

Rnf112 Cas9-KO Strategy

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Design Date:

2020-2-11

Project Overview

Project Name

Rnf112

Project type

Cas9-KO

Strain background

C57BL/6JGpt

Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *Rnf112* gene. The schematic diagram is as follows:



- The *Rnf112* gene has 7 transcripts. According to the structure of *Rnf112* gene, exon1-exon14 of *Rnf112-203* (ENSMUST00000102661.3) transcript is recommended as the knockout region. The region contains all of the coding sequence. Knock out the region will result in disruption of protein function.
- In this project we use CRISPR/Cas9 technology to modify *Rnf112* gene. The brief process is as follows: CRISPR/Cas9 system

- According to the existing MGI data, Mice homozygous for a knock-out allele exhibit reduced dendritic spines, functional synapses and paired pulse facilitation.
- The *Rnfl112* 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)

Rnf112 ring finger protein 112 [Mus musculus (house mouse)]

Gene ID: 22671, updated on 31-Jan-2019

Summary



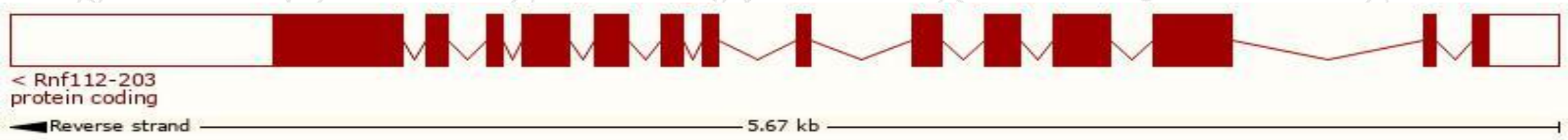
Official Symbol	Rnf112 provided by MGI
Official Full Name	ring finger protein 112 provided by MGI
Primary source	MGI:MGI:106611
See related	Ensembl:ENSMUSG00000010086
Gene type	protein coding
RefSeq status	VALIDATED
Organism	Mus musculus
Lineage	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Myomorpha; Muroidea; Muridae; Murinae; Mus; Mus
Also known as	ZNF179, Zfp179, bfp, neurolastin
Expression	Biased expression in cerebellum adult (RPKM 117.7), cortex adult (RPKM 98.5) and 5 other tissues See more
Orthologs	human all

Transcript information (Ensembl)

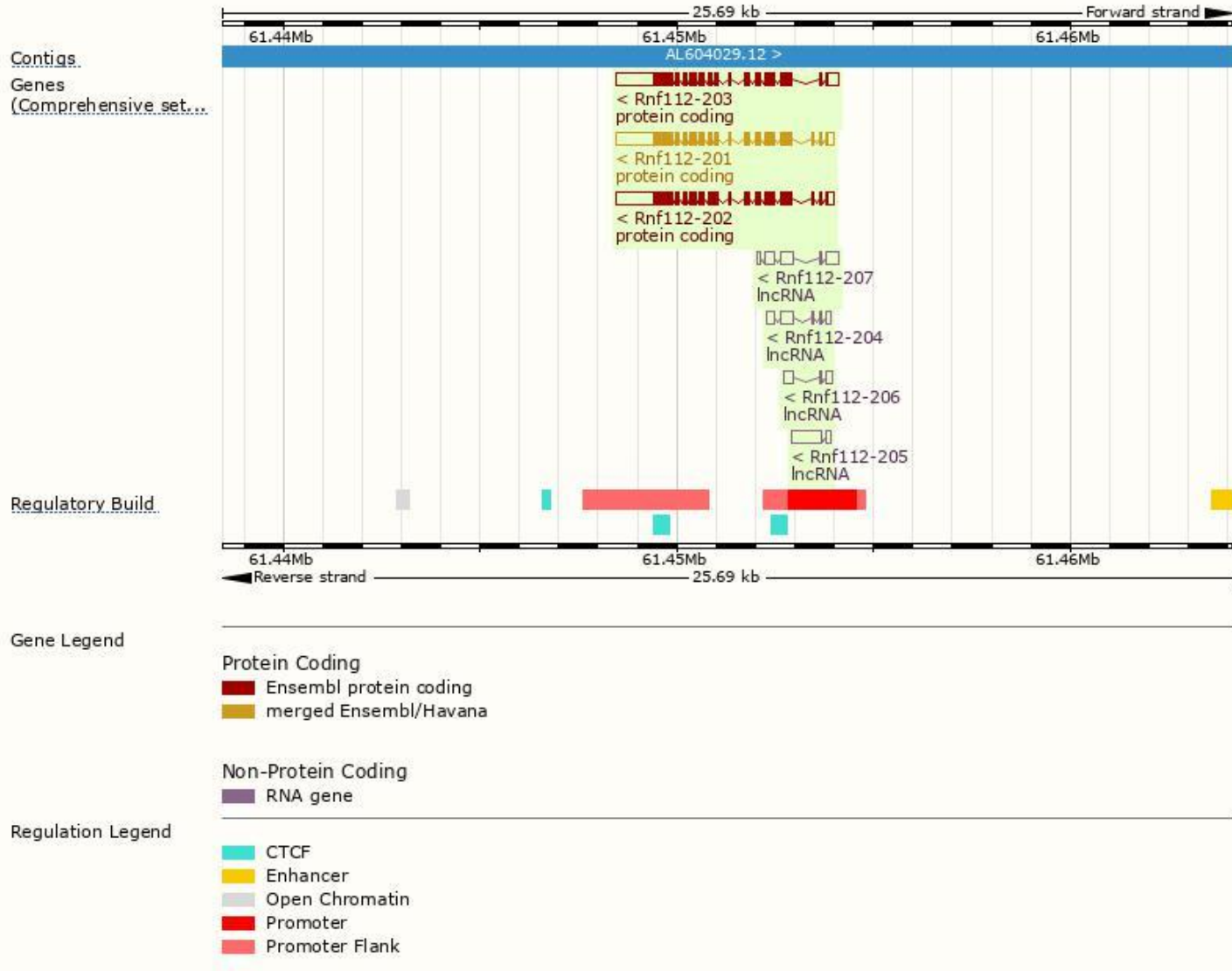
The gene has 7 transcripts,all transcripts are shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Rnf112-203	ENSMUST00000102661.3	3118	631aa	Protein coding	CCDS78960	Q96DY5	TSL:1 GENCODE basic APPRIS P1
Rnf112-201	ENSMUST00000054927.13	3086	654aa	Protein coding	CCDS24812	Q96DY5	TSL:1 GENCODE basic
Rnf112-202	ENSMUST00000060255.13	3161	679aa	Protein coding	-	Q96DY5	TSL:1 GENCODE basic
Rnf112-207	ENSMUST00000152137.7	1001	No protein	lncRNA	-	-	TSL:3
Rnf112-205	ENSMUST00000130648.1	882	No protein	lncRNA	-	-	TSL:2
Rnf112-204	ENSMUST00000126859.7	758	No protein	lncRNA	-	-	TSL:2
Rnf112-206	ENSMUST00000136966.1	425	No protein	lncRNA	-	-	TSL:2

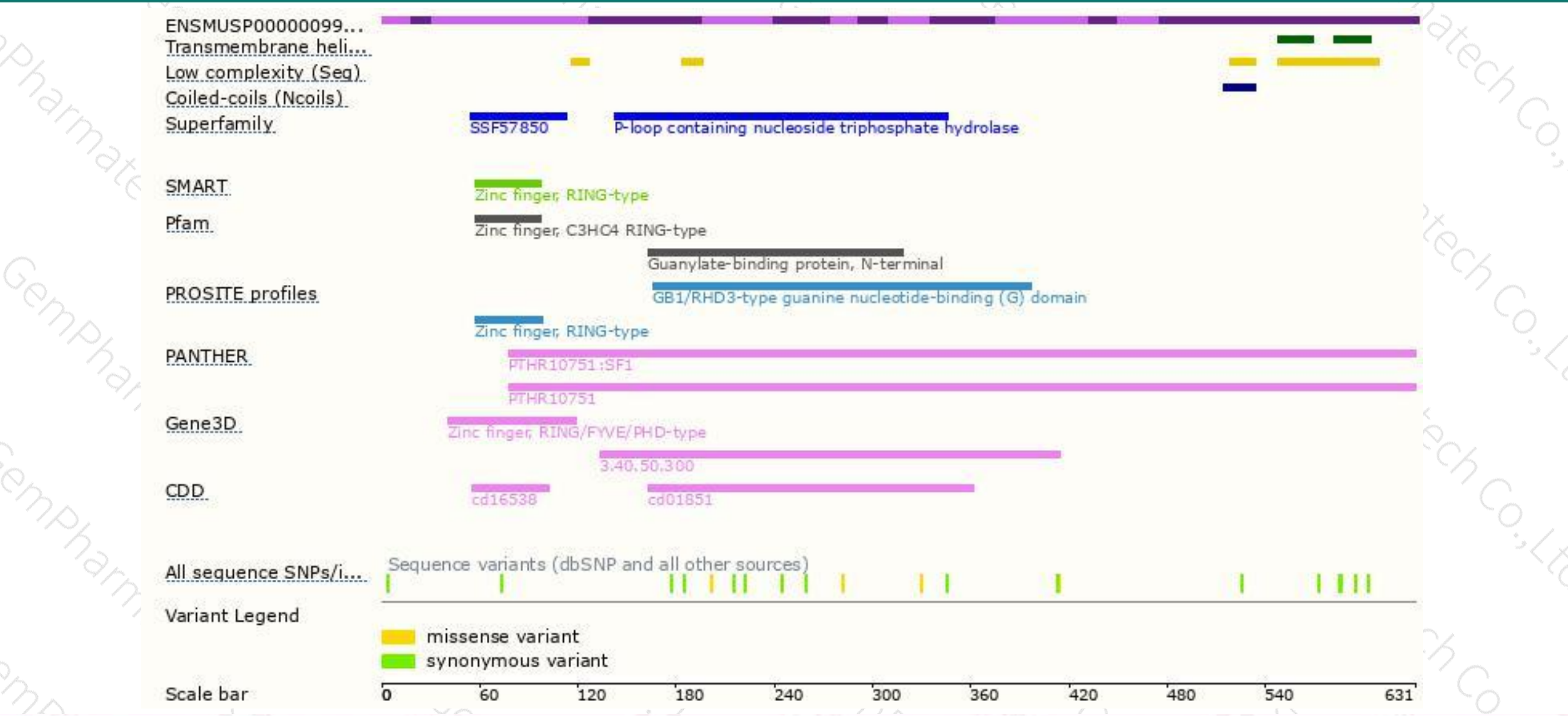
The strategy is based on the design of *Rnf112-203* transcript,The transcription is shown below



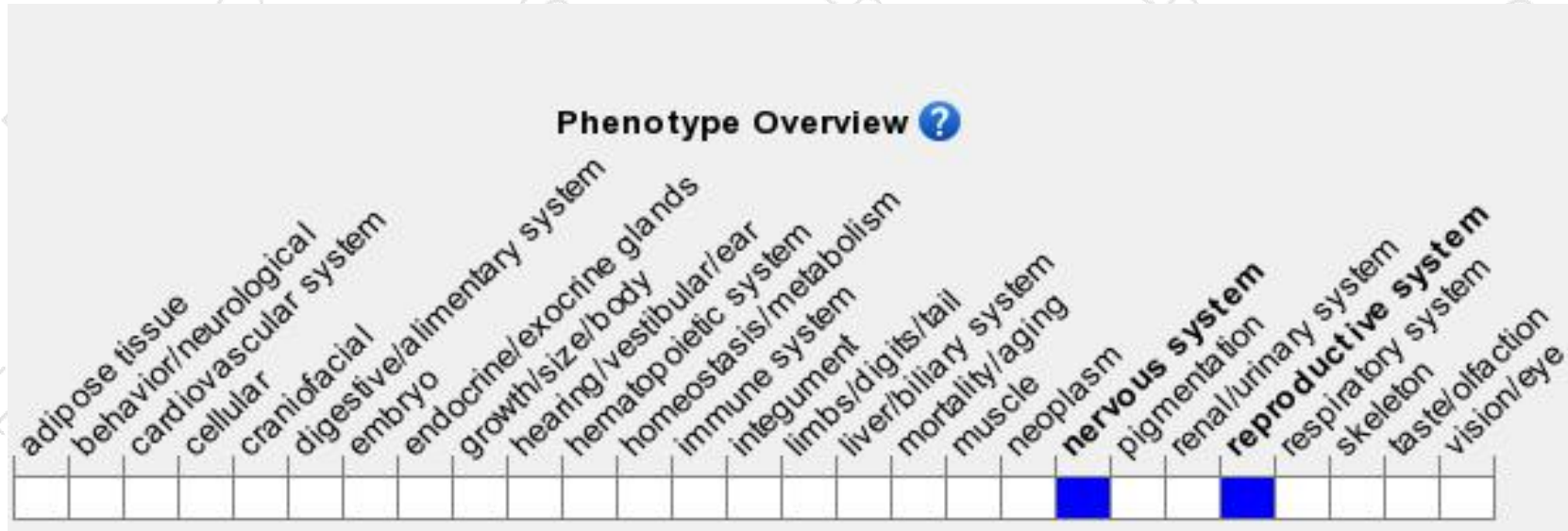
Genomic location distribution



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 reduced dendritic spines, functional synapses and paired pulse facilitation.

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

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