

***Mettl8* Cas9-KO Strategy**

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Project Overview

Project Name

Mettl8

Project type

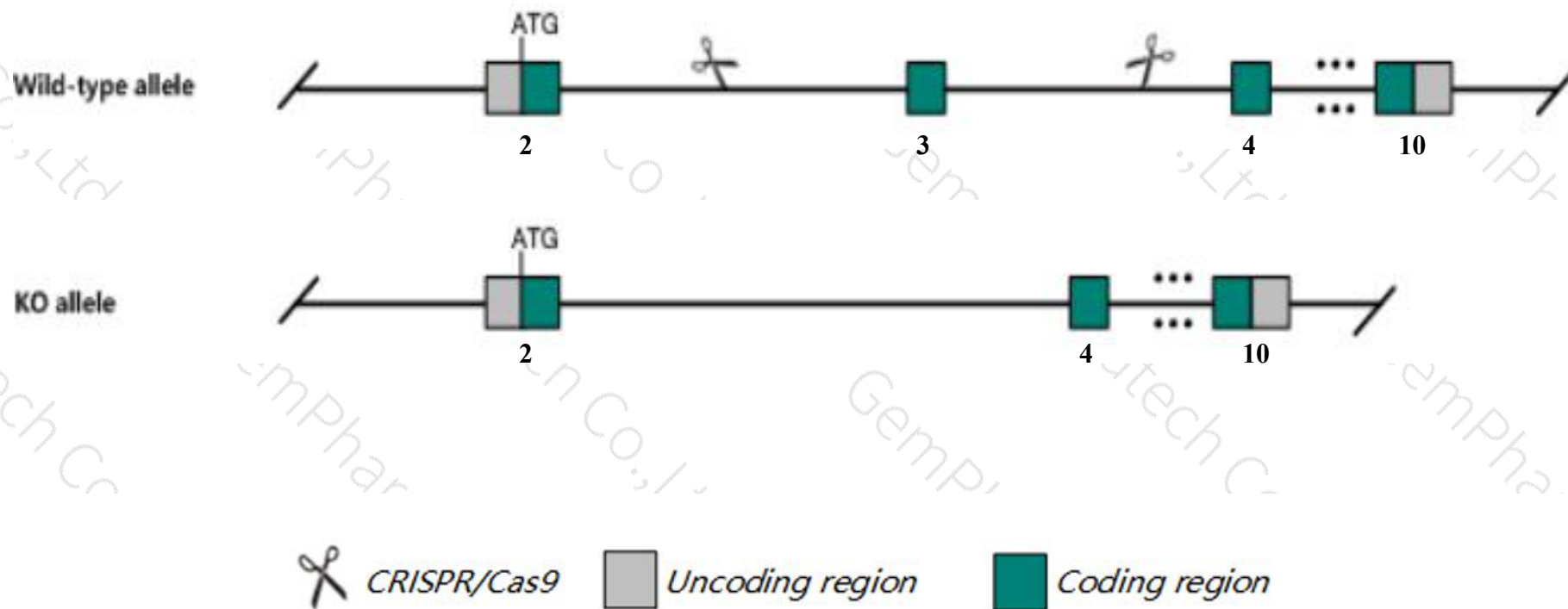
Cas9-KO

Strain background

C57BL/6JGpt

Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *Mettl8* gene. The schematic diagram is as follows:



- The *Mettl8* gene has 11 transcripts. According to the structure of *Mettl8* gene, exon3 of *Mettl8*-204(ENSMUST00000112186.8) transcript is recommended as the knockout region. The region contains 92bp coding sequence. Knock out the region will result in disruption of protein function.
- In this project we use CRISPR/Cas9 technology to modify *Mettl8* gene. The brief process is as follows: CRISPR/Cas9 system 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.

- According to the existing MGI data, mice homozygous for a knock-out allele exhibit reduced 3-methylcytidine (m3C) methyltransferases modification of mRNA.
- The *Mettl8* gene is located on the Chr2. 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)

Mettl8 methyltransferase like 8 [Mus musculus (house mouse)]

Gene ID: 228019, updated on 13-Mar-2020

Summary



Official Symbol Mettl8 provided by [MGI](#)

Official Full Name methyltransferase like 8 provided by [MGI](#)

Primary source [MGI:MGI:2385142](#)

See related [Ensembl:ENSMUSG00000041975](#)

Gene type protein coding

RefSeq status REVIEWED

Organism [Mus musculus](#)

Lineage Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Myomorpha; Muroidea; Muridae; Murinae; Mus; Mus

Also known as BC004636, Tip

Summary This locus encodes a member of the methyltransferase family, and is involved in chromatin remodeling. Transcripts from this locus can be induced or inhibited by cell stretch and affect cell differentiation in the myogenic or adipogenic pathways. Multiple transcript variants encoding different isoforms have been found for this gene. Additional splice variants have been described in the literature but they meet nonsense-mediated decay (NMD) criteria and are likely to be degraded as soon as they are transcribed. [provided by RefSeq, Jul 2008]

Expression Ubiquitous expression in thymus adult (RPKM 2.3), CNS E11.5 (RPKM 2.1) and 28 other tissues [See more](#)

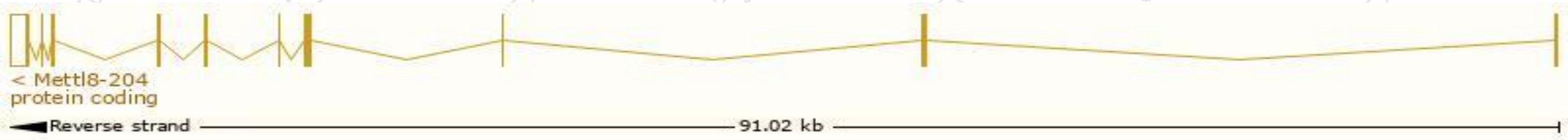
Orthologs [human](#) [all](#)

Transcript information (Ensembl)

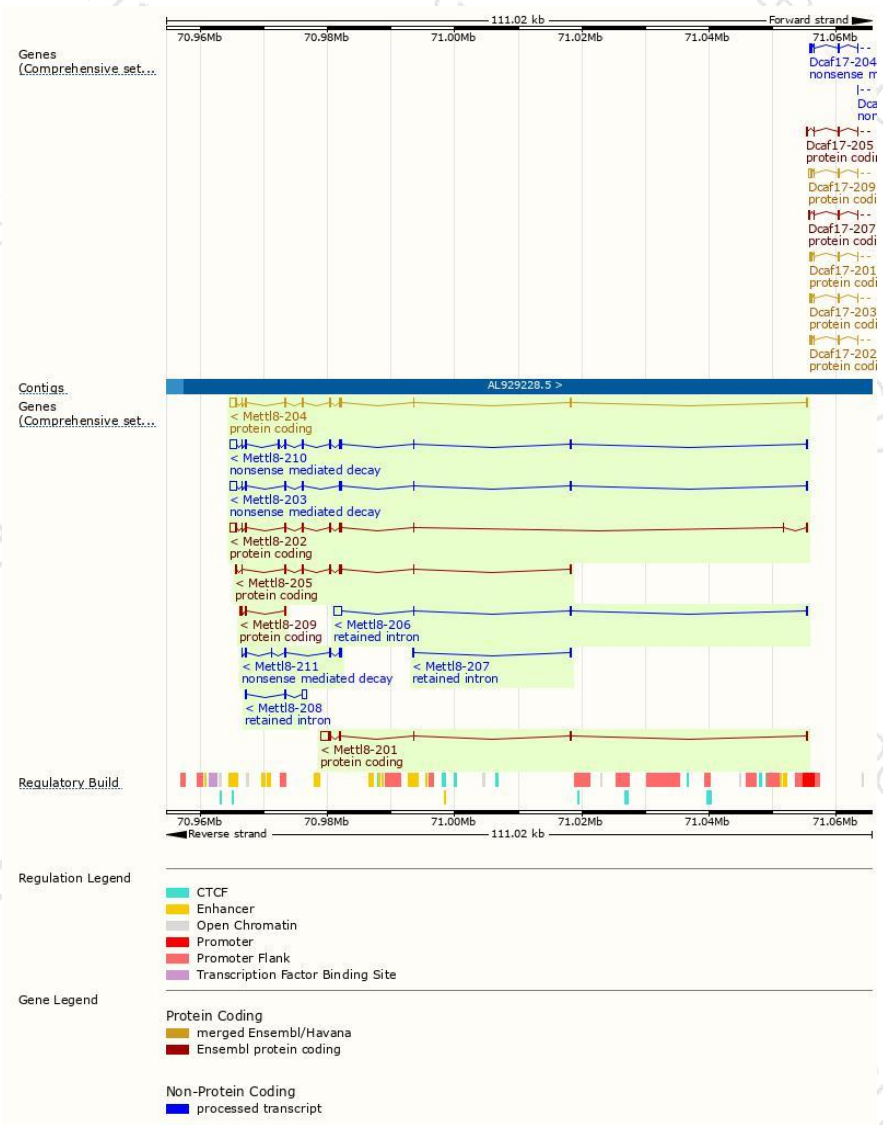
The gene has 11 transcripts,all transcripts are shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Mettl8-204	ENSMUST00000112186.8	2347	388aa	Protein coding	CCDS50600	A2AUU0	TSL:2 GENCODE basic APPRIS P2
Mettl8-202	ENSMUST00000100037.8	2254	341aa	Protein coding	-	B0R0U1	TSL:1 GENCODE basic APPRIS ALT2
Mettl8-201	ENSMUST00000090849.5	1842	163aa	Protein coding	-	Q8CA70	TSL:1 GENCODE basic
Mettl8-205	ENSMUST00000121586.7	1151	281aa	Protein coding	-	A2AUU0	TSL:5 GENCODE basic
Mettl8-209	ENSMUST00000140293.1	592	110aa	Protein coding	-	F6W103	CDS 5' incomplete TSL:3
Mettl8-210	ENSMUST00000148876.7	2473	304aa	Nonsense mediated decay	-	A2AUU0	TSL:1
Mettl8-203	ENSMUST00000112179.8	2297	206aa	Nonsense mediated decay	-	A2AUU0	TSL:2
Mettl8-211	ENSMUST00000149181.7	743	148aa	Nonsense mediated decay	-	F6Q7P7	CDS 5' incomplete TSL:5
Mettl8-206	ENSMUST00000124208.1	1597	No protein	Retained intron	-	-	TSL:1
Mettl8-208	ENSMUST00000124781.1	833	No protein	Retained intron	-	-	TSL:5
Mettl8-207	ENSMUST00000124273.1	390	No protein	Retained intron	-	-	TSL:5

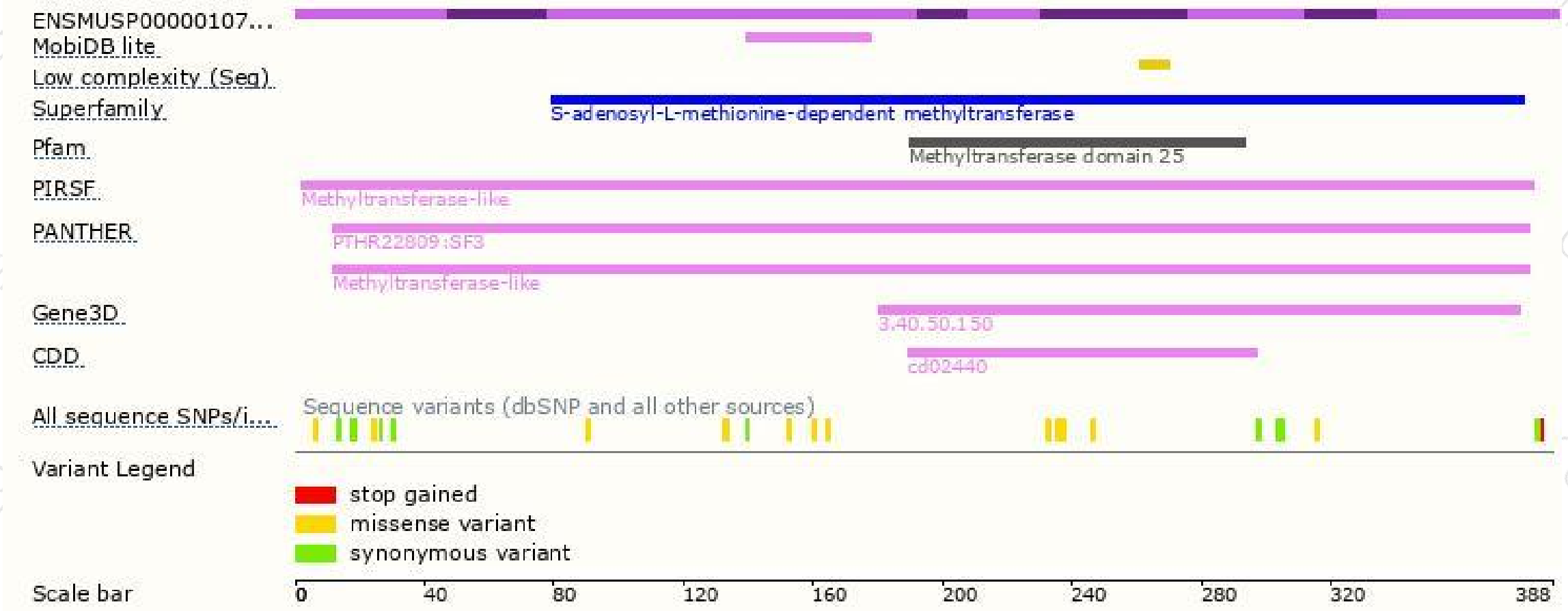
The strategy is based on the design of *Mettl8-204* transcript,the transcription is shown below:



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, mice homozygous for a knock-out allele exhibit reduced 3-methylcytidine (m3C) methyltransferases modification of mRNA.

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

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