Setd7 Cas9-KO Strategy

Designer: Daohua Xu

Design Date: 2019-8-7

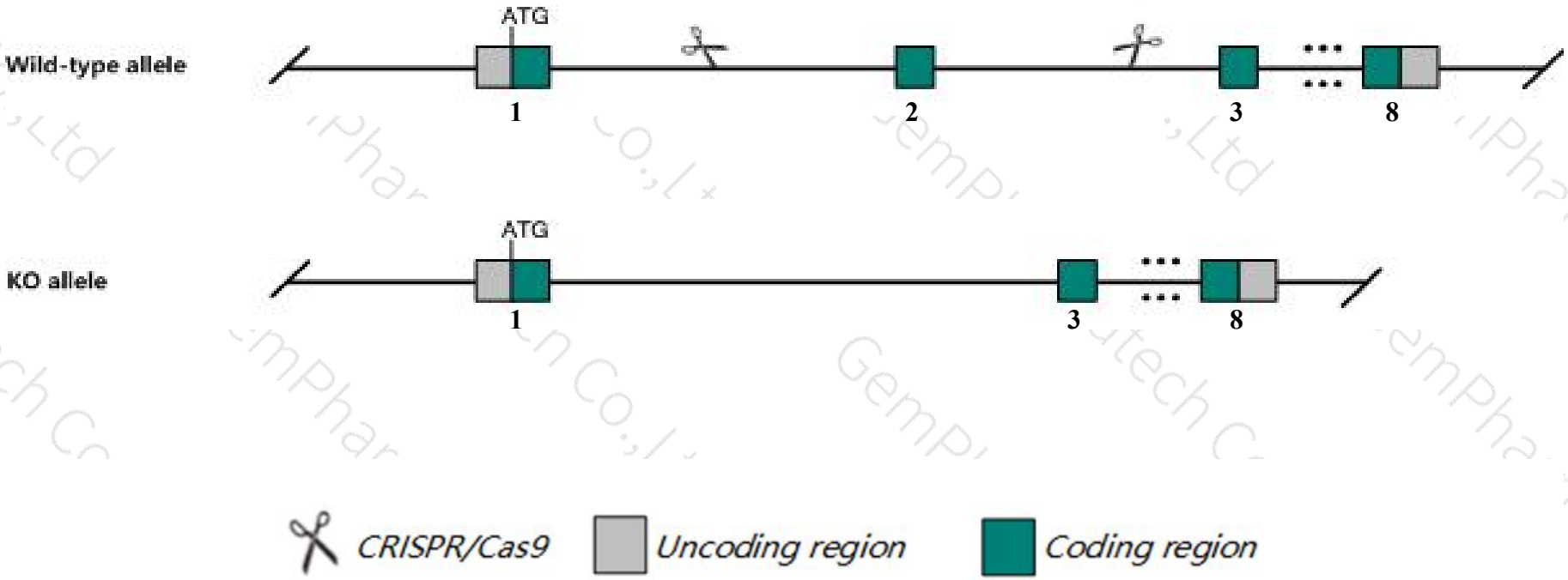
GemPharmatech Co.,Ltd

Project Overview

Project Name	***Setd7***
Project type	**Cas9-KO**
Strain background	**C57BL/6JGpt**

Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *Setd7* gene. The schematic diagram is as follows:



Technical routes

➢ The *Setd7* gene has 4 transcripts. According to the structure of *Setd7* gene, exon2 of *Setd7-201* (ENSMUST00000037141.8) transcript is recommended as the knockout region.The region contains 130bp coding sequence. Knock out the region will result in disruption of protein function.

➢ In this project we use CRISPR/Cas9 technology to modify *Setd7* gene. The brief process is as follows: CRISPR/Cas9 system

Notice

- According to the existing MGI data,Homozygotes for a knock-out allele exhibit partial prenatal lethality and failure of mouse embryonic fibroblasts and spleen cells to arrest after doxorubicin treatment. Homozygotes for a different knock-out allele show resistance to bleomycin- or adenovirus-TGFbeta-induced pulmonary fibrosis.

- The *Setd7* gene is located on the Chr3. 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）

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Setd7 SET domain containing (lysine methyltransferase) 7 [Mus musculus (house mouse)]

Gene ID: 73251, updated on 19-Feb-2019

Summary

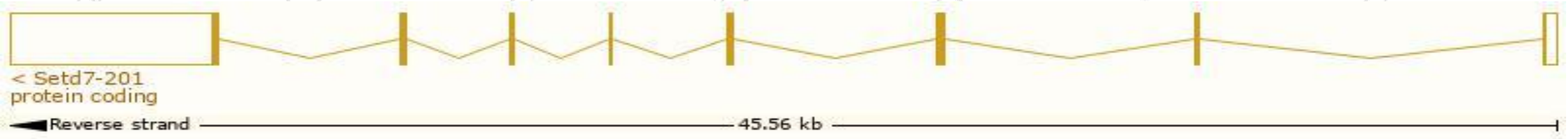
Official Symbol	Setd7 provided by MGI
Official Full Name	SET domain containing (lysine methyltransferase) 7 provided by MGI
Primary source	MGI:MGI:1920501
See related	Ensembl:ENSMUSG00000037111
Gene type	protein coding
RefSeq status	PROVISIONAL
Organism	Mus musculus
Lineage	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Myomorpha; Muroidea; Muridae; Murinae; Mus; Mus
Also known as	1600028F23Rik, H3K4MT, KMT7, Set7, Set7/9, mKIAA1717
Expression	Ubiquitous expression in cerebellum adult (RPKM 24.0), bladder adult (RPKM 20.7) and 26 other tissues See more
Orthologs	human all

Transcript information（Ensembl）

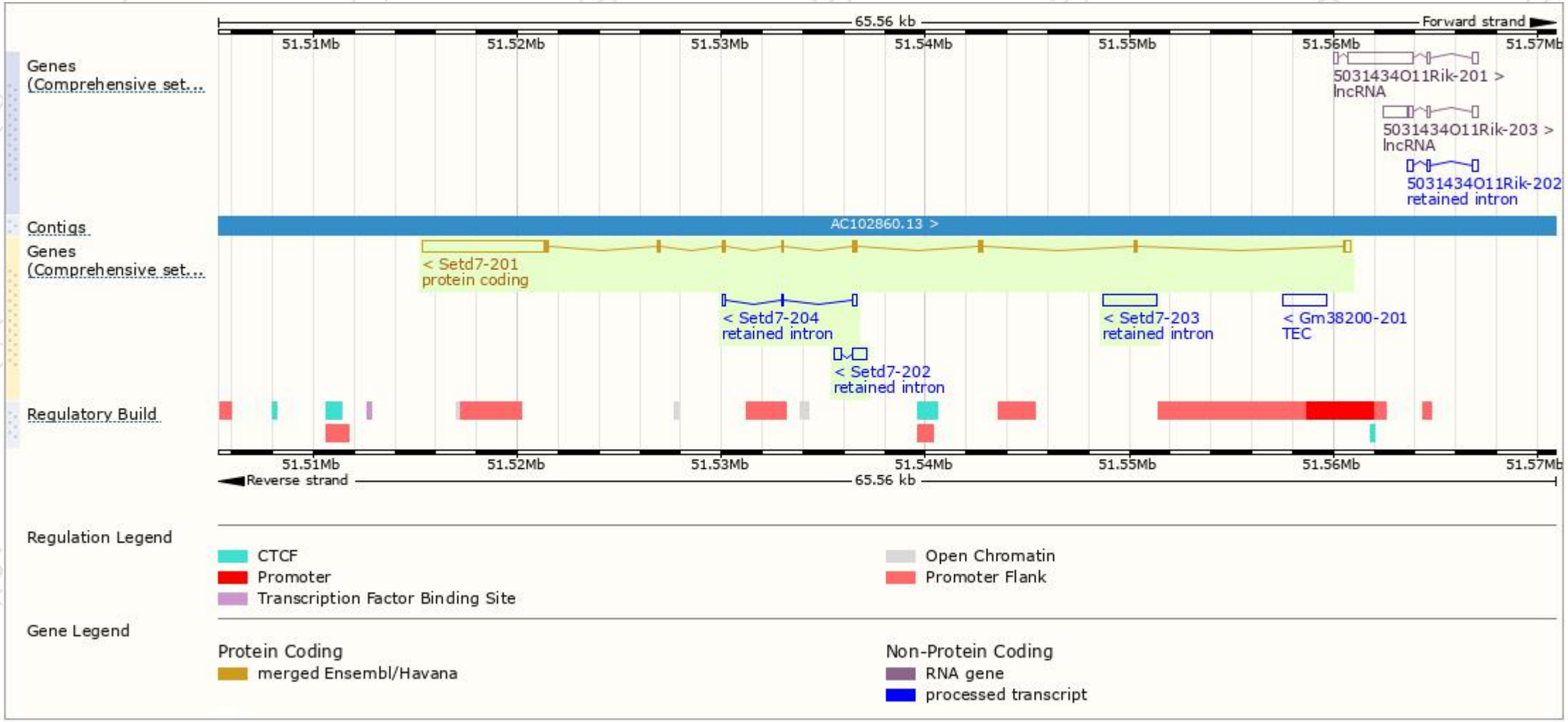
The gene has 4 transcripts,all transcripts are shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Setd7-201	ENSMUST00000037141.8	7411	366aa	Protein coding	CCDS17341	Q8VHL1	TSL:1 GENCODE basic APPRIS P1
Setd7-203	ENSMUST00000194828.1	2638	No protein	Retained intron	-	-	TSL:NA
Setd7-202	ENSMUST00000161755.2	1043	No protein	Retained intron	-	-	TSL:2
Setd7-204	ENSMUST00000195080.1	423	No protein	Retained intron	-	-	TSL:3

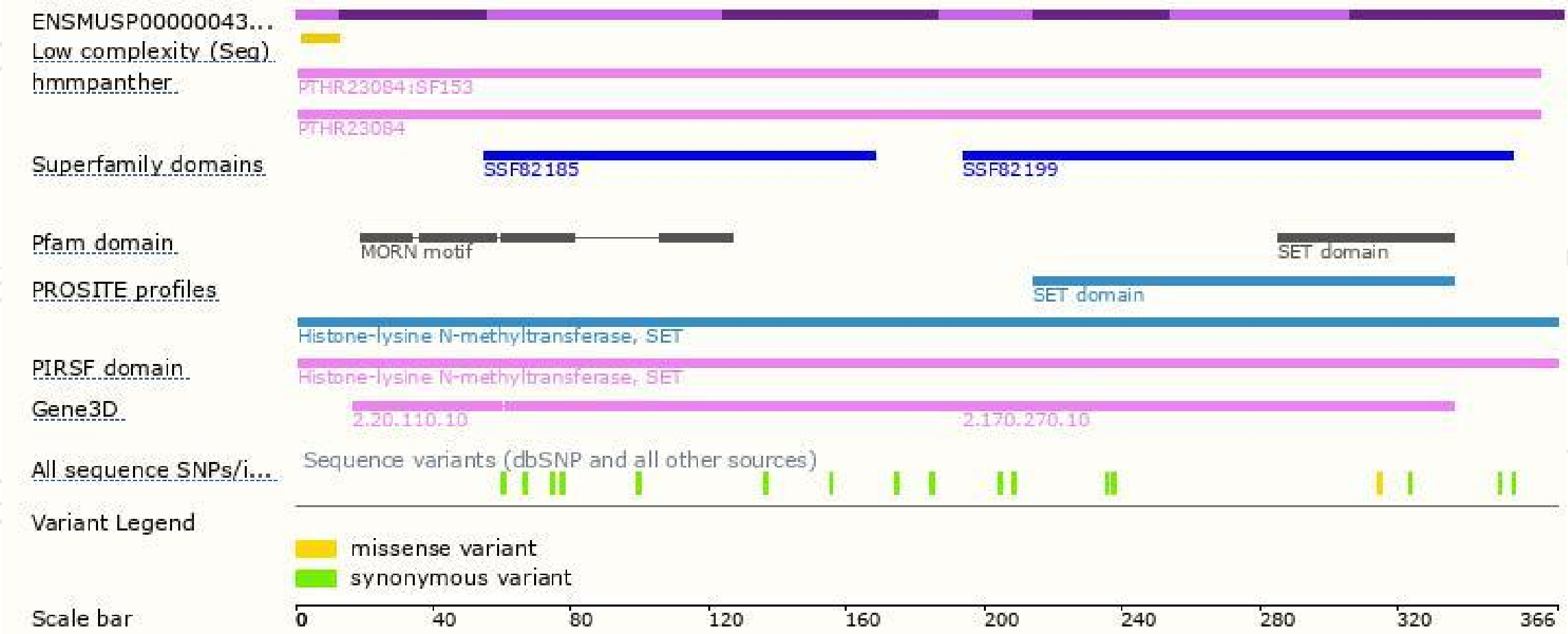
The strategy is based on the design of *Setd7-201* transcript,The transcription is shown below



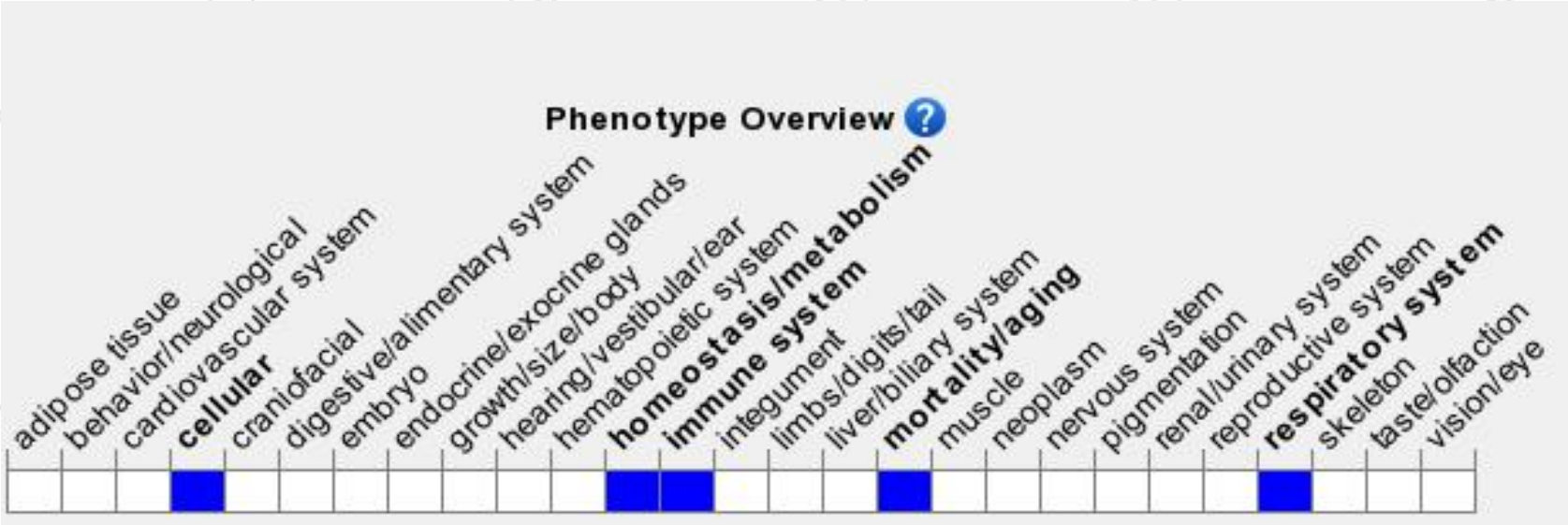
Genomic location distribution



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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