

Katnal2 Cas9-CKO Strategy

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Reviewer:

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Project Overview

Project Name

Katnal2

Project type

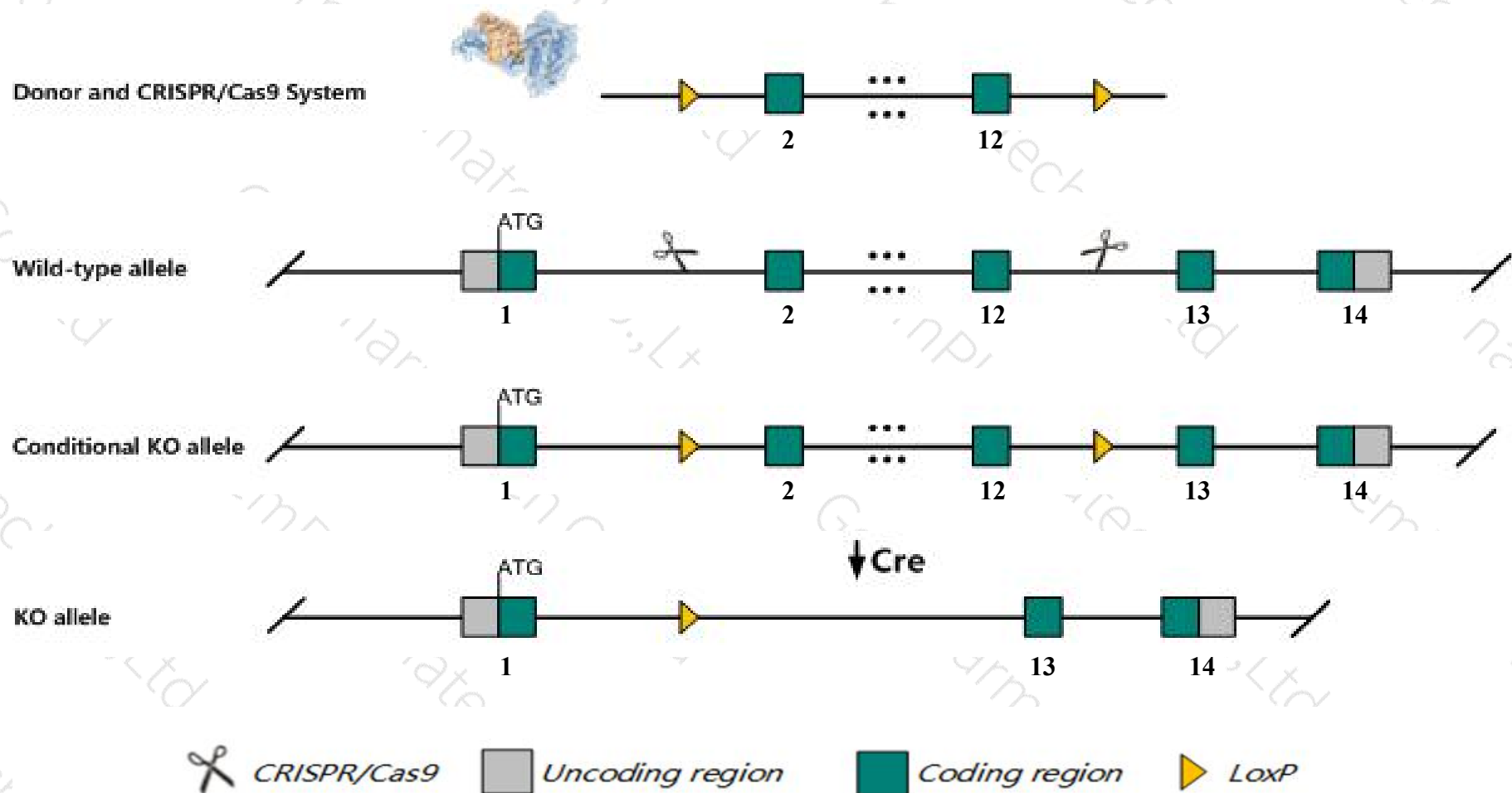
Cas9-CKO

Strain background

C57BL/6JGpt

Conditional Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *Katnal2* gene. The schematic diagram is as follows:



Technical routes

- The *Katnal2* gene has 11 transcripts. According to the structure of *Katnal2* gene, exon2-exon12 of *Katnal2-201* (ENSMUST00000026486.12) transcript is recommended as the knockout region. The region contains 1052bp coding sequence. Knock out the region will result in disruption of protein function.
- In this project we use CRISPR/Cas9 technology to modify *Katnal2* 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, Homozygous null mutations in this gene result in male sterility associated with defects in several aspects of spermatogenesis, including abnormalities in the initiation of sperm tail growth from the basal body, sperm head shaping, manchette movement and dissolution, acrosome attachment to the nucleus, and sperm release via spermiation.
- The *Katnal2* gene is located on the Chr18. 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)

Katnal2 katanin p60 subunit A-like 2 [*Mus musculus* (house mouse)]

Gene ID: 71206, updated on 21-Aug-2019

Summary

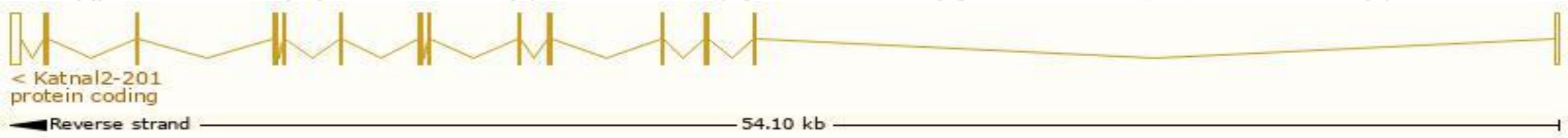
Official Symbol	Katnal2 provided by MGI
Official Full Name	katanin p60 subunit A-like 2 provided by MGI
Primary source	MGI:MGI:1924234
See related	Ensembl:ENSMUSG000000025420
Gene type	protein coding
RefSeq status	VALIDATED
Organism	Mus musculus
Lineage	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Myomorpha; Muroidea; Muridae; Murinae; Mus; Mus
Also known as	3110023G01Rik; 4933439B08Rik
Expression	Biased expression in testis adult (RPKM 8.9), CNS E11.5 (RPKM 2.5) and 5 other tissues See more
Orthologs	human all

Transcript information (Ensembl)

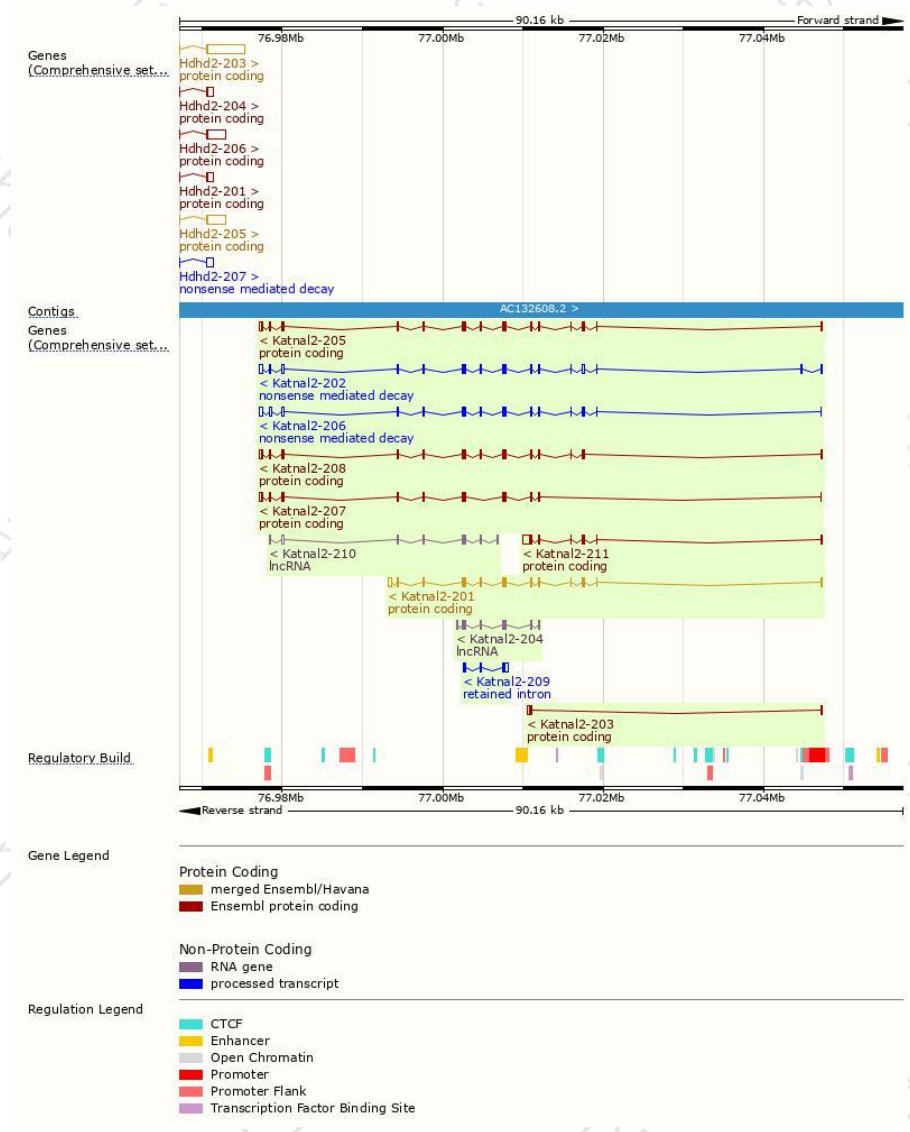
The gene has 11 transcripts,all transcripts are shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Katnal2-201	ENSMUST00000026486.12	1674	409aa	Protein coding	CCDS37865	Q9D3R6	TSL:1 GENCODE basic
Katnal2-205	ENSMUST00000126153.7	1942	539aa	Protein coding	-	Q9D3R6	TSL:1 GENCODE basic APPRIS P1
Katnal2-208	ENSMUST00000137498.7	1824	495aa	Protein coding	-	D3Z4J2	TSL:5 GENCODE basic
Katnal2-211	ENSMUST00000154665.1	1515	217aa	Protein coding	-	Q9D3R6	TSL:1 GENCODE basic
Katnal2-207	ENSMUST00000137354.7	1482	277aa	Protein coding	-	D3Z0U5	TSL:5 GENCODE basic
Katnal2-203	ENSMUST00000123650.1	638	85aa	Protein coding	-	D3Z087	TSL:1 GENCODE basic
Katnal2-202	ENSMUST00000122984.7	2039	39aa	Nonsense mediated decay	-	D6RI39	TSL:5
Katnal2-206	ENSMUST00000135029.7	2003	372aa	Nonsense mediated decay	-	D6RGM7	TSL:2
Katnal2-209	ENSMUST00000138336.1	668	No protein	Retained intron	-	-	TSL:2
Katnal2-210	ENSMUST00000154053.7	792	No protein	lncRNA	-	-	TSL:3
Katnal2-204	ENSMUST00000125744.7	768	No protein	lncRNA	-	-	TSL:5

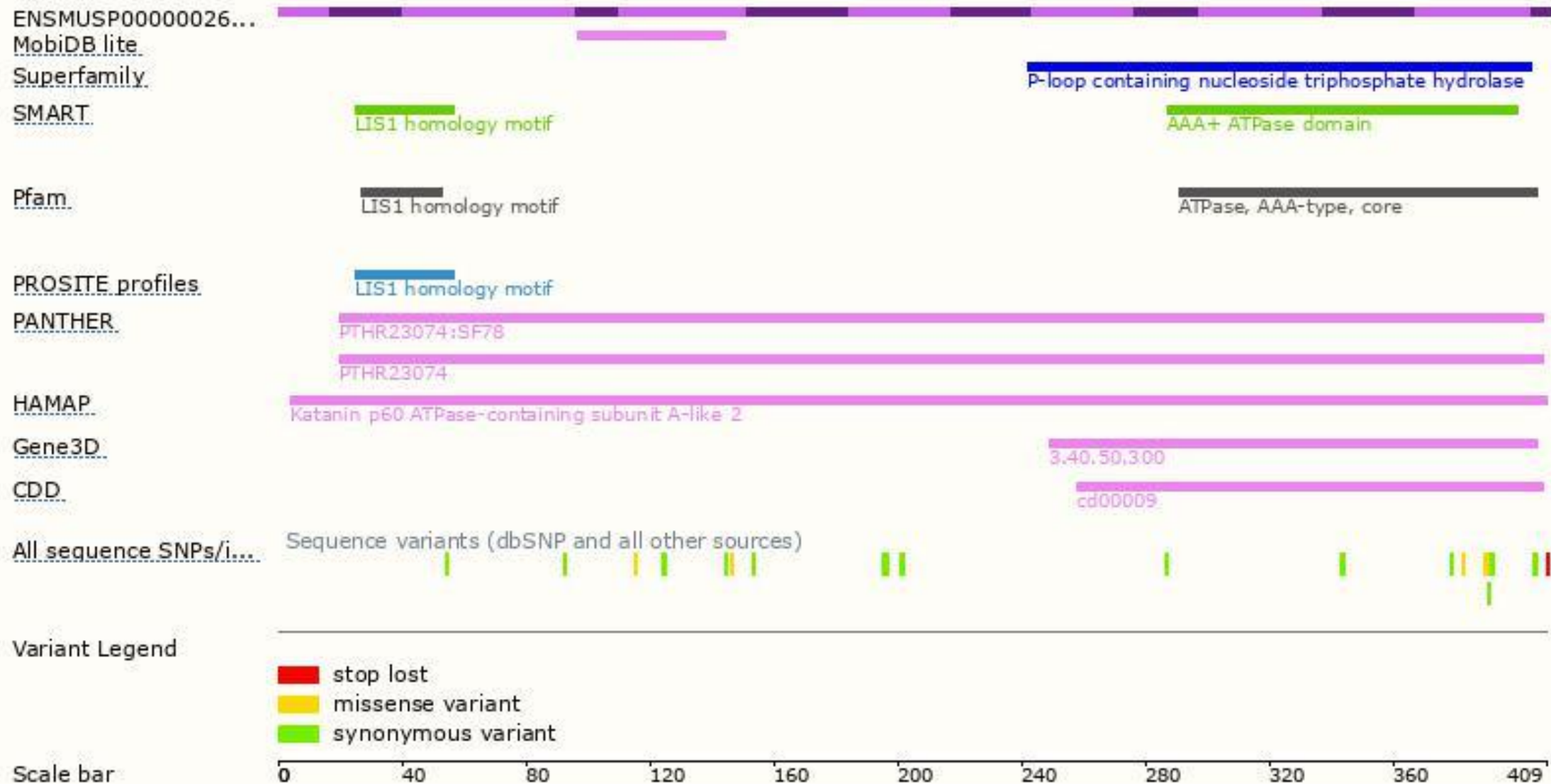
The strategy is based on the design of *Katnal2-201* transcript,The transcription is shown below



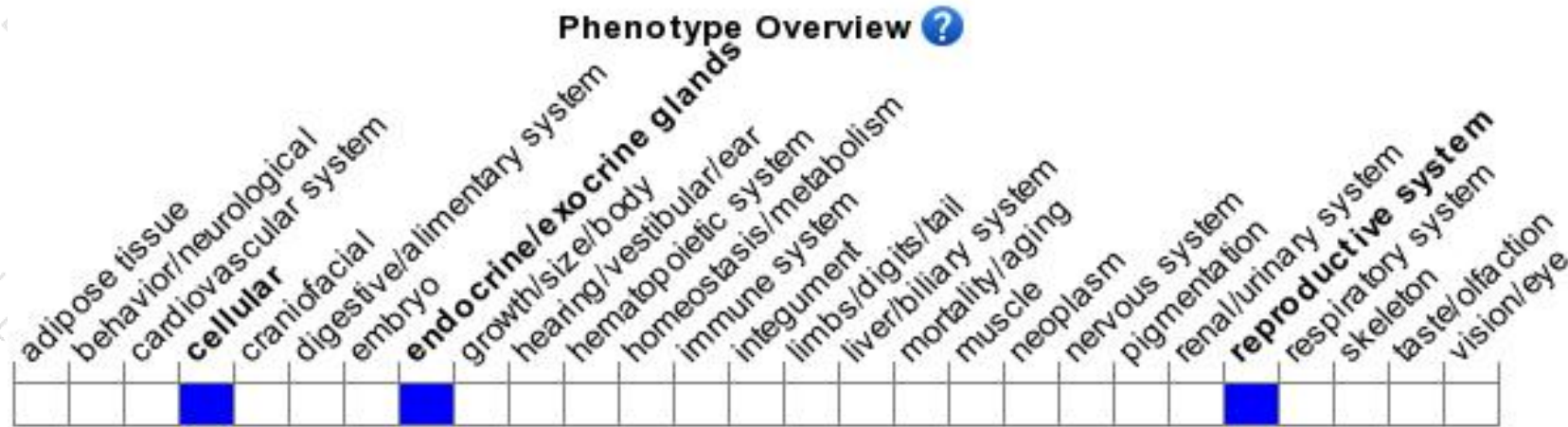
Genomic location distribution



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

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