Supt7l Cas9-KO Strategy

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Project Overview

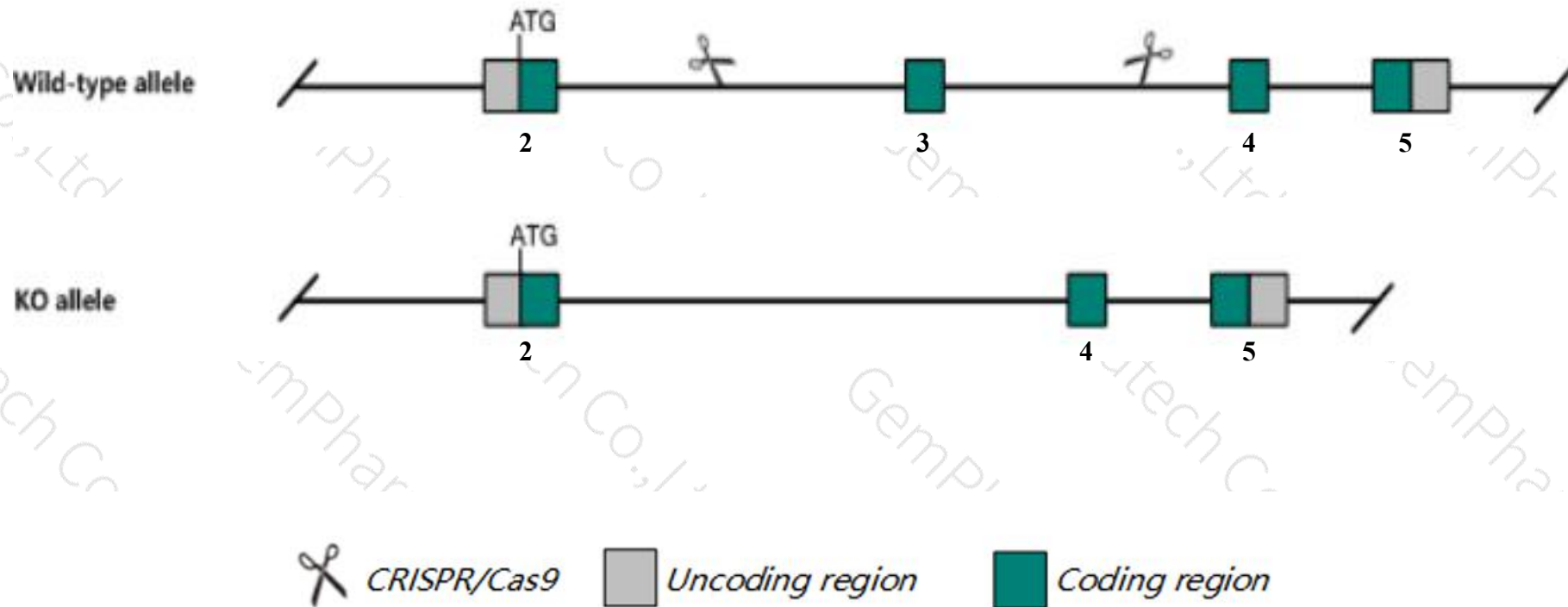|	
Project Name	*Supt7l*
Project type	**Cas9-KO**
Strain background	**C57BL/6JGpt**

Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *Supt7l* gene. The schematic diagram is as follows:

Technical routes

➤ The *Supt7l* gene has 6 transcripts. According to the structure of *Supt7l* gene, exon3 of *Supt7l-201*(ENSMUST00000065388.10) transcript is recommended as the knockout region.The region contains 325bp coding sequence. Knock out the region will result in disruption of protein function.

➤ In this project we use CRISPR/Cas9 technology to modify *Supt7l* gene. The brief process is as follows: CRISPR/Cas9 system 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

➢ The *Supt7l* gene is located on the Chr5. 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.

➢ The knockout region is near to the N-terminal of *Slc4a1ap* gene. this strategy may influence the regulatory function of the N-terminal of *Slc4a1ap* gene.

➢ Transcript *Supt7l*-203&206 may not be affected.

➢ 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）

Supt7l SPT7-like, STAGA complex gamma subunit [Mus musculus (house mouse)]
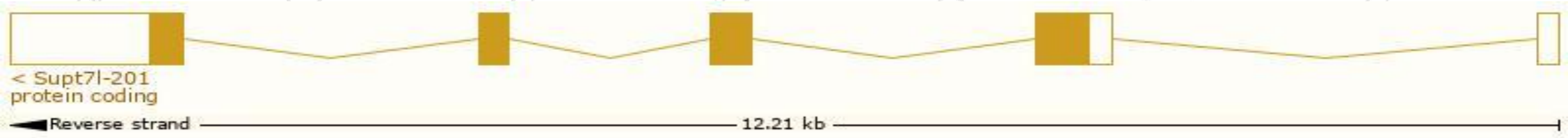
Gene ID: 72195, updated on 13-Mar-2020

▲Summary

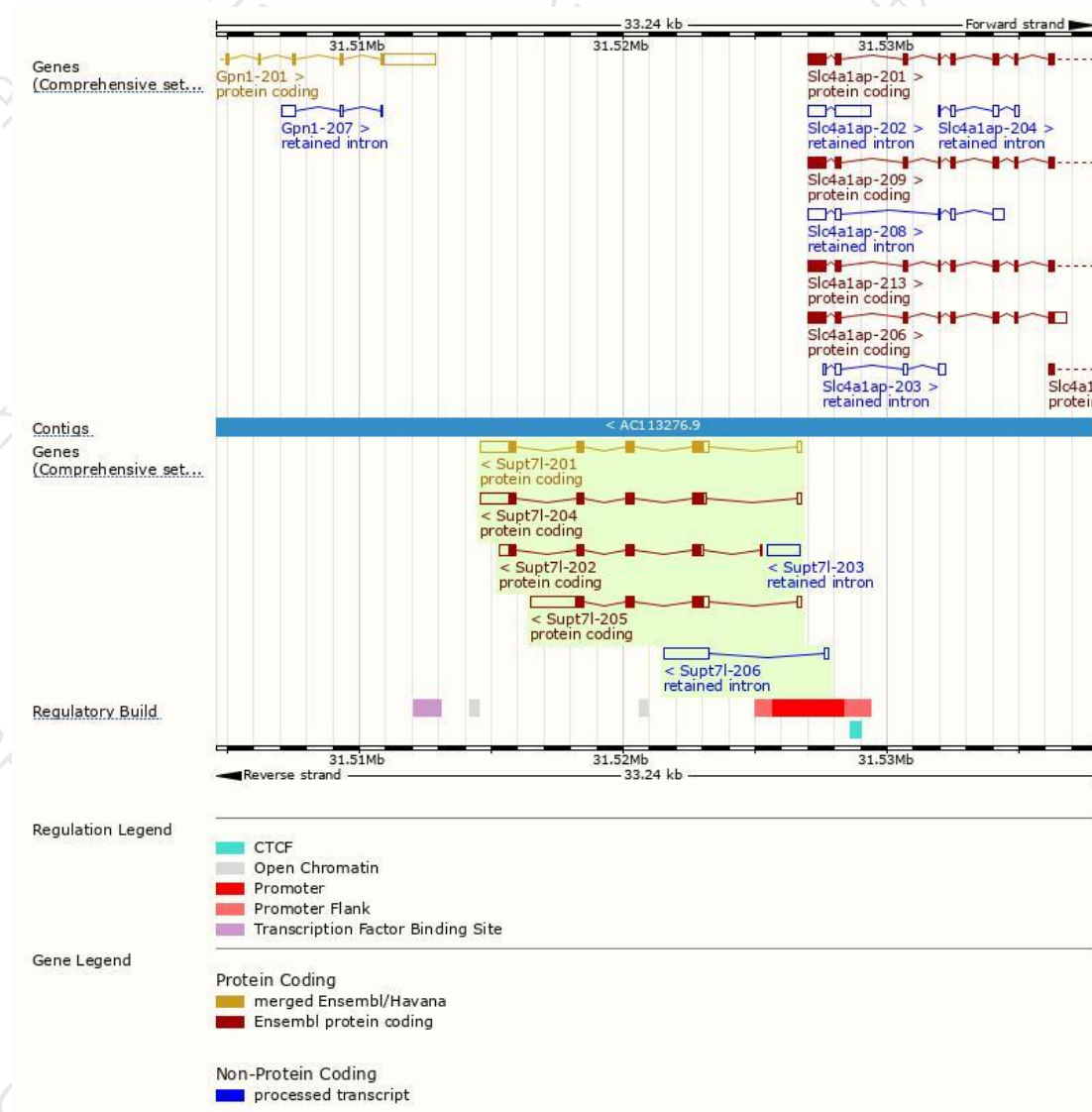|	
Official Symbol	Supt7l provided by MGI
Official Full Name	SPT7-like, STAGA complex gamma subunit provided by MGI
Primary source	MGI:MGI:1919445
See related	Ensembl:ENSMUSG00000053134
Gene type	protein coding
RefSeq status	VALIDATED
Organism	Mus musculus
Lineage	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Myomorpha; Muroidea; Muridae; Murinae; Mus; Mus
Also known as	2610524B01Rik, 6030455L14Rik
Expression	Ubiquitous expression in subcutaneous fat pad adult (RPKM 6.3), kidney adult (RPKM 6.1) and 28 other tissuesSee more
Orthologs	human all

Transcript information（Ensembl）

The gene has 6 transcripts,all transcripts are shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Supt7l-201	ENSMUST00000065388.10	2693	412aa	Protein coding	CCDS19186	Q9CZV5	TSL:1 GENCODE basic APPRIS P1
Supt7l-204	ENSMUST00000201769.3	2548	412aa	Protein coding	CCDS19186	Q9CZV5	TSL:1 GENCODE basic APPRIS P1
Supt7l-205	ENSMUST00000202421.1	3056	344aa	Protein coding	-	E9PX66	TSL:1 GENCODE basic
Supt7l-202	ENSMUST00000200721.3	1657	363aa	Protein coding	-	D3Z6Y8	TSL:5 GENCODE basic
Supt7l-206	ENSMUST00000202932.1	1899	No protein	Retained intron	-	-	TSL:1
Supt7l-203	ENSMUST00000201692.1	1246	No protein	Retained intron	-	-	TSL:NA

The strategy is based on the design of *Supt7l-201* transcript,the transcription is shown below:
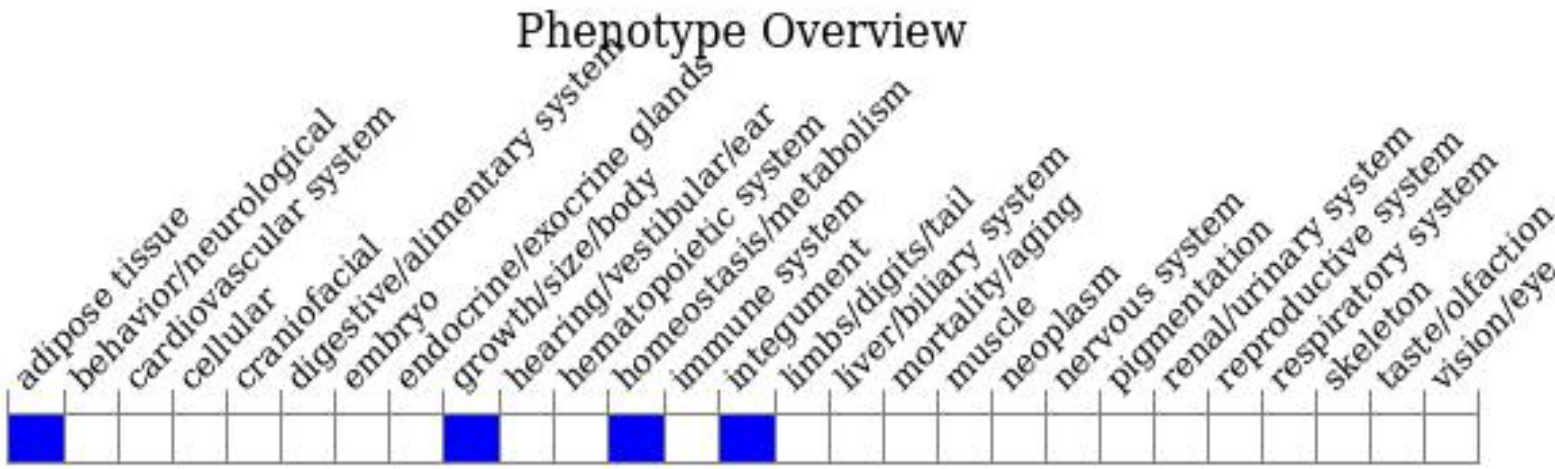

< Supt7l-201
protein coding

◀ Reverse strand

12.21 kb

Genomic location distribution

Protein domain

ENSMUSP00000144...											
MobiDB lite											
Low complexity (Seg)											
SMART					Bromodomain associated domain						
Pfam					Bromodomain associated domain						
PANTHER	STAGA complex 65 subunit gamma										
Gene3D					Histone-fold						
All sequence SNPs/i...	Sequence variants (dbSNP and all other sources)										

Variant Legend

■ missense variant
■ synonymous variant

Scale bar: 0 40 80 120 160 200 240 280 320 360 412
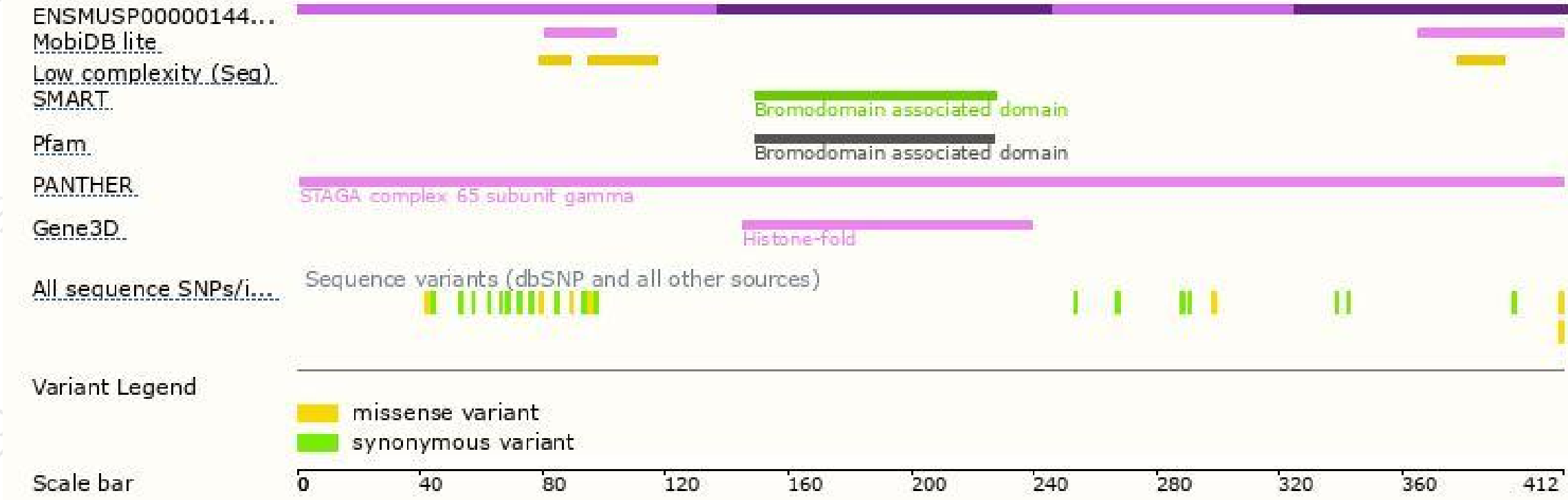
Mouse phenotype description(MGI)

Phenotypes affected by the gene are marked in blue.Data quoted from MGI database(http://www.informatics.jax.org/).

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