

Hoxc9 Cas9-KO Strategy

Designer:

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Reviewer:

Design Date:

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Project Overview

Project Name

Hoxc9

Project type

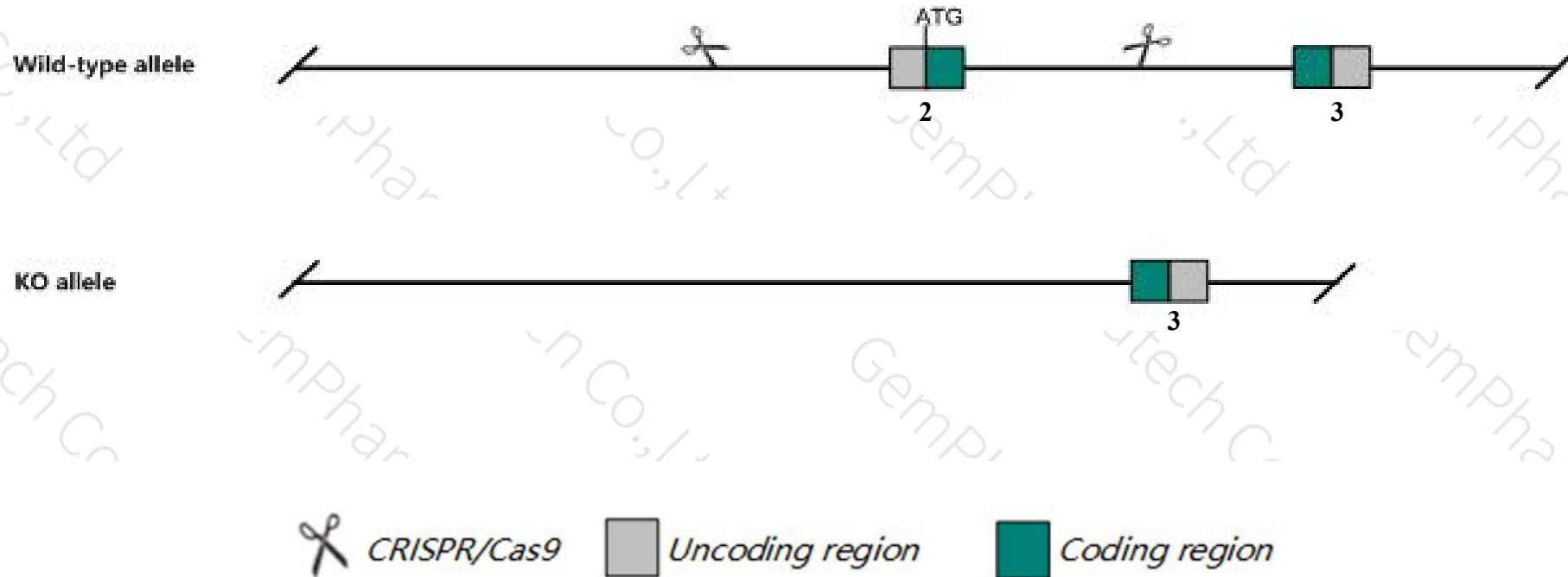
Cas9-KO

Strain background

C57BL/6JGpt

Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *Hoxc9* gene. The schematic diagram is as follows:



- The *Hoxc9* gene has 2 transcripts. According to the structure of *Hoxc9* gene, exon2 of *Hoxc9-201* (ENSMUST00000001706.6) transcript is recommended as the knockout region. The region contains start codon ATG. Knock out the region will result in disruption of protein function.
- In this project we use CRISPR/Cas9 technology to modify *Hoxc9* gene. The brief process is as follows: CRISPR/Cas9 system

- According to the existing MGI data, Mice homozygous for disruptions in this gene grow more slowly than normal and develop hunched backs. Forward transformations seen in vertebrae from L1 and forward to around T10. Abnormalities in the sternum and ribs attachments to the sternum are also seen.
- The KO region overlaps with intron1 of *Hoxc5-202* transcript. Knockout the region may affect the function of *Hoxc5-202* transcript.
- The *Hoxc9* gene is located on the Chr15. 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)

Hoxc9 homeobox C9 [*Mus musculus* (house mouse)]

Gene ID: 15427, updated on 12-Nov-2019

Summary

| | |
|---------------------------|---|
| Official Symbol | Hoxc9 provided by MGI |
| Official Full Name | homeobox C9 provided by MGI |
| Primary source | MGI:MGI:96199 |
| See related | Ensembl:ENSMUSG00000036139 |
| 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 | Hox-3.2 |
| Expression | Biased expression in ovary adult (RPKM 7.9), mammary gland adult (RPKM 7.9) and 7 other tissues See more |
| Orthologs | human all |

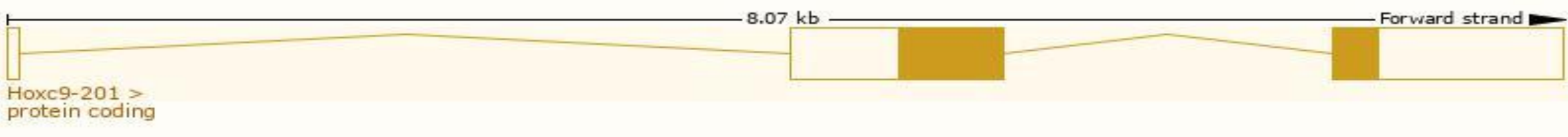


Transcript information (Ensembl)

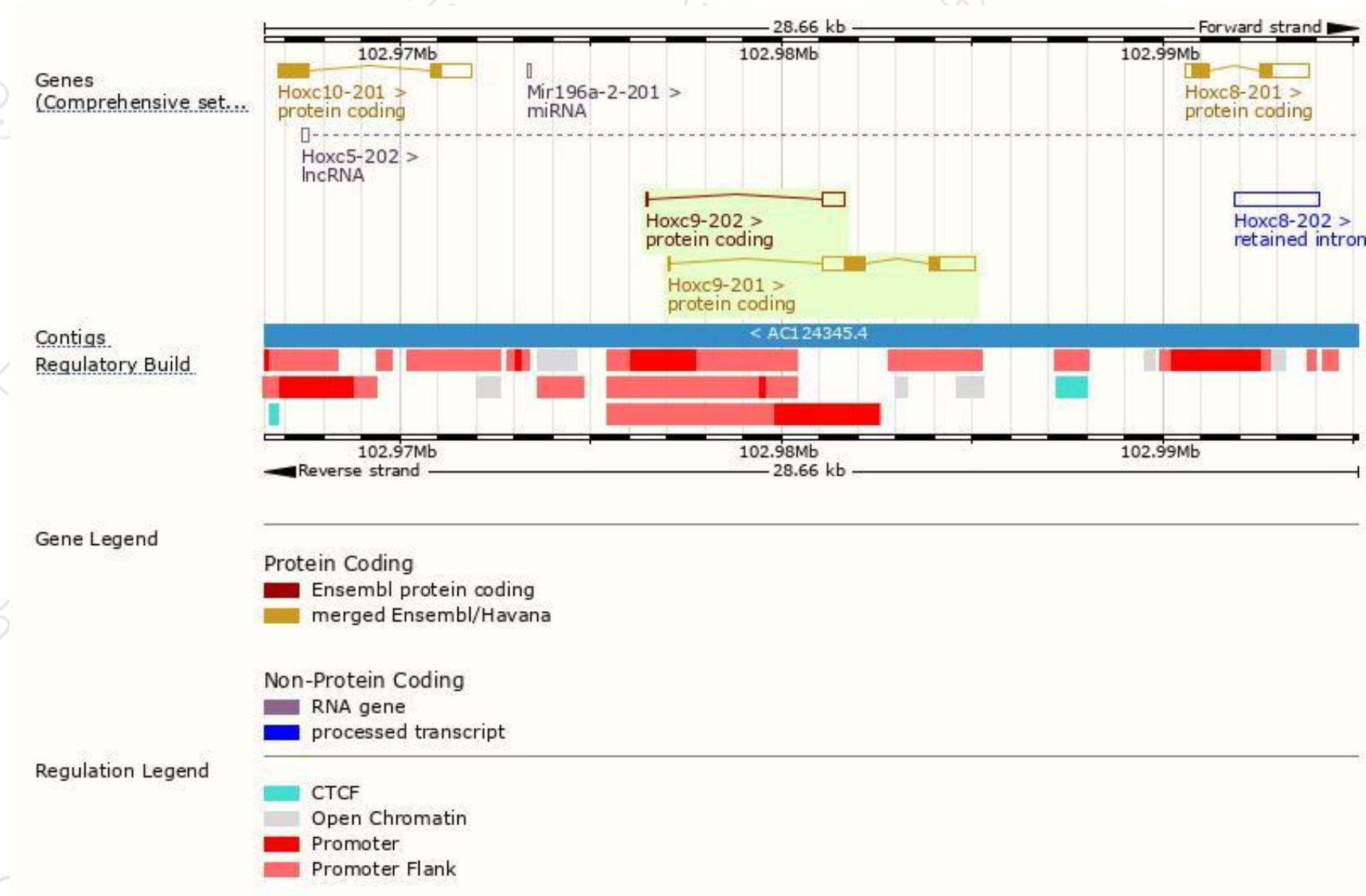
The gene has 2 transcripts,all transcripts are shown below:

| Name | Transcript ID | bp | Protein | Translation ID | Biotype | CCDS | UniProt | Flags |
|-----------|--------------------------------------|------|-----------------------|---------------------------------------|----------------|---------------------------|------------------------|-------------------------------|
| Hoxc9-201 | ENSMUST00000001706.6 | 2374 | 260aa | ENSMUSP000000001706.6 | Protein coding | CCDS27893 | P09633 | TSL:1 Gencode basic APPRIS P1 |
| Hoxc9-202 | ENSMUST00000173306.1 | 634 | 5aa | ENSMUSP00000134197.1 | Protein coding | - | - | CDS 3' incomplete TSL:3 |

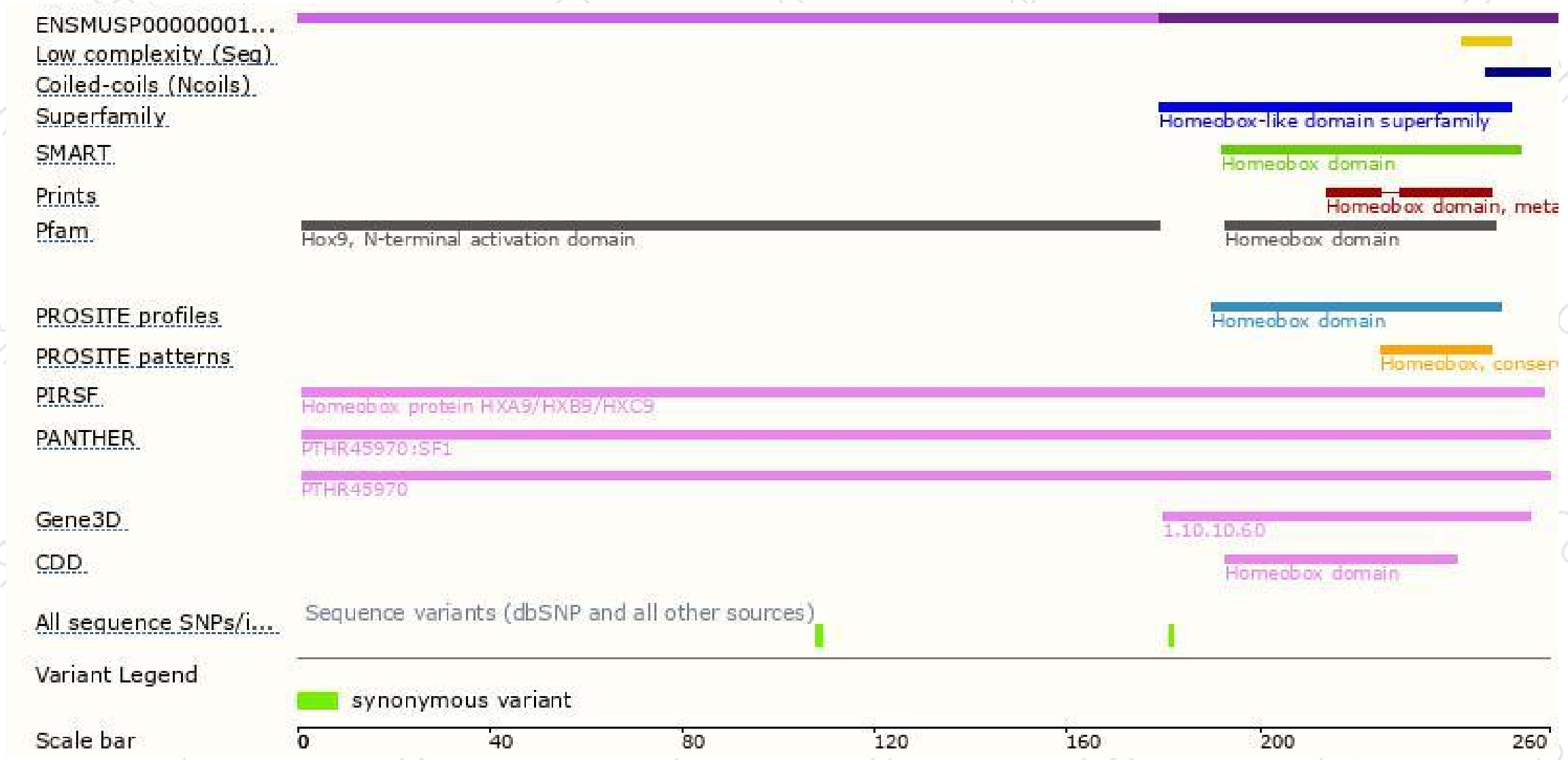
The strategy is based on the design of *Hoxc9-201* transcript,The transcription is shown below



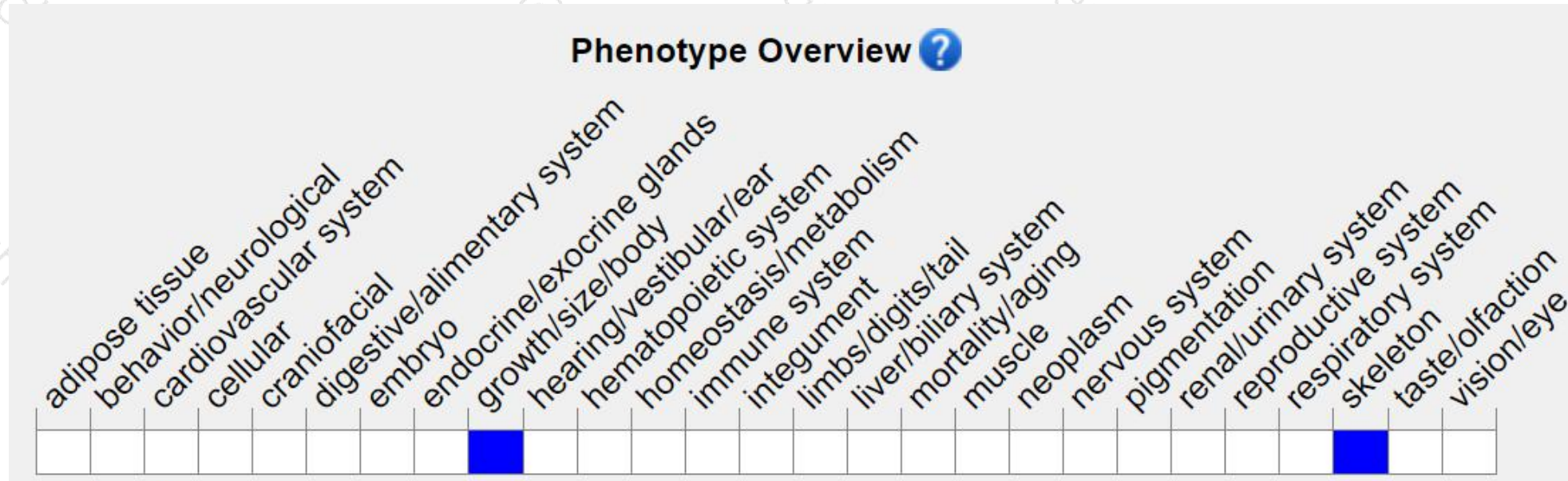
Genomic location distribution



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 disruptions in this gene grow more slowly than normal and develop hunched backs. Forward transformations seen in vertebrae from L1 and forward to around T10. Abnormalities in the sternum and ribs attachments to the sternum are also seen.

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

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