

Eef2k Cas9-CKO Strategy

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Reviewer:

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Project Overview

Project Name

Eef2k

Project type

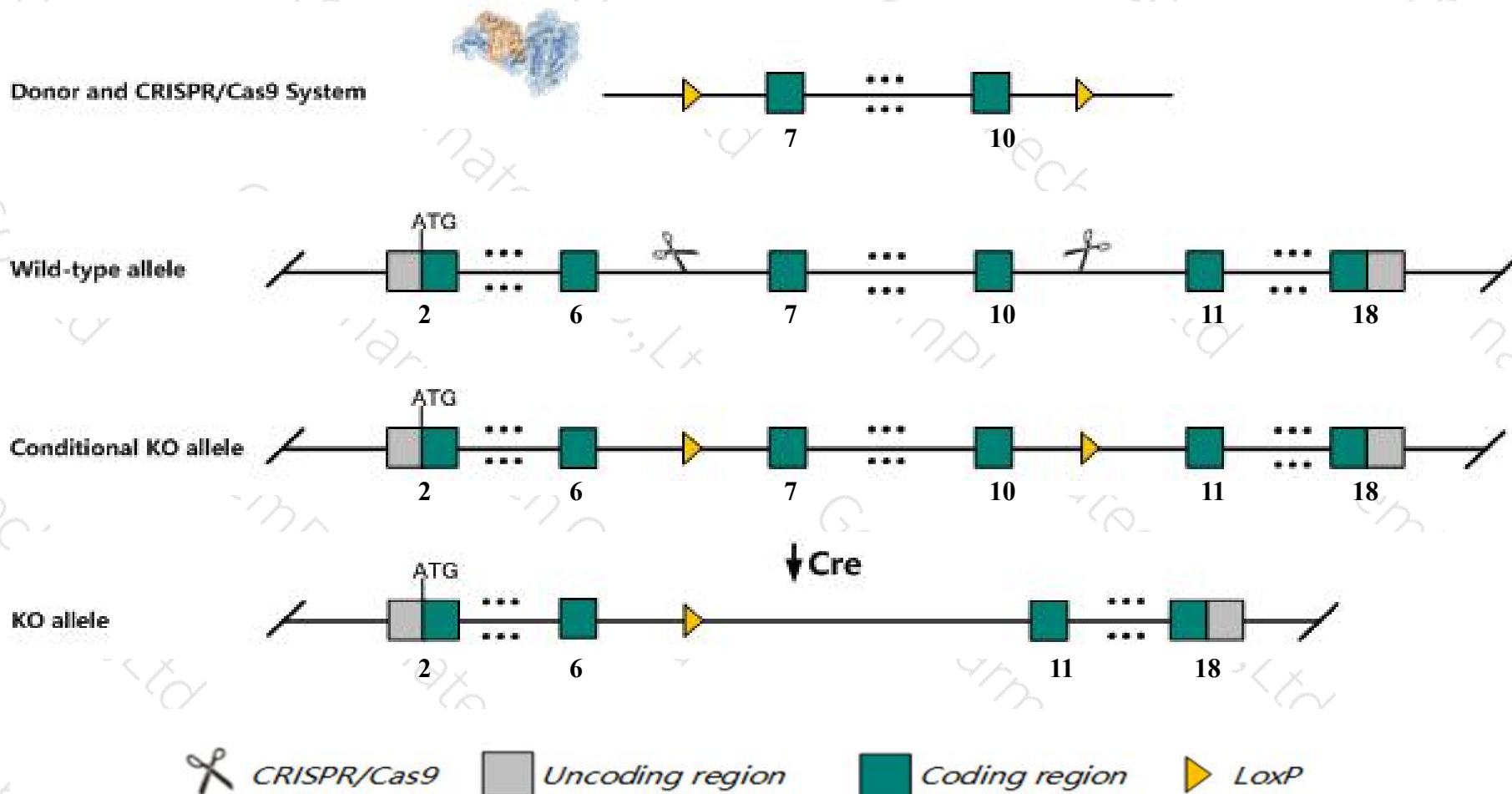
Cas9-CKO

Strain background

C57BL/6JGpt

Conditional Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *Eef2k* gene. The schematic diagram is as follows:



Technical routes

- The *Eef2k* gene has 9 transcripts. According to the structure of *Eef2k* gene, exon7-exon10 of *Eef2k-201* (ENSMUST00000047875.15) transcript is recommended as the knockout region. The region contains 613bp coding sequence. Knock out the region will result in disruption of protein function.
- In this project we use CRISPR/Cas9 technology to modify *Eef2k* 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 knock-out allele exhibit impaired regulation of ovarian follicular degeneration and apoptosis, prolonged estrus, and increased ovarian follicle numbers in aged females.
- The *Eef2k* 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)

Eef2k eukaryotic elongation factor-2 kinase [Mus musculus (house mouse)]

Gene ID: 13631, updated on 26-Feb-2019

Summary



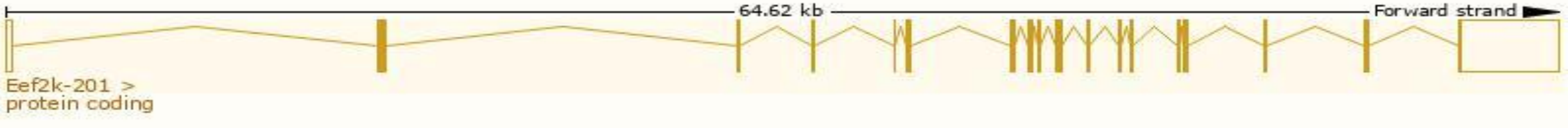
Official Symbol	Eef2k provided by MGI
Official Full Name	eukaryotic elongation factor-2 kinase provided by MGI
Primary source	MGI:MGI:1195261
See related	Ensembl:ENSMUSG00000035064
Gene type	protein coding
RefSeq status	VALIDATED
Organism	Mus musculus
Lineage	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Myomorpha; Muroidea; Muridae; Murinae; Mus; Mus
Also known as	C86191, eEF-2K
Expression	Ubiquitous expression in bladder adult (RPKM 19.4), colon adult (RPKM 10.7) and 28 other tissues See more
Orthologs	human all

Transcript information (Ensembl)

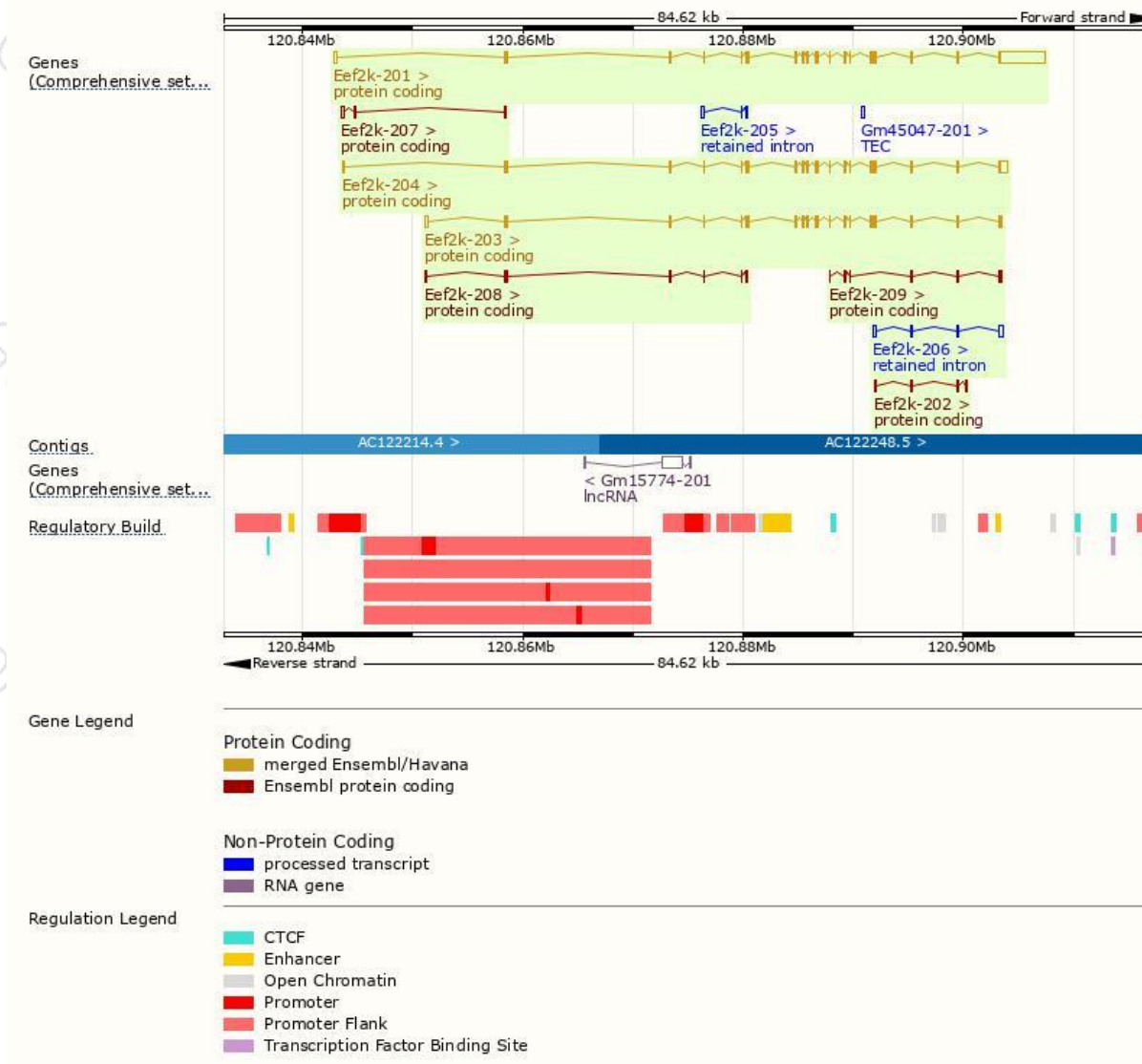
The gene has 9 transcripts,all transcripts are shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Eef2k-201	ENSMUST00000047875.15	6580	724aa	Protein coding	CCDS21796	O08796	TSL:1 GENCODE basic APPRIS P1
Eef2k-204	ENSMUST00000106489.8	3047	724aa	Protein coding	CCDS21796	O08796	TSL:1 GENCODE basic APPRIS P1
Eef2k-203	ENSMUST00000106488.2	2537	724aa	Protein coding	CCDS21796	O08796	TSL:1 GENCODE basic APPRIS P1
Eef2k-209	ENSMUST00000146482.2	672	185aa	Protein coding	-	F6ZEU2	CDS 5' incomplete TSL:5
Eef2k-208	ENSMUST00000143322.8	667	164aa	Protein coding	-	D3Z088	CDS 3' incomplete TSL:2
Eef2k-207	ENSMUST00000143279.2	504	38aa	Protein coding	-	D3Z1Y3	CDS 3' incomplete TSL:5
Eef2k-202	ENSMUST00000106487.8	485	140aa	Protein coding	-	F7A9F2	CDS 5' incomplete TSL:3
Eef2k-206	ENSMUST00000128813.1	800	No protein	Retained intron	-	-	TSL:2
Eef2k-205	ENSMUST00000125828.2	334	No protein	Retained intron	-	-	TSL:2

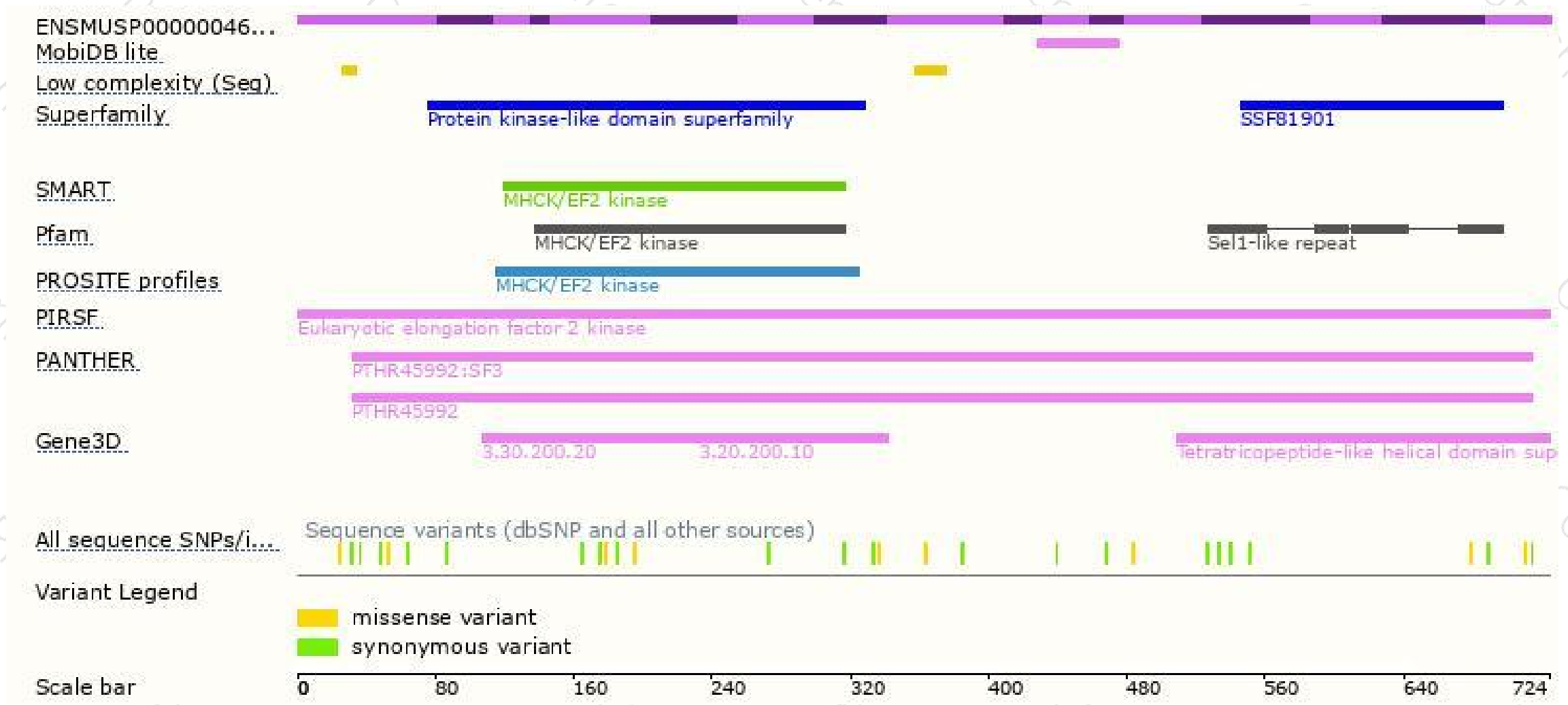
The strategy is based on the design of *Eef2k-201* transcript,The transcription is shown below



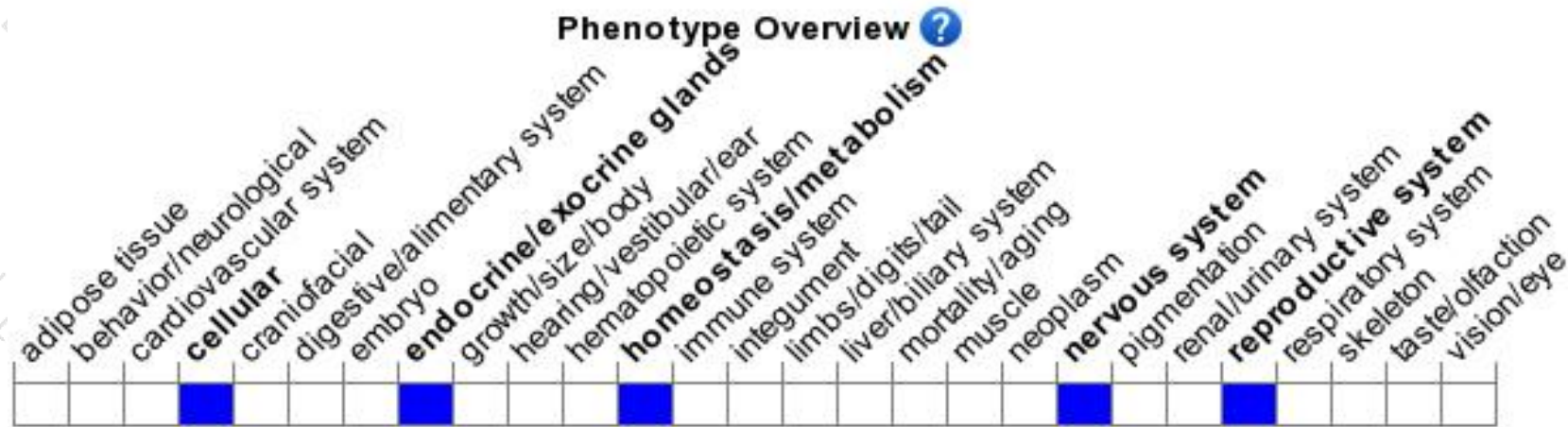
Genomic location distribution



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, Mice homozygous for a knock-out allele exhibit impaired regulation of ovarian follicular degeneration and apoptosis, prolonged estrus, and increased ovarian follicle numbers in aged females.

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

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