

# *Lep* Cas9-KO Strategy

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# Project Overview

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**Project Name**

*Lep*

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**Project type**

**Cas9-KO**

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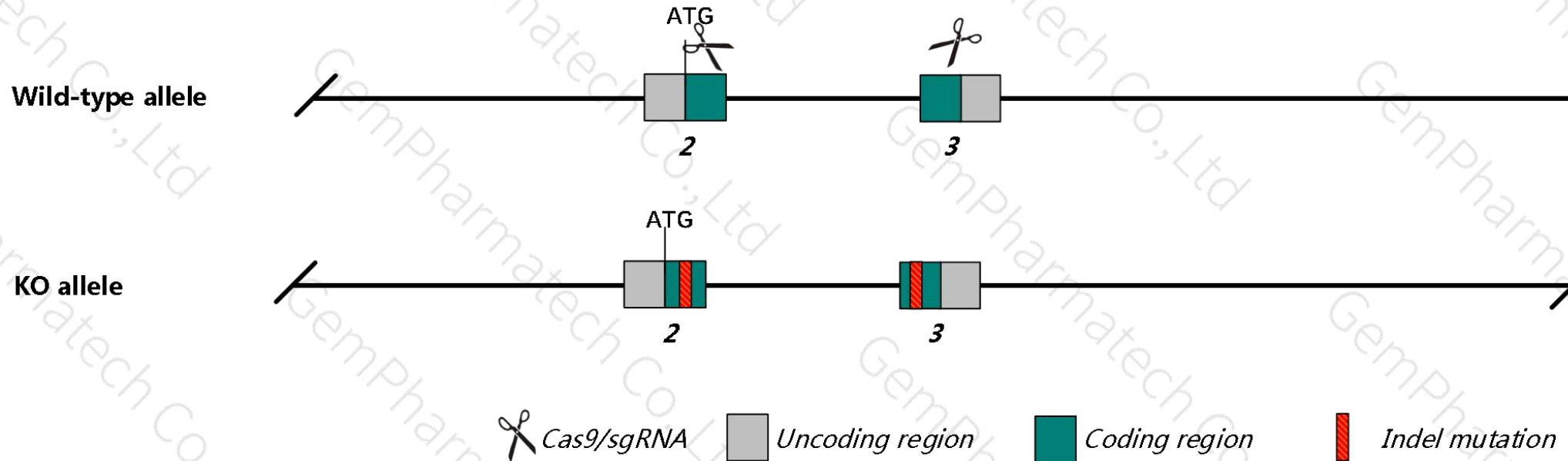
**Strain background**

**C57BL/6J**

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# Knockout strategy

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



- The *Lep* gene has 2 transcripts. According to the structure of *Lep* gene, partial exon2 and exon3 of *Lep-201* (ENSMUST00000069789.11) transcript is recommended as the knockout region, result in indel mutation and disruption of protein function.
- In this project we use CRISPR/Cas9 technology to modify *Lep* gene. The brief process is as follows: sgRNA was transcribed in vitro. Cas9 and sgRNA were microinjected into the fertilized eggs of C57BL/6J 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/6J mice.

- According to the existing MGI data, Homozygotes are obese, hyperphagic, have low activity, high metabolic efficiency, impaired thermogenesis, infertility and short lifespan in addition to varying other abnormalities. Strain background affects severity and course of diabetes. Heterozygotes survive fasting longer than control mice.
- The *Lep* gene is located on the Chr6. 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)

## Lep leptin [Mus musculus (house mouse)]

Gene ID: 16846, updated on 2-Apr-2019

### Summary



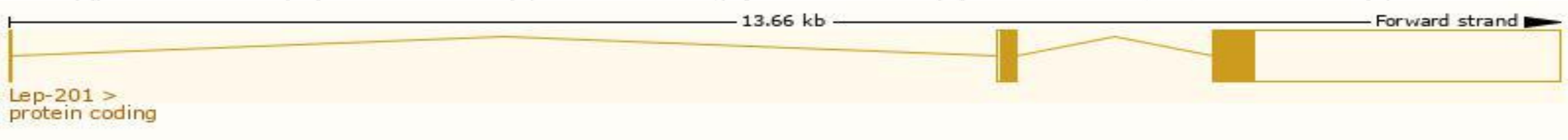
<b>Official Symbol</b>	Lep provided by <a href="#">MGI</a>
<b>Official Full Name</b>	leptin provided by <a href="#">MGI</a>
<b>Primary source</b>	<a href="#">MGI:MGI:104663</a>
<b>See related</b>	<a href="#">Ensembl:ENSMUSG00000059201</a>
<b>Gene type</b>	protein coding
<b>RefSeq status</b>	VALIDATED
<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>	ob, obese
<b>Expression</b>	Biased expression in subcutaneous fat pad adult (RPKM 267.7), genital fat pad adult (RPKM 183.5) and 1 other tissue <a href="#">See more</a>
<b>Orthologs</b>	<a href="#">human</a> <a href="#">all</a>

# Transcript information (Ensembl)

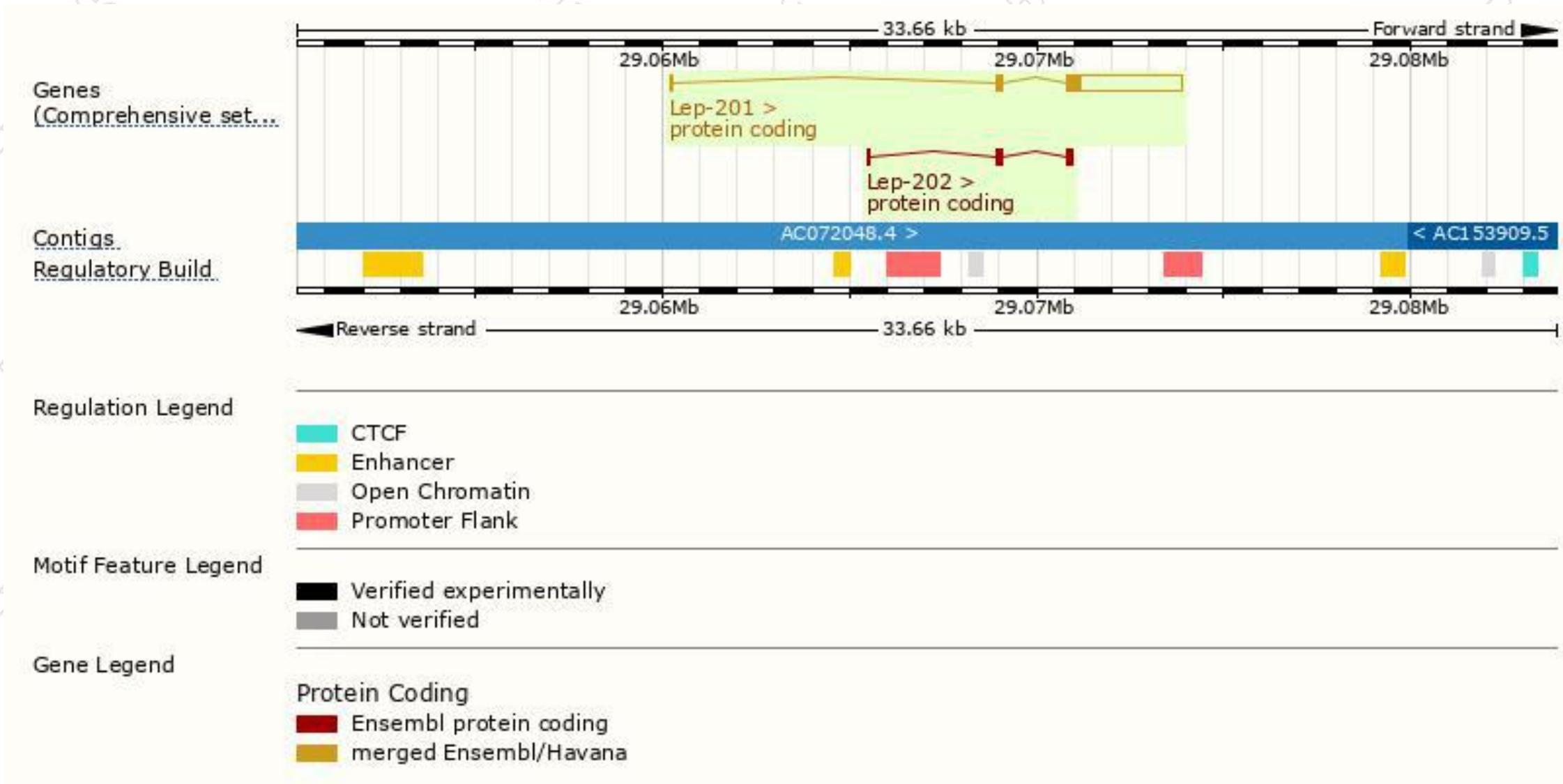
The gene has 2 transcripts,all transcripts are shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Lep-201	<a href="#">ENSMUST00000069789.11</a>	3259	<a href="#">167aa</a>	Protein coding	<a href="#">CCDS19955</a>	<a href="#">P41160 Q544U0</a>	TSL:1 GENCODE basic APPRIS P1
Lep-202	<a href="#">ENSMUST00000169505.1</a>	420	<a href="#">98aa</a>	Protein coding	-	<a href="#">E9Q7Z0</a>	CDS 3' incomplete TSL:3

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

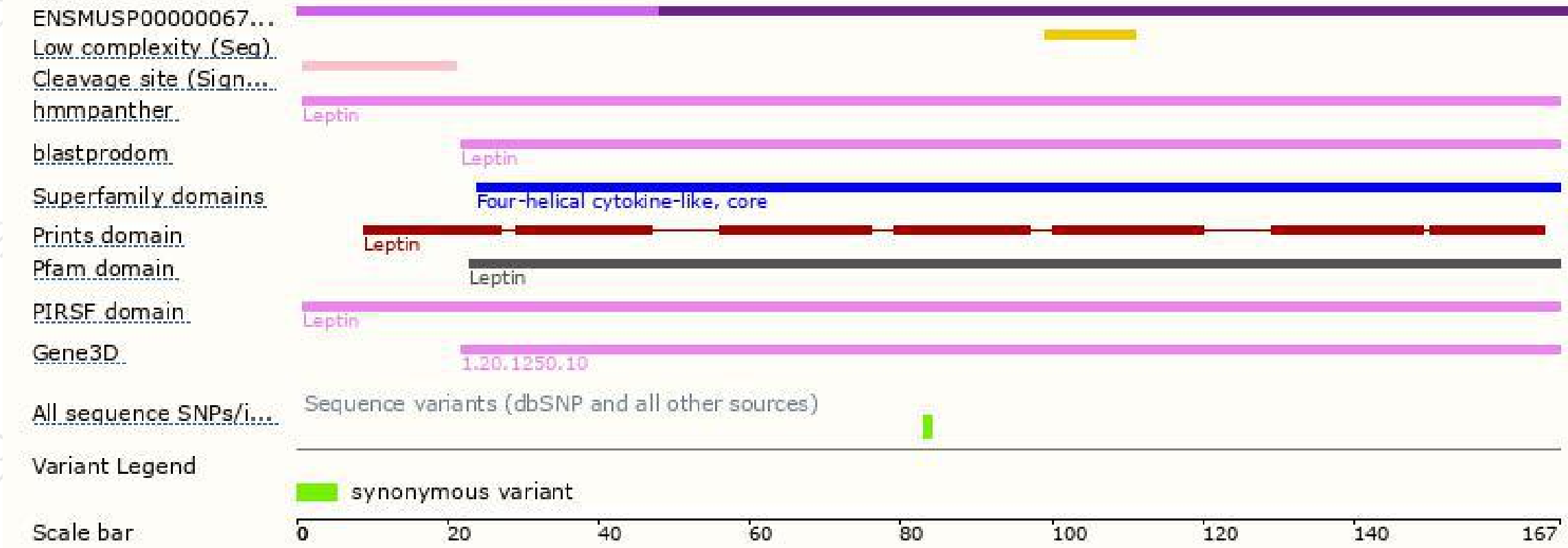


# Genomic location distribution

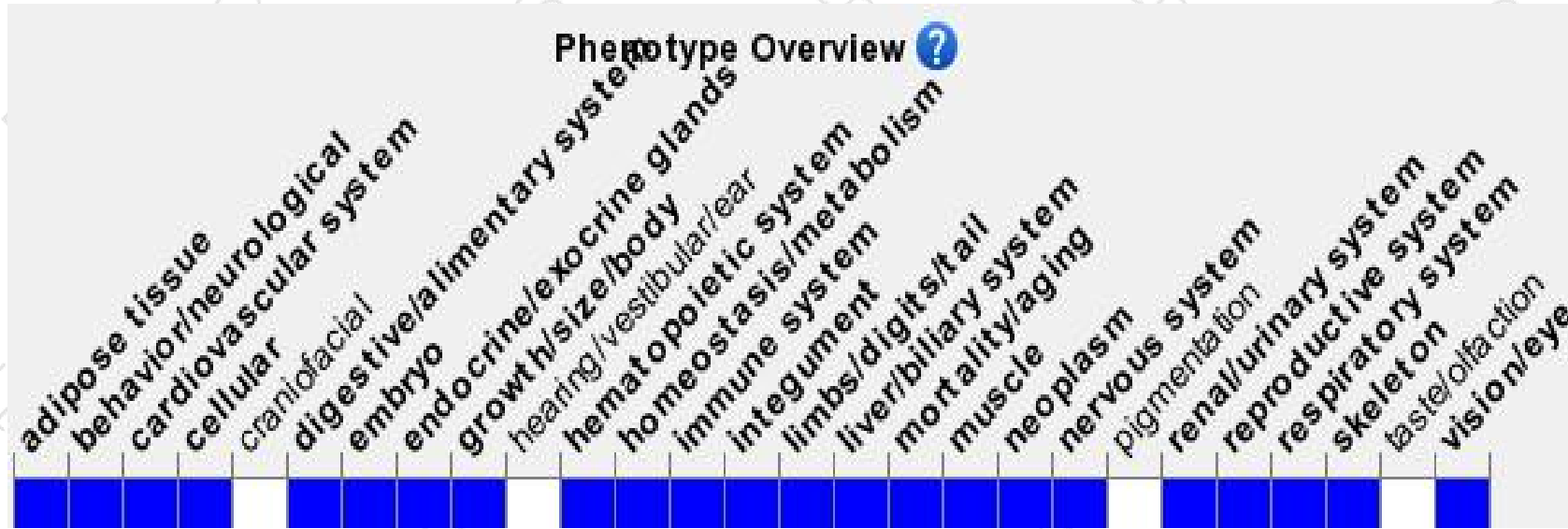




# Protein domain



# 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 are obese, hyperphagic, have low activity, high metabolic efficiency, impaired thermogenesis, infertility and short lifespan in addition to varying other abnormalities. Strain background affects severity and course of diabetes. Heterozygotes survive fasting longer than control mice.

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

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