

Cnot6l Cas9-CKO Strategy

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Project Overview

Project Name

Cnot6l

Project type

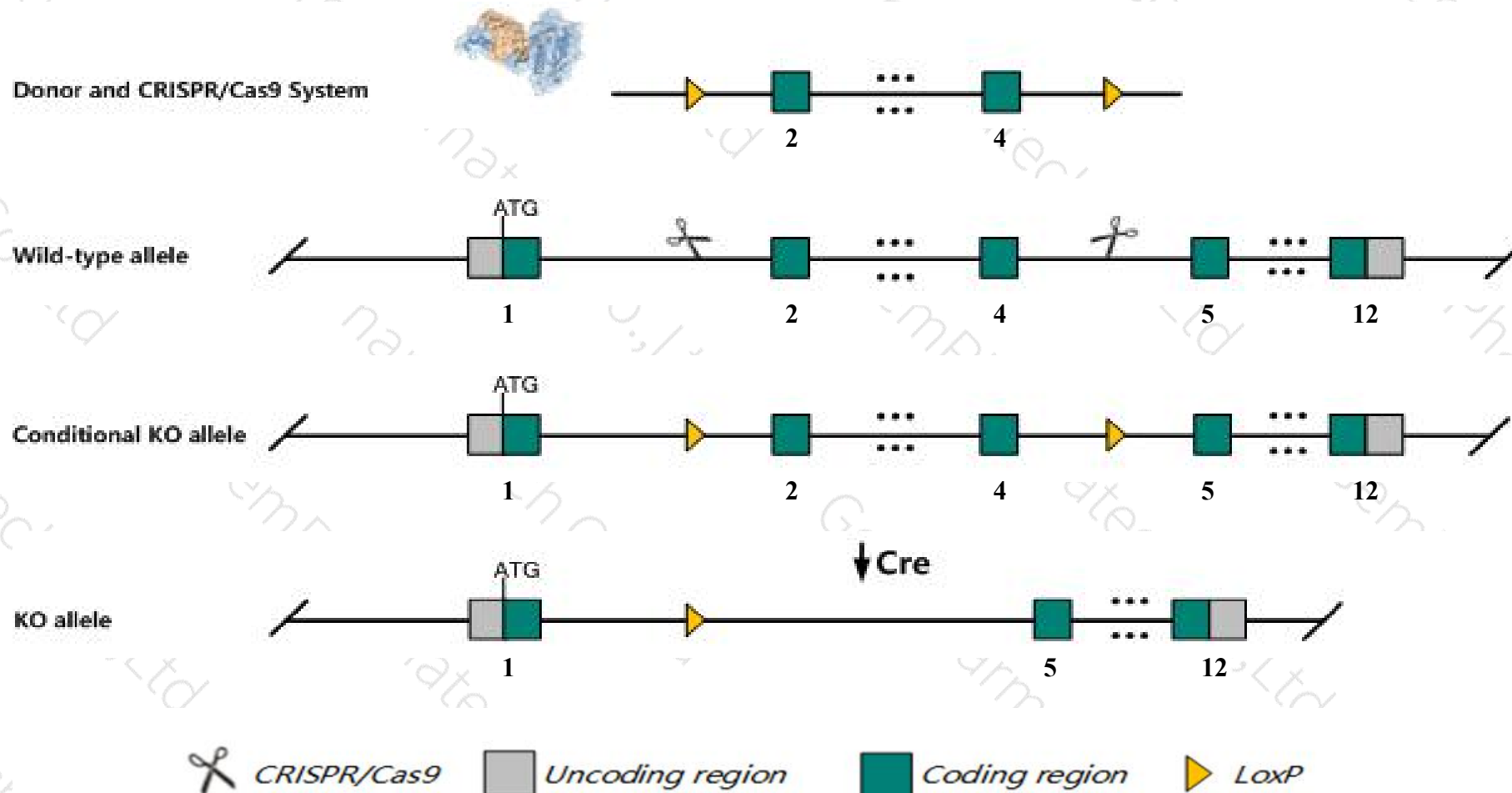
Cas9-CKO

Strain background

C57BL/6JGpt

Conditional Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *Cnot6l* gene. The schematic diagram is as follows:



- The *Cnot6l* gene has 10 transcripts. According to the structure of *Cnot6l* gene, exon2-exon4 of *Cnot6l*-202 (ENSMUST00000113005.8) transcript is recommended as the knockout region. The region contains 395bp coding sequence. Knock out the region will result in disruption of protein function.
- In this project we use CRISPR/Cas9 technology to modify *Cnot6l* 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 protection from diet-induced obesity and metabolic disruptions.
- The *Cnot6l* gene is located on the Chr5. 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)

Cnot6l CCR4-NOT transcription complex, subunit 6-like [Mus musculus (house mouse)]

Gene ID: 231464, updated on 13-Mar-2020

Summary



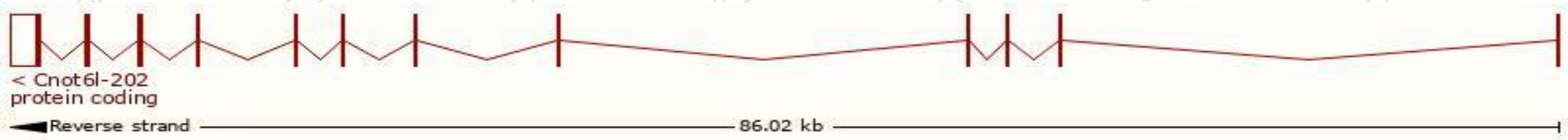
Official Symbol	Cnot6l provided by MGI
Official Full Name	CCR4-NOT transcription complex, subunit 6-like provided by MGI
Primary source	MGI:MGI:2443154
See related	Ensembl:ENSMUSG000000034724
Gene type	protein coding
RefSeq status	VALIDATED
Organism	Mus musculus
Lineage	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Myomorpha; Muroidea; Muridae; Murinae; Mus; Mus
Also known as	4932442K20Rik
Expression	Ubiquitous expression in limb E14.5 (RPKM 4.5), bladder adult (RPKM 3.7) and 27 other tissues See more
Orthologs	human all

Transcript information (Ensembl)

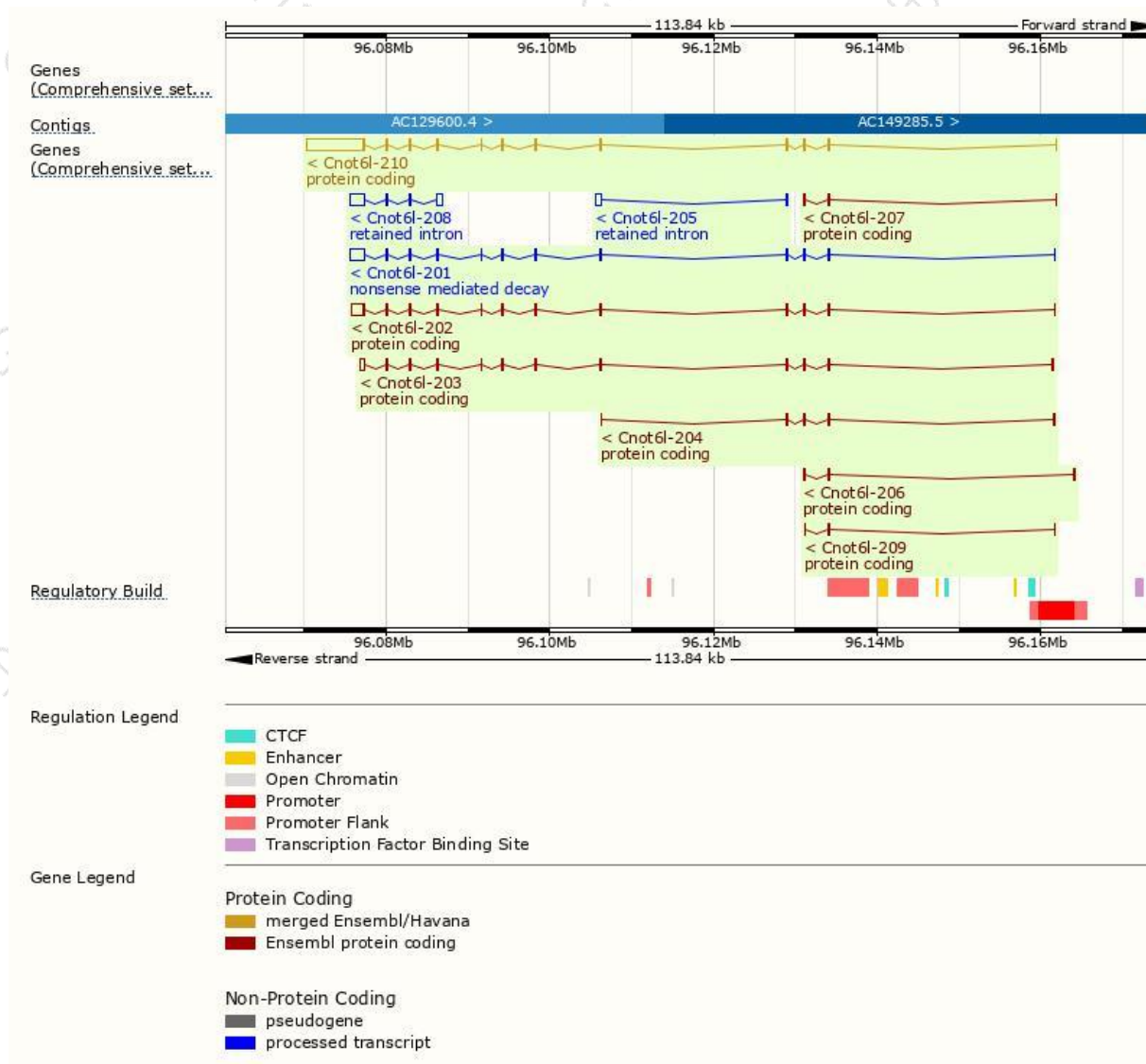
The gene has 10 transcripts,all transcripts are shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Cnot6l-210	ENSMUST00000155901.7	8564	550aa	Protein coding	CCDS19448	Q8VEG6	TSL:1 GENCODE basic APPRIS P3
Cnot6l-202	ENSMUST00000113005.8	3170	555aa	Protein coding	CCDS51566	Q8VEG6	TSL:5 GENCODE basic APPRIS ALT1
Cnot6l-203	ENSMUST00000122003.7	2089	435aa	Protein coding	-	Q8VEG6	TSL:1 GENCODE basic
Cnot6l-204	ENSMUST00000129646.7	526	130aa	Protein coding	-	D3YXZ0	CDS 3' incomplete TSL:5
Cnot6l-206	ENSMUST00000137207.1	421	87aa	Protein coding	-	D3Z2G5	CDS 3' incomplete TSL:3
Cnot6l-207	ENSMUST00000141383.7	329	99aa	Protein coding	-	D3YVH6	CDS 3' incomplete TSL:5
Cnot6l-209	ENSMUST00000154500.1	232	55aa	Protein coding	-	D3Z5R3	CDS 3' incomplete TSL:5
Cnot6l-201	ENSMUST00000036646.13	3314	46aa	Nonsense mediated decay	-	F8WJG1	TSL:1
Cnot6l-208	ENSMUST00000152490.7	3040	No protein	Retained intron	-	-	TSL:1
Cnot6l-205	ENSMUST00000137066.2	782	No protein	Retained intron	-	-	TSL:5

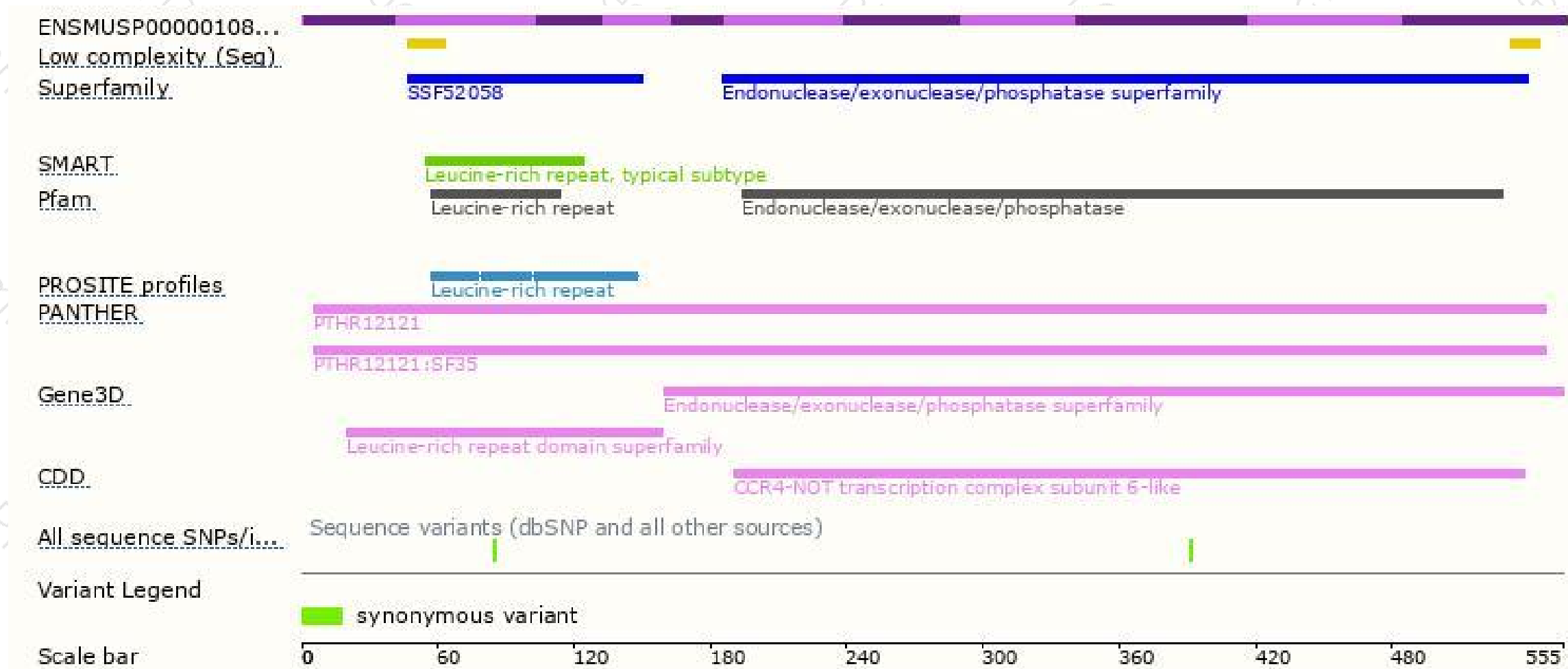
The strategy is based on the design of *Cnot6l-202* transcript,the transcription is shown below:



Genomic location distribution

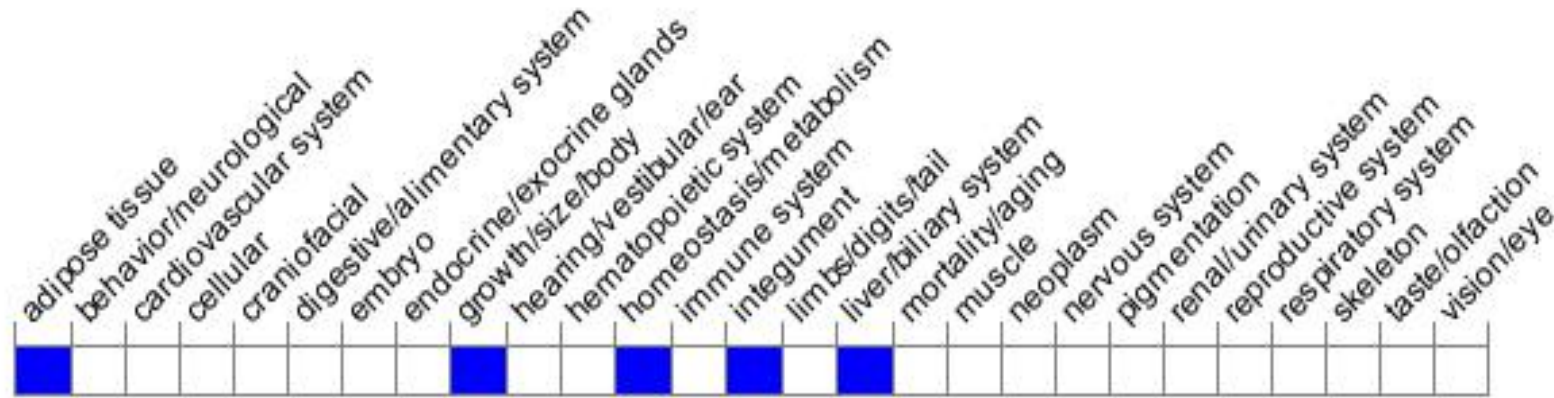


Protein domain



Mouse phenotype description(MGI)

Phenotype Overview



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 protection from diet-induced obesity and metabolic disruptions.

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

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