Supt20 Cas9-KO Strategy

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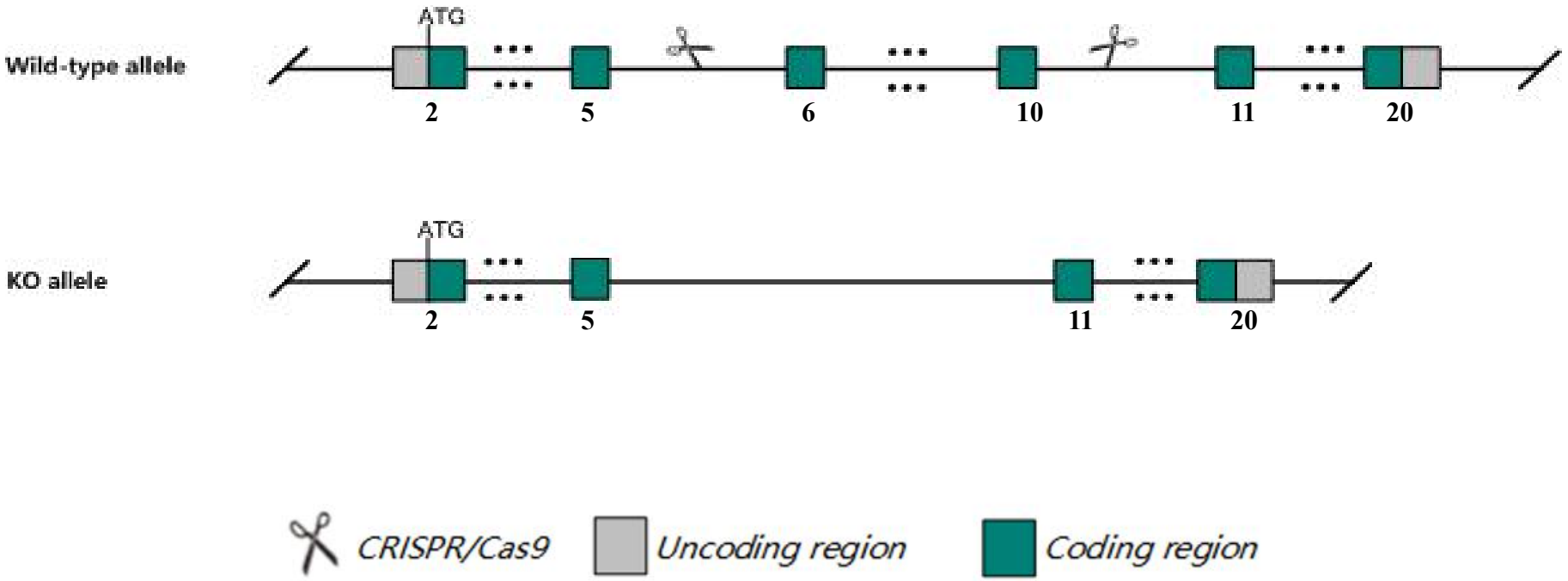
Project Overview

Project Name	***Supt20***
Project type	**Cas9-KO**
Strain background	**C57BL/6JGpt**

Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *Supt20* gene. The schematic diagram is as follows:



Technical routes

The *Supt20* gene has 12 transcripts. According to the structure of *Supt20* gene, exon6-exon10 of *Supt20-202* (ENSMUST00000170552.5) transcript is recommended as the knockout region.The region contains 545bp coding sequence. Knock out the region will result in disruption of protein function.

In this project we use CRISPR/Cas9 technology to modify *Supt20* gene. The brief process is as follows: CRISPR/Cas9 systen

Notice

According to the existing MGI data,The incompletely penetrant homozygous phenotype of a splice-site mutation may include retinal epithelium expansion over the dorsal half of the eye, exencephaly, spina bifida, gastrulation defects and/or aberrant somite and mesoderm development. A few mutants survive postnatally and appear normal.

The *Supt20* gene is located on the Chr3. 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

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Supt20 suppressor of Ty 20 [Mus musculus (house mouse)]

Gene ID: 56790, updated on 31-Jan-2019

Summary

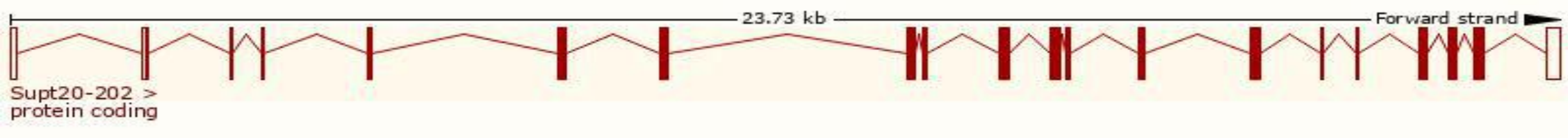
Official Symbol	Supt20 provided by MGI
Official Full Name	suppressor of Ty 20 provided by MGI
Primary source	MGI:MGI:1929651
See related	Ensembl:ENSMUSG00000027751
Gene type	protein coding
RefSeq status	VALIDATED
Organism	Mus musculus
Lineage	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Myomorpha; Muroidea; Muridae; Murinae; Mus; Mus
Also known as	AA667204, AI450544, D3Ertd300e, Fam48a, Supt20h, p38IP
Expression	Ubiquitous expression in testis adult (RPKM 74.7), limb E14.5 (RPKM 29.1) and 27 other tissues See more
Orthologs	human all

Transcript information Ensembl

The gene has 12 transcripts,all transcripts are shown below:

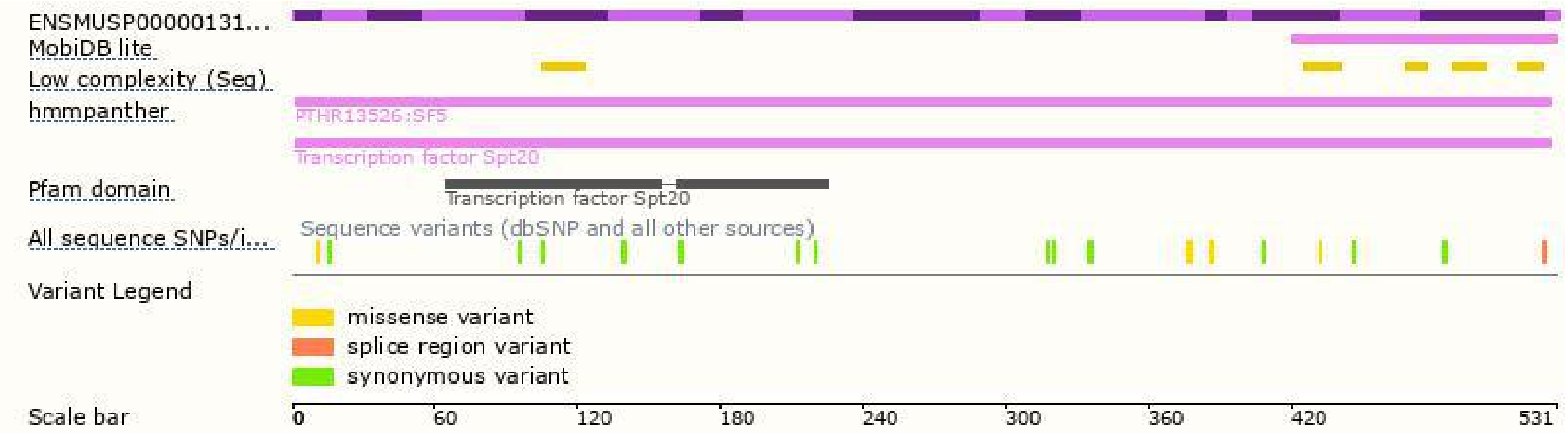
Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Supt20-202	ENSMUST00000170552.5	1968	531aa	Protein coding	CCDS38431	Q7TT00	TSL:1 GENCODE basic APPRIS P2
Supt20-203	ENSMUST00000197502.4	2751	784aa	Protein coding	-	A0A0G2JGY6	TSL:5 GENCODE basic APPRIS ALT2
Supt20-211	ENSMUST00000200441.4	2154	275aa	Protein coding	-	A0A0G2JFM5	TSL:5 GENCODE basic
Supt20-201	ENSMUST00000029315.12	2112	263aa	Protein coding	-	Z4YJG1	TSL:1 GENCODE basic
Supt20-207	ENSMUST00000199655.4	836	141aa	Protein coding	-	A0A0G2JGD1	CDS 3' incomplete TSL:5
Supt20-206	ENSMUST00000199652.4	682	181aa	Protein coding	-	A0A0G2JE63	CDS 3' incomplete TSL:5
Supt20-210	ENSMUST00000200439.1	3753	530aa	Nonsense mediated decay	-	Q7TT00	TSL:1
Supt20-208	ENSMUST00000199674.4	3700	529aa	Nonsense mediated decay	-	A0A0G2JEY3	TSL:5
Supt20-212	ENSMUST00000200450.1	1866	No protein	Retained intron	-	-	TSL:1
Supt20-209	ENSMUST00000200024.4	1341	No protein	Retained intron	-	-	TSL:1
Supt20-205	ENSMUST00000198745.1	660	No protein	Retained intron	-	-	TSL:5
Supt20-204	ENSMUST00000197568.4	364	No protein	Retained intron	-	-	TSL:3

The strategy is based on the design of *Supt20-202* transcript,The transcription is shown below

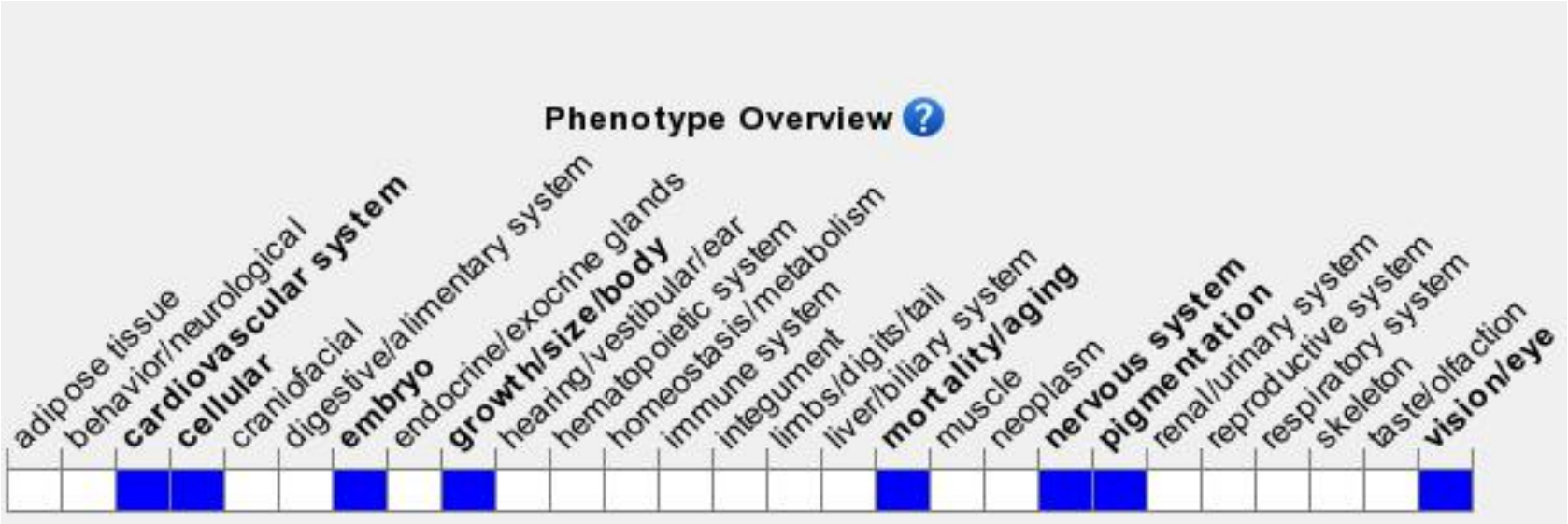


Genomic location distribution

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,The incompletely penetrant homozygous phenotype of a splice-site mutation may include retinal epithelium expansion over the dorsal half of the eye, exencephaly, spina bifida, gastrulation defects and/or aberrant somite and mesoderm development. A few mutants survive postnatally and appear normal.

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