Kdm1a Cas9-CKO Strategy

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Design Date: 2019-9-11
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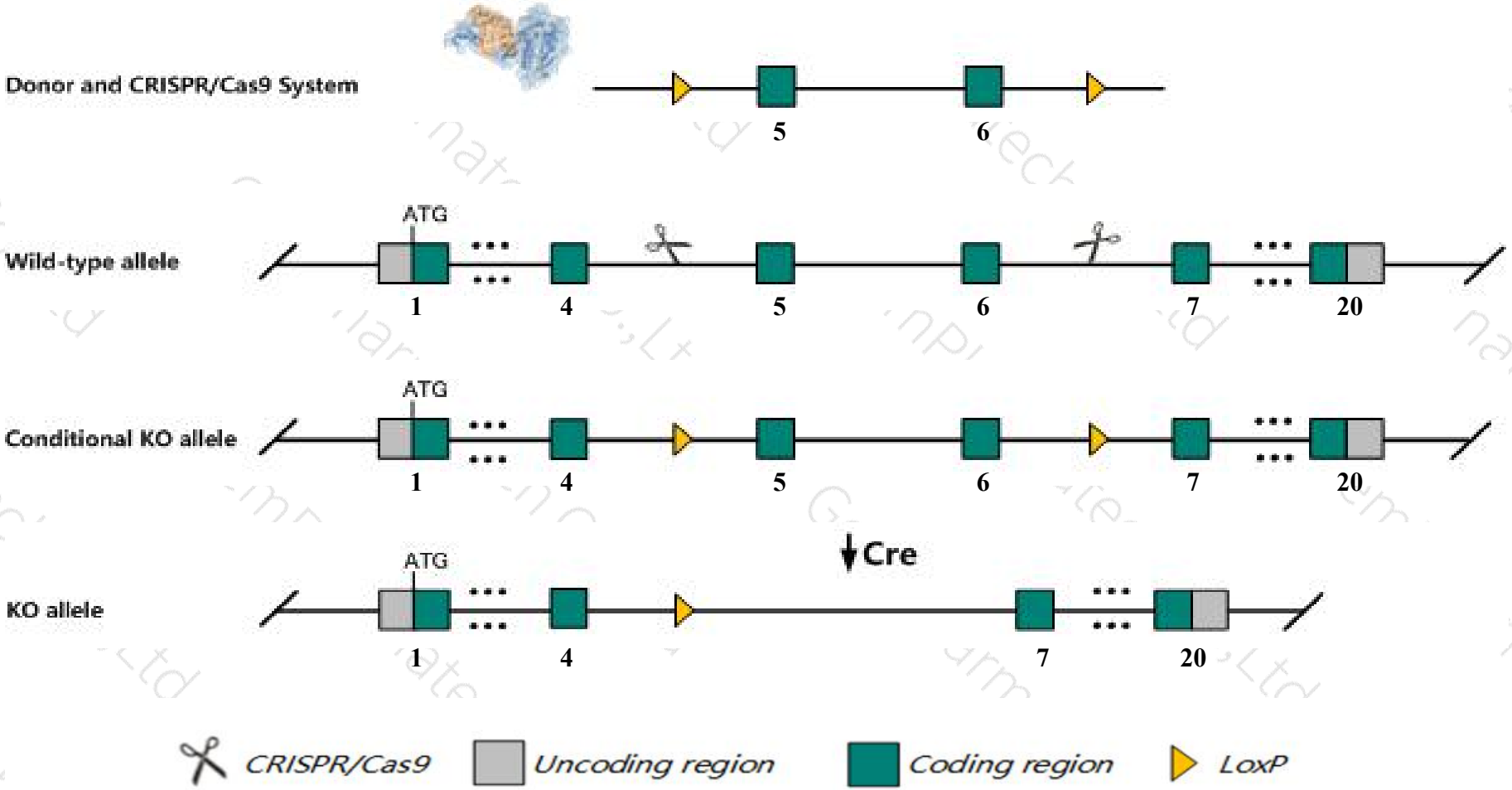
Project Overview

Project Name	***Kdm1a***
Project type	**Cas9-CKO**
Strain background	**C57BL/6JGpt**

Conditional Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *Kdm1a* gene. The schematic diagram is as follows:



Technical routes

- The *Kdm1a* gene has 9 transcripts. According to the structure of *Kdm1a* gene, exon5-exon6 of *Kdm1a-202* (ENSMUST00000105847.7) transcript is recommended as the knockout region.The region contains 172bp coding sequence. Knock out the region will result in disruption of protein function.

- In this project we use CRISPR/Cas9 technology to modify *Kdm1a* 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,Homozygous disruption of this gene results in abnormal gastrulation and early embryonic lethality. Homozygotes lacking the neurospecific isoform are hypoexcitable and display decreased susceptibility to pharmacologically induced seizures.

➢ The *Kdm1a* gene is located on the Chr4. 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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Kdm1a lysine (K)-specific demethylase 1A [Mus musculus (house mouse)]

Gene ID: 99982, updated on 17-Feb-2019

Summary

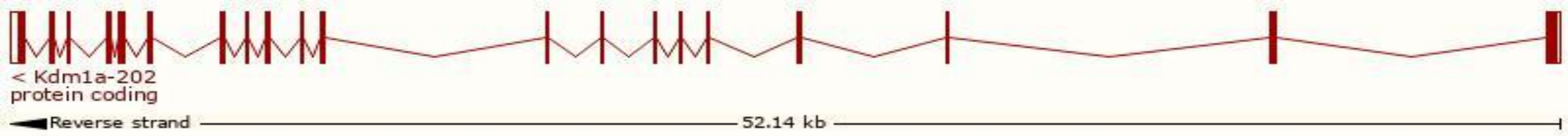
Official Symbol	Kdm1a provided by MGI
Official Full Name	lysine (K)-specific demethylase 1A provided by MGI
Primary source	MGI:MGI:1196256
See related	Ensembl:ENSMUSG00000036940
Gene type	protein coding
RefSeq status	VALIDATED
Organism	Mus musculus
Lineage	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Myomorpha; Muroidea; Muridae; Murinae; Mus; Mus
Also known as	1810043O07Rik, AA408884, Aof2, D4Ertd478e, Kdm1, Lsd1, mKIAA0601
Expression	Ubiquitous expression in CNS E14 (RPKM 42.5), whole brain E14.5 (RPKM 40.5) and 28 other tissues See more
Orthologs	human all

Transcript information（Ensembl）

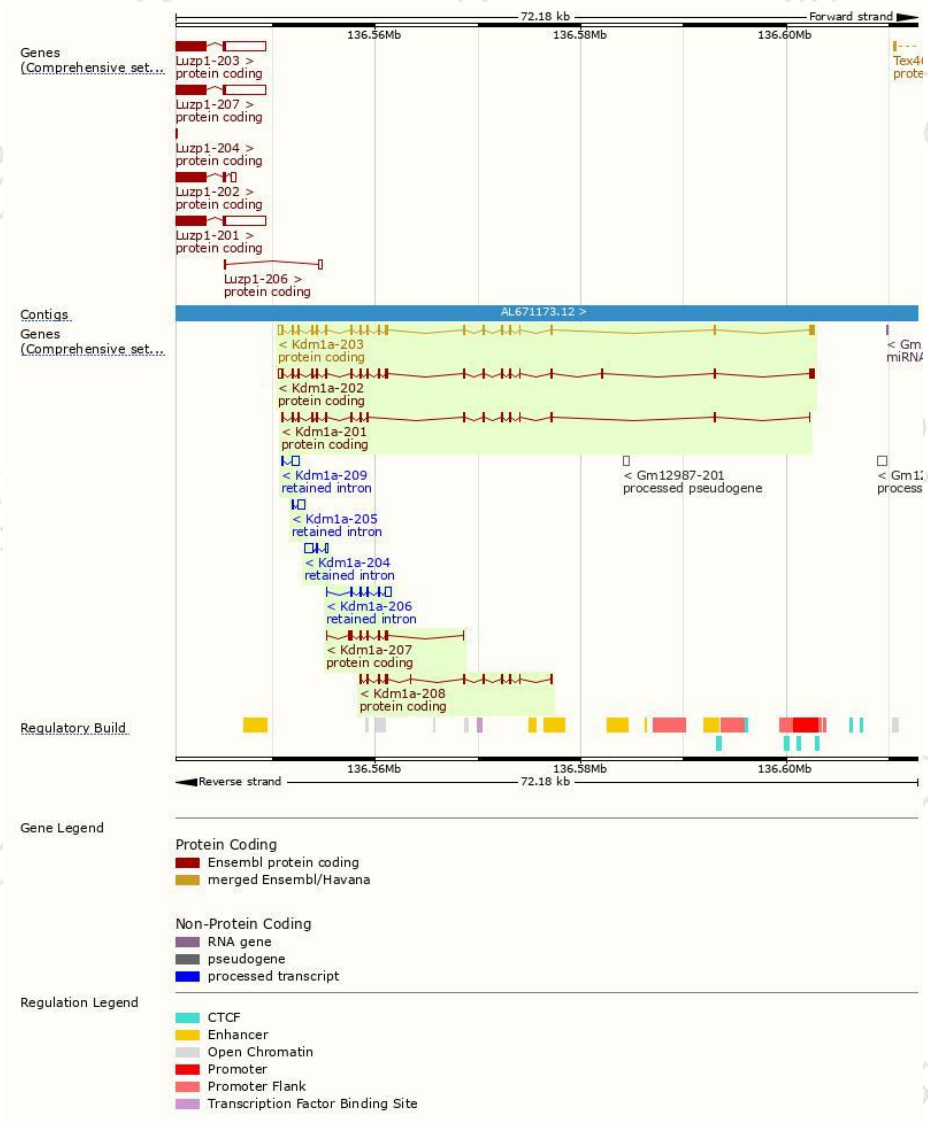
The gene has 9 transcripts,all transcripts are shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Kdm1a-202	ENSMUST00000105847.7	3028	873aa	Protein coding	CCDS84806	A3KG93	TSL:5 GENCODE basic APPRIS ALT2
Kdm1a-203	ENSMUST00000116273.8	3008	853aa	Protein coding	CCDS51331	Q6ZQ88	TSL:1 GENCODE basic APPRIS P3
Kdm1a-201	ENSMUST00000046846.13	2051	683aa	Protein coding	-	G8JL40	CDS 5' incomplete TSL:5
Kdm1a-208	ENSMUST00000170979.1	965	322aa	Protein coding	-	F6Z4I3	5' and 3' truncations in transcript evidence prevent annotation of the start and the end of the CDS. CDS 5' and 3' incomplete TSL:5
Kdm1a-207	ENSMUST00000155354.7	751	250aa	Protein coding	-	F6ZC60	5' and 3' truncations in transcript evidence prevent annotation of the start and the end of the CDS. CDS 5' and 3' incomplete TSL:3
Kdm1a-204	ENSMUST00000125111.1	1130	No protein	Retained intron	-	-	TSL:3
Kdm1a-206	ENSMUST00000147886.1	995	No protein	Retained intron	-	-	TSL:2
Kdm1a-205	ENSMUST00000139690.1	858	No protein	Retained intron	-	-	TSL:3
Kdm1a-209	ENSMUST00000171424.1	828	No protein	Retained intron	-	-	TSL:2

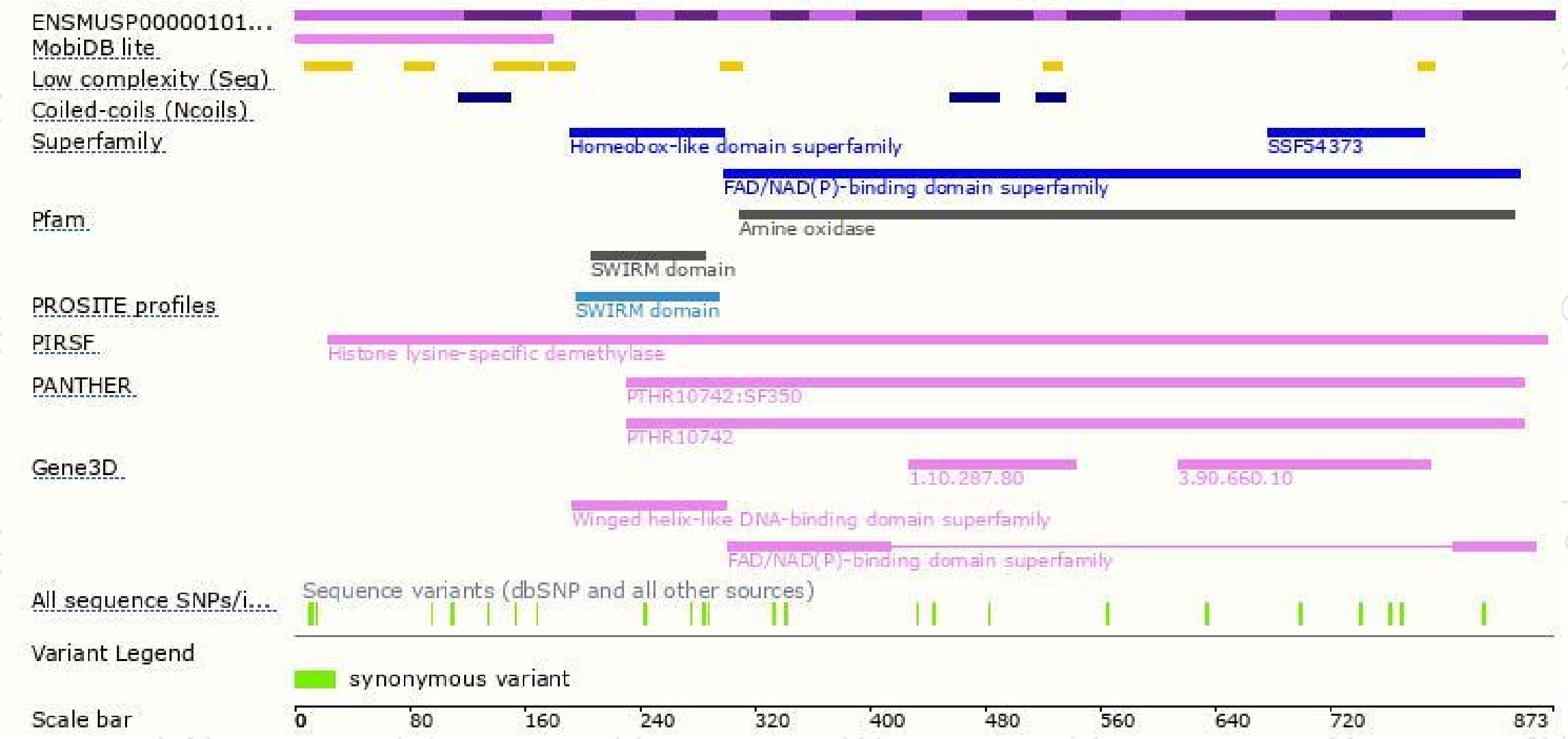
The strategy is based on the design of *Kdm1a-202* transcript,The transcription is shown below



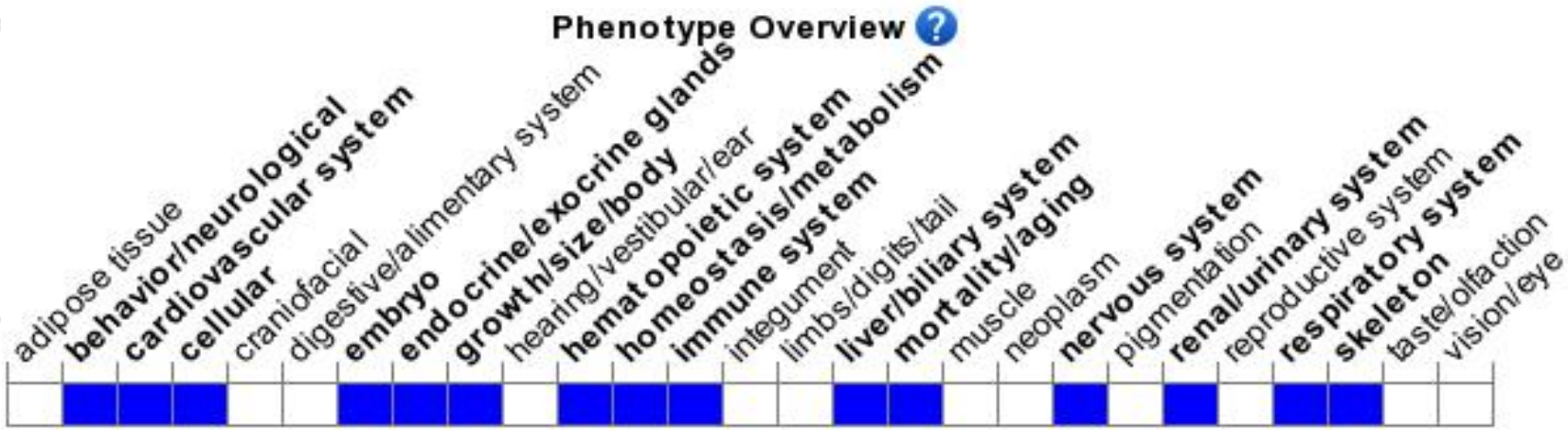
Genomic location distribution



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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