Phf20 Cas9-CKO Strategy

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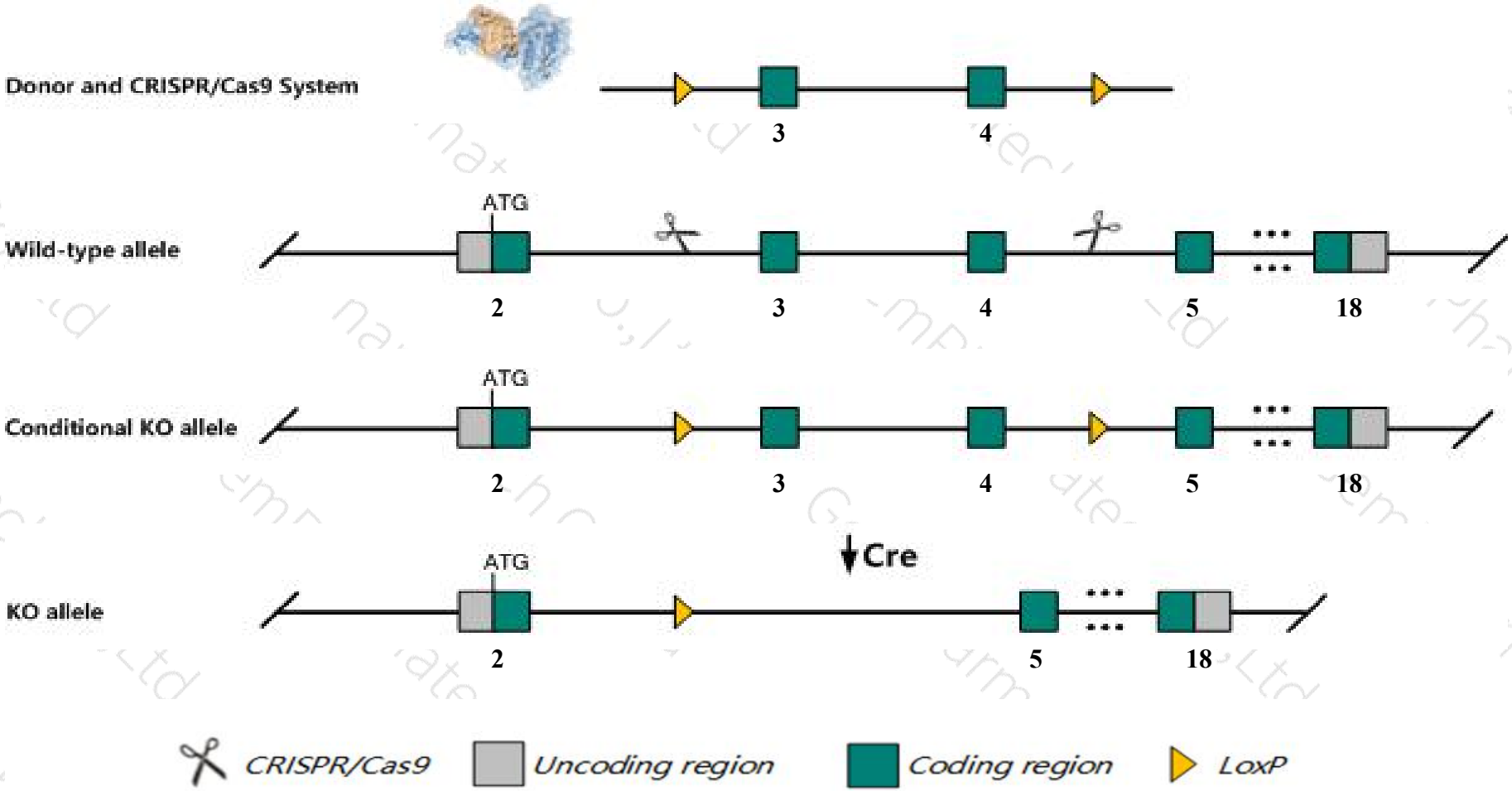
Project Overview

Project Name	***Phf20***
Project type	**Cas9-CKO**
Strain background	**C57BL/6JGpt**

Conditional Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *Phf20* gene. The schematic diagram is as follows:



Technical routes

➢ The *Phf20* gene has 11 transcripts. According to the structure of *Phf20* gene, exon3-exon4 of *Phf20-201*(ENSMUST00000037401.9) transcript is recommended as the knockout region.The region contains 257bp coding sequence. Knock out the region will result in disruption of protein function.

➢ In this project we use CRISPR/Cas9 technology to modify *Phf20* 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,mice homozygous for a knock-out allele exhibit neonatal lethality, decreased body size and total body fat amount, and abnormal skeletal and hematopoietic development.

➢Transcript 207 CDS 3' incomplete the influences is unknown.

➢ The *Phf20* 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 loxp insertion on gene transcription, RNA splicing and protein translation cannot be predicted at existing technological level.

Gene information （NCBI）

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Phf20 PHD finger protein 20 [Mus musculus (house mouse)]

Gene ID: 228829, updated on 13-Mar-2020

Summary

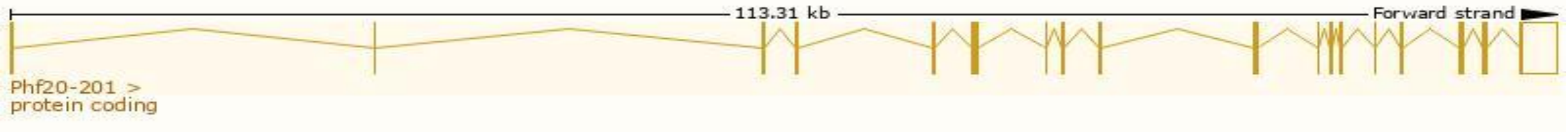
Official Symbol	Phf20 provided by MGI
Official Full Name	PHD finger protein 20 provided byMGI
Primary source	MGI:MGI:2444148
See related	Ensembl:ENSMUSG00000038116
Gene type	protein coding
RefSeq status	VALIDATED
Organism	Mus musculus
Lineage	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Myomorpha; Muroidea; Muridae; Murinae; Mus; Mus
Also known as	6820402O20Rik
Expression	Ubiquitous expression in cerebellum adult (RPKM 9.8), CNS E18 (RPKM 9.6) and 28 other tissuesSee more
Orthologs	human all

Transcript information（Ensembl）

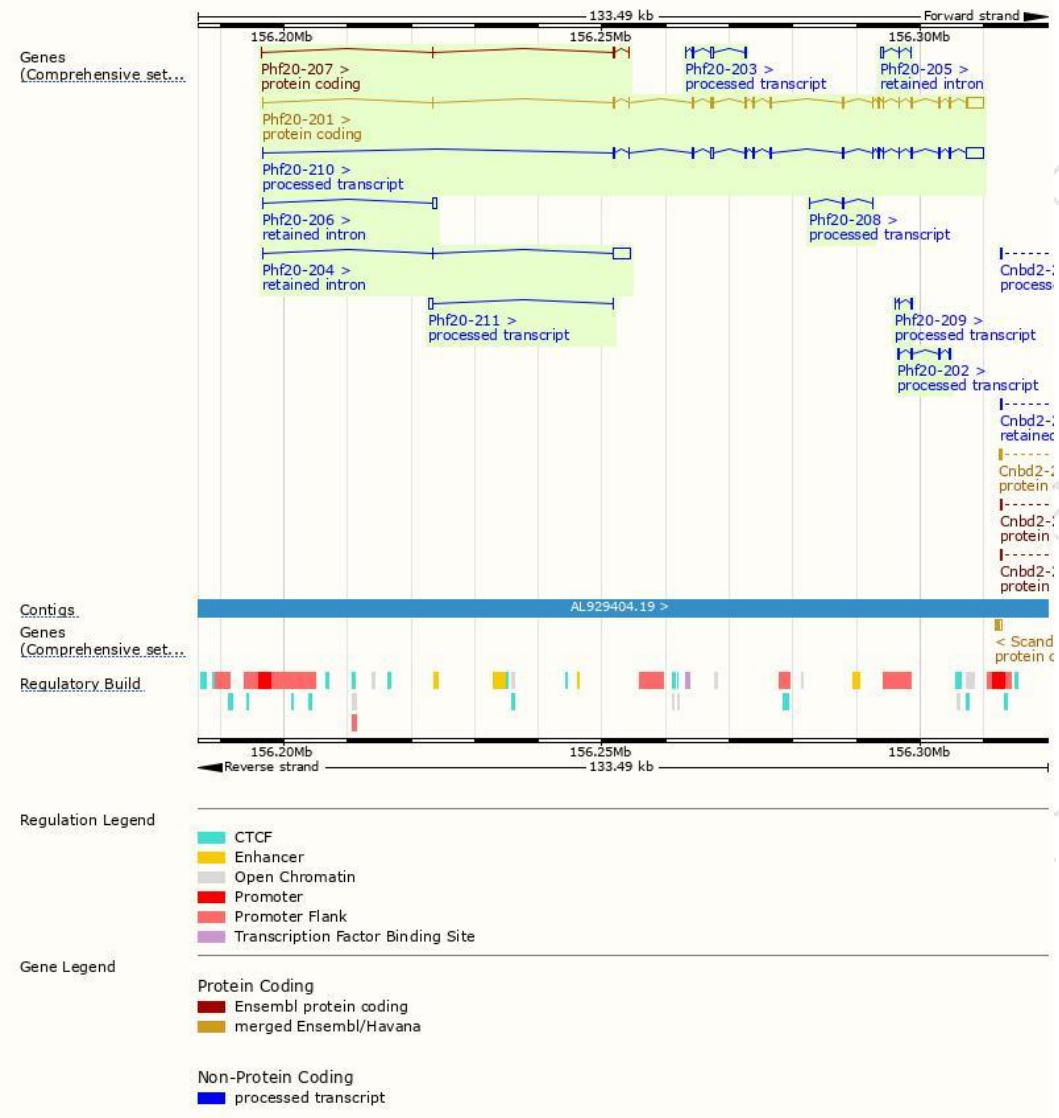
The gene has 11 transcripts,all transcripts are shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Phf20-201	ENSMUST00000037401.9	5737	1010aa	Protein coding	CCDS38297	Q8BLG0	TSL:1 GENCODE basic APPRIS P1
Phf20-207	ENSMUST00000145731.7	453	113aa	Protein coding	-	A2AV92	CDS 3' incomplete TSL:3
Phf20-210	ENSMUST00000152617.7	5524	No protein	Processed transcript	-	-	TSL:5
Phf20-202	ENSMUST00000122814.1	903	No protein	Processed transcript	-	-	TSL:5
Phf20-203	ENSMUST00000131479.1	605	No protein	Processed transcript	-	-	TSL:3
Phf20-211	ENSMUST00000153822.1	605	No protein	Processed transcript	-	-	TSL:2
Phf20-208	ENSMUST00000147234.1	377	No protein	Processed transcript	-	-	TSL:3
Phf20-209	ENSMUST00000147242.7	368	No protein	Processed transcript	-	-	TSL:5
Phf20-204	ENSMUST00000132129.1	2896	No protein	Retained intron	-	-	TSL:1
Phf20-205	ENSMUST00000132352.1	703	No protein	Retained intron	-	-	TSL:5
Phf20-206	ENSMUST00000135796.1	702	No protein	Retained intron	-	-	TSL:3

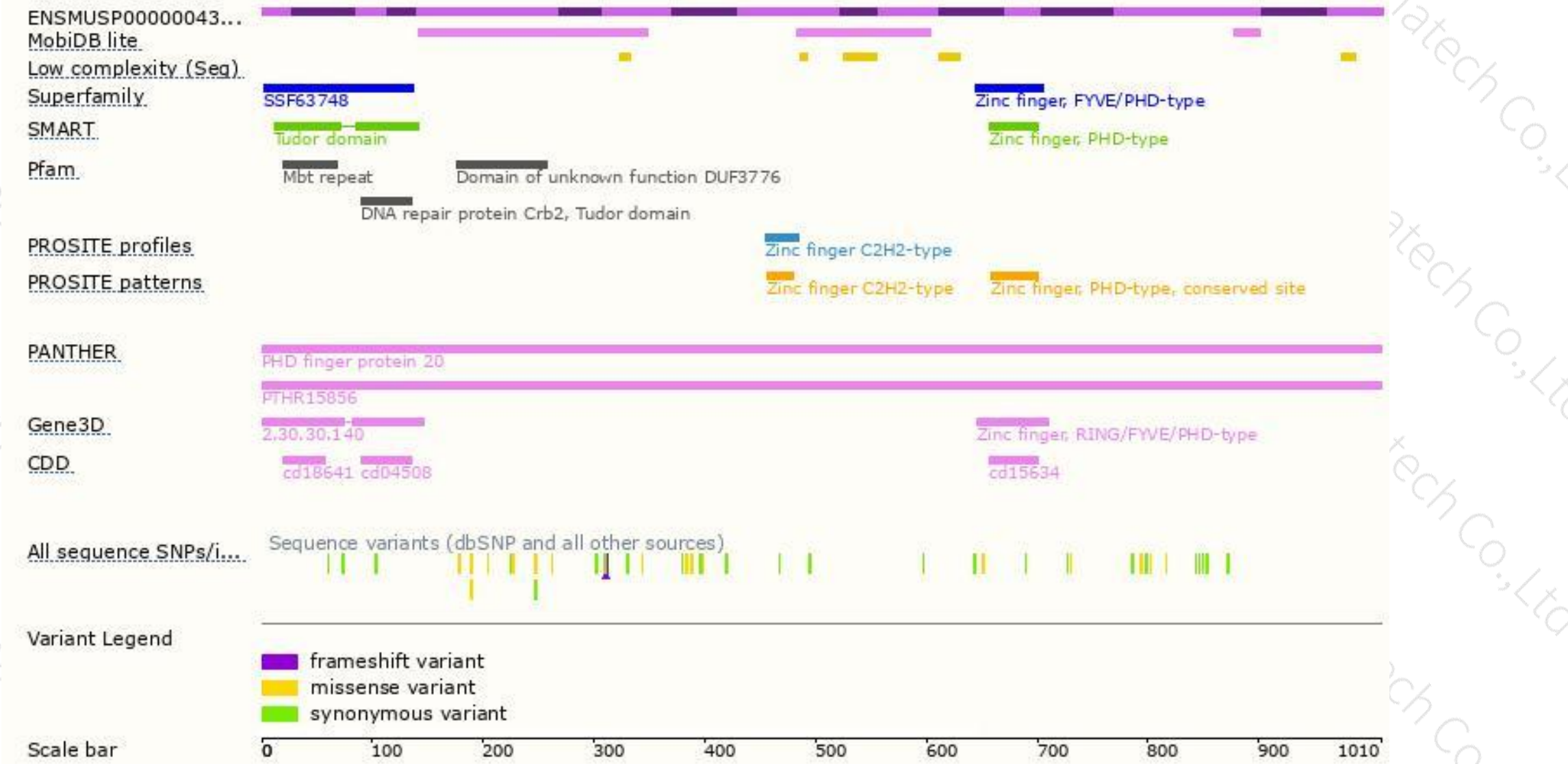
The strategy is based on the design of *Phf20-201* transcript,the transcription is shown below:



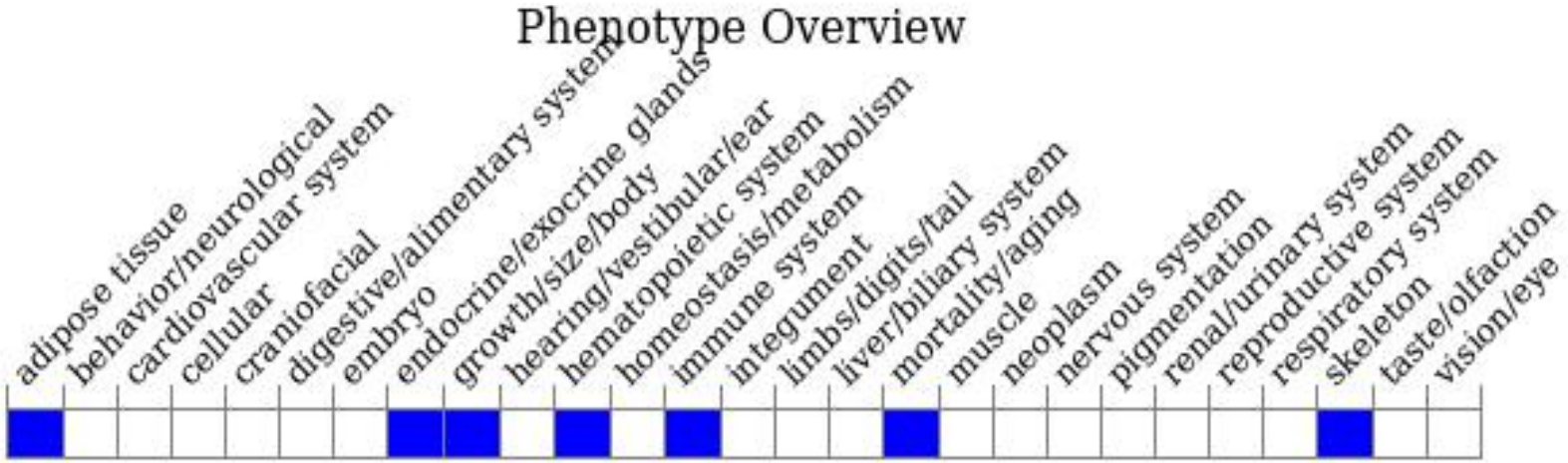
Genomic location distribution



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,mice homozygous for a knock-out allele exhibit neonatal lethality, decreased body size and total body fat amount, and abnormal skeletal and hematopoietic development.

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

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