

Hoxb13 Cas9-KO Strategy

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Reviewer :

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Project Overview

Project Name

Hoxb13

Project type

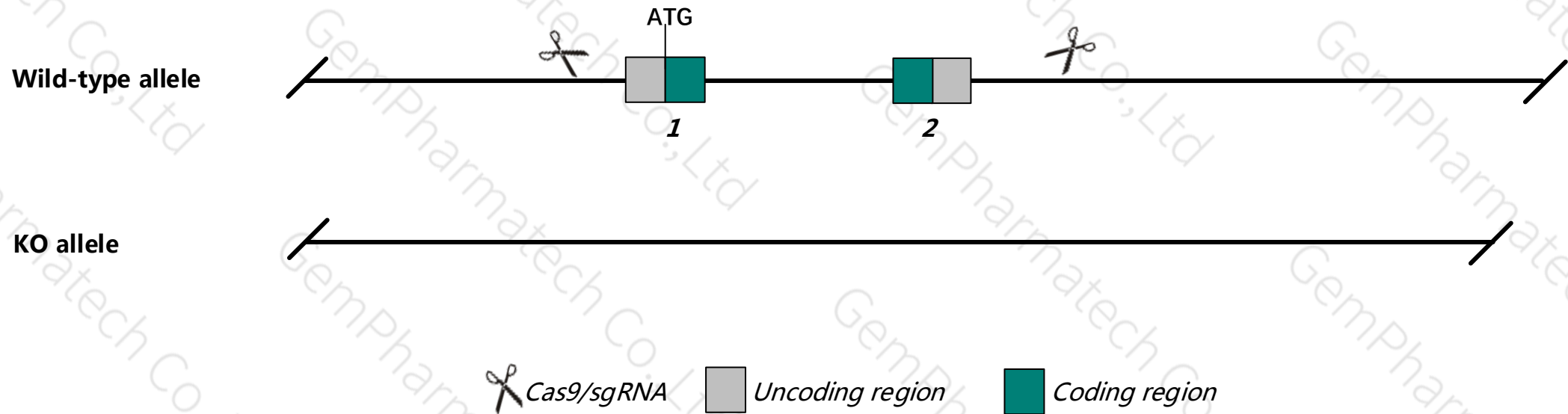
Cas9-KO

Strain background

C57BL/6JGpt

Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *Hoxb13* gene. The schematic diagram is as follows:



Technical routes

- The *Hoxb13* gene has 1 transcript. According to the structure of *Hoxb13* gene, exon1-exon2 of *Hoxb13*-201 (ENSMUST00000062709.3) transcript is recommended as the knockout region. The region contains all 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 *Hoxb13* gene. The brief process is as follows: sgRNA was transcribed in vitro. Cas9, sgRNA 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 , Mice homozygous for loss of function mutations show overgrowth in all major structures derived from the tail bud.
- The *Hoxb13* gene is located on the Chr11. 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.

Hoxb13 homeobox B13 [*Mus musculus* (house mouse)]

Gene ID: 15408, updated on 12-Aug-2019

Summary

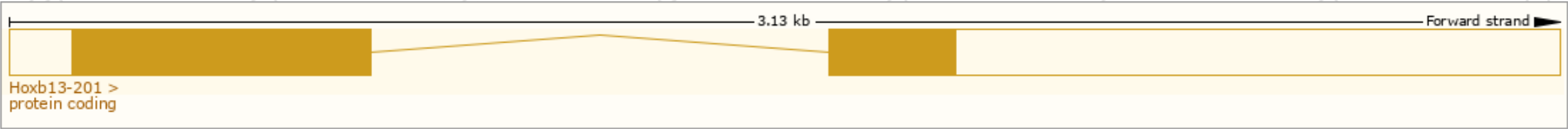
| | |
|--------------------|---------------------------------------------------------------------------------------------------------------------------------------------------------------------------|
| Official Symbol | Hoxb13 provided by MGI |
| Official Full Name | homeobox B13 provided by MGI |
| Primary source | MGI:MGI:107730 |
| See related | Ensembl:ENSMUSG00000049604 |
| 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 |
| Expression | Restricted expression toward colon adult (RPKM 258.3) See more |
| Orthologs | human all |

Transcript information (Ensembl)

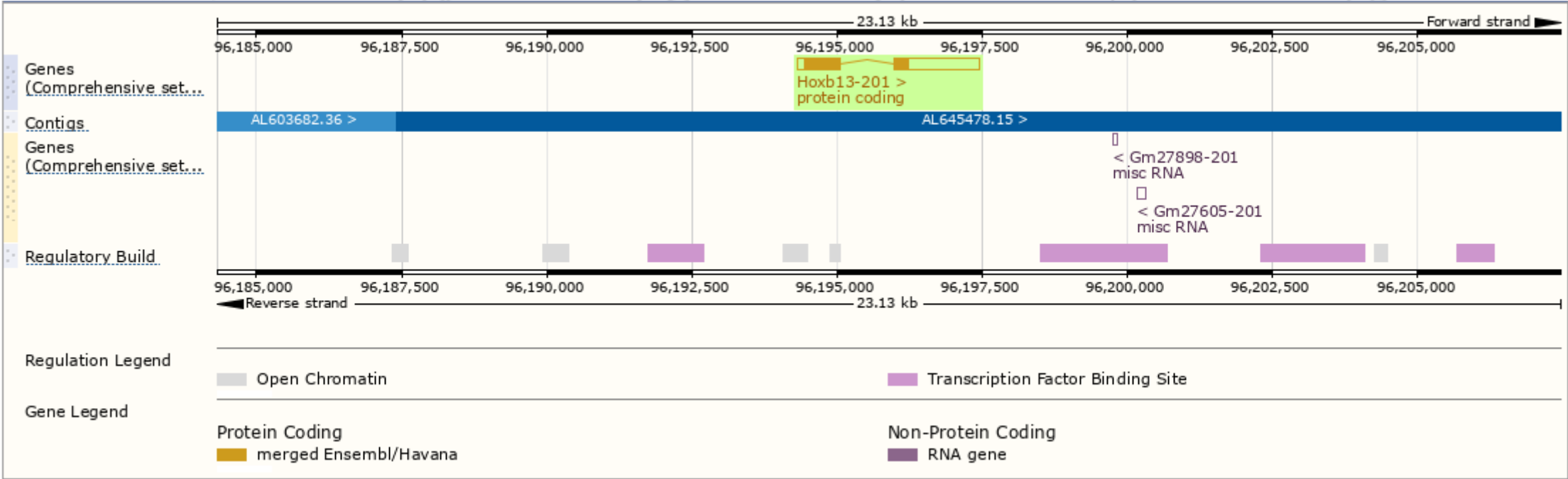
The gene has 1 transcript, and the transcripts is shown below:

| Name | Transcript ID | bp | Protein | Biotype | CCDS | UniProt | Flags |
|------------|--------------------------------------|------|-----------------------|----------------|---------------------------|------------------------|-------------------------------|
| Hoxb13-201 | ENSMUST00000062709.3 | 2206 | 286aa | Protein coding | CCDS25291 | P70321 | TSL:1 Gencode basic APPRIS P1 |

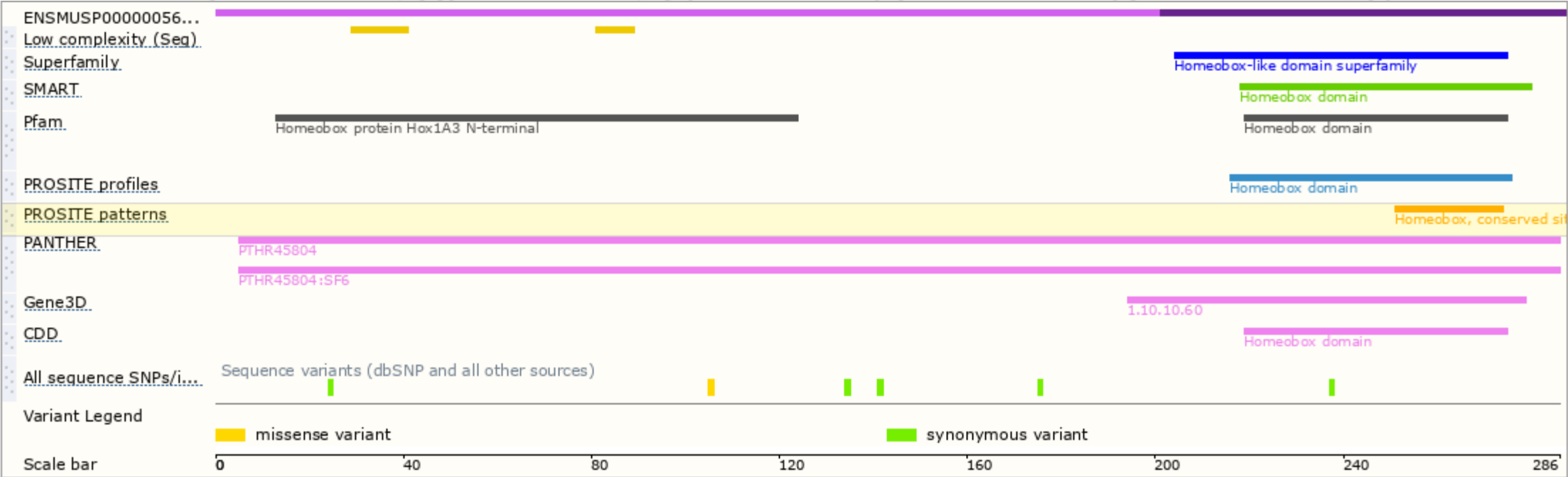
The strategy is based on the design of *Hoxb13*-201 transcript, The transcription is shown below



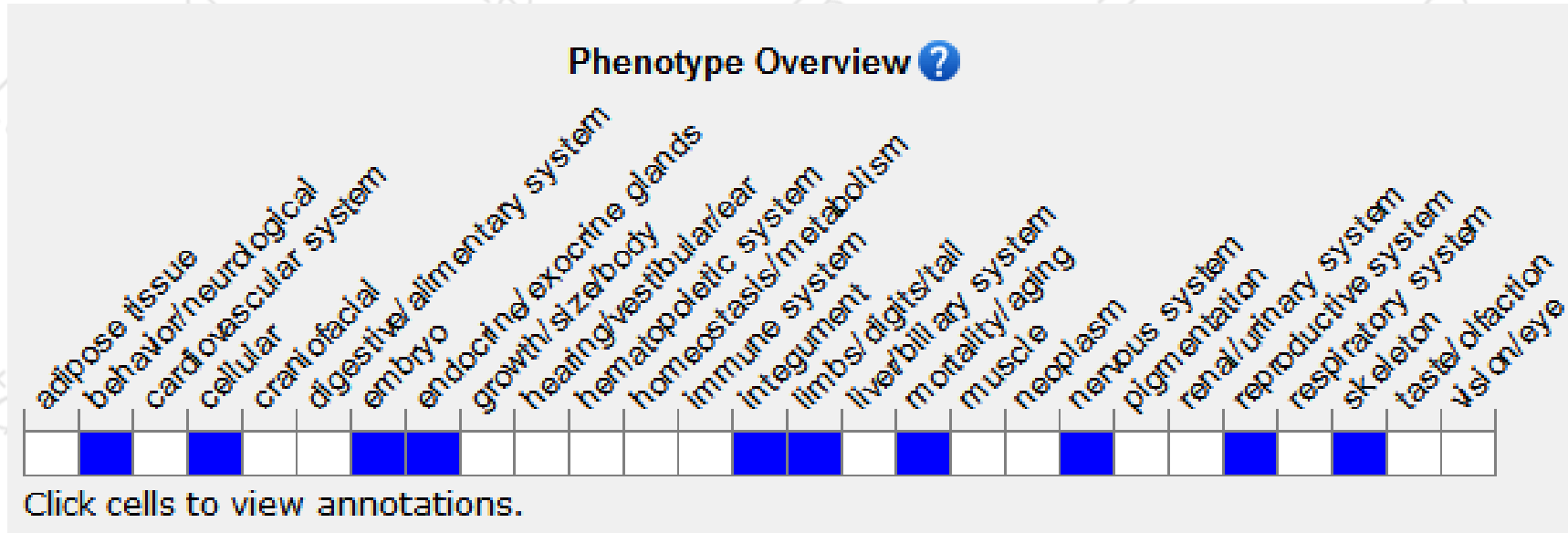
Genomic location distribution



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 loss of function mutations show overgrowth in all major structures derived from the tail bud.

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