Sp7 Cas9-KO *Strategy*

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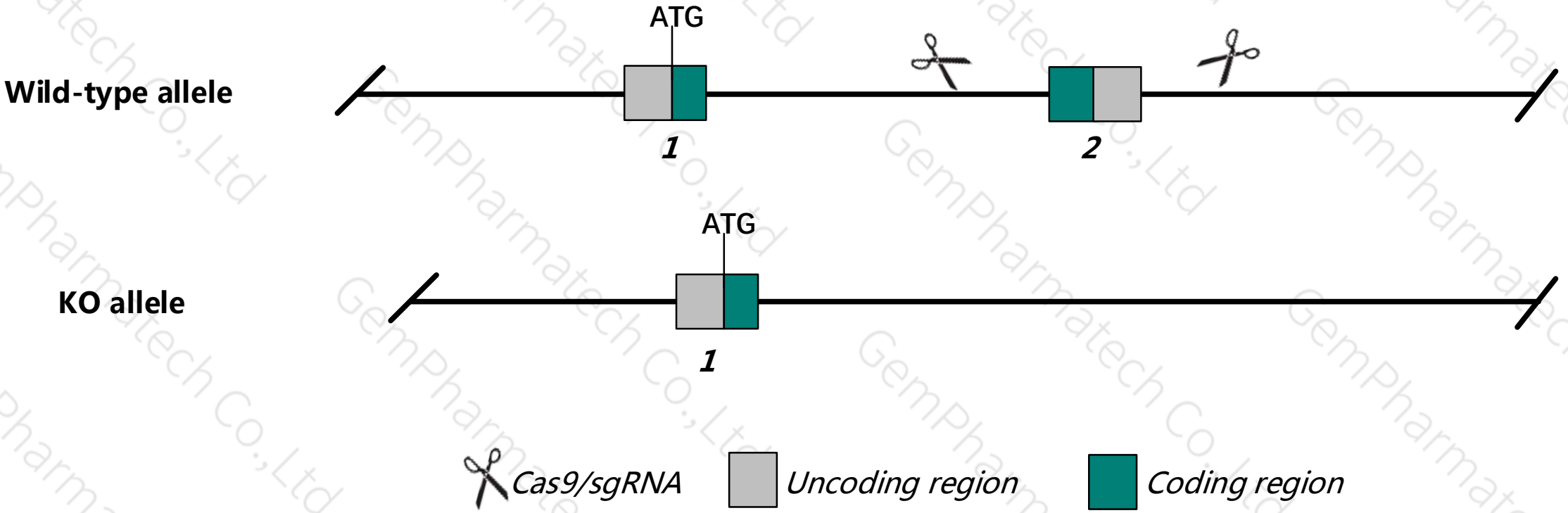
Project Overview

Project Name	***Sp7***
Project type	**Cas9-KO**
Strain background	**C57BL/6JGpt**

Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *Sp7* gene. The schematic diagram is as follows:



Technical routes

- The *Sp7* gene has 3 transcripts. According to the structure of *Sp7* gene, exon2 of *Sp7-201* 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 *Sp7* gene. The brief process is as follows: sgRNA was transcribed in vitro.Cas9 and 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.

Notice

- According to the existing MGI data, mice homozygous for a reporter allele die within minutes of birth displaying cyanosis, respiratory distress, arrested osteoblast differentiation, and failure of endochondral and intramembranous bone formation. Mice homozygous for a knock-out allele exhibit failure of bone ossification.

- The *Sp7* 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 gene transcription and translation processes, all risks cannot be predicted under existing information.

Gene information （NCBI）

集萃药康 GemPharmatech

Sp7 Sp7 transcription factor 7 [*Mus musculus* (house mouse)]

Gene ID: 170574, updated on 15-Apr-2019

Summary

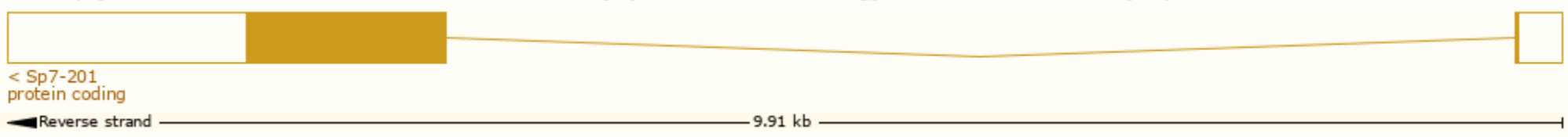
Official Symbol	Sp7 provided by MGI
Official Full Name	Sp7 transcription factor 7 provided by MGI
Primary source	MGI:MGI:2153568
See related	Ensembl:ENSMUSG00000060284
Gene type	protein coding
RefSeq status	VALIDATED
Organism	Mus musculus
Lineage	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Myomorpha; Muroidea; Muridae; Murinae; Mus; Mus
Also known as	C22; Osx; 6430578P22Rik
Expression	Biased expression in limb E14.5 (RPKM 8.9), frontal lobe adult (RPKM 5.1) and 5 other tissues See more
Orthologs	human all

Transcript information（Ensembl）

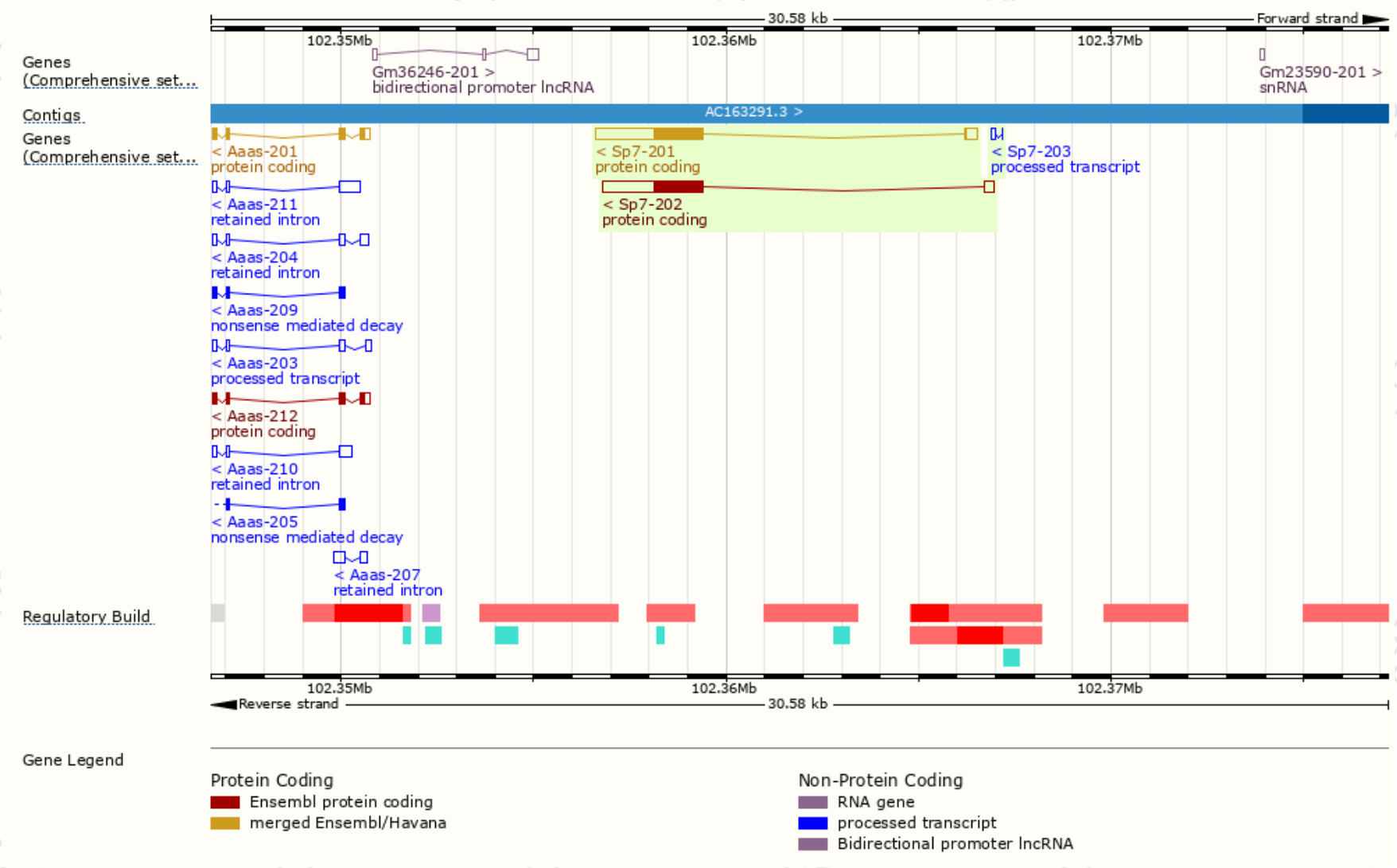
The gene has 3 transcripts, and all transcripts are shown below ：

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Sp7-201	ENSMUST00000078508.6	3097	428aa	Protein coding	CCDS37228	Q2KHK9 Q8VI67	TSL:1 GENCODE basic APPRIS P2
Sp7-202	ENSMUST00000229464.1	2873	410aa	Protein coding	-	Q5RM08	GENCODE basic APPRIS ALT2
Sp7-203	ENSMUST00000231100.1	117	No protein	Processed transcript	-	-	-

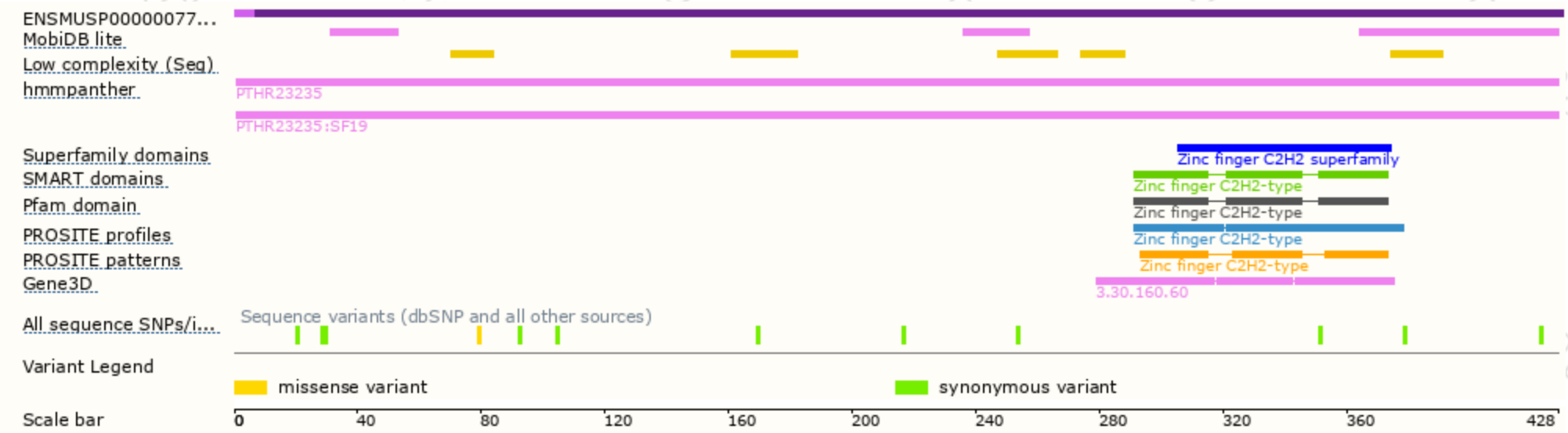
The strategy is based on the design of *Sp7-201* transcript,The transcription is shown below



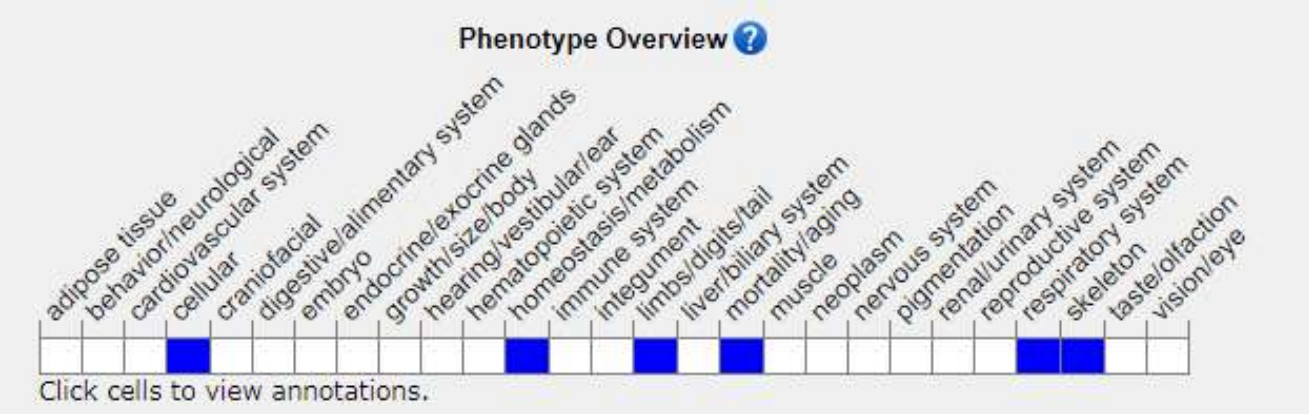
Genomic location distribution



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,Mutations in this locus affect cell-cycle regulation and apoptos is. Null homozygotes show high, early-onset tumor incidence; some have persistent hyaloid vasculature and cataracts. Truncated or temperature-sensitive alleles cause early aging phenotypes.

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

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