

Egr2 Cas9-CKO Strategy

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Project Overview

Project Name

Egr2

Project type

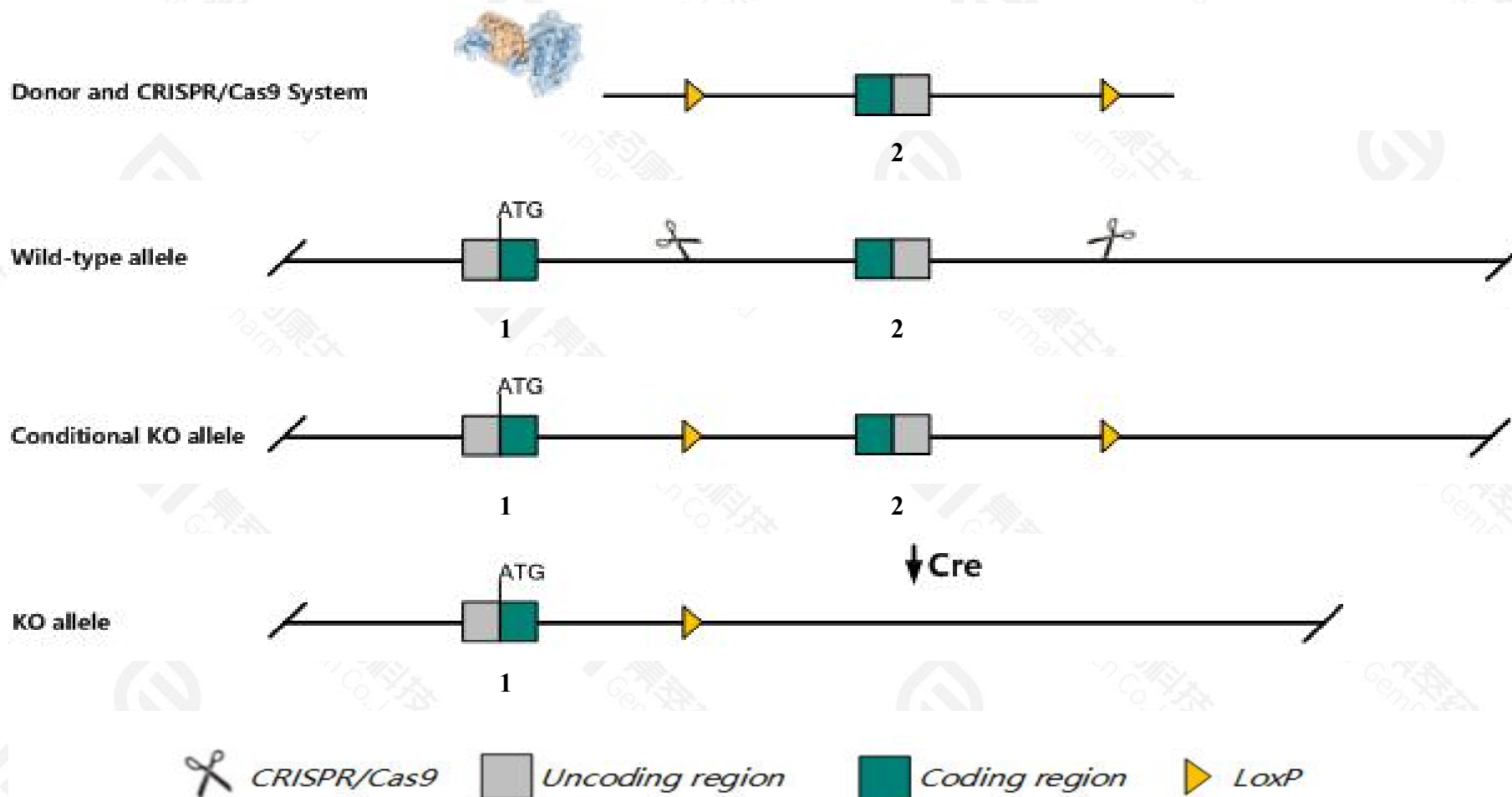
Cas9-CKO

Strain background

C57BL/6JGpt

Conditional Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *Egr2* gene. The schematic diagram is as follows:



- The *Egr2* gene has 7 transcripts. According to the structure of *Egr2* gene, exon2 of *Egr2-201*(ENSMUST00000048289.14) 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 *Egr2* 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.

- According to the existing MGI data, homozygotes for targeted mutations exhibit absence of rhombomeres 3 and 5 of the hindbrain affecting axonal migration, disrupted myelination of Schwann cells, slow respiratory and jaw opening rhythms, skeletal abnormalities, and perinatal lethality.
- The *Egr2* gene is located on the Chr10. 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)

Egr2 early growth response 2 [Mus musculus (house mouse)]

Gene ID: 13654, updated on 13-Mar-2020

Summary

Official Symbol Egr2 provided by [MGI](#)

Official Full Name early growth response 2 provided by [MGI](#)

Primary source [MGI:MGI:95296](#)

See related [Ensembl:ENSMUSG00000037868](#)

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 Egr-2, Krox-20, Krox20, NGF1-B, Zfp-25, Zfp-6

Expression Biased expression in genital fat pad adult (RPKM 22.3), thymus adult (RPKM 4.2) and 14 other tissues [See more](#)

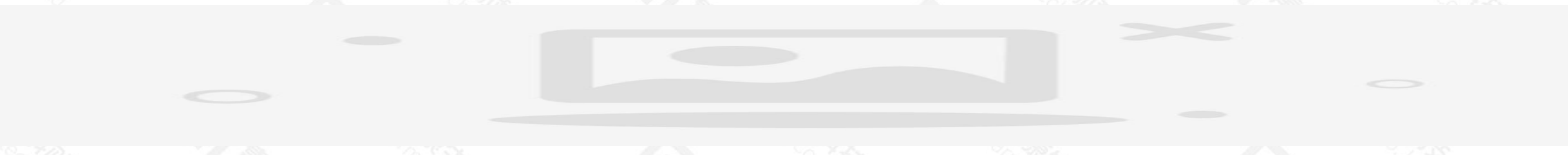
Orthologs [human](#) [all](#)

Transcript information (Ensembl)

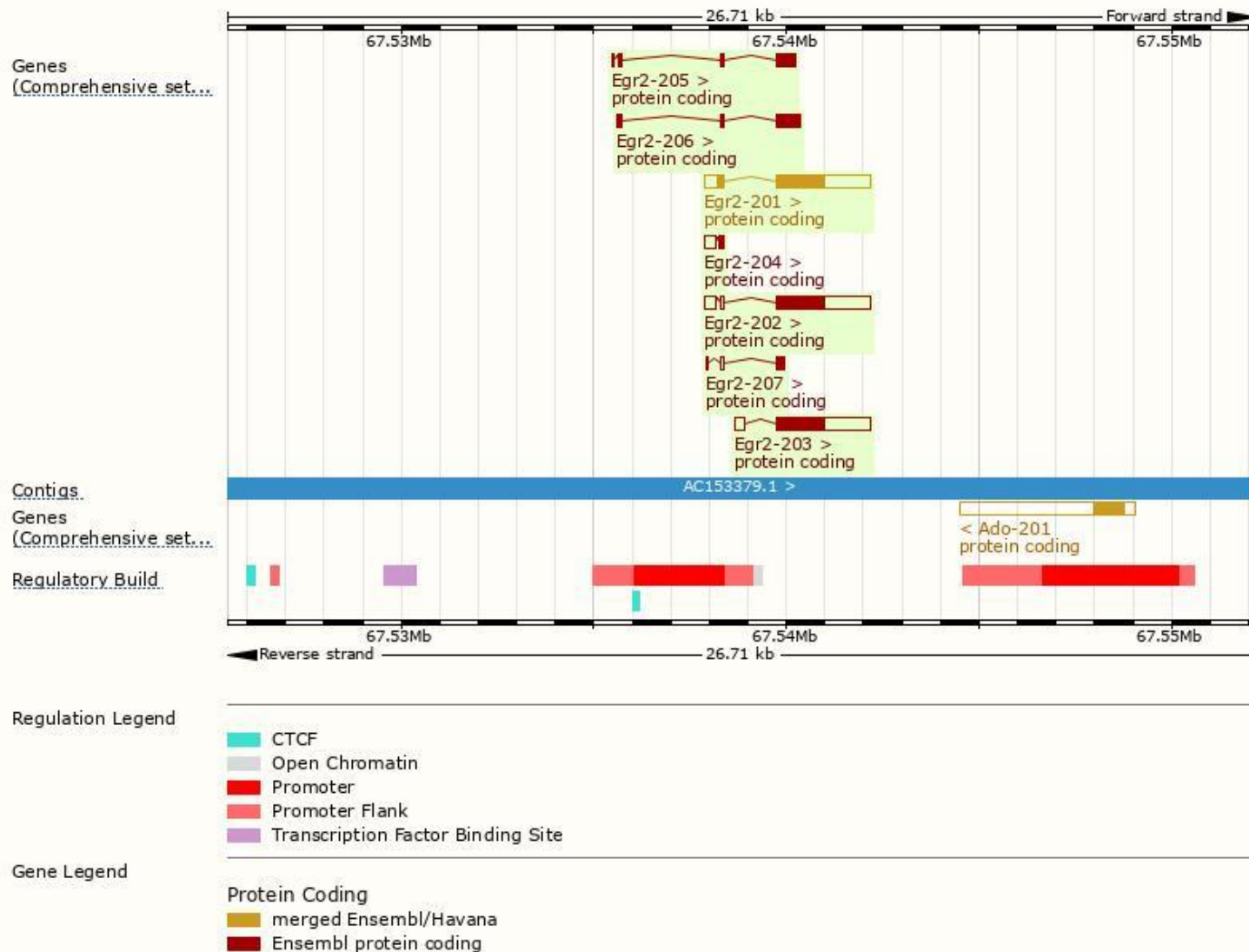
The gene has 7 transcripts, all transcripts are shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Egr2-201	ENSMUST00000048289.13	2965	470aa	Protein coding	CCDS35927	P08152_Q3U207	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
Egr2-202	ENSMUST00000105438.8	2864	420aa	Protein coding	CCDS83706	P08152	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
Egr2-203	ENSMUST00000127820.1	2665	412aa	Protein coding	-	D3Z3K7	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
Egr2-206	ENSMUST00000145936.1	902	281aa	Protein coding	-	D3YYY2	CDS 3' incomplete TSL:3
Egr2-205	ENSMUST00000145754.7	773	236aa	Protein coding	-	D3Z4G7	CDS 3' incomplete TSL:2
Egr2-204	ENSMUST00000130933.1	427	36aa	Protein coding	-	D3Z4X9	CDS 3' incomplete TSL:2
Egr2-207	ENSMUST00000146986.1	356	72aa	Protein coding	-	D3YXS2	CDS 3' incomplete TSL:2

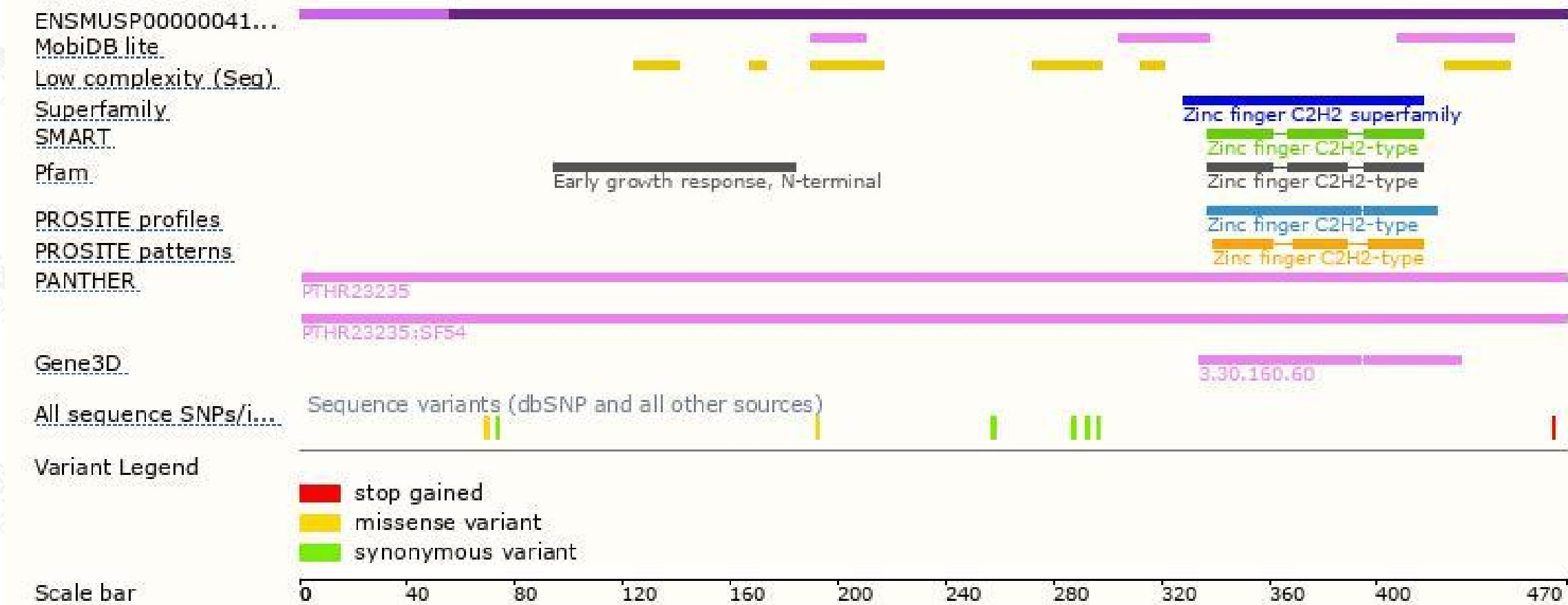
The strategy is based on the design of *Egr2-201* transcript, the transcription is shown below:



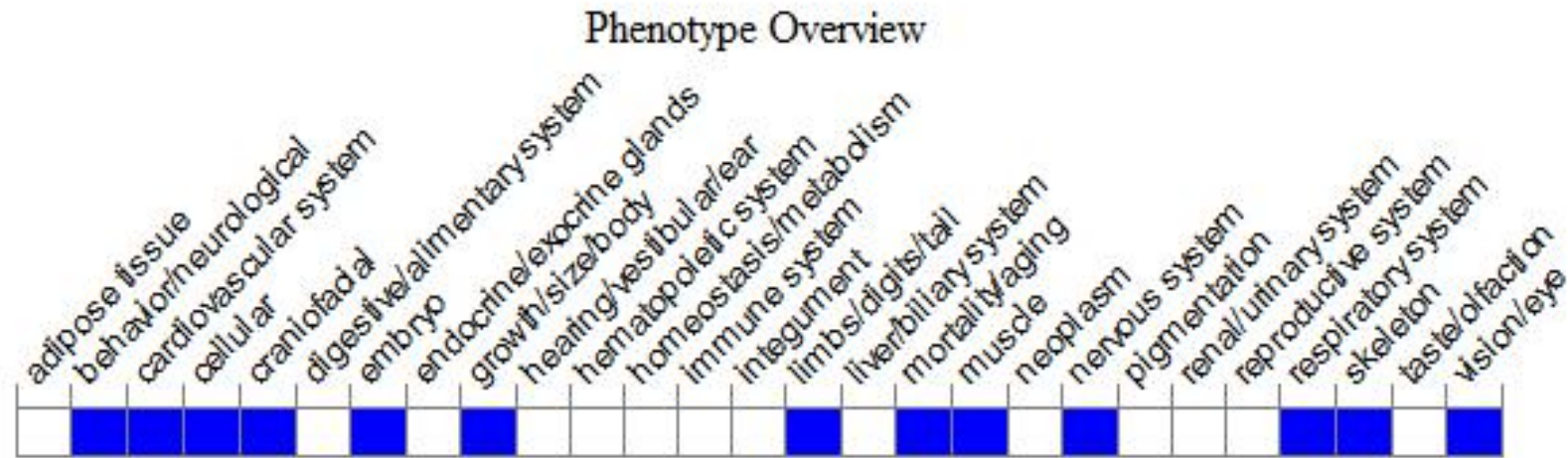
Genomic location distribution



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 targeted mutations exhibit absence of rhombomeres 3 and 5 of the hindbrain affecting axonal migration, disrupted myelination of Schwann cells, slow respiratory and jaw opening rhythms, skeletal abnormalities, and perinatal lethality.

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

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