

Rnf141 Cas9-CKO Strategy

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Project Overview

Project Name

Rnf141

Project type

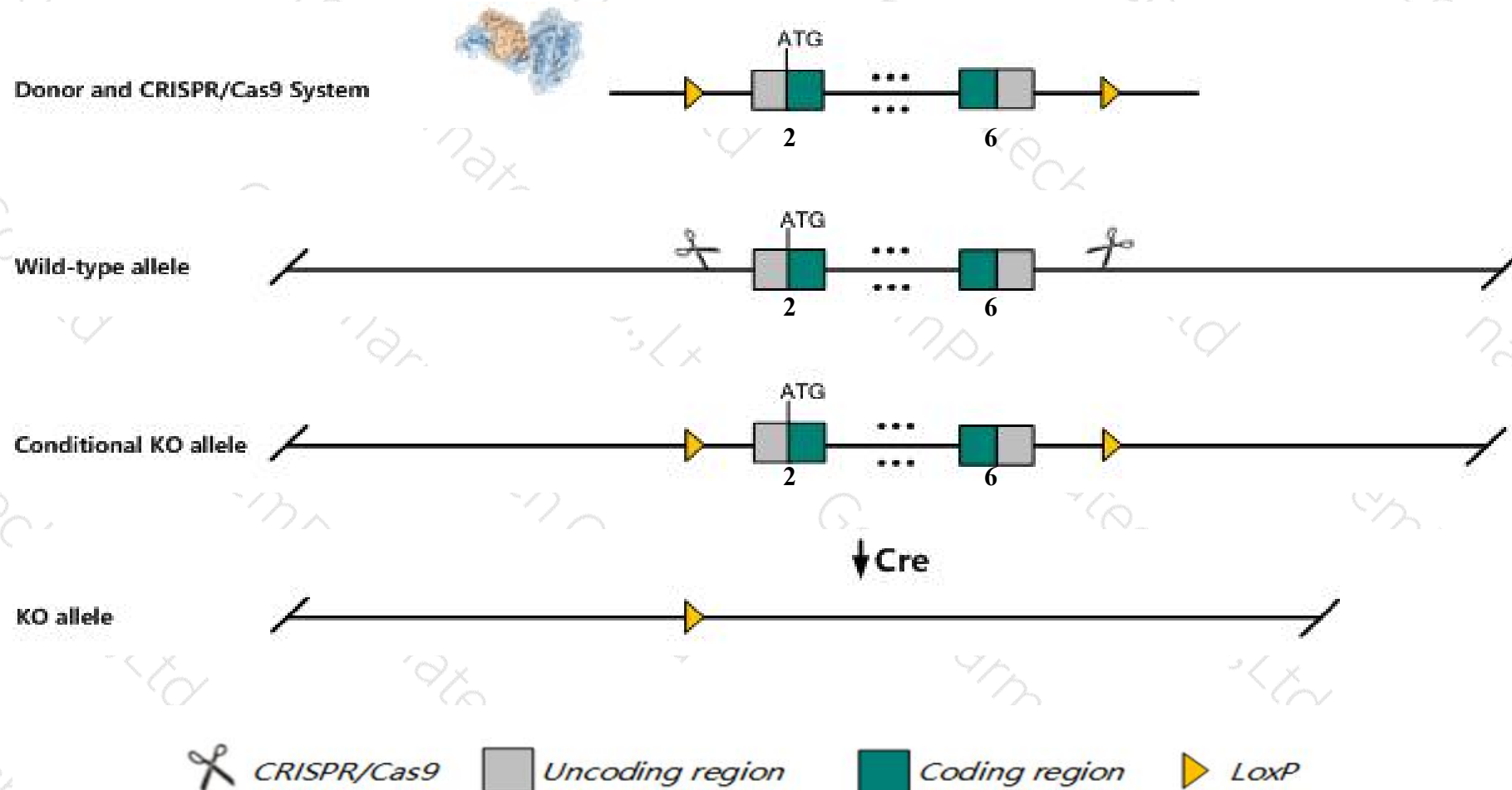
Cas9-CKO

Strain background

C57BL/6JGpt

Conditional Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *Rnfl41* gene. The schematic diagram is as follows:



- The *Rnf141* gene has 12 transcripts. According to the structure of *Rnf141* gene, exon2-exon6 of *Rnf141-209* (ENSMUST00000177236.7) 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 *Rnf141* 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.

- According to the existing MGI data, Mice homozygous for a targeted allele exhibit decreased litter size but normal spermatogenesis and testes weight.
- The flox region is about 1 kb from the 3' end of the *Ampd3* gene, which may affect the 3-terminal regulation of the gene.
- Transcripts 202, 212 are unaffected.
- The *Rnf141* 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)

Rnf141 ring finger protein 141 [*Mus musculus* (house mouse)]

Gene ID: 67150, updated on 12-Aug-2019

Summary

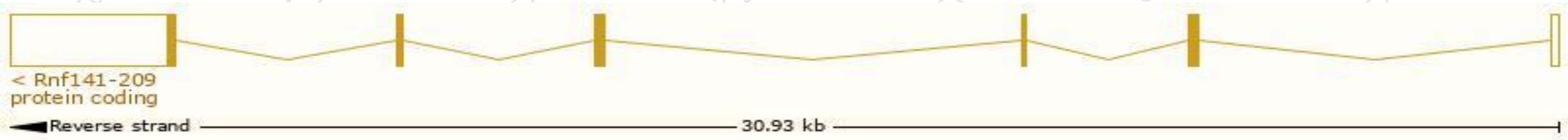
Official Symbol	Rnf141 provided by MGI
Official Full Name	ring finger protein 141 provided by MGI
Primary source	MGI:MGI:1914400
See related	Ensembl:ENSMUSG00000030788
Gene type	protein coding
RefSeq status	PROVISIONAL
Organism	Mus musculus
Lineage	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Myomorpha; Muroidea; Muridae; Murinae; Mus; Mus
Also known as	ZFP36; ZNF230; AA792898; AU022812; 2610110L04Rik
Expression	Ubiquitous expression in lung adult (RPKM 5.5), subcutaneous fat pad adult (RPKM 5.1) and 28 other tissues See more
Orthologs	human all

Transcript information (Ensembl)

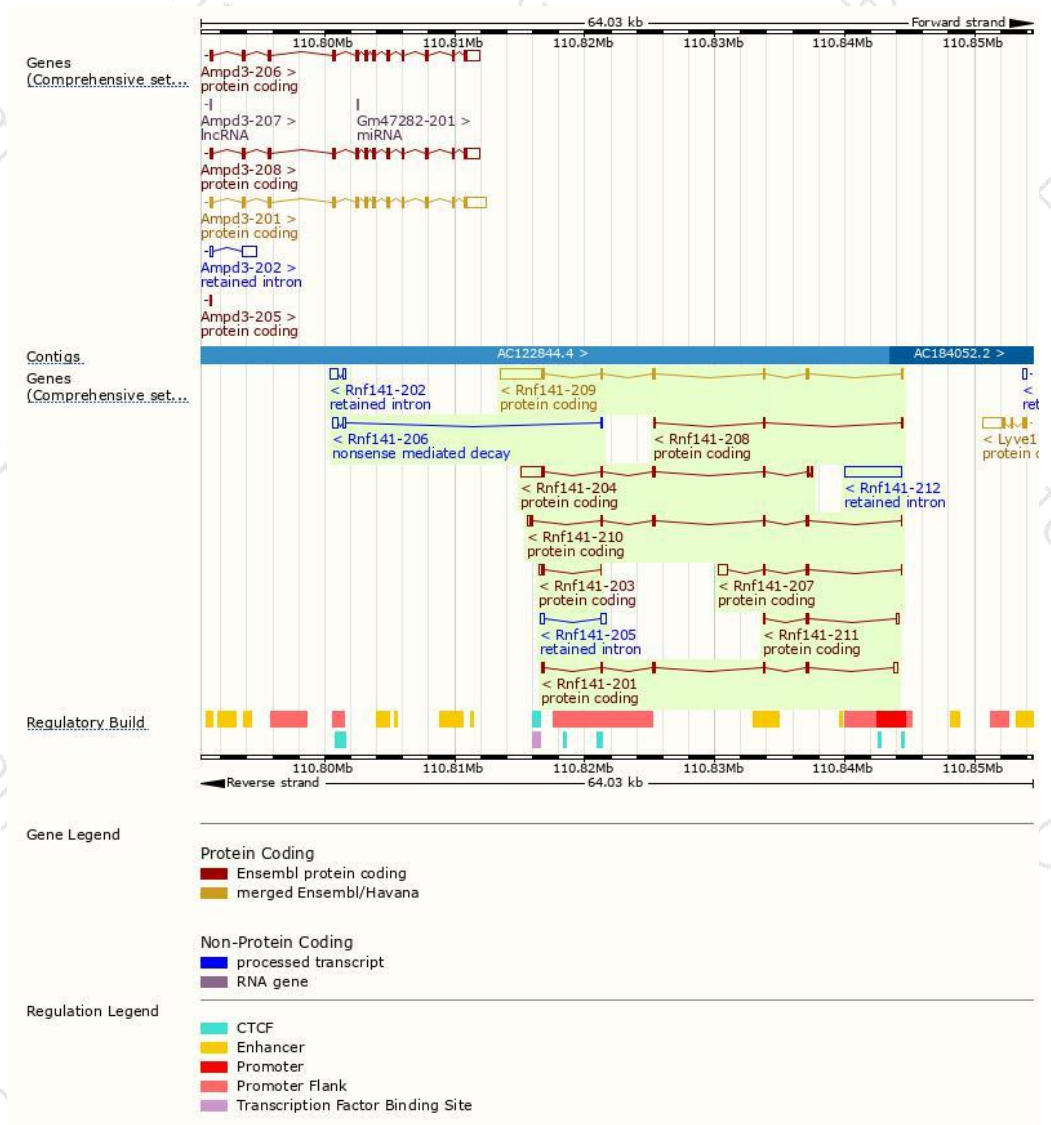
The gene has 12 transcripts,all transcripts are shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Rnf141-209	ENSMUST00000177236.7	4032	230aa	Protein coding	CCDS40086	Q99MB7	TSL:1 GENCODE basic APPRIS P1
Rnf141-201	ENSMUST00000106682.9	1101	230aa	Protein coding	CCDS40086	Q99MB7	TSL:3 GENCODE basic APPRIS P1
Rnf141-204	ENSMUST00000175981.7	2333	133aa	Protein coding	-	H3BJU0	TSL:1 GENCODE basic
Rnf141-207	ENSMUST00000176716.2	1080	87aa	Protein coding	-	A0A1B0GT51	TSL:2 GENCODE basic
Rnf141-210	ENSMUST00000177462.7	859	180aa	Protein coding	-	H3BJB4	TSL:5 GENCODE basic
Rnf141-203	ENSMUST00000175648.1	422	59aa	Protein coding	-	H3BJX9	CDS 5' incomplete TSL:3
Rnf141-211	ENSMUST00000177520.1	419	75aa	Protein coding	-	H3BJE9	CDS 3' incomplete TSL:3
Rnf141-208	ENSMUST00000176746.7	317	21aa	Protein coding	-	H3BKH1	CDS 3' incomplete TSL:2
Rnf141-206	ENSMUST00000176210.1	647	28aa	Nonsense mediated decay	-	H3BK28	CDS 5' incomplete TSL:2
Rnf141-212	ENSMUST00000210070.1	4423	No protein	Retained intron	-	-	TSL:NA
Rnf141-202	ENSMUST00000148367.1	793	No protein	Retained intron	-	-	TSL:1
Rnf141-205	ENSMUST00000176048.1	614	No protein	Retained intron	-	-	TSL:2

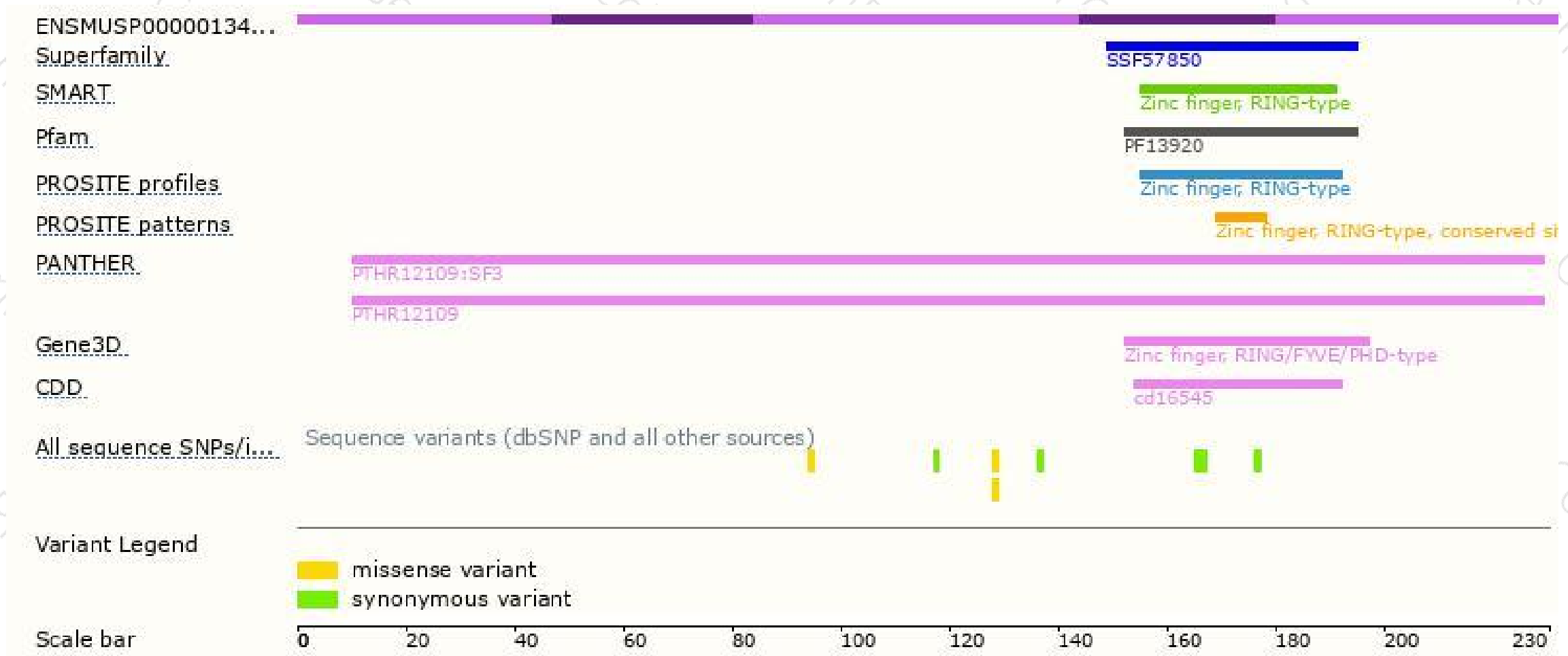
The strategy is based on the design of *Rnf141-209* transcript,The transcription is shown below



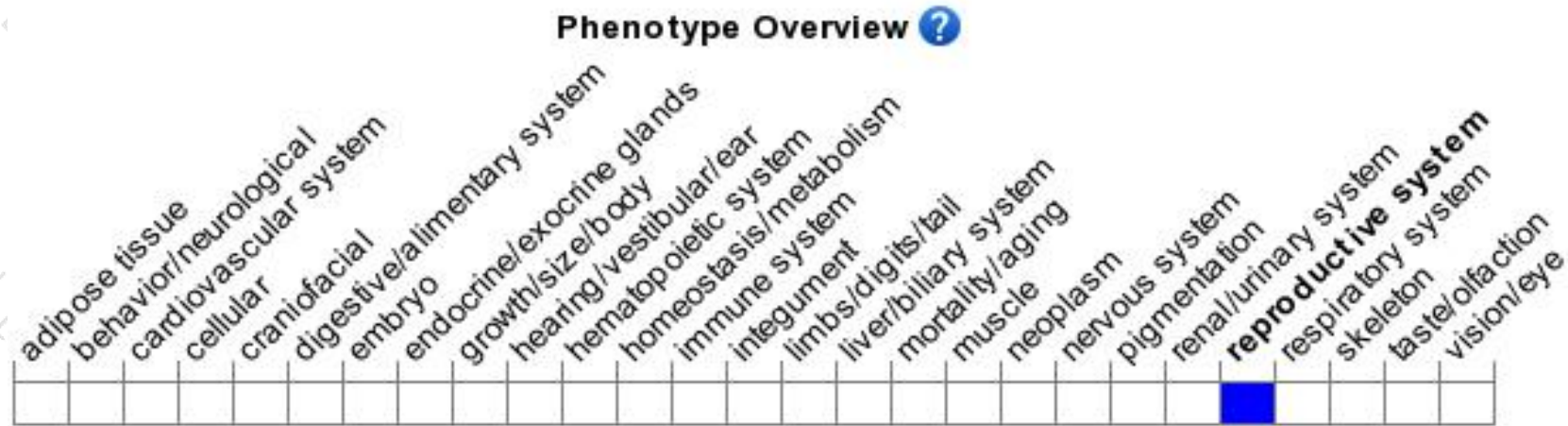
Genomic location distribution



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, Mice homozygous for a targeted allele exhibit decreased litter size but normal spermatogenesis and testes weight.

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

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