

Recql Cas9-CKO Strategy

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Project Overview

Project Name

Recql

Project type

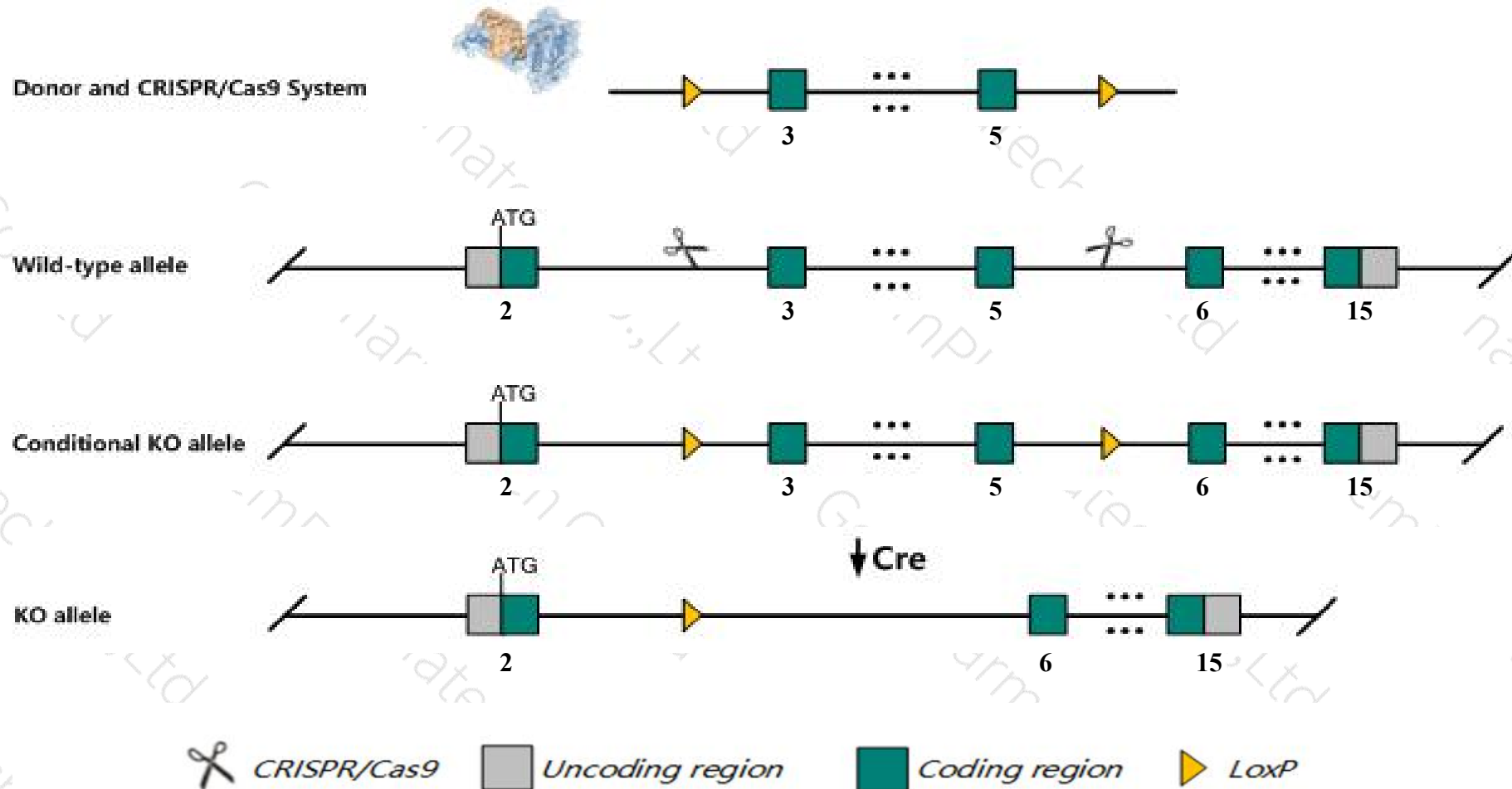
Cas9-CKO

Strain background

C57BL/6JGpt

Conditional Knockout strategy

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



- The *Recql* gene has 12 transcripts. According to the structure of *Recql* gene, exon3-exon5 of *Recql*-203 (ENSMUST00000111803.8) transcript is recommended as the knockout region. The region contains 485bp coding sequence. Knock out the region will result in disruption of protein function.
- In this project we use CRISPR/Cas9 technology to modify *Recql* 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 mutation of this gene results in chromosomal instability, with embryonic fibroblasts exhibiting aneuploidy, spontaneous chromosomal breakage, frequent translocation events, increased sensitivity to ionizing radiation, and increased frequency of sister chromatid exchange.
- The effect on transcript *Recql-204&205&206&208&212* is unknown.
- Transcript *Recql-207&209&210&211* may not be affected.
- The floxed region is near to the N-terminal of *Golt1b* gene, this strategy may influence the regulatory function of the N-terminal of *Golt1b* gene.
- The *Recql* gene is located on the Chr6. 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)

Recql RecQ protein-like [*Mus musculus* (house mouse)]

Gene ID: 19691, updated on 27-Feb-2020

Summary

Official Symbol Recql provided by [MGI](#)
Official Full Name RecQ protein-like provided by [MGI](#)
Primary source [MGI:MGI:103021](#)
See related [Ensembl:ENSMUSG00000030243](#)
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 RecQ1
Expression Ubiquitous expression in CNS E11.5 (RPKM 4.8), CNS E14 (RPKM 3.9) and 28 other tissues [See more](#)
Orthologs [human](#) [all](#)

Genomic context

Location: 6 G2; 6 73.91 cM

See Recql in [Genome Data Viewer](#)

Exon count: 18

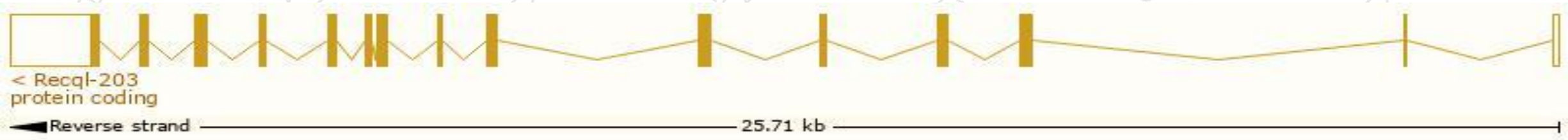
Annotation release	Status	Assembly	Chr	Location
108	current	GRCm38.p6 (GCF_000001635.26)	6	NC_000072.6 (142350342..142387100, complement)
Build 37.2	previous assembly	MGSCv37 (GCF_000001635.18)	6	NC_000072.5 (142310420..142335607, complement)

Transcript information (Ensembl)

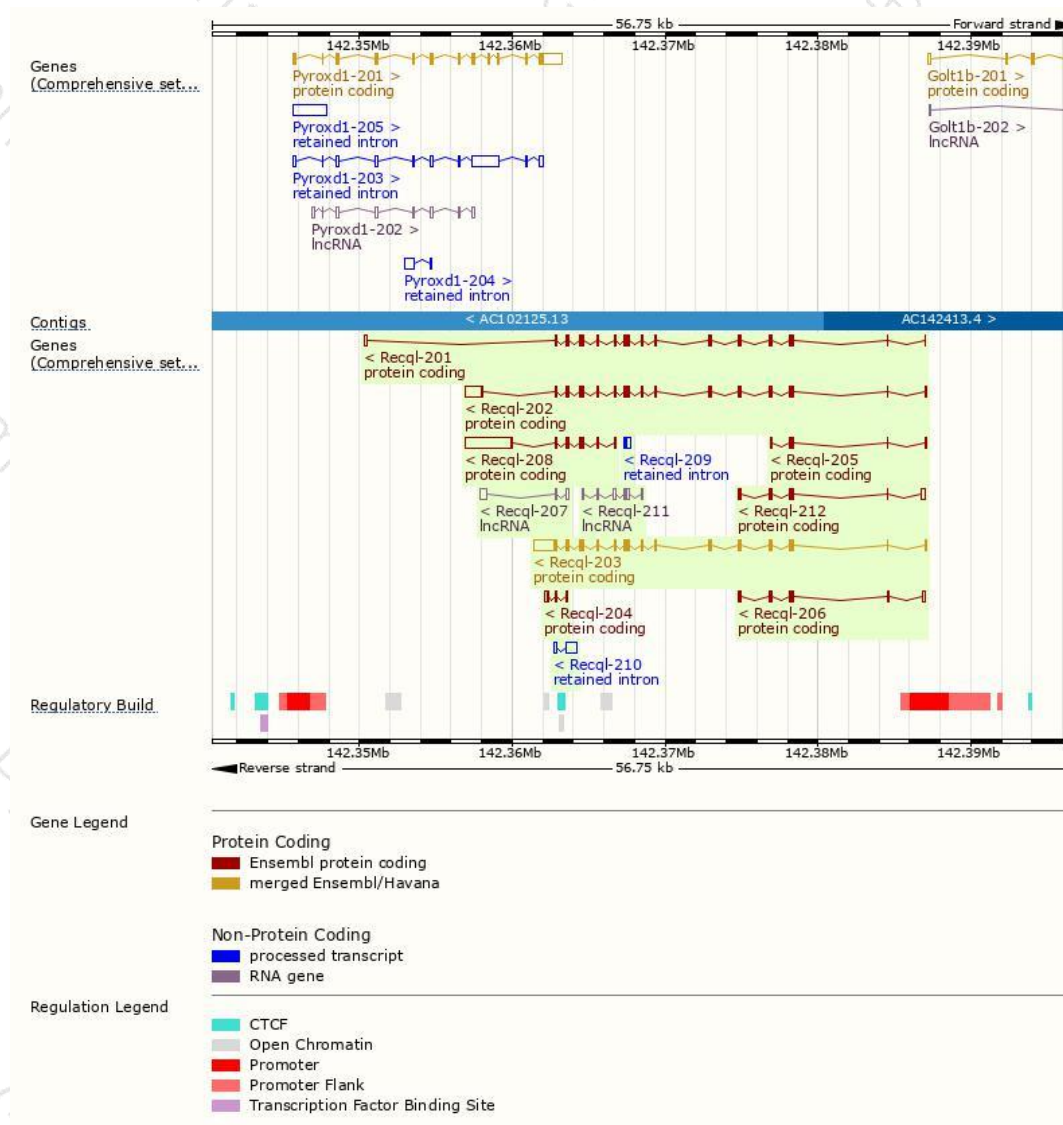
The gene has 12 transcripts,all transcripts are shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Recql-203	ENSMUST00000111803.8	3389	648aa	Protein coding	CCDS39695	Q9Z129	TSL:1 GENCODE basic APPRIS P3
Recql-202	ENSMUST00000100832.9	3054	634aa	Protein coding	CCDS57466	E9Q3N0	TSL:1 GENCODE basic APPRIS ALT2
Recql-201	ENSMUST00000032370.12	2112	631aa	Protein coding	CCDS57465	Q3UUK0 Q9Z129	TSL:1 GENCODE basic APPRIS ALT2
Recql-208	ENSMUST00000141504.7	3671	235aa	Protein coding	-	F6S4D9	CDS 5' incomplete TSL:1
Recql-212	ENSMUST00000203772.2	824	167aa	Protein coding	-	D3Z6T0	CDS 3' incomplete TSL:5
Recql-206	ENSMUST00000129694.7	710	167aa	Protein coding	-	D3Z6T0	CDS 3' incomplete TSL:5
Recql-205	ENSMUST00000128082.1	349	85aa	Protein coding	-	D3YZW9	CDS 3' incomplete TSL:2
Recql-204	ENSMUST00000123912.1	324	61aa	Protein coding	-	F7DB73	CDS 5' incomplete TSL:3
Recql-210	ENSMUST00000154870.1	783	No protein	Retained intron	-	-	TSL:2
Recql-209	ENSMUST00000143102.1	323	No protein	Retained intron	-	-	TSL:5
Recql-211	ENSMUST00000155149.1	667	No protein	lncRNA	-	-	TSL:5
Recql-207	ENSMUST00000138578.1	647	No protein	lncRNA	-	-	TSL:3

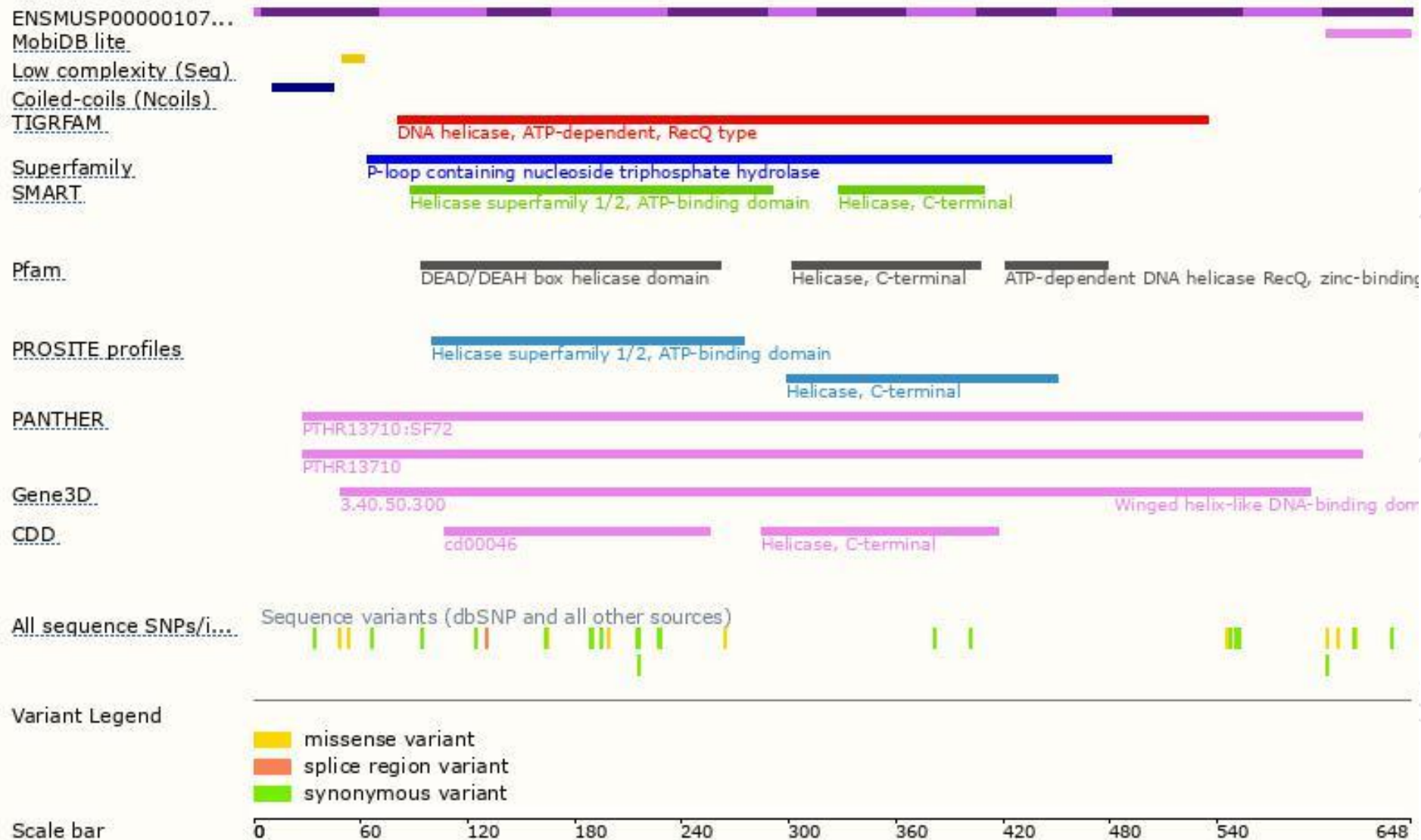
The strategy is based on the design of *Recql-203* transcript,The transcription is shown below



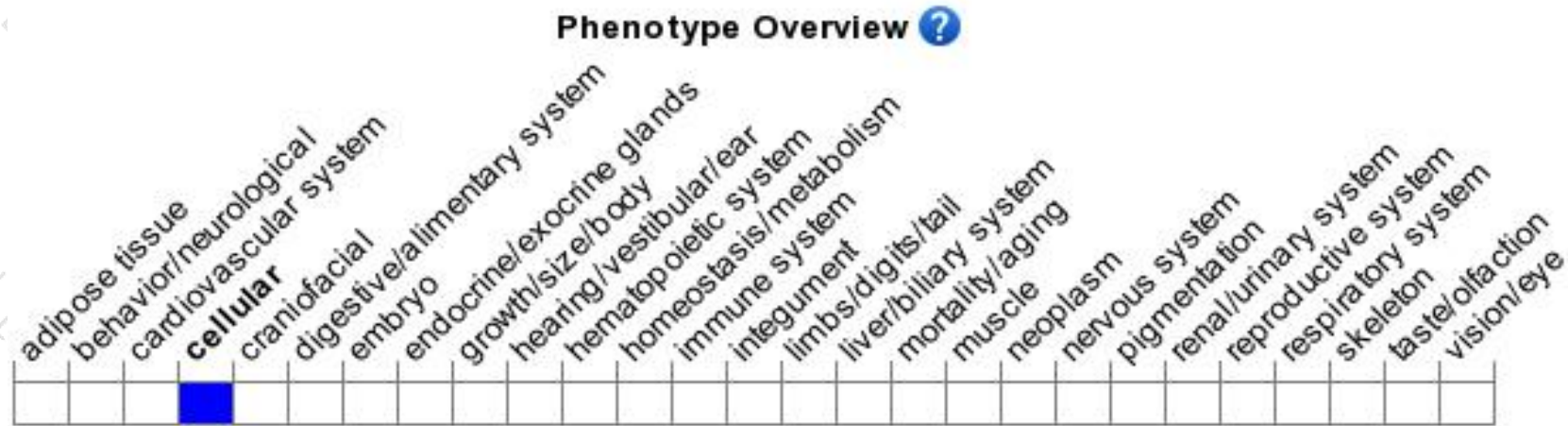
Genomic location distribution



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 chromosomal instability, with embryonic fibroblasts exhibiting aneuploidy, spontaneous chromosomal breakage, frequent translocation events, increased sensitivity to ionizing radiation, and increased frequency of sister chromatid exchange.

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

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