Smarcc1 Cas9-CKO Strategy

Designer: Daohua Xu
Reviewer: Huimin Su

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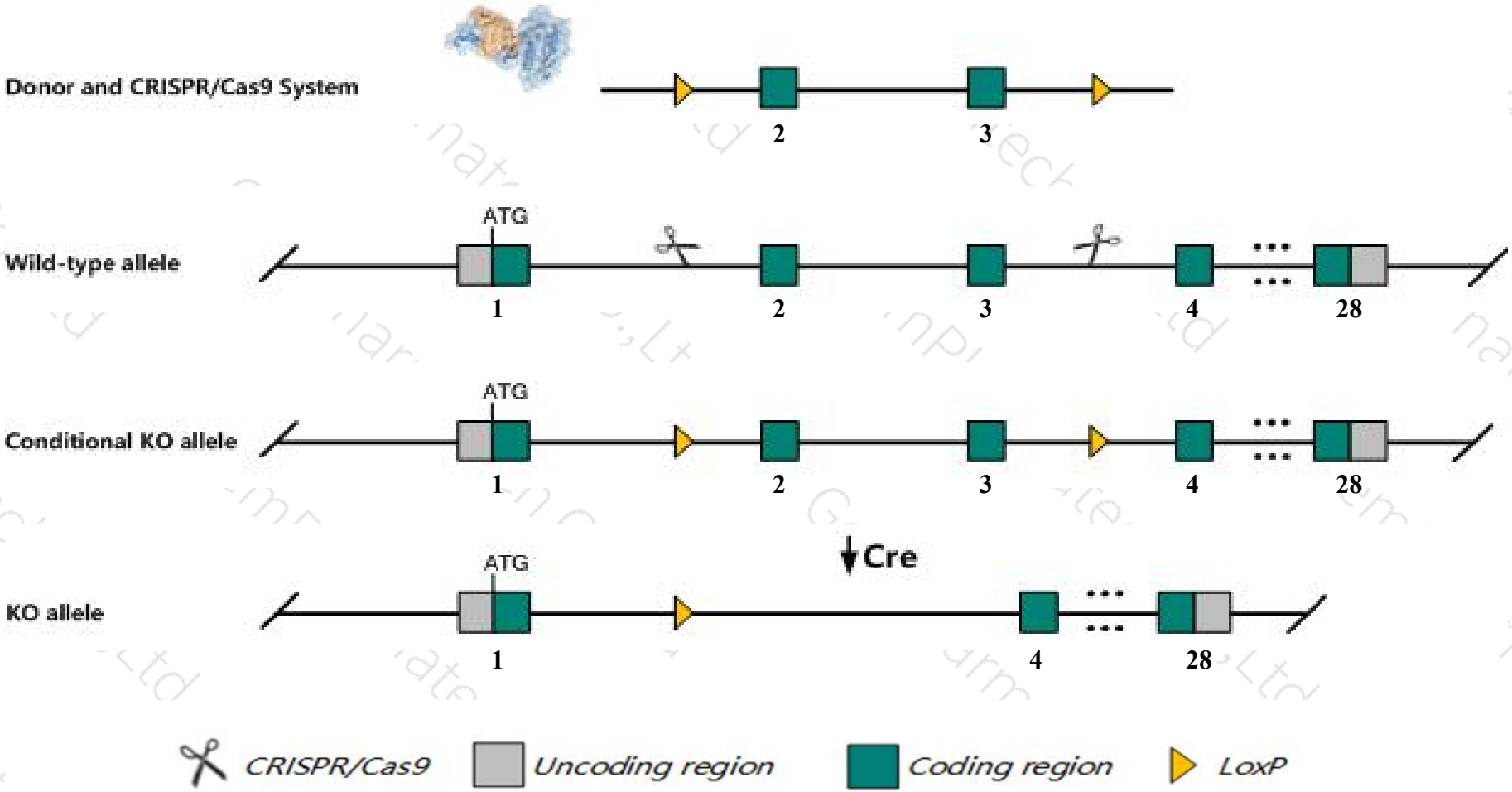
Project Overview

Project Name	***Smarcc1***
Project type	**Cas9-CKO**
Strain background	**C57BL/6JGpt**

Conditional Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *Smarcc1* gene. The schematic diagram is as follows:



Technical routes

- The *Smarcc1* gene has 9 transcripts. According to the structure of *Smarcc1* gene, exon2-exon3 of *Smarcc1-201* (ENSMUST00000088716.11) transcript is recommended as the knockout region.The region contains 206bp coding sequence. Knock out the region will result in disruption of protein function.

- In this project we use CRISPR/Cas9 technology to modify *Smarcc1* 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 a knock-out mutation display early embryonic lethality soon after decidualization due to failed egg cylinder formation and defects in the inner cell mass and primitive endoderm. About 20% of heterozygous mutant embryos show exencephaly caused by failure in neural fold elevation.

- The *Smarcc1* gene is located on the Chr9. 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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Smarcc1 SWI/SNF related, matrix associated, actin dependent regulator of chromatin, subfamily c, member 1 [Mus musculus (house mouse)]

Gene ID: 20588, updated on 19-Feb-2019

Summary

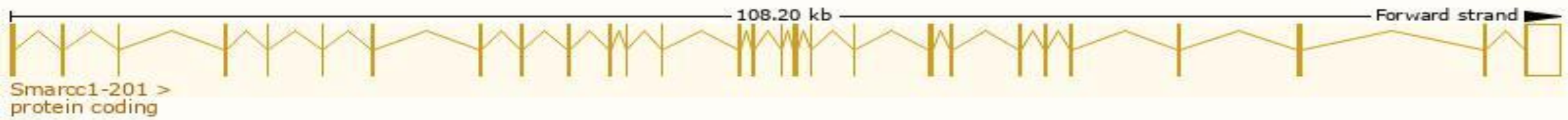
Official Symbol	Smarcc1 provided by MGI
Official Full Name	SWI/SNF related, matrix associated, actin dependent regulator of chromatin, subfamily c, member 1 provided by MGI
Primary source	MGI:MGI:1203524
See related	Ensembl:ENSMUSG00000032481
Gene type	protein coding
RefSeq status	VALIDATED
Organism	Mus musculus
Lineage	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Myomorpha; Muroidea; Muridae; Murinae; Mus; Mus
Also known as	AI115498, BAF155, Rsc8, SRG3, msp3
Expression	Ubiquitous expression in CNS E11.5 (RPKM 32.9), limb E14.5 (RPKM 21.9) and 28 other tissues See more
Orthologs	human all

Transcript information（Ensembl）

The gene has 9 transcripts,all transcripts are shown below:

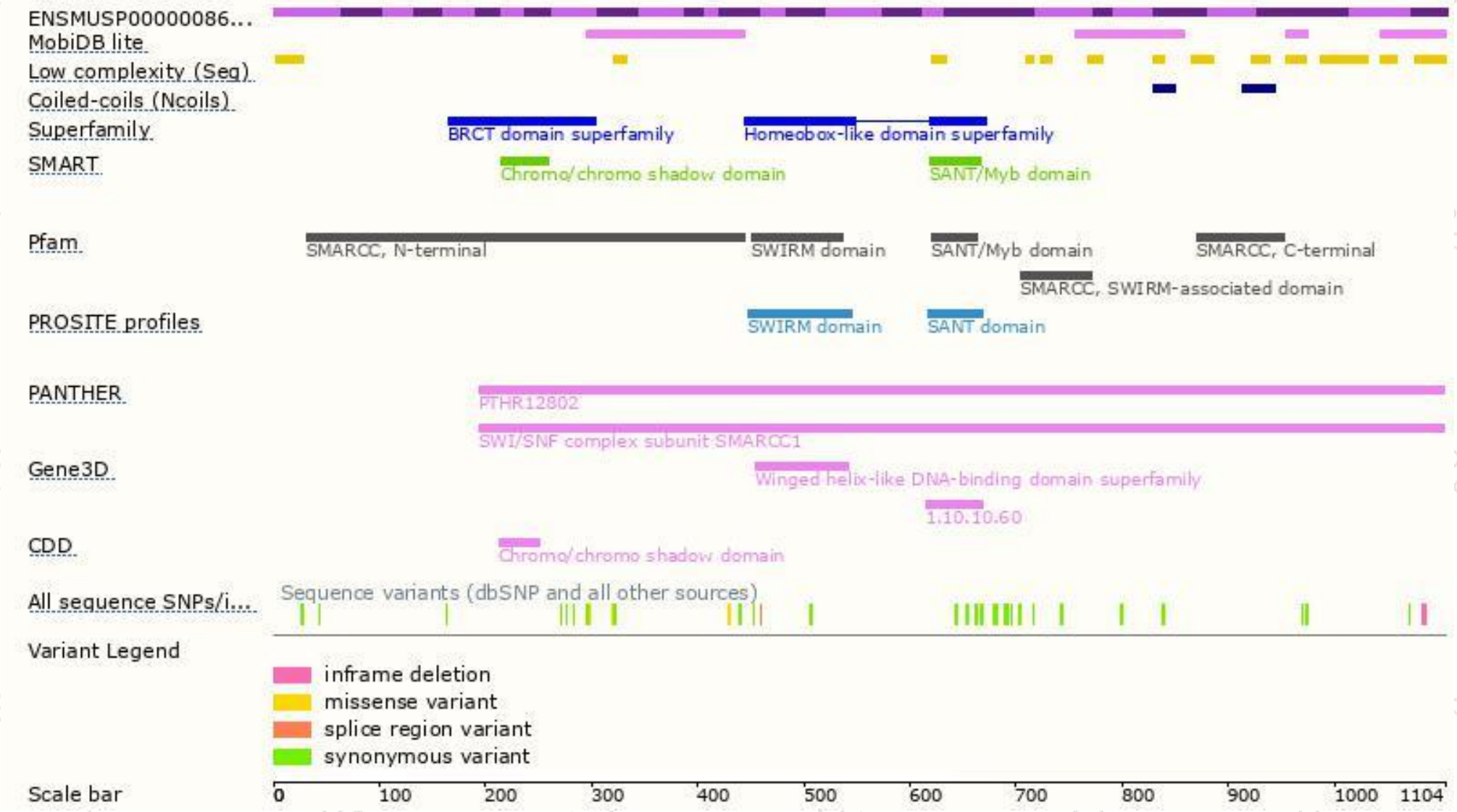
Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Smarcc1-201	ENSMUST00000088716.11	5717	1104aa	Protein coding	CCDS23561	P97496	TSL:1 GENCODE basic APPRIS P2
Smarcc1-207	ENSMUST00000199896.1	5773	1098aa	Protein coding	-	Q3UNN4	TSL:1 GENCODE basic APPRIS ALT2
Smarcc1-204	ENSMUST00000197984.4	3538	1075aa	Protein coding	-	P97496	TSL:1 GENCODE basic APPRIS ALT2
Smarcc1-203	ENSMUST00000197480.4	1949	485aa	Protein coding	-	Q3UZD0	TSL:1 GENCODE basic
Smarcc1-205	ENSMUST00000198211.1	412	49aa	Protein coding	-	A0A0G2JFJ8	CDS 5' incomplete TSL:3
Smarcc1-202	ENSMUST00000098355.5	364	49aa	Protein coding	-	F6SKR9	CDS 3' incomplete TSL:5
Smarcc1-208	ENSMUST00000200237.4	3078	No protein	Retained intron	-	-	TSL:1
Smarcc1-206	ENSMUST00000198667.1	1280	No protein	Retained intron	-	-	TSL:5
Smarcc1-209	ENSMUST00000200426.1	998	No protein	Retained intron	-	-	TSL:NA

The strategy is based on the design of *Smarcc1-201* transcript,The transcription is shown below

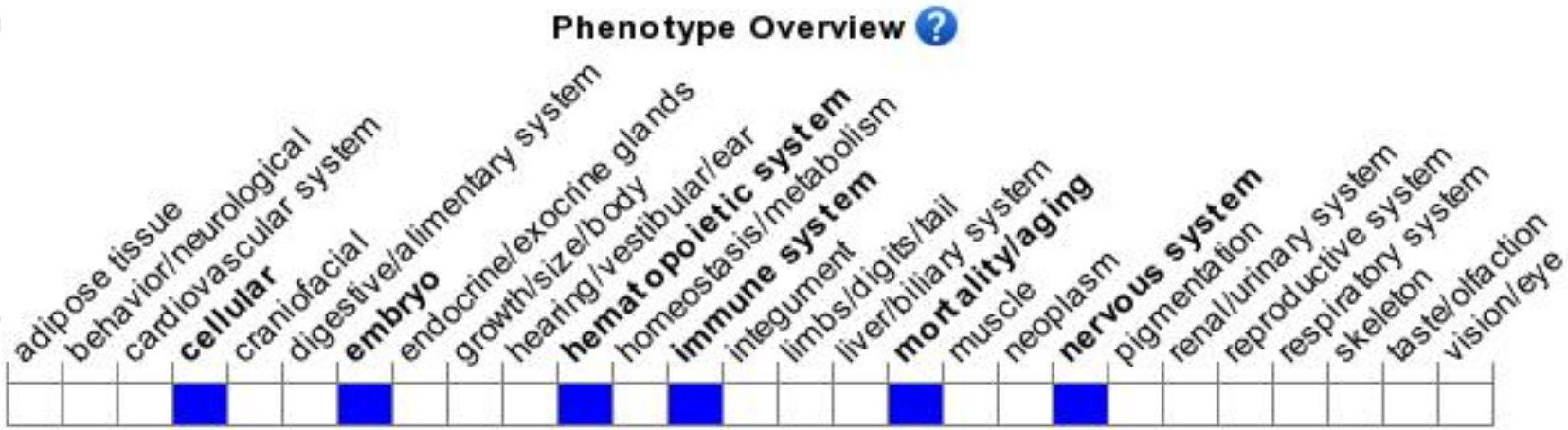


Genomic location distribution

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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集萃药康
GemPharmatech

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

Tel: 400-9660890

集萃药康生物科技
GemPharmatech Co.,Ltd