

Htatsf1 Cas9-KO Strategy

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Project Overview

Project Name

Htatsf1

Project type

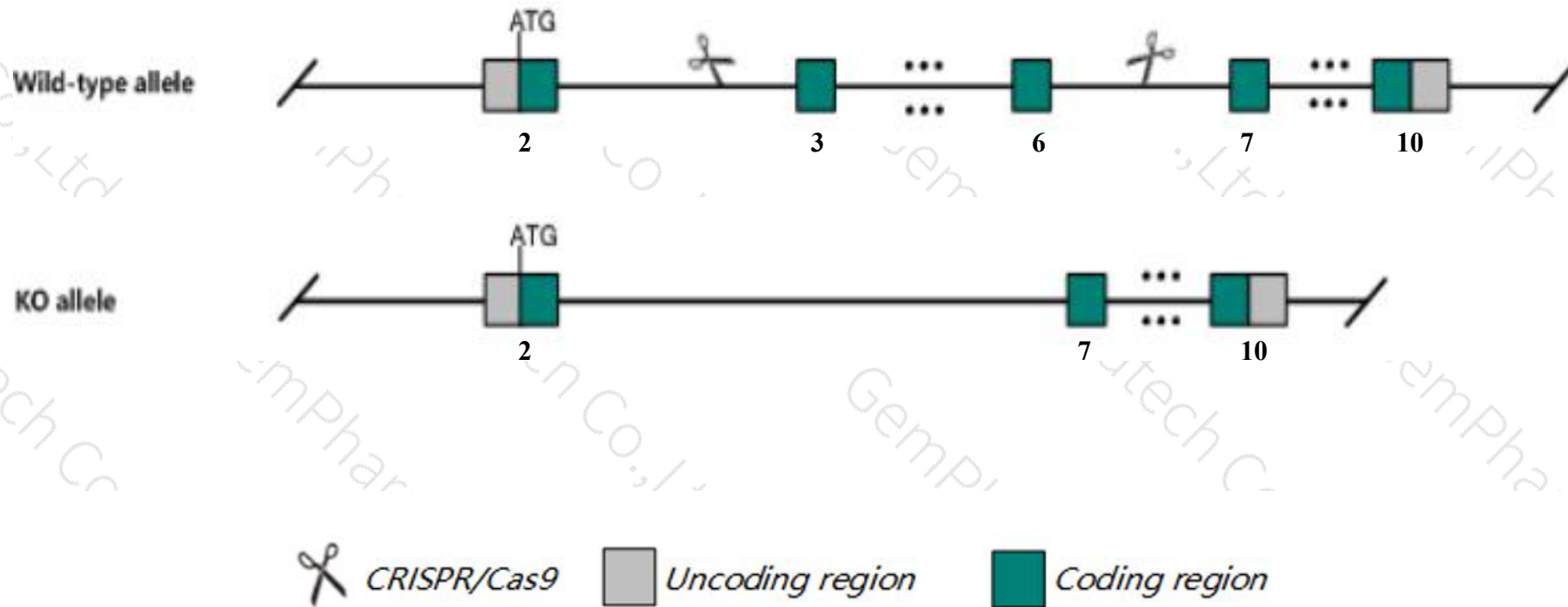
Cas9-KO

Strain background

C57BL/6JGpt

Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *Htatsf1* gene. The schematic diagram is as follows:



- The *Htatsf1* gene has 3 transcripts. According to the structure of *Htatsf1* gene, exon3-exon6 of *Htatsf1*-201 (ENSMUST00000088652.5) transcript is recommended as the knockout region. The region contains 548bp coding sequence. Knock out the region will result in disruption of protein function.
- In this project we use CRISPR/Cas9 technology to modify *Htatsf1* gene. The brief process is as follows: CRISPR/Cas9 system

- According to the existing MGI data, mice homozygous for a conditional allele activated in embryonic stem cells exhibit reduced pluripotency.
- The *Htatsf1* gene is located on the ChrX. 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)

Htatsf1 HIV TAT specific factor 1 [Mus musculus (house mouse)]

Gene ID: 72459, updated on 13-Mar-2020

Summary



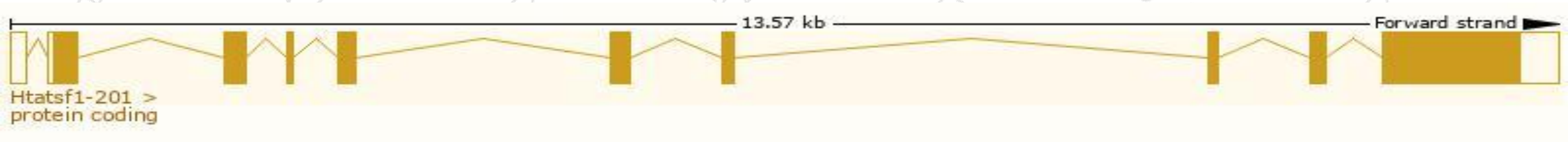
Official Symbol	Htatsf1 provided by MGI
Official Full Name	HIV TAT specific factor 1 provided by MGI
Primary source	MGI:MGI:1919709
See related	Ensembl:ENSMUSG00000067873
Gene type	protein coding
RefSeq status	VALIDATED
Organism	Mus musculus
Lineage	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Myomorpha; Muroidea; Muridae; Murinae; Mus; Mus
Also known as	1600023H17Rik, 2600017A12Rik, 2700077B20Rik, TAT-SF1
Expression	Ubiquitous expression in CNS E11.5 (RPKM 27.5), placenta adult (RPKM 19.4) and 27 other tissues See more
Orthologs	human all

Transcript information (Ensembl)

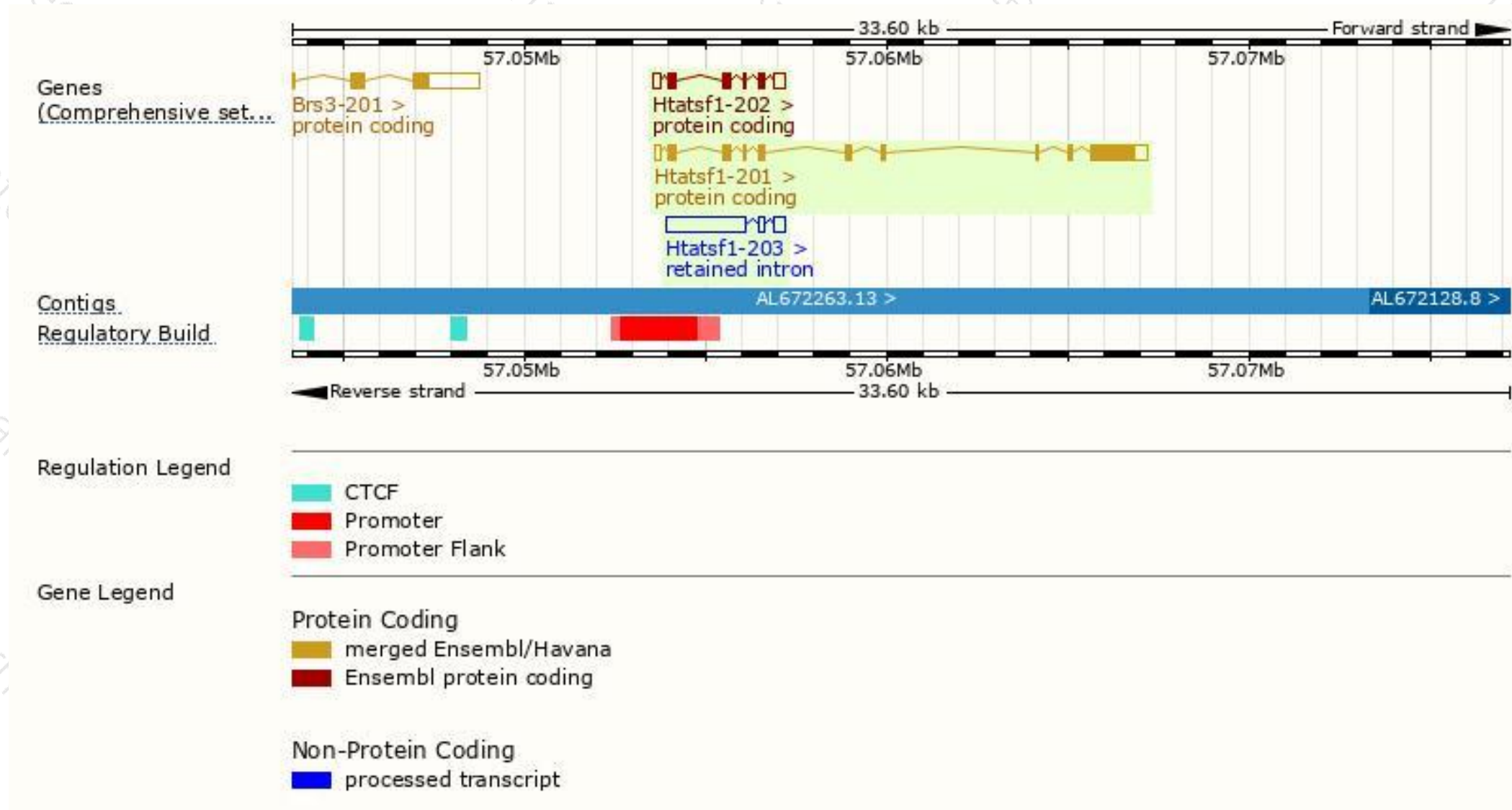
The gene has 3 transcripts,all transcripts are shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Htatsf1-201	ENSMUST00000088652.5	2810	757aa	Protein coding	CCDS40983	Q8BGC0	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
Htatsf1-202	ENSMUST00000114751.8	1128	195aa	Protein coding	-	Q8BGC0	TSL:1 GENCODE basic
Htatsf1-203	ENSMUST00000134785.1	2664	No protein	Retained intron	-	-	TSL:1

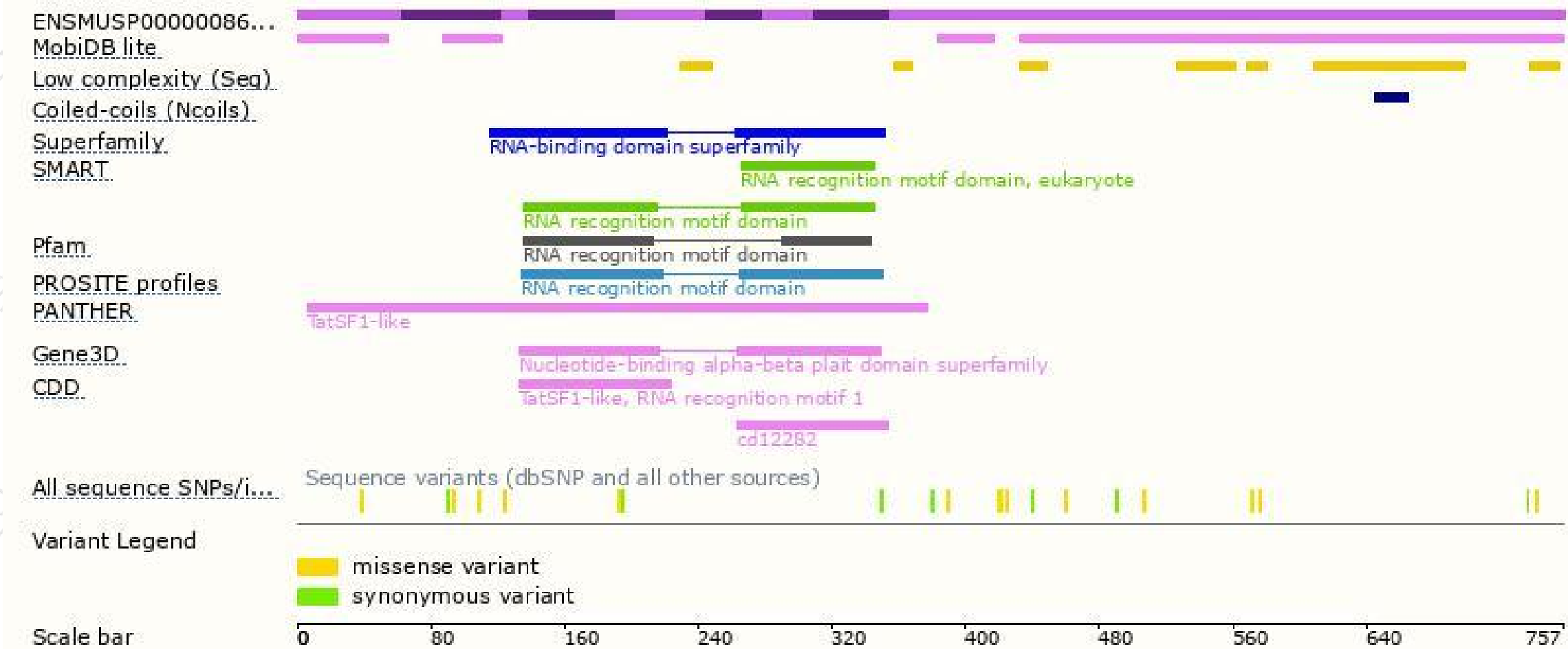
The strategy is based on the design of *Htatsf1-201* transcript,the transcription is shown below:



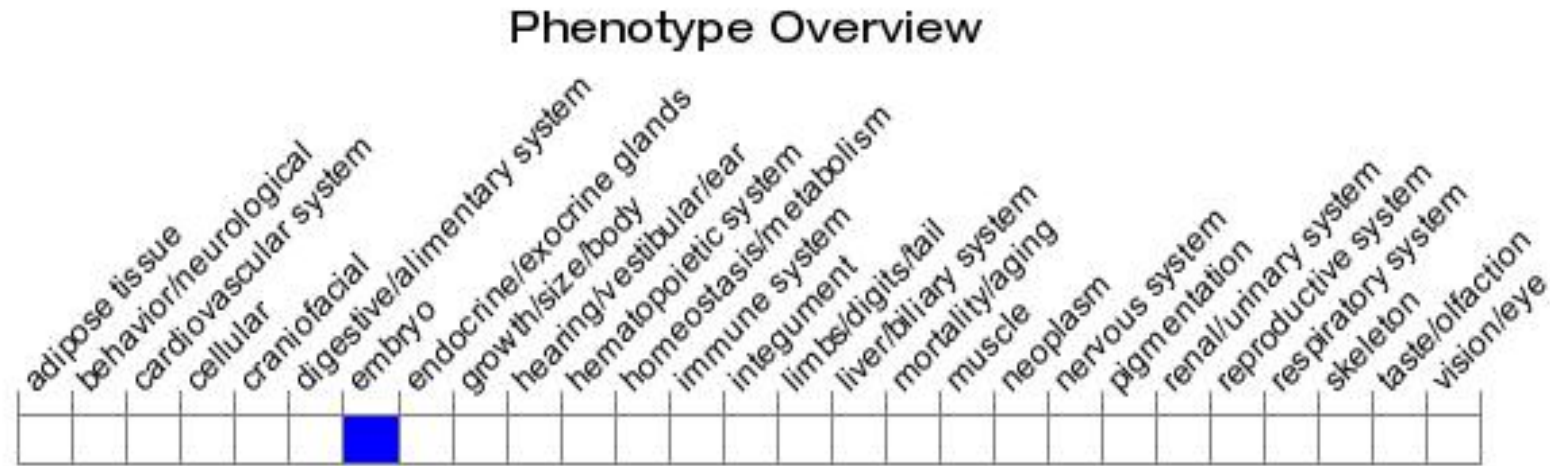
Genomic location distribution



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 conditional allele activated in embryonic stem cells exhibit reduced pluripotency.

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

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