Mettl1 Cas9-CKO Strategy

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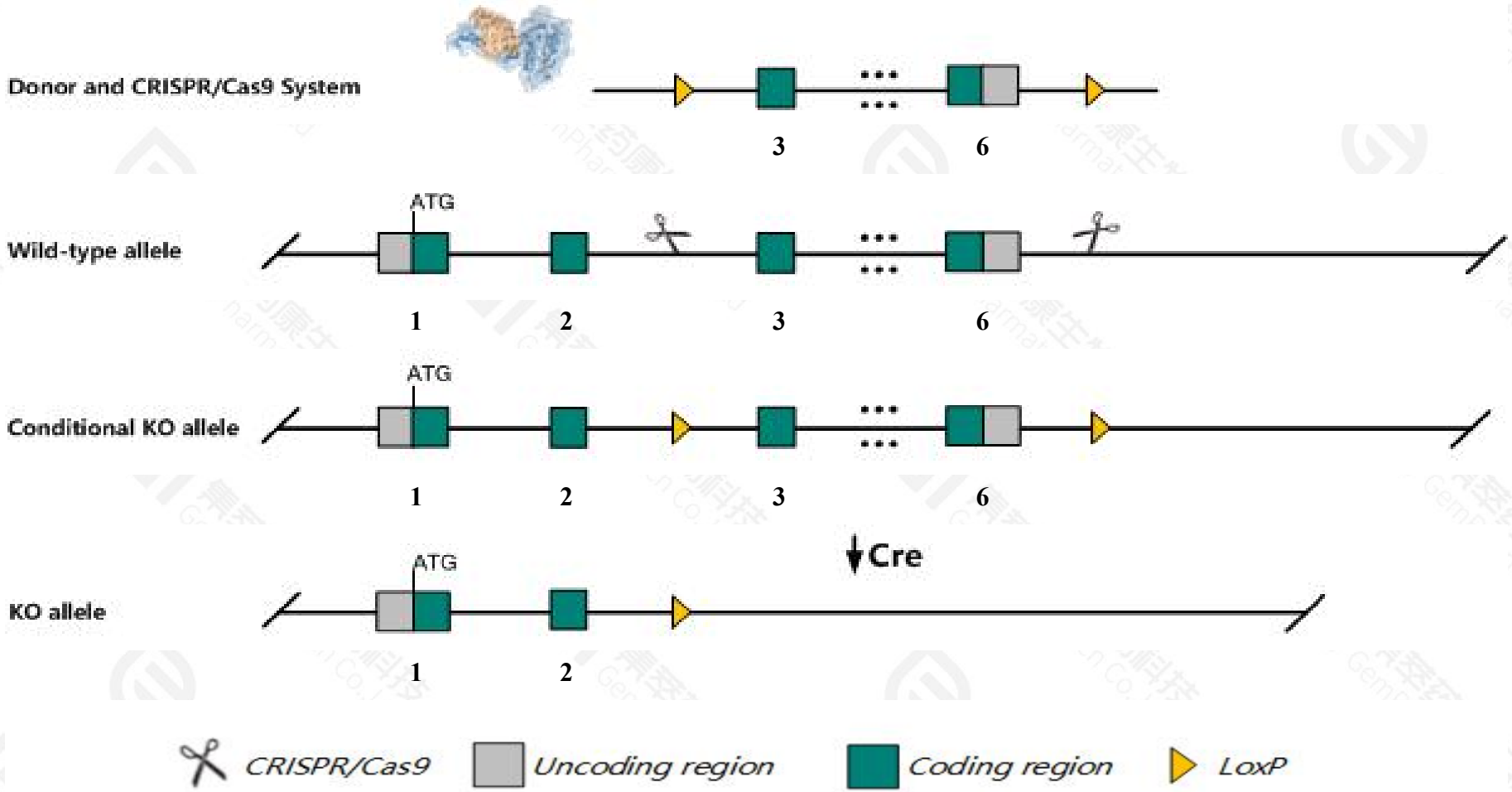
Project Overview

Project Name	***Mettl1***
Project type	**Cas9-CKO**
Strain background	**C57BL/6JGpt**

Conditional Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *Mettl1* gene. The schematic diagram is as follows:



Technical routes

➢ The *Mettl1* gene has 5 transcripts. According to the structure of *Mettl1* gene, exon3-exon6 of *Mettl1-201*(ENSMUST00000006915.14) transcript is recommended as the knockout region.The region contains most 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 *Mettl1* 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 KO region contains functional region of the *Cyp27b1* and *Eef1akmt3* gene.Knockout the region may affect the function of *Cyp27b1* and *Eef1akmt3* gene.

➢ The *Mettl1* gene is located on the Chr10. 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）

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Mettl1 methyltransferase like 1 [Mus musculus (house mouse)]

Gene ID: 17299, updated on 17-Dec-2020

Summary

Official Symbol	Mettl1 provided by MGI
Official Full Name	methyltransferase like 1 provided byMGI
Primary source	MGI:MGI:1339986
See related	Ensembl:ENSMUSG00000006732
Gene type	protein coding
RefSeq status	PROVISIONAL
Organism	Mus musculus
Lineage	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Myomorpha; Muroidea; Muridae; Murinae; Mus; Mus
Also known as	2810012D02Rik
Expression	Ubiquitous expression in limb E14.5 (RPKM 10.7), placenta adult (RPKM 9.1) and 28 other tissuesSee more
Orthologs	human all

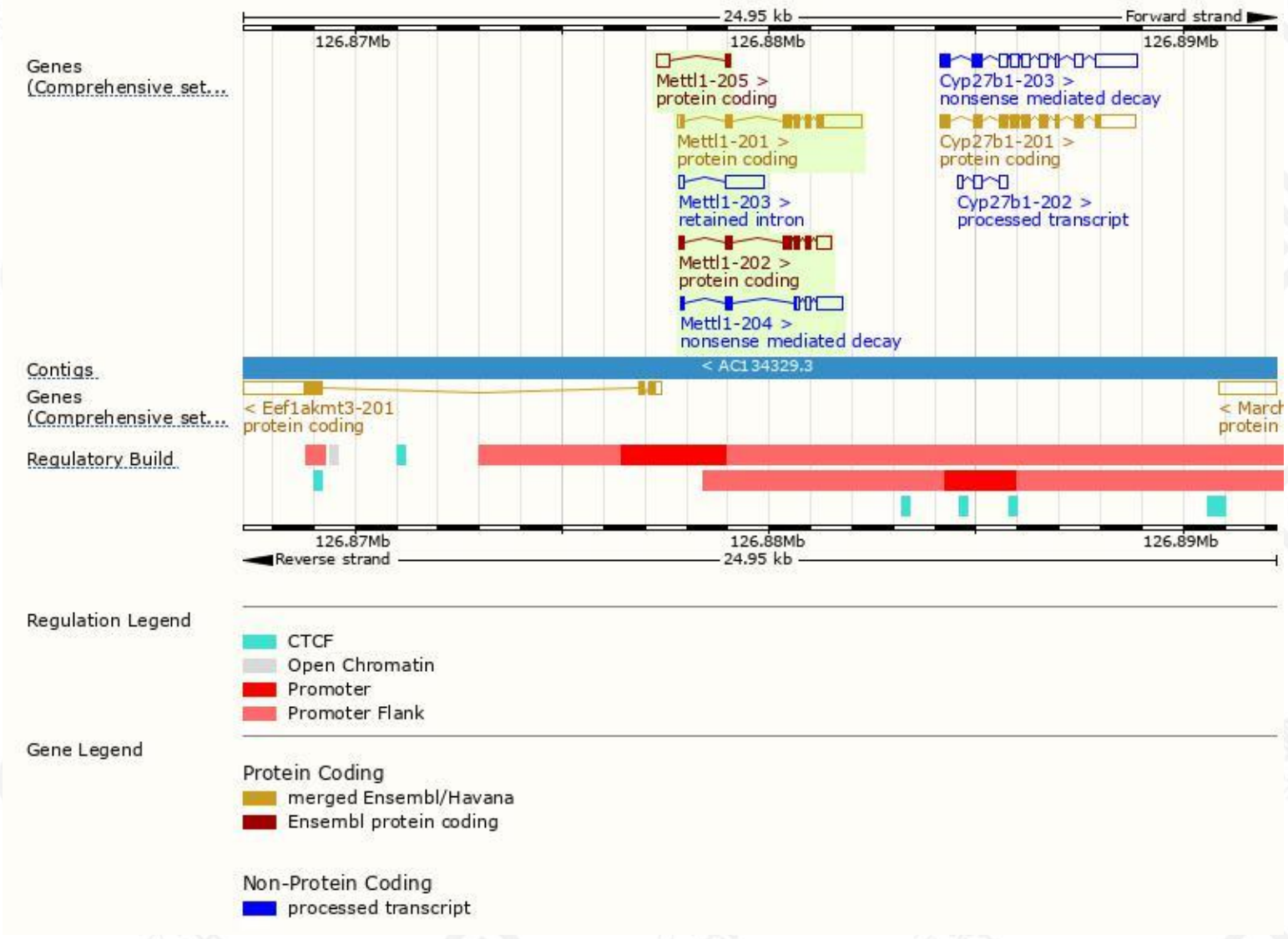
Transcript information（Ensembl）

The gene has 5 transcripts,all transcripts are shown below:

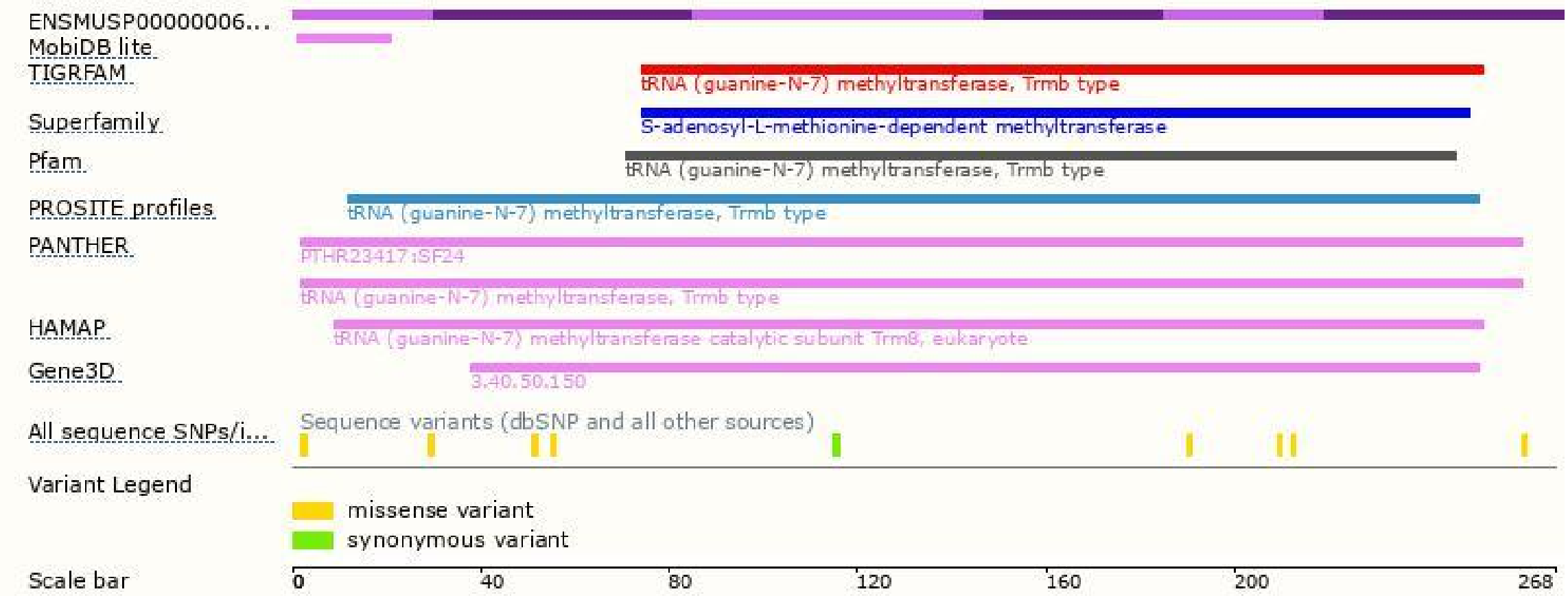
Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Mettl1-201	ENSMUST00000006915.14	1791	268aa	Protein coding	CCDS24223		TSL:1 , GENCODE basic , APPRIS P1 ,
Mettl1-202	ENSMUST00000120542.8	1044	228aa	Protein coding	-		TSL:1 , GENCODE basic ,
Mettl1-205	ENSMUST00000152960.2	431	34aa	Protein coding	-		CDS 3' incomplete , TSL:3 ,
Mettl1-204	ENSMUST00000139486.2	1089	97aa	Nonsense mediated decay	-		CDS 5' incomplete , TSL:5 ,
Mettl1-203	ENSMUST00000135655.2	1057	No protein	Retained intron	-		TSL:1 ,

The strategy is based on the design of *Mettl1-201* transcript,the transcription is shown below:

Genomic location distribution



Protein domain



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