

Smarcd2 Cas9-KO Strategy

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Project Overview

Project Name

Smarcd2

Project type

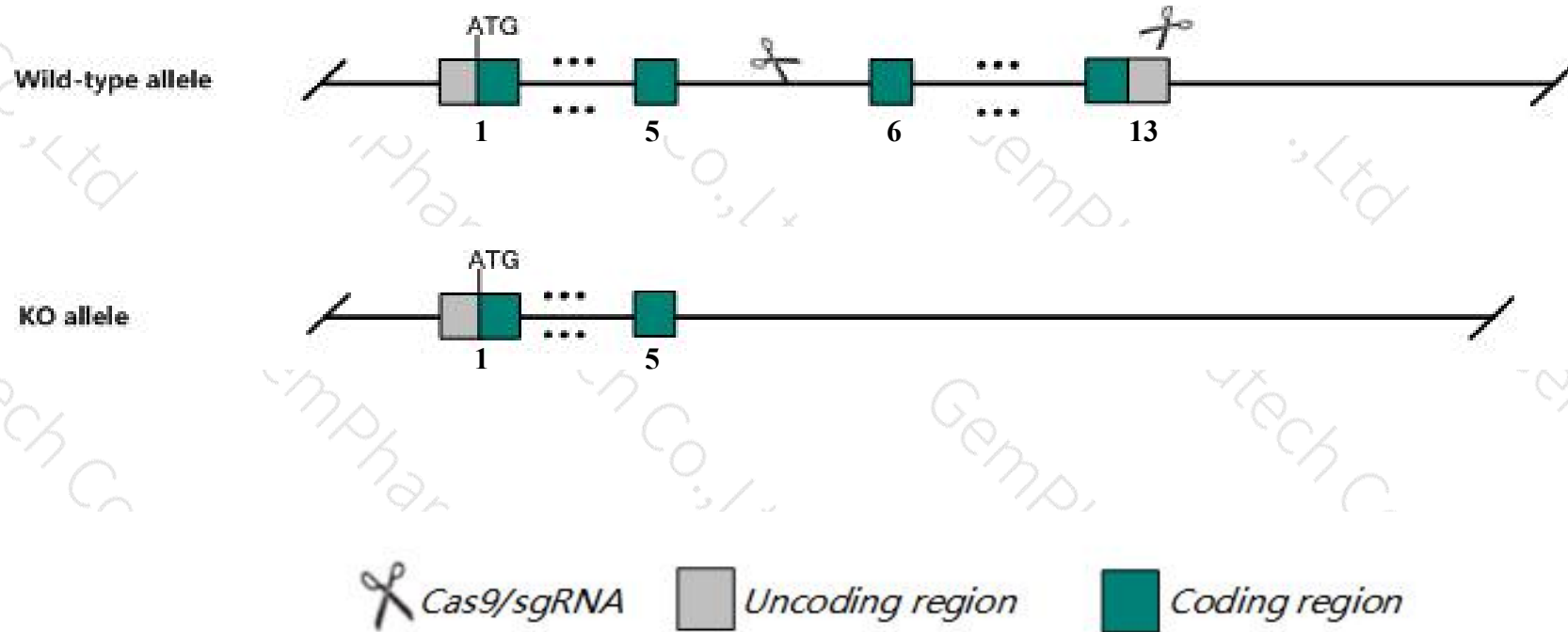
Cas9-KO

Strain background

C57BL/6J

Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *Smarcd2* gene. The schematic diagram is as follows:



- The *Smarcd2* gene has 9 transcripts. According to the structure of *Smarcd2* gene, exon6-exon13 of *Smarcd2-201* (ENSMUST00000021052.15) transcript is recommended as the knockout region. The region contains 873bp coding sequence. Knock out the region will result in disruption of protein function.
- In this project we use CRISPR/Cas9 technology to modify *Smarcd2* gene. The brief process is as follows: sgRNA was transcribed in vitro. Cas9 and sgRNA were microinjected into the fertilized eggs of C57BL/6J 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/6J mice.

- The KO region deletes most of the coding sequence, but does not result in frameshift.
- The *Smarcd2* gene is located on the Chr11. 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.

Gene information (NCBI)

Smarcd2 SWI/SNF related, matrix associated, actin dependent regulator of chromatin, subfamily d, member 2 [Mus musculus (house mouse)]

Gene ID: 83796, updated on 31-Jan-2019

Summary

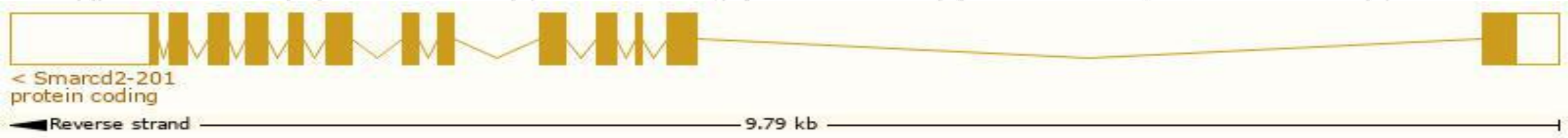
Official Symbol	Smarcd2 provided by MGI
Official Full Name	SWI/SNF related, matrix associated, actin dependent regulator of chromatin, subfamily d, member 2 provided by MGI
Primary source	MGI:MGI:1933621
See related	Ensembl:ENSMUSG00000078619
Gene type	protein coding
RefSeq status	VALIDATED
Organism	Mus musculus
Lineage	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Myomorpha; Muroidea; Muridae; Murinae; Mus; Mus
Also known as	AW322457, Baf60b
Expression	Ubiquitous expression in thymus adult (RPKM 97.9), adrenal adult (RPKM 42.3) and 26 other tissuesSee more
Orthologs	human all

Transcript information (Ensembl)

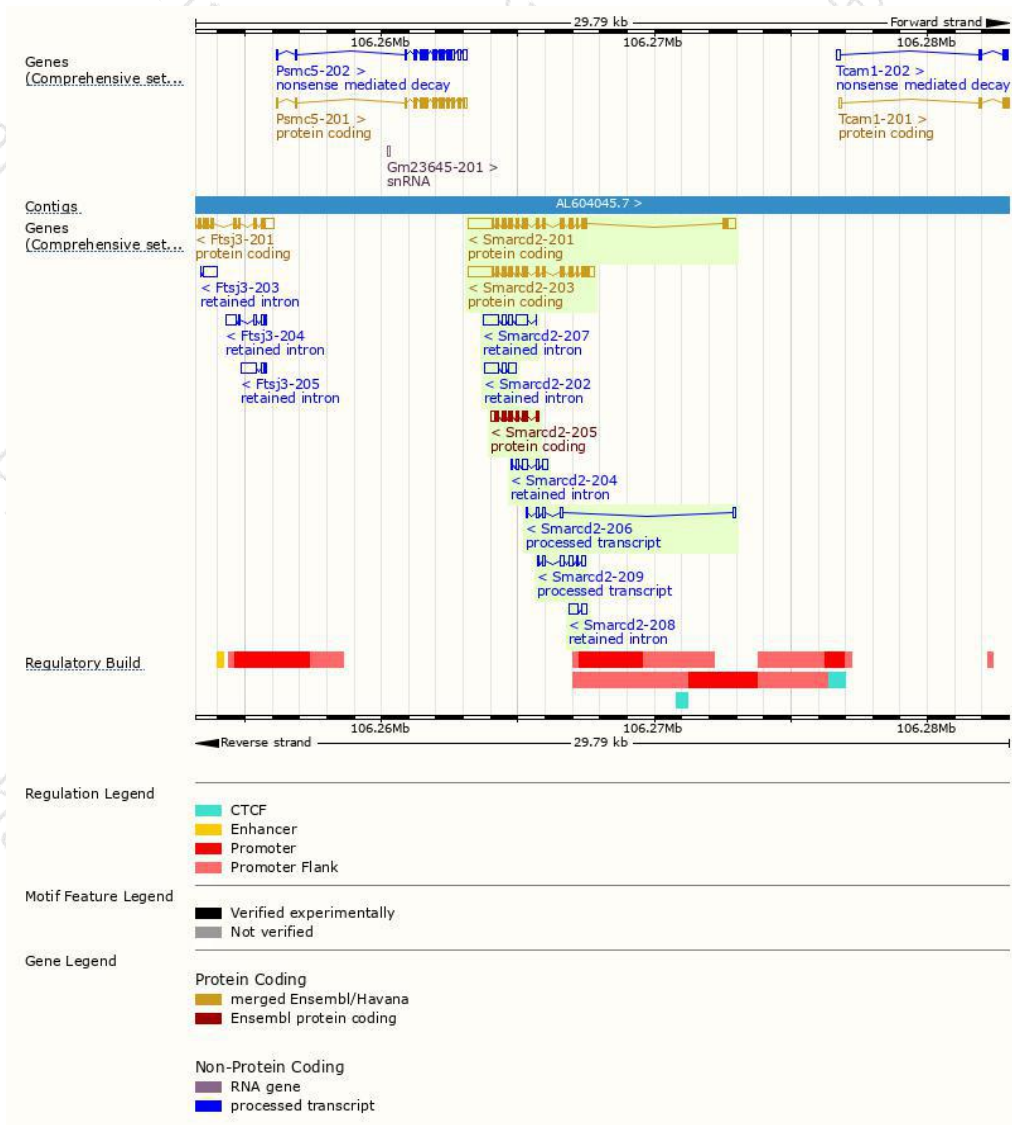
The gene has 9 transcripts,all transcripts are shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Smarcd2-201	ENSMUST00000021052.15	2747	531aa	Protein coding	CCDS48958	Q99JR8	TSL:1 GENCODE basic APPRIS P1
Smarcd2-203	ENSMUST00000106843.7	2548	484aa	Protein coding	CCDS48957	Q99JR8	TSL:1 GENCODE basic
Smarcd2-205	ENSMUST00000140255.2	884	247aa	Protein coding	-	G3UXC0	CDS 5' incomplete TSL:5
Smarcd2-209	ENSMUST00000174253.1	608	No protein	Processed transcript	-	-	TSL:3
Smarcd2-206	ENSMUST00000155243.1	405	No protein	Processed transcript	-	-	TSL:5
Smarcd2-207	ENSMUST00000155514.8	1250	No protein	Retained intron	-	-	TSL:5
Smarcd2-202	ENSMUST00000106841.1	886	No protein	Retained intron	-	-	TSL:3
Smarcd2-204	ENSMUST00000132278.7	621	No protein	Retained intron	-	-	TSL:3
Smarcd2-208	ENSMUST00000174017.1	485	No protein	Retained intron	-	-	TSL:2

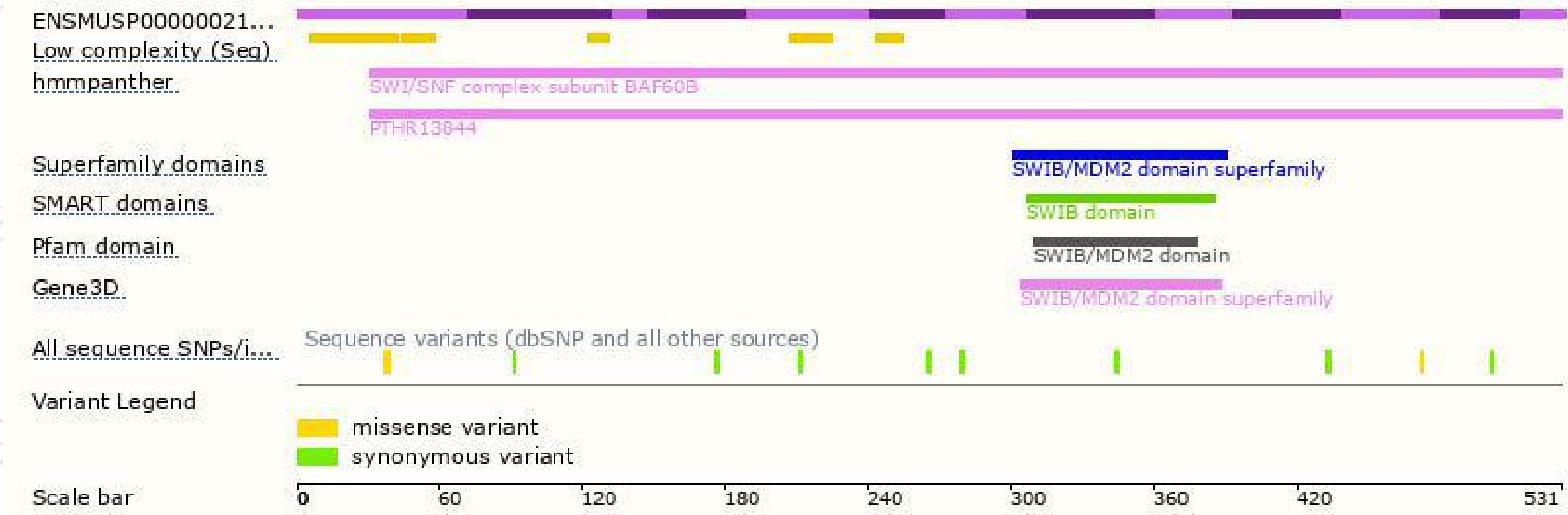
The strategy is based on the design of *Smarcd2-201* transcript,The transcription is shown below



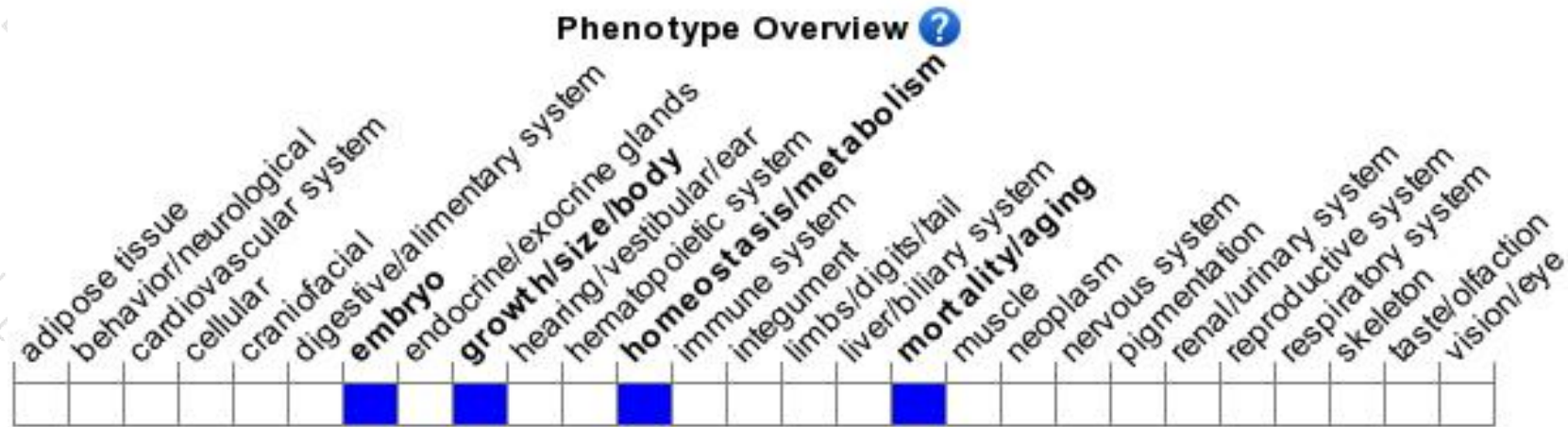
Genomic location distribution



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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