Nt5m Cas9-KO Strategy

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Project Overview

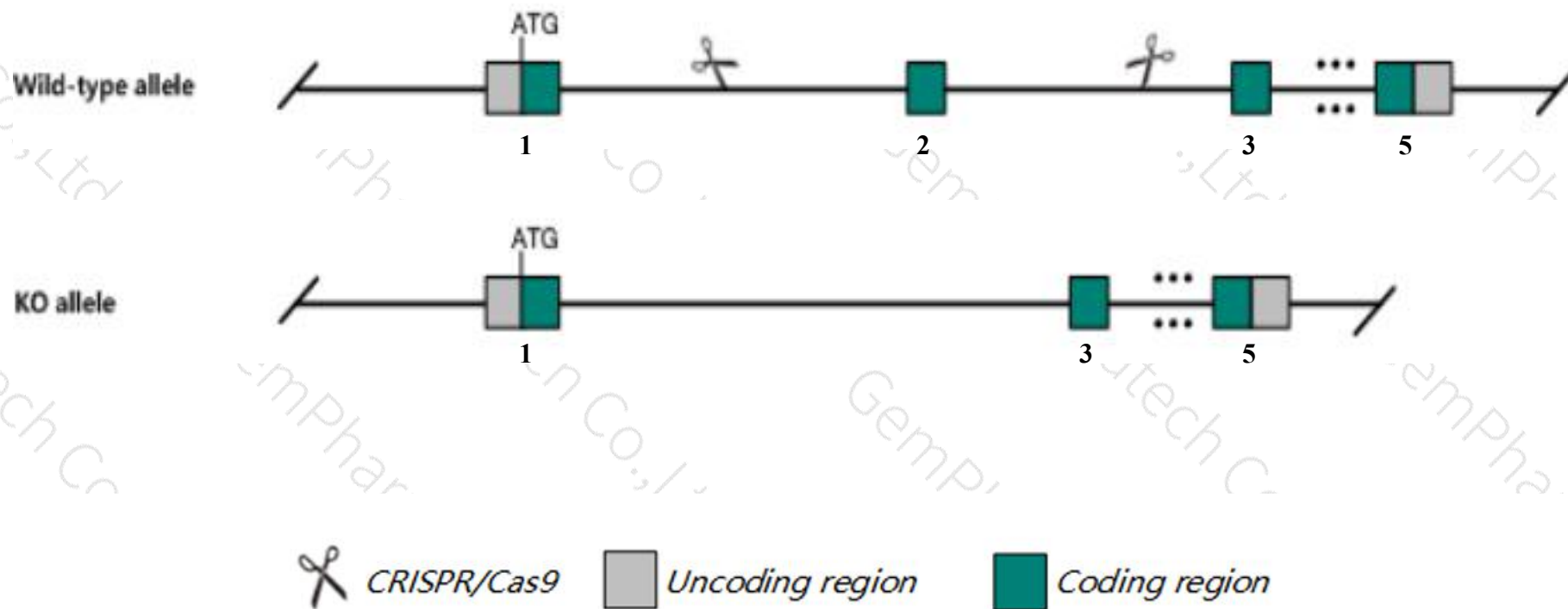|	
Project Name	*Nt5m*
Project type	**Cas9-KO**
Strain background	**C57BL/6JGpt**

Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *Nt5m* gene. The schematic diagram is as follows:

Technical routes

➢ The *Nt5m* gene has 4 transcripts. According to the structure of *Nt5m* gene, exon2 of *Nt5m-201*

(ENSMUST00000102695.3) transcript is recommended as the knockout region.The region contains 101bp coding sequence.

Knock out the region will result in disruption of protein function.

➢ In this project we use CRISPR/Cas9 technology to modify *Nt5m* gene. The brief process is as follows: CRISPR/Cas9 system

Notice

➢ The *Nt5m* 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）

Nt5m 5',3'-nucleotidase, mitochondrial [Mus musculus (house mouse)]

Gene ID: 103850, updated on 20-Mar-2020

▲Summary

Official Symbol	Nt5m provided by MGI
Official Full Name	5',3'-nucleotidase, mitochondrial provided by MGI
Primary source	MGI:MGI:1917127
See related	Ensembl:ENSMUSG00000032615
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	2010013E09Rik, AI846937, dNT-2
Expression	Ubiquitous expression in testis adult (RPKM 20.3), adrenal adult (RPKM 18.6) and 28 other tissuesSee more
Orthologs	human all

Transcript information（Ensembl）

The gene has 4 transcripts,all transcripts are shown below:

| Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Nt5m-201	ENSMUST00000102695.3	1306	220aa	Protein coding	CCDS24779	Q8VCE6	TSL:1 GENCODE basic APPRIS is a system to annotate alternatively spliced transcripts based on a range of computational methods to identify the most functionally important transcript(s) of a gene. APPRIS P1
Nt5m-204	ENSMUST00000154699.7	2220	No protein	Processed transcript	-	-	TSL:1
Nt5m-202	ENSMUST00000137695.1	1387	No protein	Processed transcript	-	-	TSL:2
Nt5m-203	ENSMUST00000149076.7	1316	No protein	Processed transcript	-	-	TSL:1

The strategy is based on the design of *Nt5m-201* transcript,The transcription is shown below
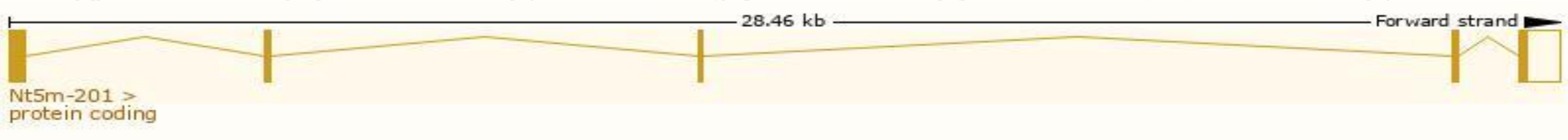
Genomic location distribution

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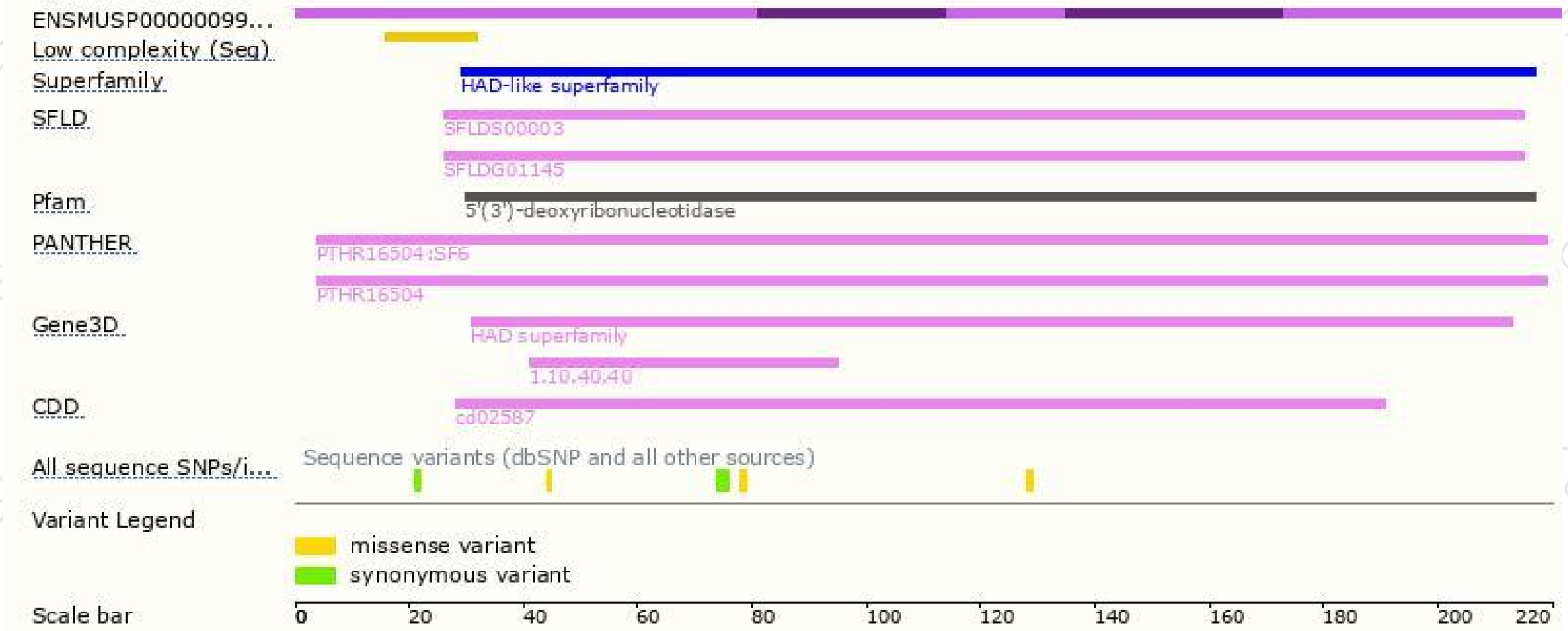
If you have any questions, you are welcome to inquire.
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