Srgn Cas9-CKO Strategy

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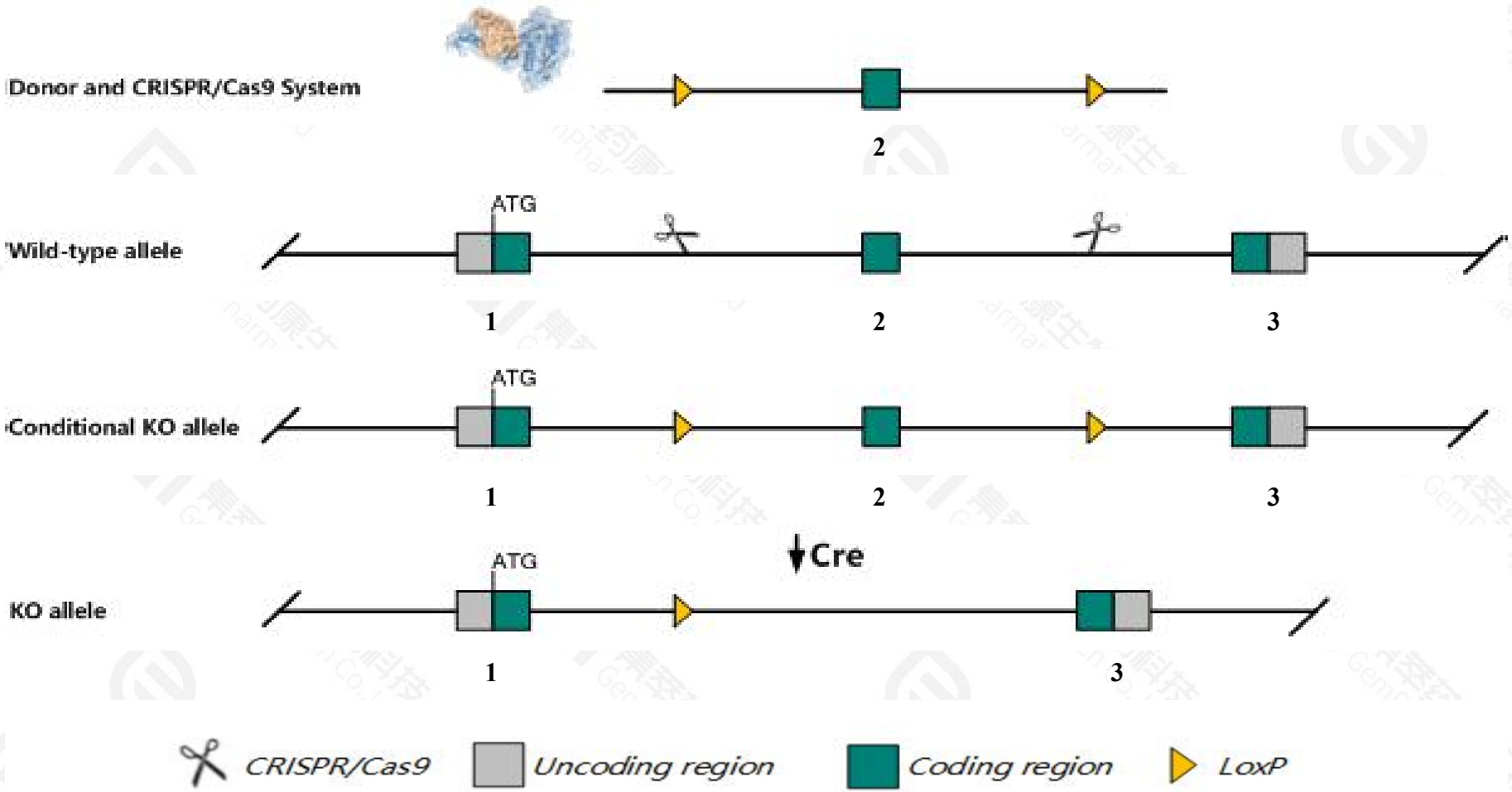
Project Overview

Project Name	***Srgn***
Project type	**Cas9-CKO**
Strain background	**C57BL/6JGpt**

Conditional Knockout strategy

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



Technical routes

➢ The *Srgn* gene has 6 transcripts. According to the structure of *Srgn* gene, exon2 of *Srgn-201*(ENSMUST00000020271.13) transcript is recommended as the knockout region.The region contains 145bp coding sequence. Knock out the region will result in disruption of protein function.

➢ In this project we use CRISPR/Cas9 technology to modify *Srgn* 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.

Notice

➢ According to the existing MGI data,mice homozygous for disruptions in this gene lack peritoneal mast cells.

➢ The *Srgn* gene is located on the Chr10. 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）

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Srgn serglycin [Mus musculus (house mouse)]

Gene ID: 19073, updated on 13-Mar-2020

Summary

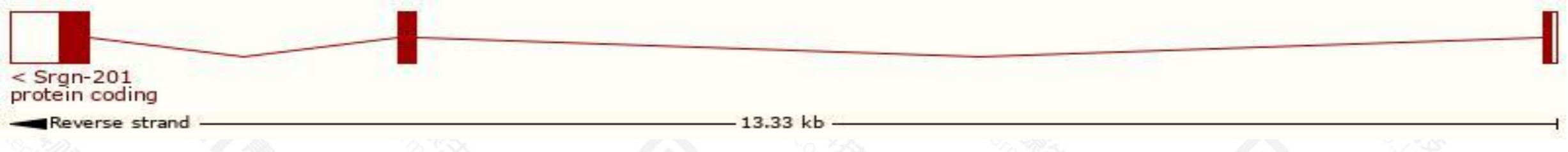
Official Symbol	Srgn provided by MGI
Official Full Name	serglycin provided byMGI
Primary source	MGI:MGI:97756
See related	Ensembl:ENSMUSG00000020077
Gene type	protein coding
RefSeq status	VALIDATED
Organism	Mus musculus
Lineage	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Myomorpha; Muroidea; Muridae; Murinae; Mus; Mus
Also known as	Prg, Prg1, Sgc
Expression	Broad expression in placenta adult (RPKM 7.7), spleen adult (RPKM 6.2) and 24 other tissuesSee more
Orthologs	human all

Transcript information（Ensembl）

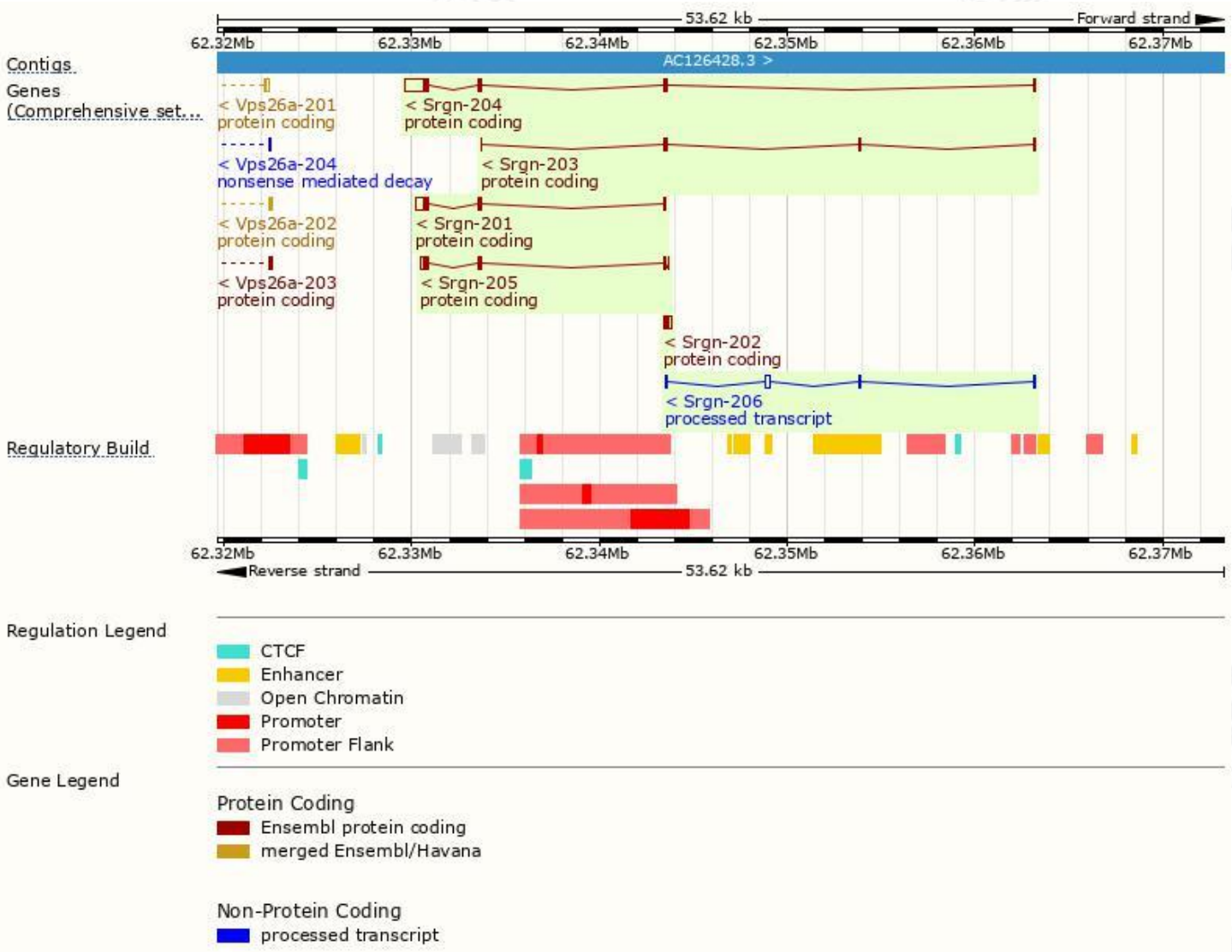
The gene has 6 transcripts,all transcripts are shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Srgn-204	ENSMUST00000160987.7	1727	152aa	Protein coding	CCDS23889	P13609	TSL:3 GENCODE basic APPRIS is a system to annotate alternatively spliced transcripts based on a range of computational methods to identify the most functionally important transcript(s) of a gene. APPRIS P1
Srgn-201	ENSMUST00000020271.12	938	152aa	Protein coding	CCDS23889	P13609	TSL:1 GENCODE basic APPRIS is a system to annotate alternatively spliced transcripts based on a range of computational methods to identify the most functionally important transcript(s) of a gene. APPRIS P1
Srgn-205	ENSMUST00000162161.1	694	152aa	Protein coding	CCDS23889	P13609	TSL:3 GENCODE basic APPRIS is a system to annotate alternatively spliced transcripts based on a range of computational methods to identify the most functionally important transcript(s) of a gene. APPRIS P1
Srgn-203	ENSMUST00000160643.7	384	27aa	Protein coding	-	E0CYA5	CDS 3' incomplete TSL:5
Srgn-202	ENSMUST00000159020.1	346	13aa	Protein coding	-	E0CZH1	CDS 3' incomplete TSL:3
Srgn-206	ENSMUST00000162956.1	466	No protein	Processed transcript	-	-	TSL:3

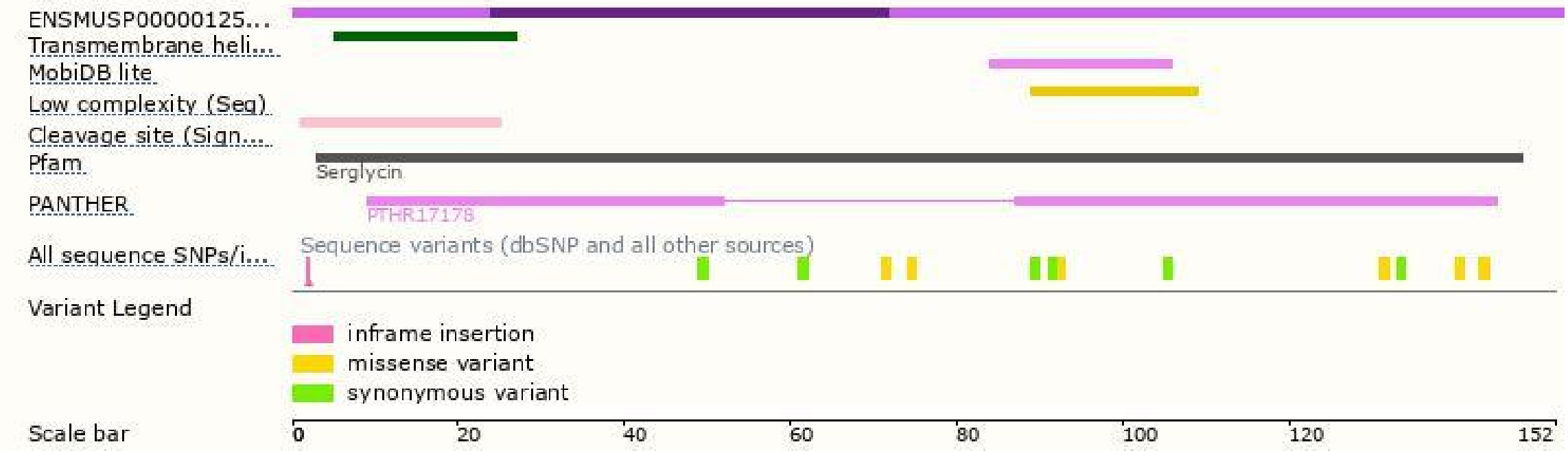
The strategy is based on the design of *Srgn-201* transcript,the transcription is shown below:



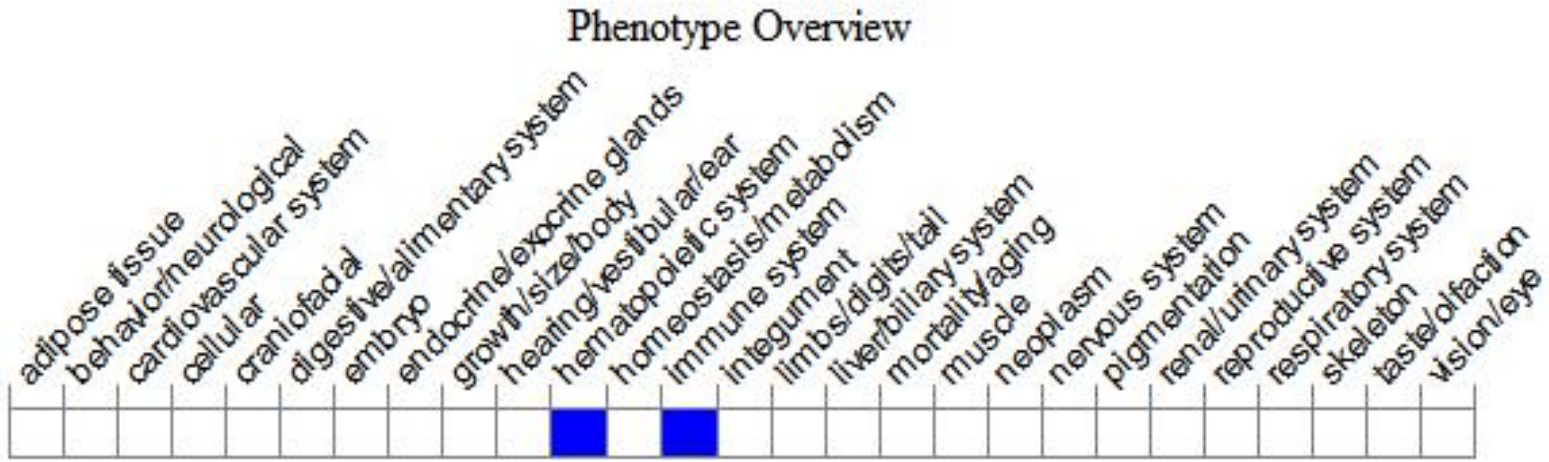
Genomic location distribution



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 disruptions in this gene lack peritoneal mast cells.

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