

Rnf138 Cas9-KO Strategy

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Design Date: 2020-4-15

Project Overview

Project Name

Rnf138

Project type

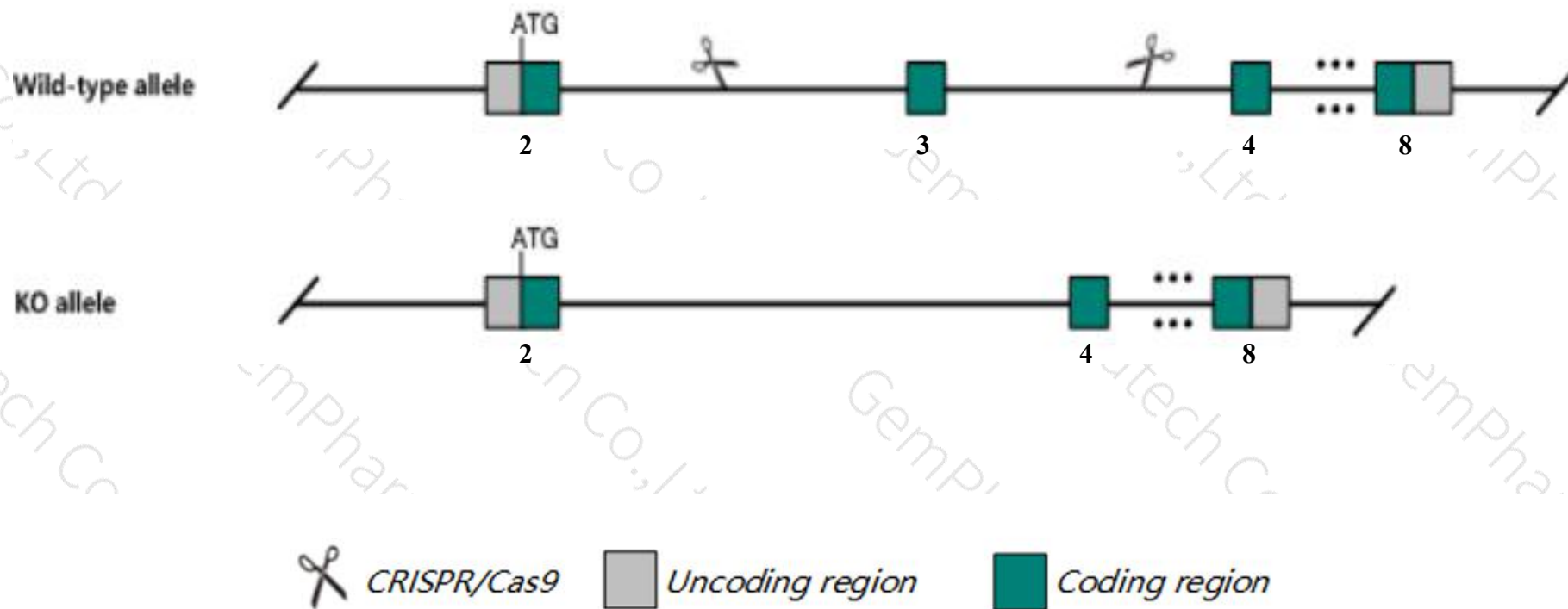
Cas9-KO

Strain background

C57BL/6JGpt

Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *Rnf138* gene. The schematic diagram is as follows:



- The *Rnfl38* gene has 6 transcripts. According to the structure of *Rnfl38* gene, exon3 of *Rnfl38-203* (ENSMUST00000234107.1) transcript is recommended as the knockout region. The region contains 166bp coding sequence. Knock out the region will result in disruption of protein function.
- In this project we use CRISPR/Cas9 technology to modify *Rnfl38* gene. The brief process is as follows: CRISPR/Cas9 system

- The *Rnf138* gene is located on the Chr18. 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)

Rnf138 ring finger protein 138 [Mus musculus (house mouse)]

Gene ID: 56515, updated on 13-Mar-2020

Summary



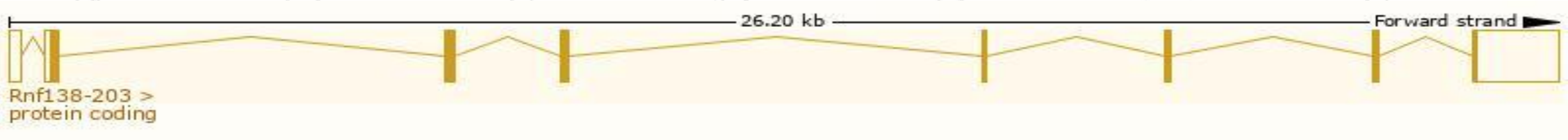
Official Symbol	Rnf138 provided by MGI
Official Full Name	ring finger protein 138 provided by MGI
Primary source	MGI:MGI:1929211
See related	Ensembl:ENSMUSG00000024317
Gene type	protein coding
RefSeq status	VALIDATED
Organism	Mus musculus
Lineage	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Myomorpha; Muroidea; Muridae; Murinae; Mus; Mus
Also known as	2410015A17Rik, 2810480D20Rik, STRIN, Trif, Trif-d
Expression	Biased expression in testis adult (RPKM 61.8), CNS E18 (RPKM 6.3) and 6 other tissues See more
Orthologs	human all

Transcript information（Ensembl）

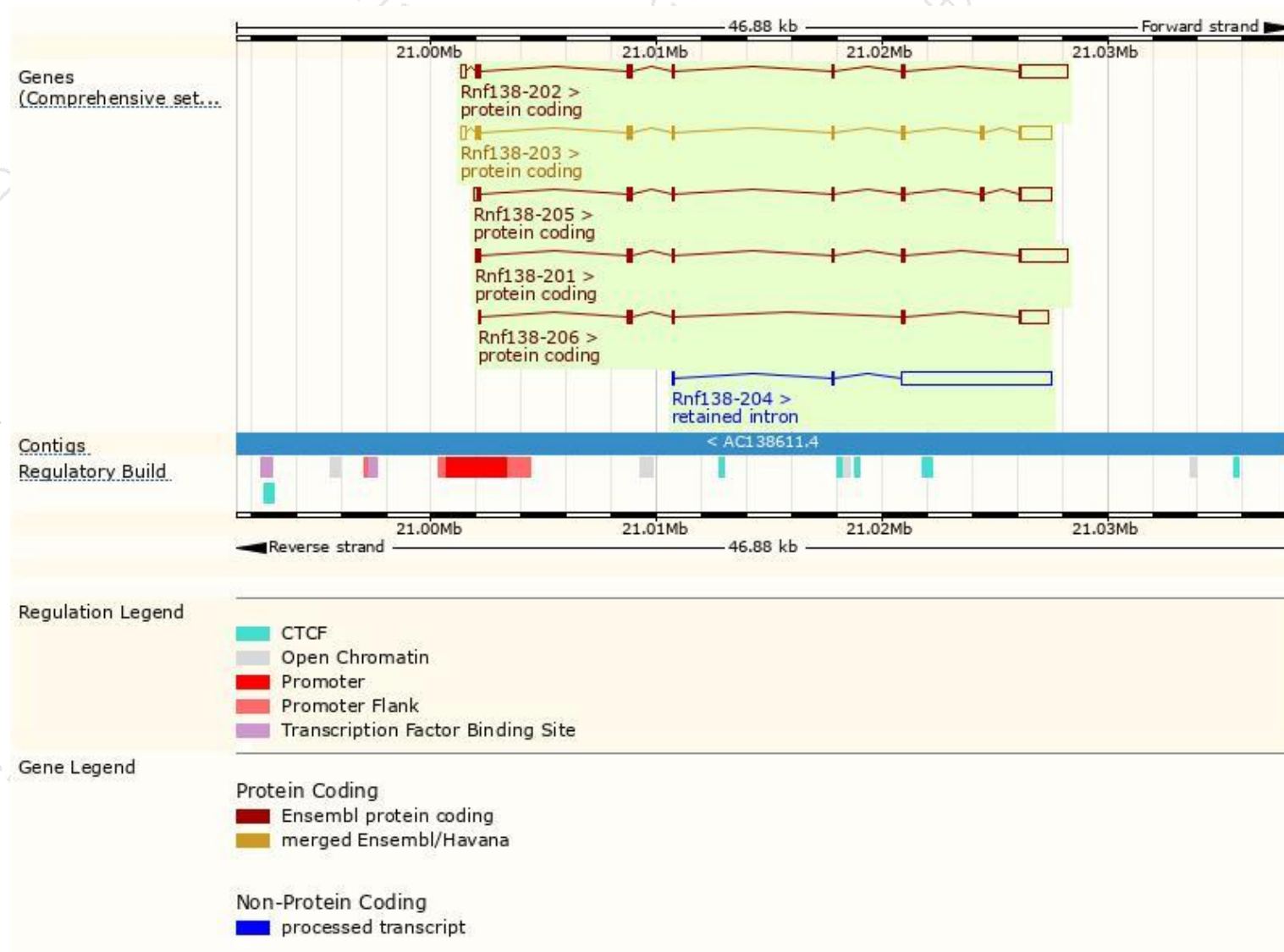
The gene has 6 transcripts,all transcripts are shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Rnf138-202	ENSMUST00000072847.11	3002	209aa	Protein coding	CCDS29089	Q9CQE0	TSL:1 GENCODE basic
Rnf138-201	ENSMUST00000052396.6	2769	209aa	Protein coding	CCDS29089	Q9CQE0	TSL:5 GENCODE basic
Rnf138-203	ENSMUST00000234107.1	2422	245aa	Protein coding	CCDS29090	Q9CQE0	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
Rnf138-205	ENSMUST00000234536.1	2271	245aa	Protein coding	CCDS29090	Q9CQE0	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
Rnf138-206	ENSMUST00000234545.1	1769	179aa	Protein coding	-	A0A3Q4EHU1	CDS 5' incomplete
Rnf138-204	ENSMUST00000234169.1	6766	No protein	Retained intron	-	-	

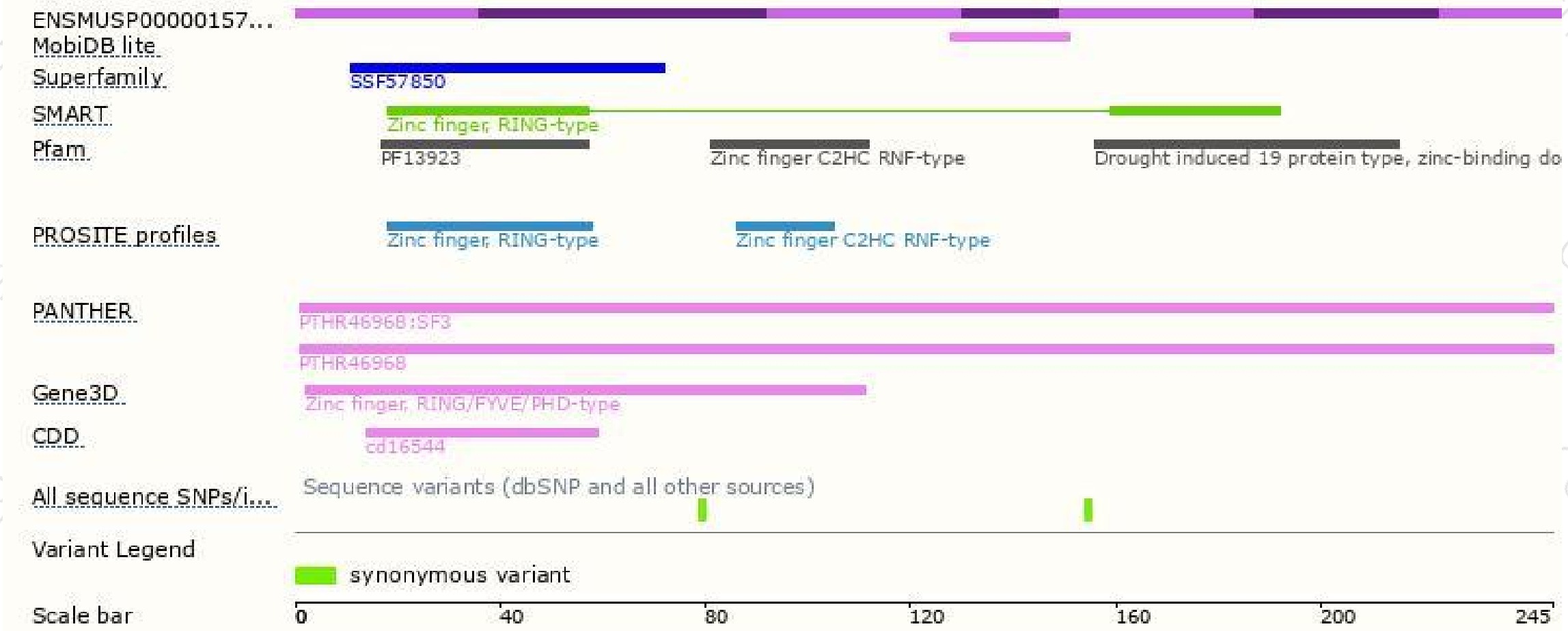
The strategy is based on the design of *Rnf138-203* transcript,the transcription is shown below:



Genomic location distribution



Protein domain



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

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