

# ***Smarcd3 Cas9-KO Strategy***

**Designer:**

**Daohua Xu**

**Reviewer:**

**Huimin Su**

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# Project Overview

**Project Name**

***Smarcd3***

**Project type**

**Cas9-KO**

**Strain background**

**C57BL/6JGpt**

# 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

- 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 the gene knockout on gene transcription, RNA splicing and protein translation cannot be predicted at the existing technology 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](#)

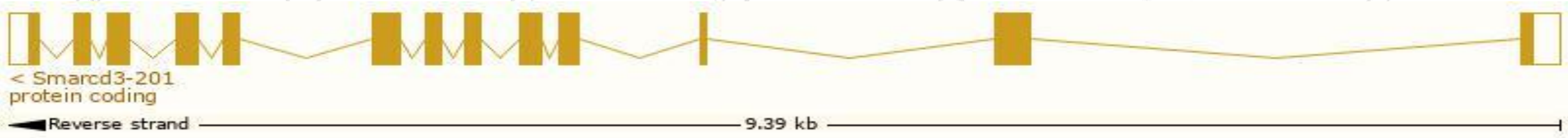
**Orthologs** [human](#) [all](#)

# Transcript information (Ensembl)

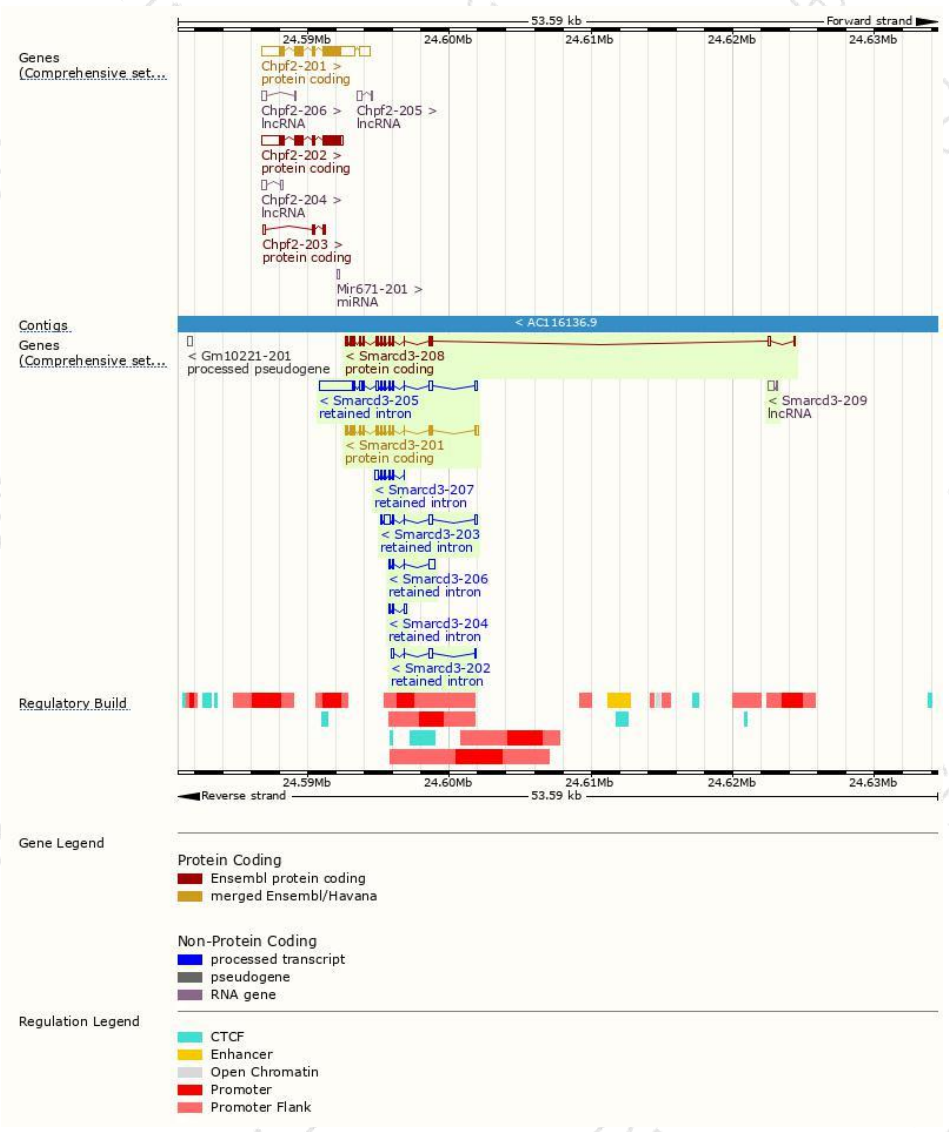
The gene has 9 transcripts,all transcripts are shown below:

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

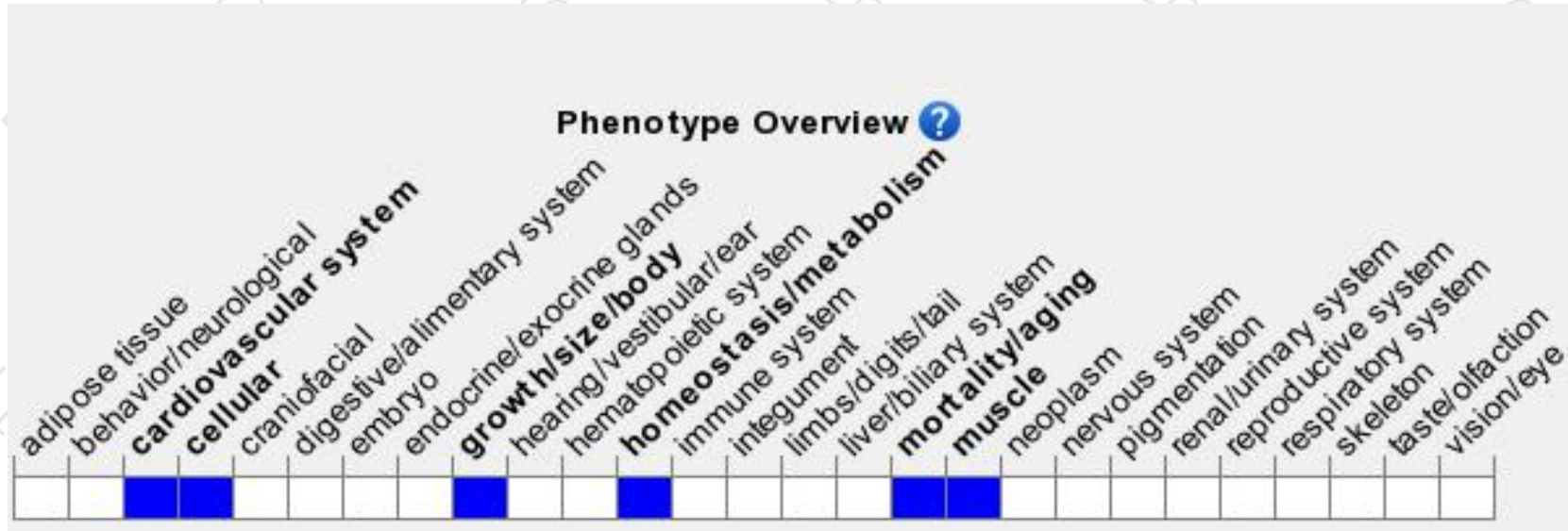




# Protein domain



# 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.

Tel: 400-9660890

