

Sympk Cas9-KO Strategy

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Project Overview

Project Name

Sympk

Project type

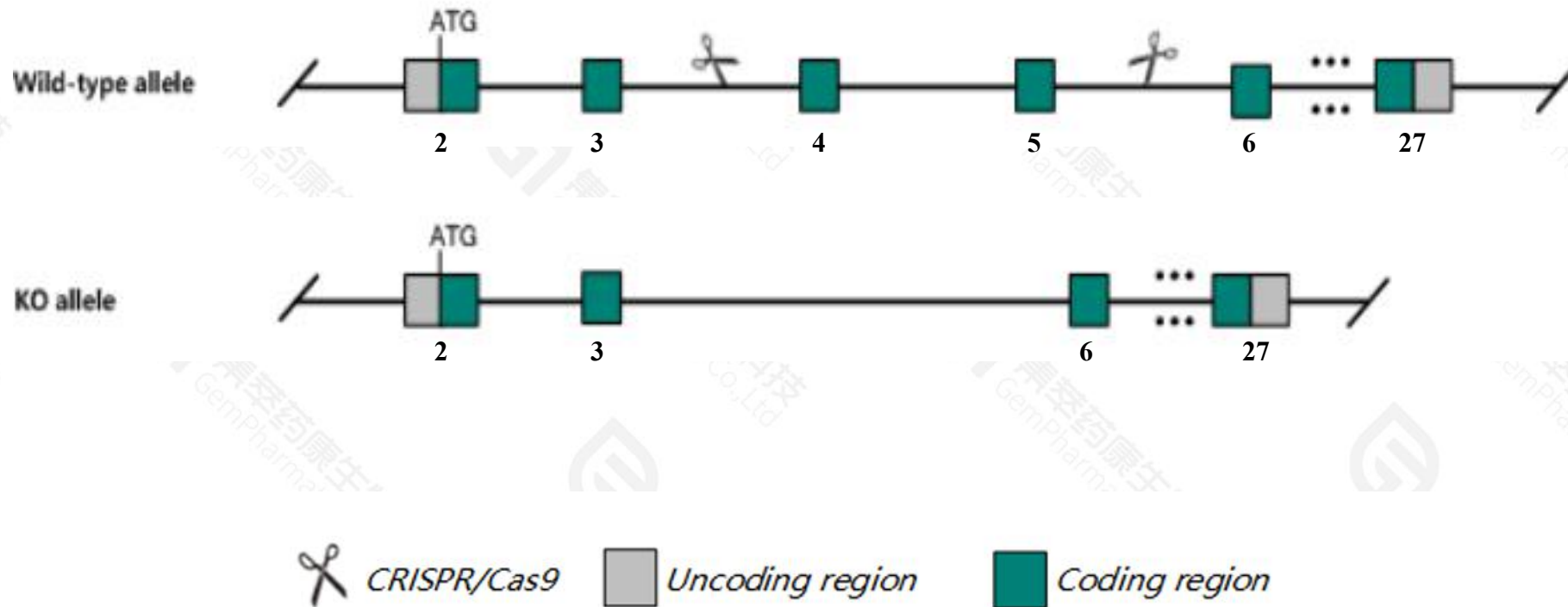
Cas9-KO

Strain background

C57BL/6JGpt

Knockout strategy

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



- The *Sympk* gene has 8 transcripts. According to the structure of *Sympk* gene, exon4-exon5 of *Sympk*-201(ENSMUST00000023882.14) transcript is recommended as the knockout region. The region contains 128bp coding sequence. Knock out the region will result in disruption of protein function.
- In this project we use CRISPR/Cas9 technology to modify *Sympk* 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.

- Transcript *Sympk-202* may not be affected.
- According to the existing MGI data, mice homozygous for a transgenic gene disruption exhibit anemia at E15 and hydrops fetalis.
- The *Sympk* gene is located on the Chr7. 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.

Sympk symplekin [Mus musculus (house mouse)]

Gene ID: 68188, updated on 29-Jan-2021

Summary



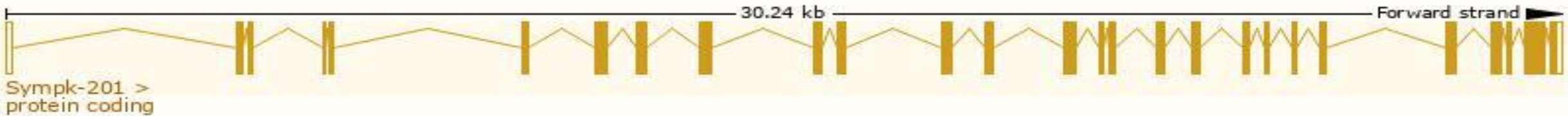
Official Symbol	Sympk provided by MGI
Official Full Name	symplekin provided by MGI
Primary source	MGI:MGI:1915438
See related	Ensembl:ENSMUSG00000023118
Gene type	protein coding
RefSeq status	VALIDATED
Organism	Mus musculus
Lineage	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Myomorpha; Muroidea; Muridae; Murinae; Mus; Mus
Also known as	1500016F02Rik, 4632415H16Rik, AA125406, AI449890, SPK, SYM
Expression	Ubiquitous expression in testis adult (RPKM 36.3), ovary adult (RPKM 34.7) and 28 other tissues See more
Orthologs	human all

Transcript information (Ensembl)

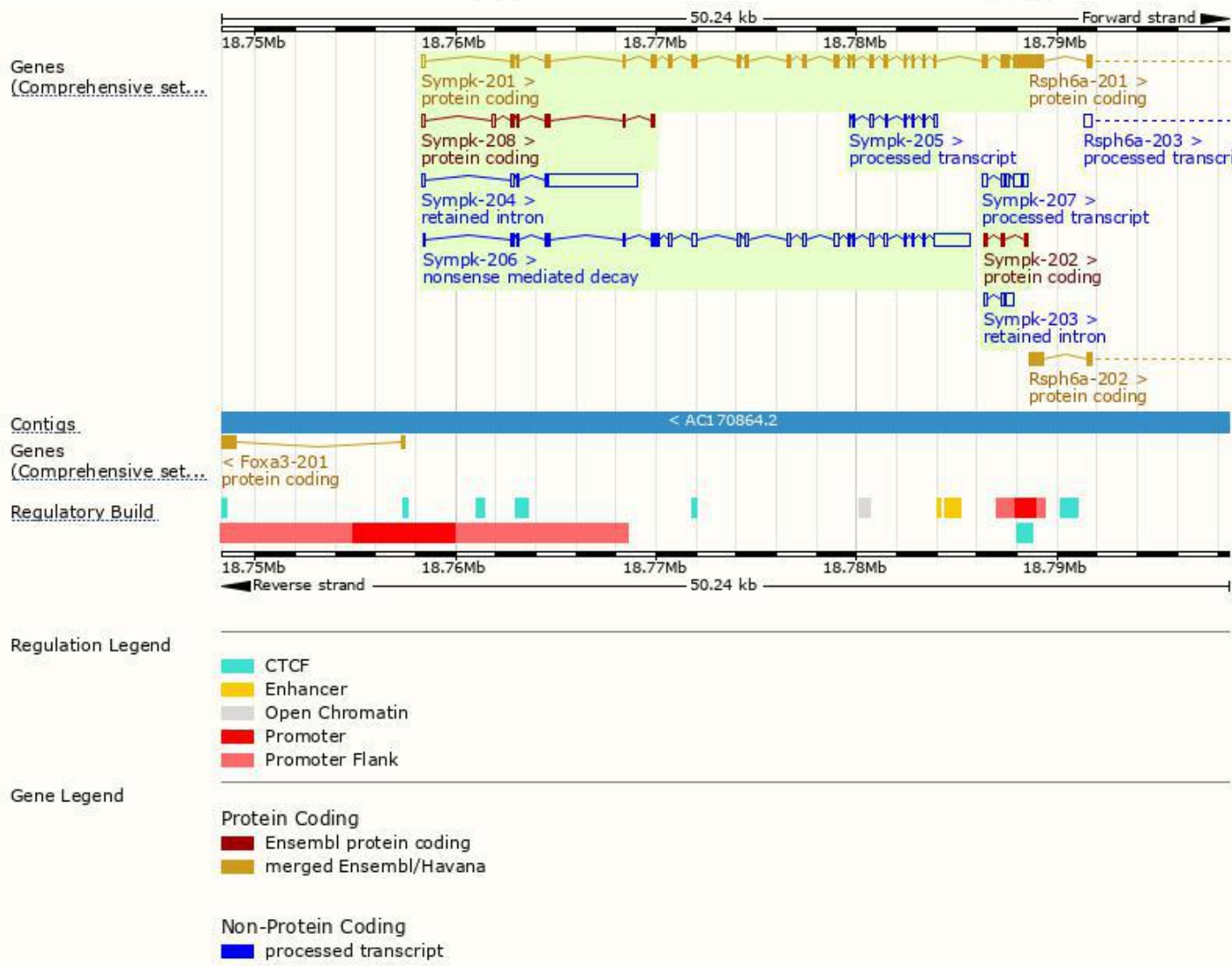
The gene has 8 transcripts,all transcripts are shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Sympk-201	ENSMUST00000023882.14	4116	1288aa	Protein coding	CCDS52051		TSL:1 , GENCODE basic , APPRIS P1 ,
Sympk-208	ENSMUST00000153976.8	827	198aa	Protein coding	-		CDS 3' incomplete , TSL:5 ,
Sympk-202	ENSMUST00000130328.2	469	143aa	Protein coding	-		CDS 5' incomplete , TSL:3 ,
Sympk-206	ENSMUST00000146903.8	4781	234aa	Nonsense mediated decay	-		TSL:1 ,
Sympk-207	ENSMUST00000148861.8	1099	No protein	Processed transcript	-		TSL:1 ,
Sympk-205	ENSMUST00000138440.2	799	No protein	Processed transcript	-		TSL:3 ,
Sympk-204	ENSMUST00000137287.3	4760	No protein	Retained intron	-		TSL:1 ,
Sympk-203	ENSMUST00000131230.2	636	No protein	Retained intron	-		TSL:2 ,

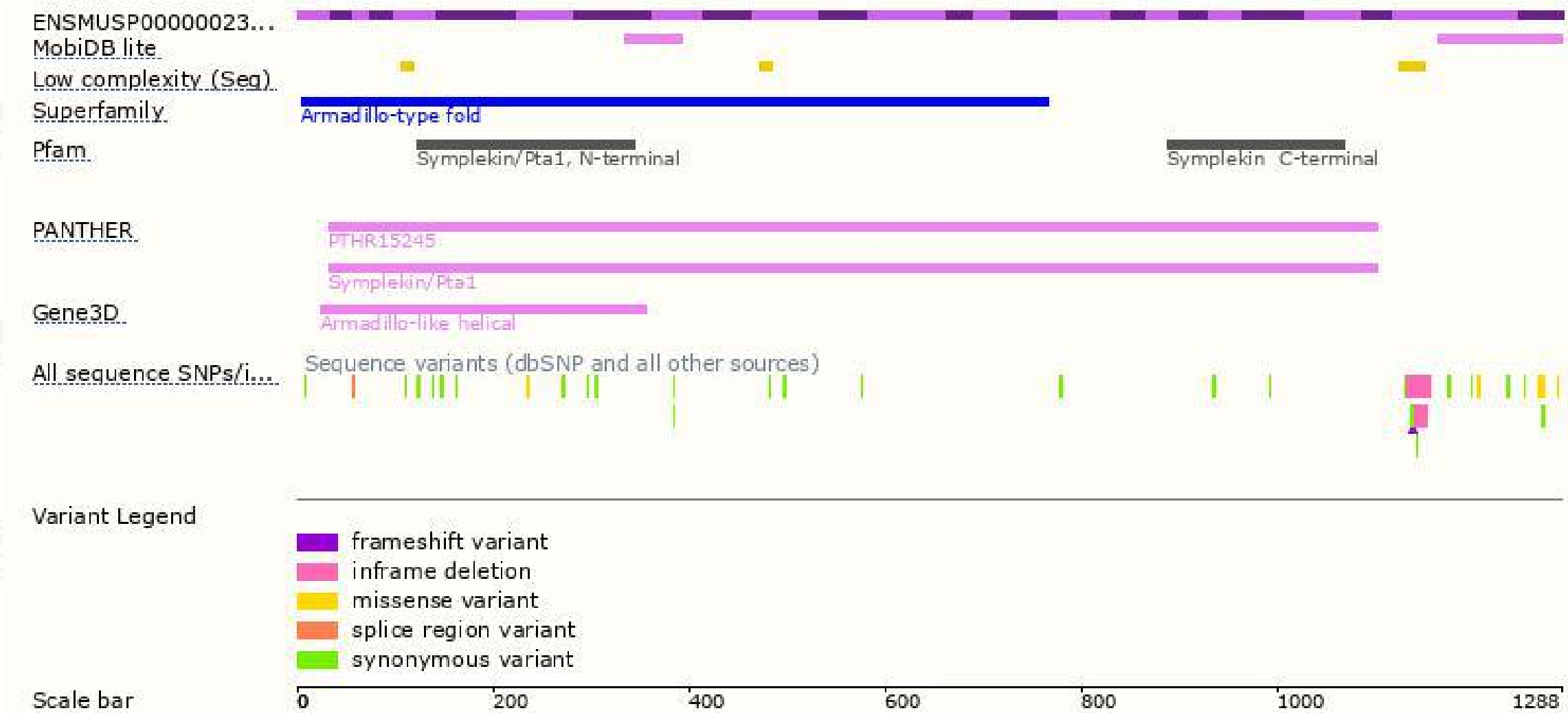
The strategy is based on the design of *Sympk-201* transcript,the transcription is shown below:



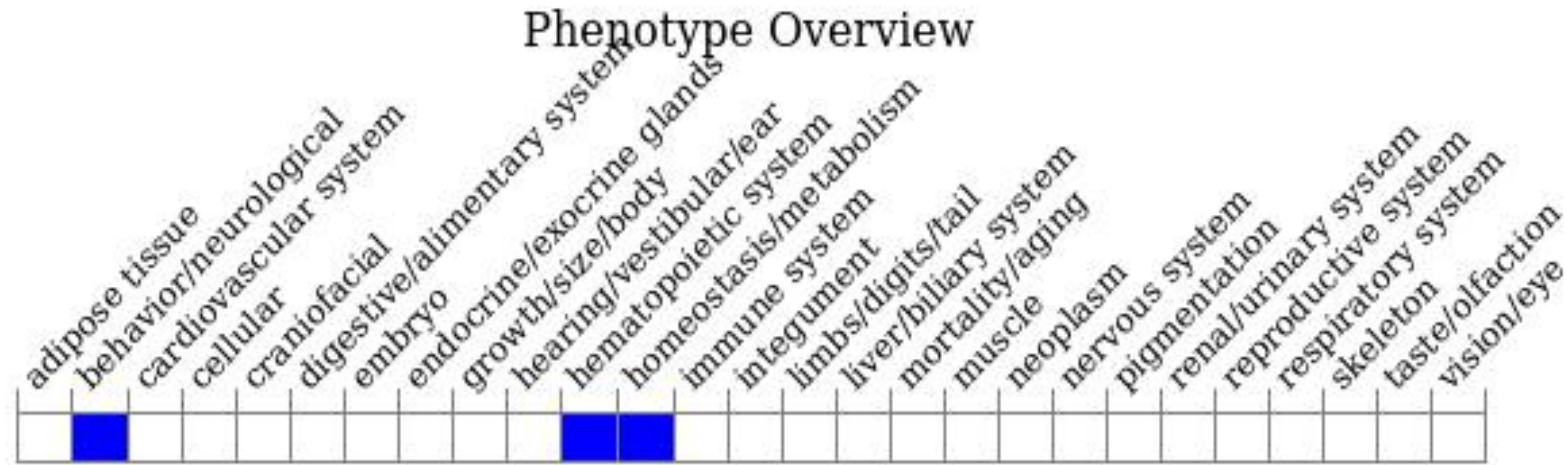
Genomic location distribution



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/>).

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