Setx Cas9-KO Strategy

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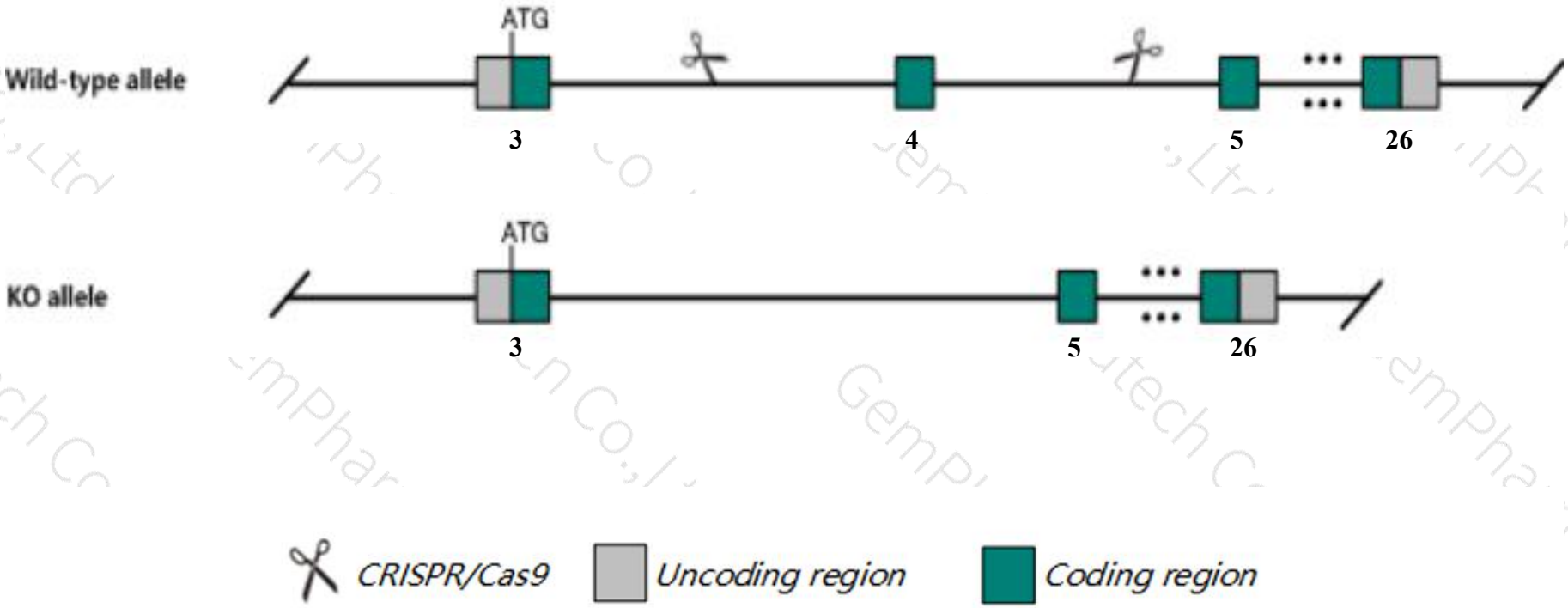
Project Overview

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

Knockout strategy

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



Technical routes

➢ The *Setx* gene has 5 transcripts. According to the structure of *Setx* gene, exon4 of *Setx-201* (ENSMUST00000061578.8) transcript is recommended as the knockout region.The region contains 211bp coding sequence. Knock out the region will result in disruption of protein function.

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

Notice

- According to the existing MGI data,mice homozygous for a knock-out allele exhibit male infertility due to arrested male meiosis and reduced female fertility.
- The *Setx* gene is located on the Chr2. 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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Setx senataxin [Mus musculus (house mouse)]

Gene ID: 269254, updated on 13-Mar-2020

Summary

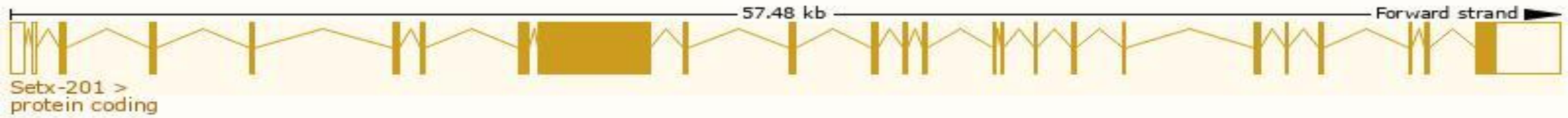
Official Symbol	Setx provided by MGI
Official Full Name	senataxin provided by MGI
Primary source	MGI:MGI:2443480
See related	Ensembl:ENSMUSG00000043535
Gene type	protein coding
RefSeq status	VALIDATED
Organism	Mus musculus
Lineage	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Myomorpha; Muroidea; Muridae; Murinae; Mus; Mus
Also known as	A130090N03, A930037J23Rik, AOA2, AW060766, Als4, SCAR1, Sen1, mKIAA0625
Expression	Broad expression in testis adult (RPKM 26.8), CNS E11.5 (RPKM 4.6) and 19 other tissues See more
Orthologs	human all

Transcript information（Ensembl）

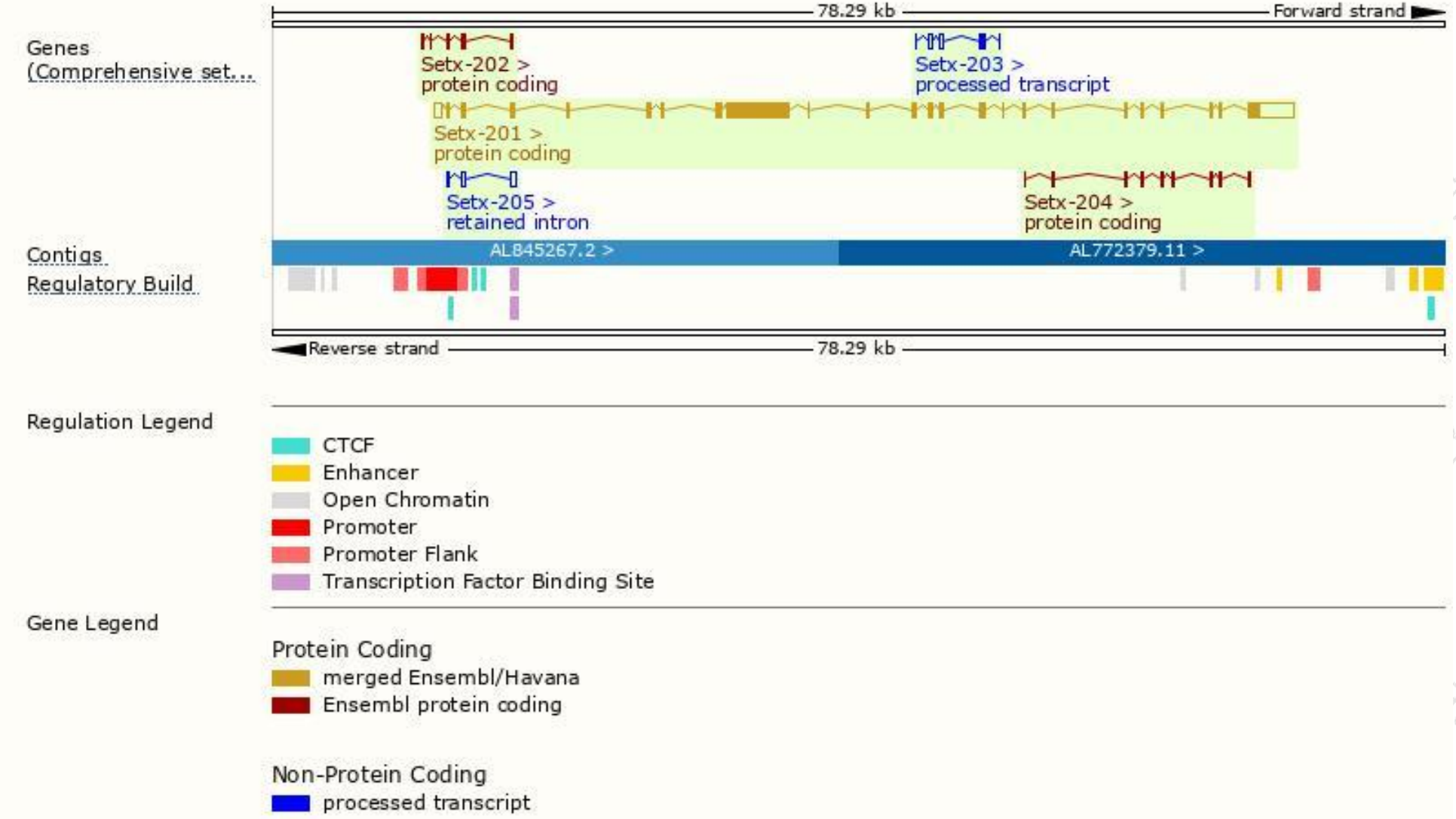
The gene has 5 transcripts,all transcripts are shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Setx-201	ENSMUST00000061578.8	10970	2646aa	Protein coding	CCDS38090	A2AKX3	TSL:5 GENCODE basic APPRIS P1
Setx-202	ENSMUST00000129544.7	525	81aa	Protein coding	-	A0A0A0MQJ0	CDS 3' incomplete TSL:3
Setx-203	ENSMUST00000135992.1	577	No protein	Processed transcript	-	-	TSL:5
Setx-204	ENSMUST00000145422.1	1141	381aa	Protein coding	-	F6R186	CDS 5' and 3' incomplete TSL:5
Setx-205	ENSMUST00000154910.1	538	No protein	Retained intron	-	-	TSL:3

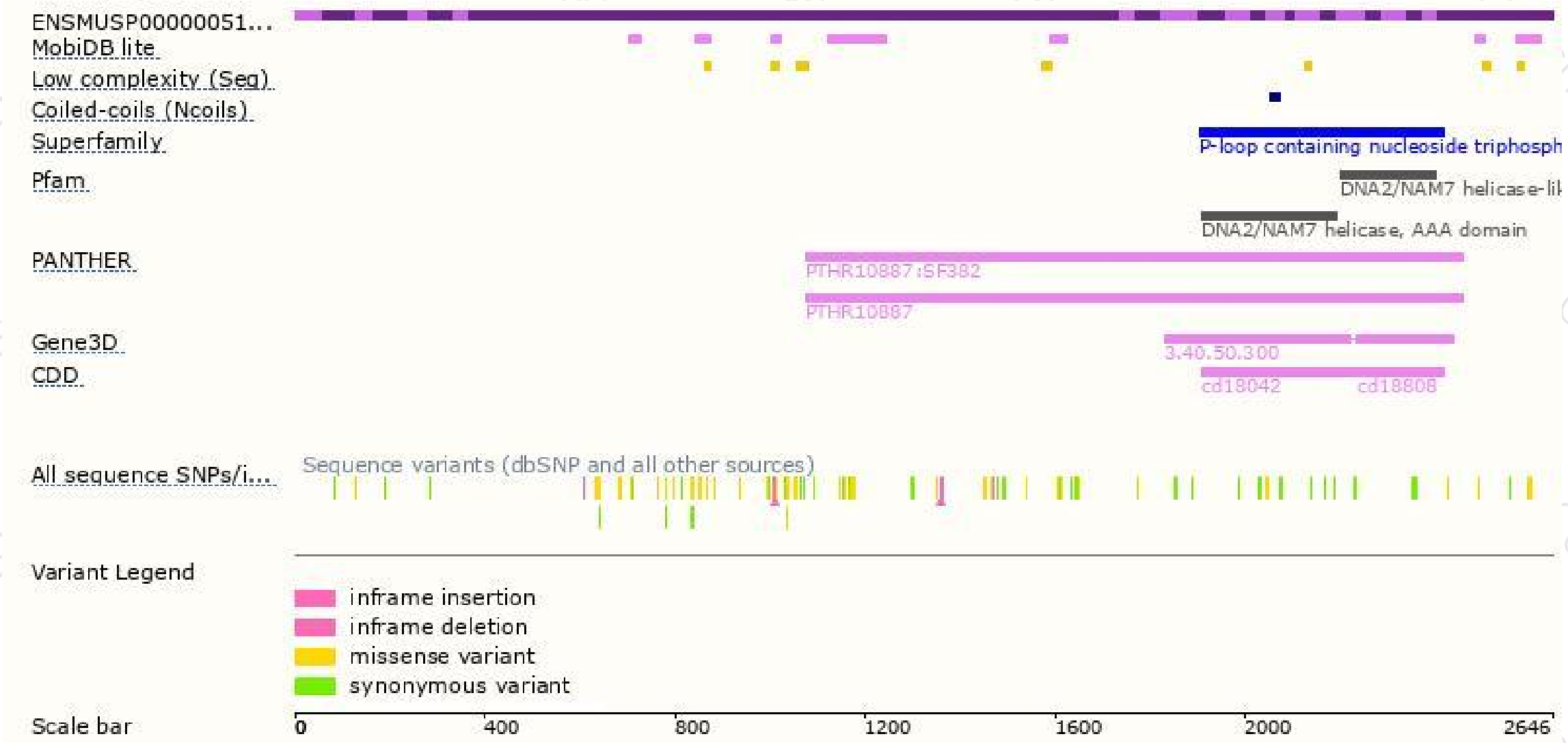
The strategy is based on the design of *Setx-201* transcript,The transcription is shown below



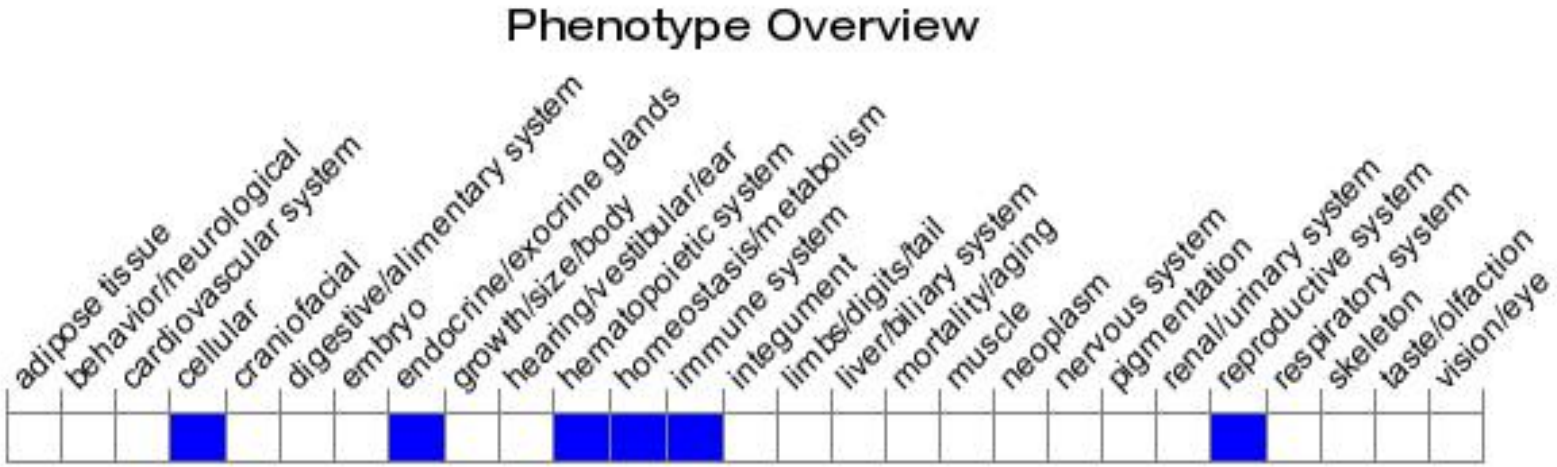
Genomic location distribution



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/).

According to the existing MGI data,Mice homozygous for a knock-out allele exhibit male infertility due to arrested male meiosis and reduced female fertility.

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

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