

# *Supt20* Cas9-CKO Strategy

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# Project Overview

**Project Name**

*Supt20*

**Project type**

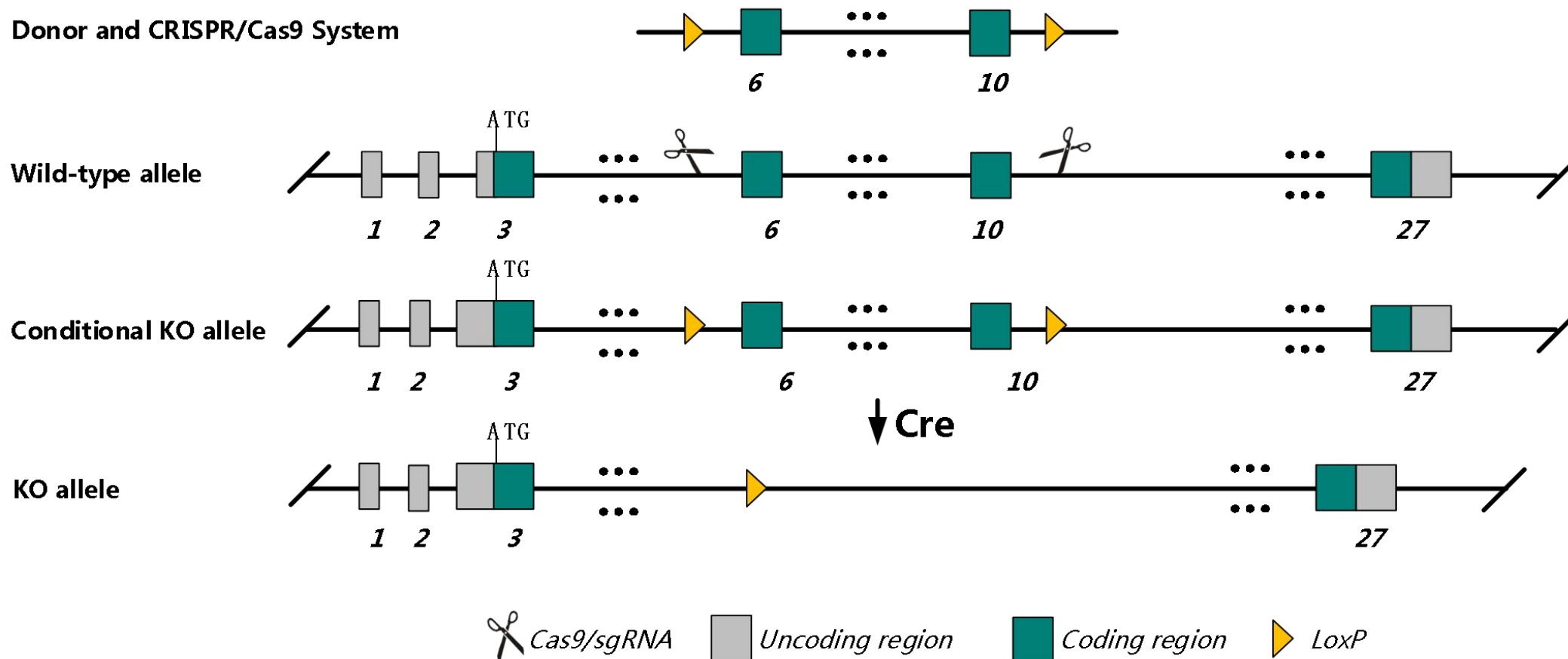
**Cas9-CKO**

**Strain background**

**C57BL/6JGpt**

# Conditional Knockout strategy

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



- The *Supt20* gene has 12 transcripts. According to the structure of *Supt20* gene, exon6-exon10 of *Supt20-203* (ENSMUST00000197502.4) 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 system and Donor 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.
- The flox mice will be knocked out after mating with mice expressing Cre recombinase, resulting in the loss of function of the target gene in specific tissues and cell types.

- 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 loxp insertion on gene transcription, RNA splicing and protein translation cannot be predicted at existing technological level.



# Gene information (NCBI)

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

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

### Summary



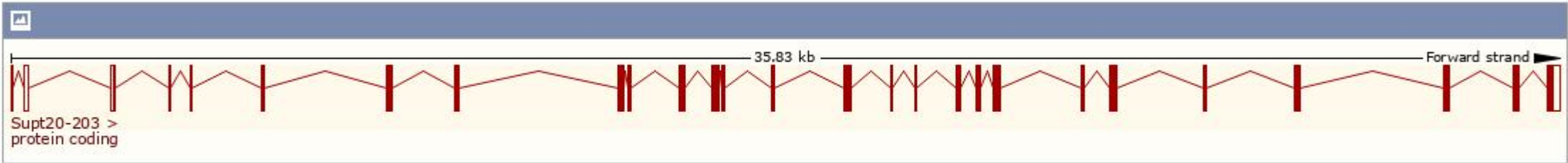
<b>Official Symbol</b>	Supt20 provided by <a href="#">MGI</a>
<b>Official Full Name</b>	suppressor of Ty 20 provided by <a href="#">MGI</a>
<b>Primary source</b>	<a href="#">MGI:MGI:1929651</a>
<b>See related</b>	<a href="#">Ensembl:ENSMUSG00000027751</a>
<b>Gene type</b>	protein coding
<b>RefSeq status</b>	VALIDATED
<b>Organism</b>	<a href="#">Mus musculus</a>
<b>Lineage</b>	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Myomorpha; Muroidea; Muridae; Murinae; Mus; Mus
<b>Also known as</b>	AA667204, AI450544, D3Ert300e, Fam48a, Supt20h, p38IP
<b>Expression</b>	Ubiquitous expression in testis adult (RPKM 74.7), limb E14.5 (RPKM 29.1) and 27 other tissues <a href="#">See more</a>
<b>Orthologs</b>	<a href="#">human</a> <a href="#">all</a>

# Transcript information (Ensembl)

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

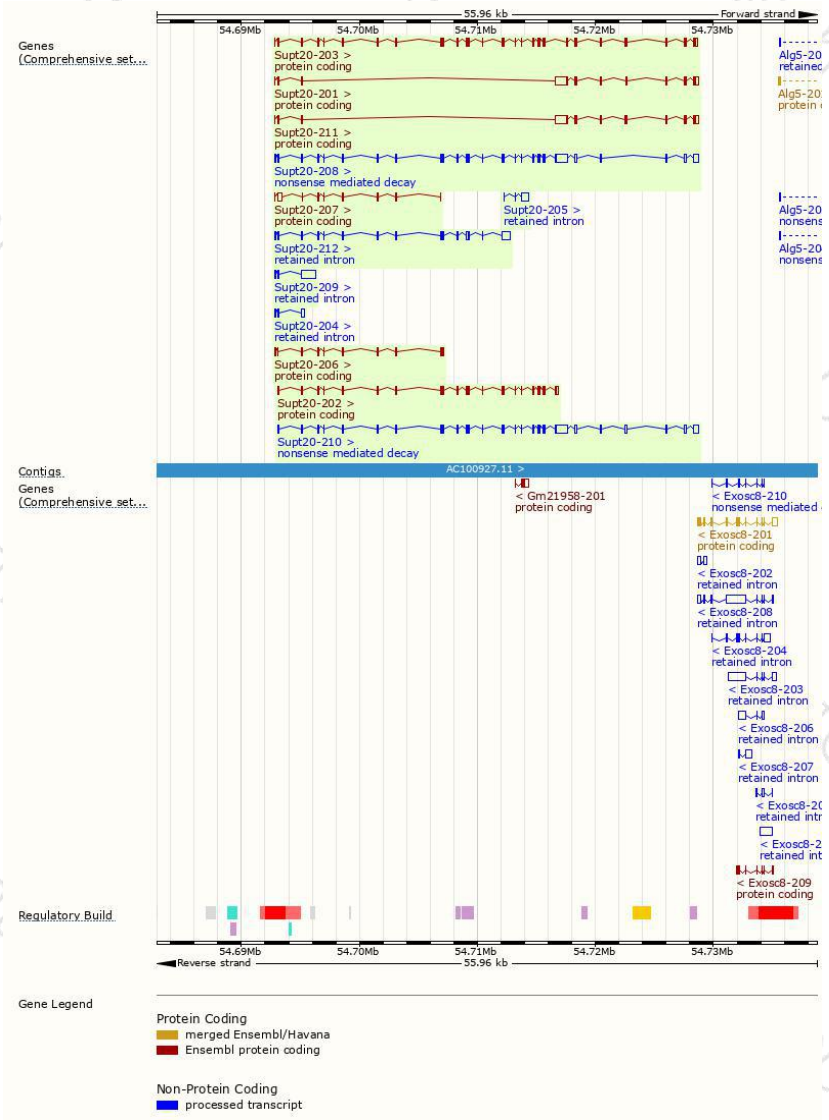
Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Supt20-202	<a href="#">ENSMUST00000170552.5</a>	1968	<a href="#">531aa</a>	Protein coding	<a href="#">CCDS38431</a>	<a href="#">Q7TT00</a>	TSL:1 GENCODE basic APPRIS P2
Supt20-203	<a href="#">ENSMUST00000197502.4</a>	2751	<a href="#">784aa</a>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

The strategy is based on the design of *Supt20-203* transcript,The transcription is shown below



Statistics Exons: 27, Coding exons: 25, Transcript length: 2,751 bps, Translation length: 784 residues

# Genomic location distribution

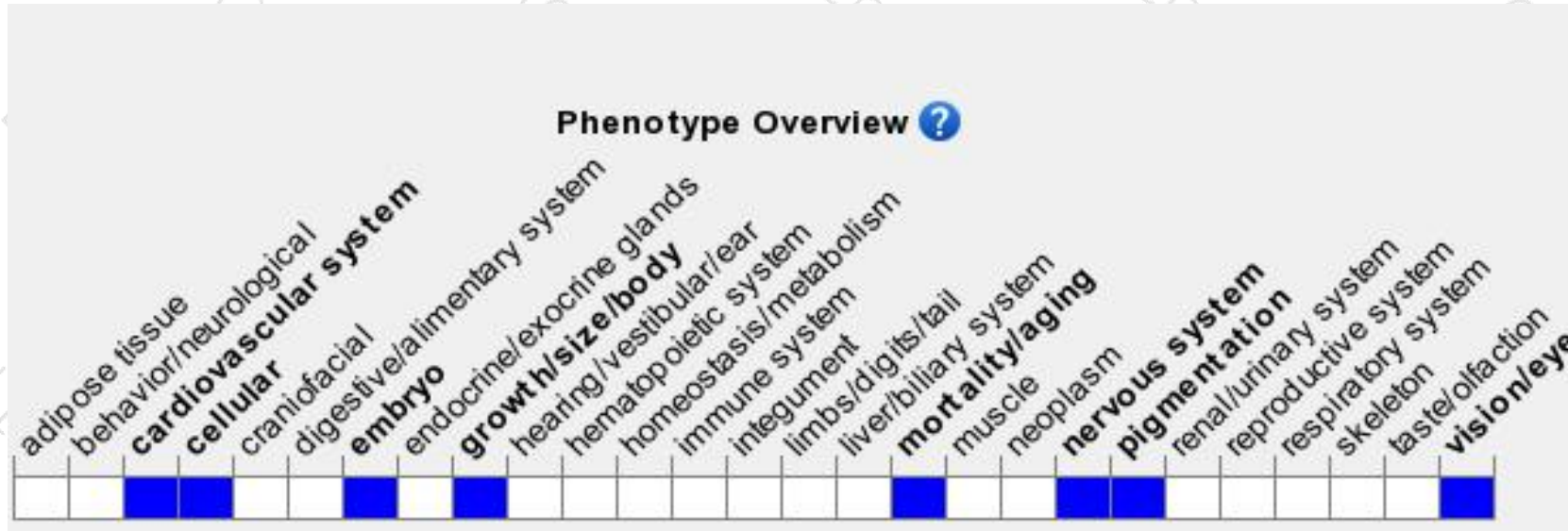




# Protein domain



# 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.

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

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