

Sars Cas9-KO Strategy

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Design Date:

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Project Overview

Project Name

Sars

Project type

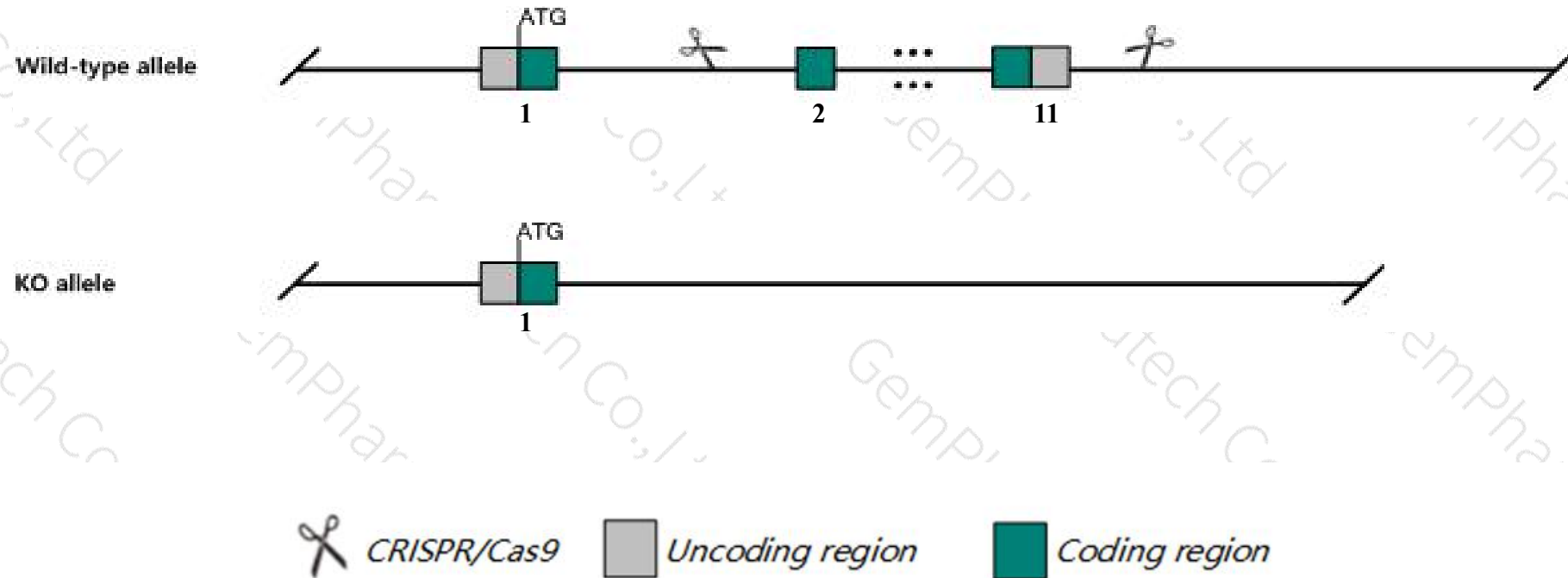
Cas9-KO

Strain background

C57BL/6JGpt

Knockout strategy

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



- The *Sars* gene has 5 transcripts. According to the structure of *Sars* gene, exon2-exon11 of *Sars-201* (ENSMUST00000090553.11) transcript is recommended as the knockout region. The region contains 1403bp coding sequence. Knock out the region will result in disruption of protein function.
- In this project we use CRISPR/Cas9 technology to modify *Sars* gene. The brief process is as follows: CRISPR/Cas9 system w

- According to the existing MGI data, Mice homozygous for a knock-out allele show complete embryonic lethality before implantation associated with abnormal morula morphology, increased cell death, and failure of blastocyst formation.
- The *Sars* 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)

Sars seryl-aminoacyl-tRNA synthetase [Mus musculus (house mouse)]

Gene ID: 20226, updated on 31-Jan-2019

Summary



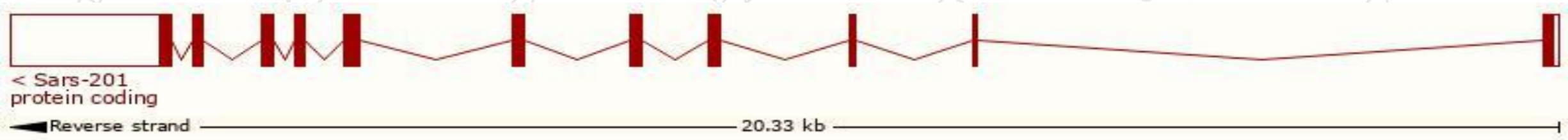
| | |
|---------------------------|---|
| Official Symbol | Sars provided by MGI |
| Official Full Name | seryl-aminoacyl-tRNA synthetase provided by MGI |
| Primary source | MGI:MGI:102809 |
| See related | Ensembl:ENSMUSG00000068739 |
| Gene type | protein coding |
| RefSeq status | VALIDATED |
| Organism | Mus musculus |
| Lineage | Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Myomorpha; Muroidea; Muridae; Murinae; Mus; Mus |
| Also known as | Sars1, Strs, serRS |
| Expression | Ubiquitous expression in CNS E14 (RPKM 31.6), CNS E11.5 (RPKM 30.2) and 28 other tissues See more |
| Orthologs | human all |

Transcript information (Ensembl)

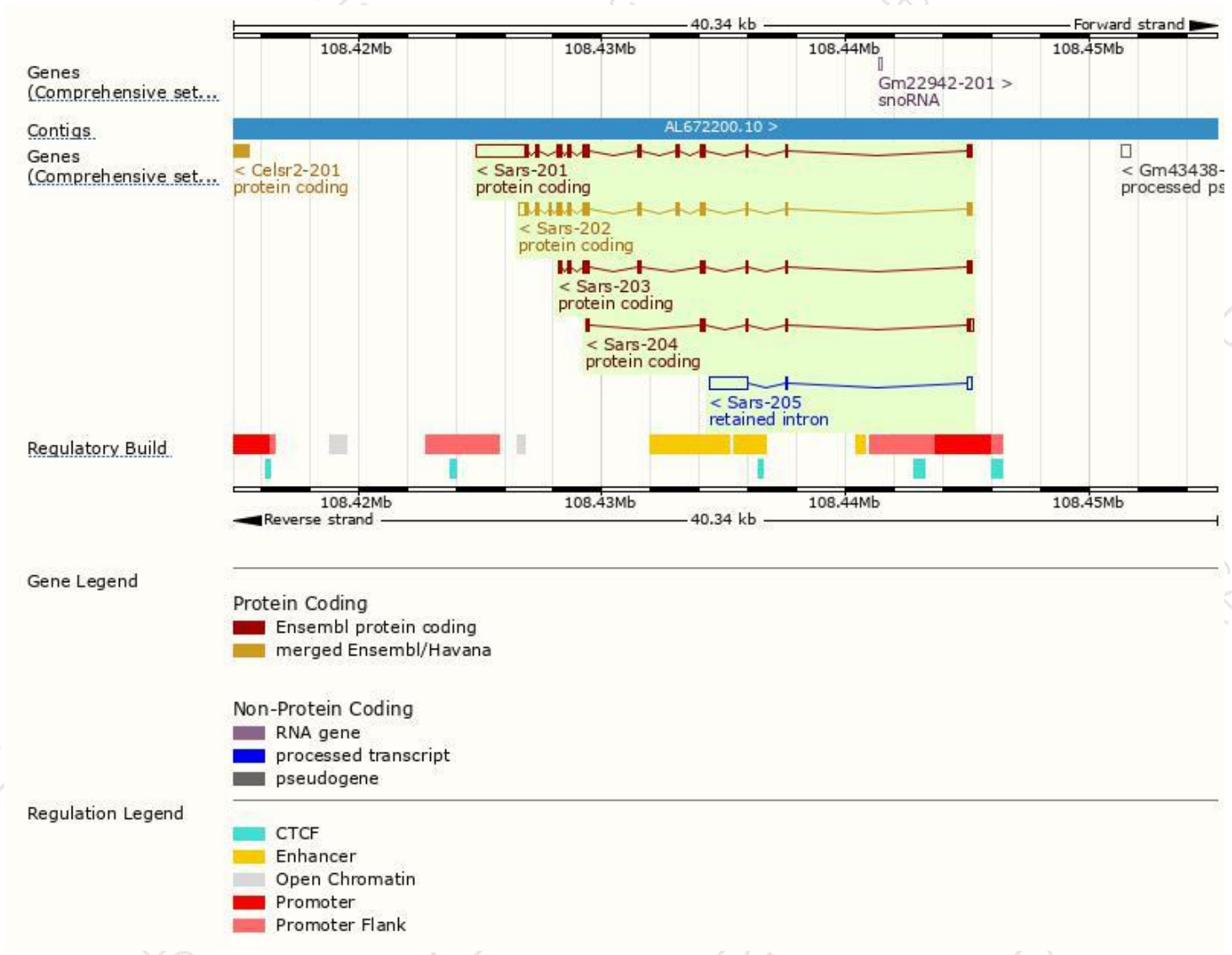
The gene has 5 transcripts,all transcripts are shown below:

| Name | Transcript ID | bp | Protein | Biotype | CCDS | UniProt | Flags |
|----------|---------------------------------------|------|-----------------------|-----------------|---------------------------|------------------------|-------------------------------|
| Sars-201 | ENSMUST00000090553.11 | 3570 | 512aa | Protein coding | CCDS57254 | P26638 | TSL:1 GENCODE basic APPRIS P1 |
| Sars-202 | ENSMUST00000102625.10 | 1866 | 536aa | Protein coding | CCDS17760 | Q8C483 | TSL:1 GENCODE basic |
| Sars-203 | ENSMUST00000132467.7 | 1067 | 352aa | Protein coding | - | A2AFS0 | CDS 3' incomplete TSL:5 |
| Sars-204 | ENSMUST00000153499.1 | 637 | 186aa | Protein coding | - | A2AFS1 | CDS 3' incomplete TSL:5 |
| Sars-205 | ENSMUST00000197647.1 | 1801 | No protein | Retained intron | - | - | TSL:1 |

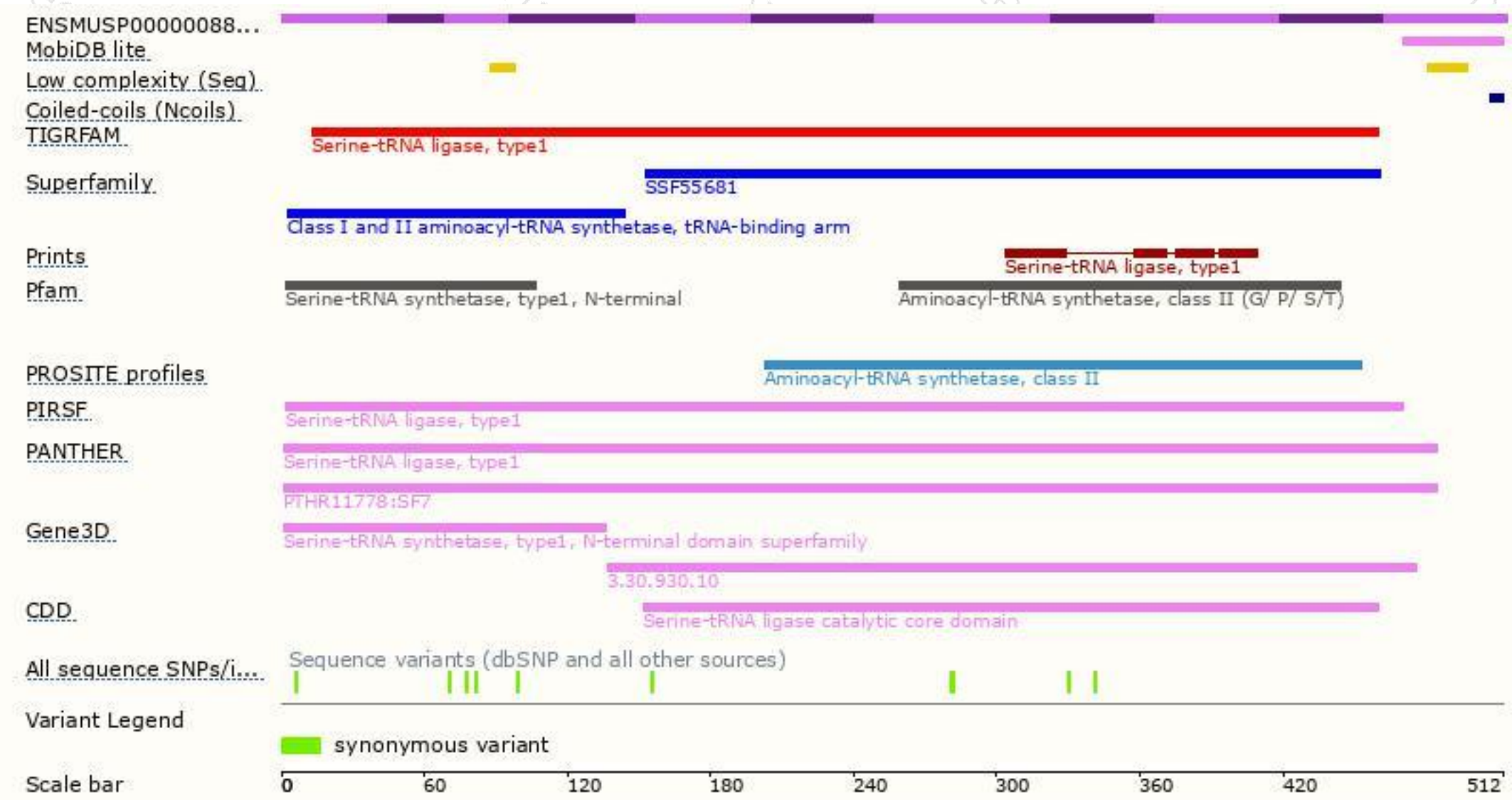
The strategy is based on the design of *Sars-201* transcript,The transcription is shown below



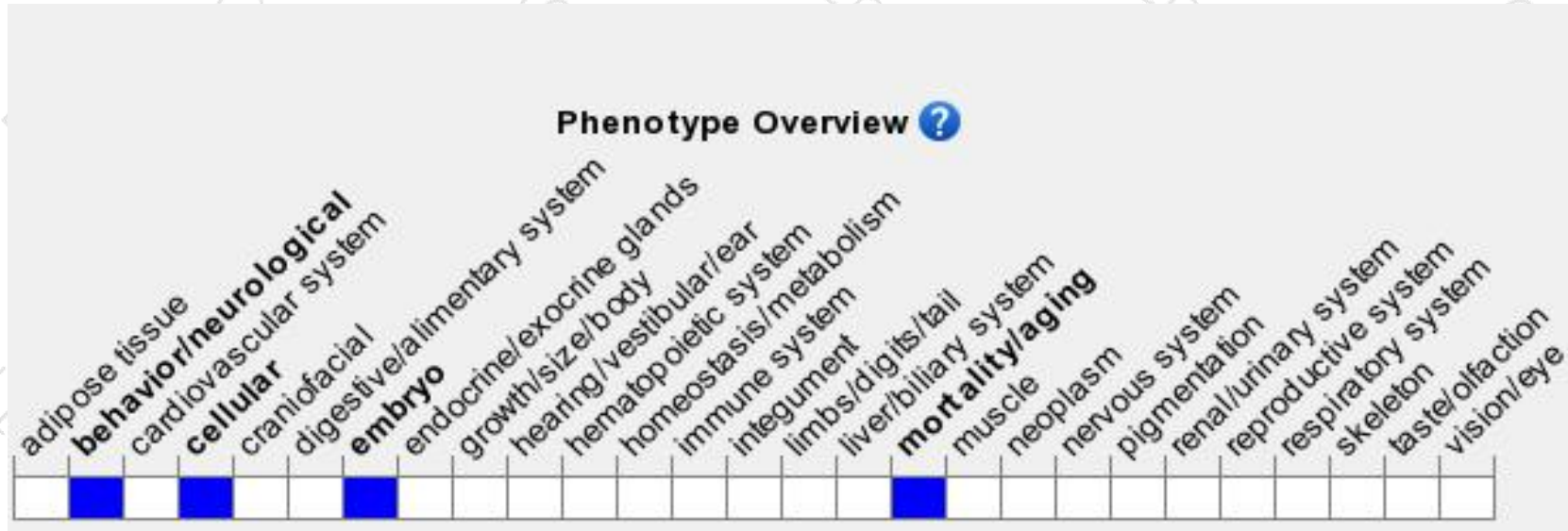
Genomic location distribution



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 show complete embryonic lethality before implantation associated with abnormal morula morphology, increased cell death, and failure of blastocyst formation.

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

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