Synpo2 Cas9-CKO Strategy

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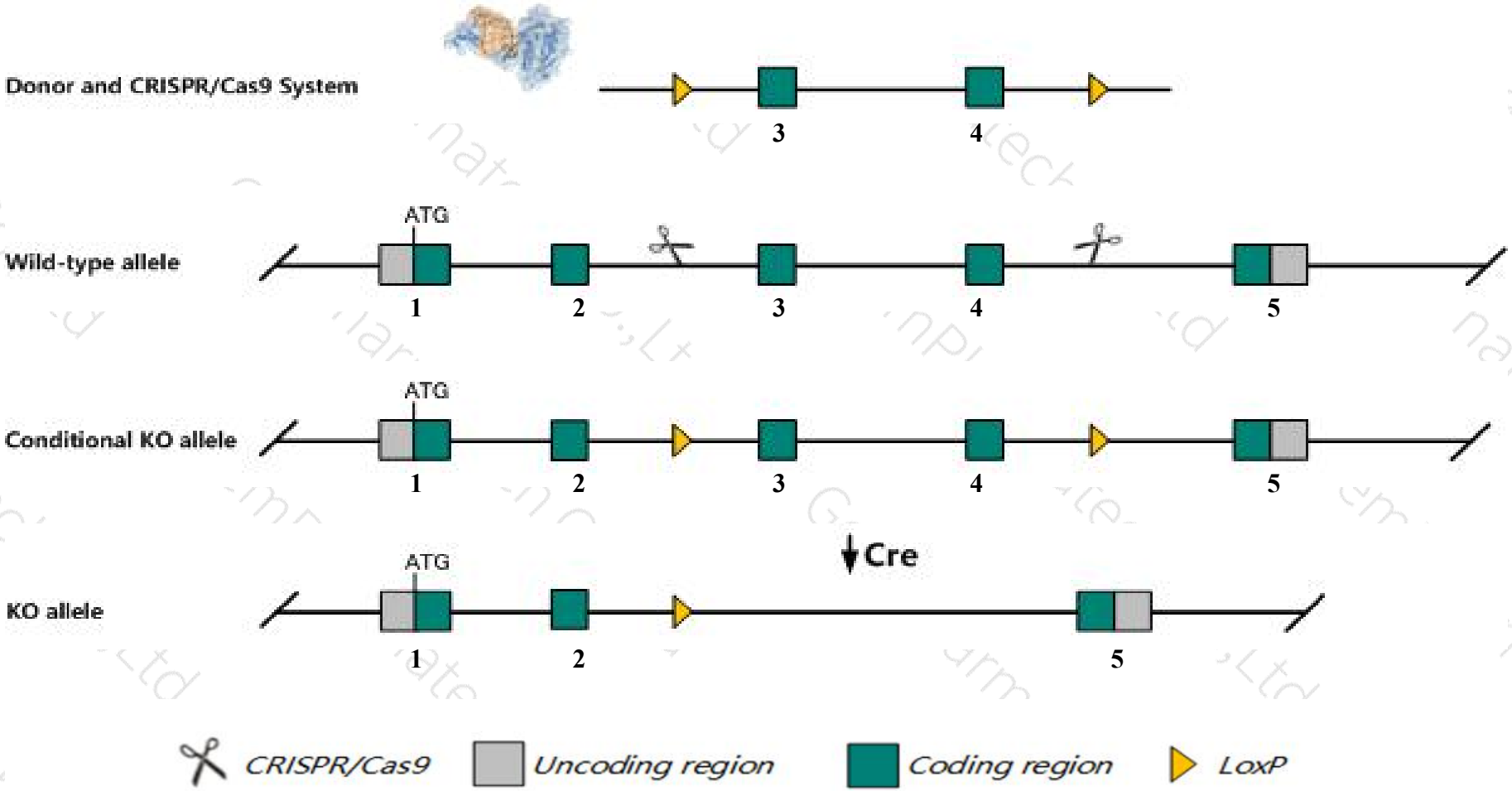
Design Date:

Project Overview

Project Name	***Synpo2***
Project type	**Cas9-CKO**
Strain background	**C57BL/6JGpt**

Conditional Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *Synpo2* gene. The schematic diagram is as follows:



Technical routes

- The *Synpo2* gene has 7 transcripts. According to the structure of *Synpo2* gene, exon3-exon4 of *Synpo2-202* (ENSMUST00000106426.7) transcript is recommended as the knockout region.The region contains 2977bp coding sequence. Knock out the region will result in disruption of protein function.

- In this project we use CRISPR/Cas9 technology to modify *Synpo2* 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

➢ The *Synpo2* 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）

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Synpo2 synaptopodin 2 [Mus musculus (house mouse)]

Gene ID: 118449, updated on 31-Jan-2019

Summary

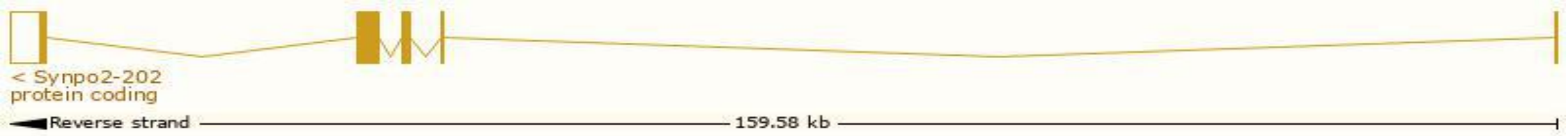
Official Symbol	Synpo2 provided by MGI
Official Full Name	synaptopodin 2 provided by MGI
Primary source	MGI:MGI:2153070
See related	Ensembl:ENSMUSG00000050315
Gene type	protein coding
RefSeq status	VALIDATED
Organism	Mus musculus
Lineage	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Myomorpha; Muroidea; Muridae; Murinae; Mus; Mus
Also known as	1110069I04Rik, 2310068J10Rik, 9530006G20Rik, AI848603, Myo
Expression	Biased expression in bladder adult (RPKM 58.2), subcutaneous fat pad adult (RPKM 12.4) and 8 other tissues See more
Orthologs	human all

Transcript information（Ensembl）

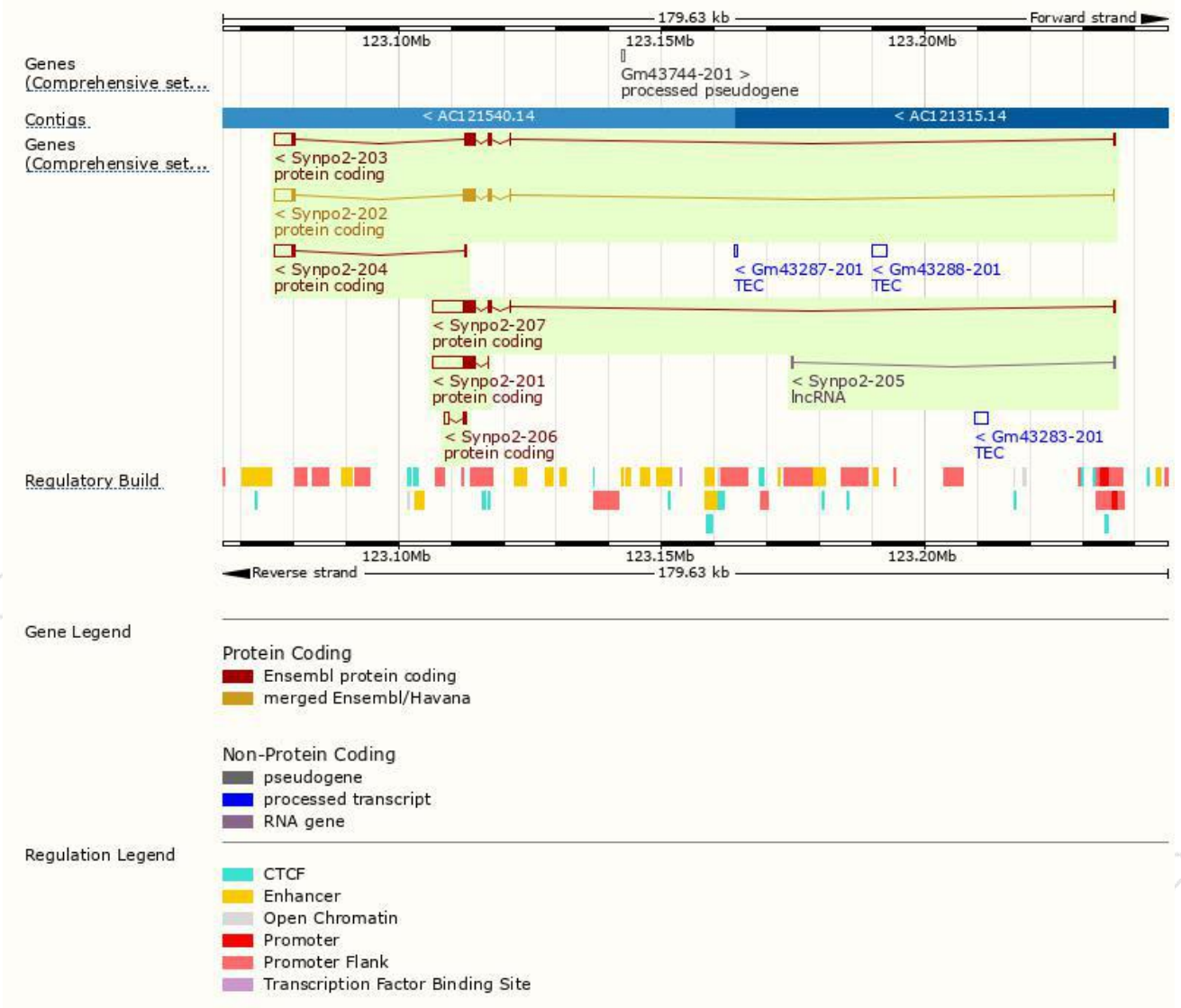
The gene has 7 transcripts,all transcripts are shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Synpo2-202	ENSMUST00000106426.7	7063	1257aa	Protein coding	CCDS51063	E9Q1U2	TSL:1 GENCODE basic APPRIS P2
Synpo2-207	ENSMUST00000198584.1	9203	1087aa	Protein coding	-	Q91YE8	TSL:5 GENCODE basic APPRIS ALT2
Synpo2-201	ENSMUST00000051443.7	8121	702aa	Protein coding	-	Q91YE8	TSL:NA GENCODE basic
Synpo2-203	ENSMUST00000106427.7	6937	1198aa	Protein coding	-	D3YVV9	TSL:5 GENCODE basic APPRIS ALT2
Synpo2-204	ENSMUST00000139160.7	3849	216aa	Protein coding	-	F6WWS1	CDS 5' incomplete TSL:3
Synpo2-206	ENSMUST00000184590.2	1297	185aa	Protein coding	-	A0A0G2JDM5	CDS 5' incomplete TSL:1
Synpo2-205	ENSMUST00000184403.1	391	No protein	lncRNA	-	-	TSL:3

The strategy is based on the design of *Synpo2-202* transcript,The transcription is shown below

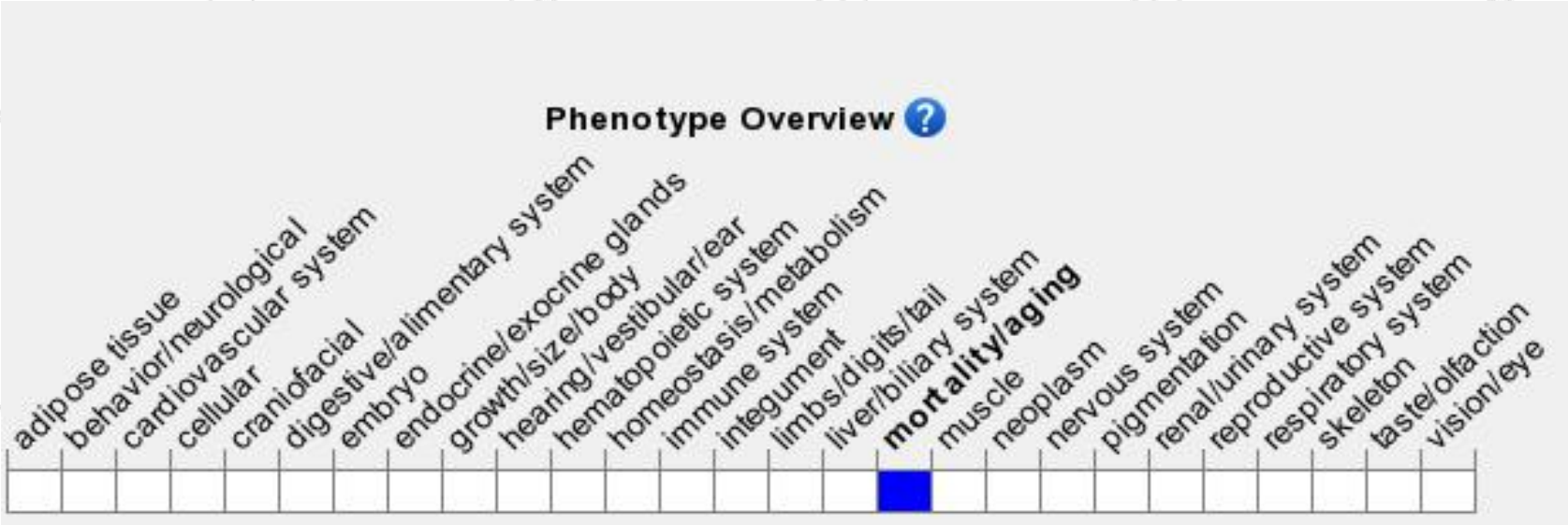


Genomic location distribution



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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