

Rnf213 Cas9-KO Strategy

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Design Date: 2018/11/22

Project Overview

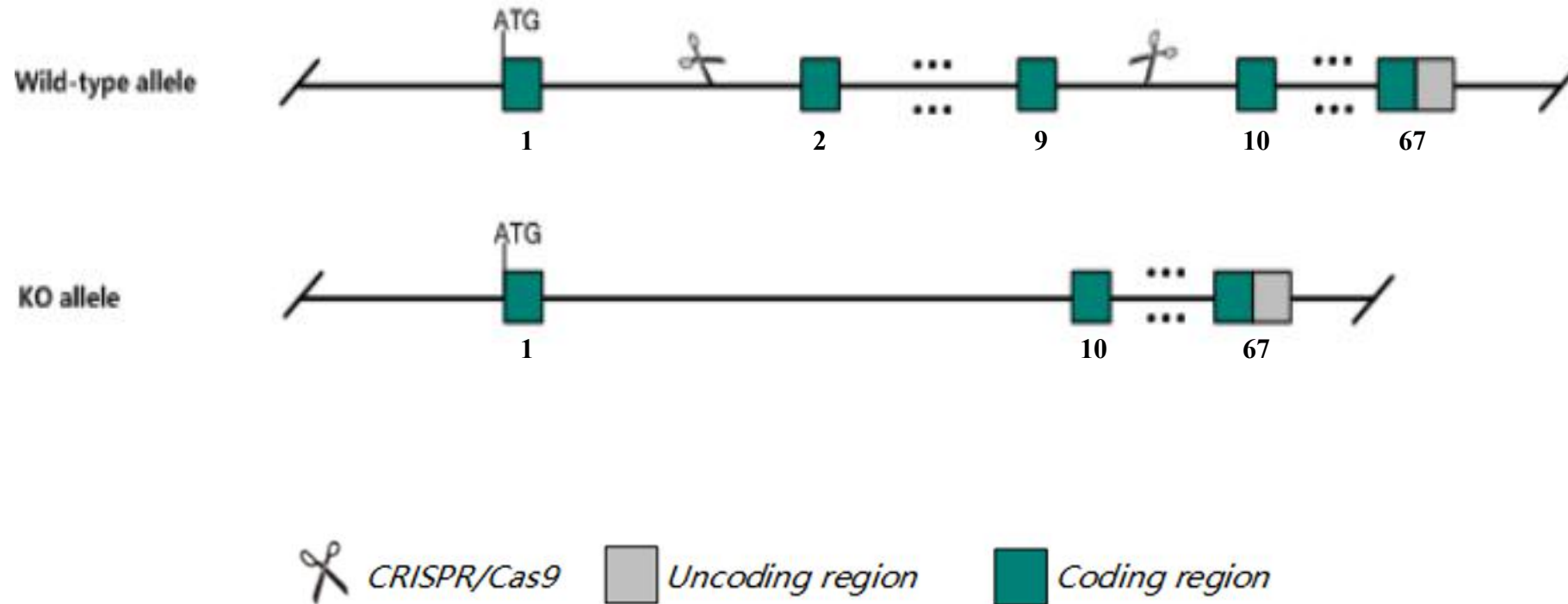
Project Name	<i>Rnf213</i>
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Project type	Cas9-KO
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Strain background	C57BL/6JGpt
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Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *Rnf213* gene. The schematic diagram is as follows:



The *Rnf213* gene has 3 transcripts. According to the structure of *Rnf213* gene, exon2-exon9 of *Rnf213-201*(ENSMUST00000093902.11) transcript is recommended as the knockout region. The region contains 1834bp coding sequence. Knock out the region will result in disruption of protein function.

In this project we use CRISPR/Cas9 technology to modify *Rnf213* 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 decreased body weight and circulating glucose level but normal glucose tolerance, insulin sensitivity, insulin plasma levels and leptin plasma levels.

The *Rnf213* 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.

Rnf213 ring finger protein 213 [Mus musculus (house mouse)]

Gene ID: 672511, updated on 13-Mar-2020

Summary



Official Symbol Rnf213 provided by [MGI](#)

Official Full Name ring finger protein 213 provided by [MGI](#)

Primary source [MGI:MGI:1289196](#)

See related [Ensembl:ENSMUSG00000070327](#)

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 6030403J01, D11Ert759e, mysterin

Expression Broad expression in ovary adult (RPKM 12.0), thymus adult (RPKM 11.4) and 26 other tissues [See more](#)

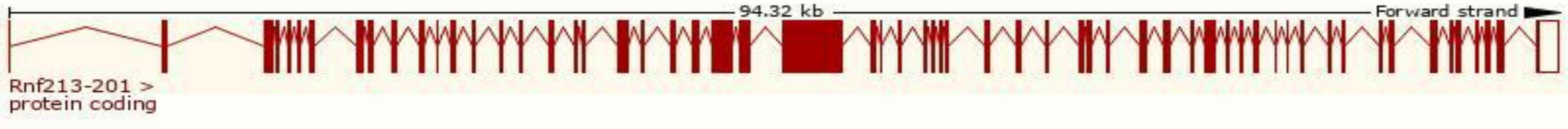
Orthologs [human](#) [all](#)

Transcript information Ensembl

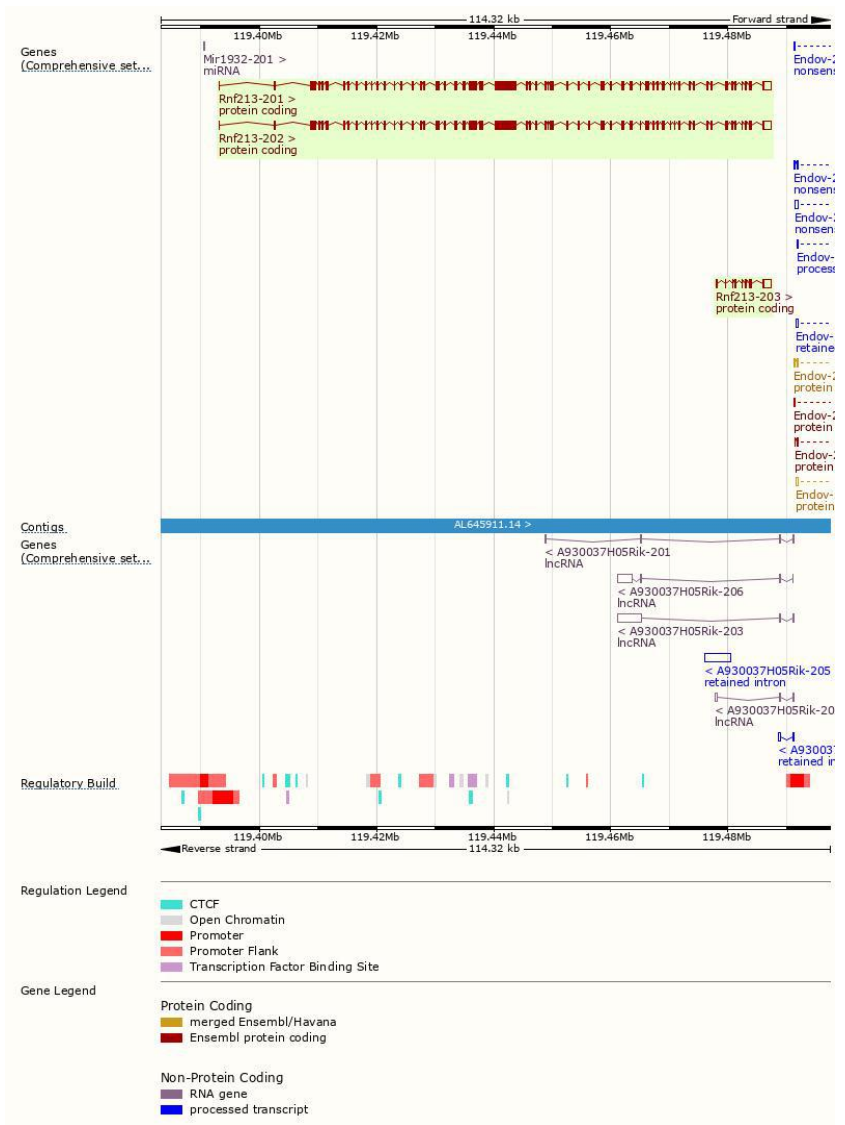
The gene has 3 transcripts,all transcripts are shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Rnf213-201	ENSMUST00000093902.11	16716	5152aa	Protein coding	-	E9Q555	TSL:5 GENCODE basic APPRIS P5
Rnf213-202	ENSMUST00000131035.9	16716	5151aa	Protein coding	-	A0A171EBL2	TSL:5 GENCODE basic APPRIS ALT2
Rnf213-203	ENSMUST00000172235.1	2422	312aa	Protein coding	-	Q3U0U2	TSL:5 GENCODE basic

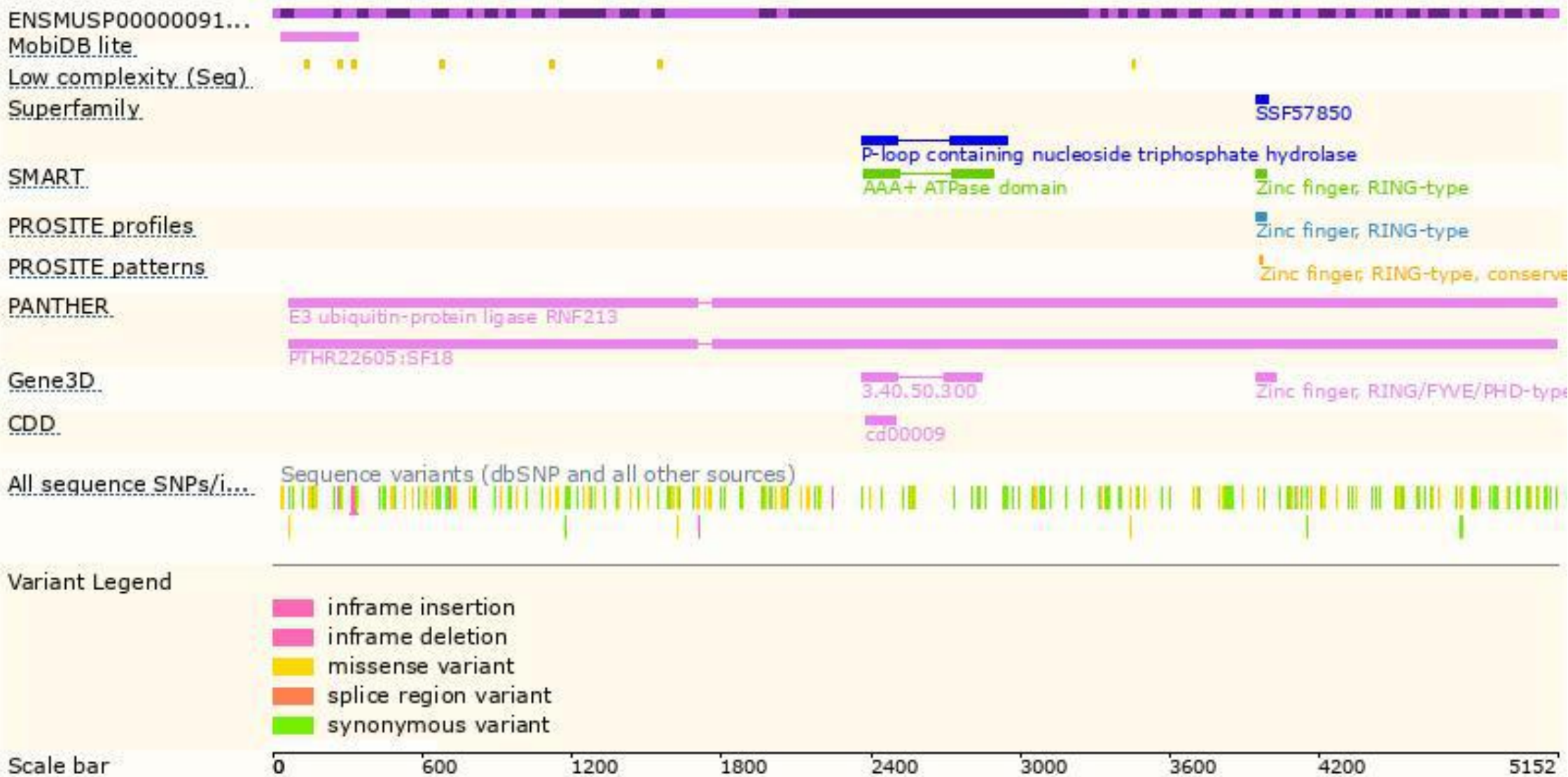
The strategy is based on the design of *Rnf213-201* transcript,the transcription is shown below:



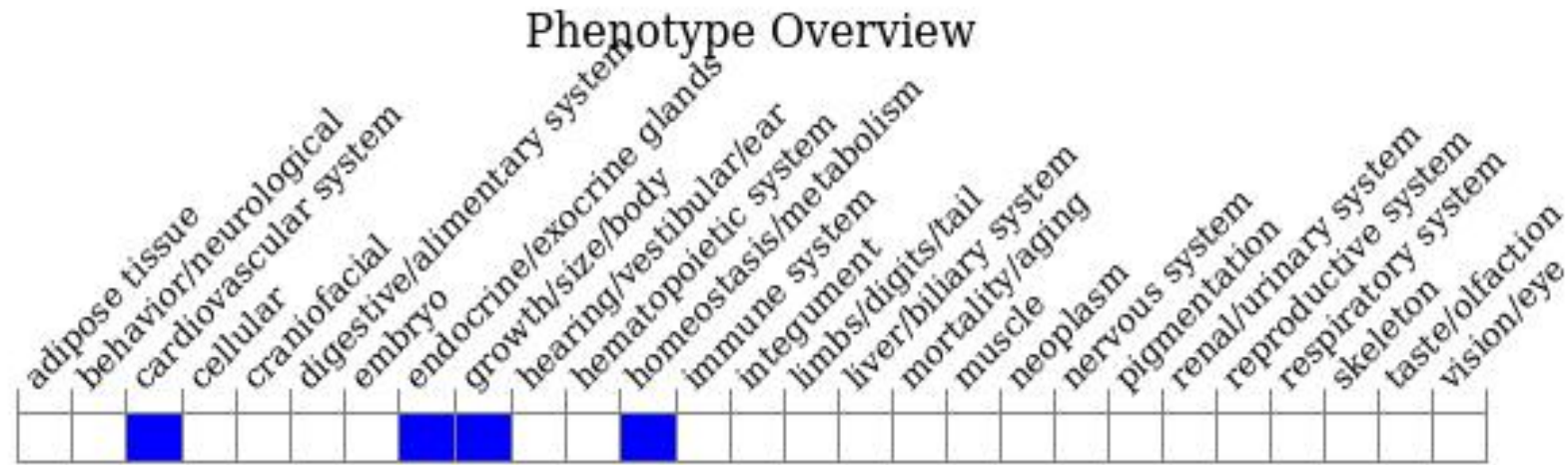
Genomic location distribution



Protein domain



集萃药康
GemPharmatech



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 decreased body weight and circulating glucose level but normal glucose tolerance, insulin sensitivity, insulin plasma levels and leptin plasma levels.

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