

Smarcd3 Cas9-CKO Strategy

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Reviewer:

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Design Date:

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Project Overview

Project Name

Smarcd3

Project type

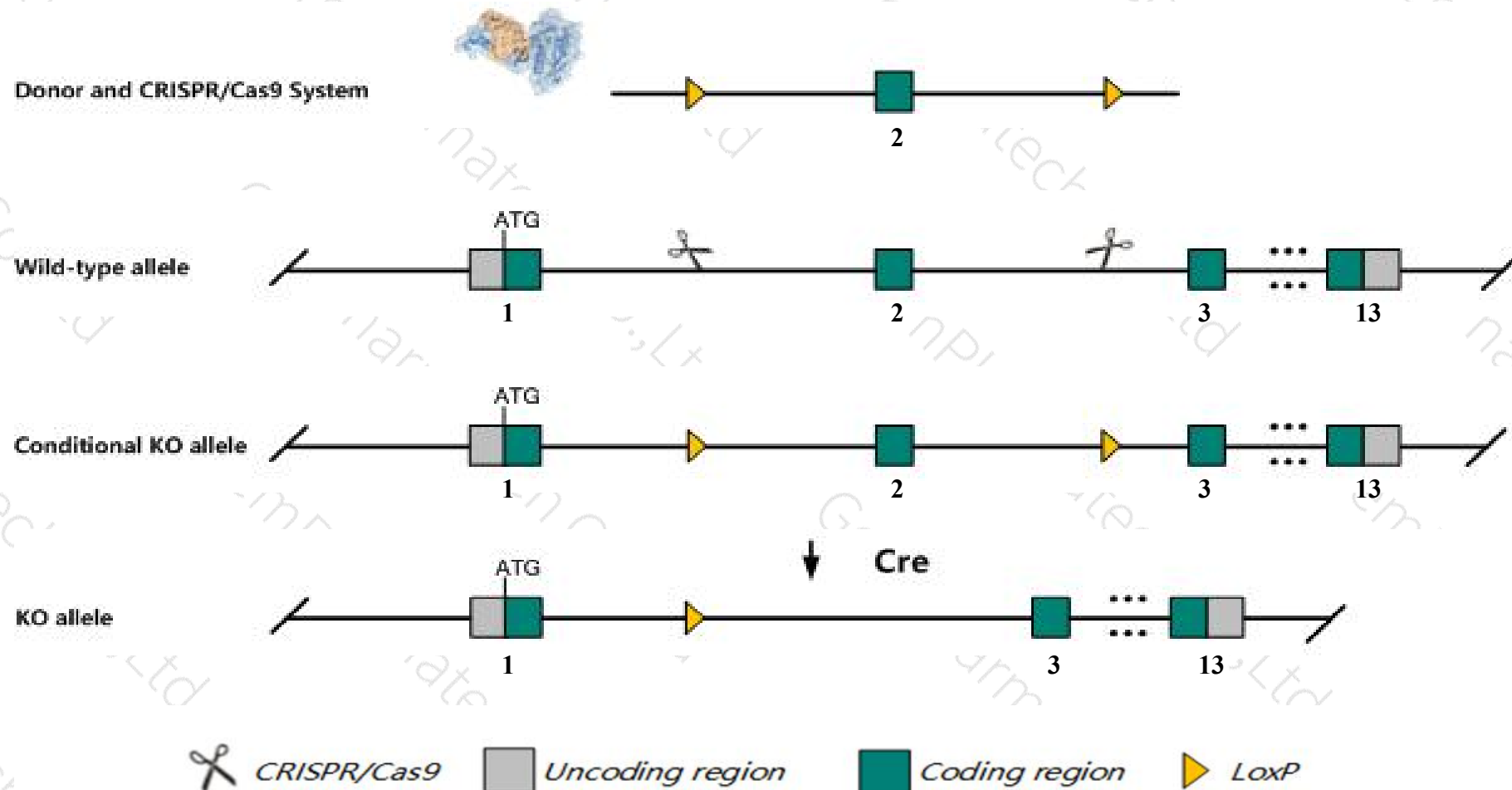
Cas9-CKO

Strain background

C57BL/6JGpt

Conditional Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *Smarcd3* gene. The schematic diagram is as follows:



- The *Smarcd3* gene has 9 transcripts. According to the structure of *Smarcd3* gene, exon2 of *Smarcd3-201* (ENSMUST00000030791.11) transcript is recommended as the knockout region. The region contains 212bp coding sequence. Knock out the region will result in disruption of protein function.
- In this project we use CRISPR/Cas9 technology to modify *Smarcd3* 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 *Smarcd3* gene is located on the Chr5. 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)

Smarcd3 SWI/SNF related, matrix associated, actin dependent regulator of chromatin, subfamily d, member 3 [Mus musculus (house mouse)]

Gene ID: 66993, updated on 31-Jan-2019

Summary



Official Symbol Smarcd3 provided by [MGI](#)

Official Full Name SWI/SNF related, matrix associated, actin dependent regulator of chromatin, subfamily d, member 3 provided by [MGI](#)

Primary source [MGI:MGI:1914243](#)

See related [Ensembl:ENSMUSG00000028949](#)

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 1500001J14Rik, 2210409C08Rik, BAF60C

Expression Broad expression in genital fat pad adult (RPKM 40.6), CNS E18 (RPKM 30.3) and 23 other tissues [See more](#)

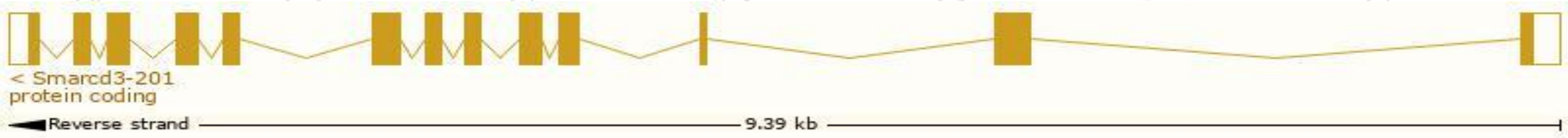
Orthologs [human](#) [all](#)

Transcript information (Ensembl)

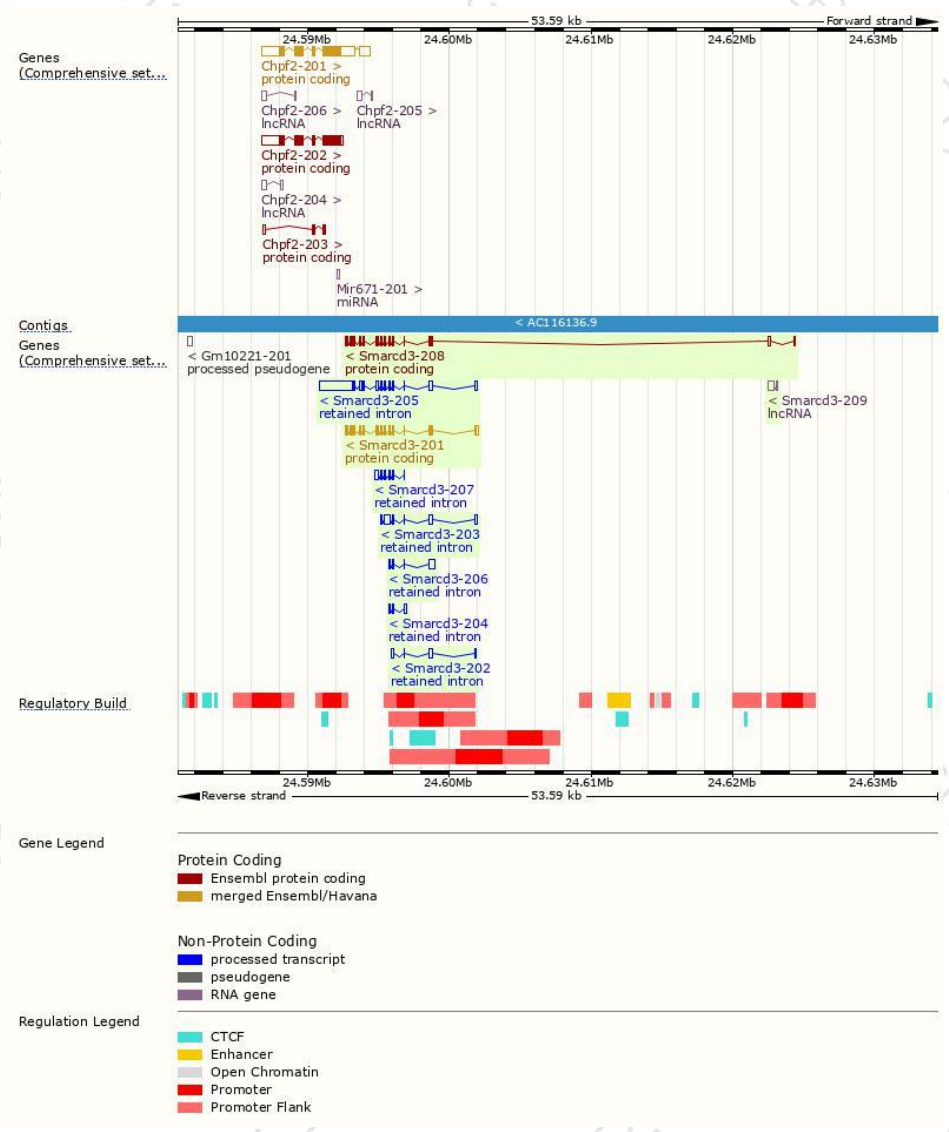
The gene has 9 transcripts,all transcripts are shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Smarcd3-201	ENSMUST00000030791.11	1735	483aa	Protein coding	CCDS19126	Q6P9Z1	TSL:1 GENCODE basic APPRIS P1
Smarcd3-208	ENSMUST00000195943.1	1712	454aa	Protein coding	-	A0A0G2JG60	TSL:5 GENCODE basic
Smarcd3-205	ENSMUST00000144995.7	3774	No protein	Retained intron	-	-	TSL:5
Smarcd3-203	ENSMUST00000143501.7	1070	No protein	Retained intron	-	-	TSL:5
Smarcd3-207	ENSMUST00000147857.7	786	No protein	Retained intron	-	-	TSL:2
Smarcd3-206	ENSMUST00000145565.7	624	No protein	Retained intron	-	-	TSL:2
Smarcd3-202	ENSMUST00000140744.1	583	No protein	Retained intron	-	-	TSL:2
Smarcd3-204	ENSMUST00000144518.1	406	No protein	Retained intron	-	-	TSL:3
Smarcd3-209	ENSMUST00000199393.1	510	No protein	lncRNA	-	-	TSL:3

The strategy is based on the design of *Smarcd3-201* transcript,The transcription is shown below



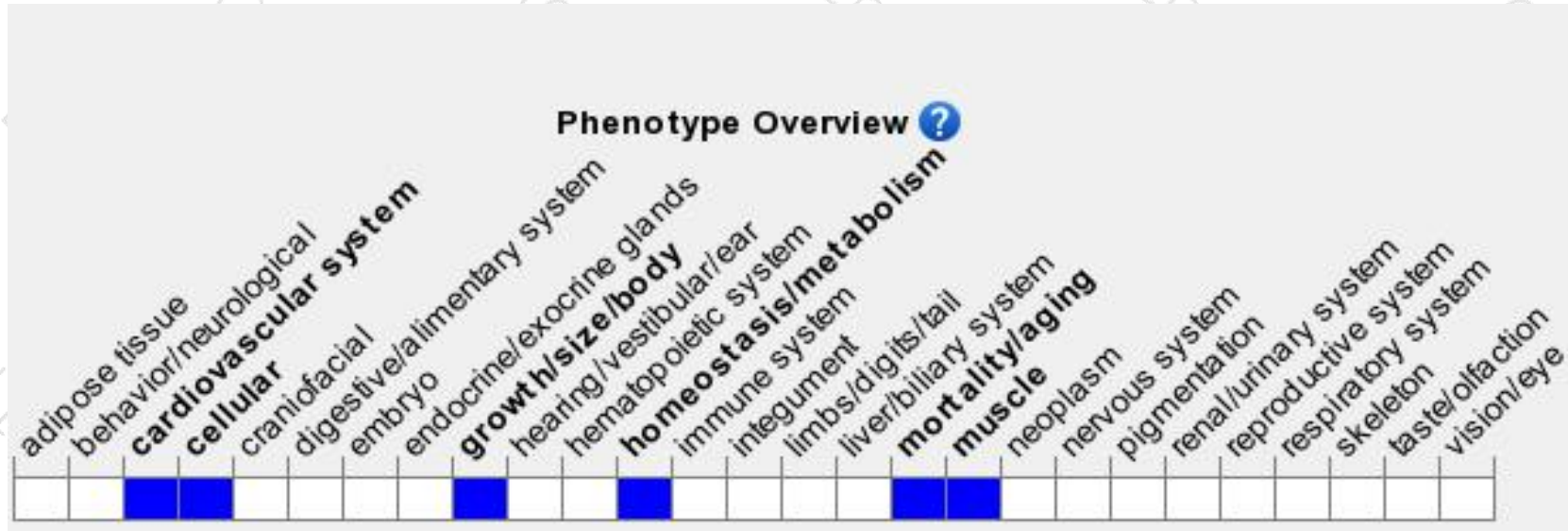
Genomic location distribution



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/>).

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

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