Ercc1 Cas9-CKO Strategy

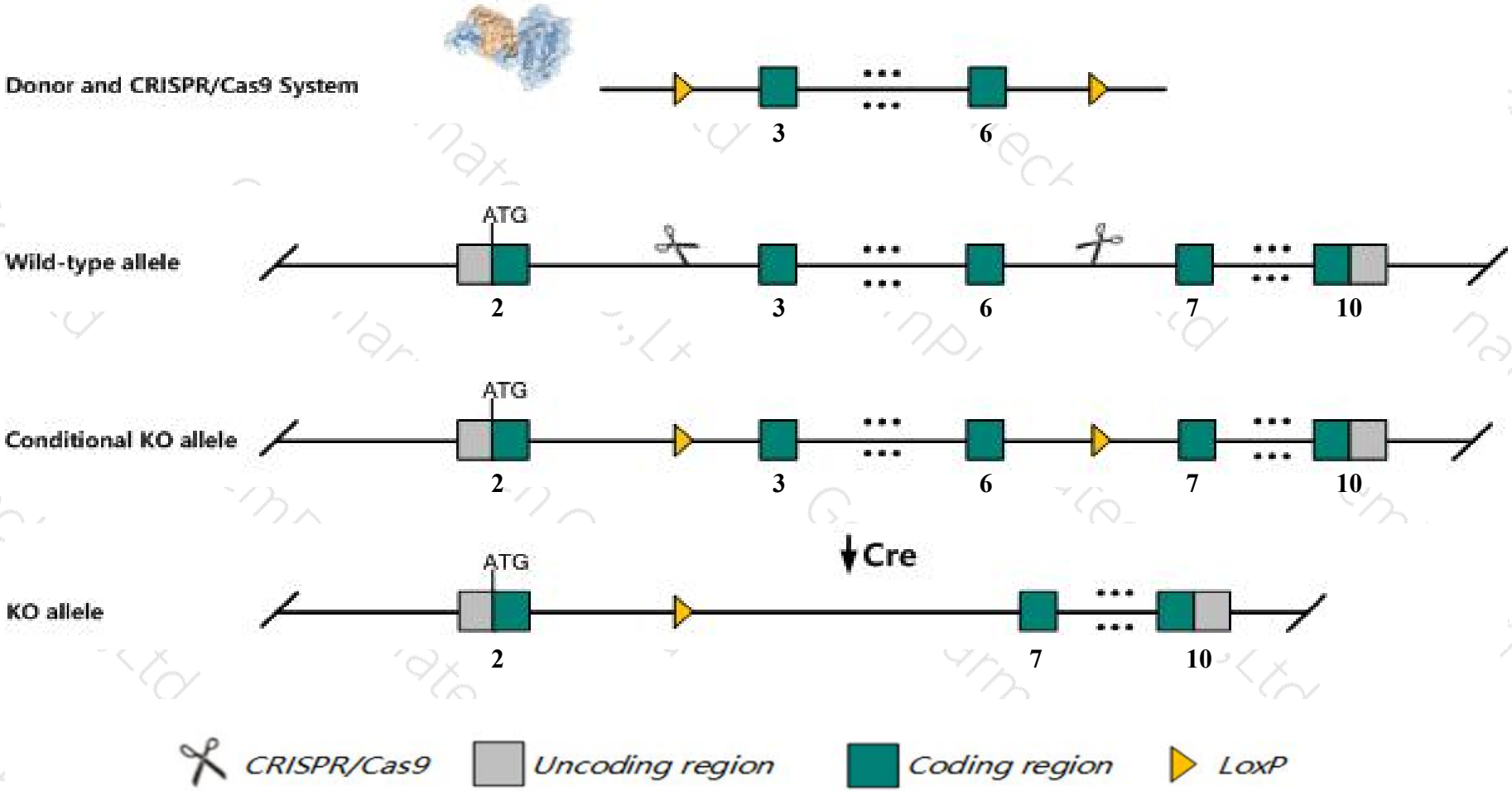
Designer: JiaYu

Project Overview

Project Name	***Ercc1***
Project type	**Cas9-CKO**
Strain background	**C57BL/6JGpt**

Conditional Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *Ercc1* gene. The schematic diagram is as follows:



Technical routes

- The *Ercc1* gene has 10 transcripts. According to the structure of *Ercc1* gene, exon3-exon6 of *Ercc1-201* (ENSMUST00000003645.8) transcript is recommended as the knockout region.The region contains 497bp coding sequence. Knock out the region will result in disruption of protein function.

- In this project we use CRISPR/Cas9 technology to modify *Ercc1* 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,Nullizygous mutations result in growth and liver failure, nuclear anomalies and postnatal death, and may lead to spleen hypoplasia, altered isotype switching, B cell hypoproliferation, dystonia, ataxia, renal failure, sarcopenia, kyphosis, early replicative aging and sensitivity to oxidative stress.

- The *Ercc1* gene is located on the Chr7. 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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Ercc1 excision repair cross-complementing rodent repair deficiency, complementation group 1 [Mus musculus (house mouse)]

Gene ID: 13870, updated on 31-Jan-2019

Summary

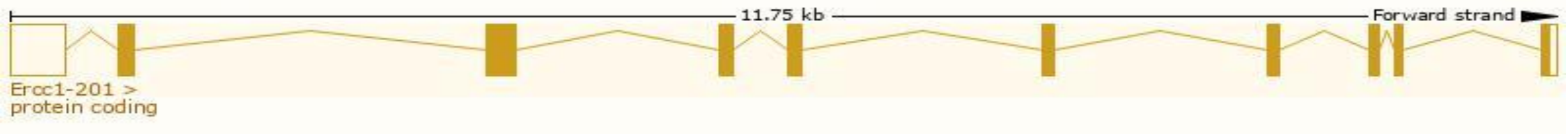
Official Symbol	Ercc1 provided by MGI
Official Full Name	excision repair cross-complementing rodent repair deficiency, complementation group 1 provided by MGI
Primary source	MGI:MGI:95412
See related	Ensembl:ENSMUSG00000003549
Gene type	protein coding
RefSeq status	VALIDATED
Organism	Mus musculus
Lineage	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Myomorpha; Muroidea; Muridae; Murinae; Mus; Mus
Also known as	Ercc-1
Expression	Ubiquitous expression in limb E14.5 (RPKM 10.9), subcutaneous fat pad adult (RPKM 10.0) and 28 other tissues See more
Orthologs	human all

Transcript information（Ensembl）

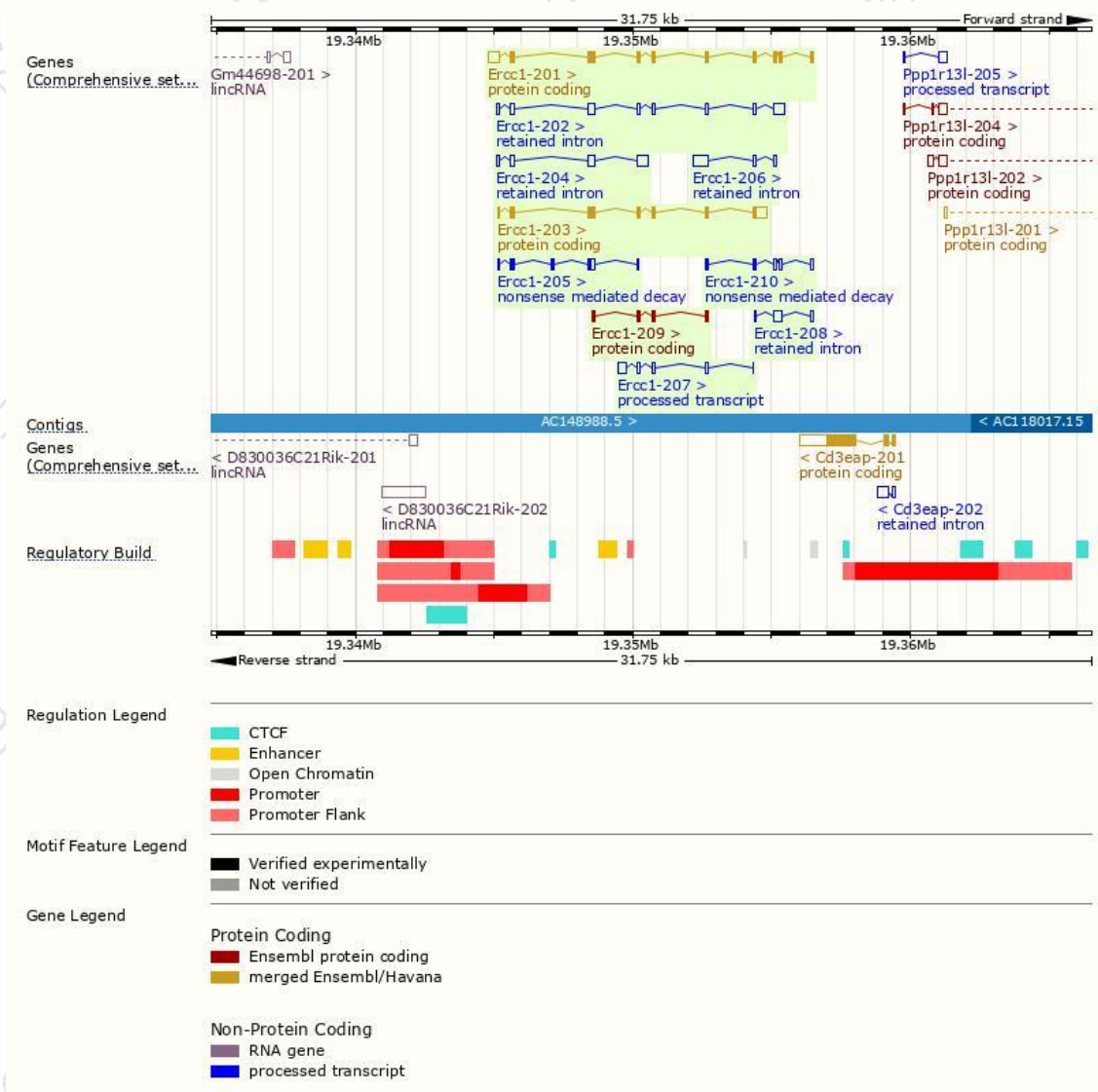
The gene has 10 transcripts,all transcripts are shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Ercc1-201	ENSMUST00000003645.8	1375	298aa	Protein coding	CCDS20898	P07903	TSL:1 GENCODE basic APPRIS P1
Ercc1-203	ENSMUST00000160369.7	1175	245aa	Protein coding	CCDS52057	E9PUM0	TSL:1 GENCODE basic
Ercc1-209	ENSMUST00000176818.1	370	123aa	Protein coding	-	H3BLF5	5' and 3' truncations in transcript evidence prevent annotation of the start and the end of the CDS. CDS 5' and 3' incomplete TSL:3
Ercc1-205	ENSMUST00000161378.1	467	86aa	Nonsense mediated decay	-	H3BJK4	TSL:5
Ercc1-210	ENSMUST00000177486.1	413	37aa	Nonsense mediated decay	-	H3BJX2	CDS 5' incomplete TSL:2
Ercc1-207	ENSMUST00000162992.1	584	No protein	Processed transcript	-	-	TSL:3
Ercc1-202	ENSMUST00000160192.7	1179	No protein	Retained intron	-	-	TSL:3
Ercc1-204	ENSMUST00000160909.1	797	No protein	Retained intron	-	-	TSL:2
Ercc1-206	ENSMUST00000162197.2	712	No protein	Retained intron	-	-	TSL:3
Ercc1-208	ENSMUST00000176723.1	421	No protein	Retained intron	-	-	TSL:5

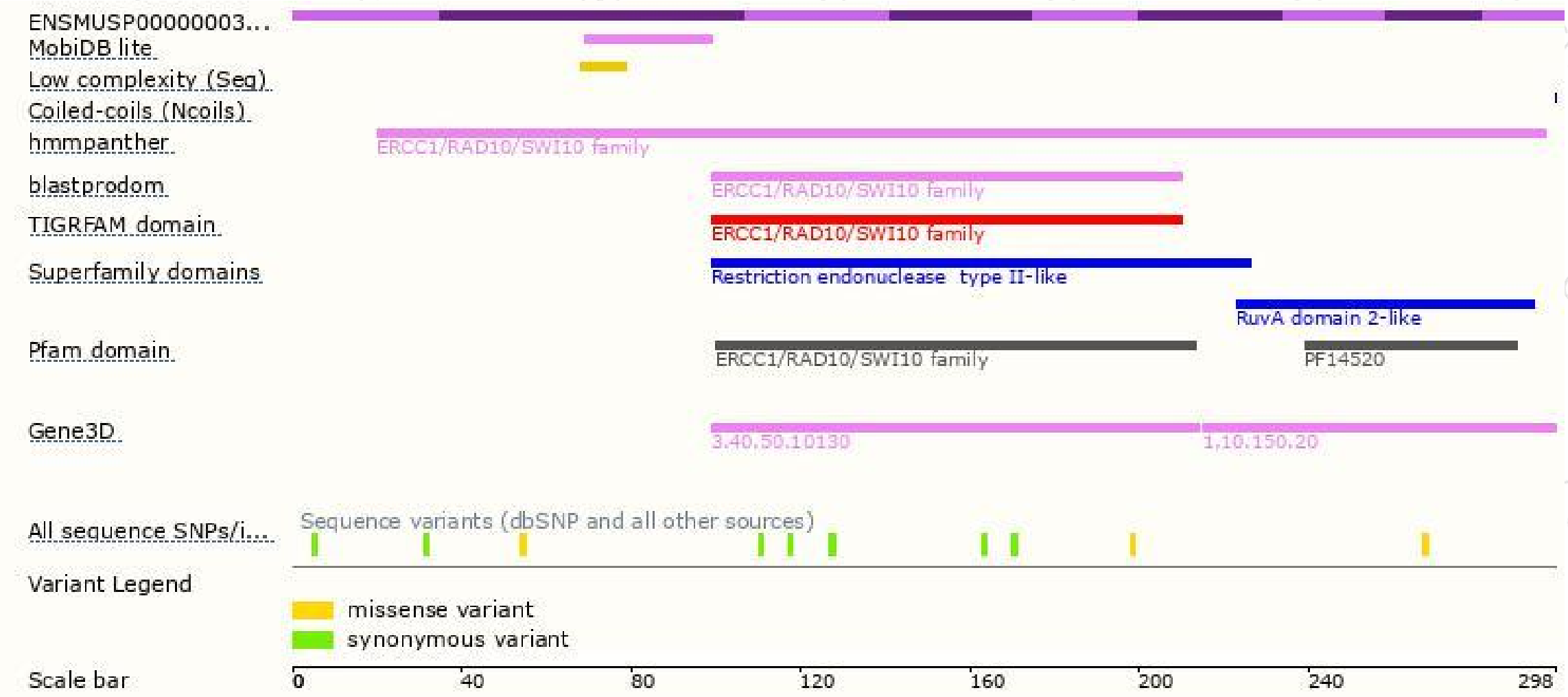
The strategy is based on the design of *Ercc1-201* transcript,The transcription is shown below



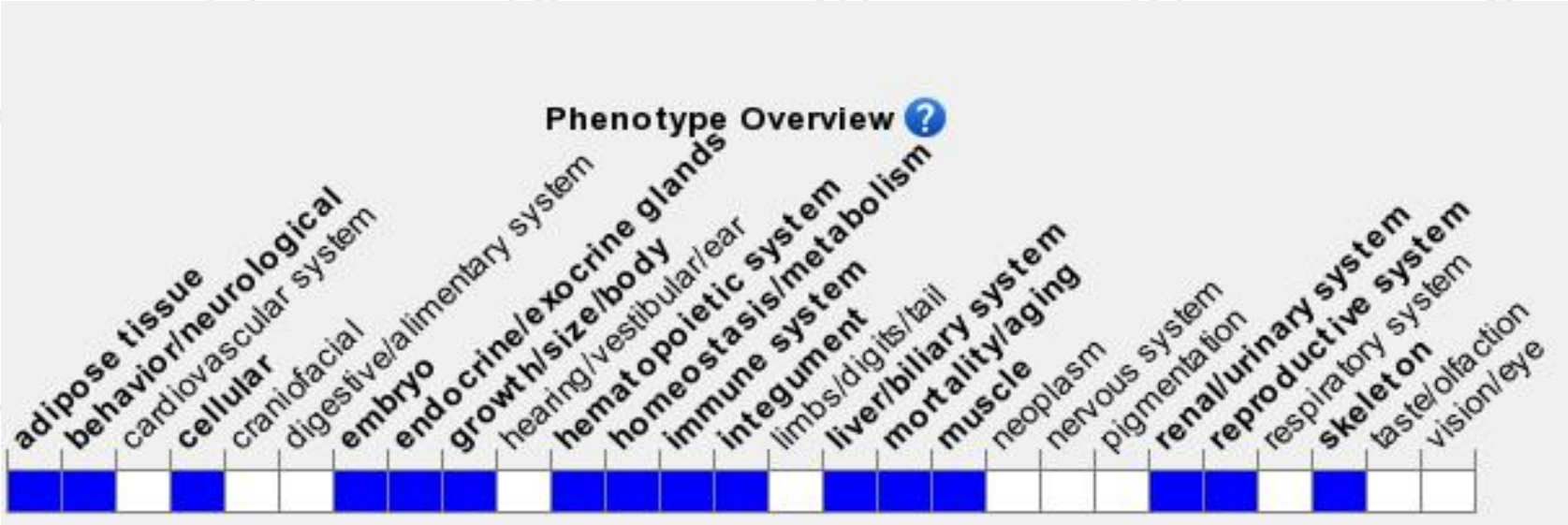
Genomic location distribution



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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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