Kif2c Cas9-CKO Strategy

集萃药康 GemPharmatech

Project Overview

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Project Name	***Kif2c***
Project type	**Cas9-CKO**
Strain background	**C57BL/6JGpt**

Conditional Knockout strategy

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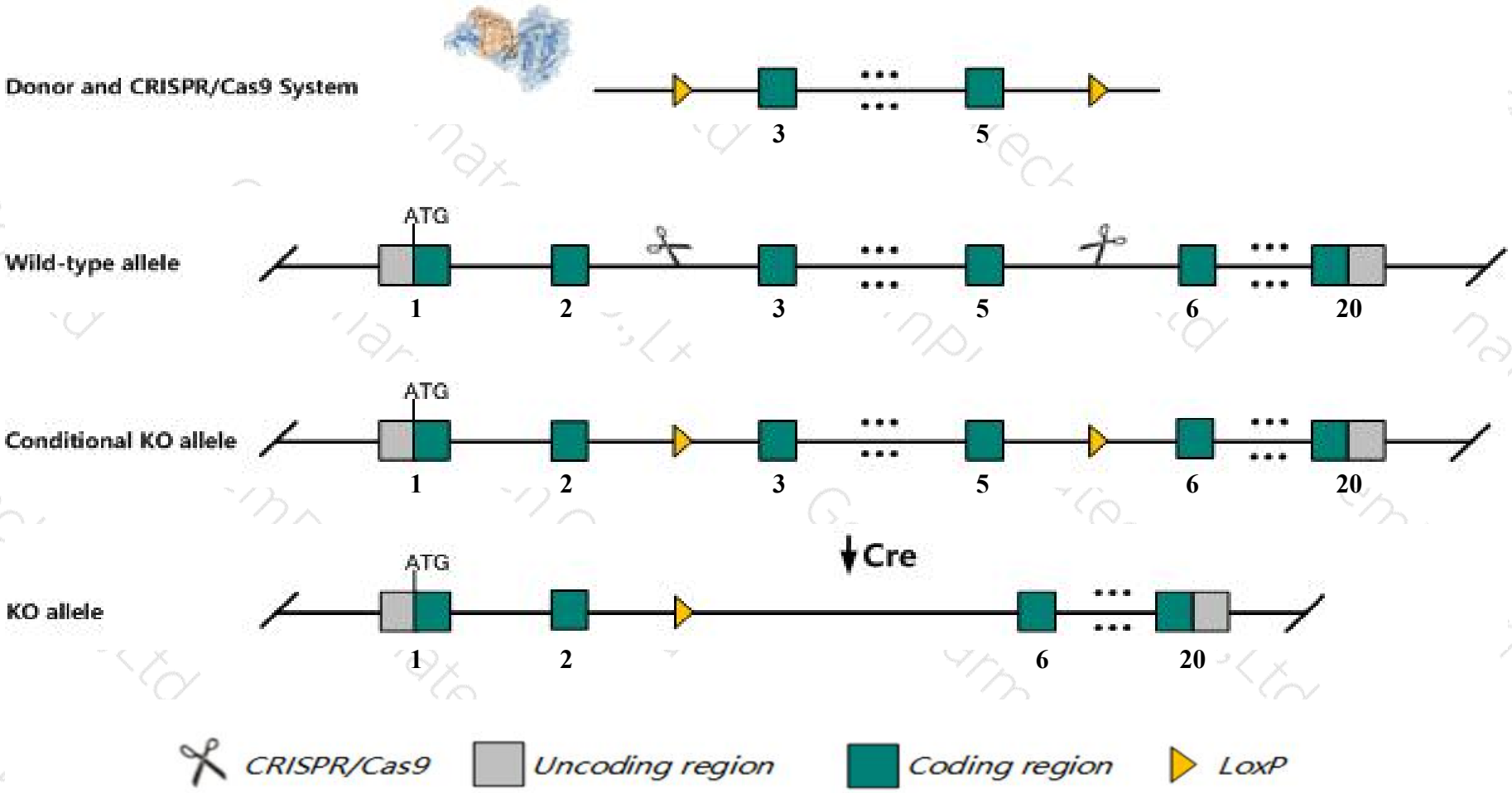
This model will use CRISPR/Cas9 technology to edit the *Kif2c* gene. The schematic diagram is as follows:



Technical routes

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- The *Kif2c* gene has 8 transcripts. According to the structure of *Kif2c* gene, exon3-exon5 of *Kif2c-201* (ENSMUST00000065896.8) transcript is recommended as the knockout region.The region contains 274bp coding sequence. Knock out the region will result in disruption of protein function.

- In this project we use CRISPR/Cas9 technology to modify *Kif2c* 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

- The *Kif2c* gene is located on the Chr4. 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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Kif2c kinesin family member 2C [Mus musculus (house mouse)]

Gene ID: 73804, updated on 31-Jan-2019

Summary

Official Symbol	Kif2c provided by MGI
Official Full Name	kinesin family member 2C provided byMGI
Primary source	MGI:MGI:1921054
See related	Ensembl:ENSMUSG00000028678
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	4930402F02Rik, ESTM5, Knsl6, MCAK, X83316
Expression	Biased expression in testis adult (RPKM 63.2), CNS E11.5 (RPKM 19.8) and 8 other tissuesSee more
Orthologs	human all

Transcript information（Ensembl）

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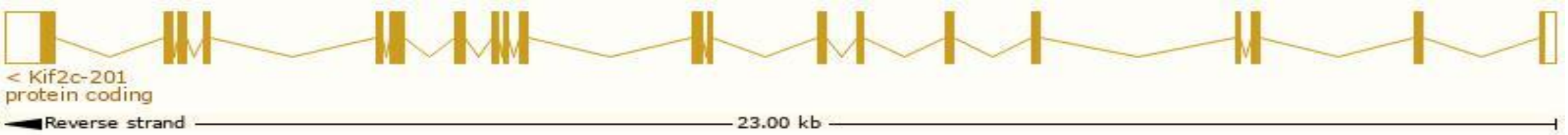
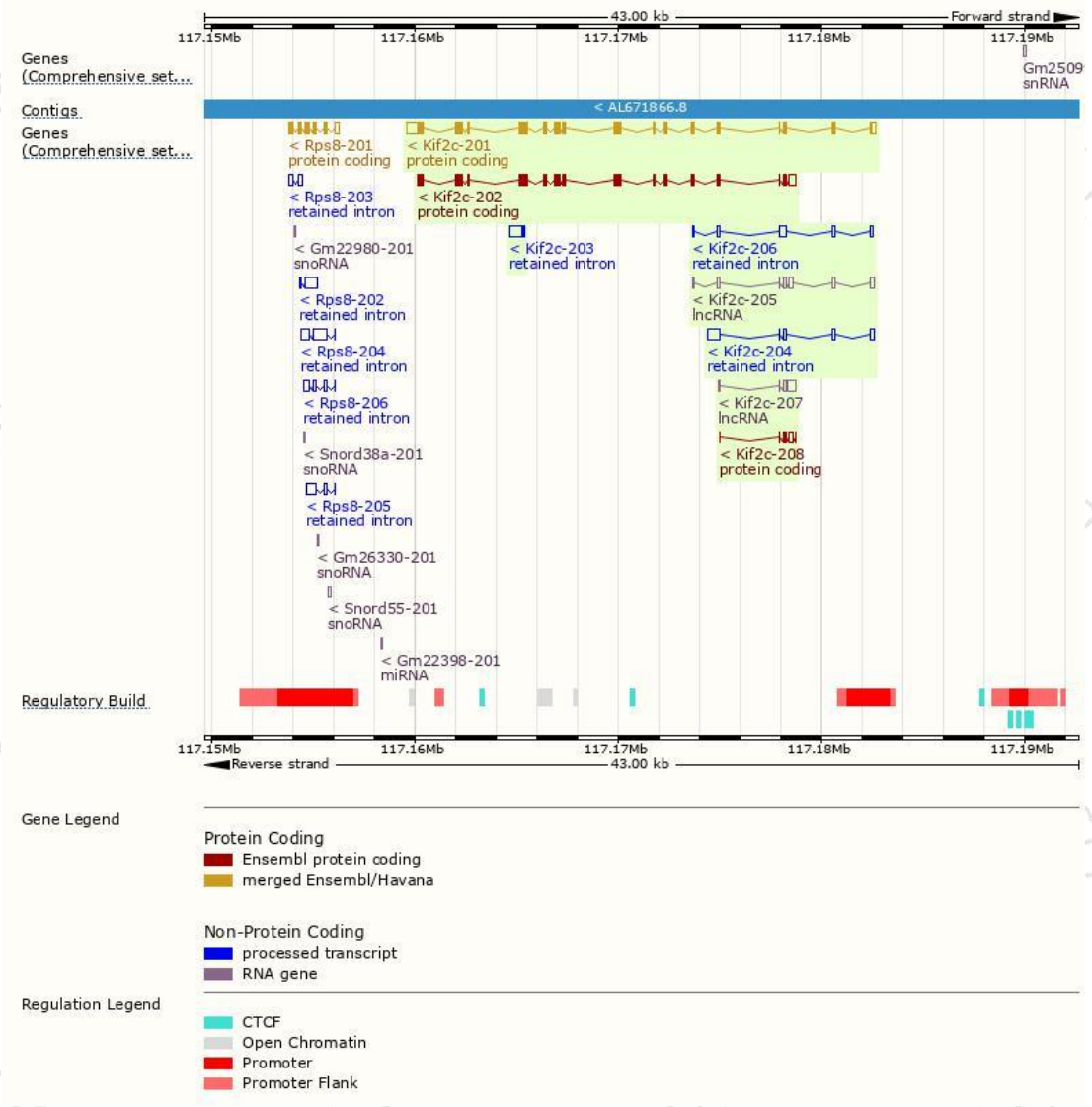
The gene has 8 transcripts,all transcripts are shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Kif2c-201	ENSMUST00000065896.8	2842	721aa	Protein coding	CCDS18531	Q922S8	TSL:1 GENCODE basic APPRIS P3
Kif2c-202	ENSMUST00000106436.7	2378	670aa	Protein coding	CCDS71452	Q3TTL2	TSL:5 GENCODE basic APPRIS ALT2
Kif2c-208	ENSMUST00000153953.1	390	57aa	Protein coding	-	A2AE72	CDS 3' incomplete TSL:5
Kif2c-205	ENSMUST00000142138.7	785	No protein	Processed transcript	-	-	TSL:5
Kif2c-207	ENSMUST00000148918.1	596	No protein	Processed transcript	-	-	TSL:3
Kif2c-204	ENSMUST00000141675.7	1009	No protein	Retained intron	-	-	TSL:1
Kif2c-206	ENSMUST00000142205.7	710	No protein	Retained intron	-	-	TSL:3
Kif2c-203	ENSMUST00000132868.1	629	No protein	Retained intron	-	-	TSL:3

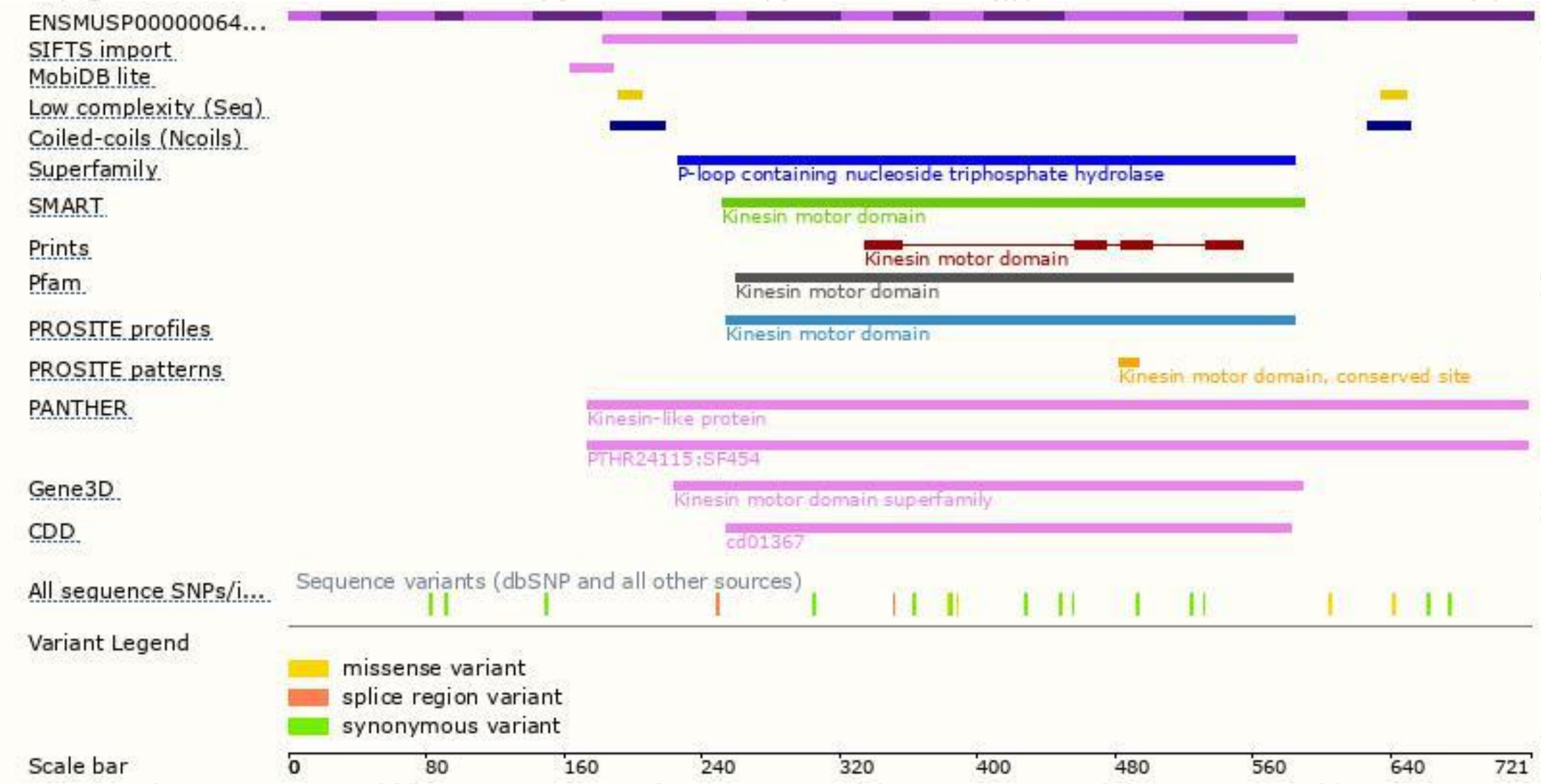
The strategy is based on the design of *Kif2c-201* transcript,The transcription is shown below



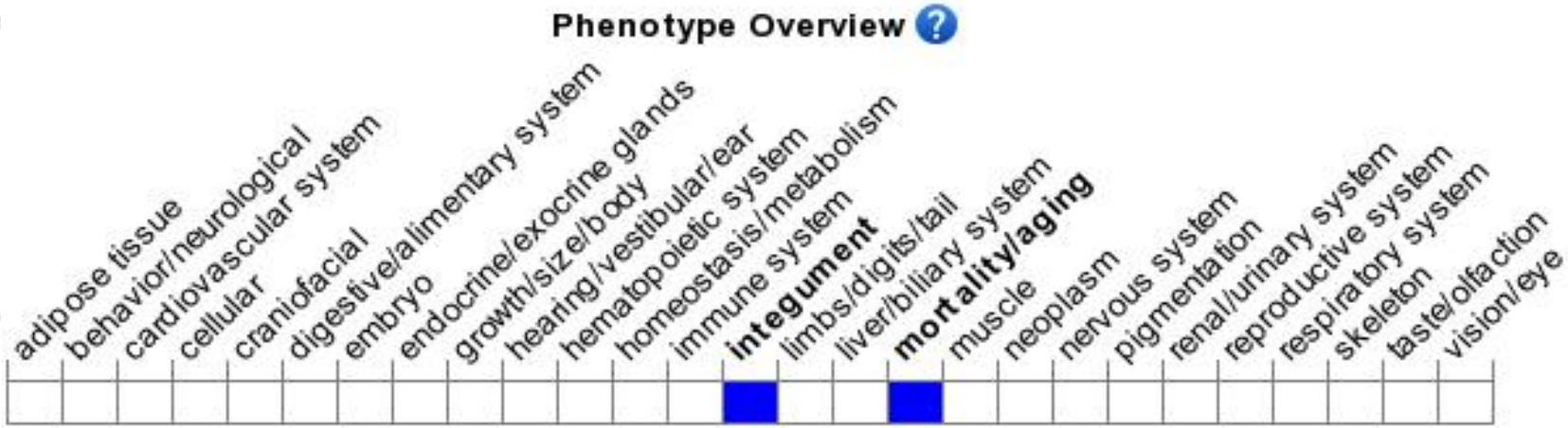
Genomic location distribution



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/).

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