Mms19 Cas9-CKO Strategy

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Date:2020-02-25

Project Overview

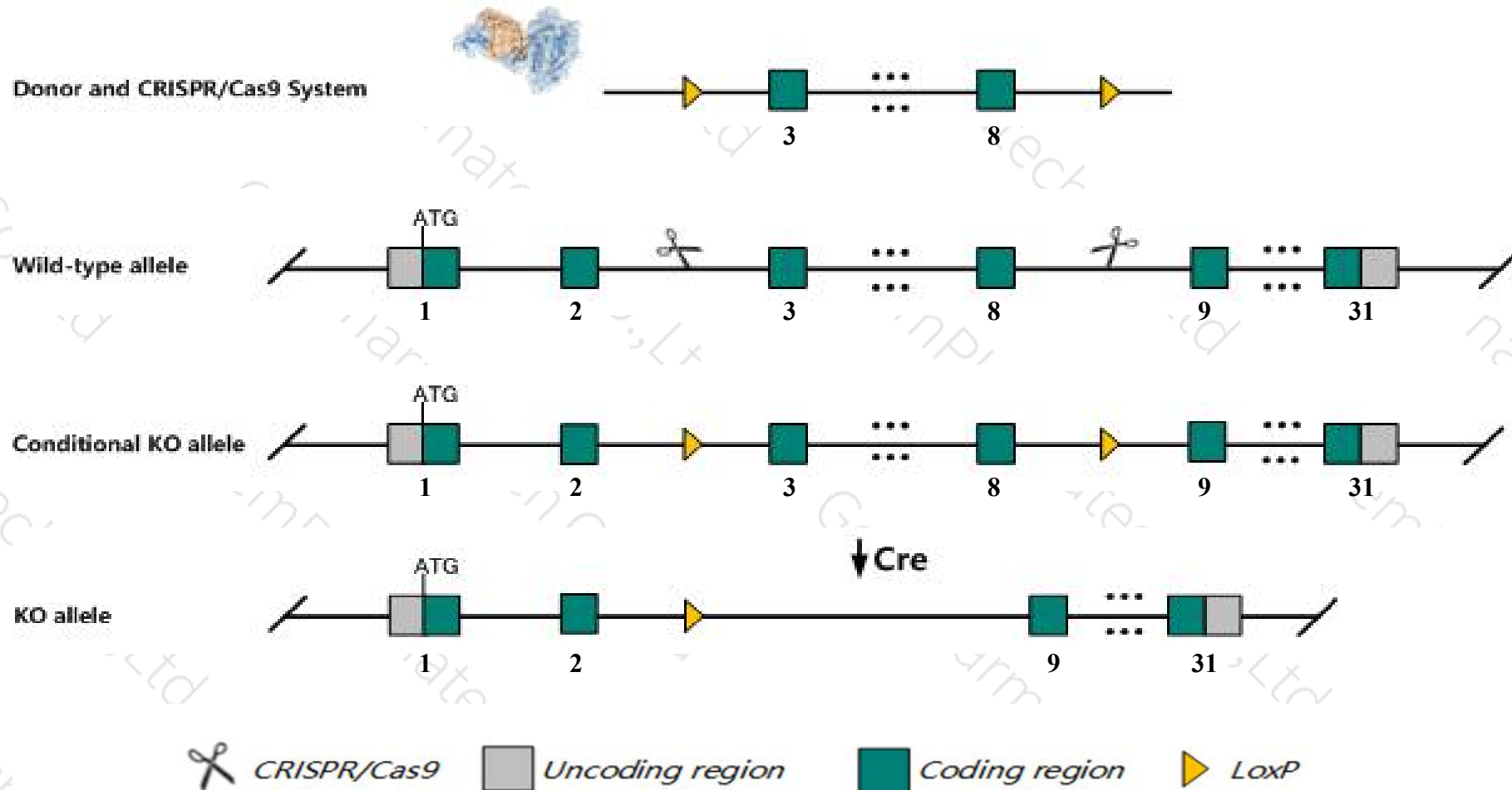|	
Project Name	*Mms19*
Project type	**Cas9-CKO**
Strain background	**C57BL/6JGpt**

Conditional Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *Mms19* gene. The schematic diagram is as follows:

Technical routes

➤ The *Mms19* gene has 18 transcripts. According to the structure of *Mms19* gene, exon3-exon8 of *Mms19-217* (ENSMUST00000171561.7) transcript is recommended as the knockout region.The region contains Ens 523bp coding sequence. Knock out the region will result in disruption of protein function.

➤ In this project we use CRISPR/Cas9 technology to modify *Mms19* 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

➤ The effect on transcript *Mms19*-208&212 is unknown.

➤ Transcript *Mms19*-205&206&207&211&214 may not be affected.

➤ The *Mms19* gene is located on the Chr19. 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）

Mms19   MMS19 cytosolic iron-sulfur assembly component [*Mus musculus* (house mouse)]

Gene ID: 72199, updated on 6-Sep-2019

▲ Summary

Official Symbol	Mms19 provided by MGI
Official Full Name	MMS19 cytosolic iron-sulfur assembly component provided by MGI
Primary source	MGI:MGI:1919449
See related	Ensembl:ENSMUSG00000025159
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	C79368; C86341; Mms19l; AI316855; 2410001K24Rik; 2610042O15Rik
Expression	Ubiquitous expression in thymus adult (RPKM 24.9), ovary adult (RPKM 20.0) and 28 other tissues See more
Orthologs	human all

▲ Genomic context

Location: 19; 19 C3

See Mms19 in Genome Data Viewer

Exon count: 32

| Annotation release	Status	Assembly	Chr	Location
108	current	GRCm38.p6 (GCF_000001635.26)	19	NC_000085.6 (41943707..41981207, complement)
Build 37.2	previous assembly	MGSCv37 (GCF_000001635.18)	19	NC_000085.5 (42018197..42055626, complement)

Transcript information（Ensembl）

The gene has 18 transcripts,all transcripts are shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Mms19-217	ENSMUST00000171561.7	6607	1031aa	Protein coding	CCDS29818	Q9D071	TSL:1 GENCODE basic APPRIS P2
Mms19-201	ENSMUST00000026168.8	3162	988aa	Protein coding	-	Q9D071	TSL:5 GENCODE basic APPRIS ALT2
Mms19-202	ENSMUST00000163287.7	3002	885aa	Protein coding	-	F7C9N6	CDS 5' incomplete TSL:5
Mms19-208	ENSMUST00000167820.1	859	286aa	Protein coding	-	F6RGK4	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
Mms19-212	ENSMUST00000169765.1	387	129aa	Protein coding	-	F6TJQ8	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
Mms19-209	ENSMUST00000167927.7	7875	357aa	Nonsense mediated decay	-	E9PW47	TSL:2
Mms19-204	ENSMUST00000164776.7	3412	75aa	Nonsense mediated decay	-	E9PUY8	TSL:5
Mms19-203	ENSMUST00000163398.7	3378	75aa	Nonsense mediated decay	-	E9PUY8	TSL:5
Mms19-213	ENSMUST00000169775.7	2630	174aa	Nonsense mediated decay	-	E9Q5T0	TSL:1
Mms19-210	ENSMUST00000168484.7	2368	357aa	Nonsense mediated decay	-	E9PW47	TSL:1
Mms19-206	ENSMUST00000166090.7	1859	501aa	Nonsense mediated decay	-	F7A0X7	CDS 5' incomplete TSL:5
Mms19-216	ENSMUST00000170209.7	3780	No protein	Retained intron	-	-	TSL:1
Mms19-218	ENSMUST00000171755.7	2810	No protein	Retained intron	-	-	TSL:1
Mms19-207	ENSMUST00000166517.1	807	No protein	Retained intron	-	-	TSL:5
Mms19-205	ENSMUST00000165043.1	599	No protein	Retained intron	-	-	TSL:3
Mms19-214	ENSMUST00000169779.1	432	No protein	Retained intron	-	-	TSL:2
Mms19-215	ENSMUST00000169933.1	240	No protein	Retained intron	-	-	TSL:3
Mms19-211	ENSMUST00000168737.1	141	No protein	Retained intron	-	-	TSL:3

The strategy is based on the design of *Mms19-217* transcript,The transcription is shown below

< Mms19-217
protein coding

◄ Reverse strand

40.07 kb
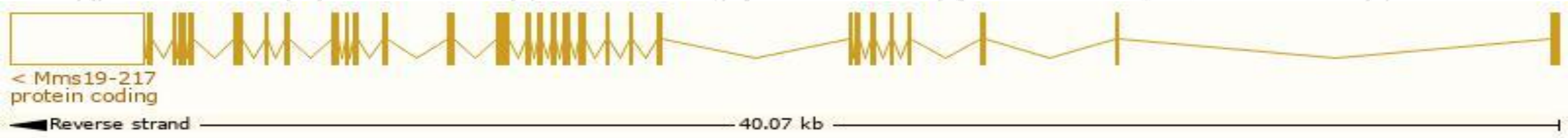
Genomic location distribution
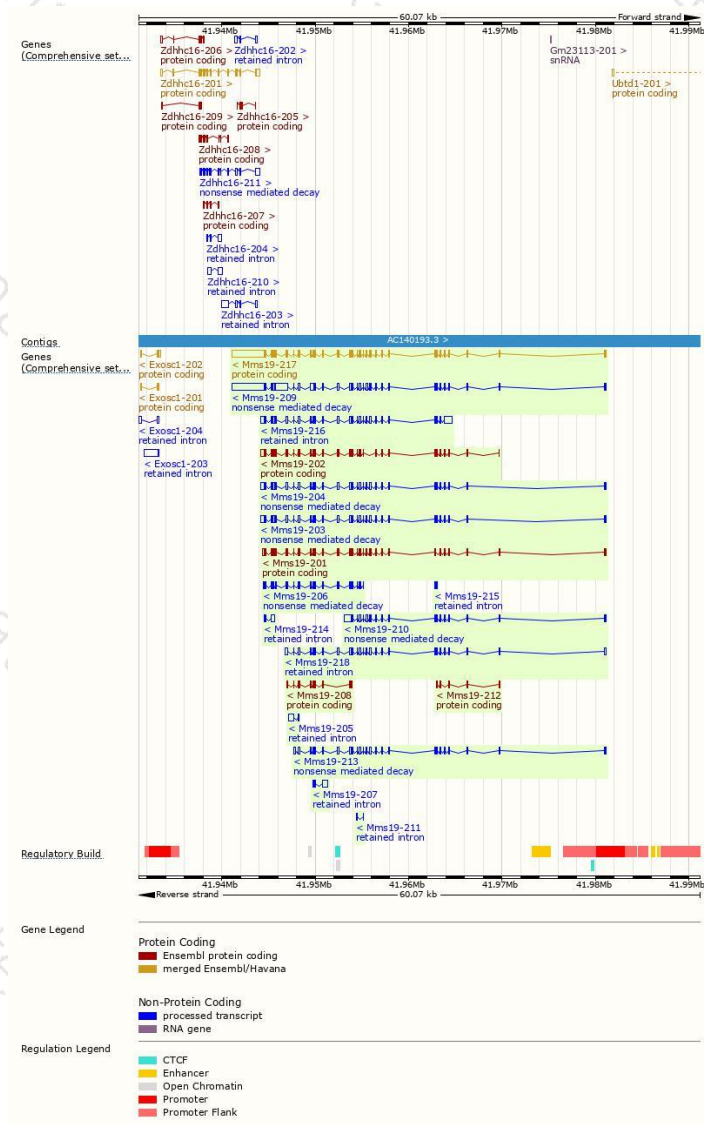
Protein domain
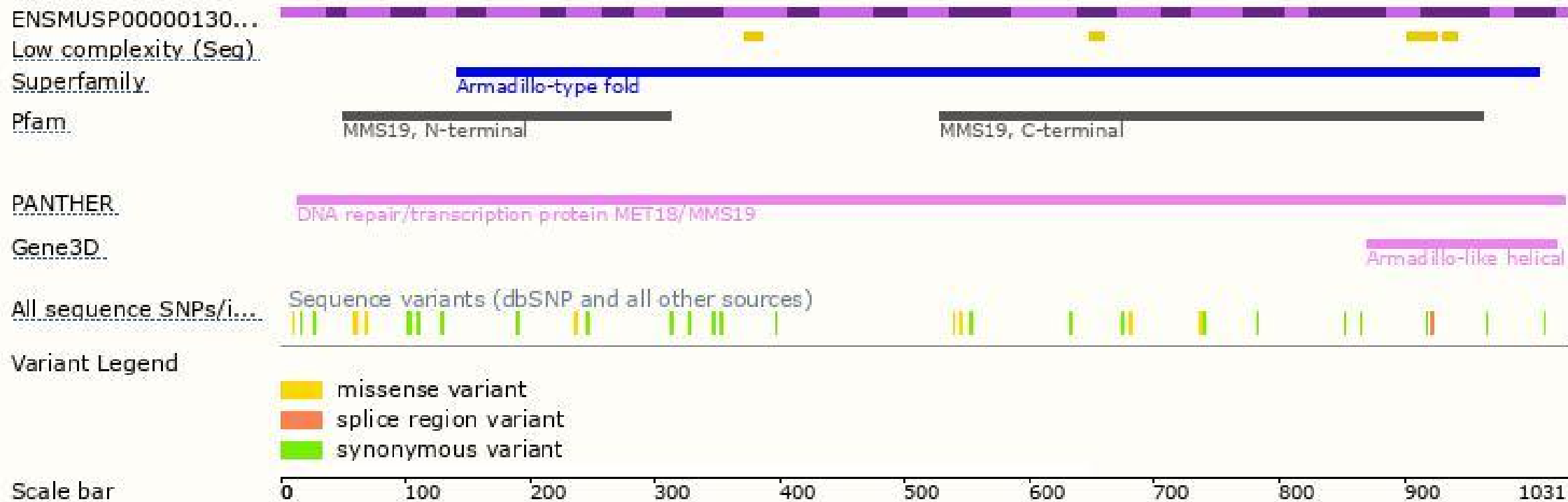
If you have any questions, you are welcome to inquire.
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