

Myt1l Cas9-CKO Strategy

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Project Overview

Project Name

Myt1l

Project type

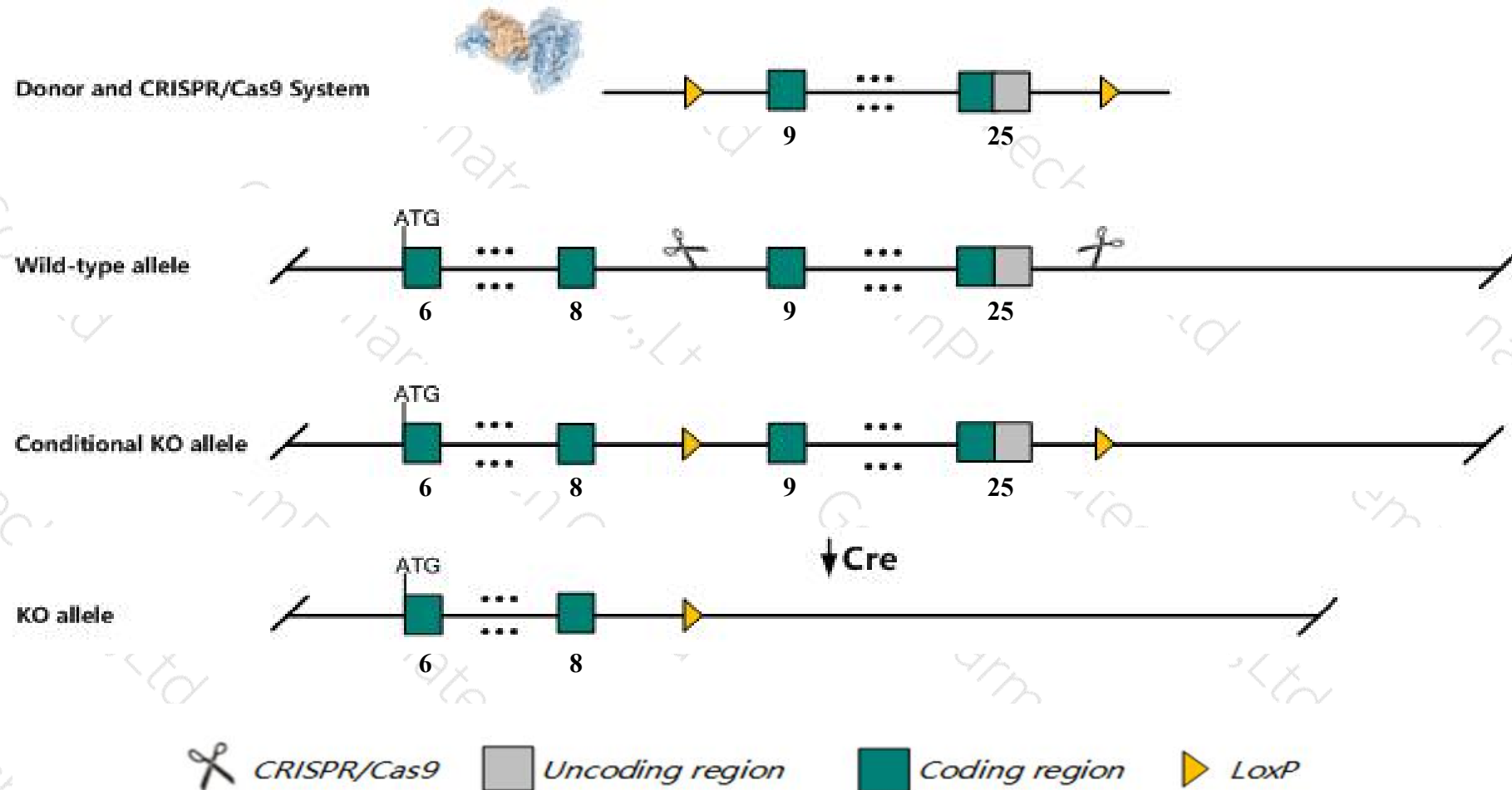
Cas9-CKO

Strain background

C57BL/6JGpt

Conditional Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *Myt1l* gene. The schematic diagram is as follows:



- The *Myt1l* gene has 11 transcripts. According to the structure of *Myt1l* gene, exon9-exon25 of *Myt1l*-202 (ENSMUST00000049784.16) transcript is recommended as the knockout region. The region contains most of the coding sequence. Knock out the region will result in disruption of protein function.
- In this project we use CRISPR/Cas9 technology to modify *Myt1l* 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.

Notice

- Transcript *Myt1l*-203&206&207&208&210 may not be affected.
- The *Myt1l* gene is located on the Chr12. 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)

Myt1l myelin transcription factor 1-like [*Mus musculus* (house mouse)]

Gene ID: 17933, updated on 24-Oct-2019

Summary

- Official Symbol** Myt1l provided by MGI
- Official Full Name** myelin transcription factor 1-like provided by MGI
- Primary source** MGI:MGI:1100511
- See related** Ensembl:ENSMUSG00000061911
- 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** Nzt1f1; Pmng1; Png-1; mKIAA1106; 2900046C06Rik; 2900093J19Rik; C630034G21Rik
- Expression** Biased expression in CNS E18 (RPKM 9.3), frontal lobe adult (RPKM 8.6) and 6 other tissues [See more](#)
- Orthologs** [human](#) [all](#)

Genomic context

Location: 12 A2; 12 11.86 cM

[See Myt1l in Genome Data Viewer](#)

Exon count: 29

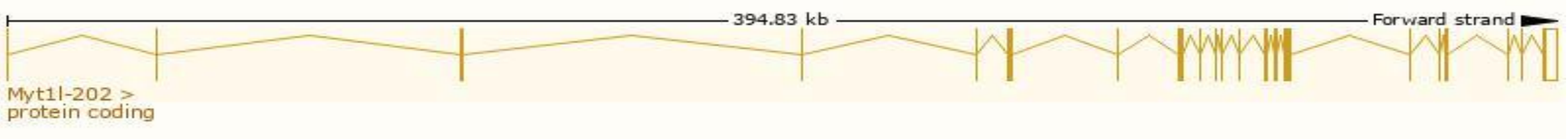
Annotation release	Status	Assembly	Chr	Location
108	current	GRCm38.p6 (GCF_000001635.26)	12	NC_000078.6 (29527590..29923216)
Build 37.2	previous assembly	MGSCv37 (GCF_000001635.18)	12	NC_000078.5 (30213249..30608074)

Transcript information (Ensembl)

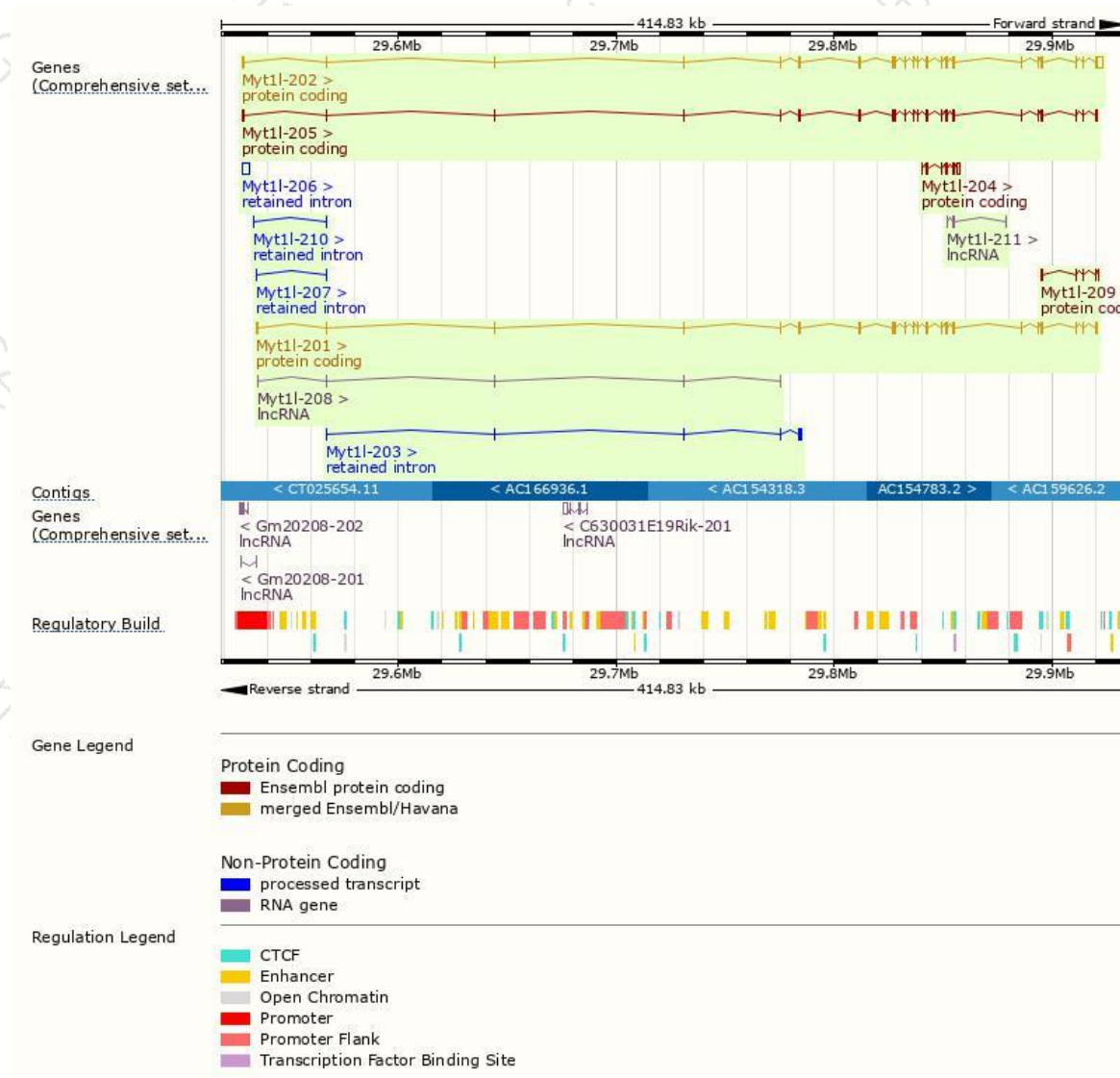
The gene has 11 transcripts,all transcripts are shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Myt1l-202	ENSMUST00000049784.16	7202	1187aa	Protein coding	CCDS49042	P97500	TSL:1 GENCODE basic APPRIS P4
Myt1l-201	ENSMUST00000021009.9	5027	1185aa	Protein coding	CCDS49041	P97500	TSL:1 GENCODE basic APPRIS ALT2
Myt1l-205	ENSMUST00000218583.1	4522	1185aa	Protein coding	CCDS49041	P97500	TSL:1 GENCODE basic APPRIS ALT2
Myt1l-204	ENSMUST00000218198.1	2735	328aa	Protein coding	-	P97500	TSL:1 GENCODE basic
Myt1l-209	ENSMUST00000219744.1	796	189aa	Protein coding	-	A0A1W2P887	CDS 5' incomplete TSL:3
Myt1l-206	ENSMUST00000219060.1	3179	No protein	Retained intron	-	-	TSL:NA
Myt1l-203	ENSMUST00000217961.1	1612	No protein	Retained intron	-	-	TSL:5
Myt1l-207	ENSMUST00000219231.1	476	No protein	Retained intron	-	-	TSL:3
Myt1l-210	ENSMUST00000219899.1	448	No protein	Retained intron	-	-	TSL:2
Myt1l-208	ENSMUST00000219463.1	632	No protein	lncRNA	-	-	TSL:3
Myt1l-211	ENSMUST00000220072.1	504	No protein	lncRNA	-	-	TSL:5

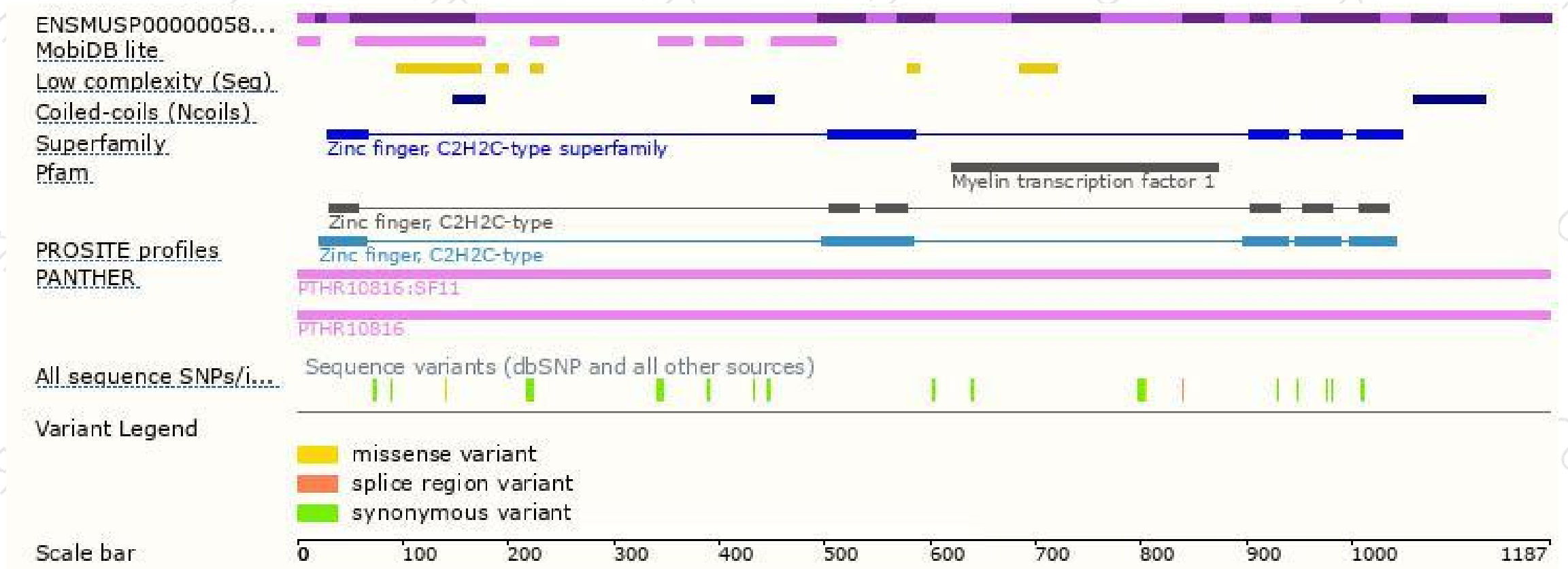
The strategy is based on the design of *Myt1l-202* transcript,The transcription is shown below



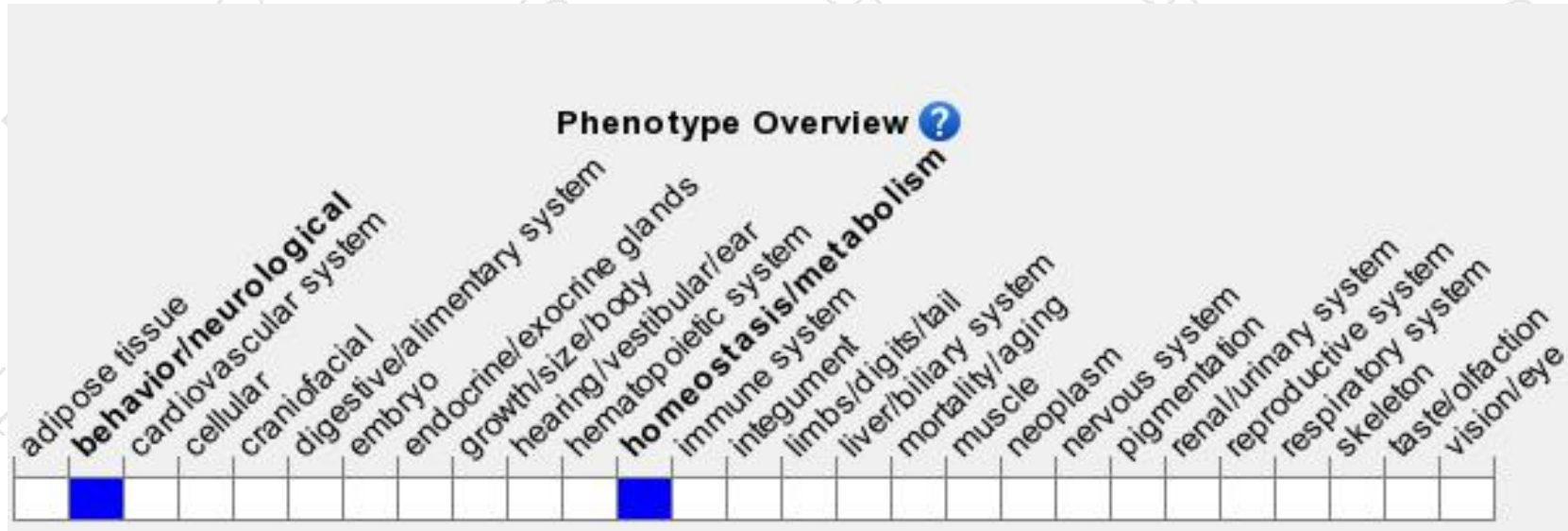
Genomic location distribution



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/>).

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

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