Ivd Cas9-KO Strategy

Designer: Huan Fan

Reviewer: Huan Wang

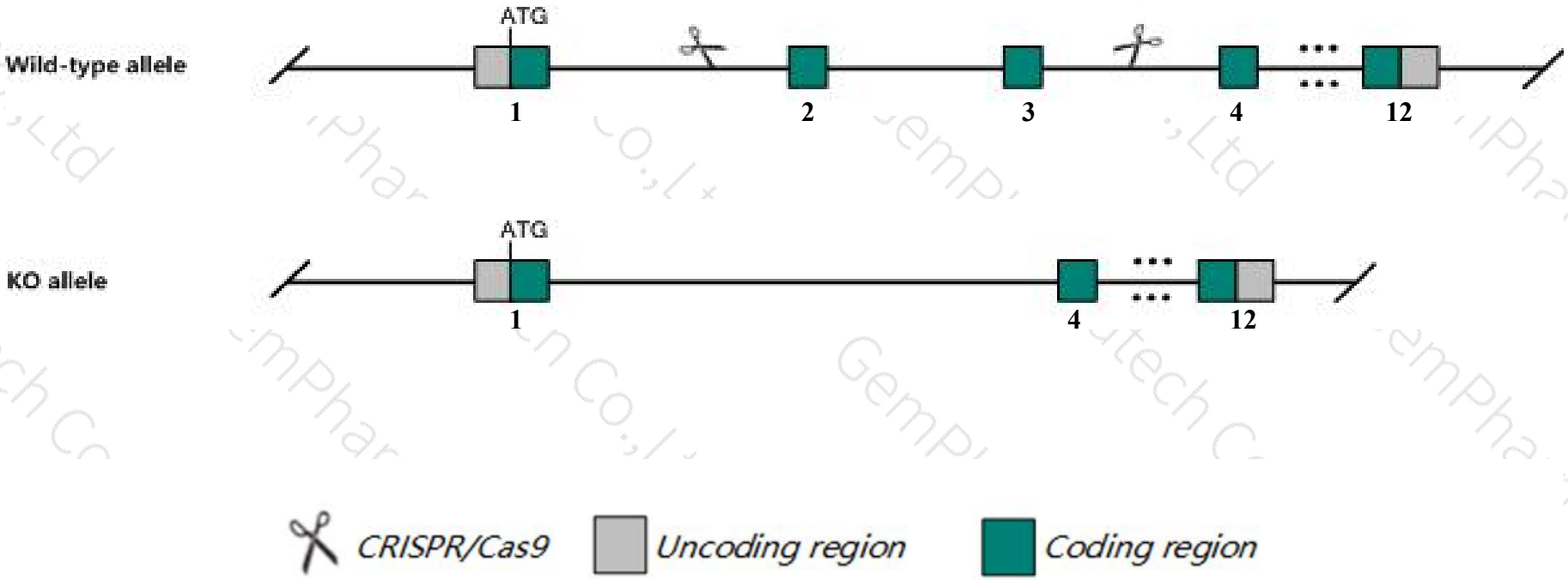
Design Date: 2019-12-11

Project Overview

Project Name	***Ivd***
Project type	**Cas9-KO**
Strain background	**C57BL/6JGpt**

Knockout strategy

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



Technical routes

➢ The *Ivd* gene has 8 transcripts. According to the structure of *Ivd* gene, exon2-exon3 of *Ivd-201* (ENSMUST00000028807.5) transcript is recommended as the knockout region.The region contains 142bp coding sequence. Knock out the region will result in disruption of protein function.

➢ In this project we use CRISPR/Cas9 technology to modify *Ivd* gene. The brief process is as follows: CRISPR/Cas9 system we

Notice

➢ The *Ivd* gene is located on the Chr2. 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）

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lvd isovaleryl coenzyme A dehydrogenase [Mus musculus (house mouse)]

Gene ID: 56357, updated on 19-Mar-2019

Summary

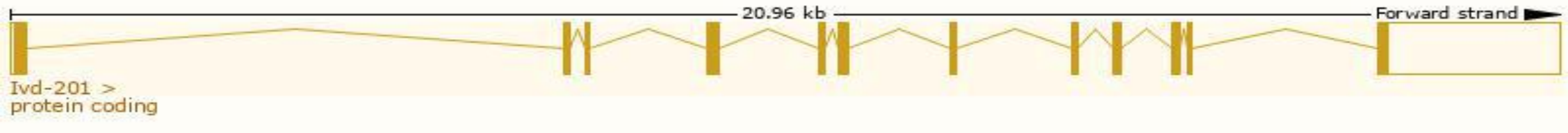
Official Symbol	lvd provided by MGI
Official Full Name	isovaleryl coenzyme A dehydrogenase provided by MGI
Primary source	MGI:MGI:1929242
See related	Ensembl:ENSMUSG00000027332
Gene type	protein coding
RefSeq status	VALIDATED
Organism	Mus musculus
Lineage	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Myomorpha; Muroidea; Muridae; Murinae; Mus; Mus
Also known as	1300016K07Rik, 6720455E18Rik, AI463340
Expression	Ubiquitous expression in adrenal adult (RPKM 99.3), heart adult (RPKM 88.5) and 28 other tissues See more
Orthologs	human all

Transcript information（Ensembl）

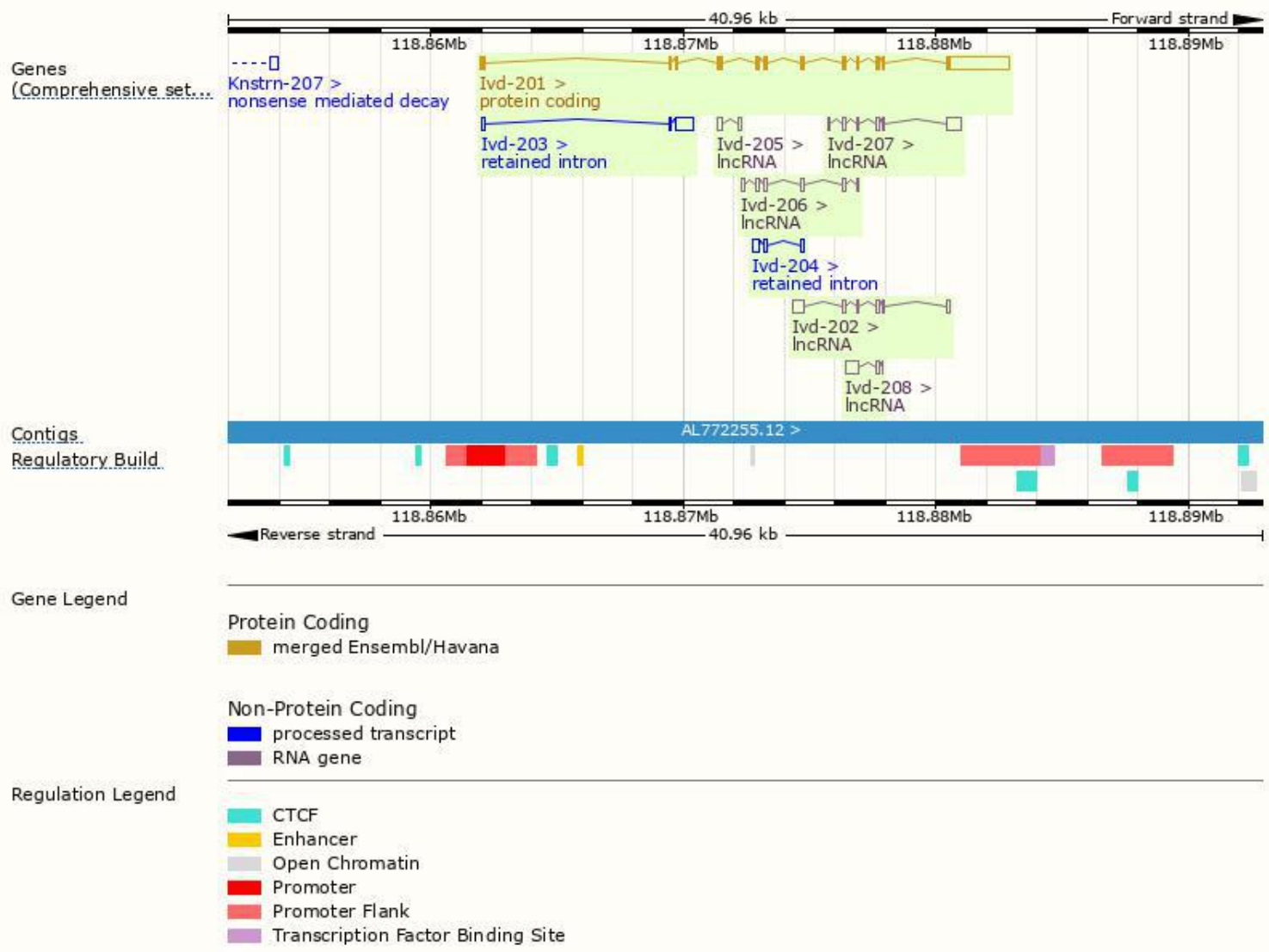
The gene has 8 transcripts,all transcripts are shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Ivd-201	ENSMUST00000028807.5	3665	424aa	Protein coding	CCDS16586	Q9JHI5	TSL:1 GENCODE basic APPRIS P1
Ivd-203	ENSMUST00000126082.1	897	No protein	Retained intron	-	-	TSL:2
Ivd-204	ENSMUST00000140282.1	446	No protein	Retained intron	-	-	TSL:2
Ivd-207	ENSMUST00000152191.7	1010	No protein	lncRNA	-	-	TSL:2
Ivd-202	ENSMUST00000125766.7	936	No protein	lncRNA	-	-	TSL:2
Ivd-208	ENSMUST00000154104.1	668	No protein	lncRNA	-	-	TSL:3
Ivd-206	ENSMUST00000150162.7	606	No protein	lncRNA	-	-	TSL:3
Ivd-205	ENSMUST00000141836.1	266	No protein	lncRNA	-	-	TSL:5

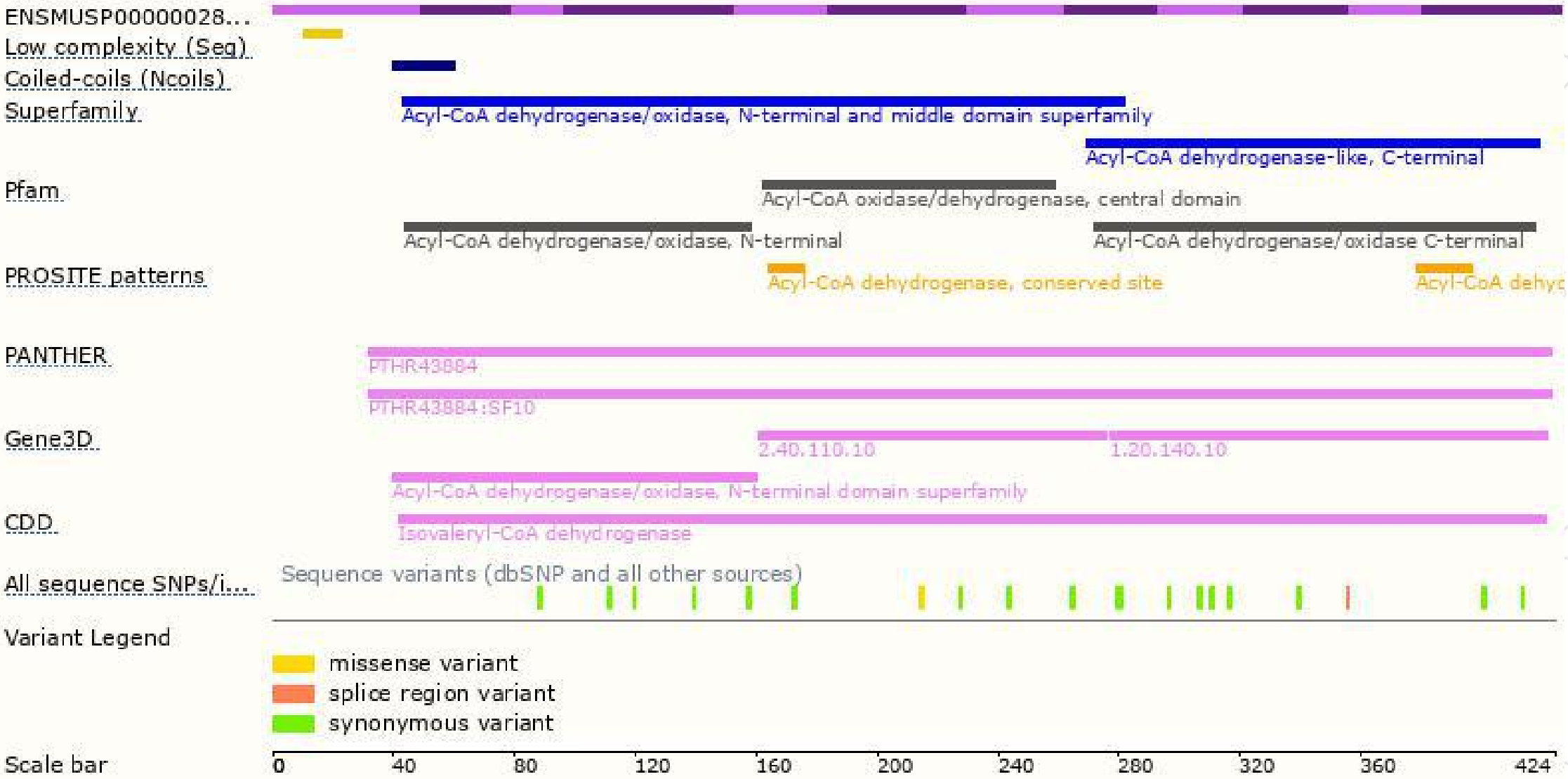
The strategy is based on the design of *Ivd-201* transcript,The transcription is shown below



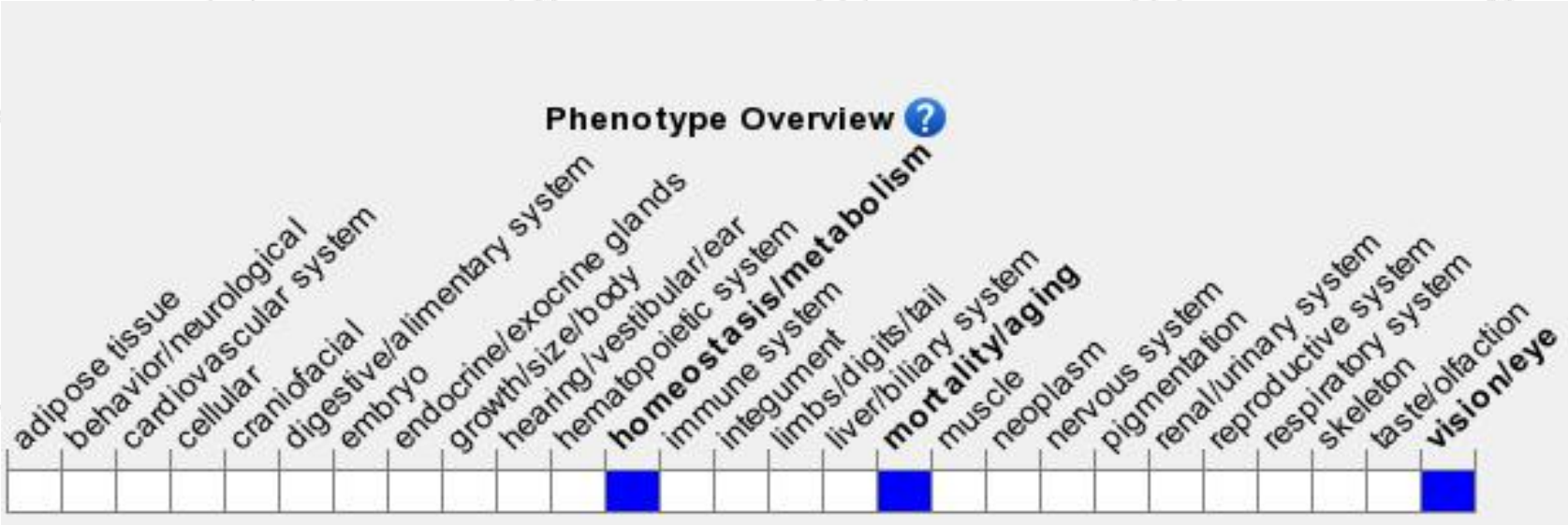
Genomic location distribution



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/).

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

Tel: 400-9660890

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