

***Mettl17* Cas9-CKO Strategy**

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Project Overview

Project Name

Mettl17

Project type

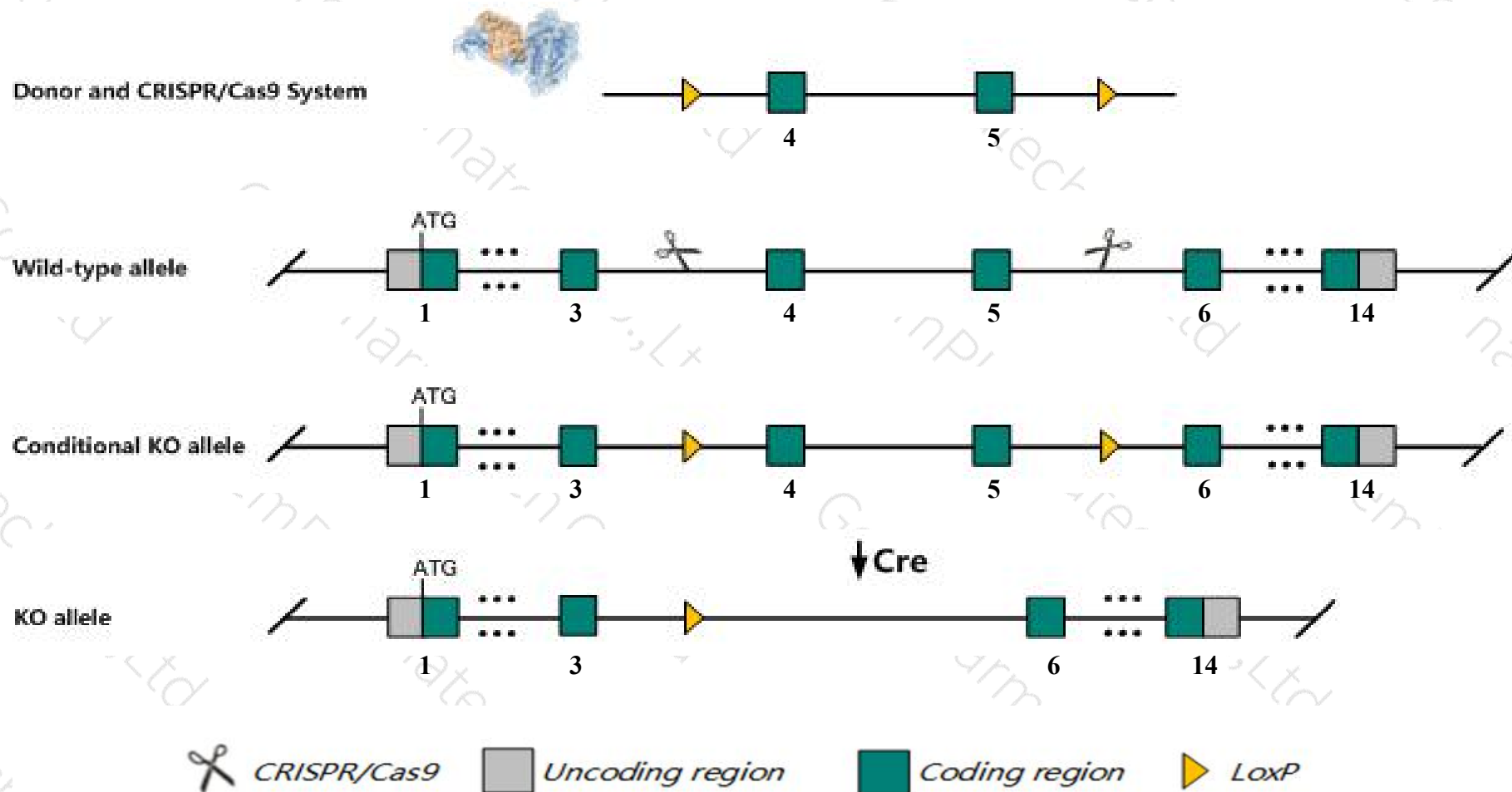
Cas9-CKO

Strain background

C57BL/6JGpt

Conditional Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *Mettl17* gene. The schematic diagram is as follows:



Technical routes

- The *Mettl17* gene has 16 transcripts. According to the structure of *Mettl17* gene, exon4-exon5 of *Mettl17-201* (ENSMUST00000047899.12) transcript is recommended as the knockout region. The region contains 164bp coding sequence. Knock out the region will result in disruption of protein function.
- In this project we use CRISPR/Cas9 technology to modify *Mettl17* 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

- Transcript *Mettl17*-211,213,216 may not be affected.
- The *Mettl17* gene is located on the Chr14. 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)

Mettl17 methyltransferase like 17 [Mus musculus (house mouse)]

Gene ID: 52535, updated on 31-Jan-2019

Summary



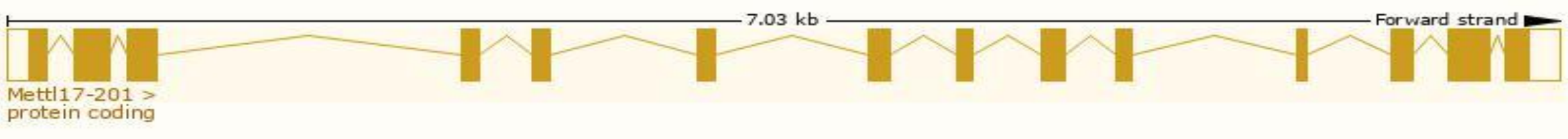
Official Symbol	Mettl17 provided by MGI
Official Full Name	methyltransferase like 17 provided by MGI
Primary source	MGI:MGI:1098577
See related	Ensembl:ENSMUSG000000004561
Gene type	protein coding
RefSeq status	VALIDATED
Organism	Mus musculus
Lineage	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Myomorpha; Muroidea; Muridae; Murinae; Mus; Mus
Also known as	2310032K15Rik, D14Ertd209e, Mett11d1
Expression	Ubiquitous expression in adrenal adult (RPKM 18.3), CNS E14 (RPKM 17.3) and 28 other tissues See more
Orthologs	human all

Transcript information (Ensembl)

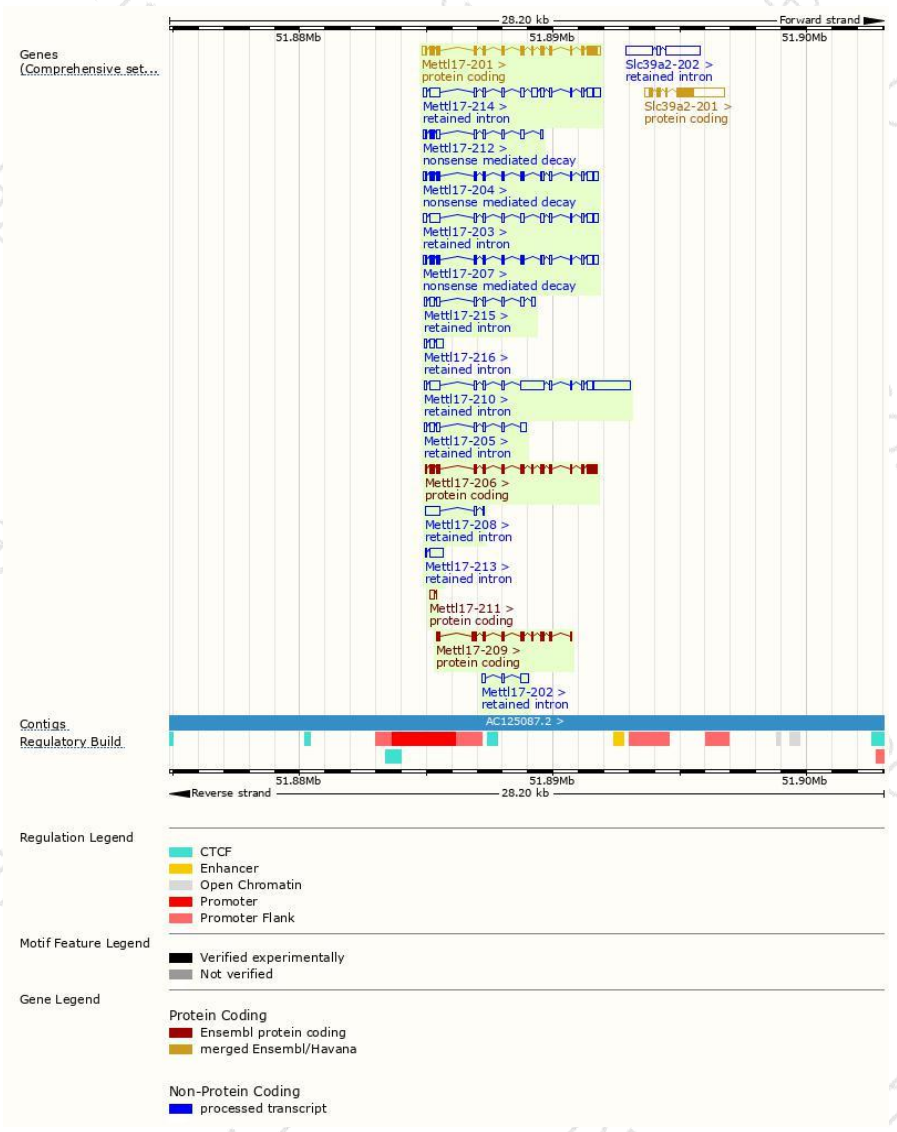
The gene has 16 transcripts,all transcripts are shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Mettl17-201	ENSMUST00000047899.12	1623	461aa	Protein coding	CCDS36913	Q3U2U7	TSL:1 GENCODE basic APPRIS P2
Mettl17-206	ENSMUST00000164902.7	1461	486aa	Protein coding	-	E9Q7K9	TSL:5 GENCODE basic APPRIS ALT2
Mettl17-209	ENSMUST00000165568.2	840	280aa	Protein coding	-	F7AGB5	5' and 3' truncations in transcript evidence prevent annotation of the start and the end of the CDS. CDS 5' and 3' incomplete TSL:5
Mettl17-211	ENSMUST00000167984.1	197	14aa	Protein coding	-	E9PYZ3	CDS 3' incomplete TSL:3
Mettl17-207	ENSMUST00000165100.7	1430	236aa	Nonsense mediated decay	-	E9Q0X9	TSL:1
Mettl17-204	ENSMUST00000164252.7	1426	236aa	Nonsense mediated decay	-	E9Q0X9	TSL:1
Mettl17-212	ENSMUST00000168217.7	809	78aa	Nonsense mediated decay	-	E9Q5R5	TSL:5
Mettl17-210	ENSMUST00000166408.7	3404	No protein	Retained intron	-	-	TSL:2
Mettl17-214	ENSMUST00000168413.7	1844	No protein	Retained intron	-	-	TSL:2
Mettl17-203	ENSMUST00000163603.7	1513	No protein	Retained intron	-	-	TSL:1
Mettl17-215	ENSMUST00000169019.7	890	No protein	Retained intron	-	-	TSL:1
Mettl17-205	ENSMUST00000164801.7	796	No protein	Retained intron	-	-	TSL:2
Mettl17-208	ENSMUST00000165150.1	703	No protein	Retained intron	-	-	TSL:2
Mettl17-213	ENSMUST00000168409.1	582	No protein	Retained intron	-	-	TSL:2
Mettl17-216	ENSMUST00000170887.7	531	No protein	Retained intron	-	-	TSL:2
Mettl17-202	ENSMUST00000077846.6	472	No protein	Retained intron	-	-	TSL:3

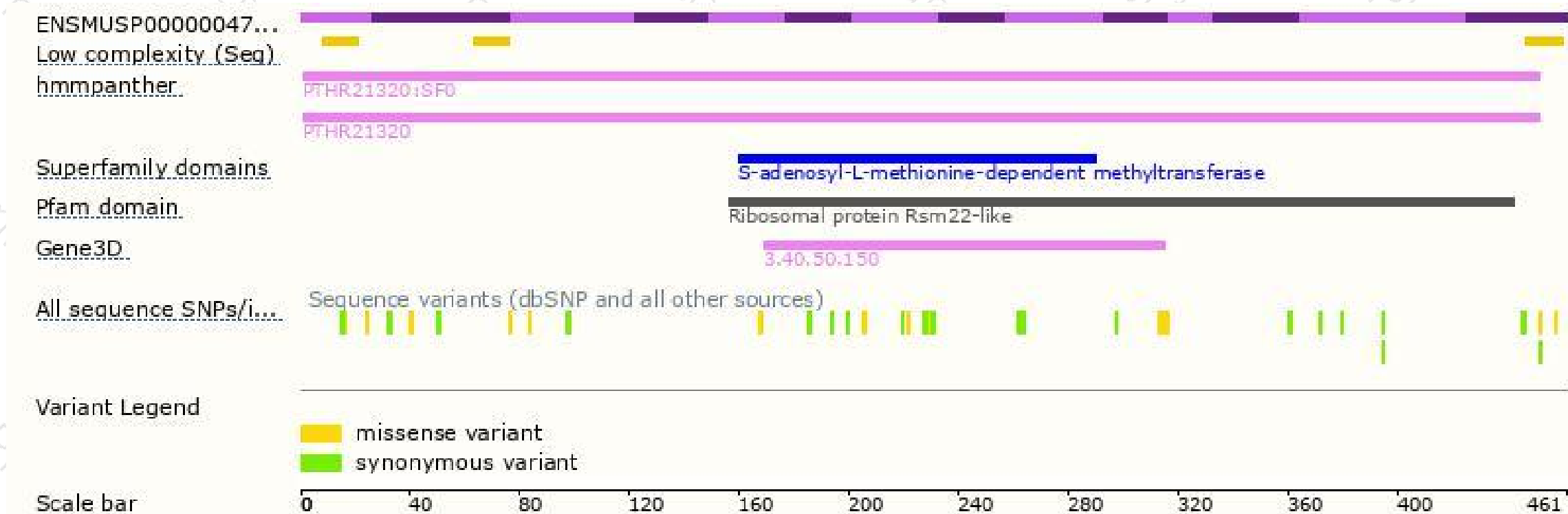
The strategy is based on the design of *Mettl17-201* transcript,The transcription is shown below



Genomic location distribution



Protein domain



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

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