

***Kmt5c* Cas9-KO Strategy**

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Reviewer:

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Project Overview

Project Name

Kmt5c

Project type

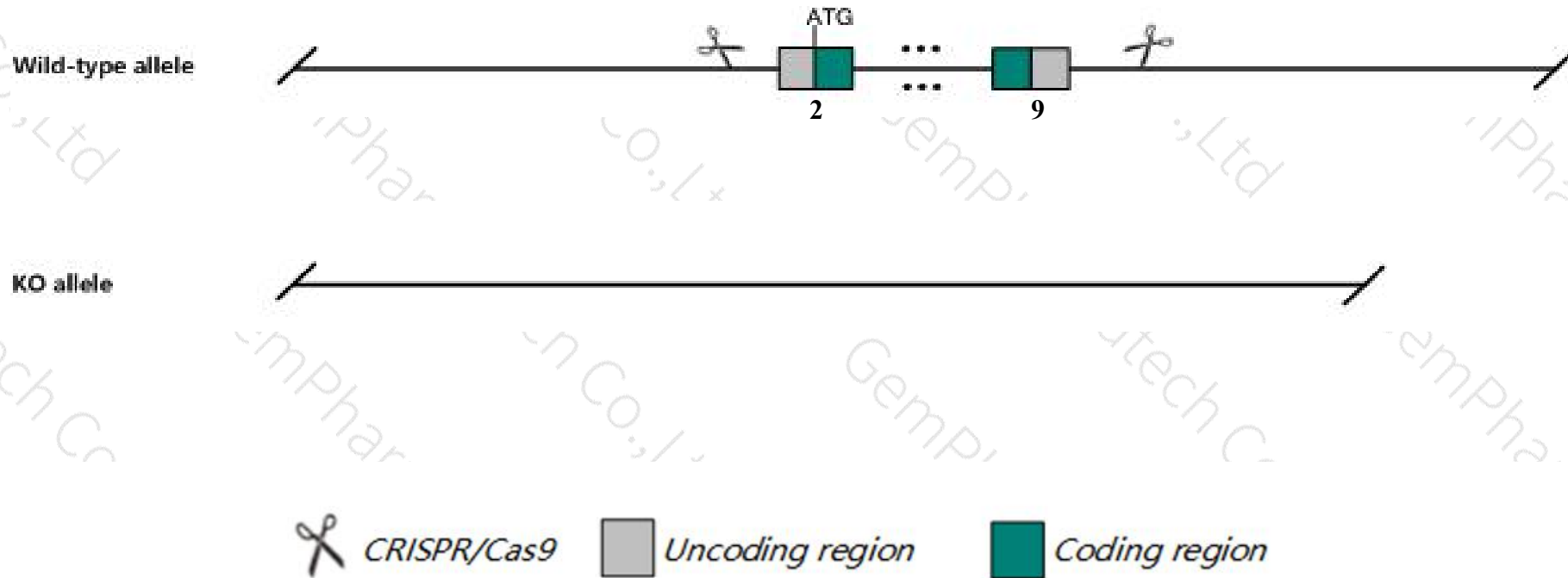
Cas9-KO

Strain background

C57BL/6JGpt

Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *Kmt5c* gene. The schematic diagram is as follows:



- The *Kmt5c* gene has 12 transcripts. According to the structure of *Kmt5c* gene, exon2-exon9 of *Kmt5c-202* (ENSMUST00000108582.9) transcript is recommended as the knockout region. The region contains all of the coding sequence. Knock out the region will result in disruption of protein function.
- In this project we use CRISPR/Cas9 technology to modify *Kmt5c* gene. The brief process is as follows: CRISPR/Cas9 system

- According to the existing MGI data, Mice homozygous for a knock-out allele exhibit no apparent defects and develop normally.
- The *Kmt5c* gene is located on the Chr7. 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)

Kmt5c lysine methyltransferase 5C [Mus musculus (house mouse)]

Gene ID: 232811, updated on 31-Jan-2019

Summary



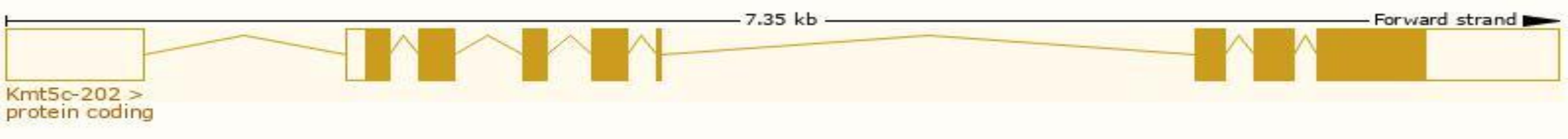
Official Symbol	Kmt5c provided by MGI
Official Full Name	lysine methyltransferase 5C provided by MGI
Primary source	MGI:MGI:2385262
See related	Ensembl:ENSMUSG00000059851
Gene type	protein coding
RefSeq status	VALIDATED
Organism	Mus musculus
Lineage	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Myomorpha; Muroidea; Muridae; Murinae; Mus; Mus
Also known as	BC024816, Suv4-20h2, Suv420h2
Expression	Ubiquitous expression in duodenum adult (RPKM 51.2), colon adult (RPKM 39.4) and 28 other tissues See more
Orthologs	human all

Transcript information (Ensembl)

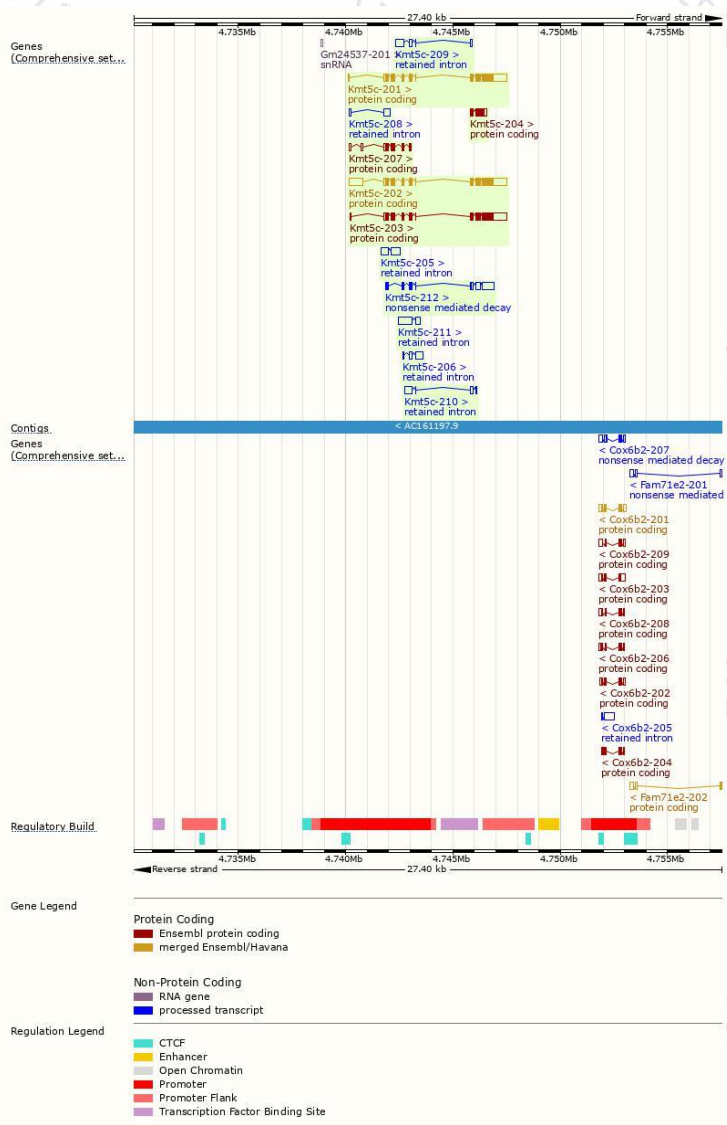
The gene has 12 transcripts,all transcripts are shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Kmt5c-202	ENSMUST00000108582.9	2774	468aa	Protein coding	CCDS20743	Q6Q783	TSL:1 GENCODE basic APPRIS P1
Kmt5c-201	ENSMUST00000098853.8	2189	468aa	Protein coding	CCDS20743	Q6Q783	TSL:1 GENCODE basic APPRIS P1
Kmt5c-203	ENSMUST00000108583.8	2177	468aa	Protein coding	CCDS20743	Q6Q783	TSL:1 GENCODE basic APPRIS P1
Kmt5c-207	ENSMUST00000130215.7	767	164aa	Protein coding	-	D3Z2F5	CDS 3' incomplete TSL:3
Kmt5c-204	ENSMUST00000128018.1	571	147aa	Protein coding	-	F6XZN9	CDS 5' incomplete TSL:2
Kmt5c-212	ENSMUST00000160480.1	1270	145aa	Nonsense mediated decay	-	E0CXW4	TSL:5
Kmt5c-211	ENSMUST00000152500.1	892	No protein	Retained intron	-	-	TSL:3
Kmt5c-205	ENSMUST00000129927.1	763	No protein	Retained intron	-	-	TSL:2
Kmt5c-209	ENSMUST00000136177.7	692	No protein	Retained intron	-	-	TSL:3
Kmt5c-206	ENSMUST00000130200.1	595	No protein	Retained intron	-	-	TSL:3
Kmt5c-210	ENSMUST00000152431.1	569	No protein	Retained intron	-	-	TSL:2
Kmt5c-208	ENSMUST00000135541.1	396	No protein	Retained intron	-	-	TSL:2

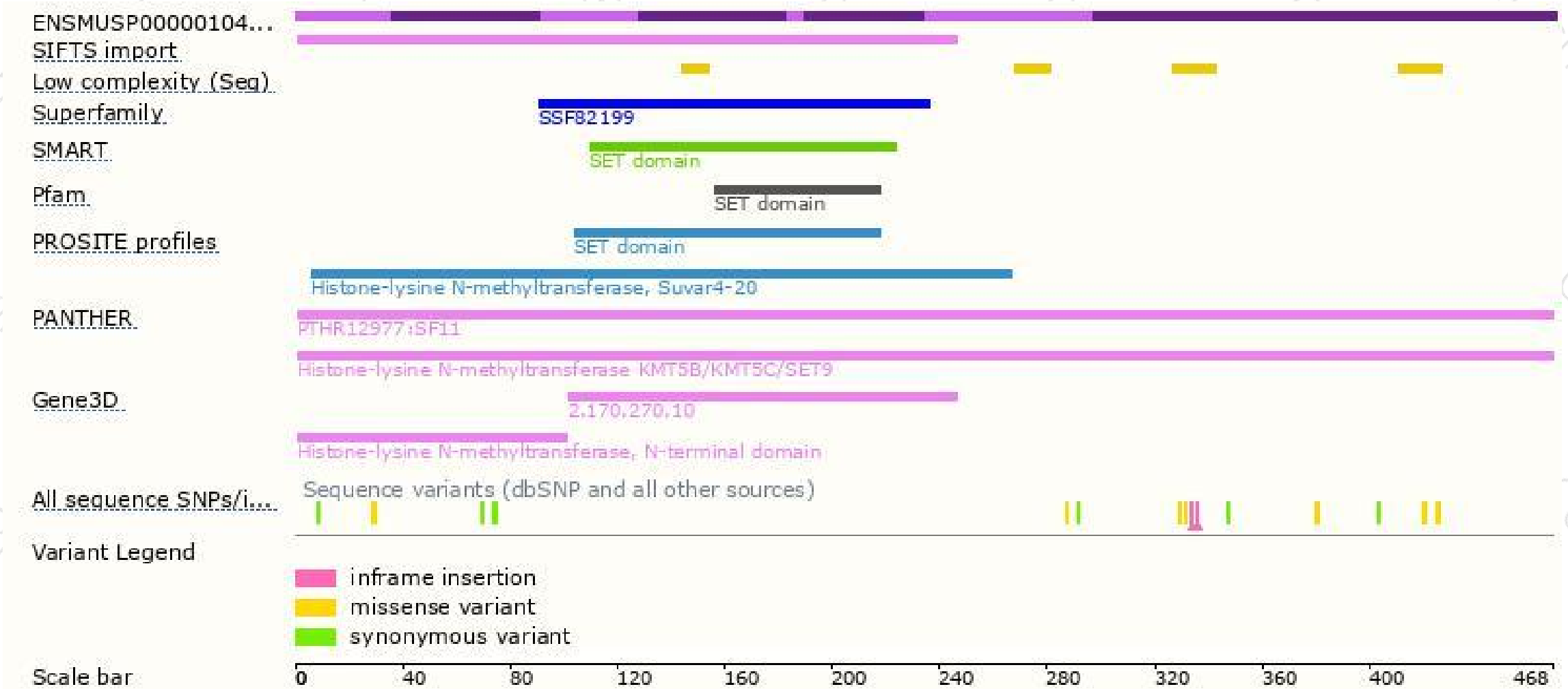
The strategy is based on the design of *Kmt5c-202* transcript,The transcription is shown below



Genomic location distribution



Protein domain



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

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