

Sox7 Cas9-KO Strategy

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Reviewer :

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Project Overview

Project Name

Sox7

Project type

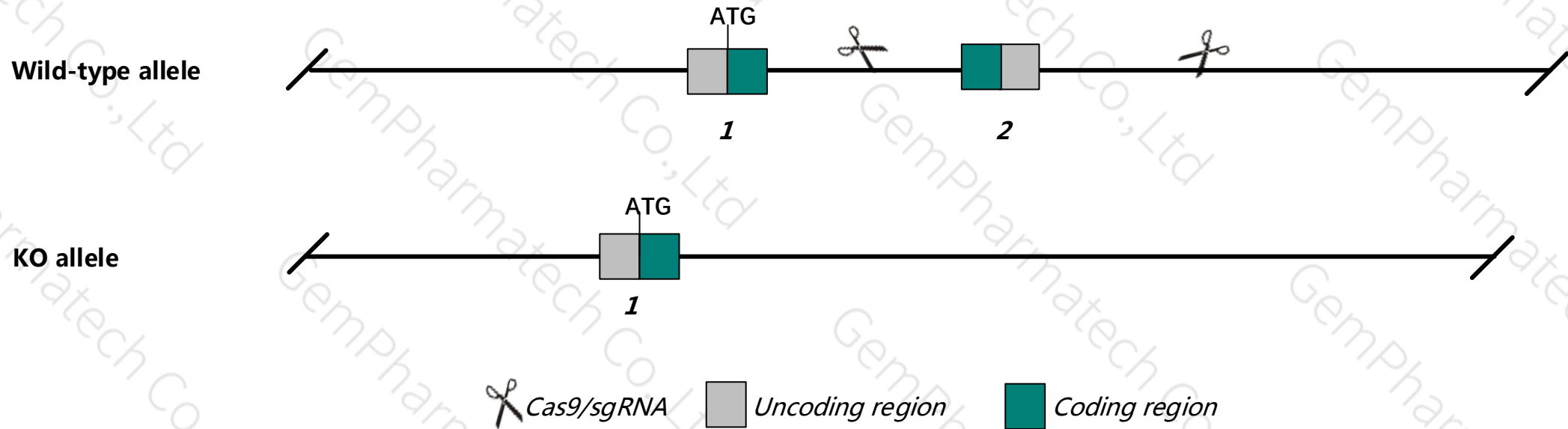
Cas9-KO

Animal background

C57BL/6JGpt

Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *Sox7* gene. The schematic diagram is as follows:



Technical routes

- The *Sox7* gene has 1 transcript, According to the structure of *Sox7* gene, exon2 of *Sox7-201* transcript is recommended as the knockout region. The region contains the most of coding sequence. Knock out the region, result in destruction of protein.
- This project uses CRISPR/Cas9 technology to modify *Sox7* gene. The brief process is as follows: sgRNA was transcribed in vitro, Cas9, sgRNA were microinjected into fertilized eggs of C57BL/6JGpt mice and homologous recombination was carried out to obtain F0 mice. A stable and hereditary F1 generation mouse model was obtained by mating F0 generation mice with C57BL/6JGpt mice which were confirmed positive by PCR-sequencing.

- According to the existing MGI data , Most embryos homozygous for a knock-out allele exhibit embryonic growth retardation, abnormal vitelline vascular remodeling and pericardial edema, and die during organogenesis. Depending on the genetic background, a portion of heterozygotes can develop congenital retrosternal diaphragmatic hernias.
- The *Sox7* gene is located in the Chr14. If the knockout mice are mixed with other mice, two target genes are avoided on the same chromosome as possible, otherwise the offspring of mice with double gene positive and homozygous gene knockout can not be obtained.
- This Strategy is designed based on genetic information in existing databases. Due to the complexity of gene transcription and translation processes, all risks cannot be predicted under existing information.

Sox7 SRY (sex determining region Y)-box 7 [*Mus musculus* (house mouse)]

Gene ID: 20680, updated on 5-Feb-2019

Summary

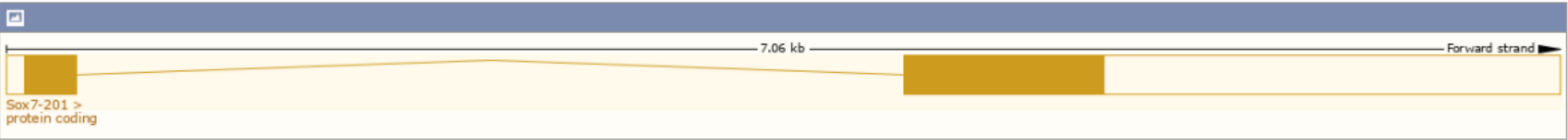
Official Symbol	Sox7 provided by MGI
Official Full Name	SRY (sex determining region Y)-box 7 provided by MGI
Primary source	MGI:MGI:98369
See related	Ensembl:ENSMUSG000000063060
Gene type	protein coding
RefSeq status	PROVISIONAL
Organism	Mus musculus
Lineage	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Myomorpha; Muroidea; Muridae; Murinae; Mus; Mus
Expression	Biased expression in lung adult (RPKM 22.4), heart adult (RPKM 6.0) and 11 other tissues See more
Orthologs	human all

Transcript information (Ensembl)

The gene has 1 transcript, and all transcripts are shown below :

Show/hide columns (1 hidden)								Filter	
Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	RefSeq	Flags	
Sox7-201	ENSMUST00000079652.6	3299	380aa	Protein coding	CCDS27206	P40646 Q3U1W5	NM_011446 NP_035576	TSL:1	GENCODE basic APPRIS P1

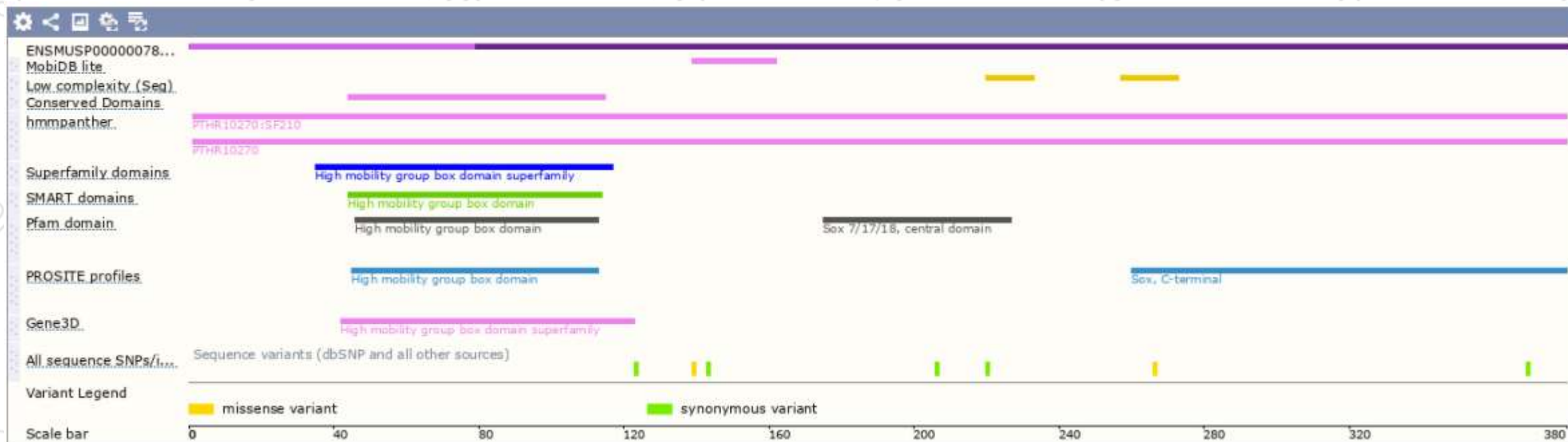
The strategy is based on the design of Sox7-201 transcript,The transcription is shown below :



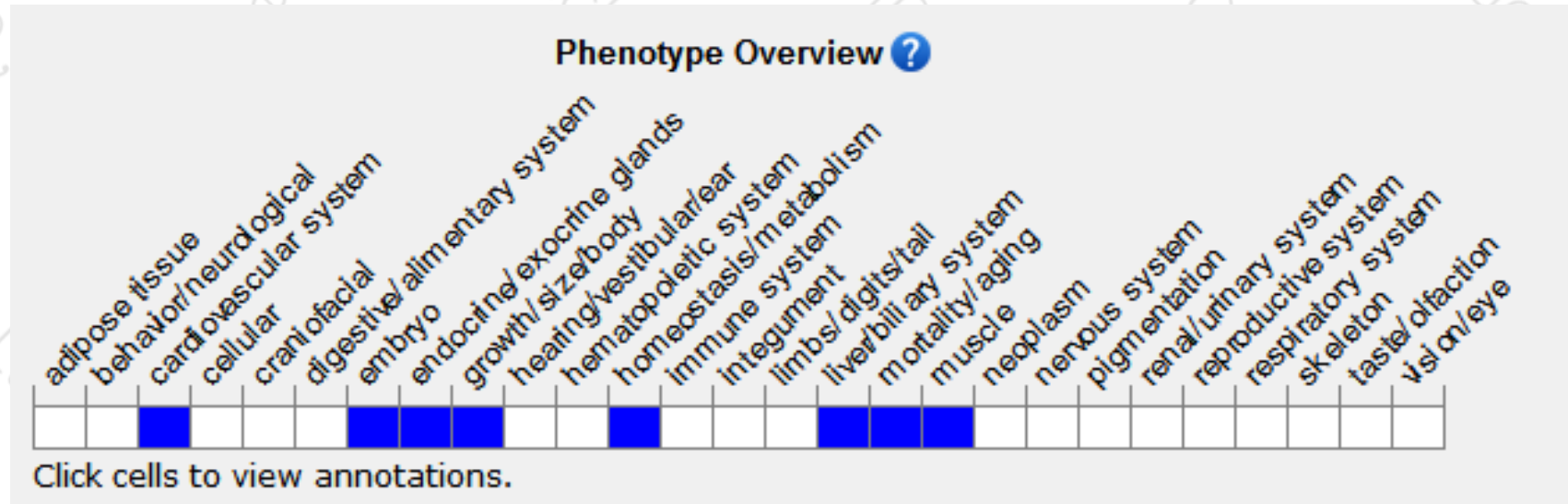
Genomic location distribution



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/>).

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Depending on the genetic background, a portion of heterozygotes can develop congenital retrosternal diaphragmatic hernias.

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