

Eif4a3 Cas9-CKO Strategy

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Project Overview

Project Name

Eif4a3

Project type

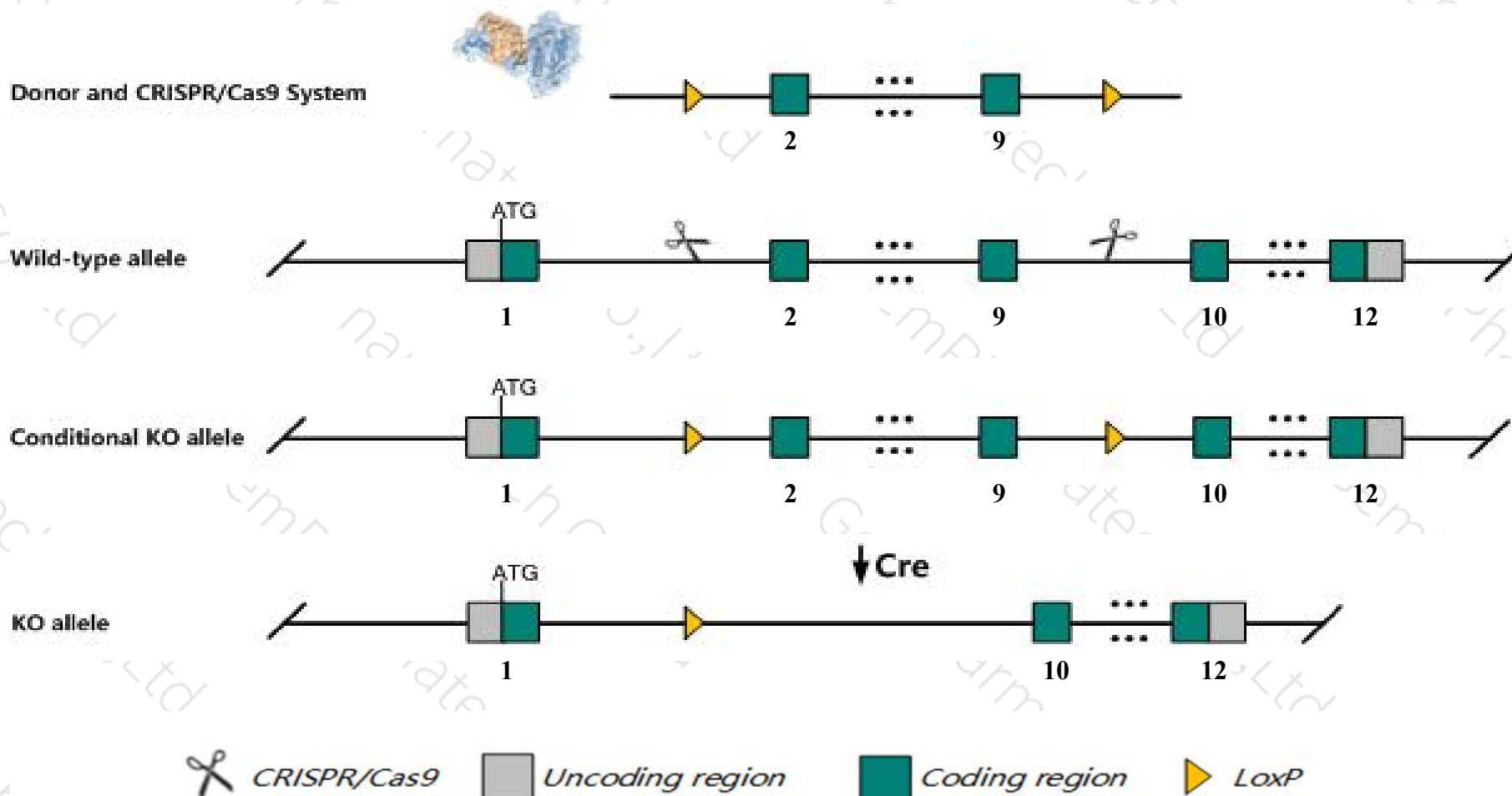
Cas9-CKO

Strain background

C57BL/6JGpt

Conditional Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *Eif4a3* gene. The schematic diagram is as follows:



Technical routes

- The *Eif4a3* gene has 6 transcripts. According to the structure of *Eif4a3* gene, exon2-exon9 of *Eif4a3-201* (ENSMUST00000026667.14) transcript is recommended as the knockout region. The region contains 814bp coding sequence. Knock out the region will result in disruption of protein function.
- In this project we use CRISPR/Cas9 technology to modify *Eif4a3* 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

- The *Eif4a3* gene is located on the Chr11. 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)

Eif4a3 eukaryotic translation initiation factor 4A3 [Mus musculus (house mouse)]

Gene ID: 192170, updated on 13-Mar-2020

Summary



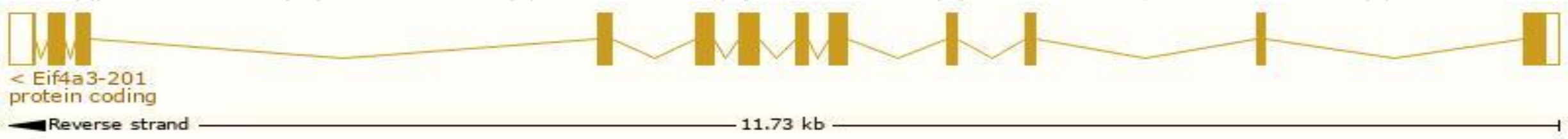
Official Symbol	Eif4a3 provided by MGI
Official Full Name	eukaryotic translation initiation factor 4A3 provided by MGI
Primary source	MGI:MGI:1923731
See related	Ensembl:ENSMUSG00000025580
Gene type	protein coding
RefSeq status	PROVISIONAL
Organism	Mus musculus
Lineage	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Myomorpha; Muroidea; Muridae; Murinae; Mus; Mus
Also known as	2400003O03Rik, Ddx48, eIF4A-III, mKIAA0111
Expression	Ubiquitous expression in CNS E11.5 (RPKM 64.0), limb E14.5 (RPKM 53.1) and 28 other tissues See more
Orthologs	human all

Transcript information (Ensembl)

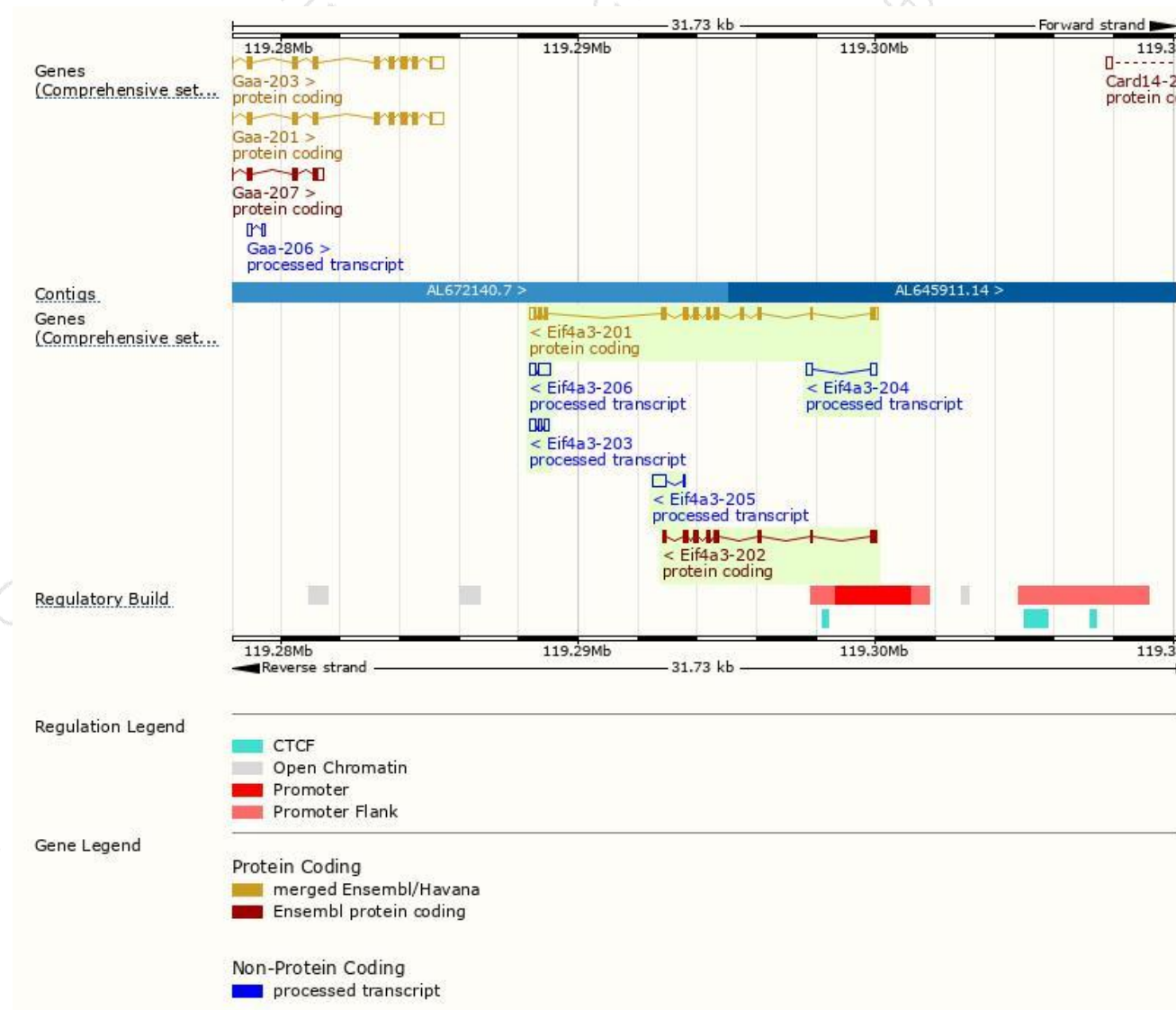
The gene has 6 transcripts,all transcripts are shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Eif4a3-201	ENSMUST00000026667.14	1509	411aa	Protein coding	CCDS25714	Q91VC3	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 P1
Eif4a3-202	ENSMUST00000106253.1	916	299aa	Protein coding	-	A2AFK7	CDS 3' incomplete TSL:5
Eif4a3-206	ENSMUST00000138849.1	613	No protein	Processed transcript	-	-	TSL:2
Eif4a3-205	ENSMUST00000135294.1	473	No protein	Processed transcript	-	-	TSL:3
Eif4a3-203	ENSMUST00000129044.7	466	No protein	Processed transcript	-	-	TSL:2
Eif4a3-204	ENSMUST00000134743.1	377	No protein	Processed transcript	-	-	TSL:2

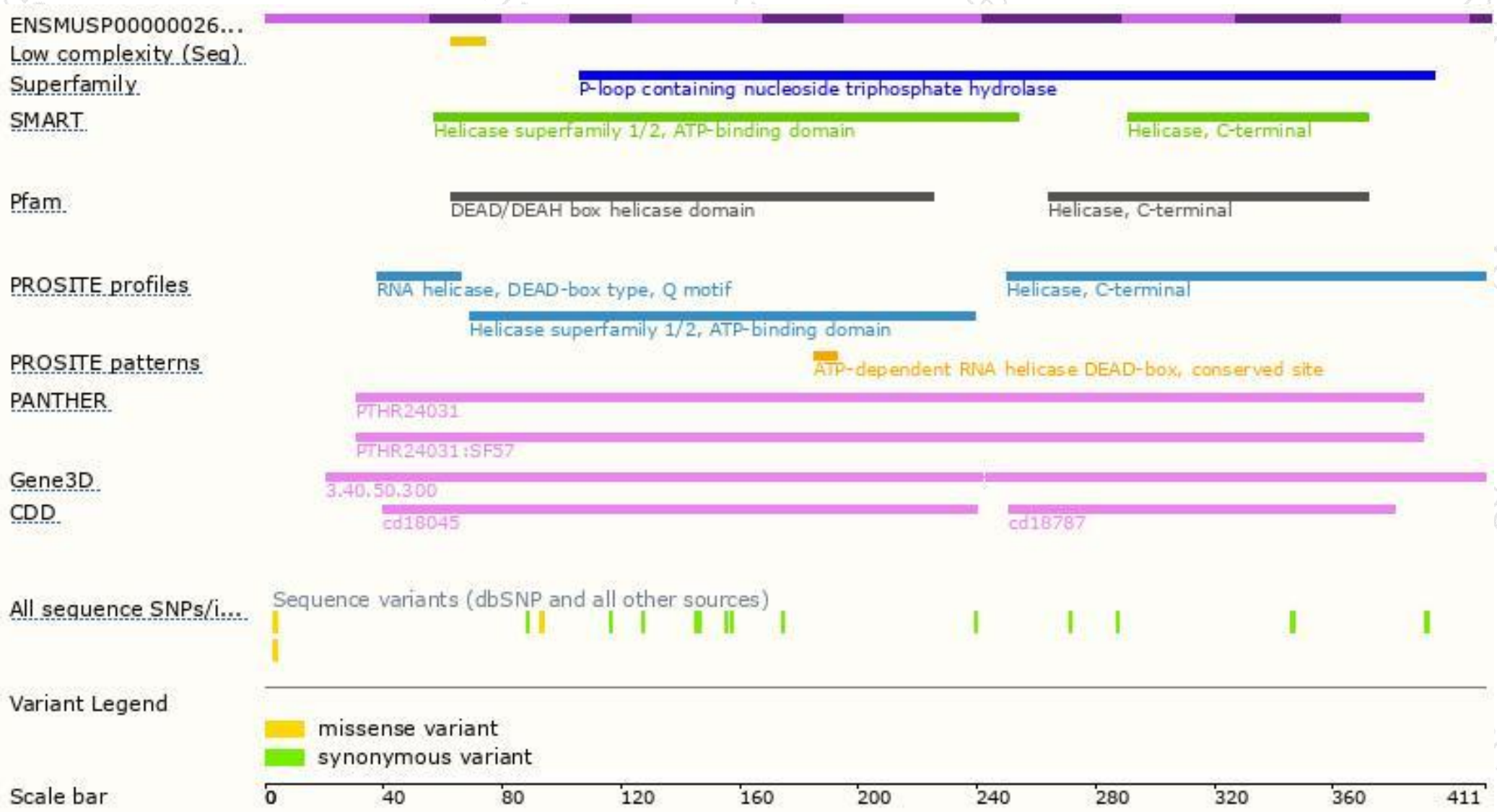
The strategy is based on the design of *Eif4a3-201* transcript,the transcription is shown below:



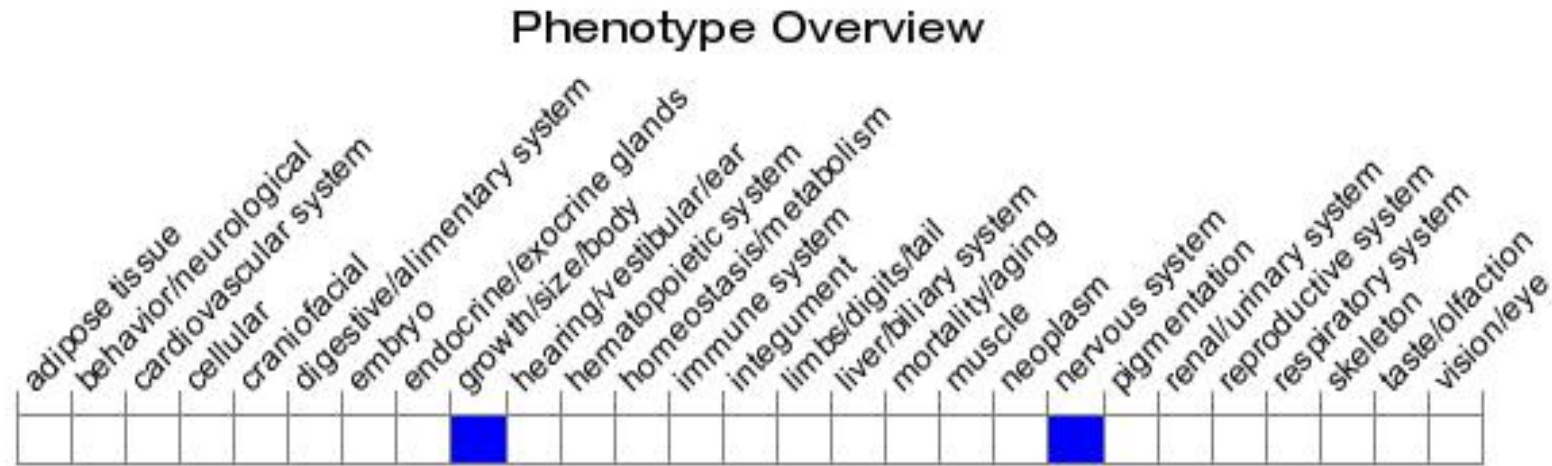
Genomic location distribution



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/>).

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

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