Septin3 Cas9-KO Strategy

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Project Overview

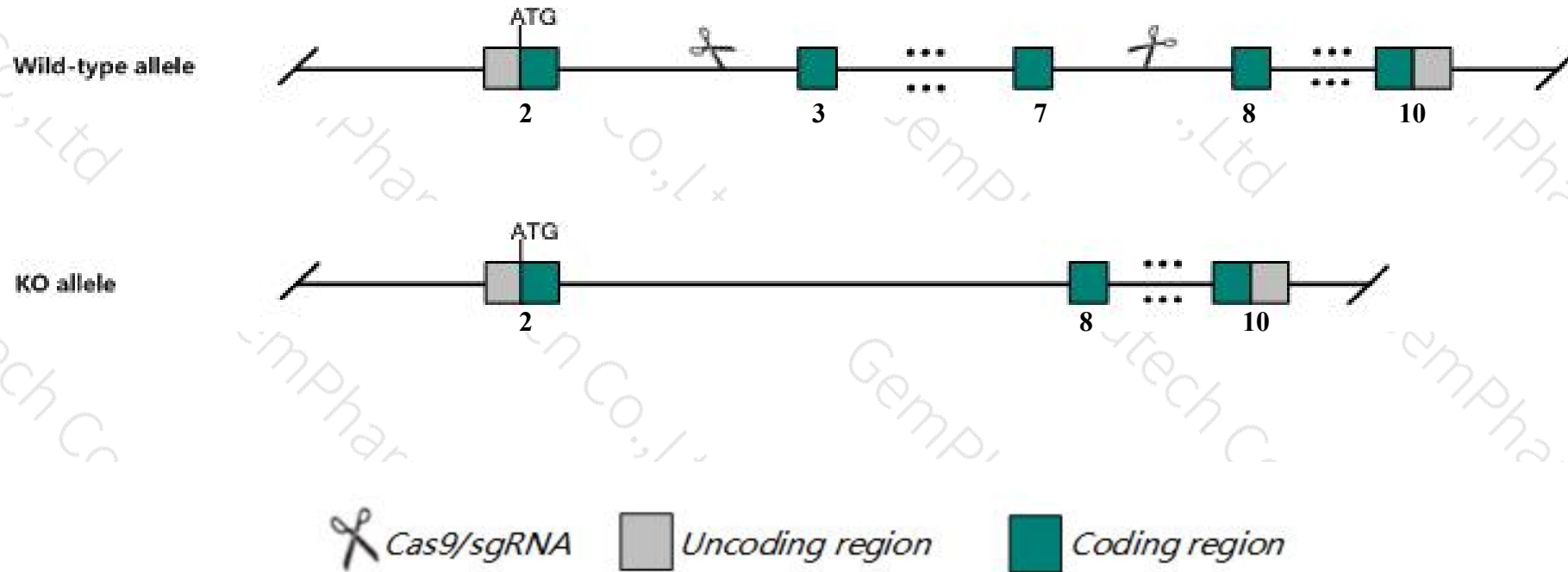|	
Project Name	*Septin3*
Project type	**Cas9-KO**
Strain background	**C57BL/6JGpt**

Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *Septin3* gene. The schematic diagram is as follows:

Technical routes

➢ The *Septin3* gene has 8 transcripts. According to the structure of *Septin3* gene, exon3-exon7 of *Septin3-201* (ENSMUST00000023095.13) transcript is recommended as the knockout region.The region contains 563bp coding sequence. Knock out the region will result in disruption of protein function.

➢ In this project we use CRISPR/Cas9 technology to modify *Septin3* 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 null allele exhibit a normal phenotype.

➤ The effect on transcript *Septin3*-205&206 is unknown.

➤ The N-terminal of *Septin3* gene will remain some amino acids,it may remain the partial function of *Septin3* gene.

➤ The *Septin3* 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 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）

Septin3   septin 3 [*Mus musculus* (house mouse)]

Gene ID: 24050, updated on 12-Nov-2019

▲ Summary

Official Symbol	Septin3 provided by MGI
Official Full Name	septin 3 provided by MGI
Primary source	MGI:MGI:1345148
See related	Ensembl:ENSMUSG00000022456
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	Sep3; Sept3; Gm46500; AV154067; 3110018K01Rik; B530002E20Rik
Expression	Biased expression in CNS E14 (RPKM 82.2), whole brain E14.5 (RPKM 81.1) and 6 other tissues See more
Orthologs	human all

▲ Genomic context

Location: 15; 15 E1

See Septin3 in Genome Data Viewer

Exon count: 15

Annotation release	Status	Assembly	Chr	Location
108	current	GRCm38.p6 (GCF_000001635.26)	15	NC_000081.6 (82268802..82294574)
Build 37.2	previous assembly	MGSCv37 (GCF_000001635.18)	15	NC_000081.5 (82105365..82124872)

Transcript information（Ensembl）

The gene has 8 transcripts,all transcripts are shown below:

| Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Septin3-201	ENSMUST00000023095.13	4992	337aa	Protein coding	CCDS37157	Q9Z1S5	TSL:1 GENCODE basic APPRIS P2
Septin3-202	ENSMUST00000116423.2	2397	337aa	Protein coding	CCDS37157	Q9Z1S5	TSL:1 GENCODE basic APPRIS P2
Septin3-209	ENSMUST00000239048.1	6443	818aa	Protein coding	-	A0A5F8MPL6	GENCODE basic APPRIS ALT2
Septin3-208	ENSMUST00000238416.2	6022	822aa	Protein coding	-	A0A571BE69	GENCODE basic APPRIS ALT2
Septin3-204	ENSMUST00000230365.1	1888	341aa	Protein coding	-	A0A2R8W6V9	GENCODE basic APPRIS ALT2
Septin3-206	ENSMUST00000230507.1	865	201aa	Protein coding	-	A0A2R8VHR7	CDS 5' incomplete
Septin3-205	ENSMUST00000230418.1	440	75aa	Protein coding	-	A0A2R8VHB2	CDS 3' incomplete
Septin3-207	ENSMUST00000230799.1	2130	No protein	Retained intron	-	-	-
Septin3-203	ENSMUST00000229067.1	1882	No protein	Retained intron	-	-	-

The strategy is based on the design of *Septin3-201* transcript,The transcription is shown below
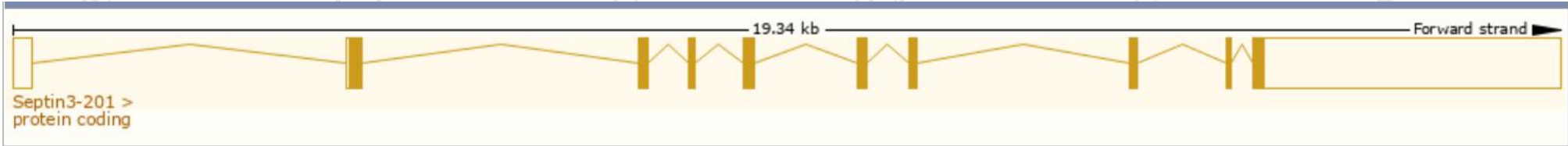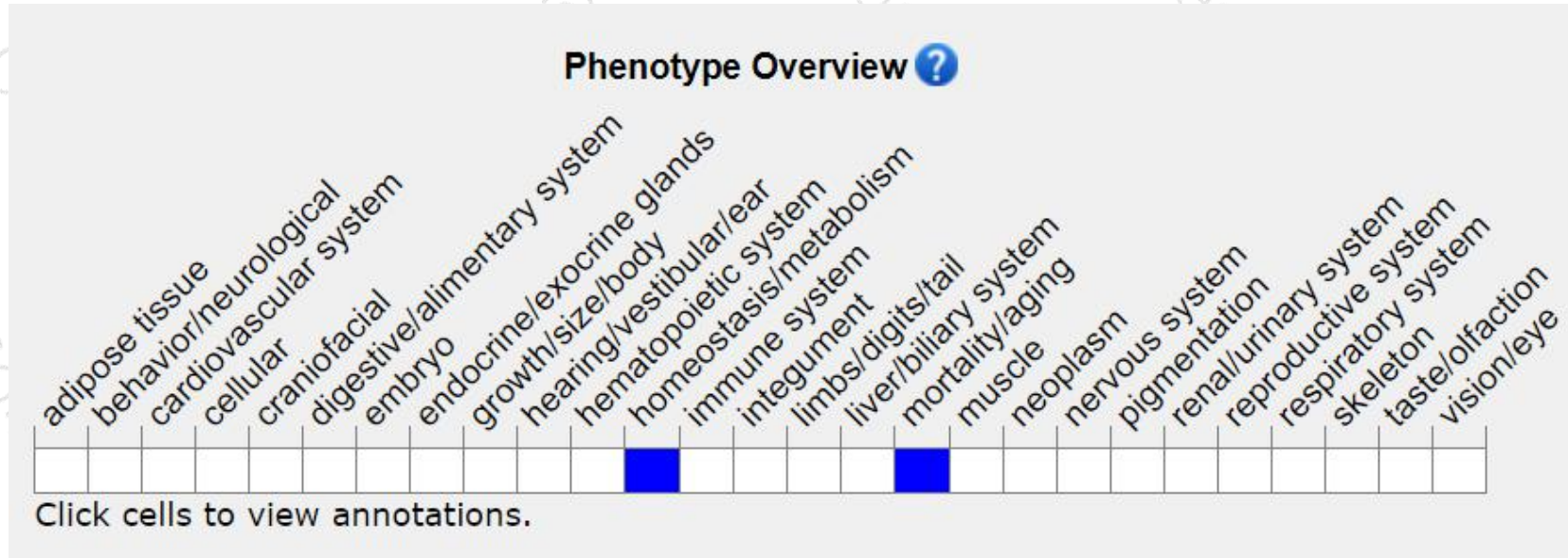
Genomic location distribution

Protein domain
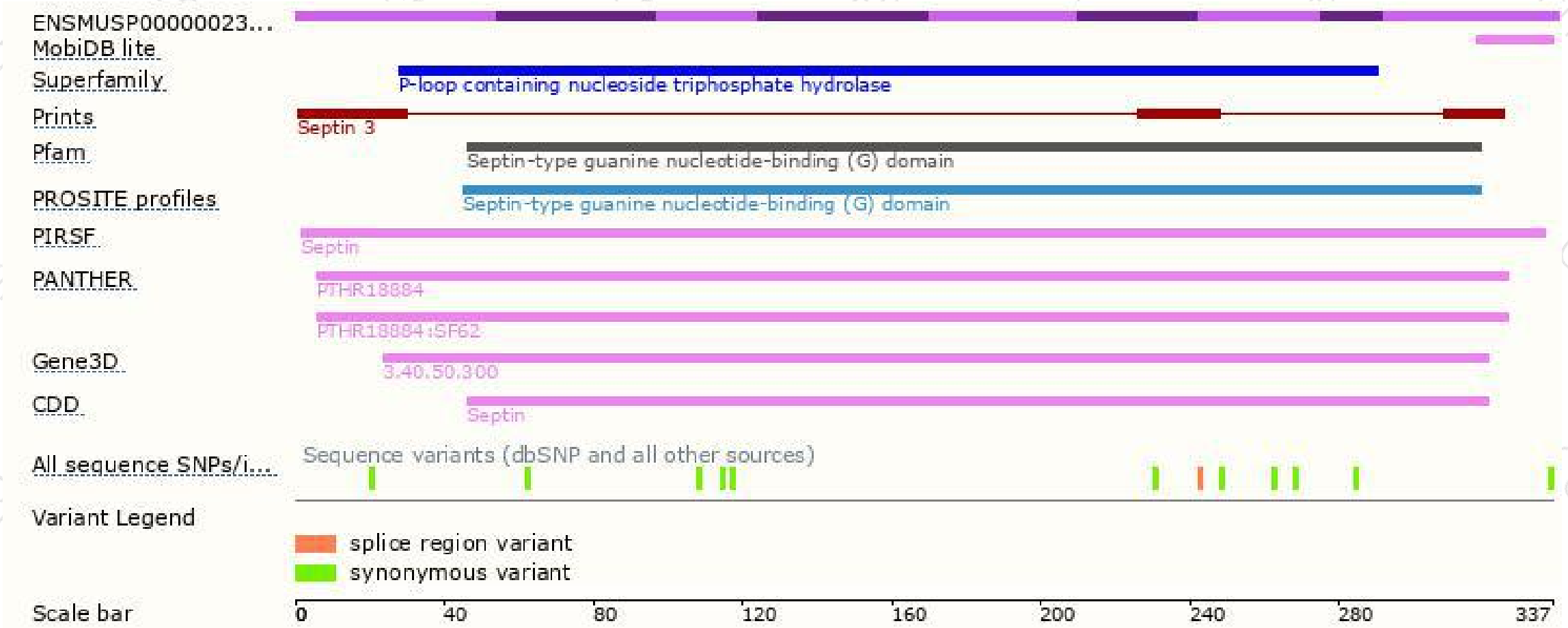
Mouse phenotype description(MGI)

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,Mice homozygous for a null allele exhibit a normal phenotype.

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