Mat2b Cas9-KO Strategy

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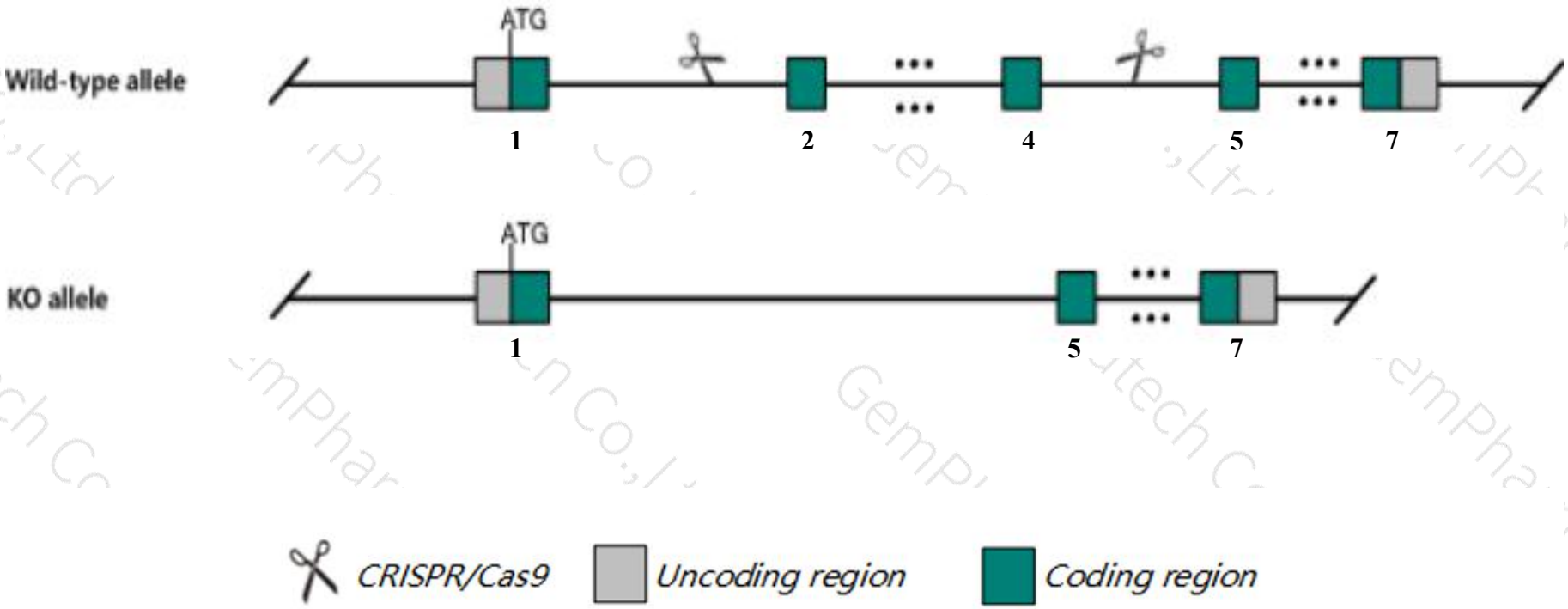
Project Overview

Project Name	***Mat2b***
Project type	**Cas9-KO**
Strain background	**C57BL/6JGpt**

Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *Mat2b* gene. The schematic diagram is as follows:



Technical routes

➢ The *Mat2b* gene has 7 transcripts. According to the structure of *Mat2b* gene, exon2-exon4 of *Mat2b-201* (ENSMUST00000040167.10) transcript is recommended as the knockout region.The region contains 463bp coding sequence. Knock out the region will result in disruption of protein function.

➢ In this project we use CRISPR/Cas9 technology to modify *Mat2b* gene. The brief process is as follows: CRISPR/Cas9 system

Notice

- The *Mat2b* gene is located on the Chr11. 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）

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Mat2b methionine adenosyltransferase II, beta [Mus musculus (house mouse)]

Gene ID: 108645, updated on 13-Mar-2020

Summary

Official Symbol	Mat2b provided by MGI
Official Full Name	methionine adenosyltransferase II, beta provided byMGI
Primary source	MGI:MGI:1913667
See related	Ensembl:ENSMUSG00000042032
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	1110064C04Rik, 2410018D16Rik, AI182287, AU022853, MAT-II, MATIIbeta, TGR
Expression	Ubiquitous expression in cortex adult (RPKM 34.1), bladder adult (RPKM 28.8) and 28 other tissuesSee more
Orthologs	human all

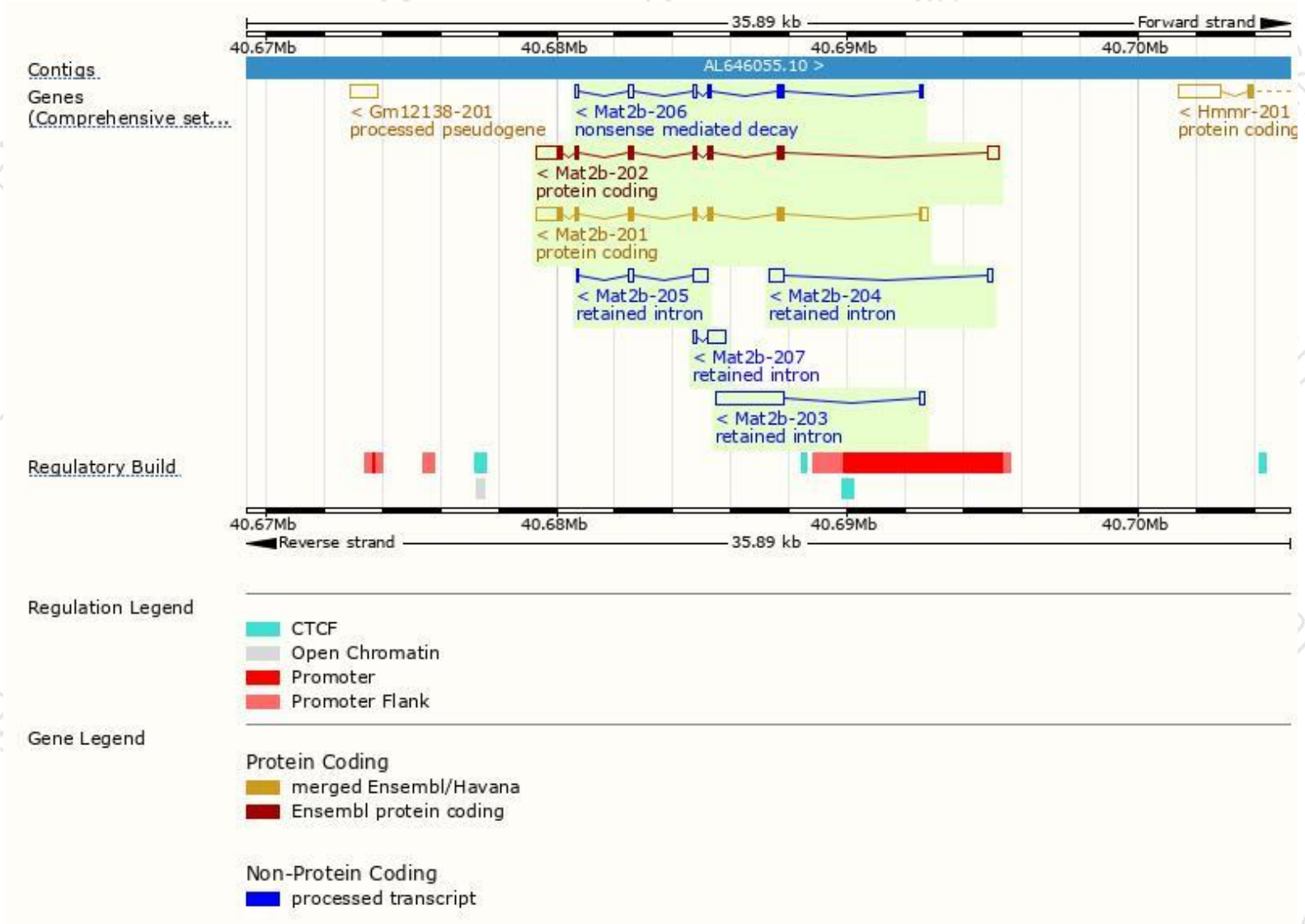
Transcript information（Ensembl）

The gene has 7 transcripts,all transcripts are shown below:

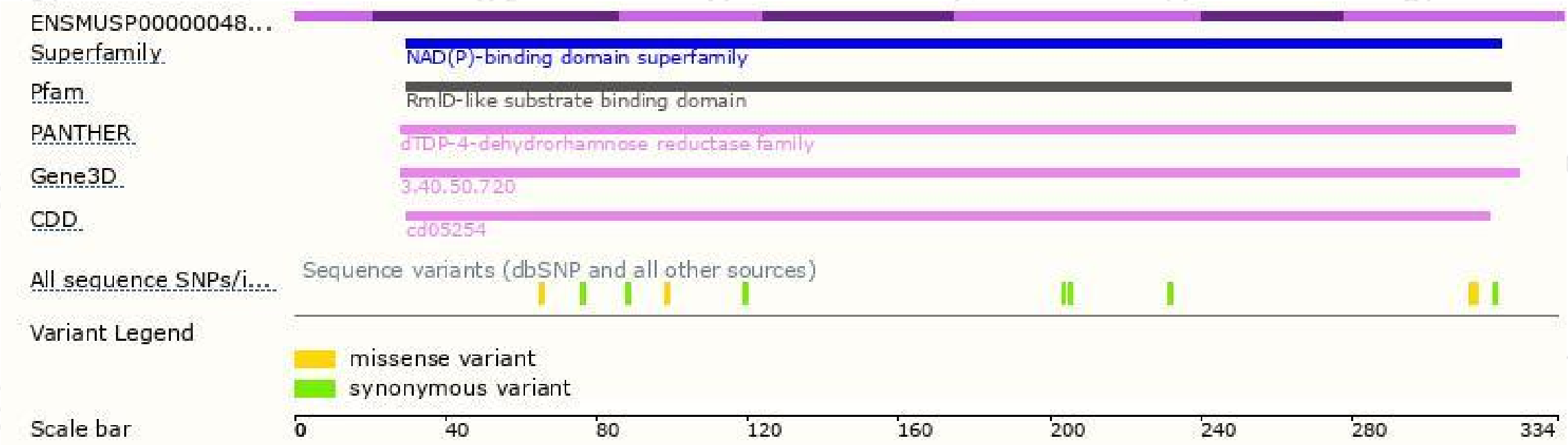
Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Mat2b-202	ENSMUST00000101347.9	2053	323aa	Protein coding	CCDS56767	Q99LB6	TSL:1 GENCODE basic APPRIS ALT1
Mat2b-201	ENSMUST00000040167.10	1949	334aa	Protein coding	CCDS24547	Q99LB6	TSL:1 GENCODE basic APPRIS P3
Mat2b-206	ENSMUST00000141830.7	887	102aa	Nonsense mediated decay	-	E0CYU5	TSL:3
Mat2b-203	ENSMUST00000109307.1	2461	No protein	Retained intron	-	-	TSL:1
Mat2b-205	ENSMUST00000137797.1	800	No protein	Retained intron	-	-	TSL:3
Mat2b-207	ENSMUST00000156867.1	732	No protein	Retained intron	-	-	TSL:3
Mat2b-204	ENSMUST00000135617.1	644	No protein	Retained intron	-	-	TSL:2

The strategy is based on the design of *Mat2b-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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