

Tet1 Cas9-KO Strategy

Designer:

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Design Date:

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Project Overview

Project Name

Tet1

Project type

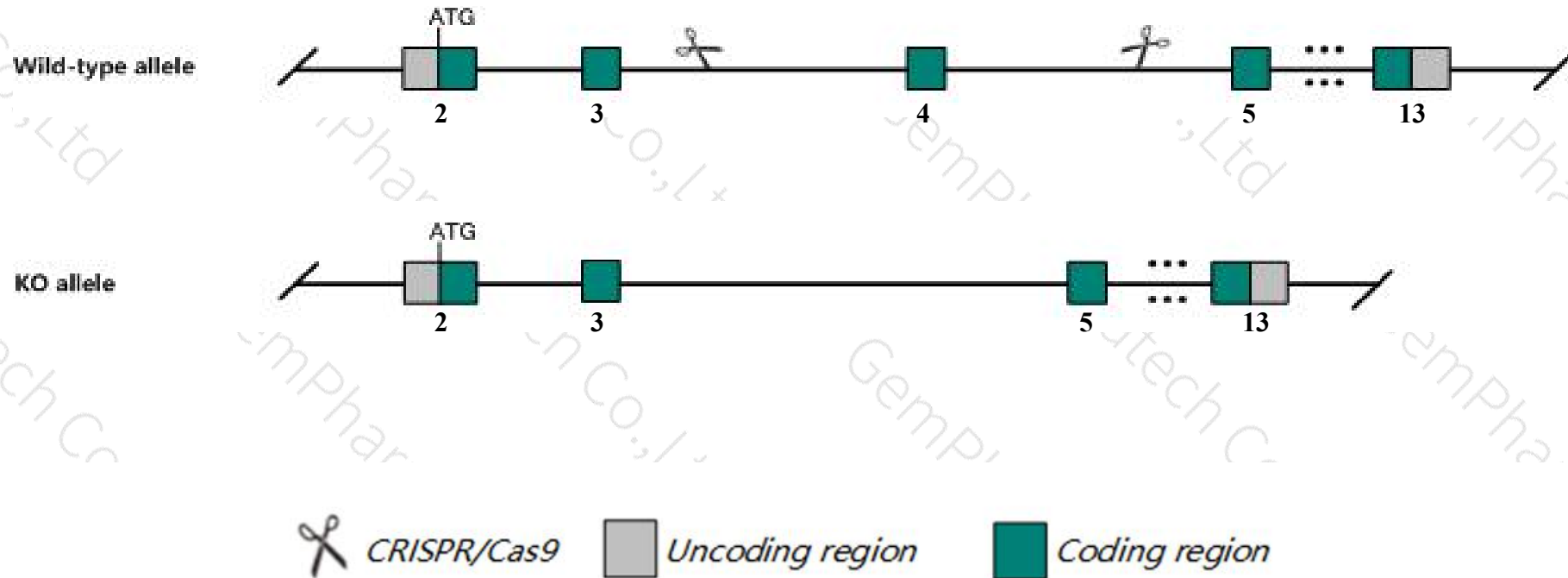
Cas9-KO

Strain background

C57BL/6JGpt

Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *Tet1* gene. The schematic diagram is as follows:



- The *Tet1* gene has 10 transcripts. According to the structure of *Tet1* gene, exon4 of *Tet1*-206 (ENSMUST00000174189.1) transcript is recommended as the knockout region. The region contains 2203bp coding sequence. Knock out the region will result in disruption of protein function.
- In this project we use CRISPR/Cas9 technology to modify *Tet1* gene. The brief process is as follows: CRISPR/Cas9 system w

- According to the existing MGI data, Mice homozygous for a knock-out allele exhibit background sensitive lethality, abnormal forebrain development, abnormal female reproductive organs and decreased litter size. Mice homozygous for a different knock-out allele exhibit impaired adult neurogenesis, impaired spatial learning and impaired short-term memory retention.
- The *Tet1* 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 the gene knockout on gene transcription, RNA splicing and protein translation cannot be predicted at the existing technology level.

Gene information (NCBI)

Tet1 tet methylcytosine dioxygenase 1 [Mus musculus (house mouse)]

Gene ID: 52463, updated on 12-Mar-2019

Summary



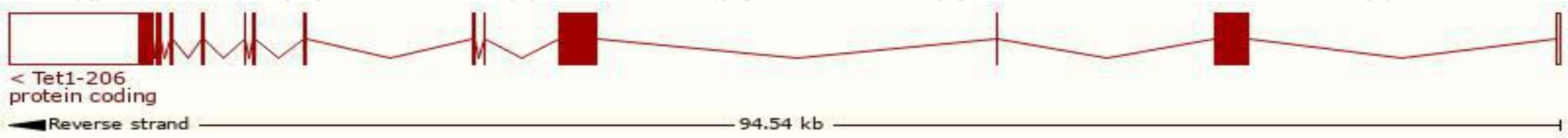
Official Symbol	Tet1 provided by MGI
Official Full Name	tet methylcytosine dioxygenase 1 provided by MGI
Primary source	MGI:MGI:1098693
See related	Ensembl:ENSMUSG00000047146
Gene type	protein coding
RefSeq status	VALIDATED
Organism	Mus musculus
Lineage	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Myomorpha; Muroidea; Muridae; Murinae; Mus; Mus
Also known as	2510010B09Rik, AA517754, BB001228, Cxxc6, D10Erd17e, LCX, mKIAA1676
Expression	Broad expression in CNS E18 (RPKM 2.2), whole brain E14.5 (RPKM 2.0) and 18 other tissues See more
Orthologs	human all

Transcript information (Ensembl)

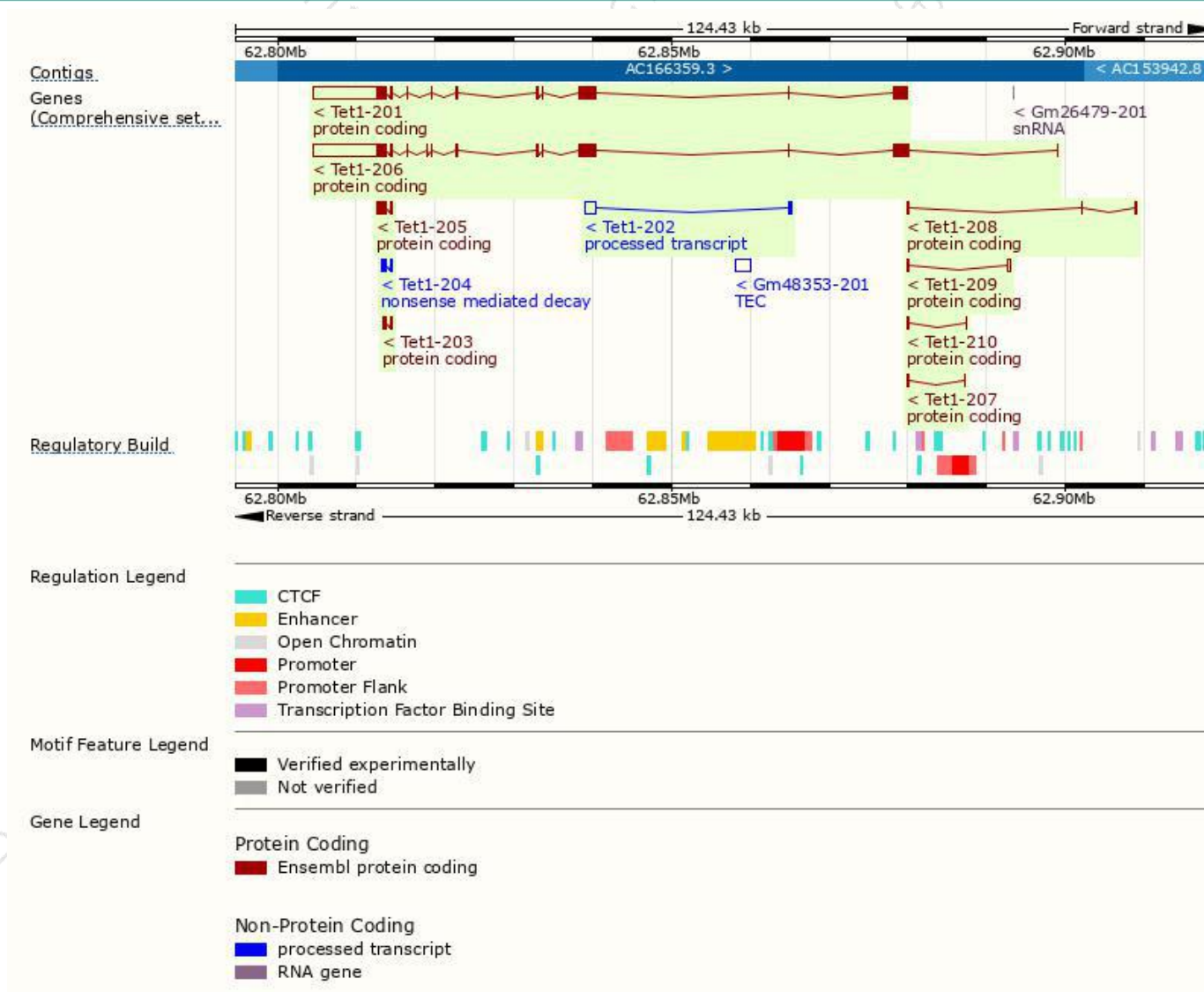
The gene has 10 transcripts,all transcripts are shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Tet1-210	ENSMUST00000228901.1	361	47aa	Protein coding	-	A0A1W2P7E3	CDS 3' incomplete
Tet1-209	ENSMUST00000227494.1	553	47aa	Protein coding	-	A0A1W2P7E3	CDS 3' incomplete
Tet1-208	ENSMUST00000218782.1	463	47aa	Protein coding	-	A0A1W2P7E3	CDS 3' incomplete TSL:1
Tet1-207	ENSMUST00000218438.1	414	47aa	Protein coding	-	A0A1W2P7E3	CDS 3' incomplete TSL:1
Tet1-206	ENSMUST00000174189.1	14369	2039aa	Protein coding	CCDS56706	E9Q9Y4	TSL:5 GENCODE basic APPRIS P2
Tet1-205	ENSMUST00000174121.1	1197	399aa	Protein coding	-	G3UZ35	CDS 5' and 3' incomplete TSL:2
Tet1-204	ENSMUST00000173905.1	618	68aa	Nonsense mediated decay	-	G3UZN8	CDS 5' incomplete TSL:3
Tet1-203	ENSMUST00000173087.1	581	138aa	Protein coding	-	G3UXI7	CDS 5' incomplete TSL:2
Tet1-202	ENSMUST00000173081.1	1505	No protein	lncRNA	-	-	TSL:1
Tet1-201	ENSMUST00000050826.13	13986	2007aa	Protein coding	-	Q3URK3	TSL:5 GENCODE basic APPRIS ALT2

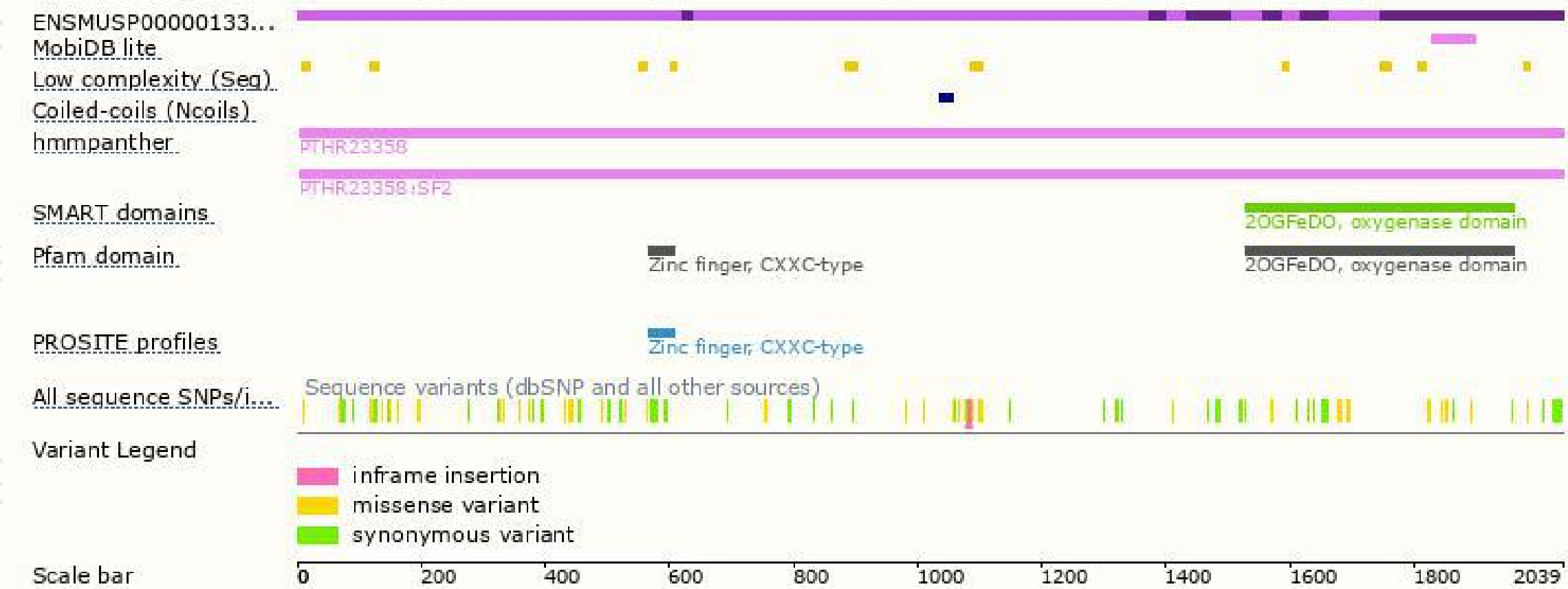
The strategy is based on the design of *Tet1-206* transcript,The transcription is shown below



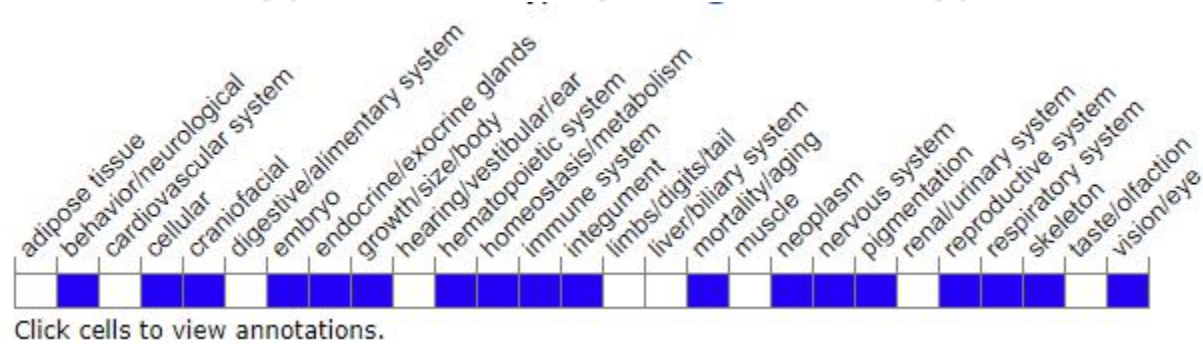
Genomic location distribution



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 background sensitive lethality, abnormal forebrain development, abnormal female reproductive organs and decreased litter size. Mice homozygous for a different knock-out allele exhibit impaired adult neurogenesis, impaired spatial learning and impaired short-term memory retention.

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

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