

Rnf212 Cas9-KO Strategy

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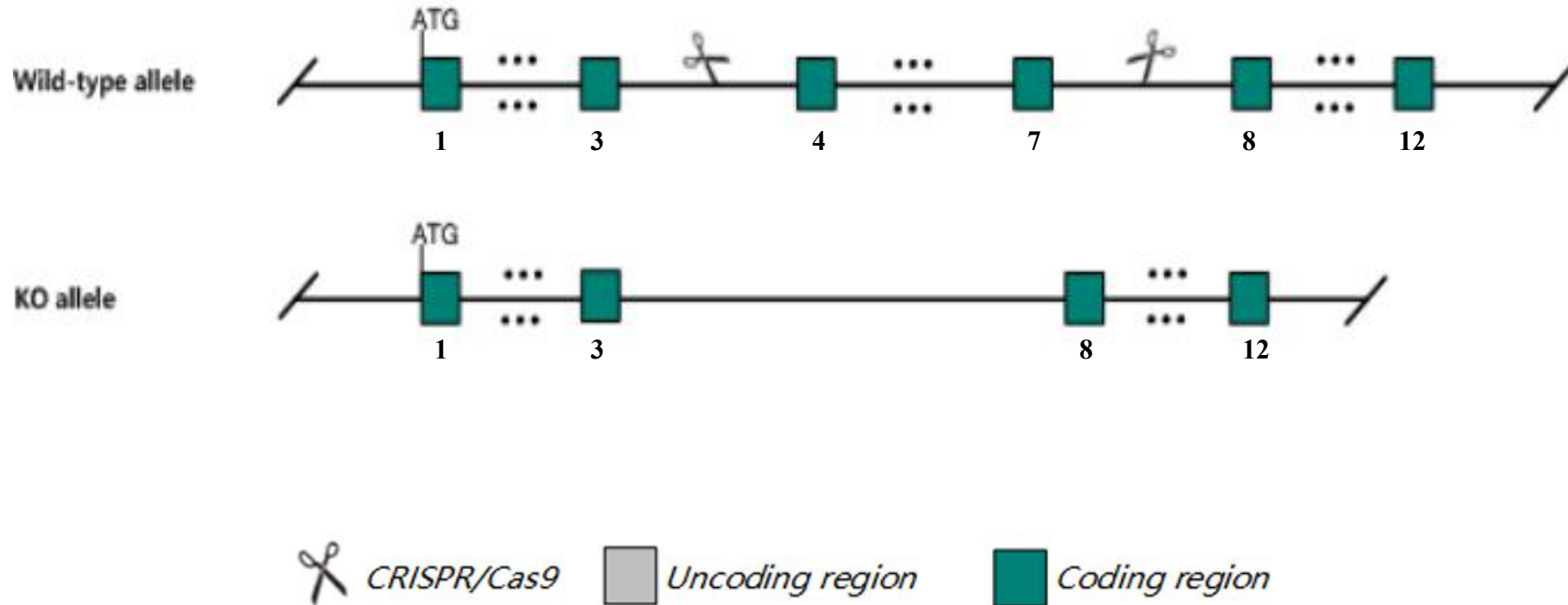
Project Name	<i>Rnf212</i>
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Project type	Cas9-KO
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Strain background	C57BL/6JGpt
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Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *Rnf212* gene. The schematic diagram is as follows:



The *Rnf212* gene has 6 transcripts. According to the structure of *Rnf212* gene, exon4-exon7 of *Rnf212*-206(ENSMUST00000212212.1) transcript is recommended as the knockout region. The region contains 221bp coding sequence. Knock out the region will result in disruption of protein function.

In this project we use CRISPR/Cas9 technology to modify *Rnf212* gene. The brief process is as follows: CRISPR/Cas9 system were microinjected into the fertilized eggs of C57BL/6JGpt mice. Fertilized eggs were transplanted to obtain positive F0 mice which were confirmed by PCR and sequencing. A stable F1 generation mouse model was obtained by mating positive F0 generation mice with C57BL/6JGpt mice.

According to the existing MGI data, mice homozygous for a knock-out allele exhibit abnormal male meiosis.

The *Rnf212* gene is located on the Chr5. 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.

Rnf212 ring finger protein 212 [*Mus musculus* (house mouse)]

Gene ID: 671564, updated on 26-Jun-2020

Summary



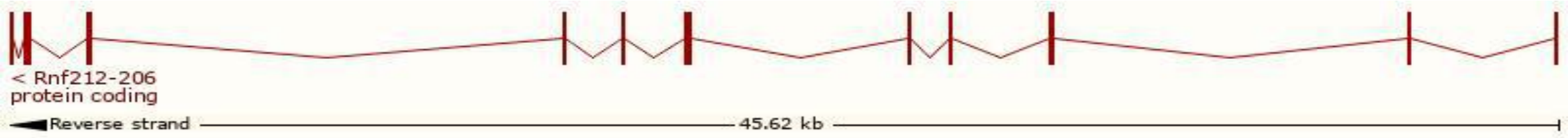
Official Symbol	Rnf212 provided by MGI
Official Full Name	ring finger protein 212 provided by MGI
Primary source	MGI:MGI:3645767
See related	Ensembl:ENSMUSG00000055385
Gene type	protein coding
RefSeq status	VALIDATED
Organism	Mus musculus
Lineage	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Myomorpha; Muroidea; Muridae; Murinae; Mus; Mus
Also known as	repro57; EG330157; F830003B07
Expression	Biased expression in testis adult (RPKM 2.5), colon adult (RPKM 0.7) and 7 other tissues See more
Orthologs	human all

Transcript information Ensembl

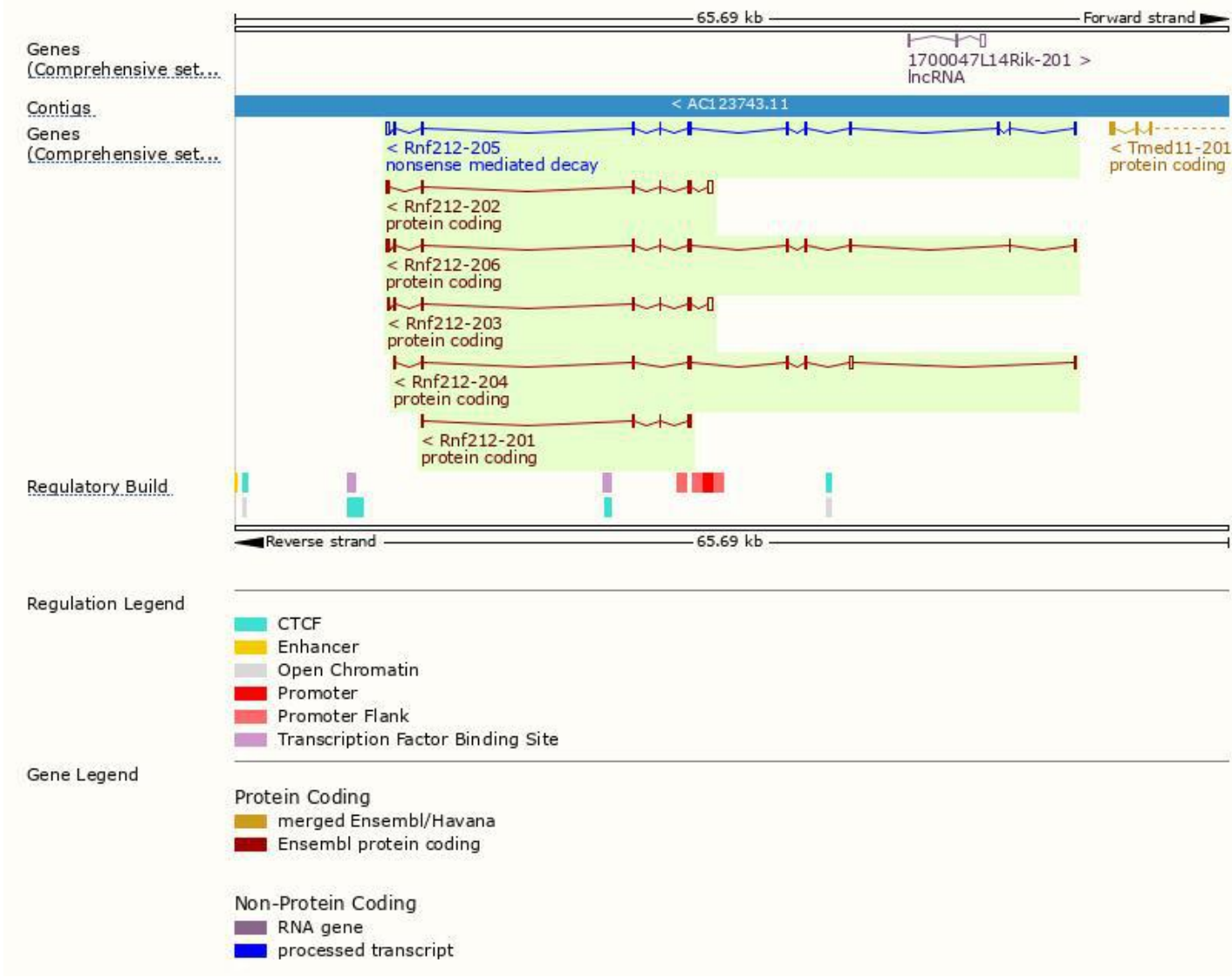
The gene has 6 transcripts,all transcripts are shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Rnf212-206	ENSMUST00000212212.1	924	307aa	Protein coding	-	F6TQD1	TSL:5 GENCODE basic APPRIS P1
Rnf212-203	ENSMUST00000197384.4	899	179aa	Protein coding	-	A0A0G2JDH3	CDS 3' incomplete TSL:1
Rnf212-202	ENSMUST00000196652.4	853	99aa	Protein coding	-	F6TQD1	TSL:2 GENCODE basic
Rnf212-204	ENSMUST00000200159.1	773	93aa	Protein coding	-	A0A0G2JFM4	CDS 3' incomplete TSL:5
Rnf212-201	ENSMUST00000068946.7	288	95aa	Protein coding	-	Z4YJP7	TSL:5 GENCODE basic
Rnf212-205	ENSMUST00000212176.1	1136	60aa	Nonsense mediated decay	-	A0A1D5RLU8	TSL:5

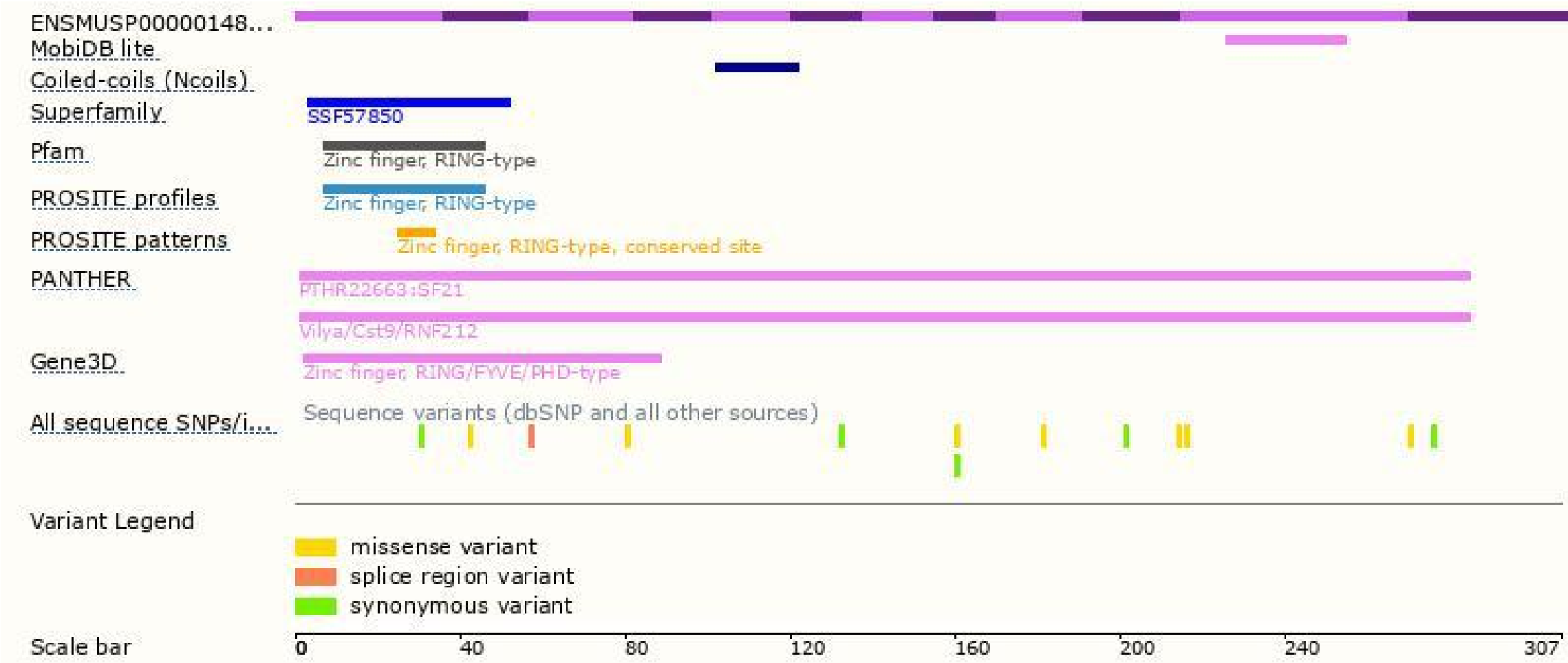
The strategy is based on the design of *Rnf212-206* transcript,the transcription is shown below:



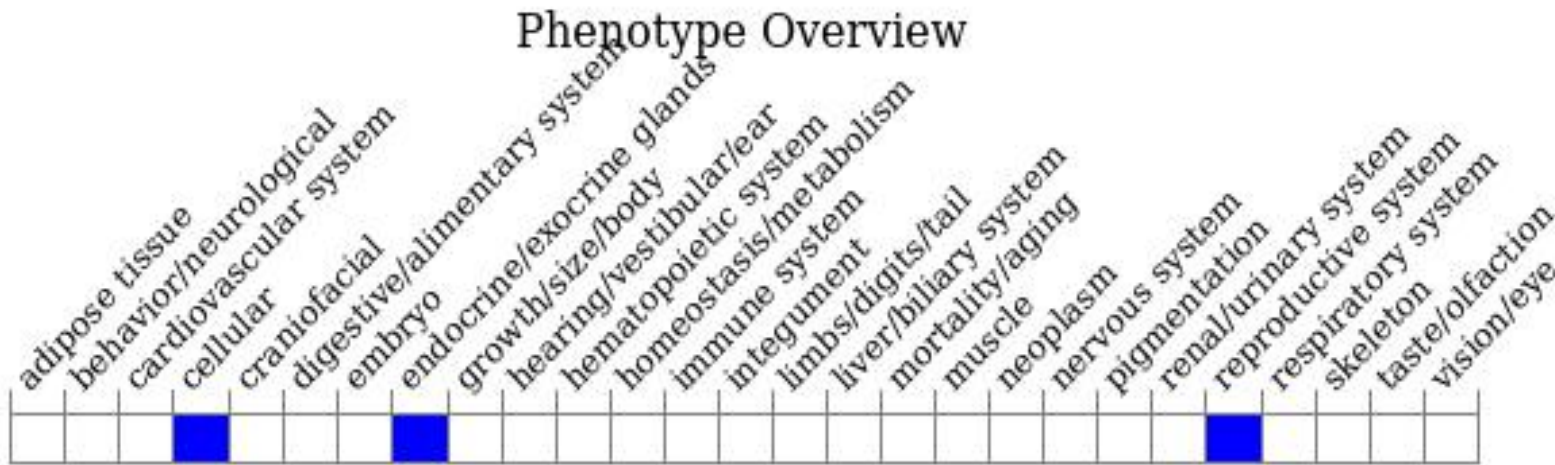
Genomic location distribution



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 abnormal male meiosis.

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