

Kdm5c Cas9-KO Strategy

Designer:

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Design Date:

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Project Overview

Project Name

Kdm5c

Project type

Cas9-KO

Strain background

C57BL/6JGpt

Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *Kdm5c* gene. The schematic diagram is as follows:



- The *Kdm5c* gene has 6 transcripts. According to the structure of *Kdm5c* gene, exon2-exon17 of *Kdm5c-203* (ENSMUST00000112588.8) transcript is recommended as the knockout region. The region contains 2366bp coding sequence. Knock out the region will result in disruption of protein function.
- In this project we use CRISPR/Cas9 technology to modify *Kdm5c* gene. The brief process is as follows: CRISPR/Cas9 system

- According to the existing MGI data, Male chimeras hemizygous for a gene trapped allele exhibit posterior patterning defects and abnormal heart morphology at E9.5. Chimeras hemizygous for a different gene trapped allele appear normal at E10.5.
- The *Kdm5c* gene is located on the ChrX. 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)

Kdm5c lysine (K)-specific demethylase 5C [Mus musculus (house mouse)]

Gene ID: 20591, updated on 31-Jan-2019

Summary



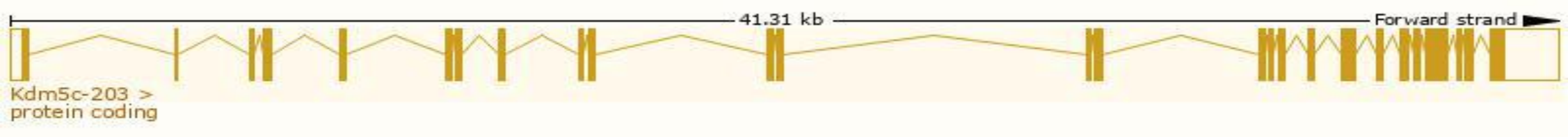
Official Symbol	Kdm5c provided by MGI
Official Full Name	lysine (K)-specific demethylase 5C provided by MGI
Primary source	MGI:MGI:99781
See related	Ensembl:ENSMUSG00000025332
Gene type	protein coding
RefSeq status	VALIDATED
Organism	Mus musculus
Lineage	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Myomorpha; Muroidea; Muridae; Murinae; Mus; Mus
Also known as	D930009K15Rik, Jarid1c, Smcx, mKIAA0234
Expression	Ubiquitous expression in CNS E11.5 (RPKM 13.0), ovary adult (RPKM 12.8) and 28 other tissues See more
Orthologs	human all

Transcript information (Ensembl)

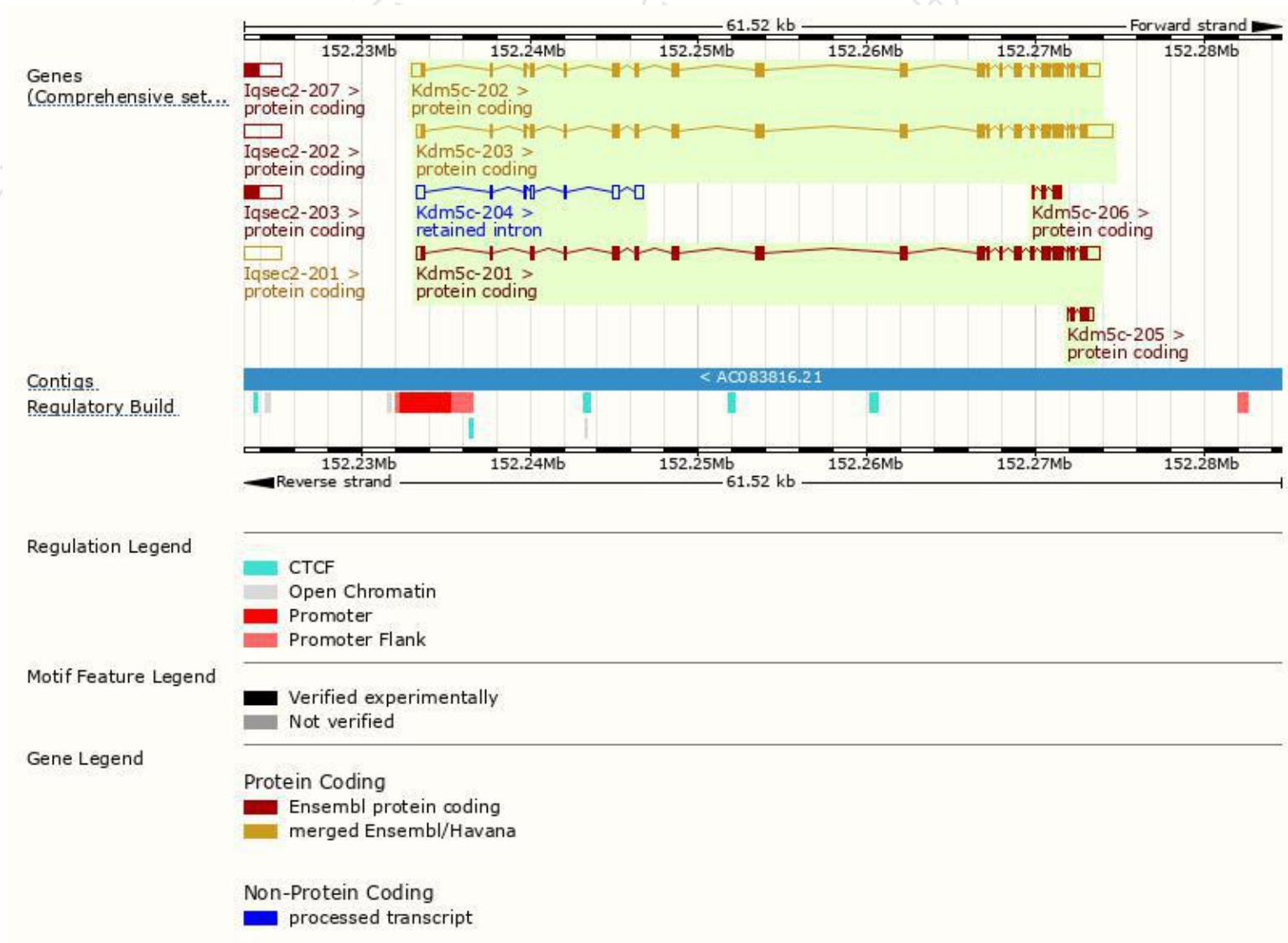
The gene has 6 transcripts,all transcripts are shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Kdm5c-203	ENSMUST00000112588.8	6449	1551aa	Protein coding	CCDS41178	P41230	TSL:1 GENCODE basic APPRIS P2
Kdm5c-202	ENSMUST00000112584.7	5900	1554aa	Protein coding	-	P41230	TSL:5 GENCODE basic APPRIS ALT2
Kdm5c-201	ENSMUST00000082177.12	5520	1510aa	Protein coding	-	P41230	TSL:5 GENCODE basic APPRIS ALT2
Kdm5c-206	ENSMUST00000156114.1	773	257aa	Protein coding	-	F7BXT3	5' and 3' truncations in transcript evidence prevent annotation of the start and the end of the CDS. CDS 5' and 3' incomplete TSL:3
Kdm5c-205	ENSMUST00000155793.1	756	177aa	Protein coding	-	F6WXI0	CDS 5' incomplete TSL:2
Kdm5c-204	ENSMUST00000154938.1	1872	No protein	Retained intron	-	-	TSL:2

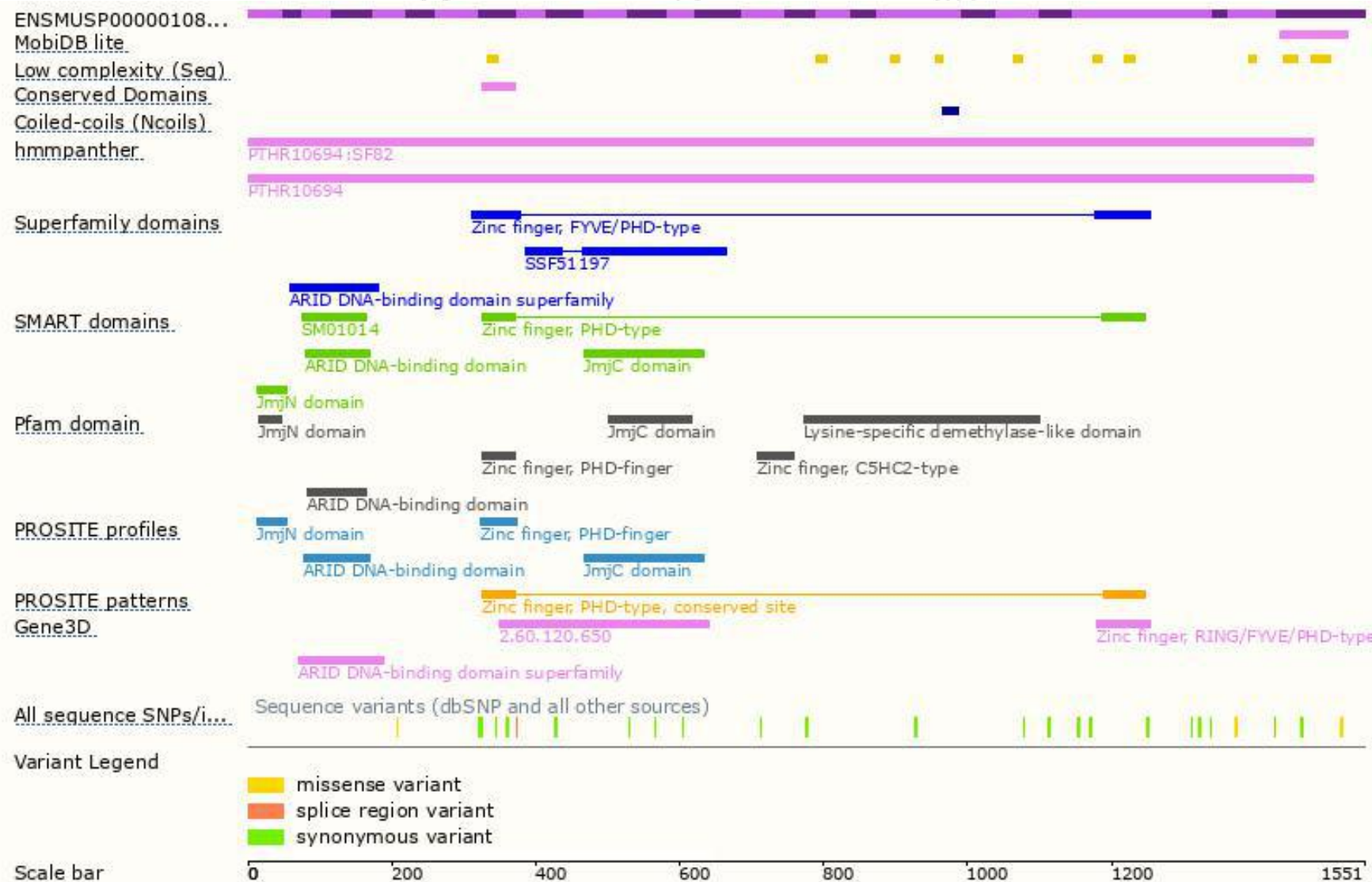
The strategy is based on the design of *Kdm5c-203* transcript,The transcription is shown below



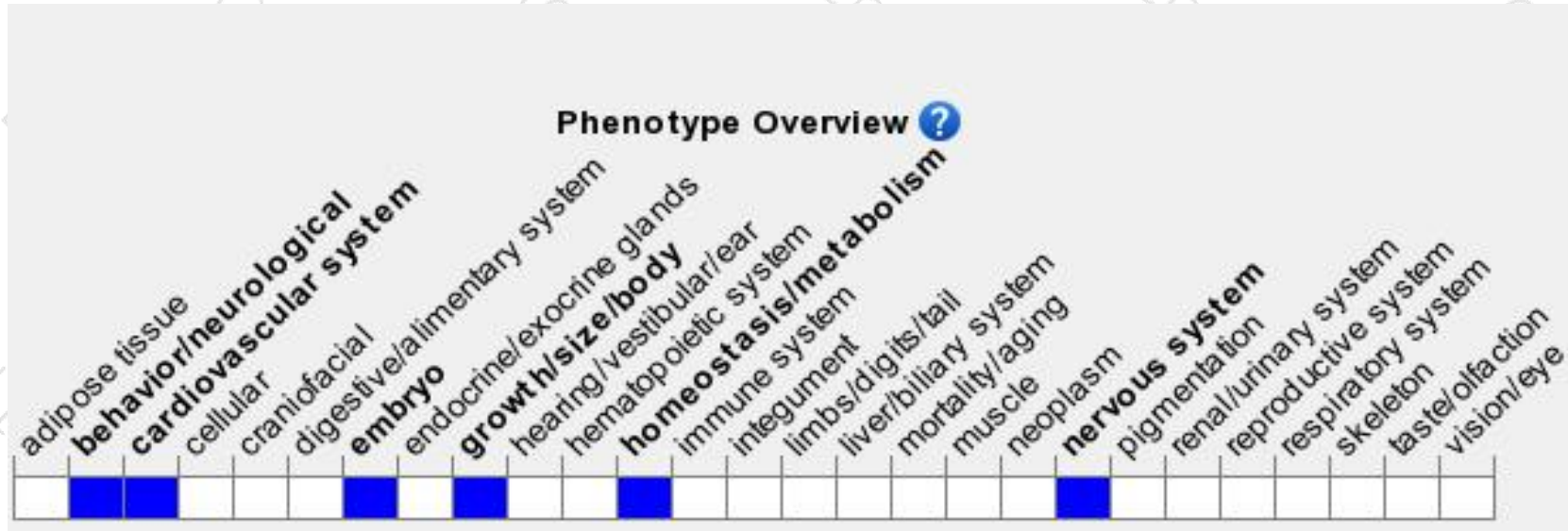
Genomic location distribution



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/>).

According to the existing MGI data, Male chimeras hemizygous for a gene trapped allele exhibit posterior patterning defects and abnormal heart morphology at E9.5. Chimeras hemizygous for a different gene trapped allele appear normal at E10.5.

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

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