Ercc8 Cas9-CKO Strategy

Designer: JiaYu

Reviewer: Xiaojing Li

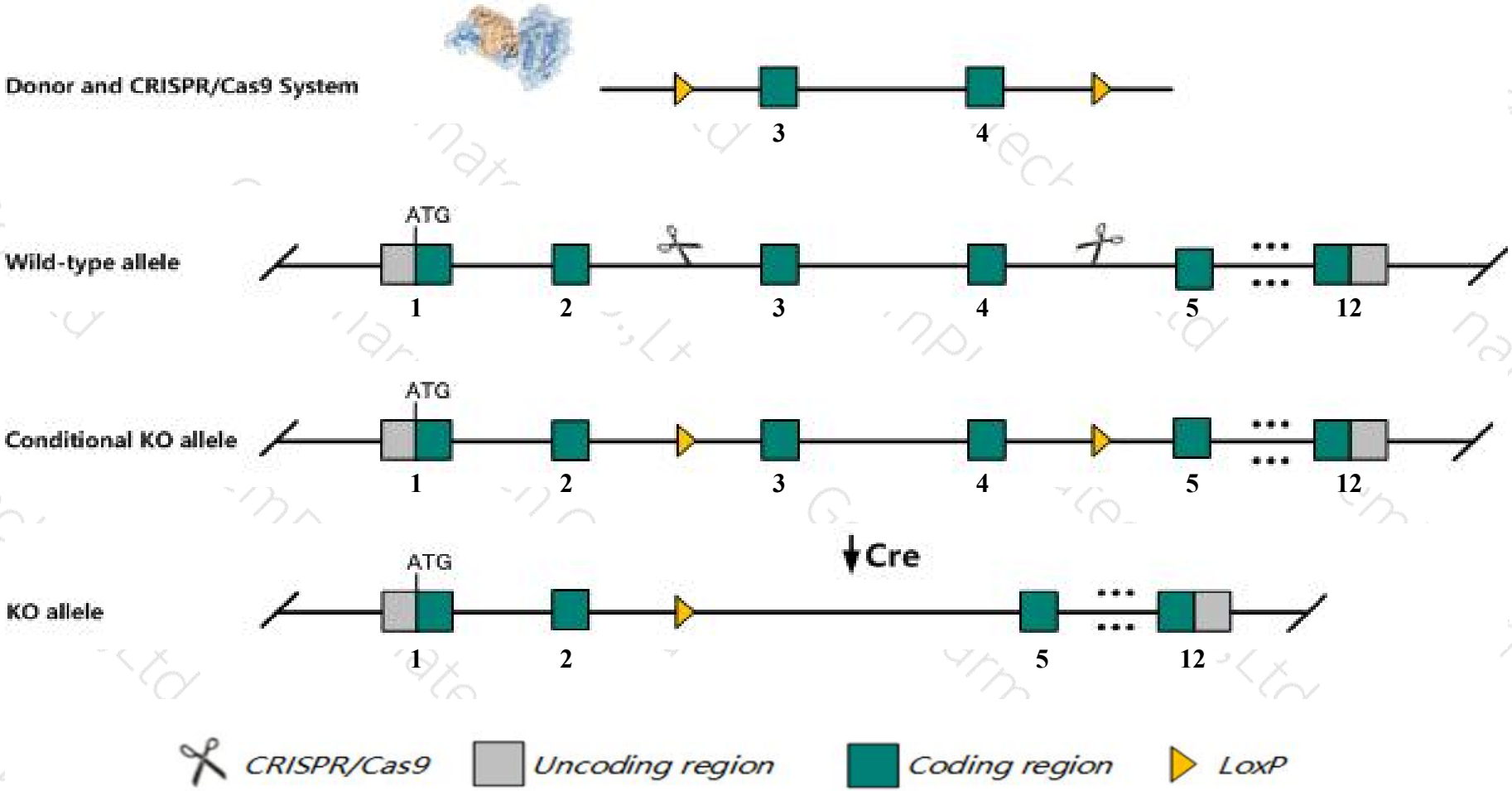
Design Date: 2020-2-20

Project Overview

Project Name	***Ercc8***
Project type	**Cas9-CKO**
Strain background	**C57BL/6JGpt**

Conditional Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *Ercc8* gene. The schematic diagram is as follows:



Technical routes

- The *Ercc8* gene has 10 transcripts. According to the structure of *Ercc8* gene, exon3-exon4 of *Ercc8-201* (ENSMUST00000054835.14) transcript is recommended as the knockout region.The region contains 226bp coding sequence. Knock out the region will result in disruption of protein function.

- In this project we use CRISPR/Cas9 technology to modify *Ercc8* 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 mutation of this gene results in skin photosensitivity, increased incidence of skin tumors after UV exposure, and progressive photoreceptor degeneration.

- The *Ercc8* gene is located on the Chr13. 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

Ercc8 excision repaiross-complementing rodent repair deficiency, complementation group 8 [Mus musculus (house mouse)]

Gene ID: 71991, updated on 31-Jan-2019

Summary

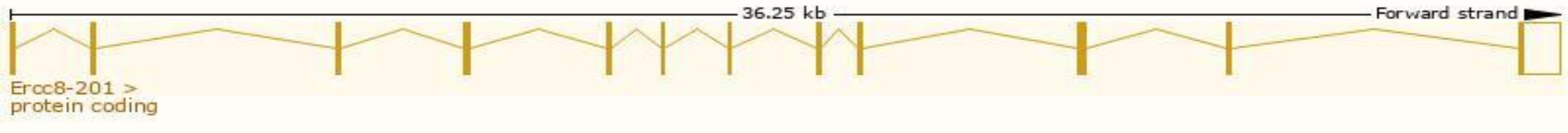
Official Symbol	Ercc8 provided by MGI
Official Full Name	excision repaiross-complementing rodent repair deficiency, complementation group 8 provided by MGI
Primary source	MGI:MGI:1919241
See related	Ensembl:ENSMUSG00000021694
Gene type	protein coding
RefSeq status	VALIDATED
Organism	Mus musculus
Lineage	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Myomorpha; Muroidea; Muridae; Murinae; Mus; Mus
Also known as	2410022P04Rik, 2810431L23Rik, 4631412O06Rik, B130065P18Rik, Ckn1, Csa
Expression	Ubiquitous expression in testis adult (RPKM 4.3), CNS E18 (RPKM 3.3) and 28 other tissues See more
Orthologs	human all

Transcript information（Ensembl）

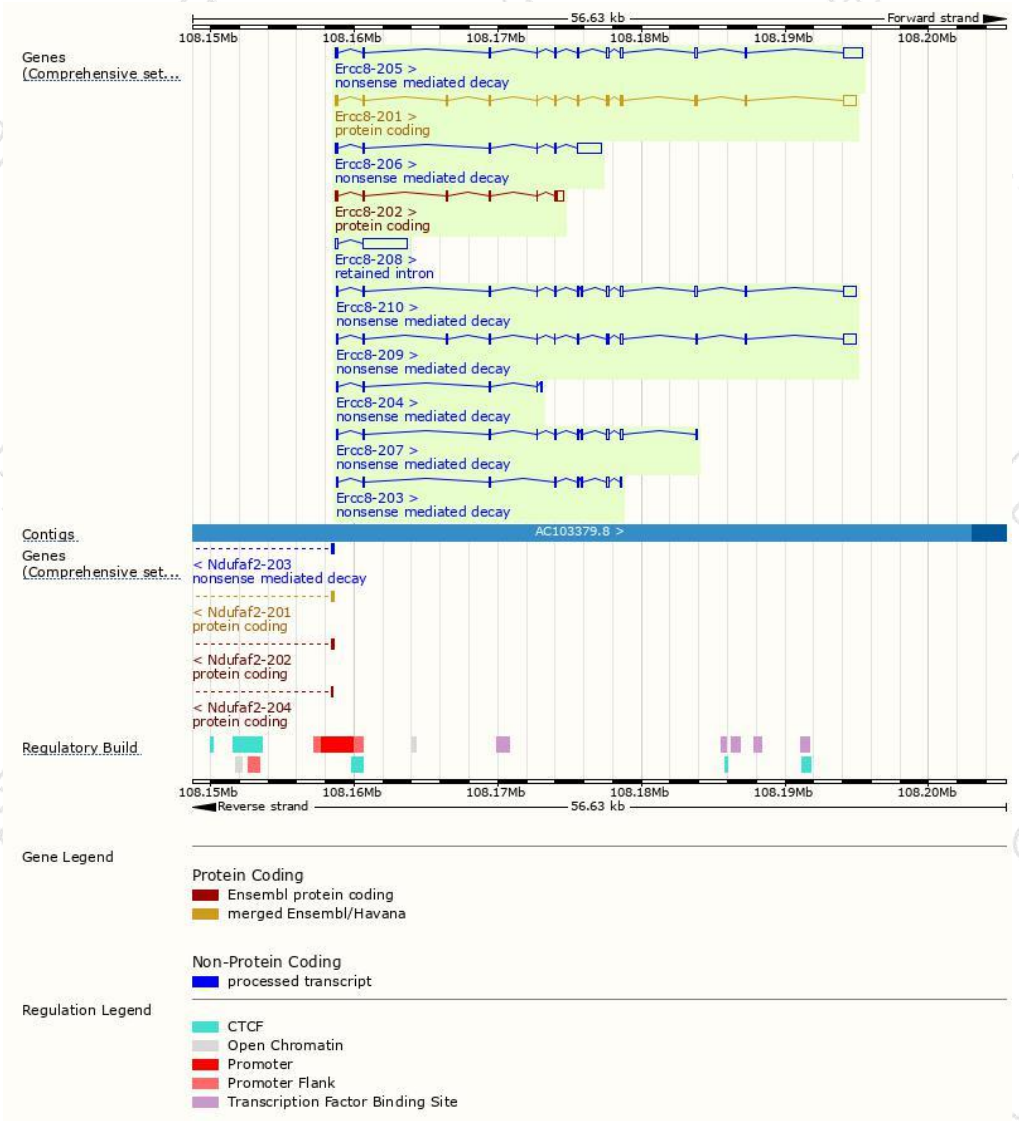
The gene has 10 transcripts,all transcripts are shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Ercc8-201	ENSMUST00000054835.14	2111	397aa	Protein coding	CCDS26761	Q8CFD5	TSL:1 GENCODE basic APPRIS P1
Ercc8-202	ENSMUST00000120672.7	1144	200aa	Protein coding	-	D3YU16	TSL:1 GENCODE basic
Ercc8-205	ENSMUST00000123657.7	2395	57aa	Nonsense mediated decay	-	D6RET0	TSL:1
Ercc8-206	ENSMUST00000129117.7	2199	57aa	Nonsense mediated decay	-	D6RET0	TSL:1
Ercc8-210	ENSMUST00000152634.7	2095	57aa	Nonsense mediated decay	-	D6RET0	TSL:1
Ercc8-209	ENSMUST00000142931.7	1923	194aa	Nonsense mediated decay	-	D6RIM0	TSL:5
Ercc8-207	ENSMUST00000133957.7	933	54aa	Nonsense mediated decay	-	F6QML7	CDS 5' incomplete TSL:5
Ercc8-203	ENSMUST00000123138.1	719	54aa	Nonsense mediated decay	-	F6QPY9	CDS 5' incomplete TSL:3
Ercc8-204	ENSMUST00000123182.7	458	57aa	Nonsense mediated decay	-	D6RET0	TSL:3
Ercc8-208	ENSMUST00000137425.1	3163	No protein	Retained intron	-	-	TSL:1

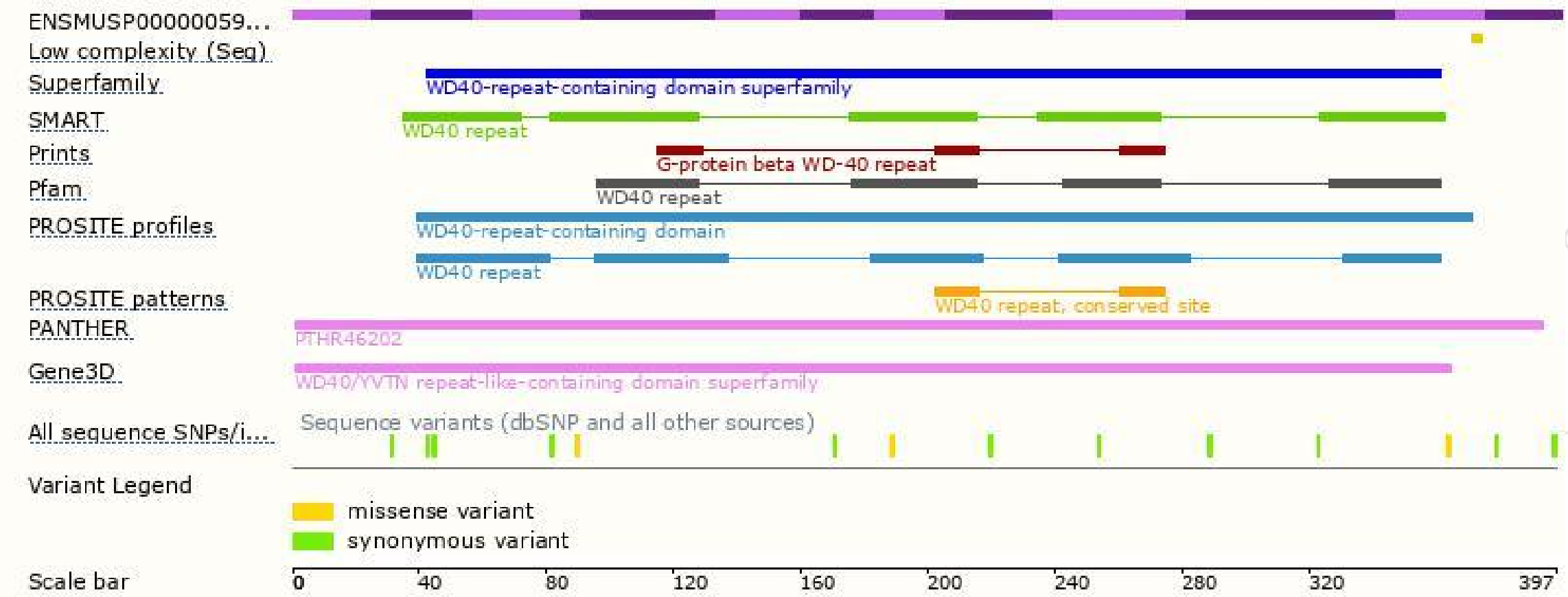
The strategy is based on the design of *Ercc8-201* transcript,The transcription is shown below



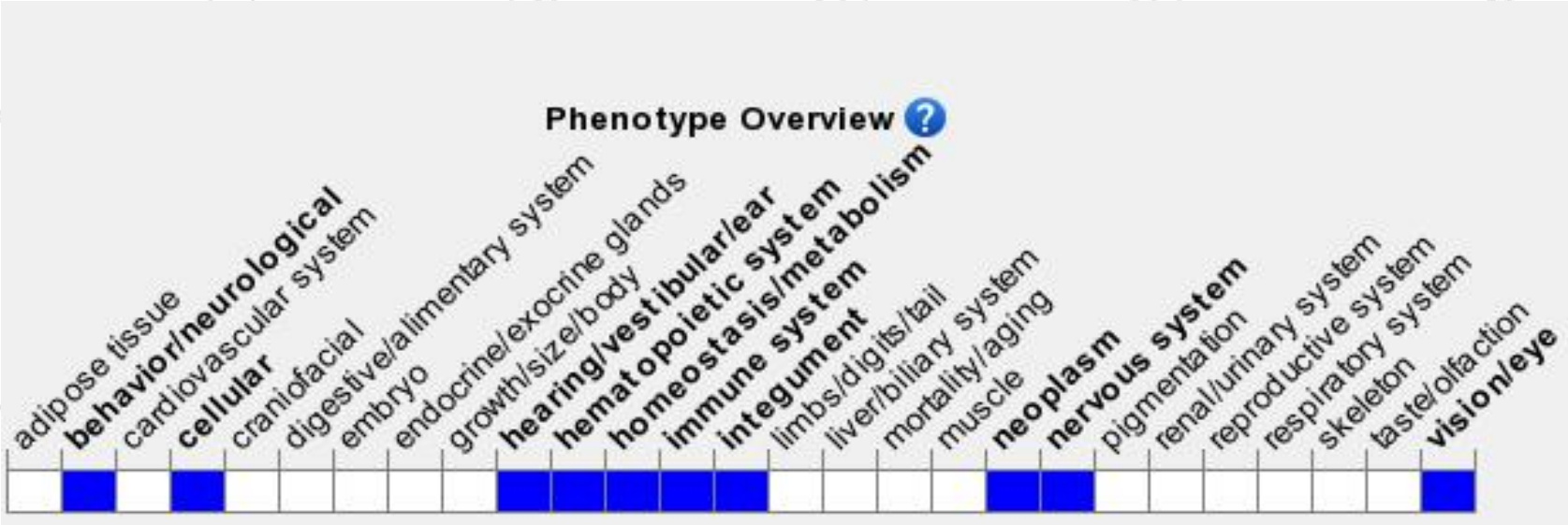
Genomic location distribution



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 mutation of this gene results in skin photosensitivity, increased incidence of skin tumors after UV exposure, and progressive photoreceptor degeneration.

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