

***Lrrc7* Cas9-CKO Strategy**

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Date: 2020-02-27

Project Overview

Project Name

Lrrc7

Project type

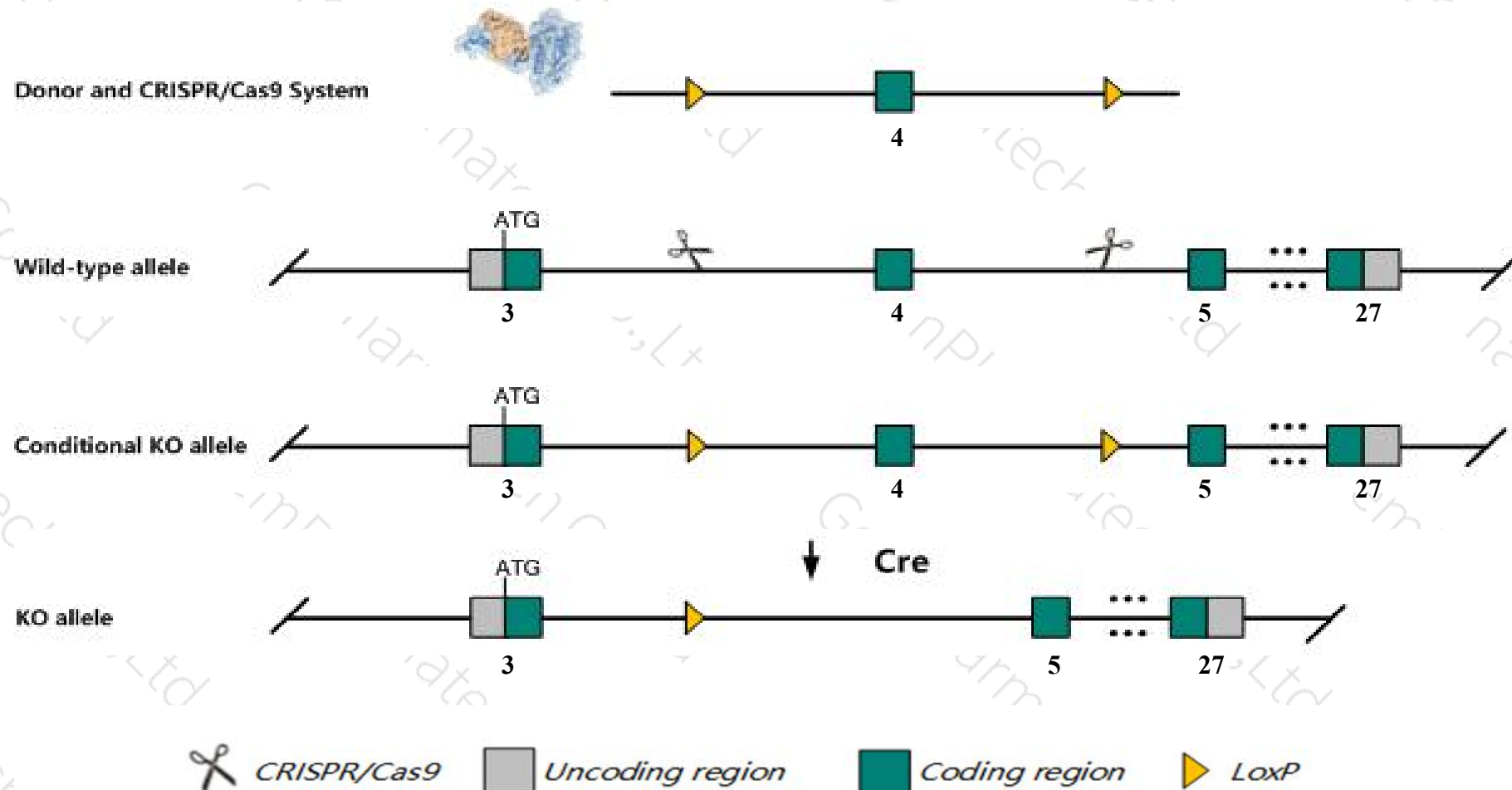
Cas9-CKO

Strain background

C57BL/6JGpt

Conditional Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *Lrrc7* gene. The schematic diagram is as follows:



Technical routes

- The *Lrrc7* gene has 7 transcripts. According to the structure of *Lrrc7* gene, exon4 of *Lrrc7-205* (ENSMUST00000200137.4) transcript is recommended as the knockout region. The region contains 203bp coding sequence. Knock out the region will result in disruption of protein function.
- In this project we use CRISPR/Cas9 technology to modify *Lrrc7* 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 limb grasping, reduced long term depression, increased anxiety, increased aggression towards other mice, impaired spatial memory, decreased prepulse inhibition, decreased nesting building behavior, and abnormal dendritic spines.
- The effect on transcript *Lrrc7*-206 is unknown.
- The *Lrrc7* gene is located on the Chr3. 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)

Lrrc7 leucine rich repeat containing 7 [*Mus musculus* (house mouse)]

Gene ID: 242274, updated on 10-Oct-2019

Summary

- Official Symbol** Lrrc7 provided by [MGI](#)
- Official Full Name** leucine rich repeat containing 7 provided by [MGI](#)
- Primary source** [MGI:MGI:2676665](#)
- See related** [Ensembl:ENSMUSG00000028176](#)
- 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** densin; AK122498; mKIAA1365
- Expression** Biased expression in frontal lobe adult (RPKM 5.5), cortex adult (RPKM 5.0) and 5 other tissues [See more](#)
- Orthologs** [human](#) [all](#)

Genomic context

Location: 3; 3 H4

See Lrrc7 in [Genome Data Viewer](#)

Exon count: 29

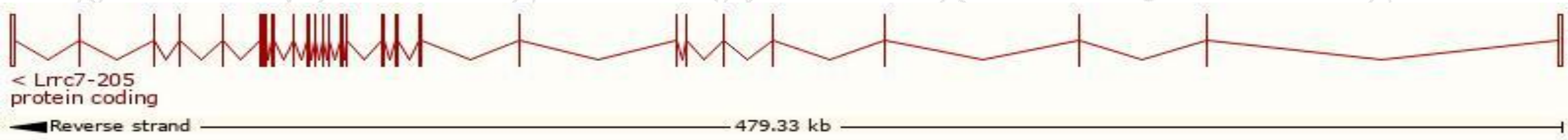
Annotation release	Status	Assembly	Chr	Location
108	current	GRCm38.p6 (GCF_000001635.26)	3	NC_000069.6 (158067186..158561983, complement)
Build 37.2	previous assembly	MGSCv37 (GCF_000001635.18)	3	NC_000069.5 (157747403..158225185, complement)

Transcript information (Ensembl)

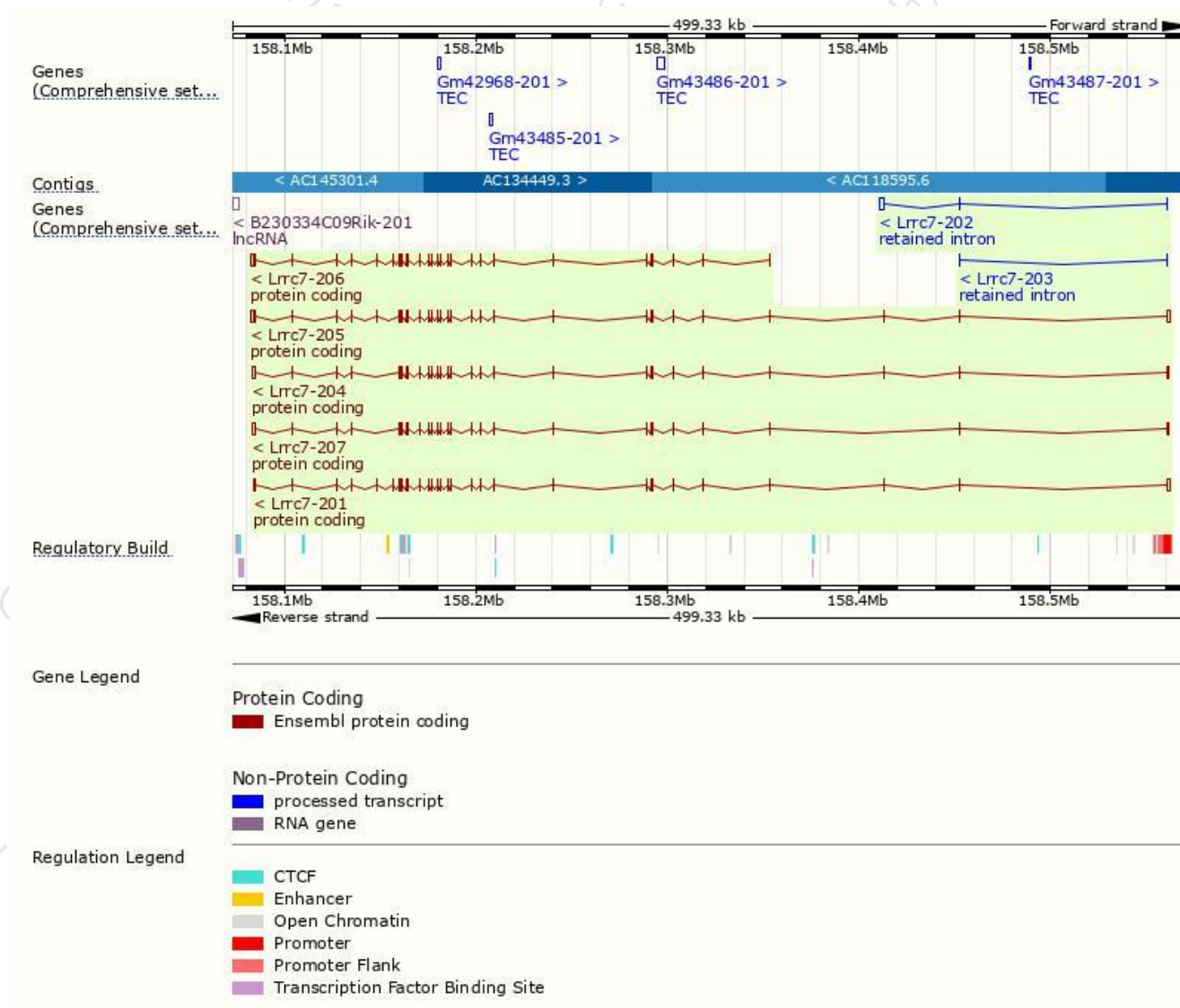
The gene has 7 transcripts,all transcripts are shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Lrrc7-205	ENSMUST00000200137.4	7321	1495aa	Protein coding	CCDS80073	A0A0G2JDT9	TSL:1 GENCODE basic APPRIS P2
Lrrc7-204	ENSMUST00000199890.4	6326	1398aa	Protein coding	CCDS80072	B9EHV0	TSL:1 GENCODE basic
Lrrc7-207	ENSMUST00000238317.1	6250	1431aa	Protein coding	-	-	GENCODE basic
Lrrc7-206	ENSMUST00000200196.4	6142	1531aa	Protein coding	-	A0A0G2JFZ5	CDS 5' incomplete TSL:5
Lrrc7-201	ENSMUST00000106044.5	5918	1542aa	Protein coding	-	E9Q6L9	TSL:5 GENCODE basic APPRIS ALT2
Lrrc7-202	ENSMUST00000197866.1	2405	No protein	Retained intron	-	-	TSL:1
Lrrc7-203	ENSMUST00000198284.1	688	No protein	Retained intron	-	-	TSL:2

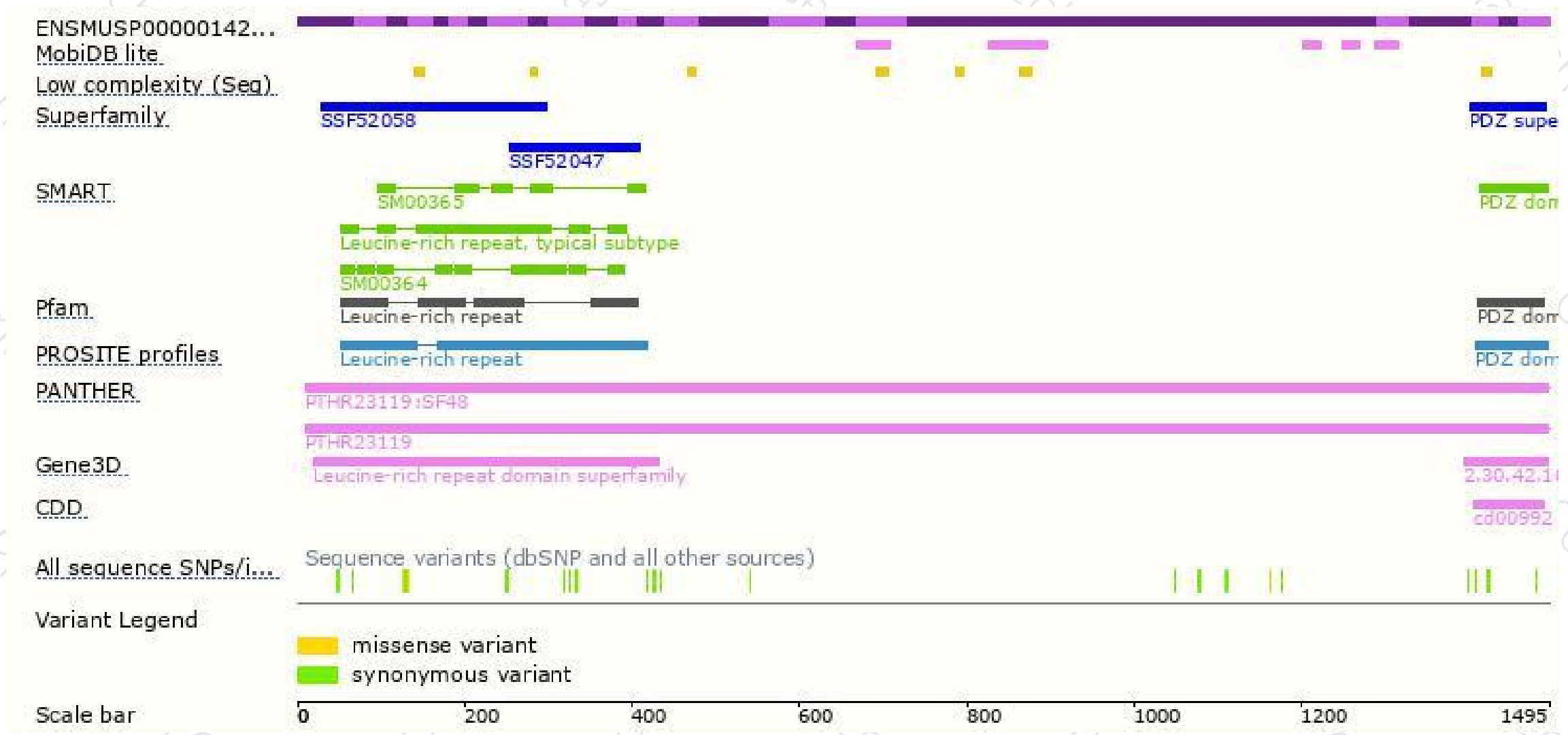
The strategy is based on the design of *Lrrc7-205* transcript,The transcription is shown below



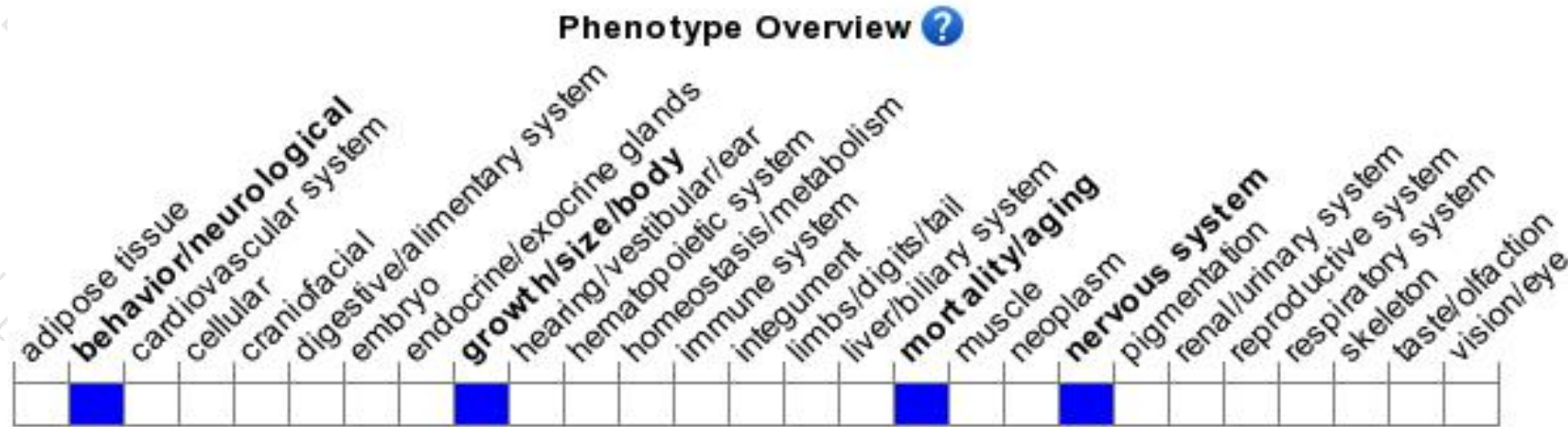
Genomic location distribution



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 limb grasping, reduced long term depression, increased anxiety, increased aggression towards other mice, impaired spatial memory, decreased prepulse inhibition, decreased nesting building behavior, and abnormal dendritic spines.

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

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