

# *Evx1* Cas9-KO Strategy

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# Project Overview

**Project Name**

*Evx1*

**Project type**

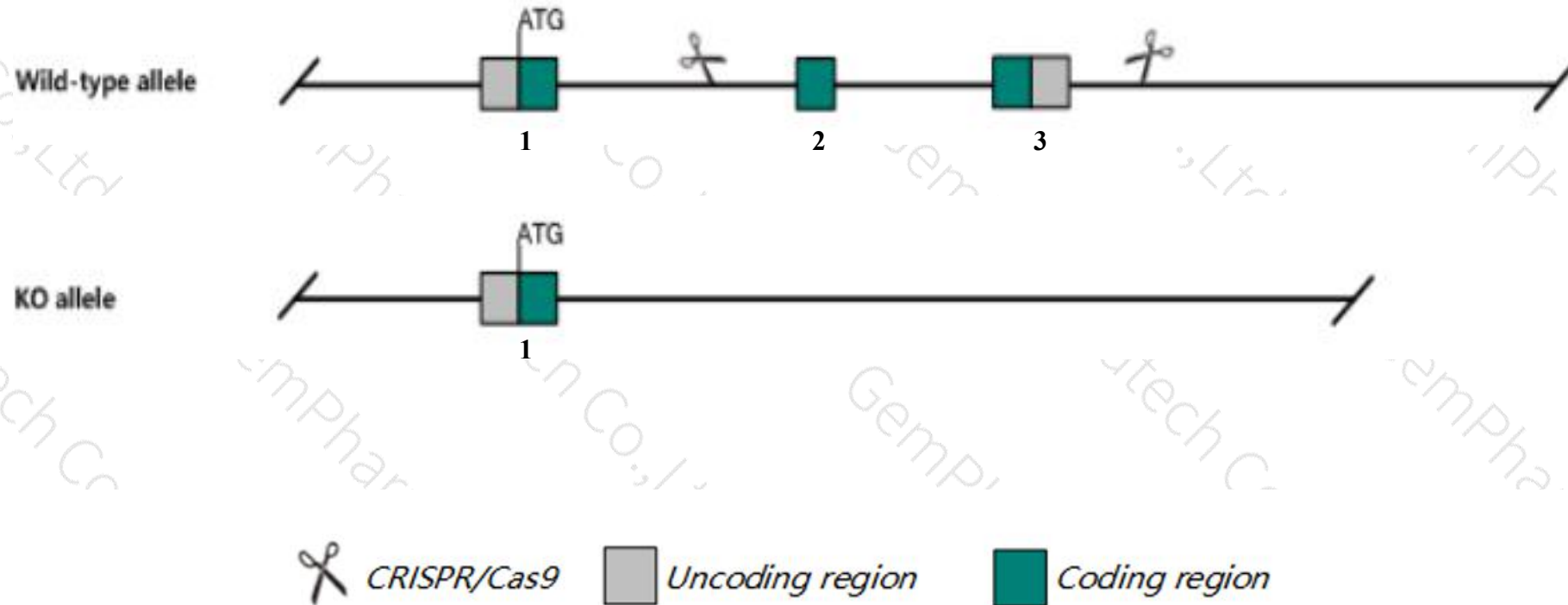
**Cas9-KO**

**Strain background**

**C57BL/6JGpt**

# Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *Evx1* gene. The schematic diagram is as follows:



- The *Evx1* gene has 2 transcripts. According to the structure of *Evx1* gene, exon2-exon3 of *Evx1-201* (ENSMUST00000031787.7) transcript is recommended as the knockout region. The region contains most of the coding sequence. Knock out the region will result in disruption of protein function.
- In this project we use CRISPR/Cas9 technology to modify *Evx1* gene. The brief process is as follows: CRISPR/Cas9 system v

- According to the existing MGI data, homozygotes for a particular targeted mutation are embryonic lethal. another heritable cre-generated allele exhibits defects of the interneurons of the ventral spinal cord, and rarely, a kinked tail.
- The knockout region is near to the N-terminal of *Evx1os* gene, this strategy may influence the regulatory function of the N-terminal of *Evx1os* gene.
- The *Evx1* gene is located on the Chr6. 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)

## Evx1 even-skipped homeobox 1 [Mus musculus (house mouse)]

Gene ID: 14028, updated on 13-Mar-2020

### Summary



**Official Symbol** Evx1 provided by [MGI](#)

**Official Full Name** even-skipped homeobox 1 provided by [MGI](#)

**Primary source** [MGI:MGI:95461](#)

**See related** [Ensembl:ENSMUSG000000005503](#)

**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** Evx-1

**Expression** Biased expression in colon adult (RPKM 1.7), ovary adult (RPKM 1.2) and 8 other tissues [See more](#)

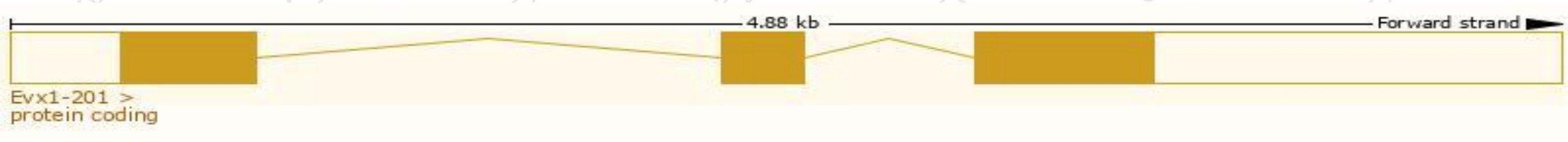
**Orthologs** [human](#) [all](#)

# Transcript information (Ensembl)

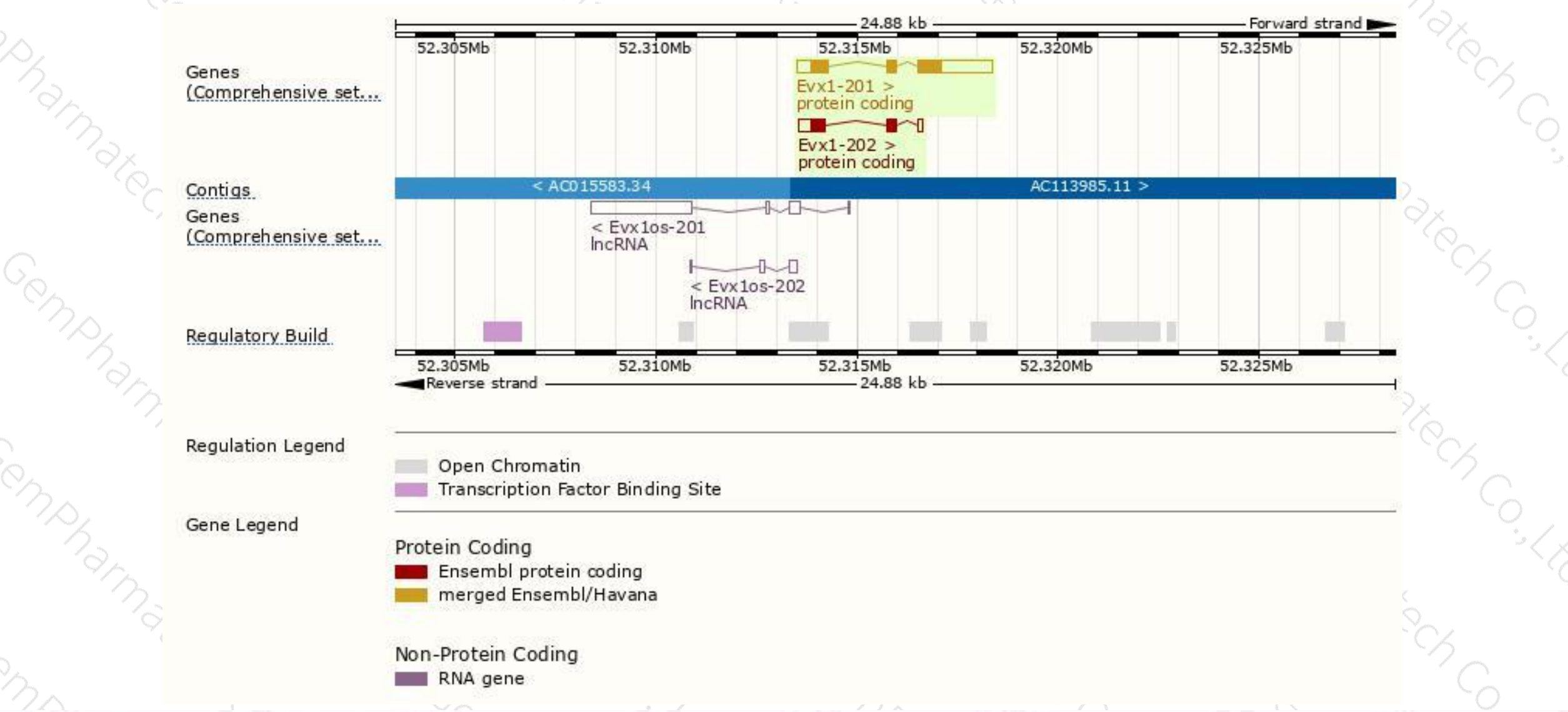
The gene has 2 transcripts,all transcripts are shown below:

| Name     | Transcript ID                        | bp   | Protein               | Biotype        | CCDS                      | UniProt                | Flags                                                                                                                                                                                                         |
|----------|--------------------------------------|------|-----------------------|----------------|---------------------------|------------------------|---------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|
| Evx1-201 | <a href="#">ENSMUST00000031787.7</a> | 2877 | <a href="#">416aa</a> | Protein coding | <a href="#">CCDS20149</a> | <a href="#">P23683</a> | 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 |
| Evx1-202 | <a href="#">ENSMUST00000129243.2</a> | 1034 | <a href="#">201aa</a> | Protein coding | -                         | <a href="#">F6R8N2</a> | TSL:3 GENCODE basic                                                                                                                                                                                           |

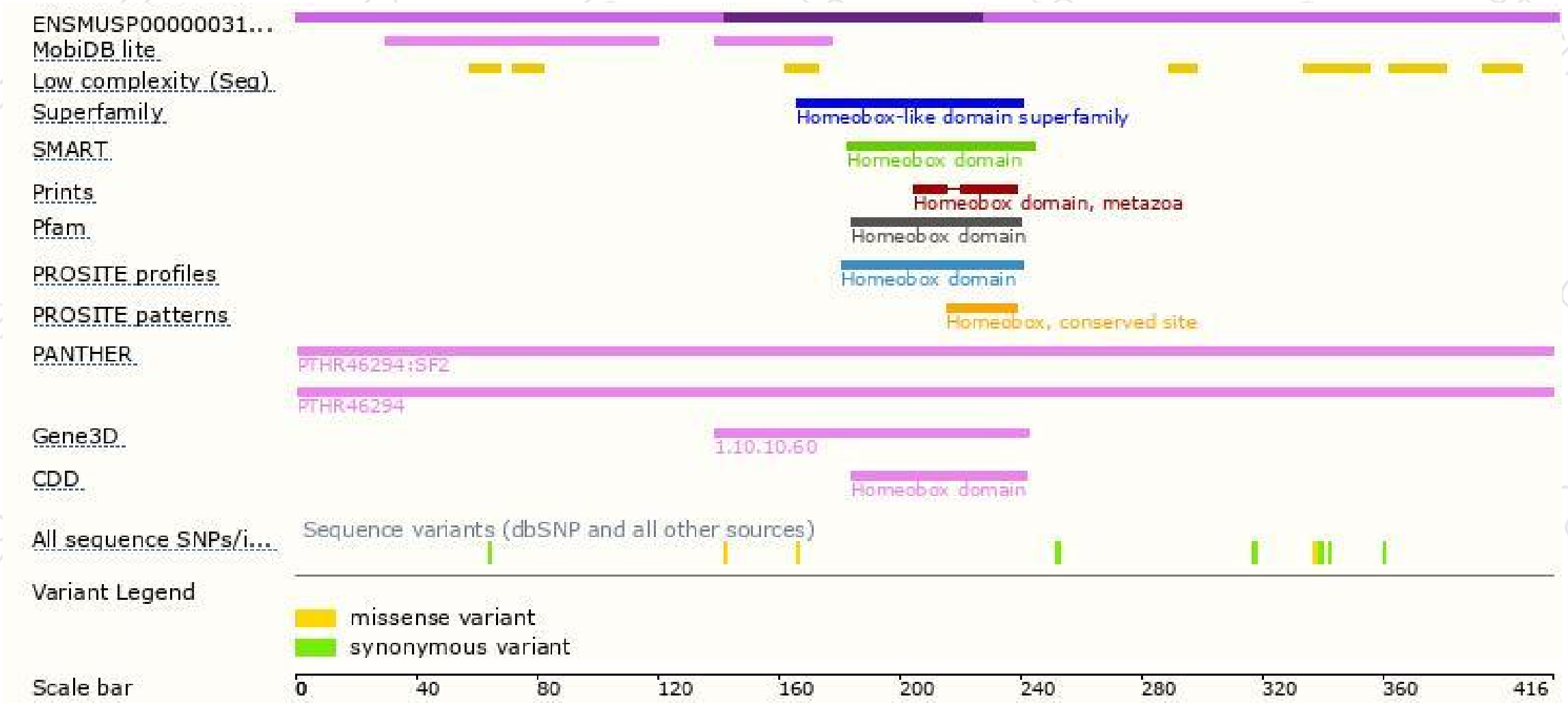
The strategy is based on the design of *Evx1-201* transcript,the transcription is shown below:



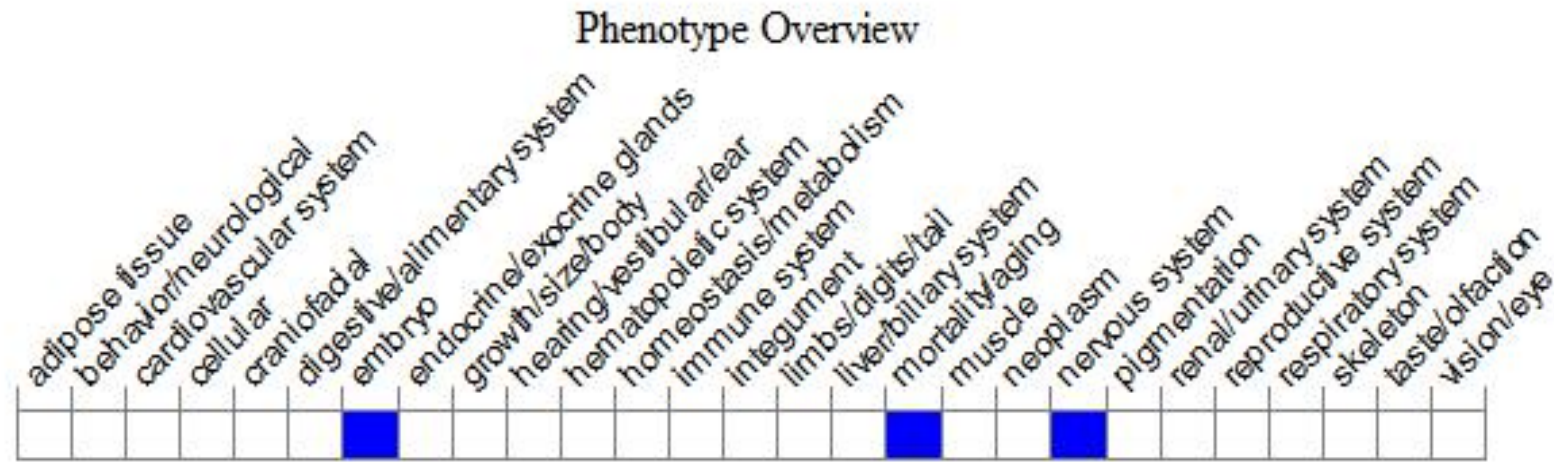
# Genomic location distribution



# 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 particular targeted mutation are embryonic lethal. Another heritable cre-generated allele exhibits defects of the interneurons of the ventral spinal cord, and rarely, a kinked tail.

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

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