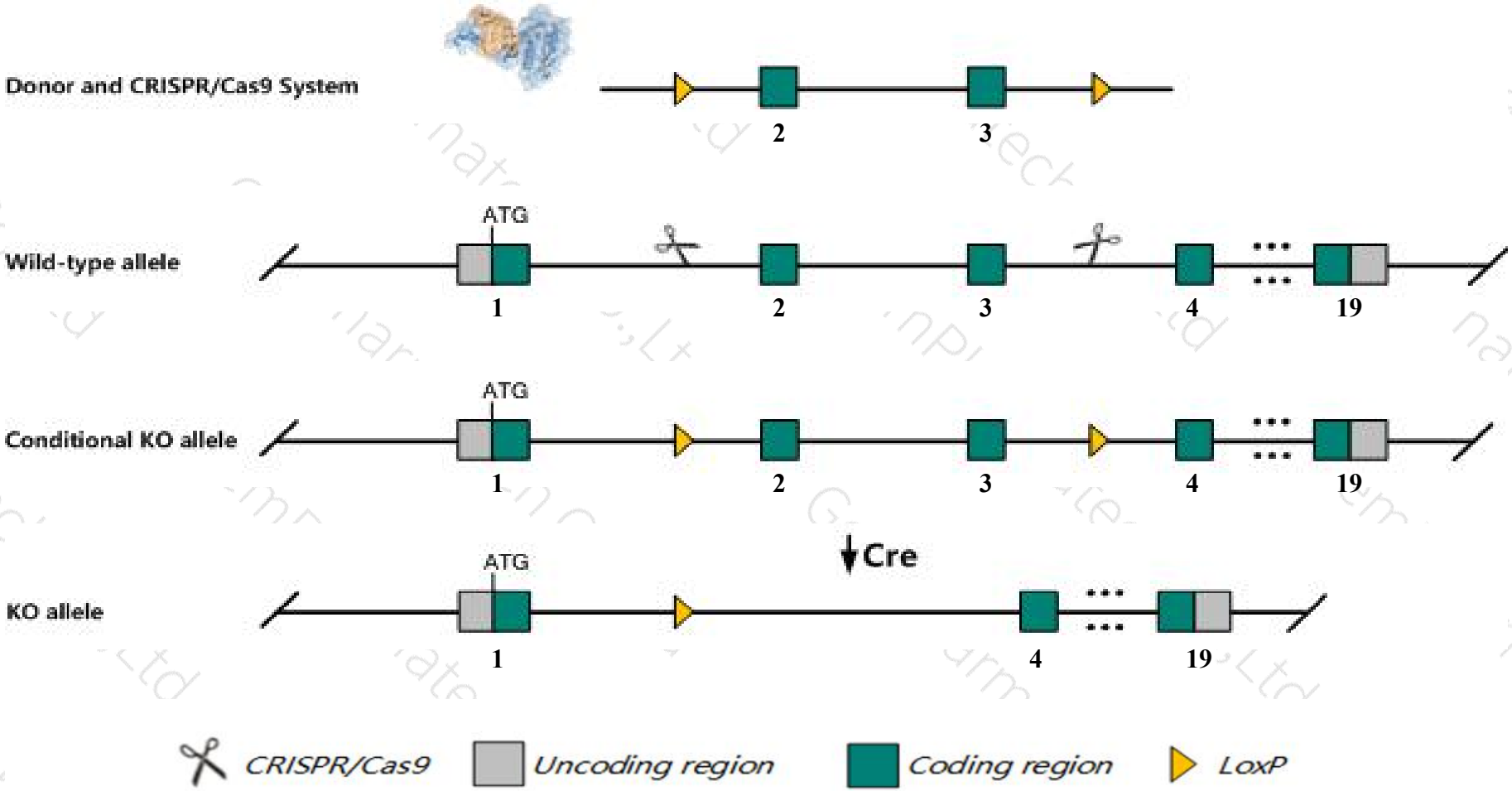
Designer: Ruirui Zhang
Reviewer: Huimin Su
Design Date: 2019-12-13

Project Overview

Project Name	***Baz1b***
Project type	**Cas9-CKO**
Strain background	**C57BL/6JGpt**

Conditional Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *Baz1b* gene. The schematic diagram is as follows:



Technical routes

- The *Baz1b* gene has 5 transcripts. According to the structure of *Baz1b* gene, exon2-exon3 of *Baz1b-201* (ENSMUST00000002825.5) transcript is recommended as the knockout region.The region contains 262bp coding sequence. Knock out the region will result in disruption of protein function.

- In this project we use CRISPR/Cas9 technology to modify *Baz1b* 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, mice homozygous for a null allele exhibit postnatal lethality by P2, small size at birth, impaired double strand DNA repair, and heart defects. Mice heterozygous for a null allele exhibit hypercalcemia and heart defects. Mice homozygous for an ENU mutation exhibit craniofacial and skeletal defects.

➢ The *Baz1b* gene is located on the Chr5. 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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Baz1b bromodomain adjacent to zinc finger domain, 1B [*Mus musculus* (house mouse)]

Gene ID: 22385, updated on 12-Aug-2019

Summary

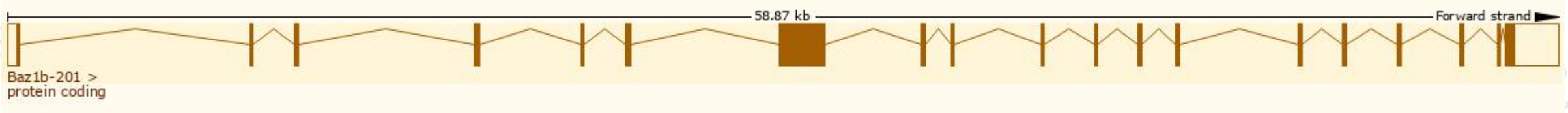
Official Symbol	Baz1b provided by MGI
Official Full Name	bromodomain adjacent to zinc finger domain, 1B provided by MGI
Primary source	MGI:MGI:1353499
See related	Ensembl:ENSMUSG00000002748
Gene type	protein coding
RefSeq status	VALIDATED
Organism	Mus musculus
Lineage	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Myomorpha; Muroidea; Muridae; Murinae; Mus; Mus
Also known as	WSTF; C87820; Wbscr9
Expression	Ubiquitous expression in CNS E11.5 (RPKM 36.9), limb E14.5 (RPKM 19.4) and 28 other tissues See more
Orthologs	human all

Transcript information（Ensembl）

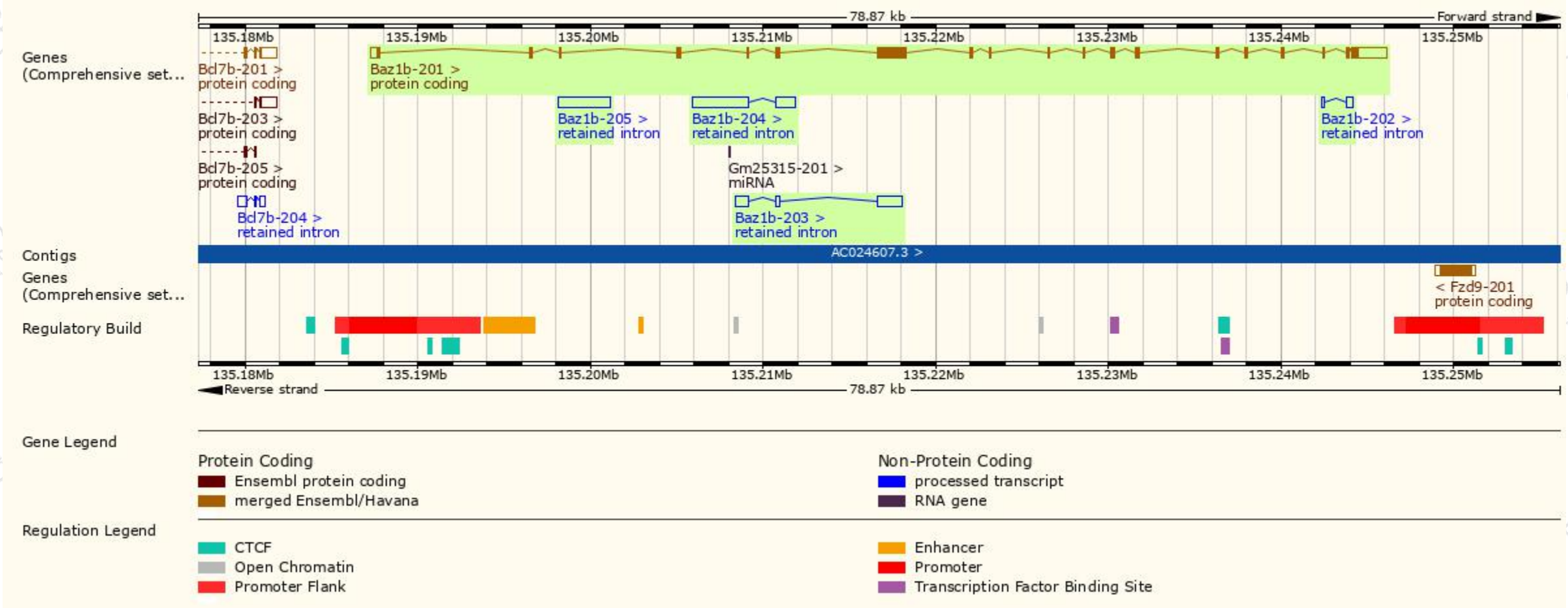
The gene has 5 transcripts,all transcripts are shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Baz1b-201	ENSMUST00000002825.5	6492	1479aa	Protein coding	CCDS19736	Q9Z277	TSL:1 GENCODE basic APPRIS P1
Baz1b-202	ENSMUST00000136947.1	528	No protein	Retained intron	-	-	TSL:3
Baz1b-203	ENSMUST00000142307.1	2423	No protein	Retained intron	-	-	TSL:2
Baz1b-204	ENSMUST00000176793.1	4406	No protein	Retained intron	-	-	TSL:5
Baz1b-205	ENSMUST00000201894.1	3018	No protein	Retained intron	-	-	TSL:NA

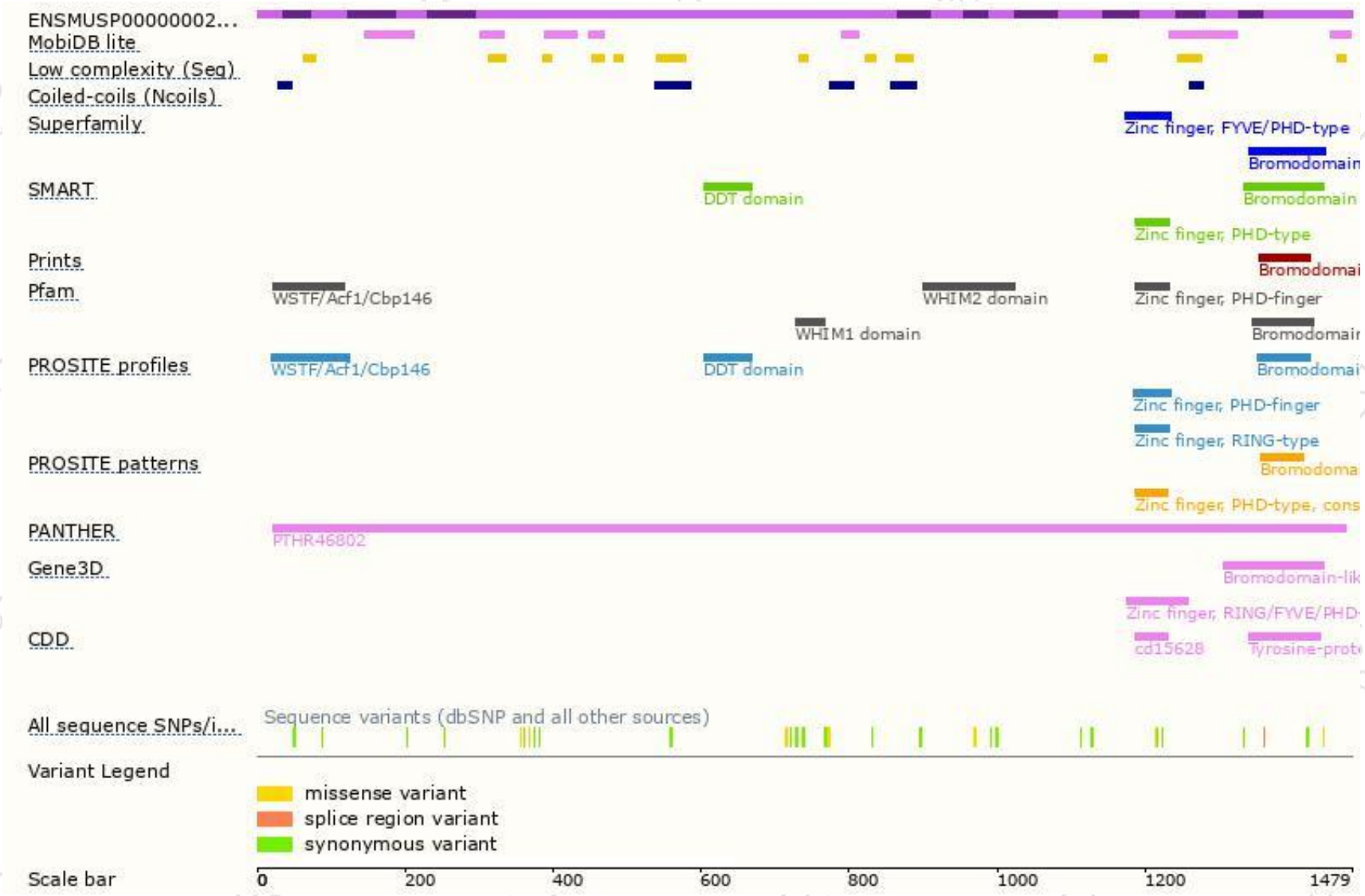
The strategy is based on the design of *Baz1b-201* transcript, the transcription is shown below:



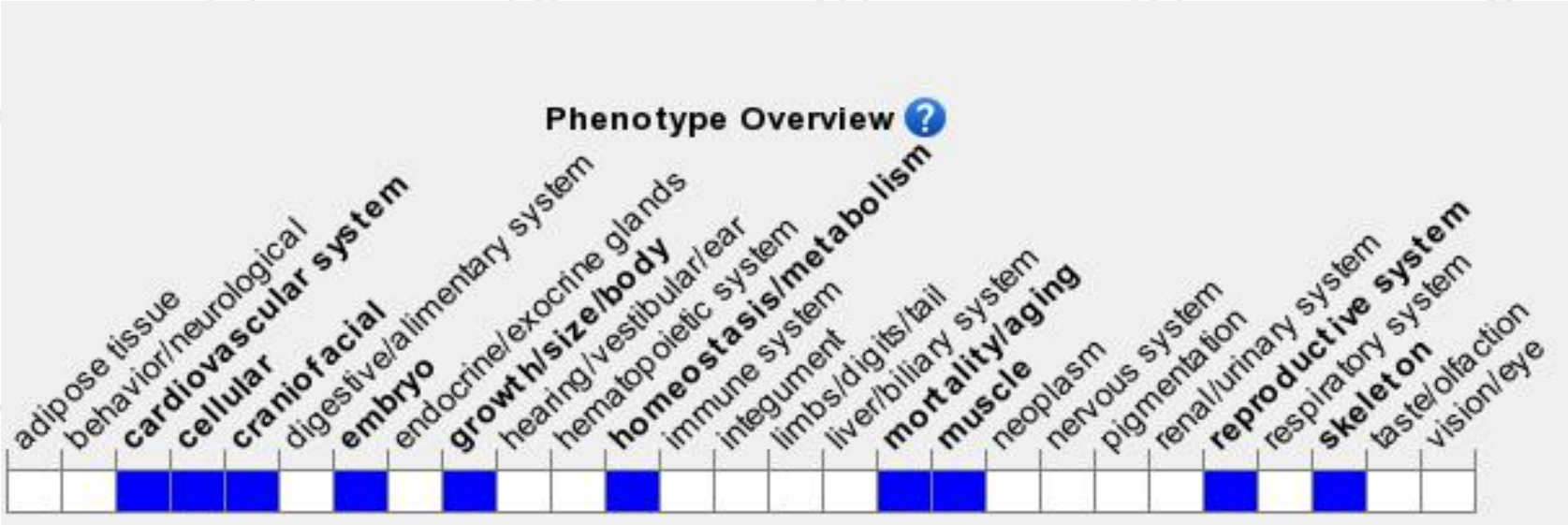
Genomic location distribution



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/).

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GemPharmatech

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

Tel: 400-9660890

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GemPharmatech Co.,Ltd