

Cd36 Cas9-CKO Strategy

Designer: Shilei Zhu

Project Overview

Project Name

Cd36

Project type

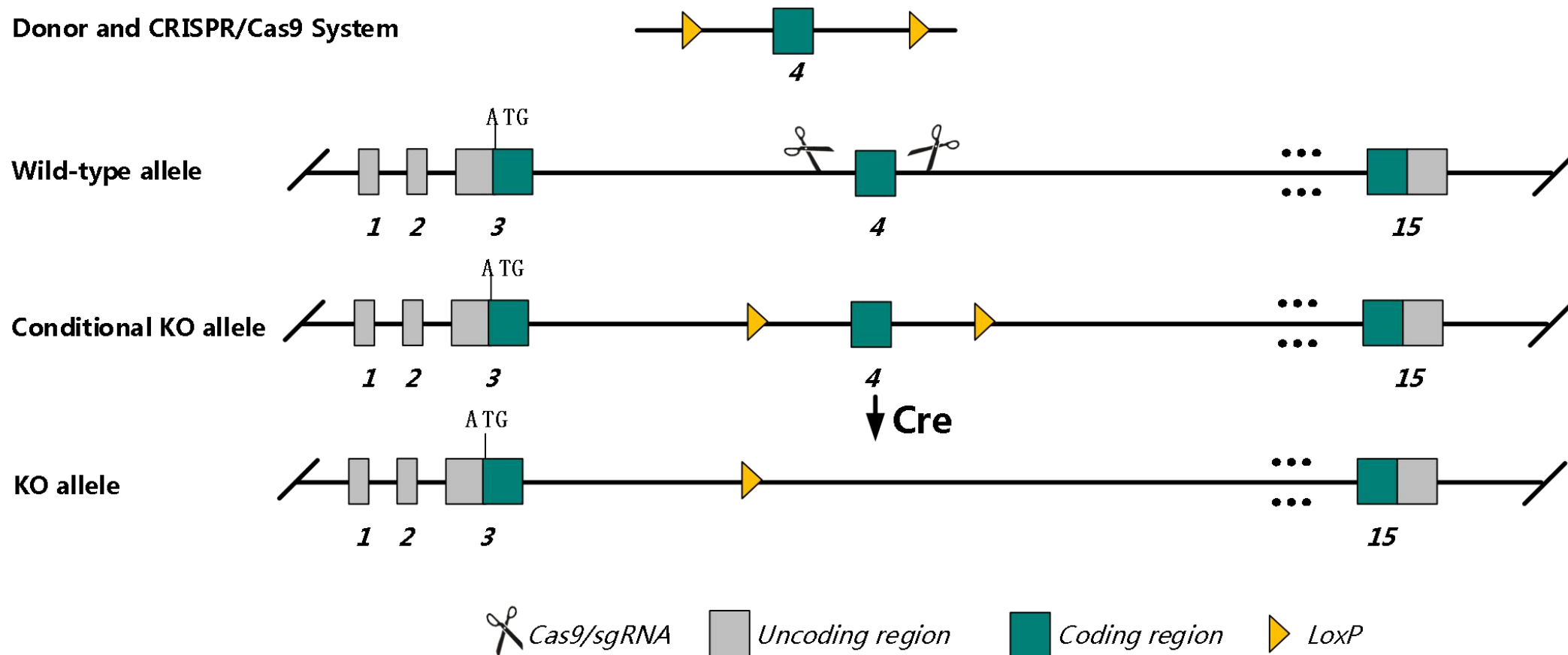
Cas9-CKO

Strain background

C57BL/6JGpt

Conditional Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *Cd36* gene. The schematic diagram is as follows:



Technical routes

The *Cd36* gene has 6 transcripts. According to the structure of *Cd36* gene, exon4 of *Cd36-204* (ENSMUST00000170051.7) transcript is recommended as the knockout region. The region contains 161bp coding sequence. Knock out the region will result in disruption of protein function.

In this project we use CRISPR/Cas9 technology to modify *Cd36* 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, Homozygous mutant mice exhibit an immunodeficiency phenotype, are susceptible to *S. aureus* infection and develop ocular pterygium. Mice homozygous for disruptions in this gene display abnormal lipid homeostasis which affects energy utilization in the heart.

The *Cd36* 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.

Cd36 CD36 molecule [Mus musculus (house mouse)]

Gene ID: 12491, updated on 2-Apr-2019

Summary



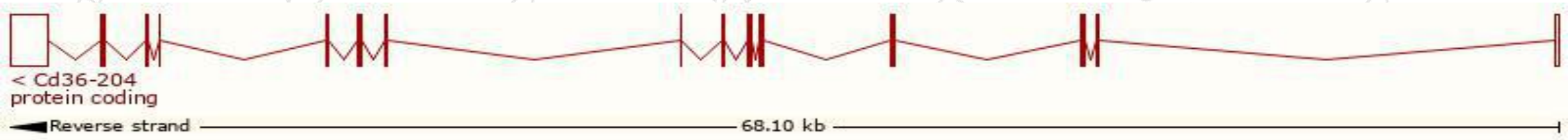
| | |
|---------------------------|---|
| Official Symbol | Cd36 provided by MGI |
| Official Full Name | CD36 molecule provided by MGI |
| Primary source | MGI:MGI:107899 |
| See related | Ensembl:ENSMUSG000000002944 |
| Gene type | protein coding |
| RefSeq status | VALIDATED |
| Organism | Mus musculus |
| Lineage | Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Myomorpha; Muroidea; Muridae; Murinae; Mus; Mus |
| Also known as | FAT, GPIV, Scarb3 |
| Expression | Biased expression in subcutaneous fat pad adult (RPKM 144.0), heart adult (RPKM 110.7) and 5 other tissues See more |
| Orthologs | human all |

Transcript information Ensembl

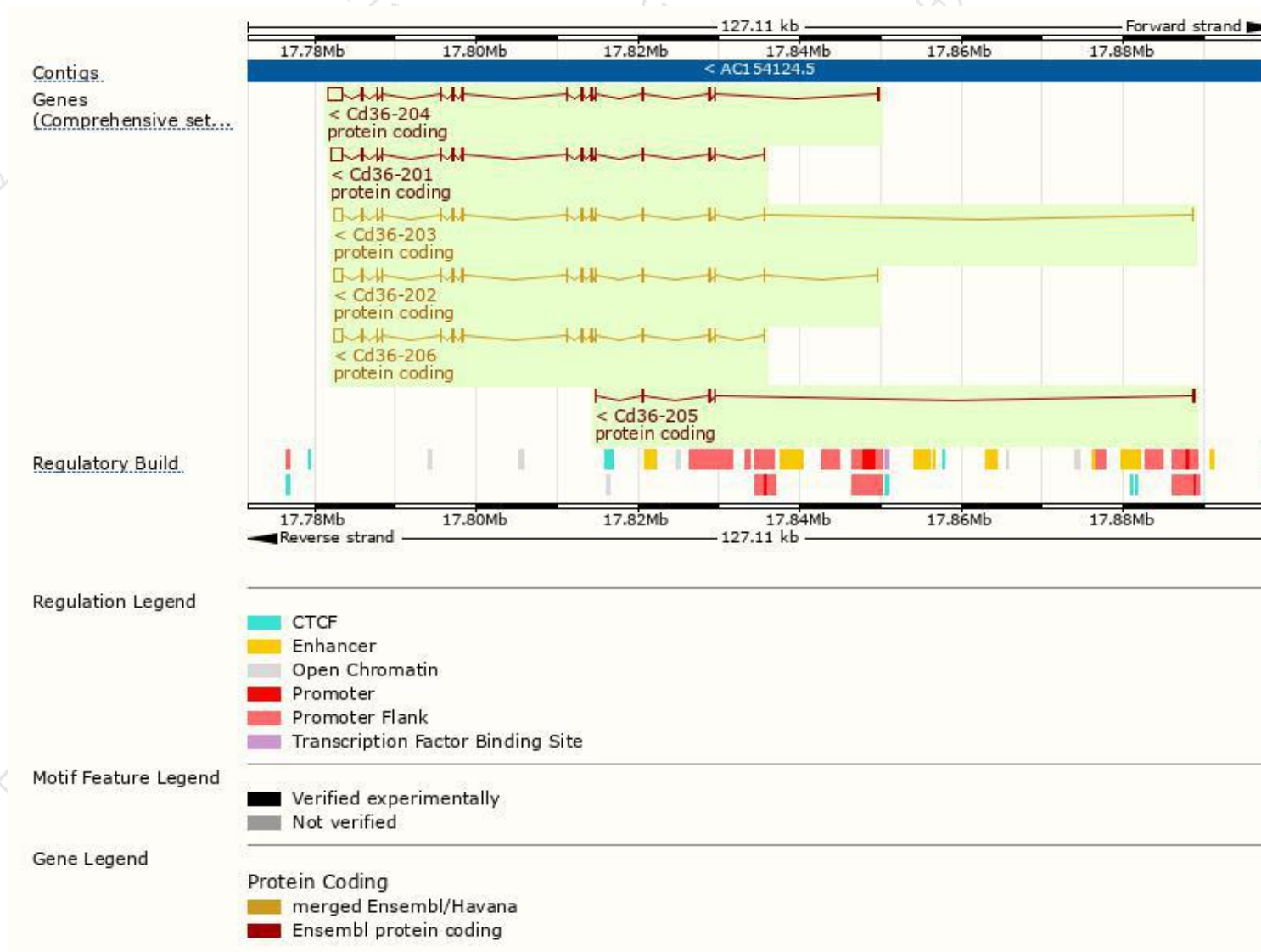
The gene has 6 transcripts,all transcripts are shown below:

| Name | Transcript ID | bp | Protein | Biotype | CCDS | UniProt | Flags |
|----------|---------------------------------------|------|-----------------------|----------------|---------------------------|-------------------------------|-------------------------------|
| Cd36-204 | ENSMUST00000170051.7 | 3399 | 472aa | Protein coding | CCDS19100 | Q08857 Q3UAI3 | TSL:1 GENCODE basic APPRIS P1 |
| Cd36-201 | ENSMUST00000082367.12 | 3016 | 472aa | Protein coding | CCDS19100 | Q08857 Q3UAI3 | TSL:1 GENCODE basic APPRIS P1 |
| Cd36-202 | ENSMUST00000165232.7 | 2708 | 472aa | Protein coding | CCDS19100 | Q08857 Q3UAI3 | TSL:1 GENCODE basic APPRIS P1 |
| Cd36-203 | ENSMUST00000169095.5 | 2677 | 472aa | Protein coding | CCDS19100 | Q08857 Q3UAI3 | TSL:1 GENCODE basic APPRIS P1 |
| Cd36-206 | ENSMUST00000197890.4 | 2564 | 472aa | Protein coding | CCDS19100 | Q08857 Q3UAI3 | TSL:1 GENCODE basic APPRIS P1 |
| Cd36-205 | ENSMUST00000197574.1 | 702 | 142aa | Protein coding | - | A0A0G2JFB7 | CDS 3' incomplete TSL:5 |

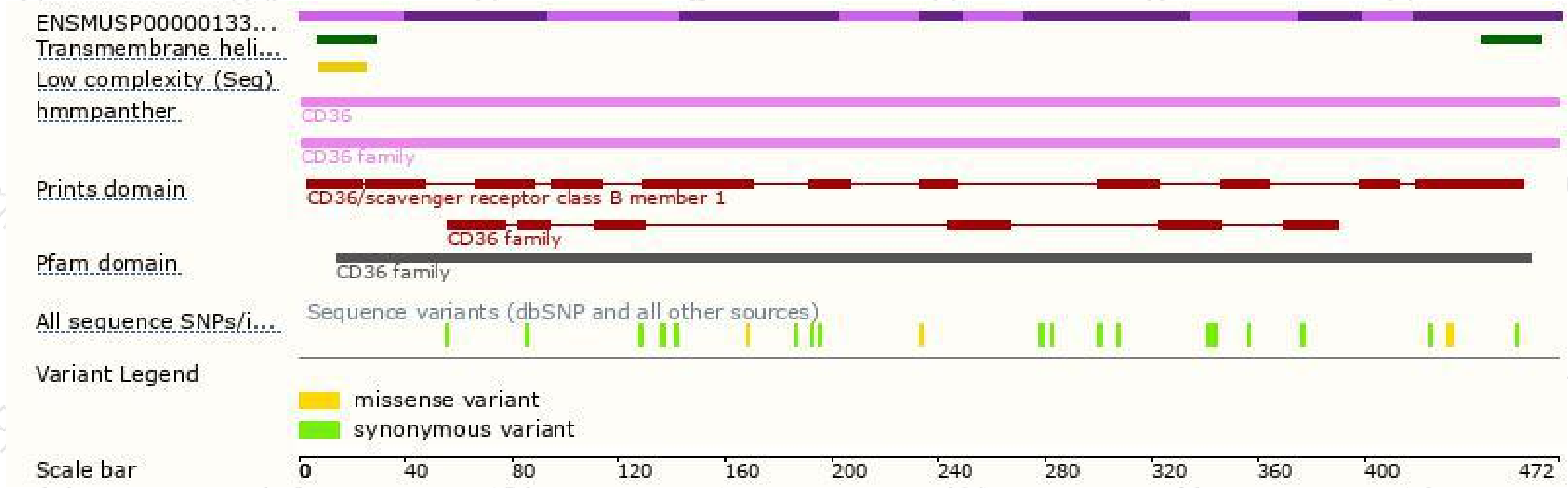
The strategy is based on the design of *Cd36-204* transcript,The transcription is shown below



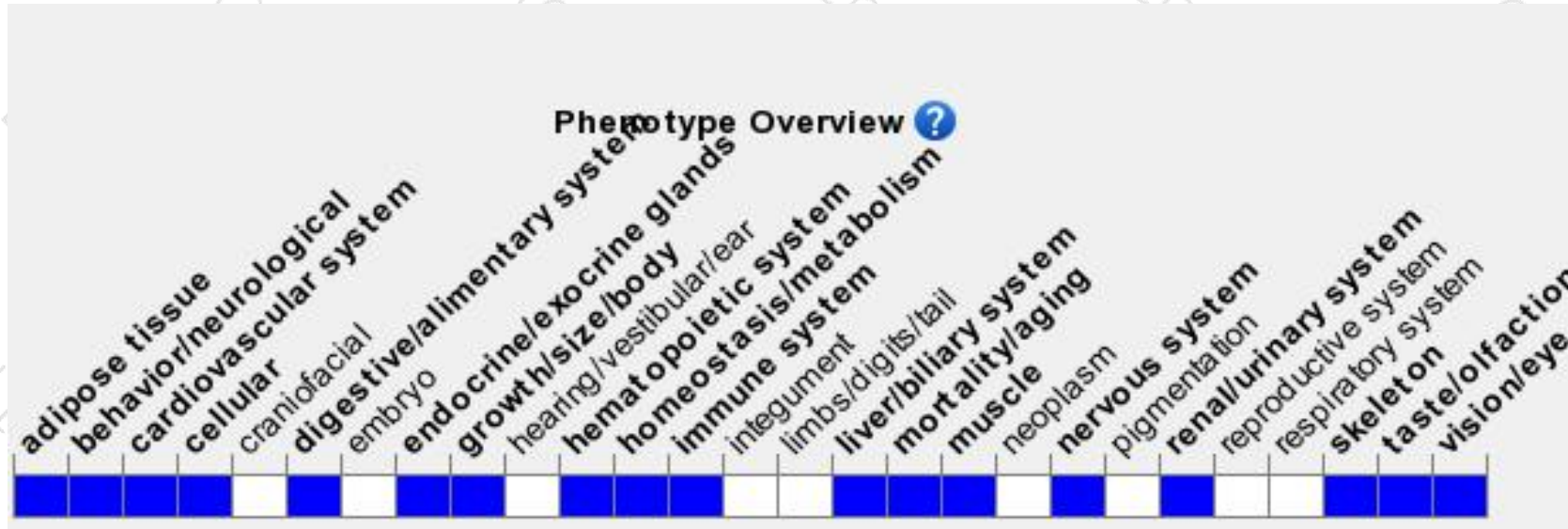
Genomic location distribution



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/>).

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

Tel: 400-9660890

