Eif2ak4 Cas9-KO Strategy

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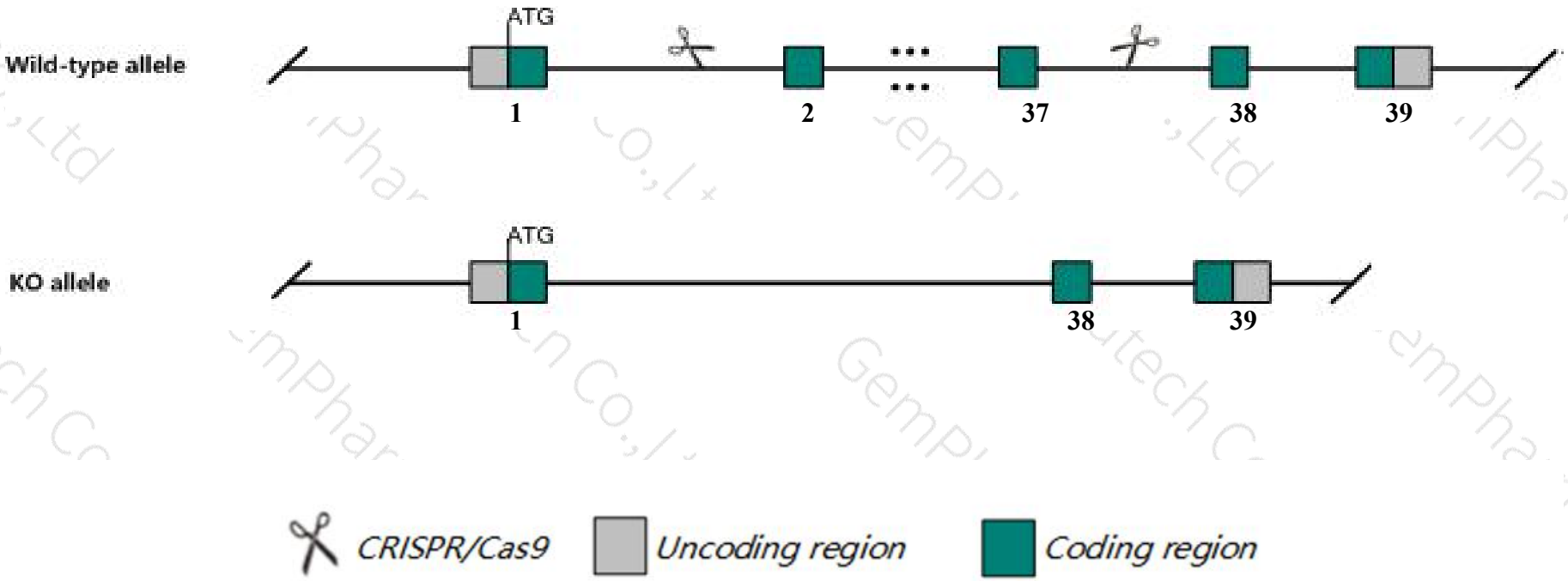
Design Date: 2019-7-18

Project Overview

Project Name	***Eif2ak4***
Project type	**Cas9-KO**
Strain background	**C57BL/6JGpt**

Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *Eif2ak4* gene. The schematic diagram is as follows:



Technical routes

➢ The *Eif2ak4* gene has 8 transcripts. According to the structure of *Eif2ak4* gene, exon2-exon37 of *Eif2ak4-201* (ENSMUST00000005233.11) transcript is recommended as the knockout region.The region contains most of the coding sequence.Knock out the region will result in disruption of protein function.

➢ In this project we use CRISPR/Cas9 technology to modify *Eif2ak4* gene. The brief process is as follows: CRISPR/Cas9 syste

Notice

- According to the existing MGI data,Homozygotes for a null allele have altered feeding behavior, synaptic plasticity and dendritic cell function. Homozygotes for another null allele show enhanced muscle loss and morbidity after amino acid deprivation. Homozygotes for an ENU-induced allele show higher susceptibility to viral infection.

- The *Eif2ak4* 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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Eif2ak4 eukaryotic translation initiation factor 2 alpha kinase 4 [Mus musculus (house mouse)]

Gene ID: 27103, updated on 31-Jan-2019

Summary

Official Symbol	Eif2ak4 provided by MGI
Official Full Name	eukaryotic translation initiation factor 2 alpha kinase 4 provided by MGI
Primary source	MGI:MGI:1353427
See related	Ensembl:ENSMUSG00000005102
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	2610011M03, GCN2, MGCN2
Expression	Ubiquitous expression in ovary adult (RPKM 8.2), limb E14.5 (RPKM 7.9) and 28 other tissues See more
Orthologs	human all

Transcript information（Ensembl）

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

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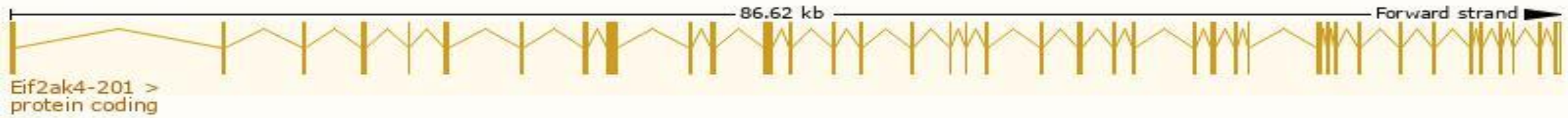
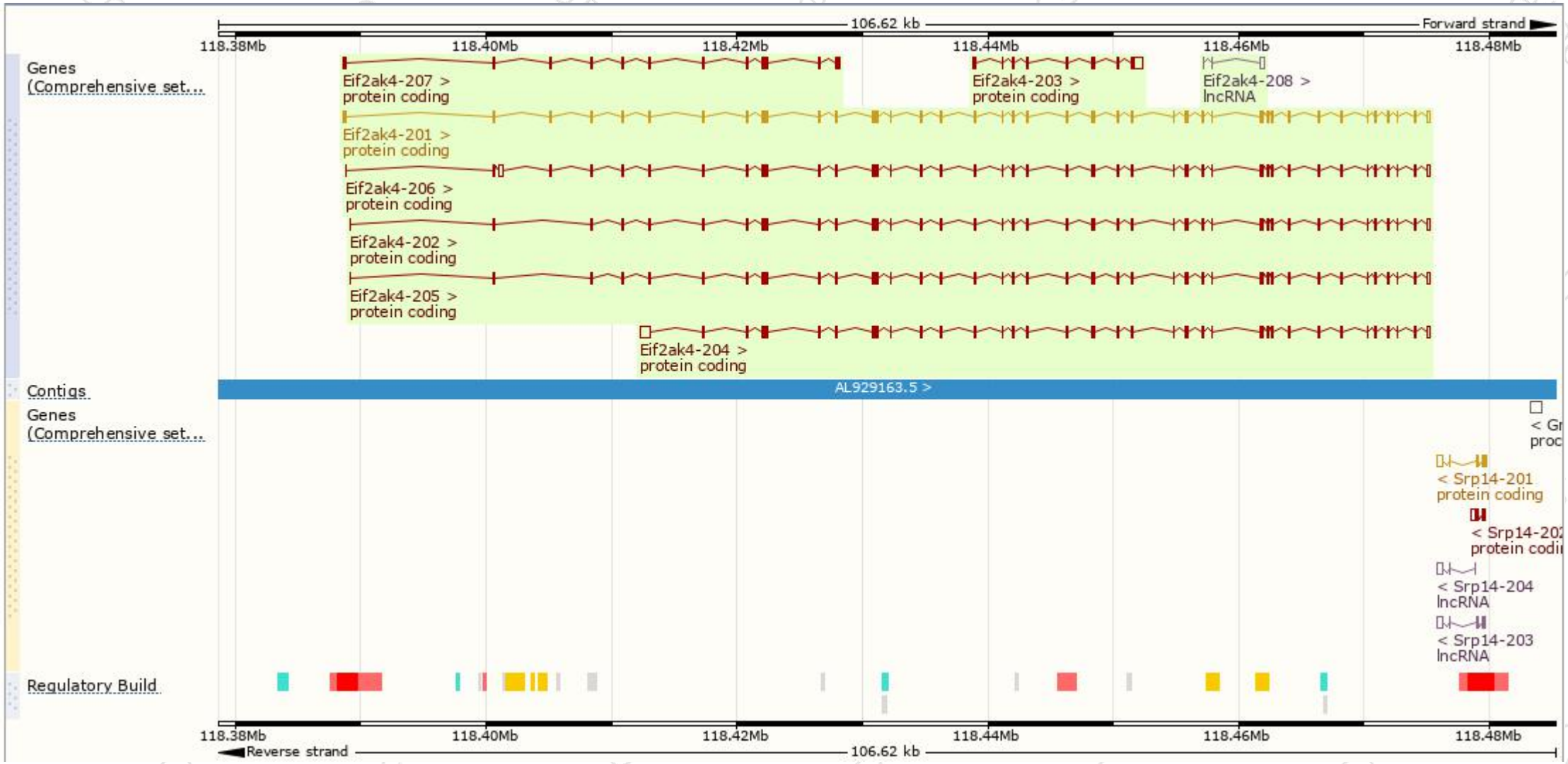
Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Eif2ak4-201	ENSMUST00000005233.11	5212	1648aa	Protein coding	CCDS16576	A2AUM0	TSL:1 GENCODE basic APPRIS P1
Eif2ak4-202	ENSMUST00000102527.9	4906	1536aa	Protein coding	CCDS50669	Q9QZ05	TSL:1 GENCODE basic
Eif2ak4-206	ENSMUST00000110874.7	5298	1570aa	Protein coding	-	A2AUM1	TSL:5 GENCODE basic
Eif2ak4-204	ENSMUST00000110870.7	5116	1370aa	Protein coding	-	Q9QZ05	TSL:1 GENCODE basic
Eif2ak4-205	ENSMUST00000110872.7	4907	1527aa	Protein coding	-	A2AUM2	TSL:1 GENCODE basic
Eif2ak4-207	ENSMUST00000110877.7	2134	653aa	Protein coding	-	A2AUL9	TSL:1 GENCODE basic
Eif2ak4-203	ENSMUST00000110869.1	1715	347aa	Protein coding	-	Q9QZ05	TSL:1 GENCODE basic
Eif2ak4-208	ENSMUST00000125281.1	517	No protein	lncRNA	-	-	TSL:2

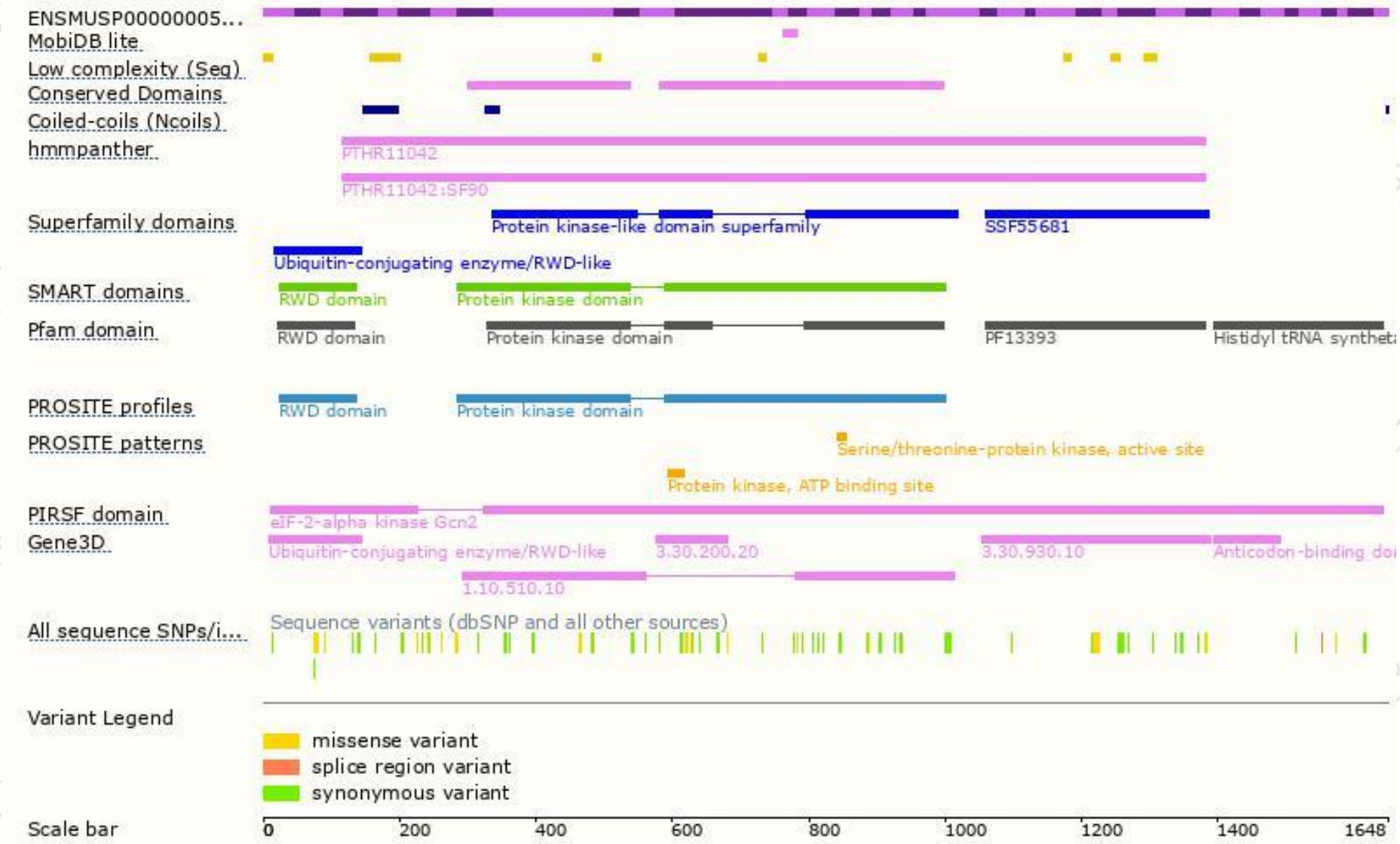
The strategy is based on the design of *Eif2ak4-201* transcript,The transcription is shown below



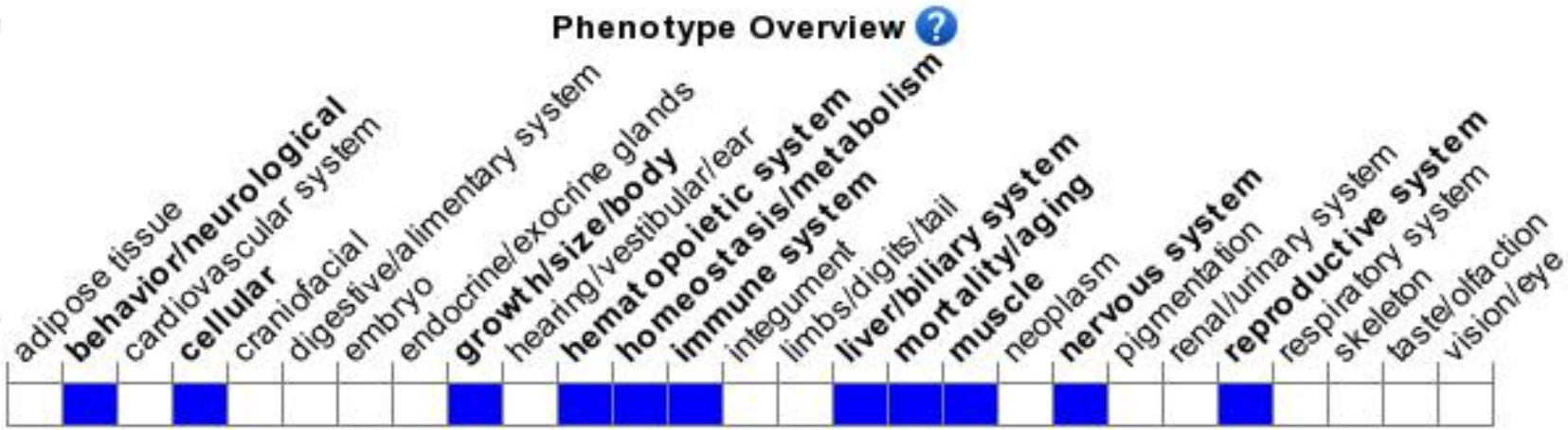
Genomic location distribution



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 have altered feeding behavior, synaptic plasticity and dendritic cell function. Homozygotes for another null allele show enhanced muscle loss and morbidity after amino acid deprivation. Homozygotes for an ENU-induced allele show higher susceptibility to viral infection.

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

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