Colec10 Cas9-KO Strategy

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Project Overview

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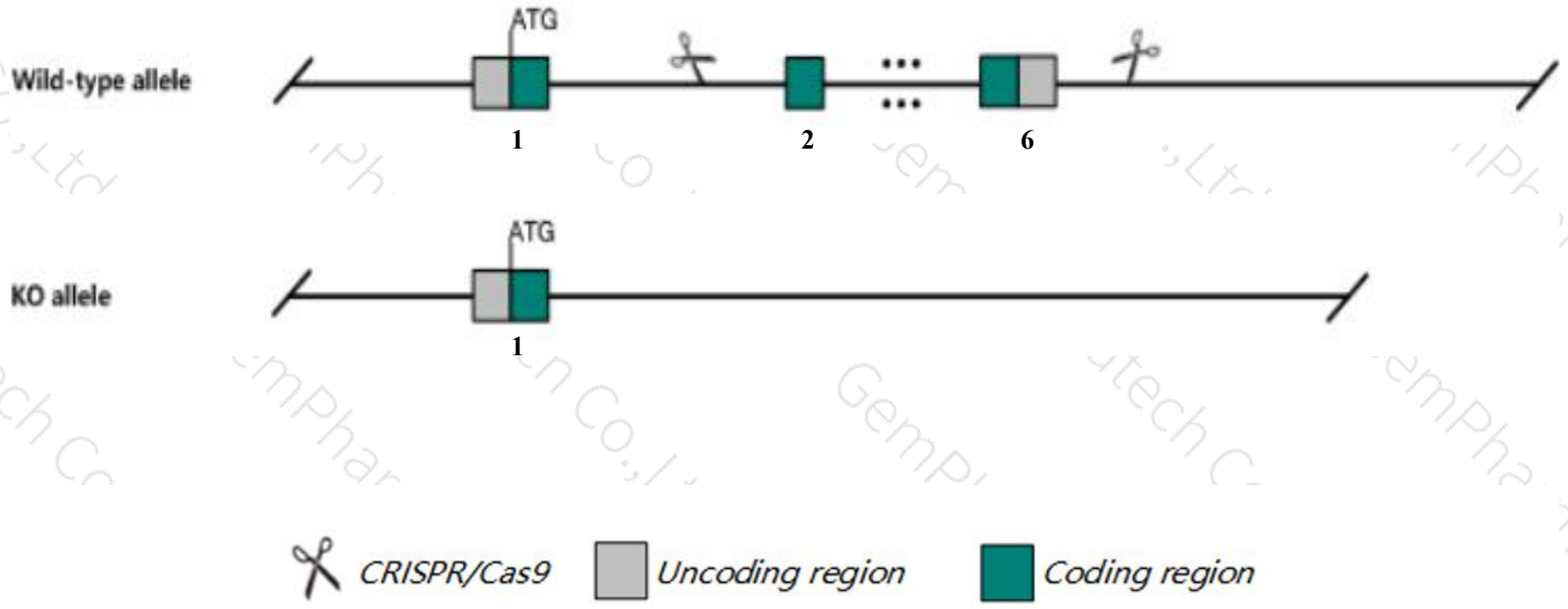
Project Name	***Colec10***
Project type	**Cas9-KO**
Strain background	**C57BL/6JGpt**

Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *Colec10* gene. The schematic diagram is as follows:



Technical routes

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- The *Colec10* gene has 1 transcript. According to the structure of *Colec10* gene, exon2-exon6 of *Colec10-201* (ENSMUST00000036737.3) 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 *Colec10* gene. The brief process is as follows: CRISPR/Cas9 syste

Notice

- The *Colec10* 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.

- *Gm18152* gene will de deleted.

- 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）

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Colec10 collectin sub-family member 10 [Mus musculus (house mouse)]

Gene ID: 239447, updated on 13-Mar-2020

Summary

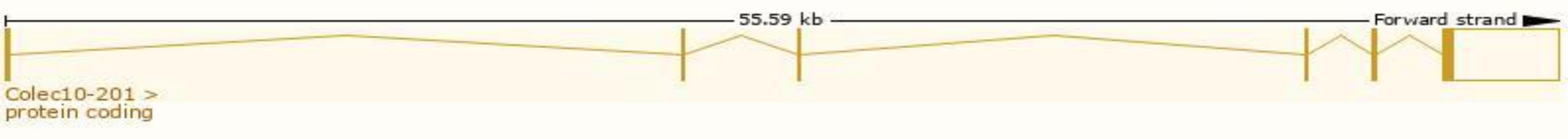
Official Symbol	Colec10 provided by MGI
Official Full Name	collectin sub-family member 10 provided byMGI
Primary source	MGI:MGI:3606482
See related	Ensembl:ENSMUSG00000038591
Gene type	protein coding
RefSeq status	VALIDATED
Organism	Mus musculus
Lineage	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Myomorpha; Muroidea; Muridae; Murinae; Mus; Mus
Also known as	CL-L1
Expression	Biased expression in liver E18 (RPKM 6.6), placenta adult (RPKM 5.0) and 5 other tissuesSee more
Orthologs	human all

Transcript information（Ensembl）

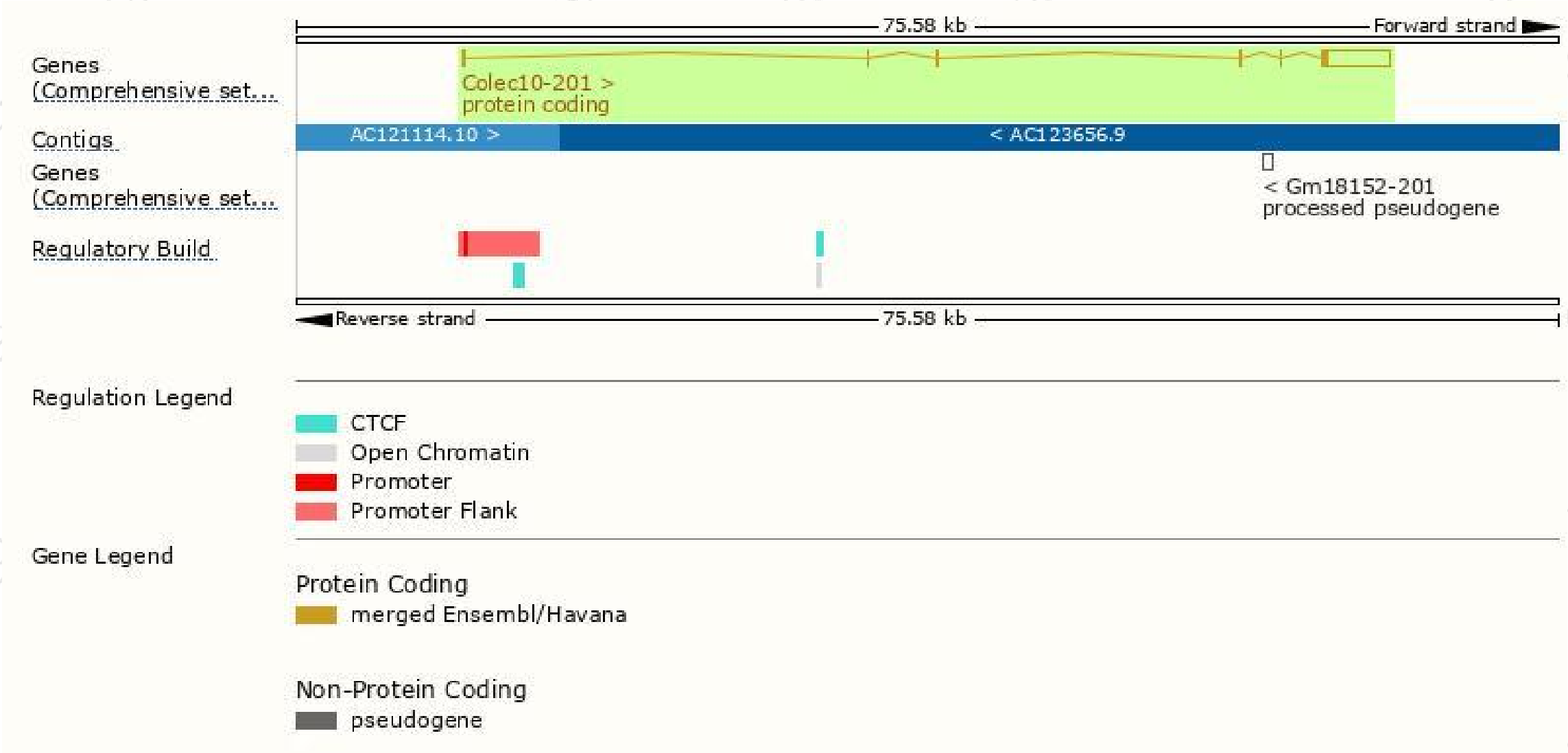
The gene has 1 transcript,and the transcript is shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Colec10-201	ENSMUST00000036737.3	4587	277aa	Protein coding	CCDS27469	Q8CF98	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 P1

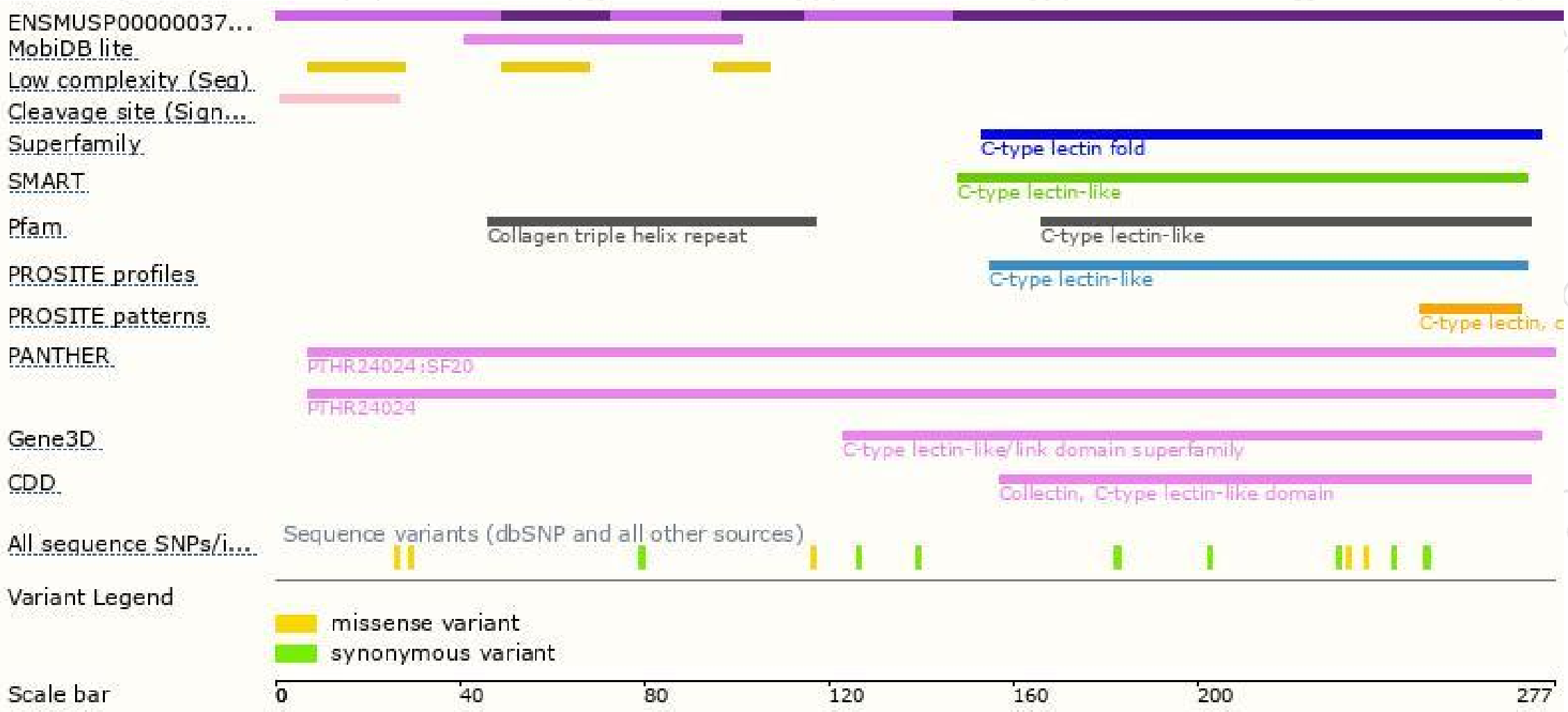
The strategy is based on the design of *Colec10-201* transcript,the transcription is shown below:



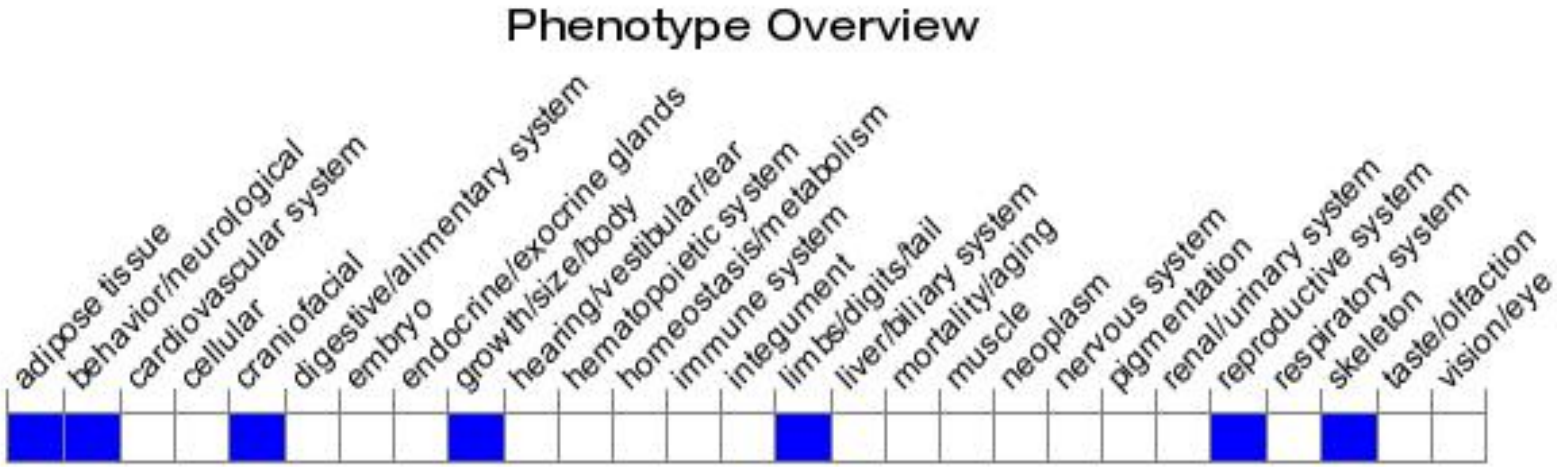
Genomic location distribution



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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