Eml1 Cas9-CKO Strategy

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Project Overview

Project Name	***Eml1***
Project type	**Cas9-CKO**
Strain background	**C57BL/6JGpt**

Conditional Knockout strategy

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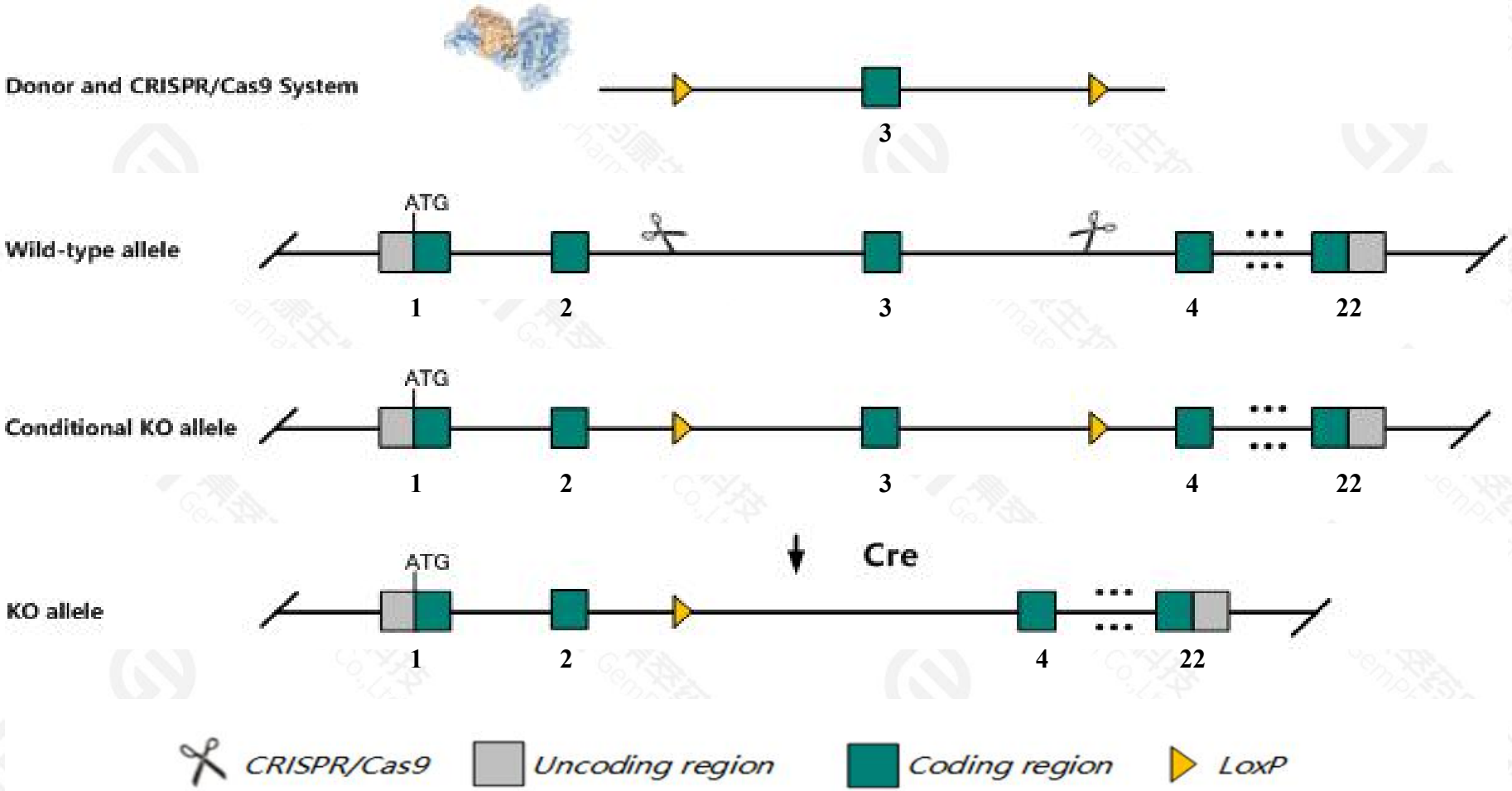
This model will use CRISPR/Cas9 technology to edit the *Eml1* gene. The schematic diagram is as follows:



Technical routes

➢ The *Eml1* gene has 8 transcripts. According to the structure of *Eml1* gene, exon3 of *Eml1-203*(ENSMUST00000109860.8) transcript is recommended as the knockout region.The region contains 133bp coding sequence. Knock out the region will result in disruption of protein function.

➢ In this project we use CRISPR/Cas9 technology to modify *Eml1* 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 spontaneous mutation exhibit subcortical band heterotopia associated with seizures, developmental delay and behavioral deficits.

➢ The *Eml1* gene is located on the Chr12. 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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Eml1 echinoderm microtubule associated protein like 1 [Mus musculus (house mouse)]

Gene ID: 68519, updated on 17-Dec-2020

Summary

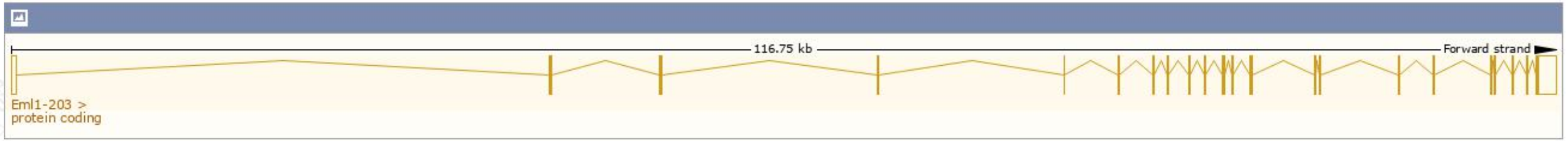
Official Symbol	Eml1 provided by MGI
Official Full Name	echinoderm microtubule associated protein like 1 provided by MGI
Primary source	MGI:MGI:1915769
See related	Ensembl:ENSMUSG00000058070
Gene type	protein coding
RefSeq status	VALIDATED
Organism	Mus musculus
Lineage	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Myomorpha; Muroidea; Muridae; Murinae; Mus; Mus
Also known as	1110008N23Rik, A930030P13Rik, AA171013, AI847476, AI853955, ELP, ELP79, EMAP, EMAP-1, EMAPL, hec, heco
Expression	Broad expression in bladder adult (RPKM 32.9), subcutaneous fat pad adult (RPKM 15.9) and 22 other tissues See more
Orthologs	human all

Transcript information（Ensembl）

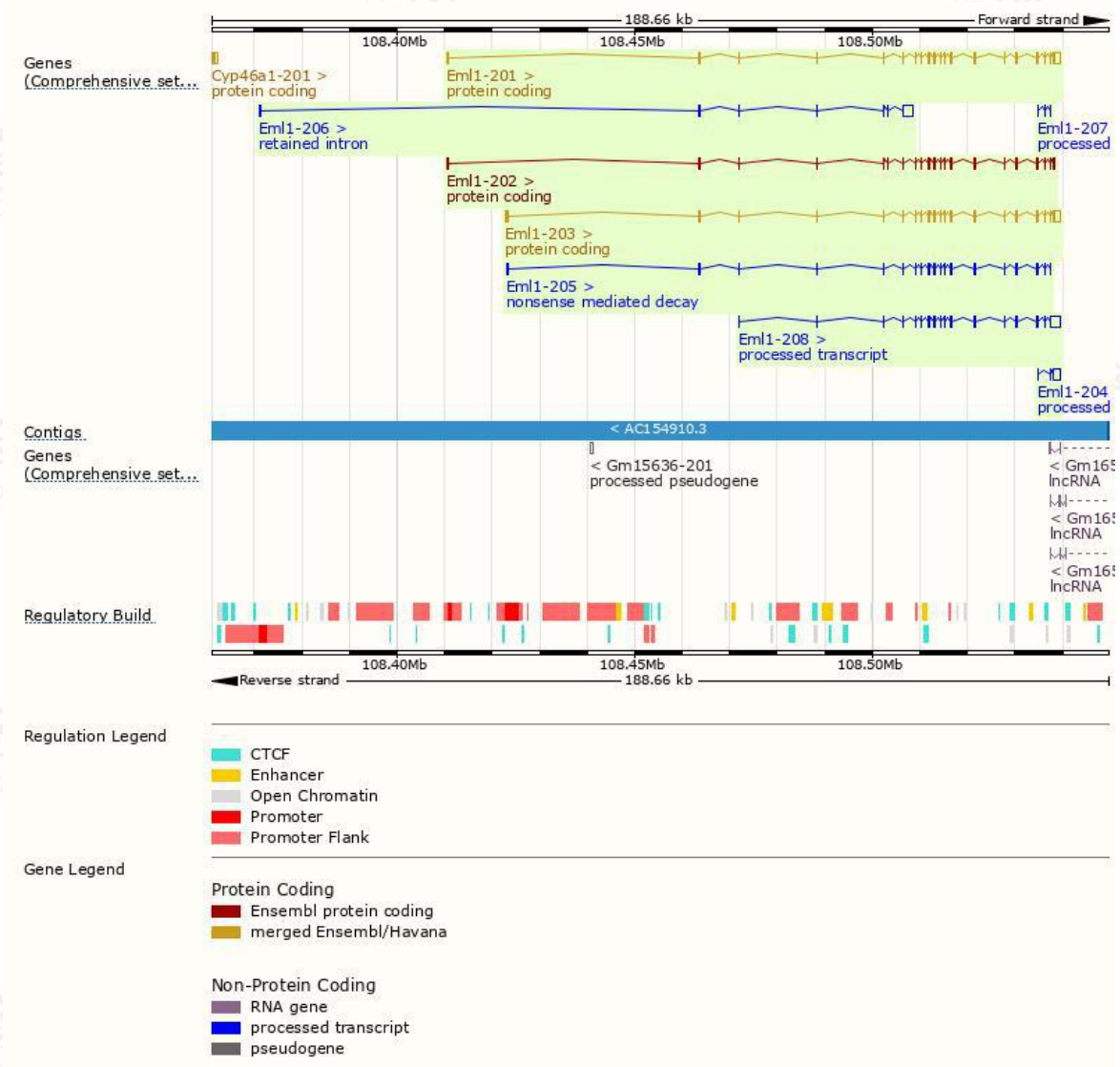
The gene has 8 transcripts,all transcripts are shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Eml1-203	ENSMUST00000109860.8	4160	814aa	Protein coding	CCDS36555		TSL:1 , GENCODE basic , APPRIS P1 ,
Eml1-201	ENSMUST00000054955.14	3879	783aa	Protein coding	CCDS36556		TSL:1 , GENCODE basic ,
Eml1-202	ENSMUST00000109857.8	2627	800aa	Protein coding	CCDS70420		TSL:1 , GENCODE basic ,
Eml1-205	ENSMUST00000130999.2	2493	699aa	Nonsense mediated decay	-		TSL:2 ,
Eml1-208	ENSMUST00000155544.8	4169	No protein	Processed transcript	-		TSL:5 ,
Eml1-204	ENSMUST00000123035.2	1730	No protein	Processed transcript	-		TSL:1 ,
Eml1-207	ENSMUST00000148186.2	332	No protein	Processed transcript	-		TSL:3 ,
Eml1-206	ENSMUST00000138456.8	2984	No protein	Retained intron	-		TSL:1 ,

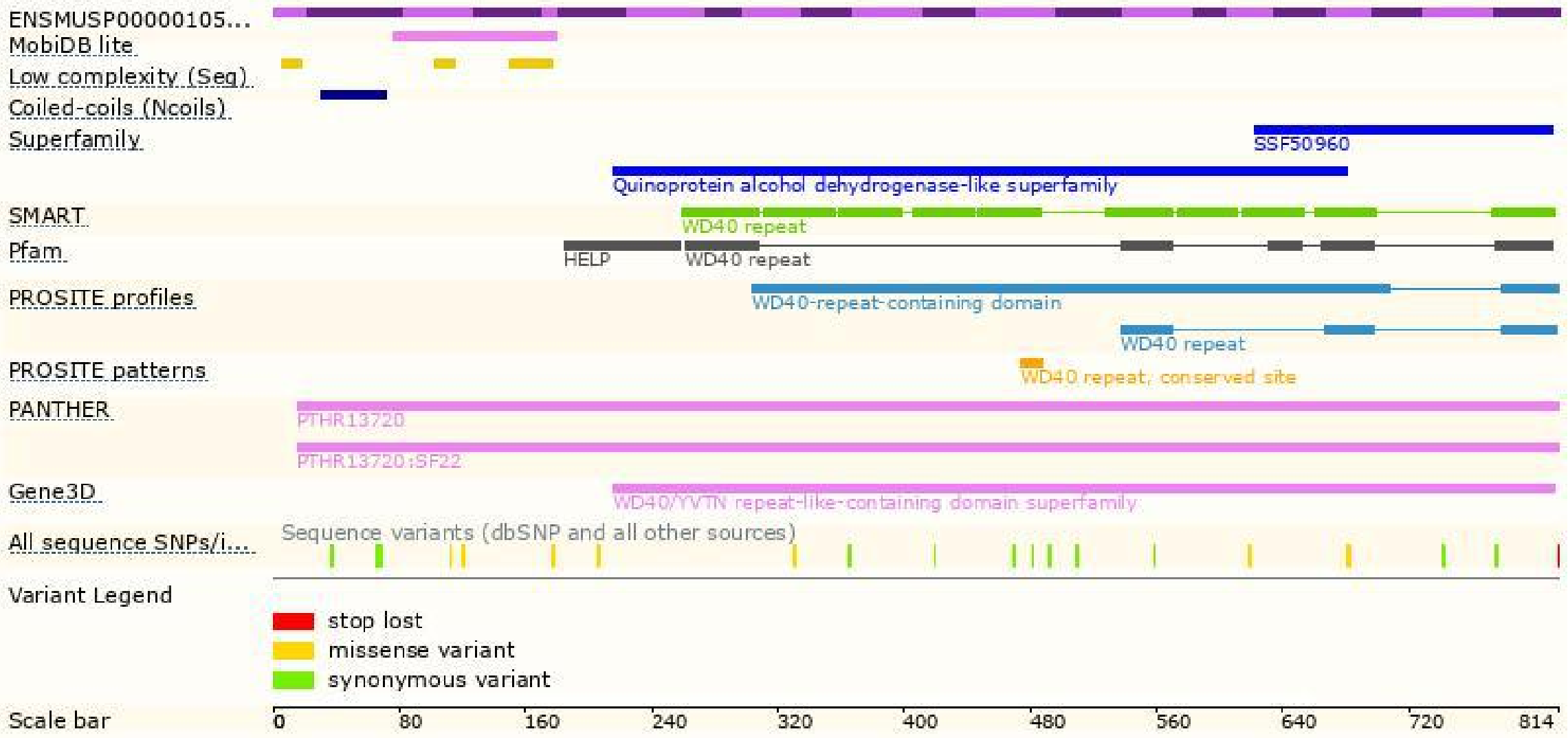
The strategy is based on the design of *Eml1-203* transcript,the transcription is shown below:



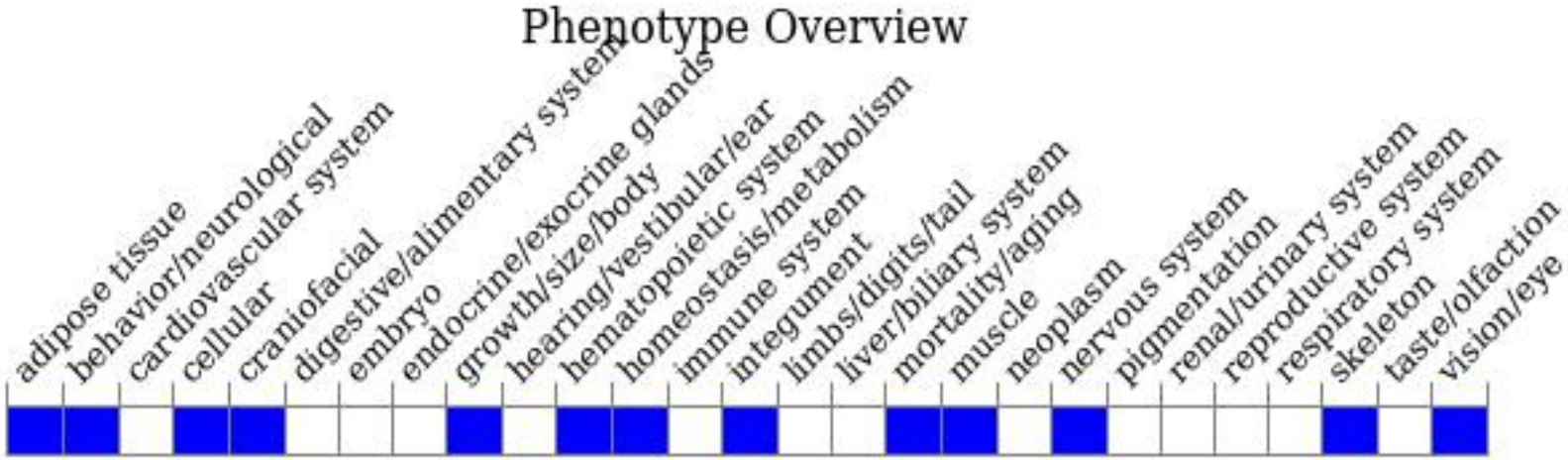
Genomic location distribution



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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