

Osbp18 Cas9-KO Strategy

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Date: 2020-02-17

Project Overview

Project Name

Osbpl8

Project type

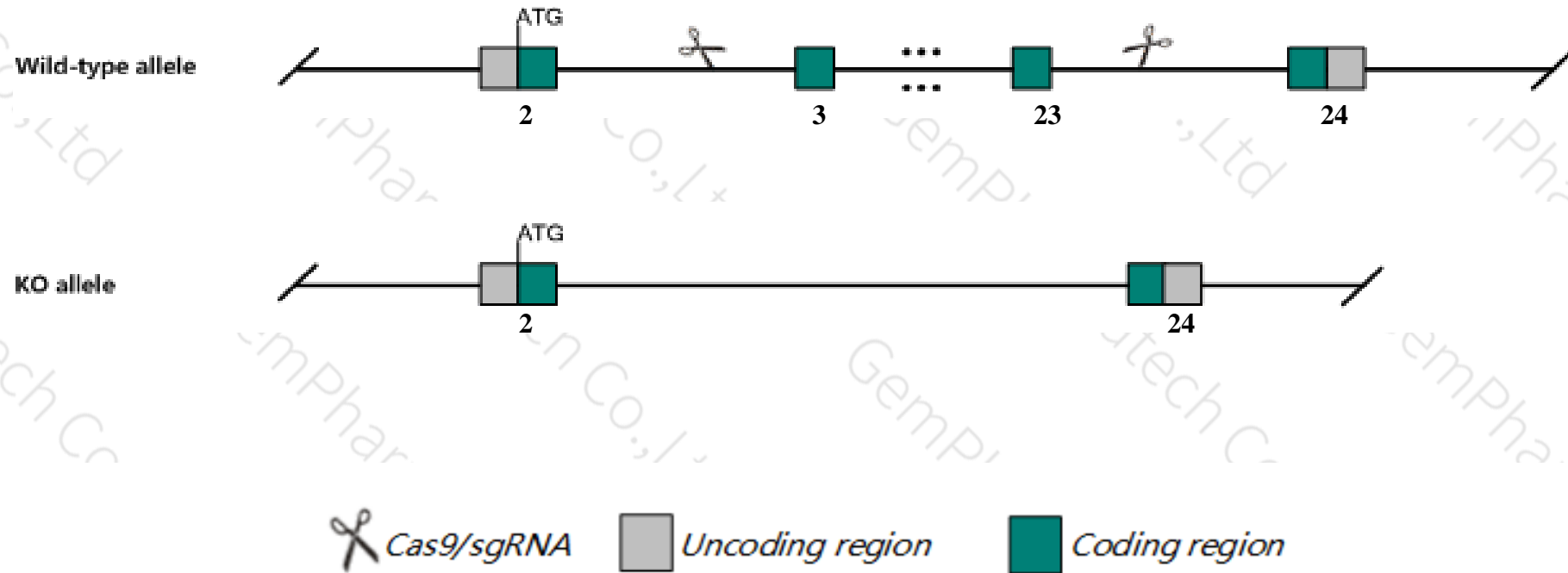
Cas9-KO

Strain background

C57BL/6JGpt

Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *Osbpl8* gene. The schematic diagram is as follows:



- The *Osbpl8* gene has 4 transcripts. According to the structure of *Osbpl8* gene, exon3-exon23 of *Osbpl8*-202 (ENSMUST00000105275.8) transcript is recommended as the knockout region. The region contains 2495bp coding sequence. Knock out the region will result in disruption of protein function.
- In this project we use CRISPR/Cas9 technology to modify *Osbpl8* gene. The brief process is as follows: sgRNA was transcribed in vitro. Cas9 and sgRNA 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.

- According to the existing MGI data, Mice homozygous for a gene trap allele exhibit elevated of HDL and gender-specific alterations in lipid metabolism.
- The knockout region is near to the N-terminal of *Bbs10* gene, this strategy may influence the regulatory function of the N-terminal of *Bbs10* gene.
- The *Osbp18* gene is located on the Chr10. 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 the gene knockout on gene transcription, RNA splicing and protein translation cannot be predicted at the existing technology level.

Gene information (NCBI)

Osbpl8 oxysterol binding protein-like 8 [*Mus musculus* (house mouse)]

Gene ID: 237542, updated on 10-Oct-2019

Summary

- Official Symbol** Osbp18 provided by [MGI](#)
- Official Full Name** oxysterol binding protein-like 8 provided by [MGI](#)
- Primary source** [MGI:MGI:2443807](#)
- See related** [Ensembl:ENSMUSG00000020189](#)
- Gene type** protein coding
- RefSeq status** REVIEWED
- Organism** [Mus musculus](#)
- Lineage** Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Myomorpha; Muroidea; Muridae; Murinae; Mus; Mus
- Also known as** ORP-8; AA536976; AA536995; C730029P18Rik; D330025H14Rik
- Summary** This gene encodes a member of the oxysterol-binding protein (Osbp) family, a group of intracellular lipid receptors. Like most members, the encoded protein contains an N-terminal pleckstrin homology domain and a highly conserved C-terminal Osbp-like sterol-binding domain. Two transcript variants encoding different isoforms have been found for this gene. [provided by RefSeq, Jul 2008]
- Expression** Ubiquitous expression in CNS E18 (RPKM 7.5), frontal lobe adult (RPKM 6.6) and 25 other tissues [See more](#)
- Orthologs** [human](#) [all](#)

Genomic context

Location: 10; 10 D1 See Osbp18 in [Genome Data Viewer](#)

Exon count: 26

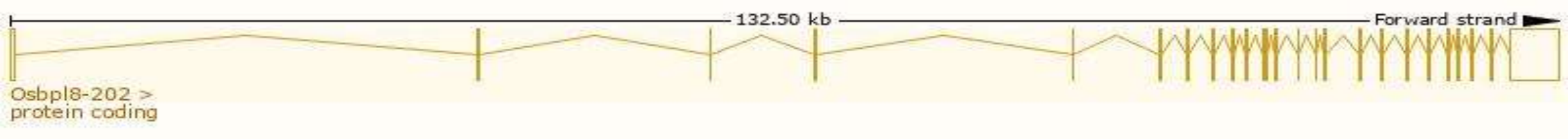
Annotation release	Status	Assembly	Chr	Location
108	current	GRCm38.p6 (GCF_000001635.26)	10	NC_000076.6 (111164742..111297249)
Build 37.2	previous assembly	MGSCv37 (GCF_000001635.18)	10	NC_000076.5 (110601858..110734303)

Transcript information (Ensembl)

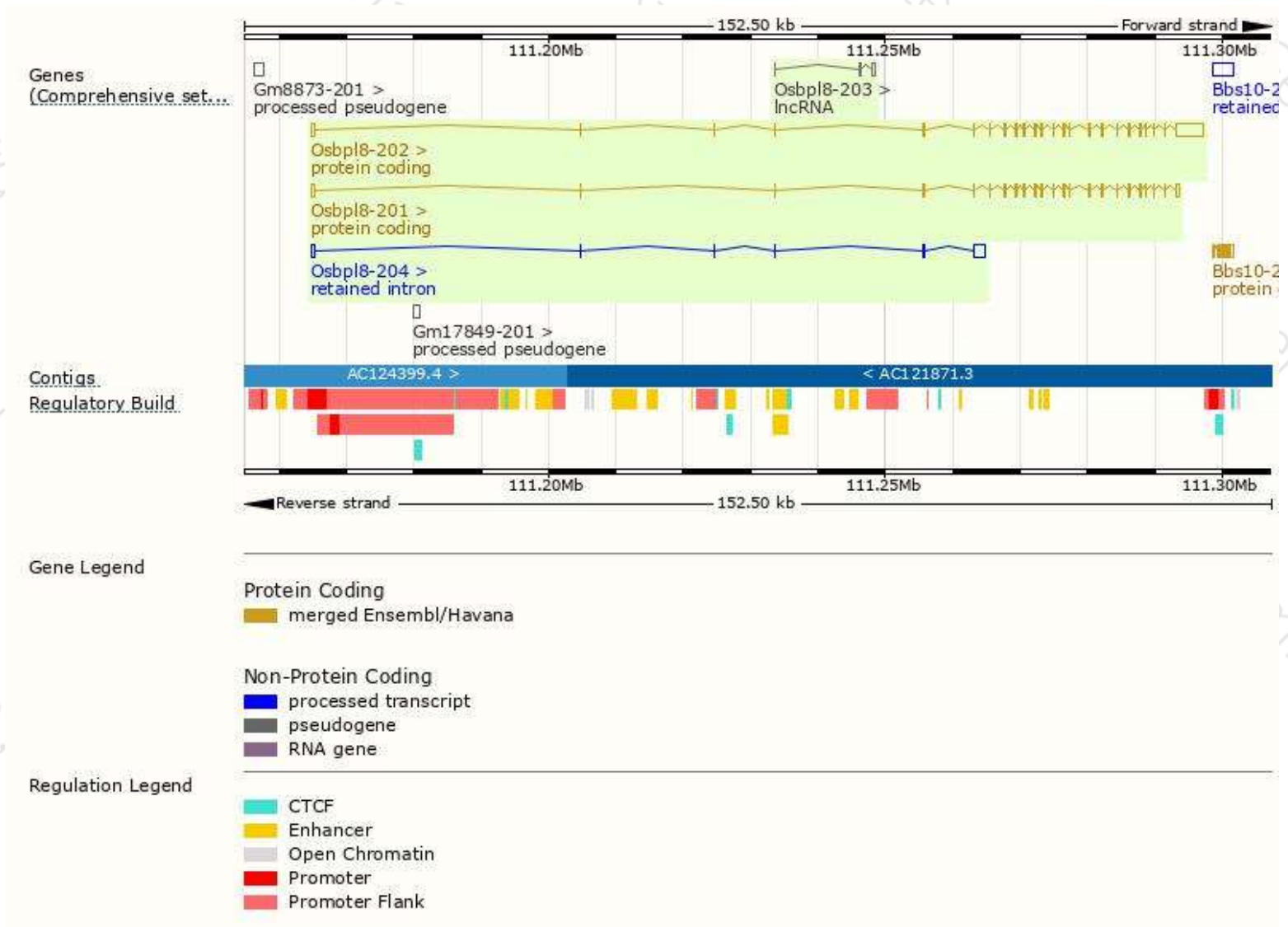
The gene has 4 transcripts,all transcripts are shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Osbpl8-202	ENSMUST00000105275.8	7204	889aa	Protein coding	CCDS36056	B9EJ86	TSL:1 GENCODE basic APPRIS ALT 1
Osbpl8-201	ENSMUST00000095310.2	3622	847aa	Protein coding	CCDS24166	A0A0R4J150	TSL:1 GENCODE basic APPRIS P3
Osbpl8-204	ENSMUST00000220139.1	2460	No protein	Retained intron	-	-	TSL:1
Osbpl8-203	ENSMUST00000217693.1	624	No protein	lncRNA	-	-	TSL:3

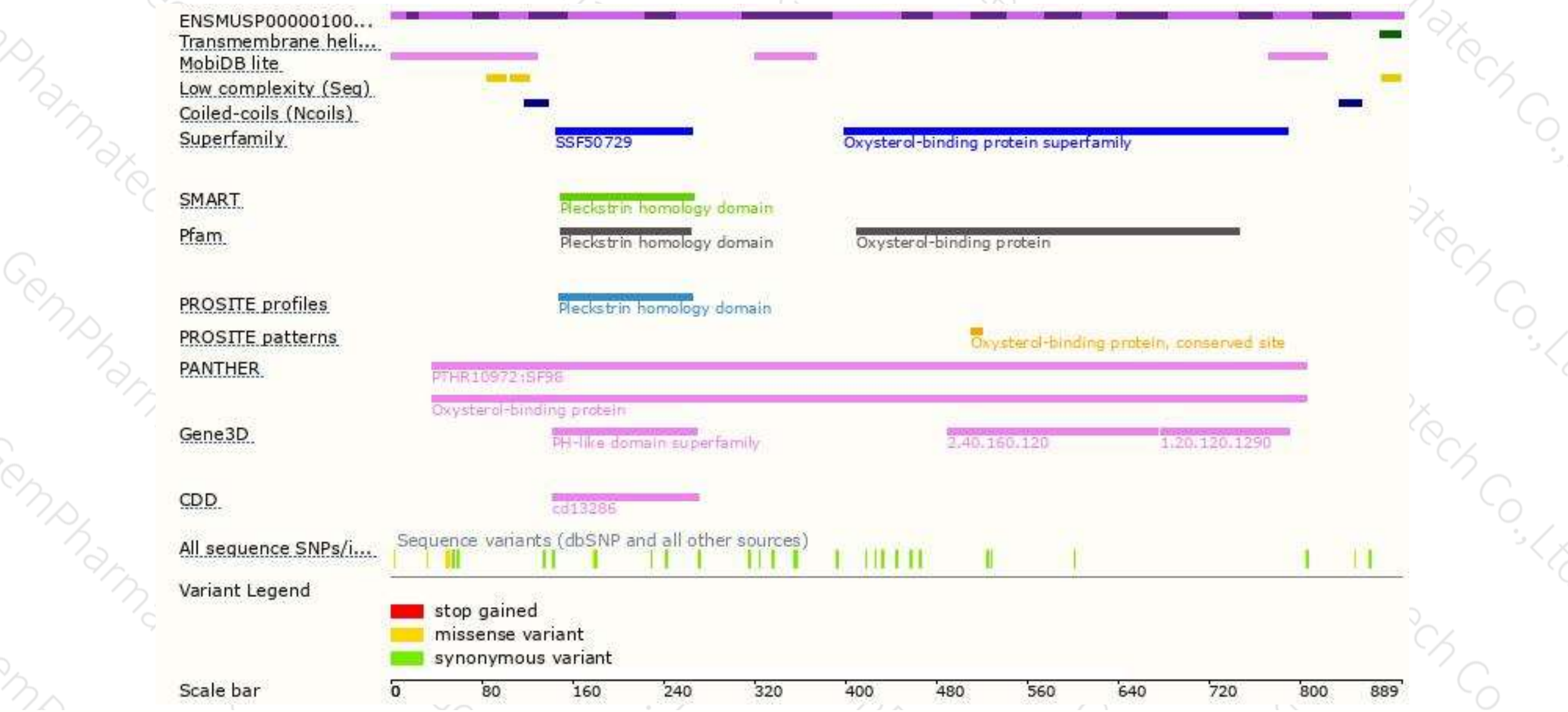
The strategy is based on the design of *Osbpl8-202* transcript,The transcription is shown below



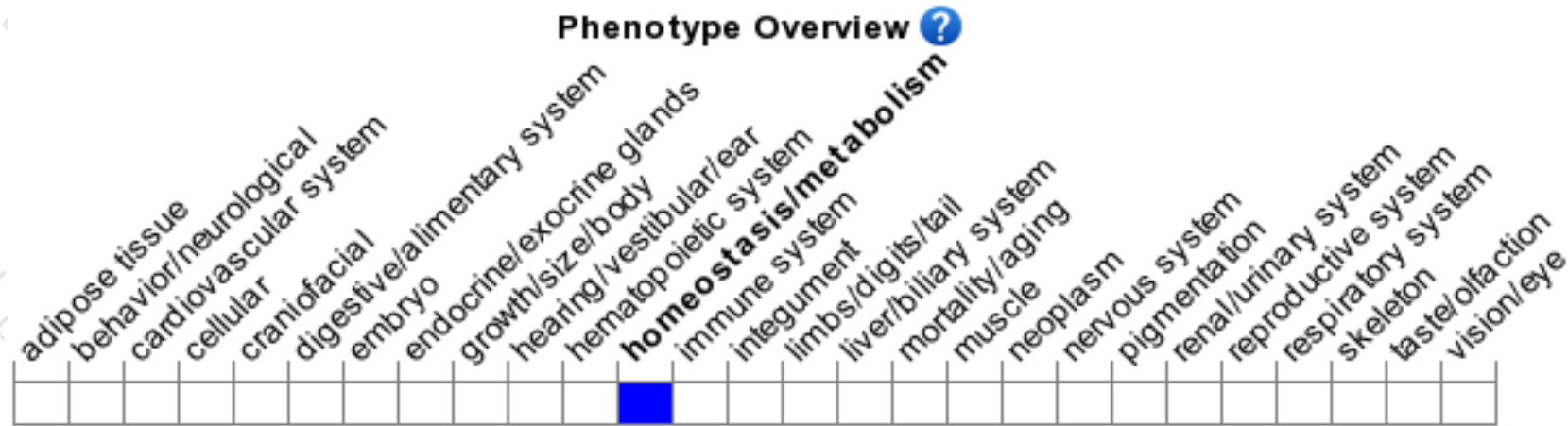
Genomic location distribution



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/>).

According to the existing MGI data, Mice homozygous for a gene trap allele exhibit elevated of HDL and gender-specific alterations in lipid metabolism.

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

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