

***Mettl14* Cas9-KO Strategy**

Designer:

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Design Date:

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Project Overview

Project Name

Mettl14

Project type

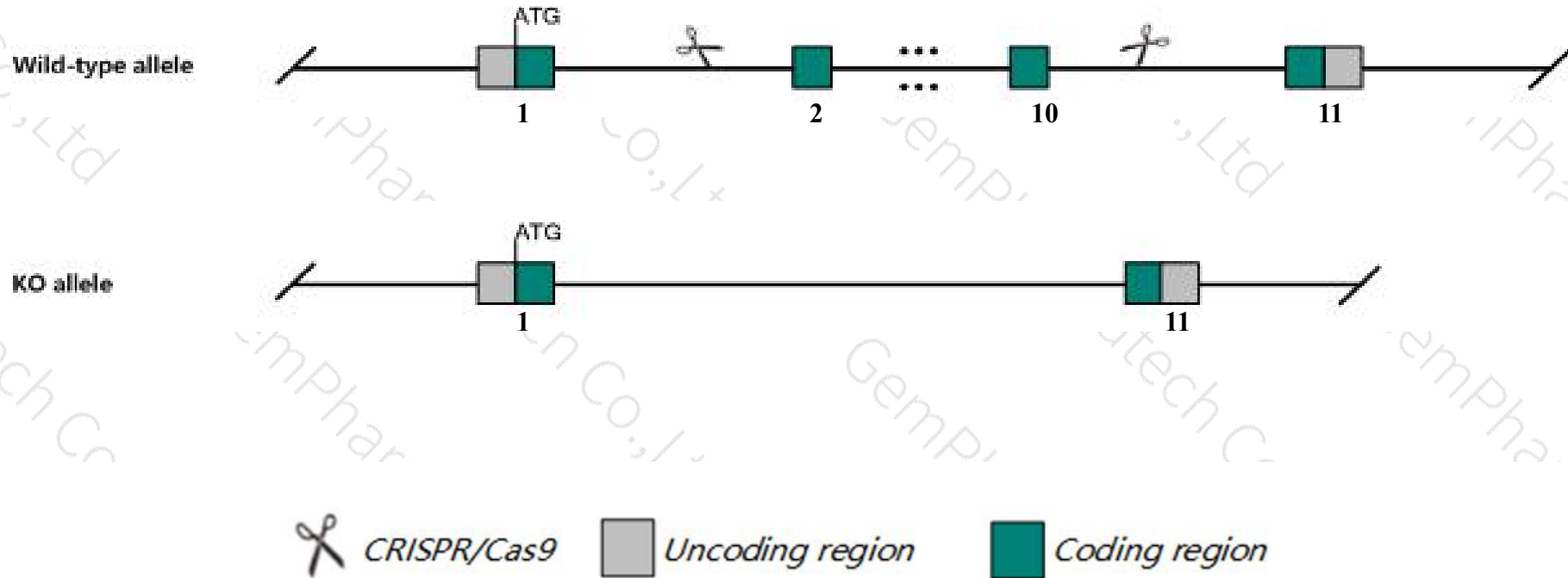
Cas9-KO

Strain background

C57BL/6JGpt

Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *Mettl14* gene. The schematic diagram is as follows:



- The *Mettl14* gene has 5 transcripts. According to the structure of *Mettl14* gene, exon2-exon10 of *Mettl14-201* (ENSMUST00000029759.15) transcript is recommended as the knockout region. The region contains 1000bp coding sequence. Knock out the region will result in disruption of protein function.
- In this project we use CRISPR/Cas9 technology to modify *Mettl14* gene. The brief process is as follows: CRISPR/Cas9 system

- The *Mettl14* gene is located on the Chr3. 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)

Mettl14 methyltransferase like 14 [Mus musculus (house mouse)]

Gene ID: 210529, updated on 12-Feb-2019

Summary



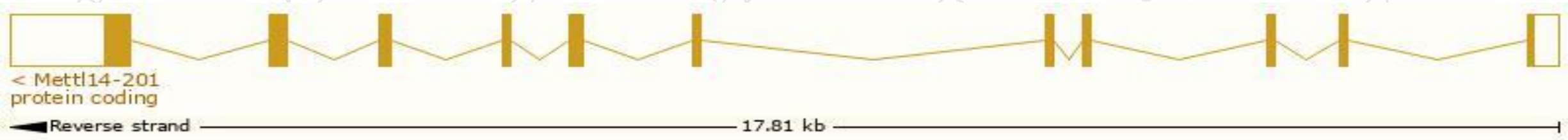
Official Symbol	Mettl14 provided by MGI
Official Full Name	methyltransferase like 14 provided by MGI
Primary source	MGI:MGI:2442926
See related	Ensembl:ENSMUSG00000028114
Gene type	protein coding
RefSeq status	VALIDATED
Organism	Mus musculus
Lineage	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Myomorpha; Muroidea; Muridae; Murinae; Mus; Mus
Also known as	G430022H21Rik, mKIAA1627
Expression	Ubiquitous expression in CNS E11.5 (RPKM 10.1), CNS E14 (RPKM 6.0) and 28 other tissues See more
Orthologs	human all

Transcript information (Ensembl)

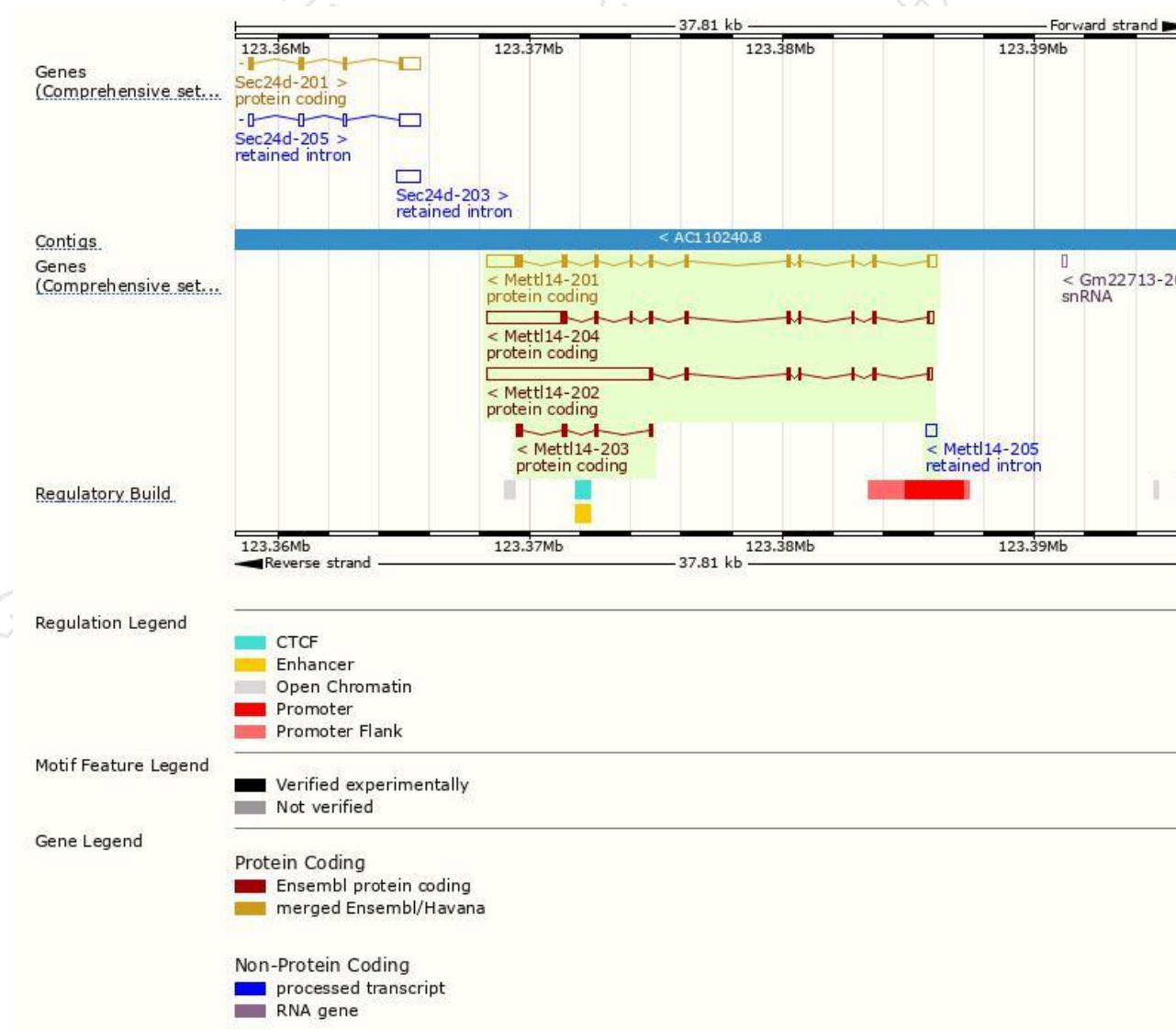
The gene has 5 transcripts,all transcripts are shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Mettl14-201	ENSMUST00000029759.15	2741	456aa	Protein coding	CCDS38622	Q3UIK4	TSL:1 GENCODE basic APPRIS P1
Mettl14-202	ENSMUST00000090371.13	7197	217aa	Protein coding	-	E9QPC5	TSL:1 GENCODE basic
Mettl14-204	ENSMUST00000174323.5	4202	377aa	Protein coding	-	G3UYS3	TSL:1 GENCODE basic
Mettl14-203	ENSMUST00000174006.4	634	211aa	Protein coding	-	G3UXL6	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
Mettl14-205	ENSMUST00000197628.1	382	No protein	Retained intron	-	-	TSL:NA

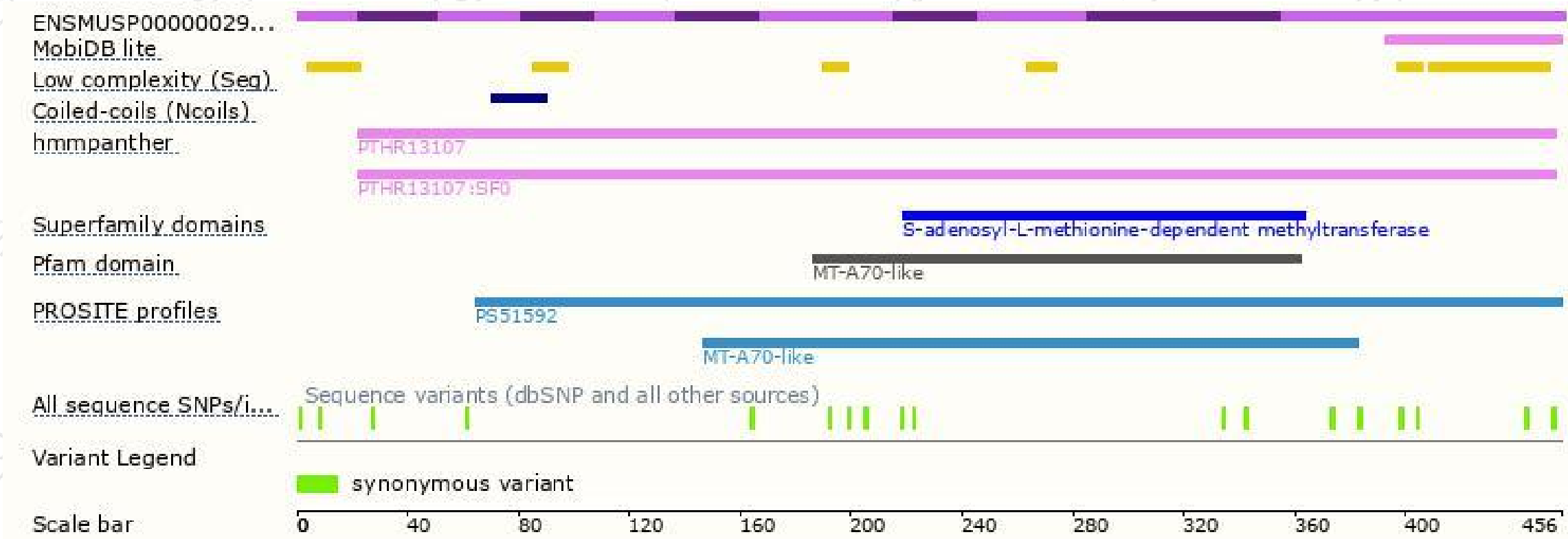
The strategy is based on the design of *Mettl14-201* transcript,The transcription is shown below



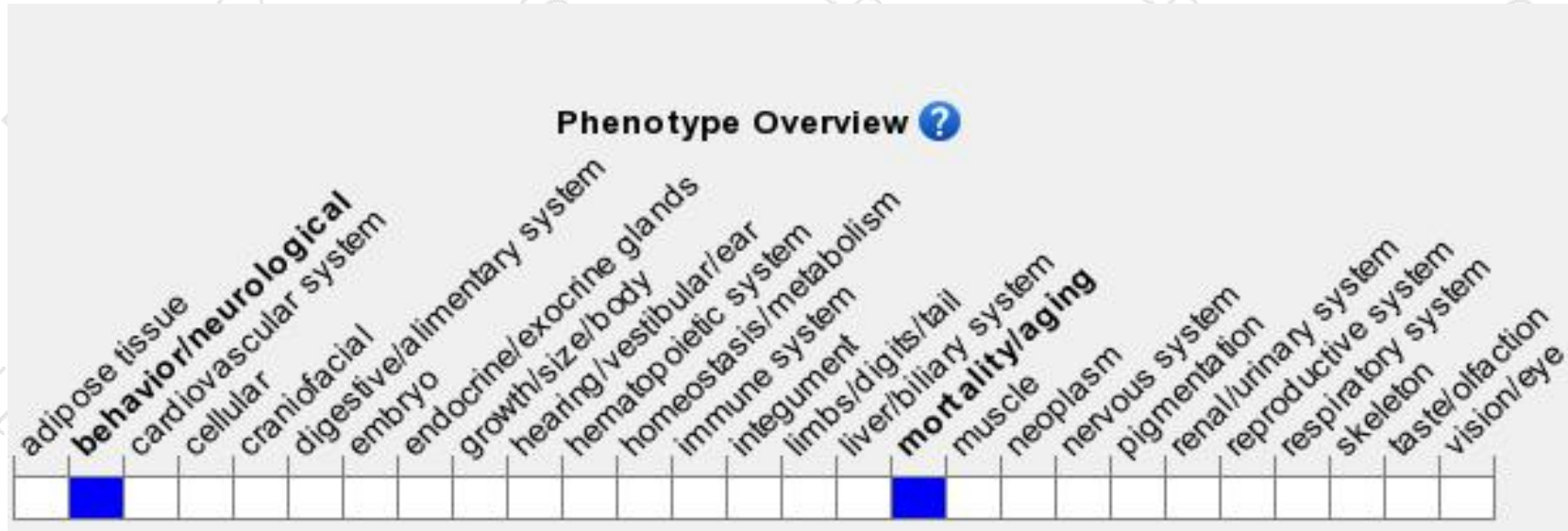
Genomic location distribution



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/>).

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

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