Foxp2 Cas9-KO Strategy

Designer:

Reviewer:

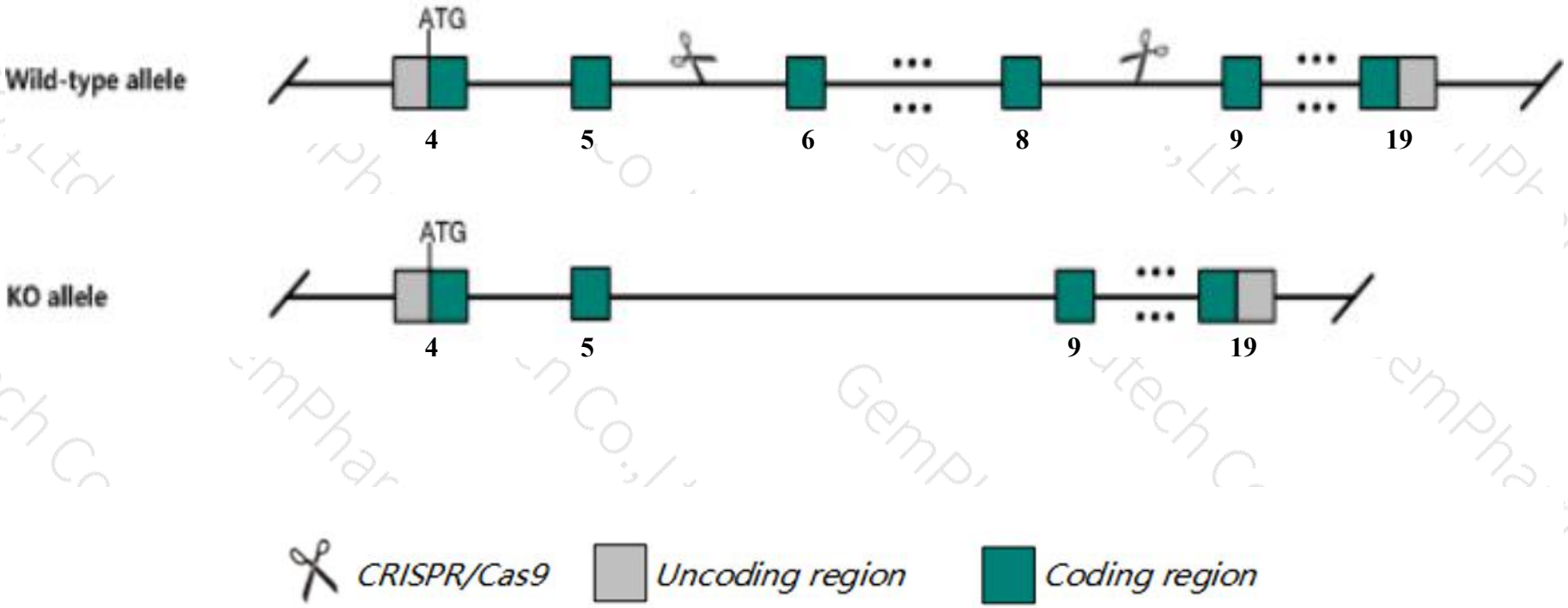
Design Date:

Project Overview

Project Name	***Foxp2***
Project type	**Cas9-KO**
Strain background	**C57BL/6JGpt**

Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *Foxp2* gene. The schematic diagram is as follows:



Technical routes

➢ The *Foxp2* gene has 20 transcripts. According to the structure of *Foxp2* gene, exon6-exon8 of *Foxp2-207*(ENSMUST00000115477.7) transcript is recommended as the knockout region.The region contains 514bp coding sequence. Knock out the region will result in disruption of protein function.

➢ In this project we use CRISPR/Cas9 technology to modify *Foxp2* gene. The brief process is as follows: CRISPR/Cas9 system 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.

Notice

➢ According to the existing MGI data,homozygous null mice display postnatal lethality, growth retardation, reduced vocalization, prolonged external granule cell layer presence, abnormal Purkinje and radial glial cells, delayed eye opening and ear emergence, negative geotaxis, impaired righting response, and hypoactivity.

➢ Transcript *Foxp2*-211&217&218&219&220 may not be affected.

➢ The effect on transcript *Foxp2*-203&208&212&216 is unknown.

➢ The *Foxp2* gene is located on the Chr6. 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 the gene knockout on gene transcription, RNA splicing and protein translation cannot be predicted at the existing technology level.

Gene information（NCBI）

Foxp2 forkhead box P2 [Mus musculus (house mouse)]

Gene ID: 114142, updated on 15-Mar-2020

Summary

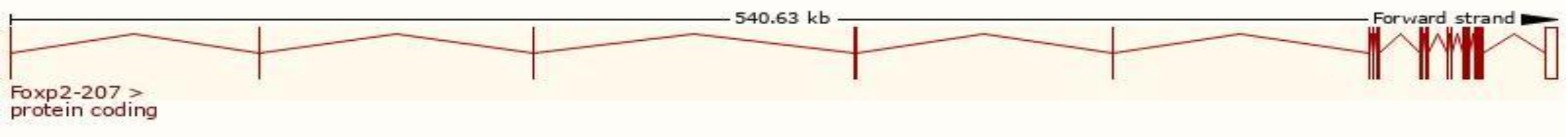
Official Symbol	Foxp2 provided by MGI
Official Full Name	forkhead box P2 provided byMGI
Primary source	MGI:MGI:2148705
See related	Ensembl:ENSMUSG00000029563
Gene type	protein coding
RefSeq status	VALIDATED
Organism	Mus musculus
Lineage	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Myomorpha; Muroidea; Muridae; Murinae; Mus; Mus
Also known as	2810043D05Rik, AI449000, CAG-16, D0Kist7
Expression	Biased expression in whole brain E14.5 (RPKM 9.5), CNS E14 (RPKM 7.9) and 13 other tissuesSee more
Orthologs	human all

Transcript information（Ensembl）

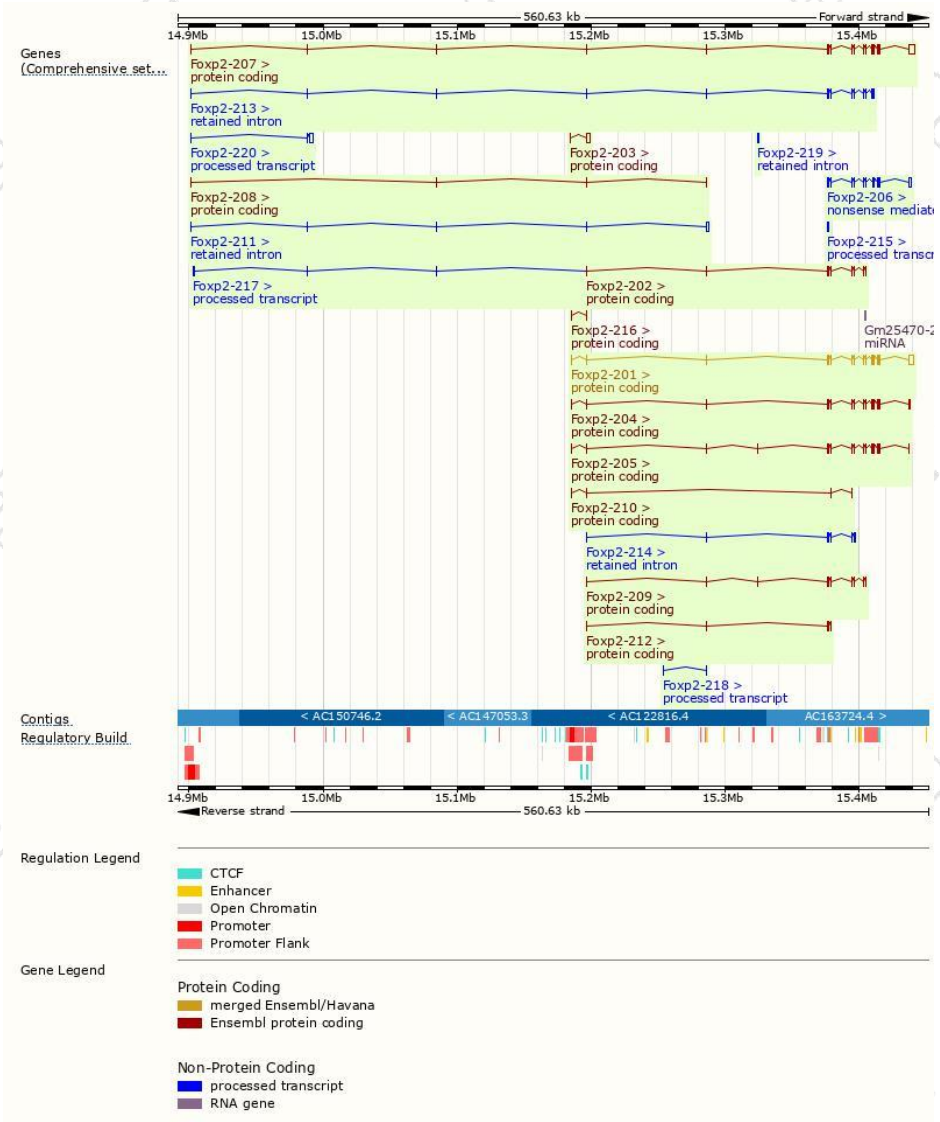
The gene has 20 transcripts,all transcripts are shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Foxp2-207	ENSMUST00000115477.7	6760	714aa	Protein coding	CCDS19918	P58463	TSL:1 GENCODE basic APPRIS P3
Foxp2-201	ENSMUST00000031545.13	5647	714aa	Protein coding	CCDS19918	P58463	TSL:1 GENCODE basic APPRIS P3
Foxp2-204	ENSMUST00000115472.7	2687	693aa	Protein coding	CCDS71726	P58463	TSL:1 GENCODE basic APPRIS ALT2
Foxp2-203	ENSMUST00000115470.2	2692	83aa	Protein coding	-	Q3TPK1	TSL:1 GENCODE basic
Foxp2-205	ENSMUST00000115474.7	2544	739aa	Protein coding	-	D3Z142	TSL:5 GENCODE basic APPRIS ALT2
Foxp2-209	ENSMUST00000131414.7	1381	456aa	Protein coding	-	D3YUQ7	TSL:5 GENCODE basic
Foxp2-202	ENSMUST00000115469.7	1293	430aa	Protein coding	-	D3Z146	TSL:5 GENCODE basic
Foxp2-212	ENSMUST00000140557.7	792	260aa	Protein coding	-	D3Z2Q6	CDS 3' incomplete TSL:5
Foxp2-210	ENSMUST00000137628.7	778	171aa	Protein coding	-	D3Z4F4	CDS 3' incomplete TSL:3
Foxp2-208	ENSMUST00000128567.7	647	86aa	Protein coding	-	D3YUM2	CDS 3' incomplete TSL:5
Foxp2-216	ENSMUST00000154448.1	352	38aa	Protein coding	-	D3Z7E9	CDS 3' incomplete TSL:2
Foxp2-206	ENSMUST00000115475.6	2762	56aa	Nonsense mediated decay	-	F6UMM1	CDS 5' incomplete TSL:5
Foxp2-220	ENSMUST00000204869.2	2849	No protein	Processed transcript	-	-	TSL:1
Foxp2-215	ENSMUST00000152563.2	407	No protein	Processed transcript	-	-	TSL:5
Foxp2-217	ENSMUST00000156883.2	349	No protein	Processed transcript	-	-	TSL:5
Foxp2-218	ENSMUST00000159788.1	265	No protein	Processed transcript	-	-	TSL:5
Foxp2-213	ENSMUST00000151060.7	2877	No protein	Retained intron	-	-	TSL:1
Foxp2-214	ENSMUST00000151301.7	2103	No protein	Retained intron	-	-	TSL:5
Foxp2-211	ENSMUST00000138273.7	1770	No protein	Retained intron	-	-	TSL:1
Foxp2-219	ENSMUST00000203227.1	1178	No protein	Retained intron	-	-	TSL:NA

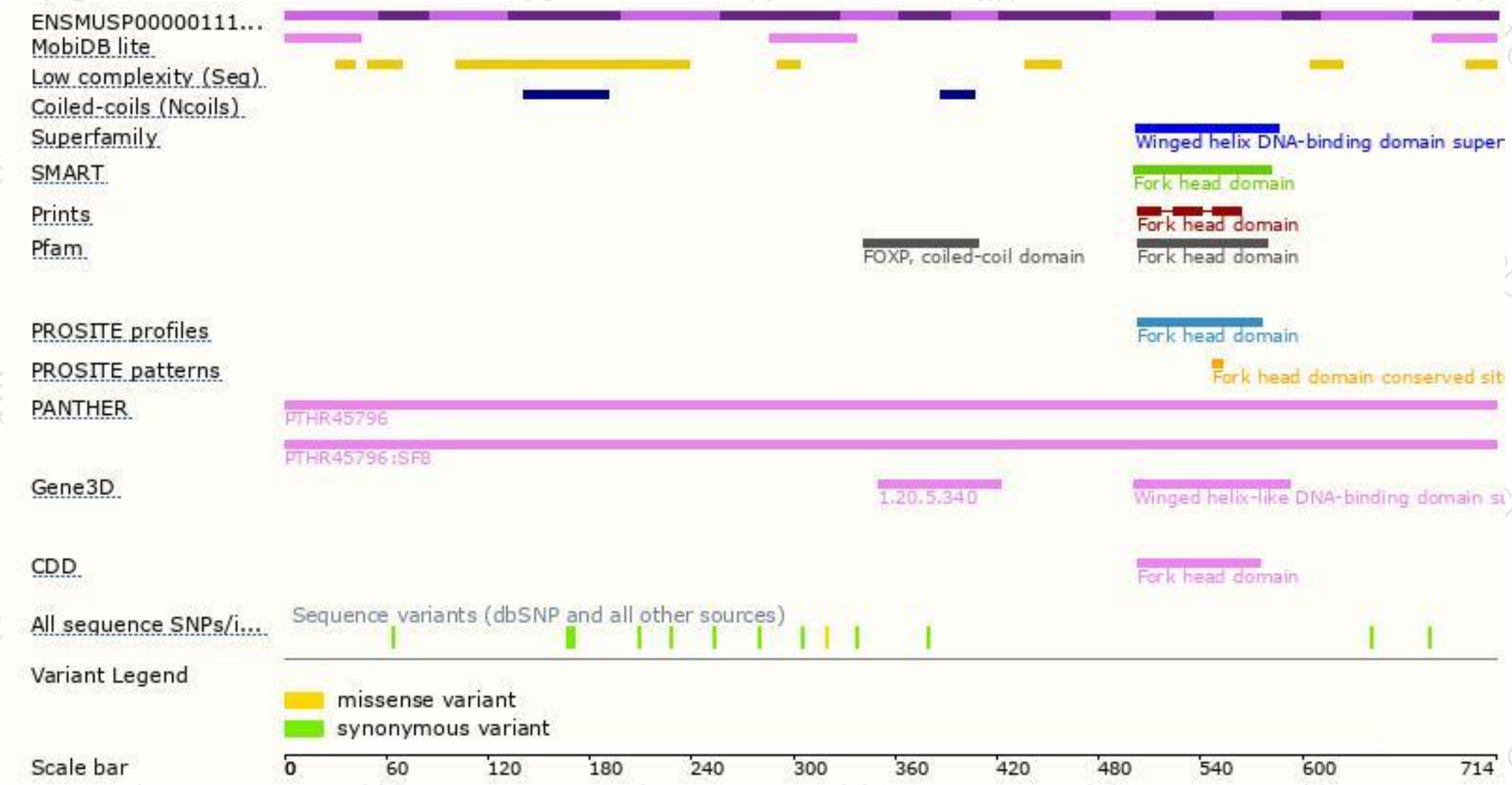
The strategy is based on the design of *Foxp2-207* transcript,the transcription is shown below:



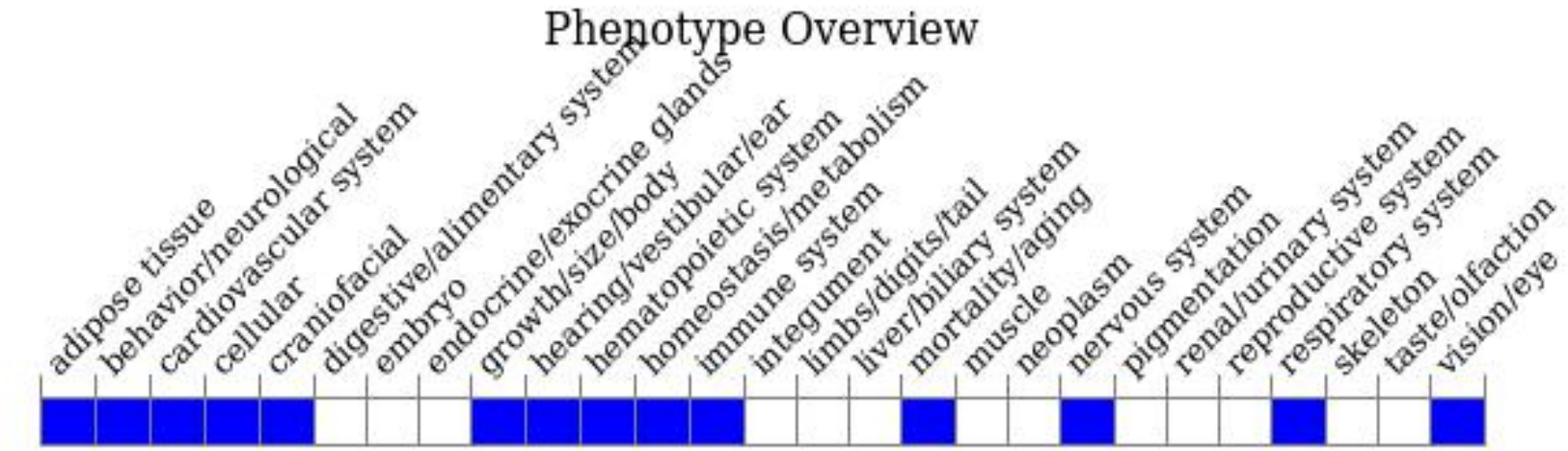
Genomic location distribution



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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