Cers5 Cas9-CKO Strategy

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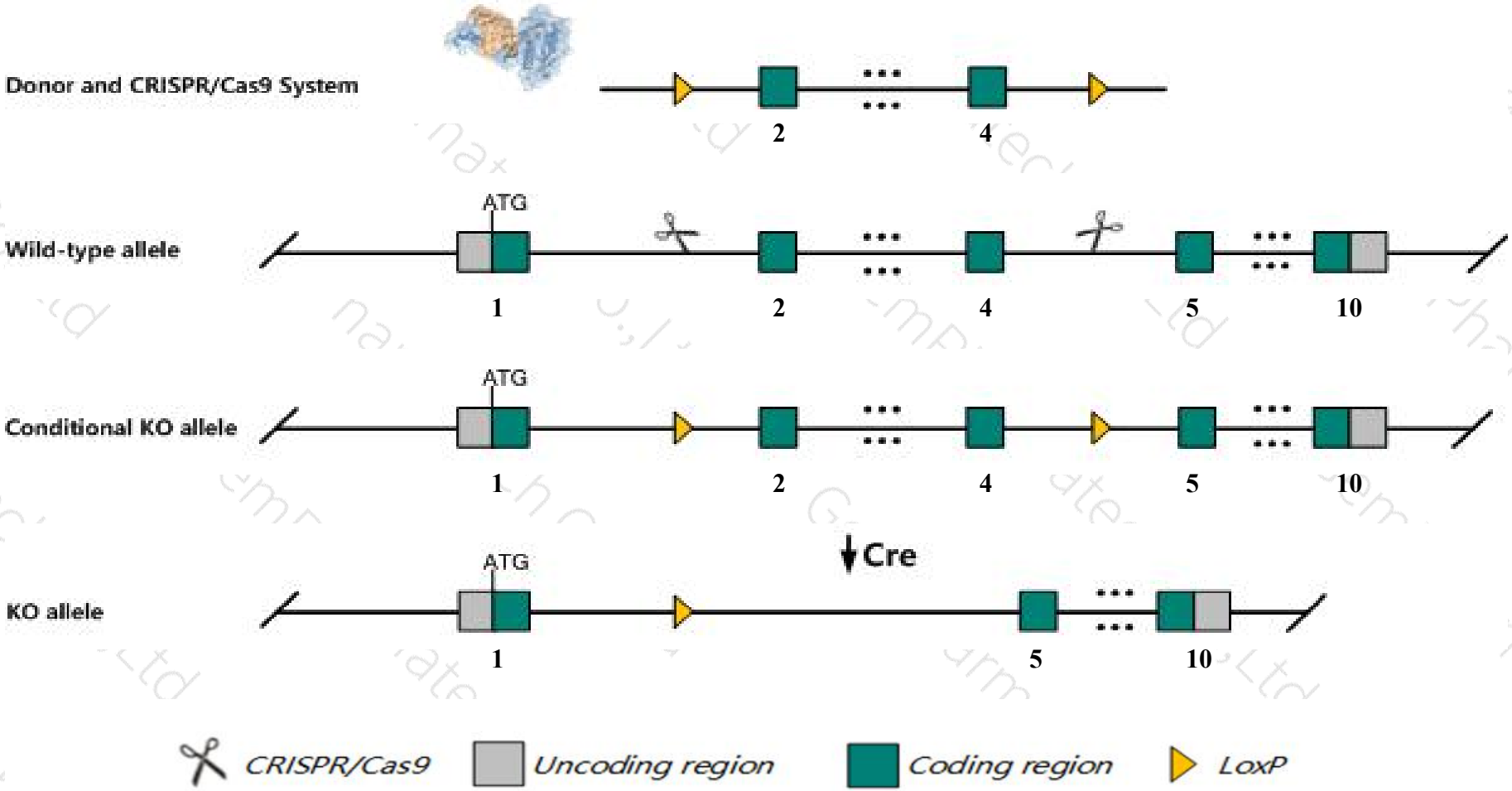
Project Overview

Project Name	***Cers5***
Project type	**Cas9-CKO**
Strain background	**C57BL/6JGpt**

Conditional Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *Cers5* gene. The schematic diagram is as follows:



Technical routes

- The *Cers5* gene has 6 transcripts. According to the structure of *Cers5* gene, exon2-exon4 of *Cers5-201* (ENSMUST00000023762.12) transcript is recommended as the knockout region.The region contains 295bp coding sequence. Knock out the region will result in disruption of protein function.

- In this project we use CRISPR/Cas9 technology to modify *Cers5* 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 *Cers5* gene is located on the Chr15. 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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Cers5 ceramide synthase 5 [Mus musculus (house mouse)]

Gene ID: 71949, updated on 31-Jan-2019

Summary

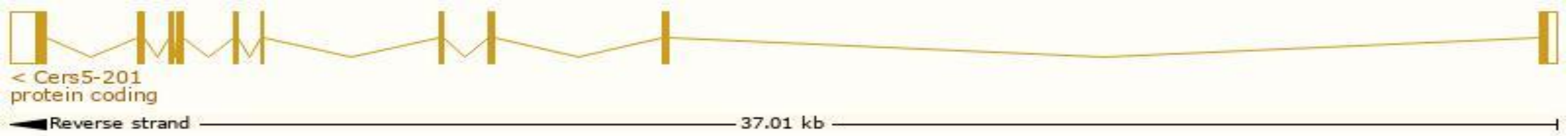
Official Symbol	Cers5 provided by MGI
Official Full Name	ceramide synthase 5 provided by MGI
Primary source	MGI:MGI:1919199
See related	Ensembl:ENSMUSG00000023021
Gene type	protein coding
RefSeq status	PROVISIONAL
Organism	Mus musculus
Lineage	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Myomorpha; Muroidea; Muridae; Murinae; Mus; Mus
Also known as	2310081H14Rik, AU045339, AW544927, Lass5, Trh4
Expression	Ubiquitous expression in limb E14.5 (RPKM 25.1), CNS E18 (RPKM 20.0) and 27 other tissues See more
Orthologs	human all

Transcript information（Ensembl）

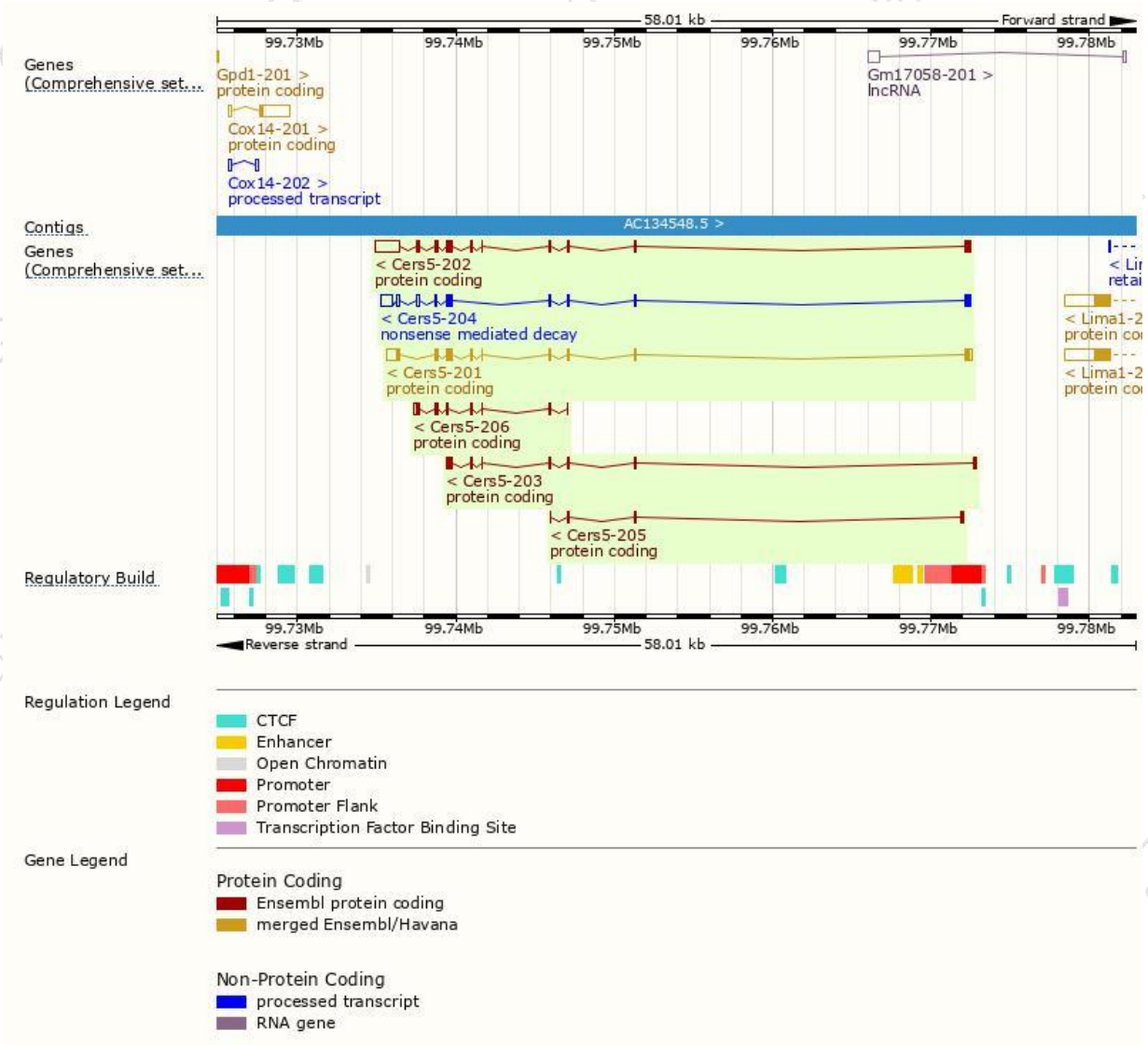
The gene has 6 transcripts,all transcripts are shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Cers5-201	ENSMUST00000023762.12	2096	414aa	Protein coding	CCDS27830	Q9D6K9	TSL:1 GENCODE basic APPRIS P2
Cers5-202	ENSMUST00000109035.10	2775	387aa	Protein coding	-	Q9D6K9	TSL:1 GENCODE basic APPRIS ALT2
Cers5-203	ENSMUST00000175876.7	884	241aa	Protein coding	-	H3BJ49	CDS 3' incomplete TSL:5
Cers5-206	ENSMUST00000176970.7	819	203aa	Protein coding	-	H3BLB3	CDS 5' incomplete TSL:5
Cers5-205	ENSMUST00000176627.2	447	95aa	Protein coding	-	H3BJH5	CDS 3' incomplete TSL:3
Cers5-204	ENSMUST00000176248.7	1883	251aa	Nonsense mediated decay	-	H3BJQ0	TSL:5

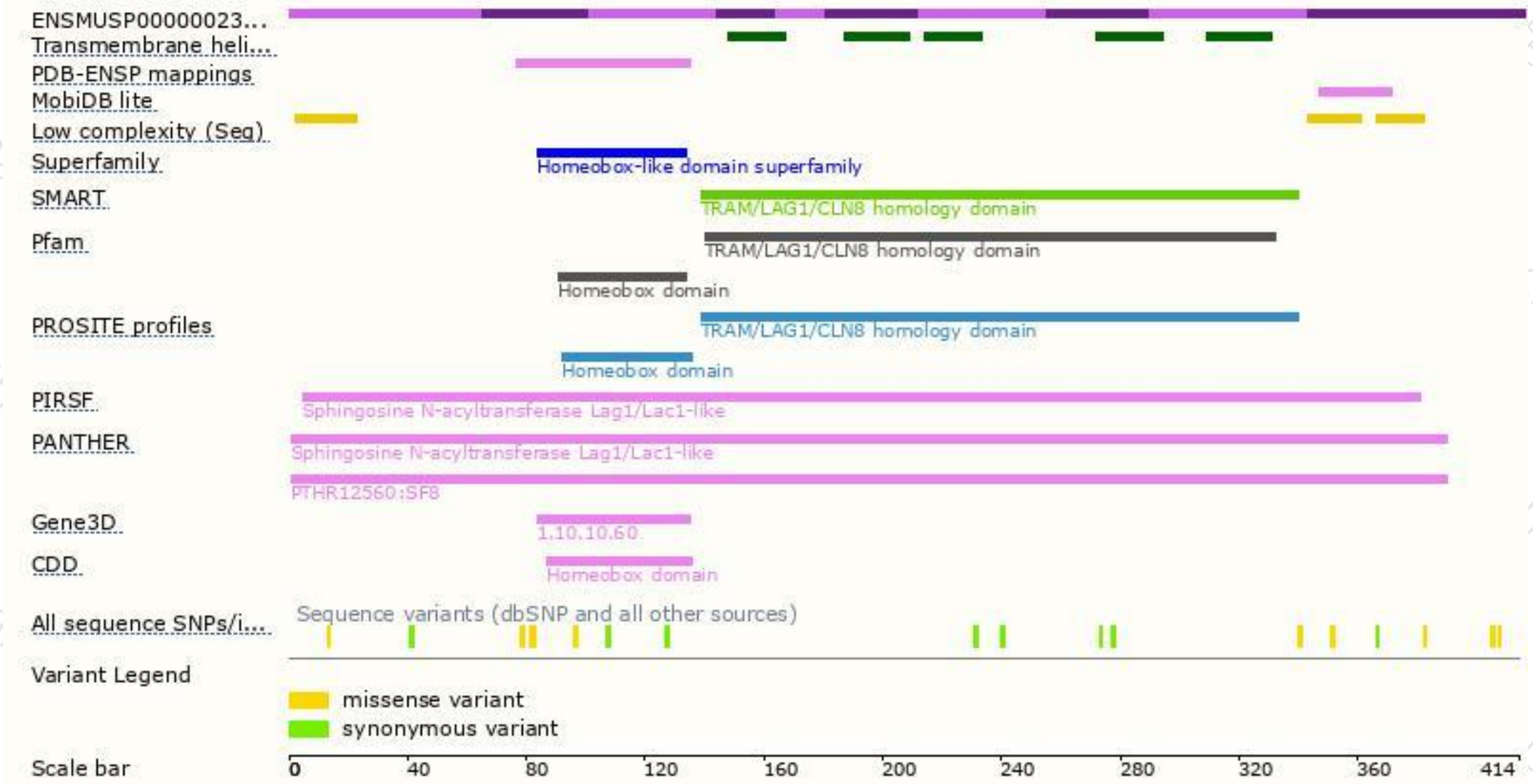
The strategy is based on the design of *Cers5-201* transcript,The transcription is shown below



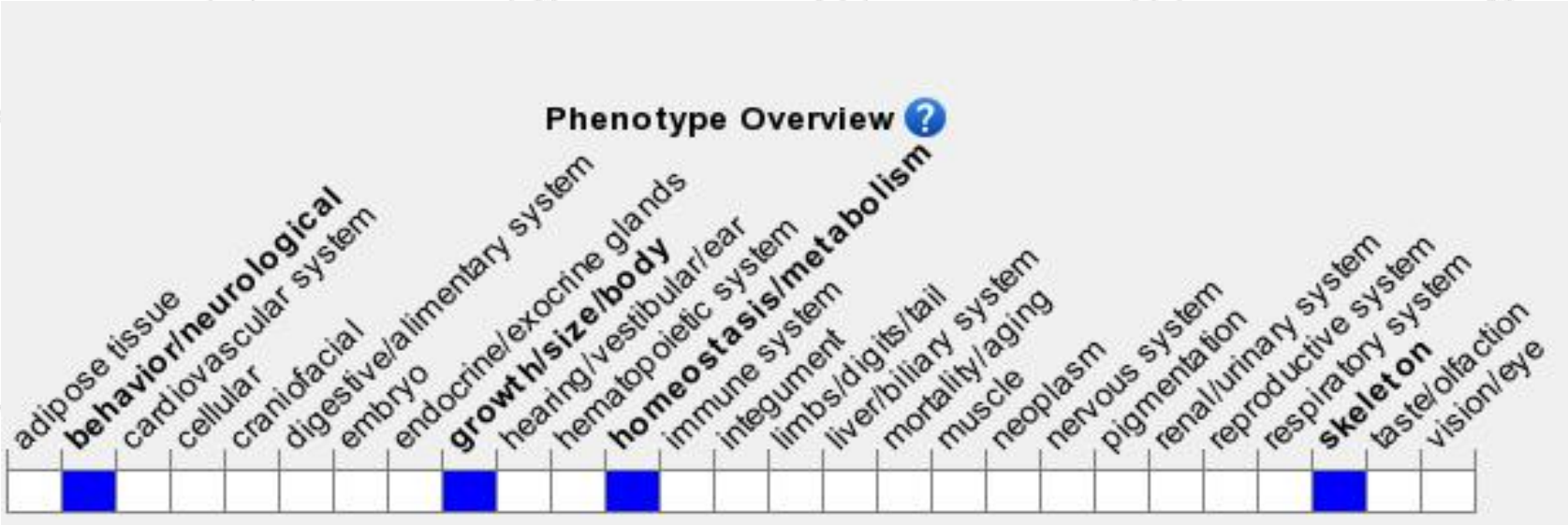
Genomic location distribution



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/).

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

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