

# ***Fa2h*** Cas9-KO Strategy

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**Reviewer:**

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# Project Overview

**Project Name**

***Fa2h***

**Project type**

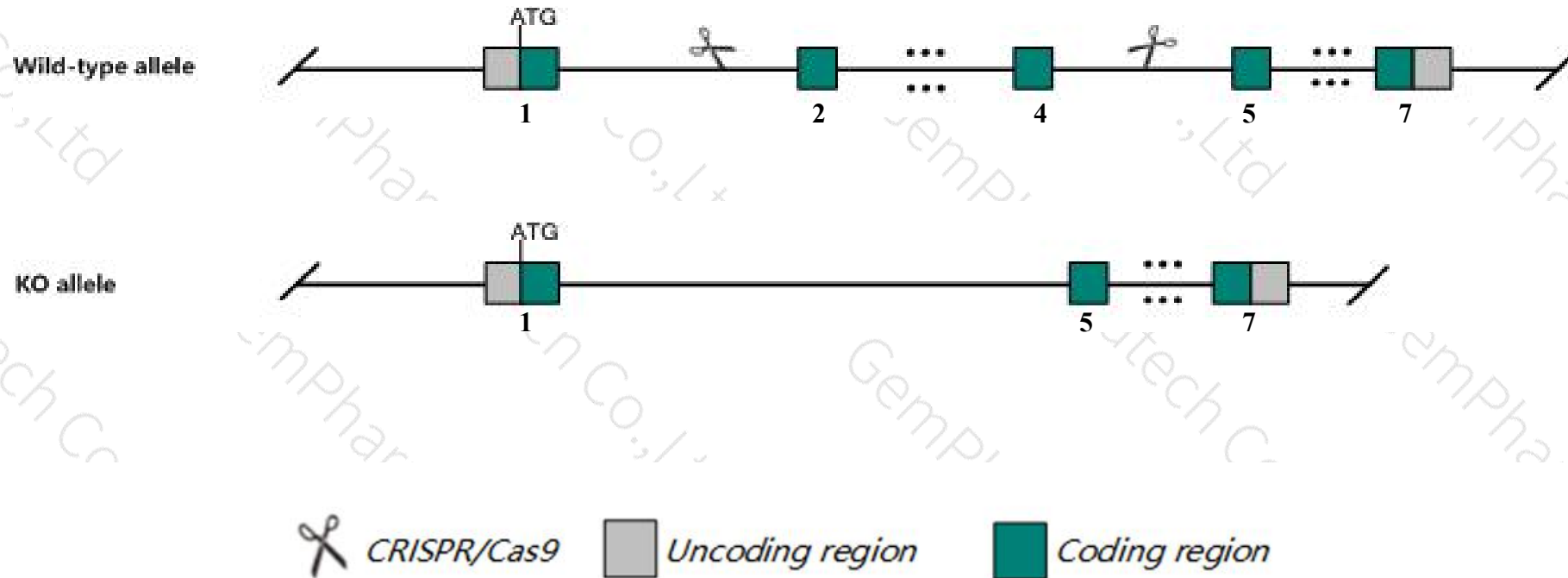
**Cas9-KO**

**Strain background**

**C57BL/6JGpt**

# Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *Fa2h* gene. The schematic diagram is as follows:



- The *Fa2h* gene has 4 transcripts. According to the structure of *Fa2h* gene, exon2-exon4 of *Fa2h-201* (ENSMUST00000038475.8) transcript is recommended as the knockout region. The region contains 343bp coding sequence. Knock out the region will result in disruption of protein function.
- In this project we use CRISPR/Cas9 technology to modify *Fa2h* gene. The brief process is as follows: CRISPR/Cas9 system v

- According to the existing MGI data, Homozygotes for a null allele show demyelination, axonal loss, and cerebellar dysfunction. Homozygotes for a different null allele show late onset axon and myelin sheath degeneration, delayed fur emergence, altered sebum composition, sebocyte hyperproliferation, and cyclic alopecia.
- The *Fa2h* gene is located on the Chr8. 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)

## Fa2h fatty acid 2-hydroxylase [Mus musculus (house mouse)]

Gene ID: 338521, updated on 19-Mar-2019

### Summary



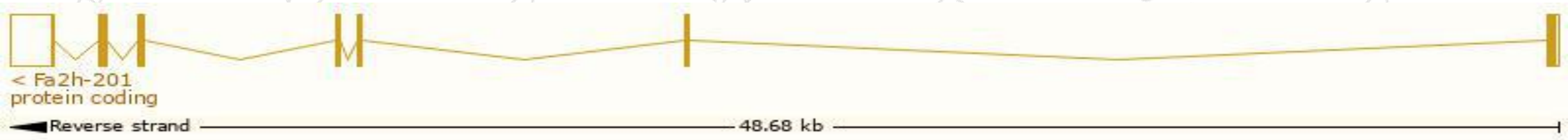
<b>Official Symbol</b>	Fa2h provided by <a href="#">MGI</a>
<b>Official Full Name</b>	fatty acid 2-hydroxylase provided by <a href="#">MGI</a>
<b>Primary source</b>	<a href="#">MGI:MGI:2443327</a>
<b>See related</b>	<a href="#">Ensembl:ENSMUSG00000033579</a>
<b>Gene type</b>	protein coding
<b>RefSeq status</b>	VALIDATED
<b>Organism</b>	<a href="#">Mus musculus</a>
<b>Lineage</b>	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Myomorpha; Muroidea; Muridae; Murinae; Mus; Mus
<b>Also known as</b>	FAAH, Faxdc1, G630055L08Rik
<b>Expression</b>	Biased expression in stomach adult (RPKM 77.1), colon adult (RPKM 59.1) and 8 other tissues <a href="#">See more</a>
<b>Orthologs</b>	<a href="#">human</a> <a href="#">all</a>

# Transcript information (Ensembl)

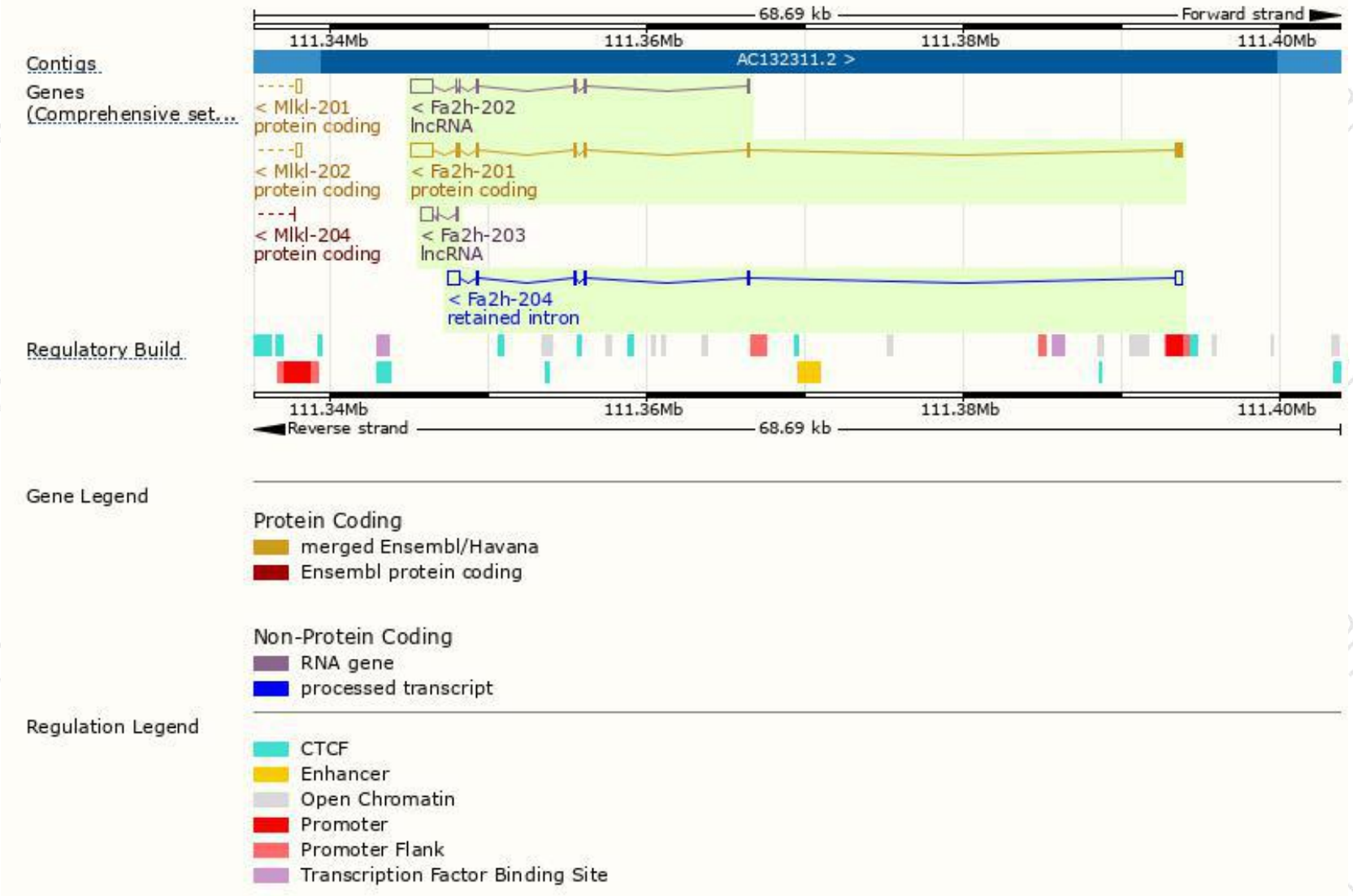
The gene has 4 transcripts,all transcripts are shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Fa2h-201	<a href="#">ENSMUST00000038475.8</a>	2492	<a href="#">372aa</a>	Protein coding	<a href="#">CCDS22674</a>	<a href="#">Q5MPP0</a>	TSL:1 GENCODE basic APPRIS P1
Fa2h-204	<a href="#">ENSMUST00000162463.1</a>	1566	No protein	Retained intron	-	-	TSL:1
Fa2h-202	<a href="#">ENSMUST00000159336.7</a>	1971	No protein	lncRNA	-	-	TSL:5
Fa2h-203	<a href="#">ENSMUST00000162216.1</a>	933	No protein	lncRNA	-	-	TSL:3

The strategy is based on the design of *Fa2h-201* transcript,The transcription is shown below

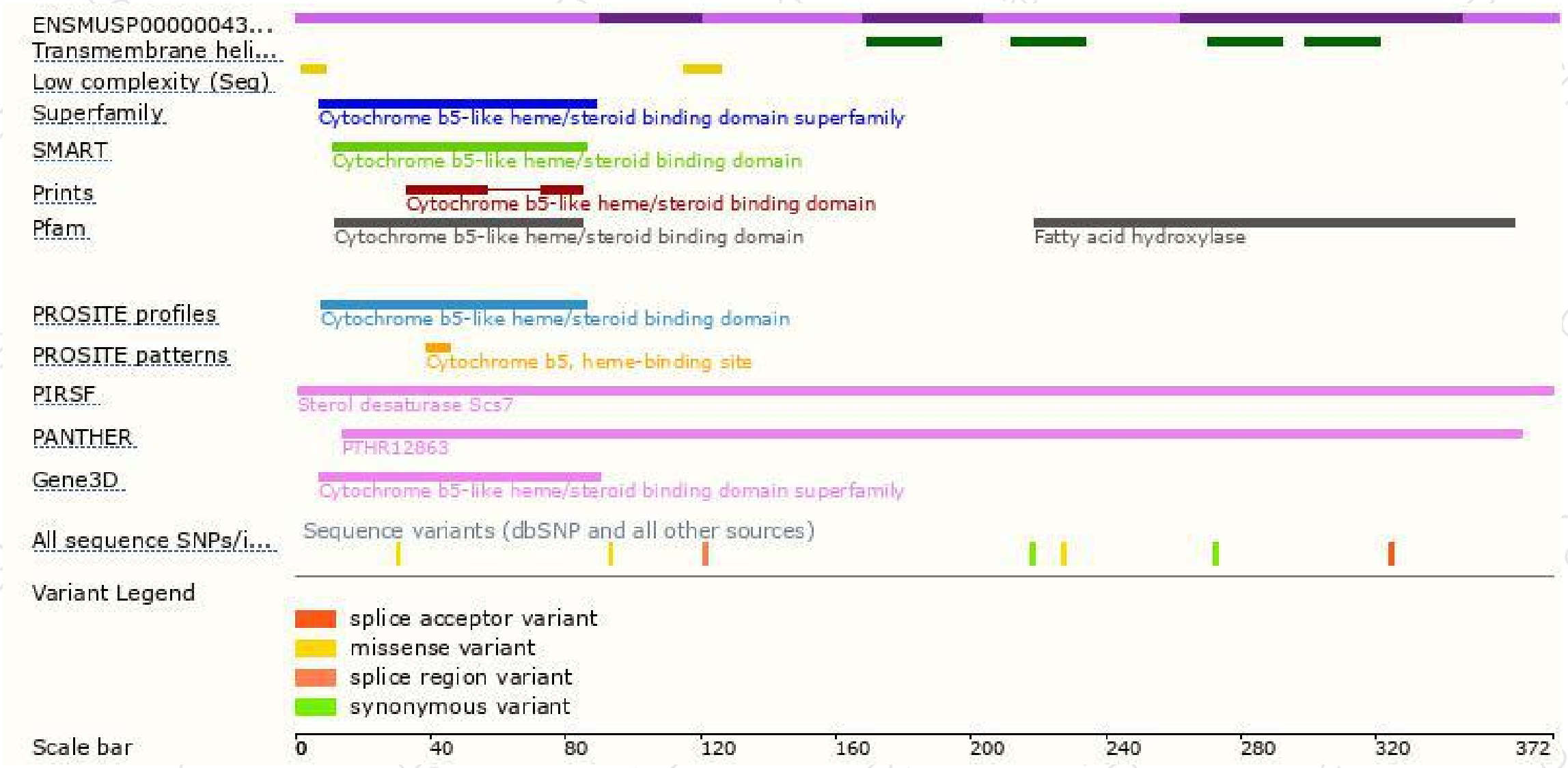


# Genomic location distribution

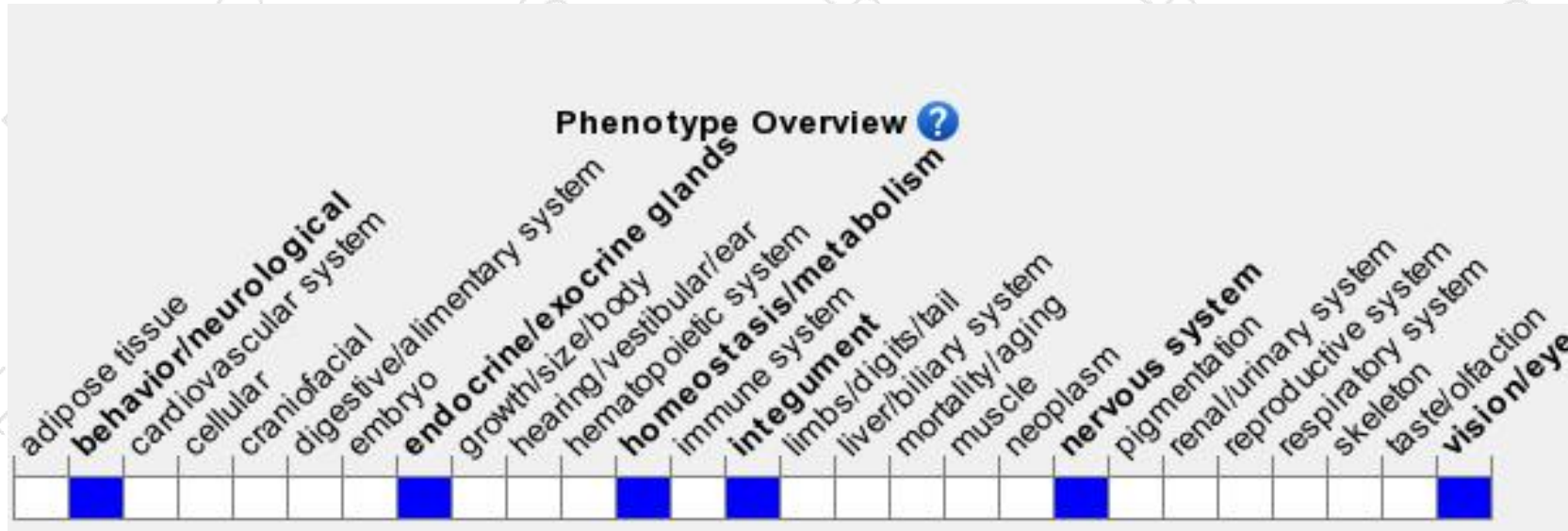




# Protein domain



# 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, Homozygotes for a null allele show demyelination, axonal loss, and cerebellar dysfunction. Homozygotes for a different null allele show late onset axon and myelin sheath degeneration, delayed fur emergence, altered sebum composition, sebocyte hyperproliferation, and cyclic alopecia.

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

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