Bgn Cas9-CKO Strategy

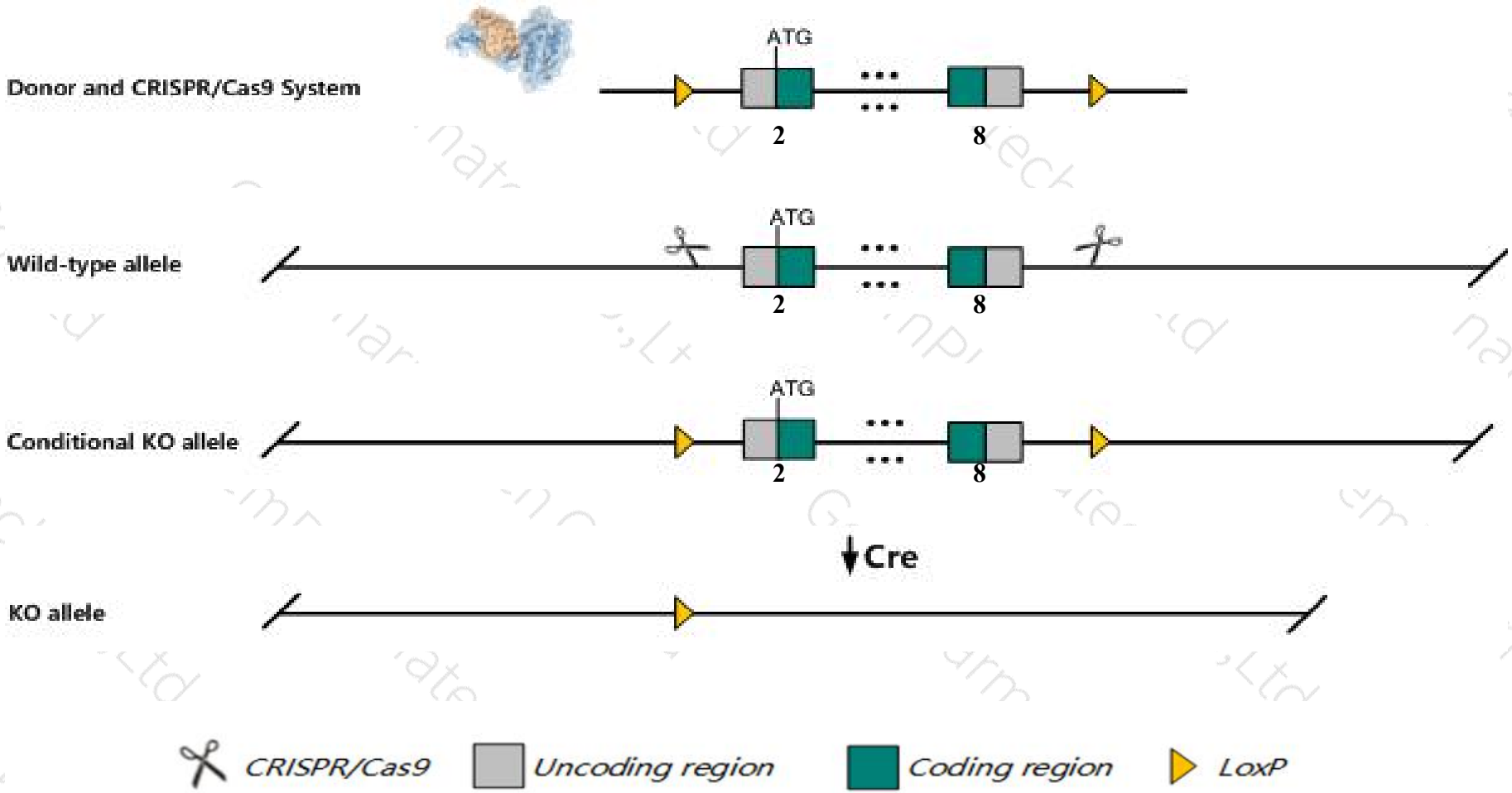
Designer: Lixin Lv

Project Overview

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

Conditional Knockout strategy

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



Technical routes

- The *Bgn* gene has 8 transcripts. According to the structure of *Bgn* gene, exon2-exon8 of *Bgn-201* (ENSMUST00000033741.14) 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 *Bgn* 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 null mutants display reduced growth and develop age-dependent osteopenia. Age-related osteoporosis is associated with defects in bone marrow stromal cells, including increased apoptosis, reduced numbers of colony-forming units-fibroblastic (CFU-F), and decreased collagen production.

- The *Bgn* gene is located on the ChrX. 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）

集萃药康 GemPharmatech

Bgn biglycan [Mus musculus (house mouse)]

Gene ID: 12111, updated on 3-Feb-2019

Summary

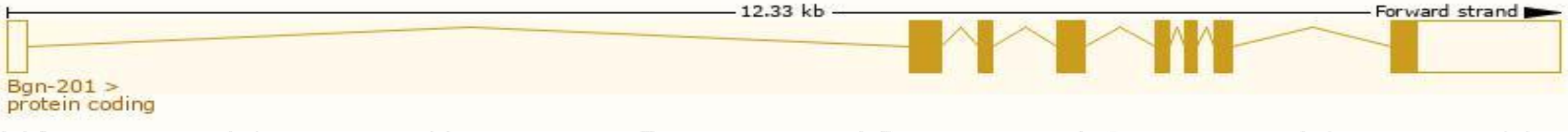
Official Symbol	Bgn provided by MGI
Official Full Name	biglycan provided byMGI
Primary source	MGI:MGI:88158
See related	Ensembl:ENSMUSG00000031375
Gene type	protein coding
RefSeq status	REVIEWED
Organism	Mus musculus
Lineage	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Myomorpha; Muroidea; Muridae; Murinae; Mus; Mus
Also known as	BG, DSPG1, PG-S1, PGI, SLRR1A
Summary	This gene encodes a small, leucine-rich repeat proteoglycan that plays important roles in bone mineralization and connective tissue metabolism. The encoded preproprotein undergoes post-translational processing during which chondroitin sulfate or dermatan sulfate chains are attached before incorporation into the extracellular matrix. Mice lacking the encoded protein exhibit reduced growth rate and acquire diminished bone mass progressively with age. [provided by RefSeq, Oct 2015]
Expression	Broad expression in bladder adult (RPKM 238.1), lung adult (RPKM 231.1) and 22 other tissuesSee more
Orthologs	human all

Transcript information（Ensembl）

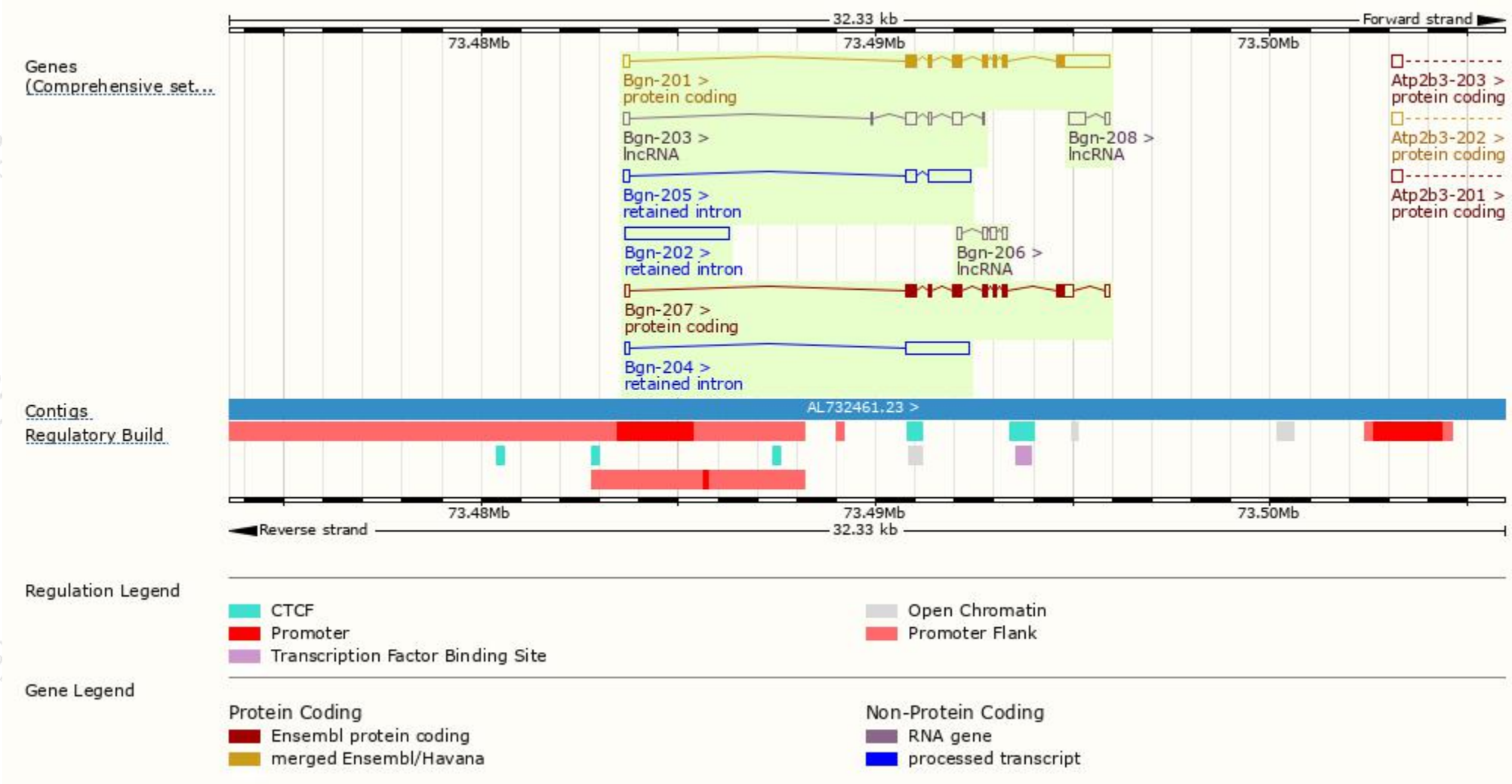
The gene has 8 transcripts,all transcripts are shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Bgn-201	ENSMUST00000033741.14	2419	369aa	Protein coding	CCDS30204	P28653 Q3TNY9	TSL:1 GENCODE basic APPRIS P1
Bgn-207	ENSMUST00000169489.1	1574	369aa	Protein coding	CCDS30204	P28653 Q3TNY9	TSL:2 GENCODE basic APPRIS P1
Bgn-203	ENSMUST00000133394.7	828	No protein	Processed transcript	-	-	TSL:3
Bgn-208	ENSMUST00000183174.1	548	No protein	Processed transcript	-	-	TSL:3
Bgn-206	ENSMUST00000155231.1	460	No protein	Processed transcript	-	-	TSL:3
Bgn-202	ENSMUST00000130873.2	2666	No protein	Retained intron	-	-	TSL:NA
Bgn-204	ENSMUST00000140803.1	1728	No protein	Retained intron	-	-	TSL:2
Bgn-205	ENSMUST00000141945.1	1473	No protein	Retained intron	-	-	TSL:2

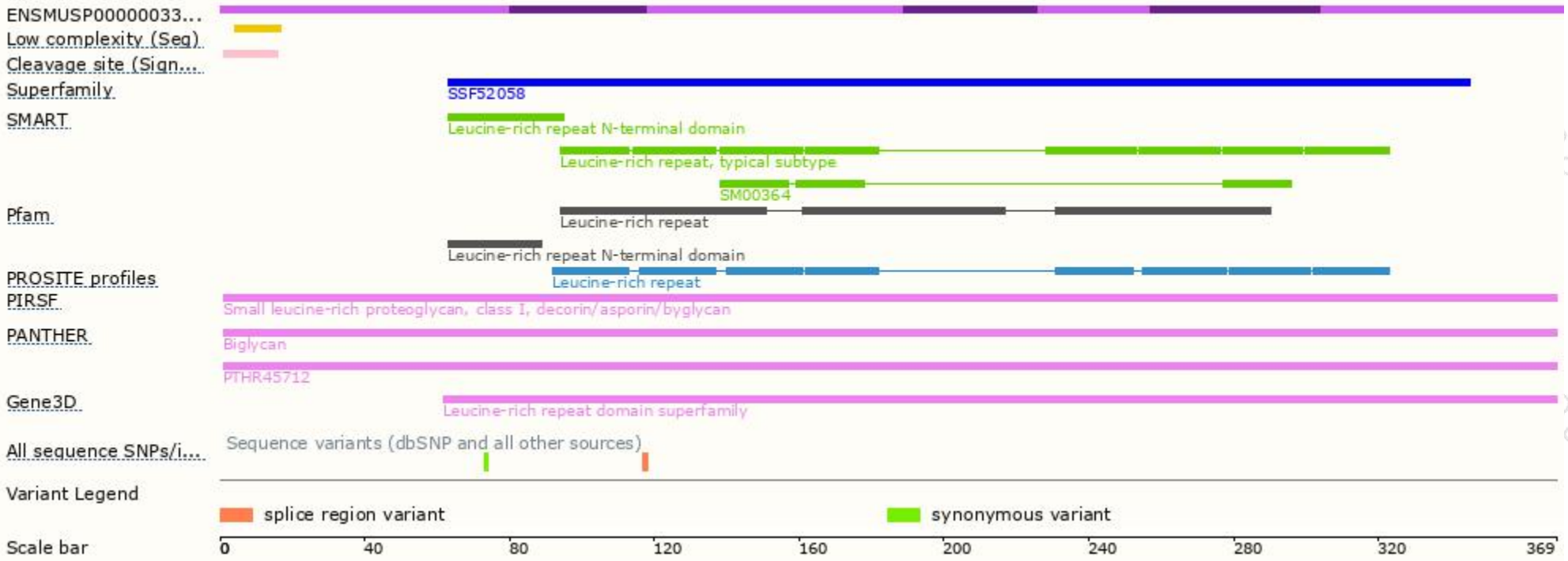
The strategy is based on the design of *Bgn-201* transcript,The transcription is shown below



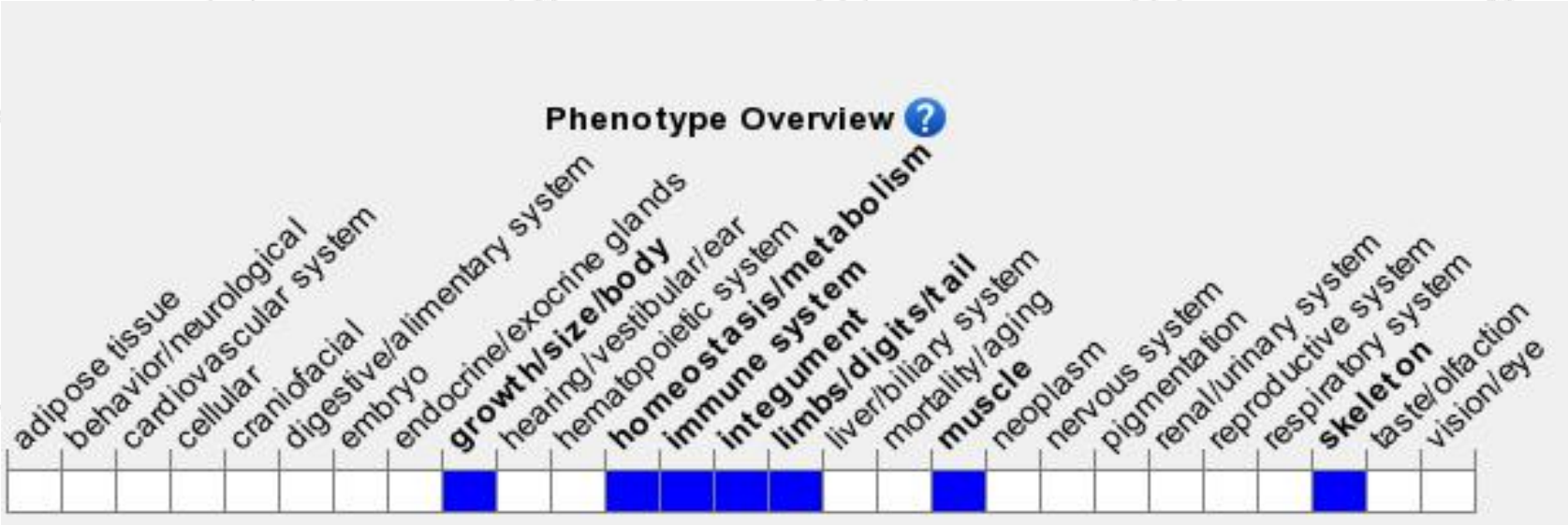
Genomic location distribution



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 null mutants display reduced growth and develop age-dependent osteopenia Age-related osteoporosis is associated with defects in bone marrow stromal cells, including increased apoptosis, reduced numbers of colony-forming units-fibroblastic (CFU-F), and decreased collagen production.

集萃药康
GemPharmatech

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

Tel: 400-9660890

集萃药康生物科技
GemPharmatech Co.,Ltd