Carm1 Cas9-CKO Strategy

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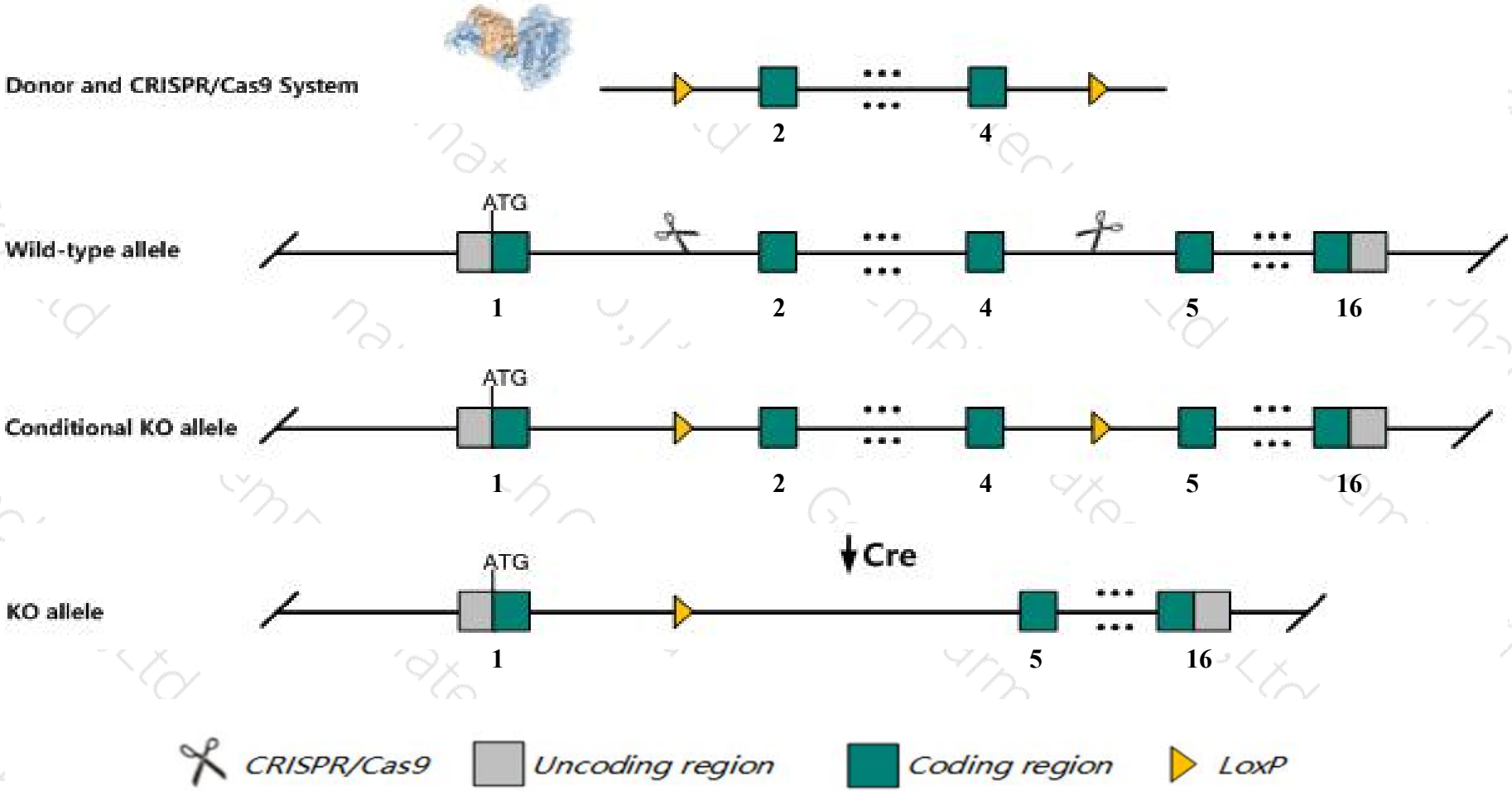
Project Overview

Project Name	***Carm1***
Project type	**Cas9-CKO**
Strain background	**C57BL/6JGpt**

Conditional Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *Carm1* gene. The schematic diagram is as follows:



Technical routes

- The *Carm1* gene has 10 transcripts. According to the structure of *Carm1* gene, exon2-exon4 of *Carm1-201* (ENSMUST00000034703.14) transcript is recommended as the knockout region.The region contains 338bp coding sequence. Knock out the region will result in disruption of protein function.

- In this project we use CRISPR/Cas9 technology to modify *Carm1* 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.

Notice

- According to the existing MGI data,homozygous null fetuses are small and die perinatally, whereas heterozygotes are born at the expected mendelian ratio but show decreased survival through weaning. mice homozygous for a kinase null allele exhibit neonatal lethality, arrested t cell development, and impaired adipogenesis.
- The *Carm1* gene is located on the Chr9. 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.

Gene information （NCBI）

集萃药康 GemPharmatech

Carm1 coactivator-associated arginine methyltransferase 1 [Mus musculus (house mouse)]

Gene ID: 59035, updated on 13-Mar-2020

Summary

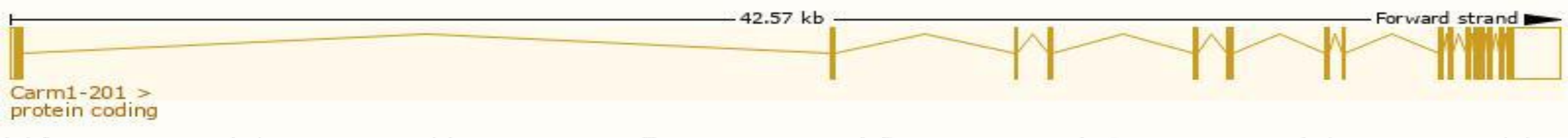
Official Symbol	Carm1 provided by MGI
Official Full Name	coactivator-associated arginine methyltransferase 1 provided by MGI
Primary source	MGI:MGI:1913208
See related	Ensembl:ENSMUSG00000032185
Gene type	protein coding
RefSeq status	VALIDATED
Organism	Mus musculus
Lineage	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Myomorpha; Muroidea; Muridae; Murinae; Mus; Mus
Also known as	Prmt4
Expression	Ubiquitous expression in testis adult (RPKM 59.4), limb E14.5 (RPKM 52.7) and 28 other tissues See more
Orthologs	human all

Transcript information（Ensembl）

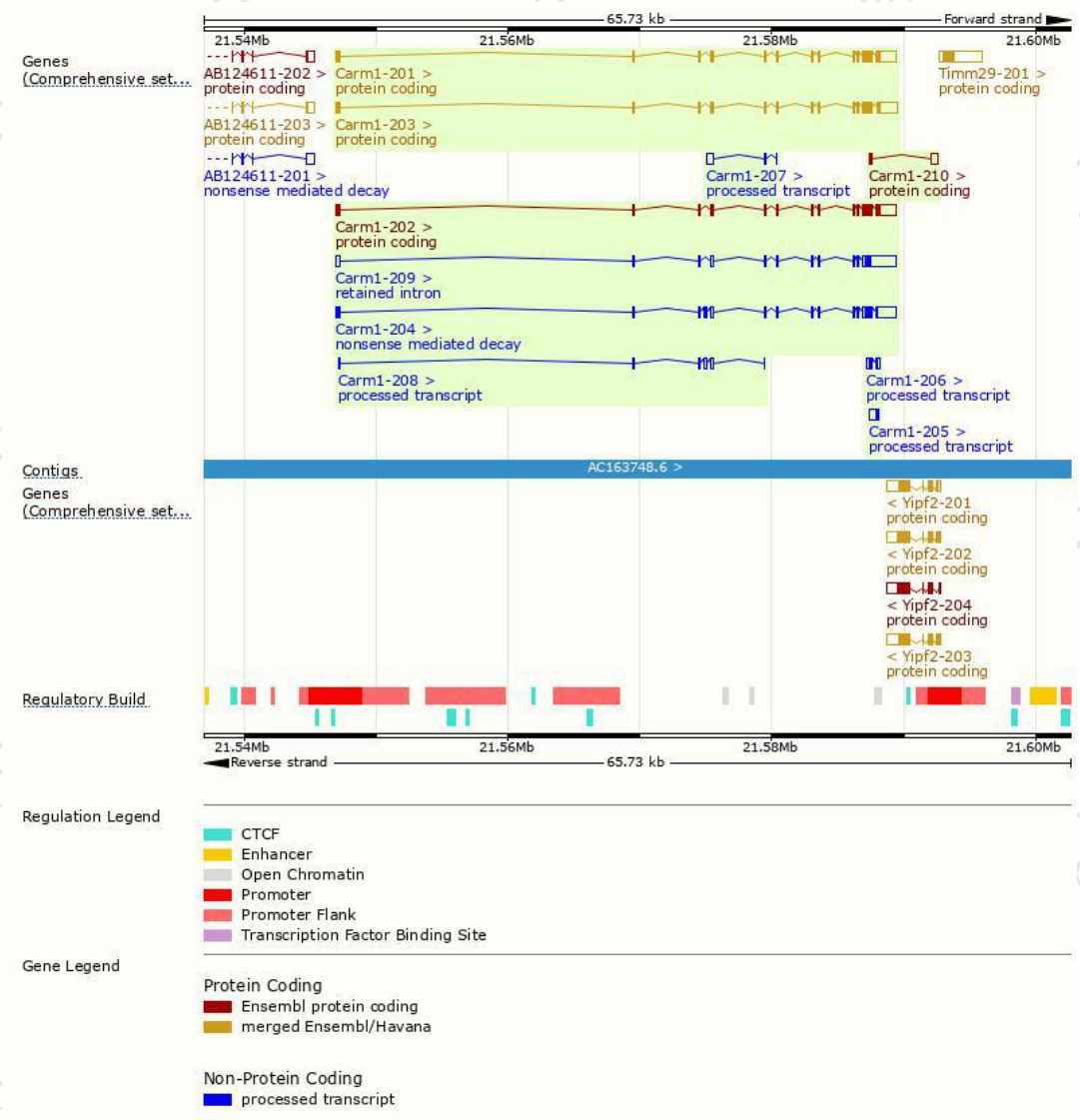
The gene has 10 transcripts,all transcripts are shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Carm1-201	ENSMUST00000034703.14	3220	608aa	Protein coding	CCDS22906	Q9WVG6	TSL:1 GENCODE basic APPRIS is a system to annotate alternatively spliced transcripts based on a range of computational methods to identify the most functionally important transcript(s) of a gene. APPRIS P3
Carm1-203	ENSMUST00000115395.9	3152	585aa	Protein coding	CCDS52736	Q9WVG6	TSL:1 GENCODE basic APPRIS is a system to annotate alternatively spliced transcripts based on a range of computational methods to identify the most functionally important transcript(s) of a gene. APPRIS ALT2
Carm1-202	ENSMUST00000115394.7	3320	651aa	Protein coding	-	D3YUP1	TSL:5 GENCODE basic APPRIS is a system to annotate alternatively spliced transcripts based on a range of computational methods to identify the most functionally important transcript(s) of a gene. APPRIS ALT2
Carm1-210	ENSMUST00000216160.1	665	48aa	Protein coding	-	A0A1L1ST60	CDS 5' incomplete TSL:2
Carm1-204	ENSMUST00000130032.7	3336	162aa	Nonsense mediated decay	-	D6RFA7	TSL:1
Carm1-208	ENSMUST00000147749.1	604	No protein	Processed transcript	-	-	TSL:5
Carm1-205	ENSMUST00000130100.1	598	No protein	Processed transcript	-	-	TSL:2
Carm1-207	ENSMUST00000139871.1	557	No protein	Processed transcript	-	-	TSL:3
Carm1-206	ENSMUST00000132011.1	485	No protein	Processed transcript	-	-	TSL:2
Carm1-209	ENSMUST00000154049.7	3585	No protein	Retained intron	-	-	TSL:5

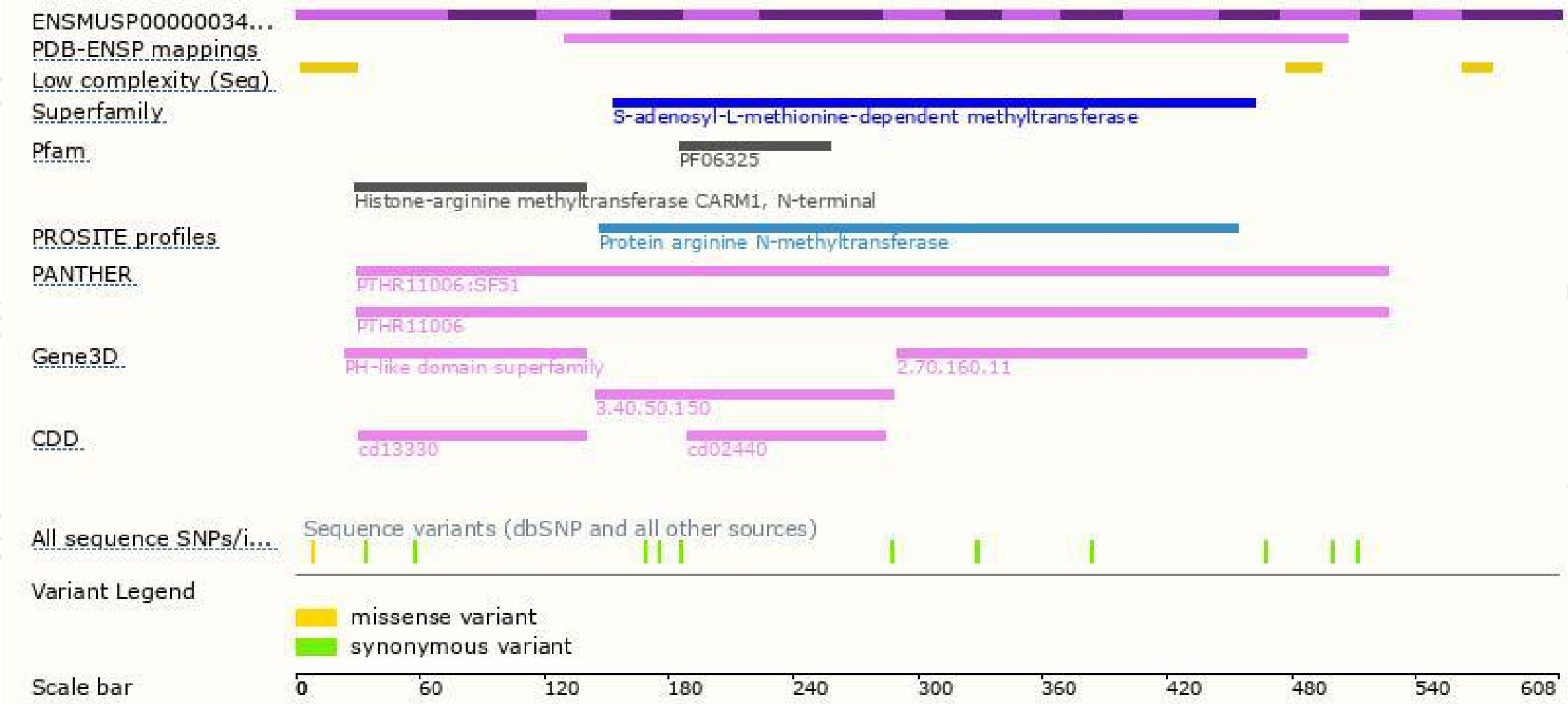
The strategy is based on the design of *Carm1-201* transcript,the transcription is shown below：



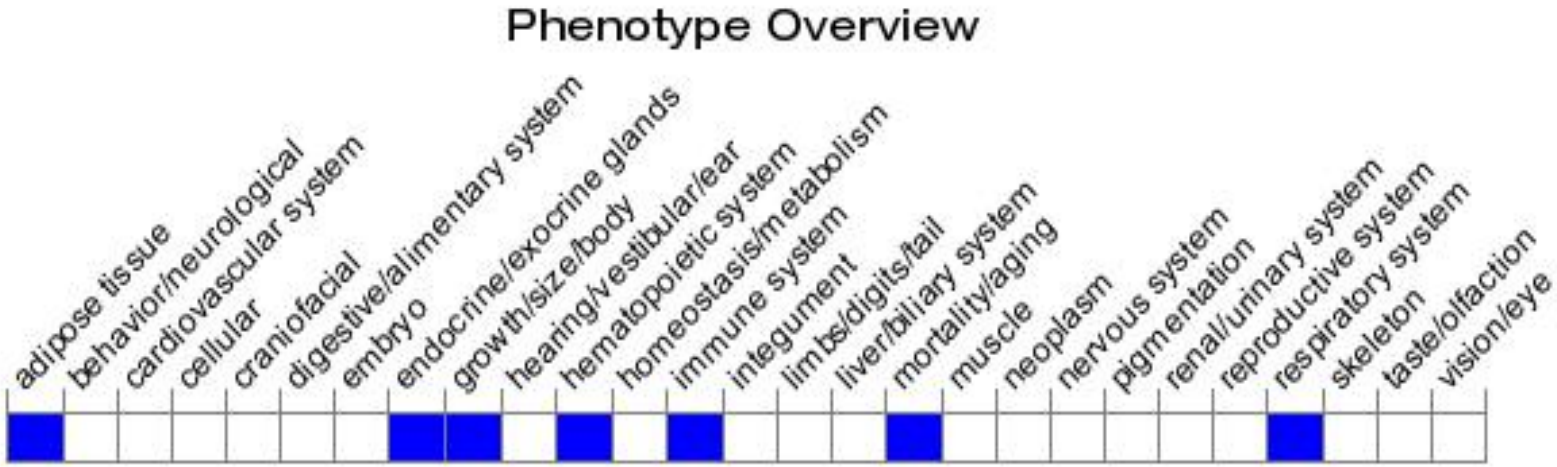
Genomic location distribution



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.

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