

Tor3a Cas9-KO Strategy

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Design Date: 2020-4-28

Project Overview

Project Name

Tor3a

Project type

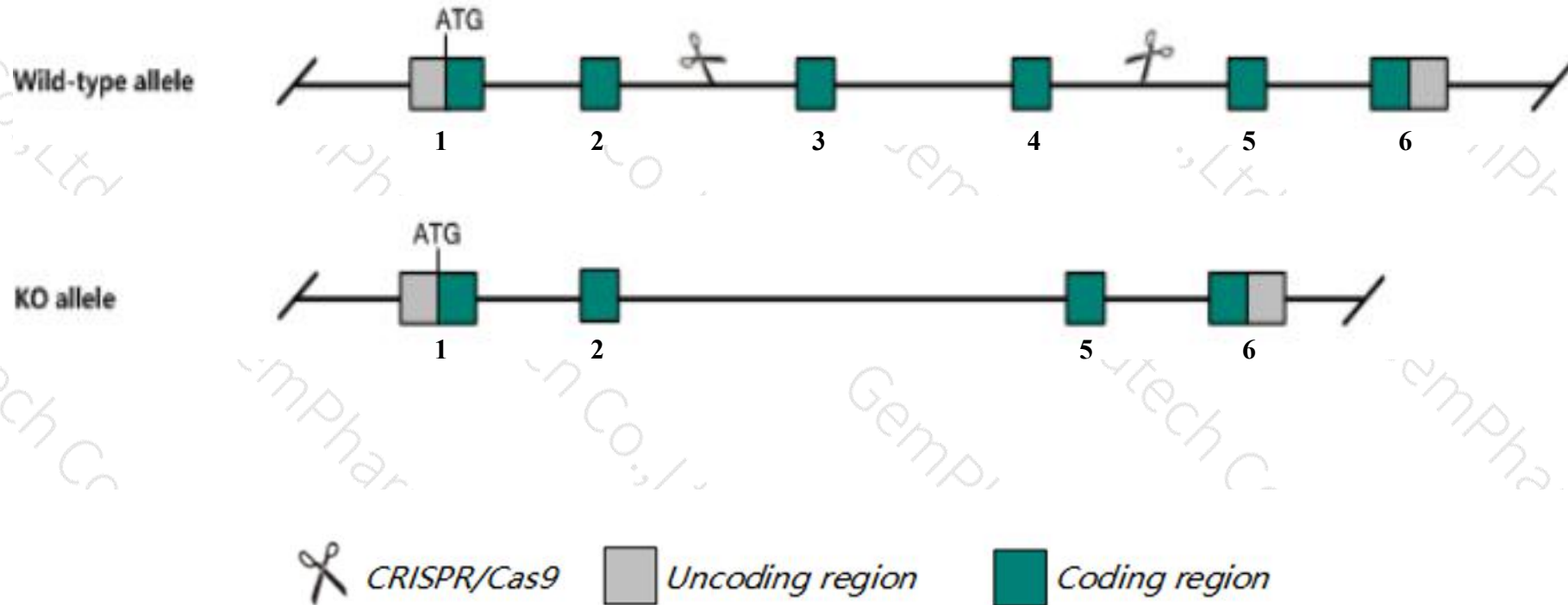
Cas9-KO

Strain background

C57BL/6JGpt

Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *Tor3a* gene. The schematic diagram is as follows:



- The *Tor3a* gene has 8 transcripts. According to the structure of *Tor3a* gene, exon3-exon4 of *Tor3a-201* (ENSMUST00000079625.10) transcript is recommended as the knockout region. The region contains 445bp coding sequence. Knock out the region will result in disruption of protein function.
- In this project we use CRISPR/Cas9 technology to modify *Tor3a* gene. The brief process is as follows: CRISPR/Cas9 system

- The N-terminal of *Tor3a* gene will remain several amino acids ,it may remain the partial function of *Tor3a* gene.
- Transcript *Tor3a*-205 may not be affected.
- The *Tor3a* gene is located on the Chr1. 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)

Tor3a torsin family 3, member A [Mus musculus (house mouse)]

Gene ID: 30935, updated on 13-Mar-2020

Summary



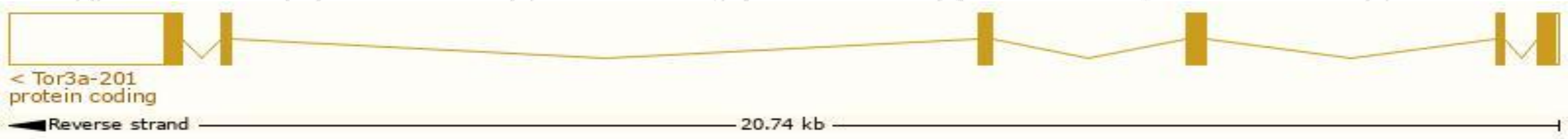
Official Symbol	Tor3a provided by MGI
Official Full Name	torsin family 3, member A provided by MGI
Primary source	MGI:MGI:1353652
See related	Ensembl:ENSMUSG00000060519
Gene type	protein coding
RefSeq status	VALIDATED
Organism	Mus musculus
Lineage	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Myomorpha; Muroidea; Muridae; Murinae; Mus; Mus
Also known as	Adir
Expression	Ubiquitous expression in lung adult (RPKM 14.2), colon adult (RPKM 10.8) and 27 other tissues See more
Orthologs	human all

Transcript information (Ensembl)

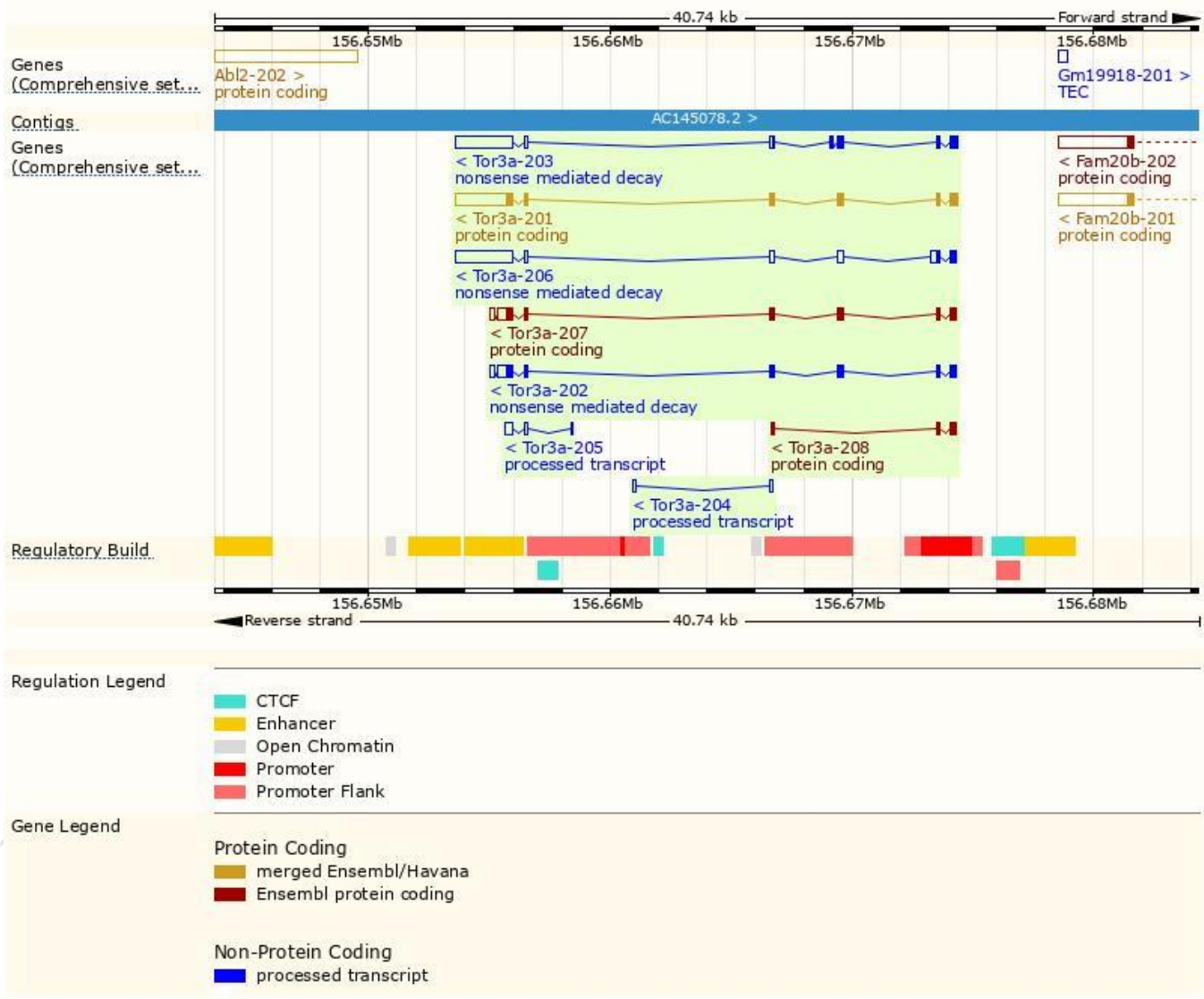
The gene has 8 transcripts,all transcripts are shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Tor3a-201	ENSMUST00000079625.10	3285	385aa	Protein coding	CCDS15394	Q9ER38	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
Tor3a-207	ENSMUST00000188964.6	1750	385aa	Protein coding	CCDS15394	Q9ER38	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
Tor3a-208	ENSMUST00000190607.1	453	133aa	Protein coding	-	A0A087WQB9	TSL:3 GENCODE basic
Tor3a-206	ENSMUST00000156861.7	3545	115aa	Nonsense mediated decay	-	A0A087WRX4	TSL:2
Tor3a-203	ENSMUST00000150557.7	3355	245aa	Nonsense mediated decay	-	M0QWH2	TSL:2
Tor3a-202	ENSMUST00000122242.7	1750	385aa	Nonsense mediated decay	-	Q9ER38	TSL:1
Tor3a-205	ENSMUST00000154353.1	491	No protein	Processed transcript	-	-	TSL:3
Tor3a-204	ENSMUST00000152604.1	284	No protein	Processed transcript	-	-	TSL:3

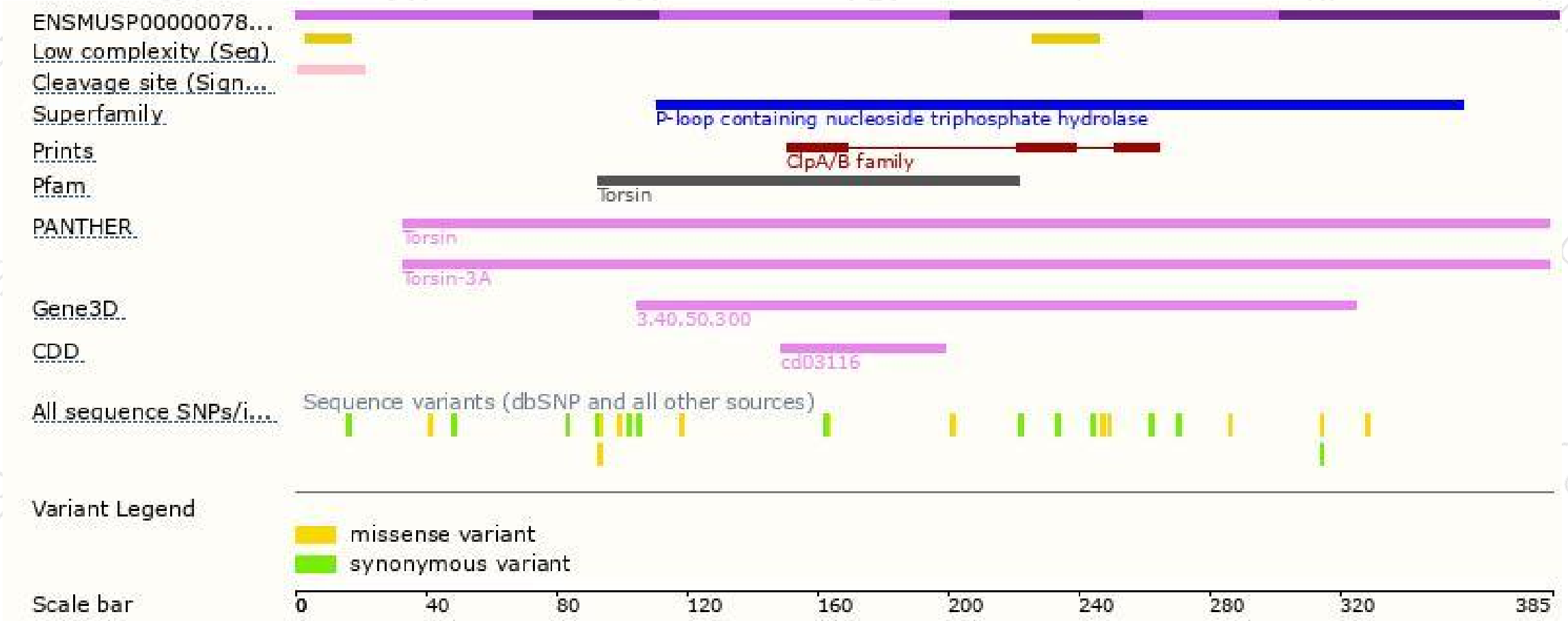
The strategy is based on the design of *Tor3a-201* transcript,the transcription is shown below:



Genomic location distribution



Protein domain



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

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