

Rc3h2 Cas9-KO Strategy

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Design Date: 2020-7-29

Project Overview

Project Name

Rc3h2

Project type

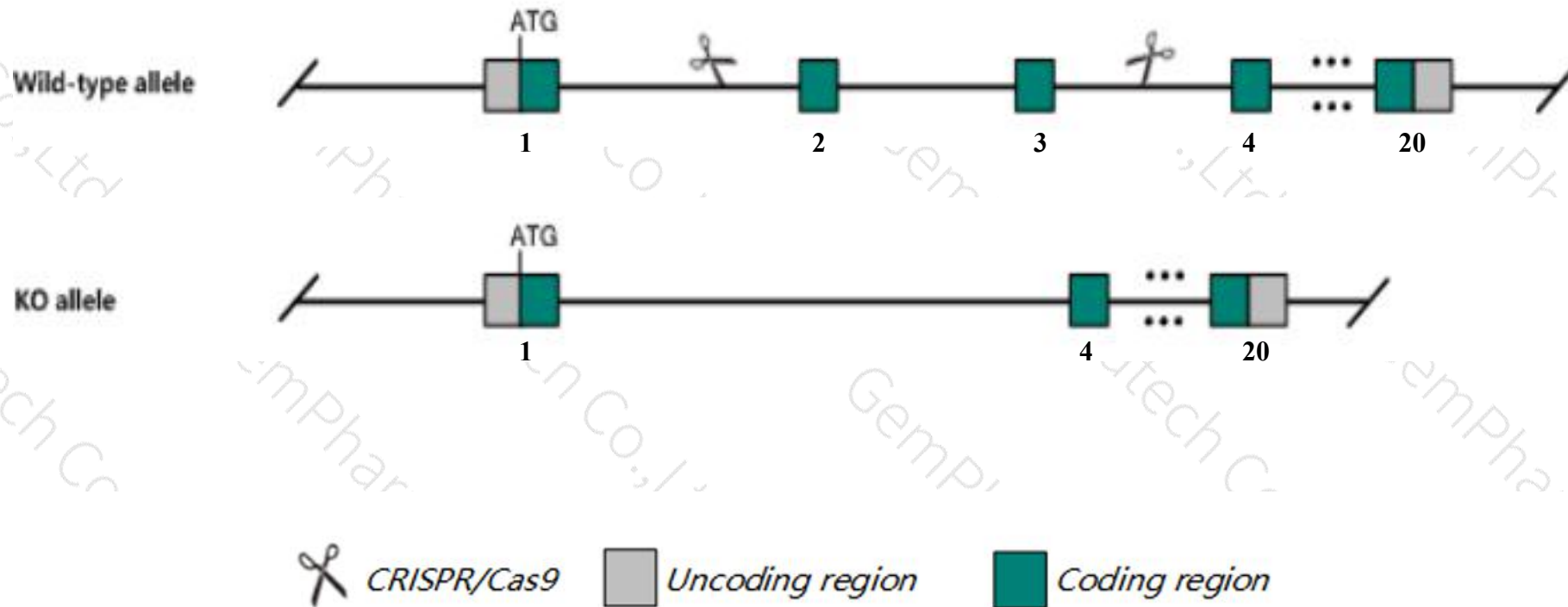
Cas9-KO

Strain background

C57BL/6JGpt

Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *Rc3h2* gene. The schematic diagram is as follows:



- The *Rc3h2* gene has 10 transcripts. According to the structure of *Rc3h2* gene, exon2-exon3 of *Rc3h2*-201(ENSMUST00000100143.9) transcript is recommended as the knockout region. The region contains 352bp coding sequence. Knock out the region will result in disruption of protein function.
- In this project we use CRISPR/Cas9 technology to modify *Rc3h2* gene. The brief process is as follows: CRISPR/Cas9 system were microinjected into the fertilized eggs of C57BL/6JGpt mice. Fertilized eggs were transplanted to obtain positive F0 mice which were confirmed by PCR and sequencing. A stable F1 generation mouse model was obtained by mating positive F0 generation mice with C57BL/6JGpt mice.

- According to the existing MGI data, homozygotes for a knock-out allele are viable and healthy but show increased TNF production by macrophages in response to LPS. Homozygotes for a different knock-out allele show postnatal lethality, decreased body size and weight, and an immature lung phenotype with decreased alveolar expansion.
- The *Rc3h2* 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)

Rc3h2 ring finger and CCCH-type zinc finger domains 2 [Mus musculus (house mouse)]

Gene ID: 319817, updated on 13-Mar-2020

Summary



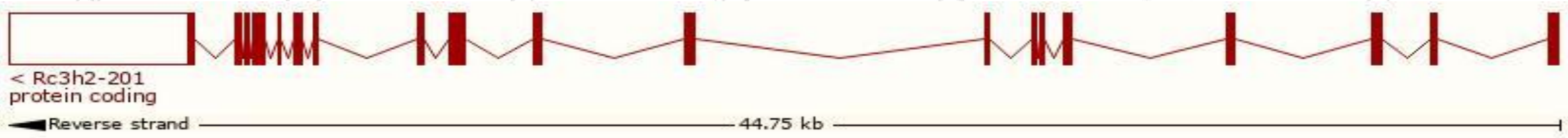
| | |
|---------------------------|---|
| Official Symbol | Rc3h2 provided by MGI |
| Official Full Name | ring finger and CCCH-type zinc finger domains 2 provided by MGI |
| Primary source | MGI:MGI:2442789 |
| See related | Ensembl:ENSMUSG00000075376 |
| Gene type | protein coding |
| RefSeq status | 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 | 2900024N03Rik, 9430019J22Rik, D930043C02Rik, Mnab, Rnf164 |
| Expression | Ubiquitous expression in whole brain E14.5 (RPKM 8.3), CNS E18 (RPKM 7.9) and 28 other tissues See more |
| Orthologs | human all |

Transcript information (Ensembl)

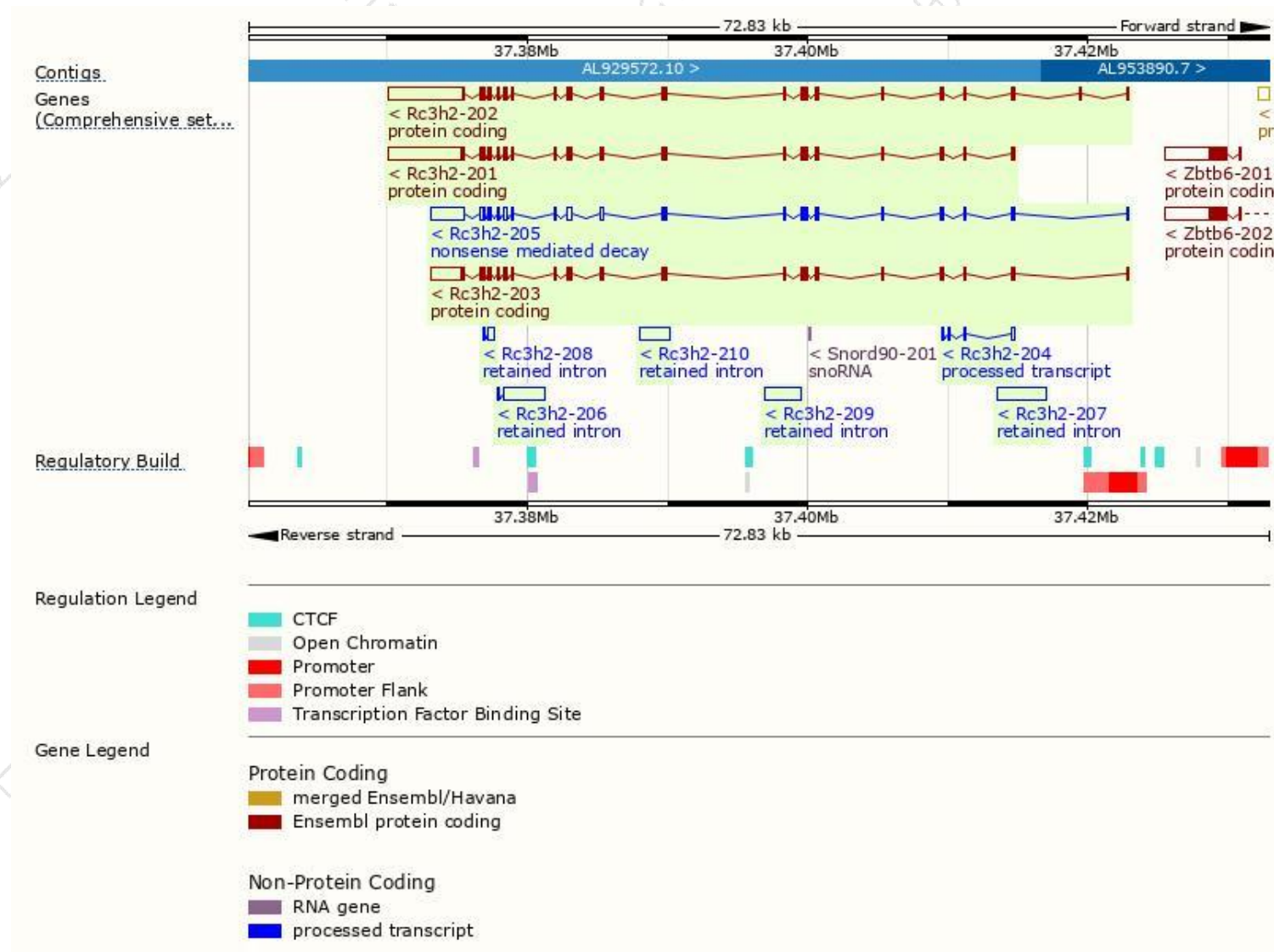
The gene has 10 transcripts,all transcripts are shown below:

| Name | Transcript ID | bp | Protein | Biotype | CCDS | UniProt | Flags |
|-----------|--------------------------------------|------|------------------------|-------------------------|---------------------------|----------------------------|---------------------------------|
| Rc3h2-202 | ENSMUST00000112934.7 | 8948 | 1125aa | Protein coding | CCDS71046 | A2AVP4 | TSL:1 GENCODE basic APPRIS ALT1 |
| Rc3h2-201 | ENSMUST00000100143.9 | 8799 | 1187aa | Protein coding | CCDS38116 | P0C090 | TSL:5 GENCODE basic APPRIS P3 |
| Rc3h2-203 | ENSMUST00000112936.3 | 5828 | 1187aa | Protein coding | CCDS38116 | P0C090 | TSL:5 GENCODE basic APPRIS P3 |
| Rc3h2-205 | ENSMUST00000125619.6 | 5754 | 478aa | Nonsense mediated decay | - | A0A0N4SVF7 | TSL:5 |
| Rc3h2-204 | ENSMUST00000124218.1 | 513 | No protein | Processed transcript | - | - | TSL:3 |
| Rc3h2-207 | ENSMUST00000204690.1 | 3479 | No protein | Retained intron | - | - | TSL:NA |
| Rc3h2-206 | ENSMUST00000143826.1 | 3083 | No protein | Retained intron | - | - | TSL:2 |
| Rc3h2-209 | ENSMUST00000204962.1 | 2698 | No protein | Retained intron | - | - | TSL:NA |
| Rc3h2-210 | ENSMUST00000205124.1 | 2236 | No protein | Retained intron | - | - | TSL:NA |
| Rc3h2-208 | ENSMUST00000204959.1 | 575 | No protein | Retained intron | - | - | TSL:2 |

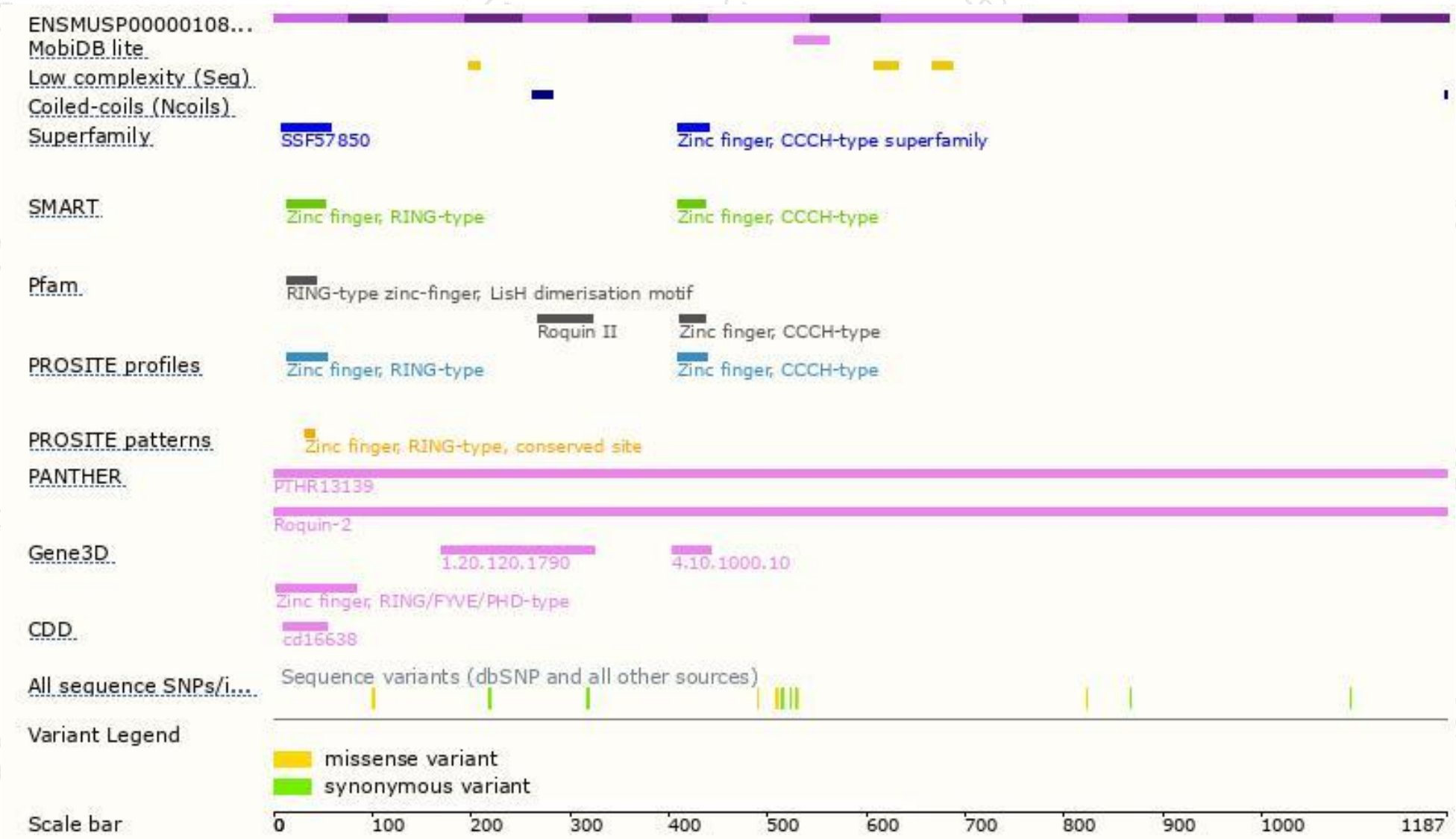
The strategy is based on the design of *Rc3h2-201* transcript,the transcription is shown below:



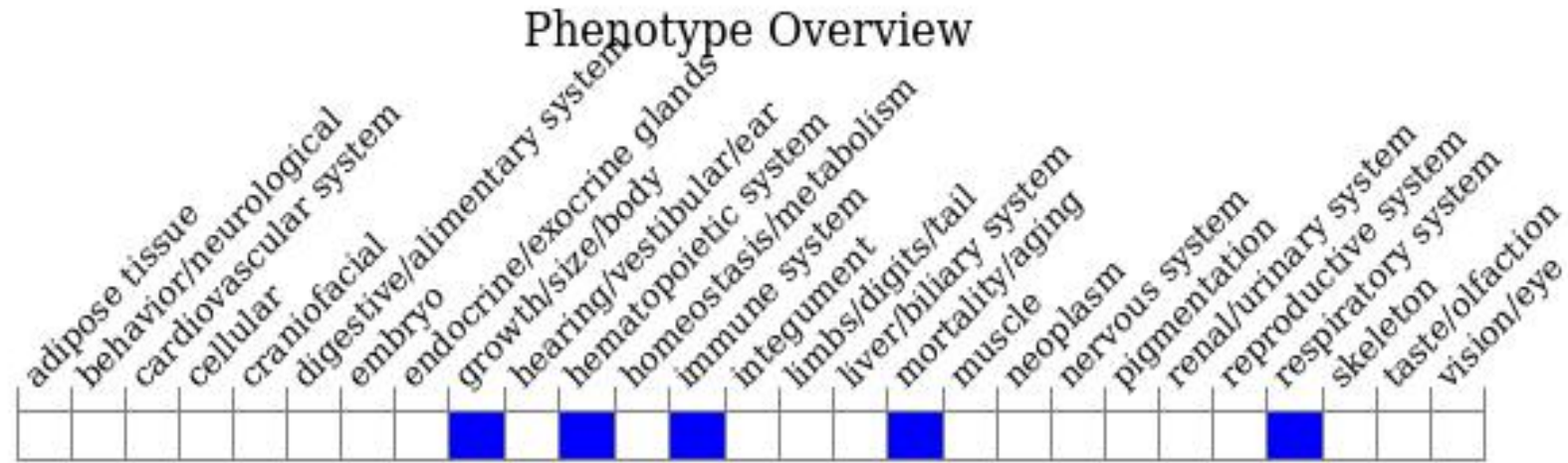
Genomic location distribution



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, homozygotes for a knock-out allele are viable and healthy but show increased TNF production by macrophages in response to LPS. Homozygotes for a different knock-out allele show postnatal lethality, decreased body size and weight, and an immature lung phenotype with decreased alveolar expansion.

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

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