Rnf180 Cas9-KO Strategy

Designer: Daohua Xu

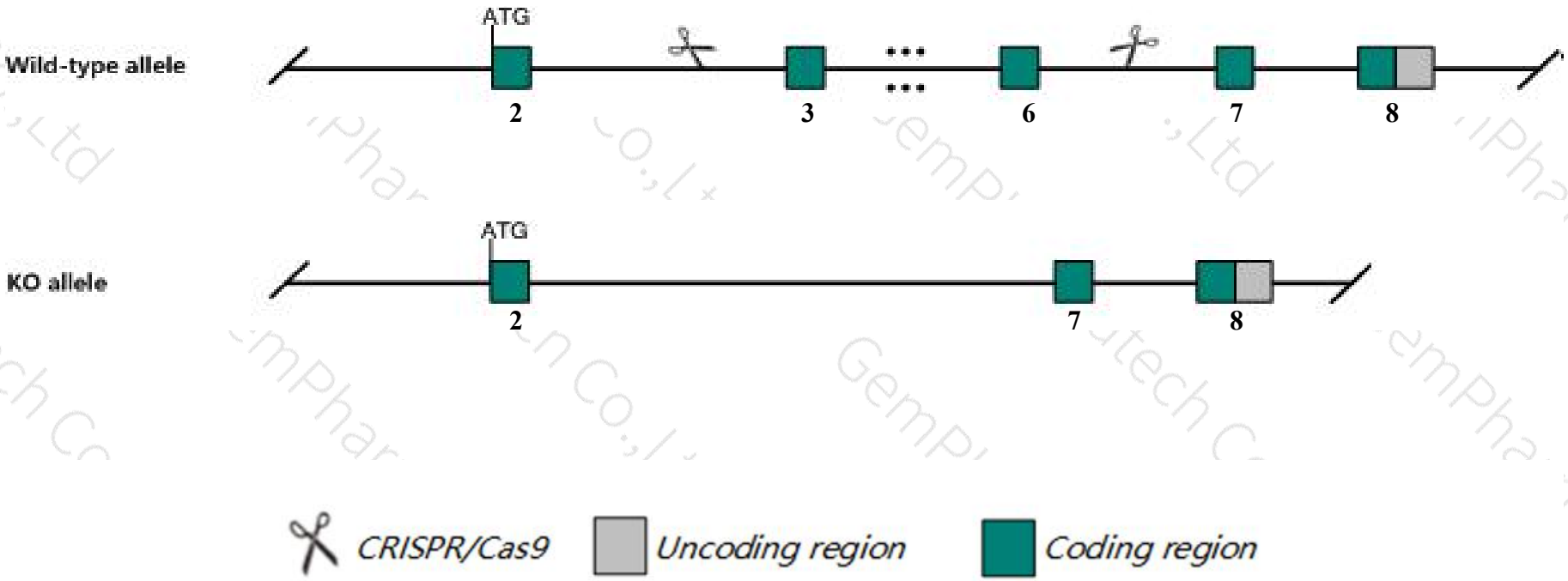
Design Date: 2019-7-30

Project Overview

Project Name	***Rnf180***
Project type	**Cas9-KO**
Strain background	**C57BL/6JGpt**

Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *Rnf180* gene. The schematic diagram is as follows:



Technical routes

➢ The *Rnf180* gene has 5 transcripts. According to the structure of *Rnf180* gene, exon3-exon6 of *Rnf180-202* (ENSMUST00000224011.1) transcript is recommended as the knockout region.The region contains 1318bp coding sequence. Knock out the region will result in disruption of protein function.

➢ In this project we use CRISPR/Cas9 technology to modify *Rnf180* gene. The brief process is as follows: CRISPR/Cas9 systen

Notice

➢ According to the existing MGI data,Knock-out mice show impaired stress responses, enhanced anxiety, and affiliative behavior. Norepinephrine and serotonin levels are decreased in the locus ceruleus, prefrontal cortex, and amygdala and MAO-A enzyme activity is enhanced in the locus ceruleus.

➢The KO region contains functional region of the *Gm25631* gene.Knockout the region may affect the function of *Gm25631* gene.

➢ The *Rnf180* gene is located on the Chr13. 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）

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Rnf180 ring finger protein 180 [Mus musculus (house mouse)]

Gene ID: 71816, updated on 31-Jan-2019

Summary

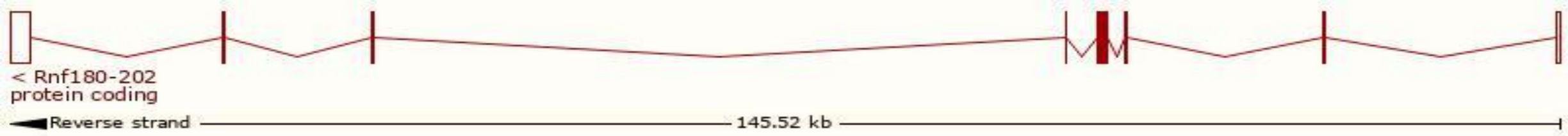
Official Symbol	Rnf180 provided by MGI
Official Full Name	ring finger protein 180 provided by MGI
Primary source	MGI:MGI:1919066
See related	Ensembl:ENSMUSG00000021720
Gene type	protein coding
RefSeq status	VALIDATED
Organism	Mus musculus
Lineage	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Myomorpha; Muroidea; Muridae; Murinae; Mus; Mus
Also known as	3110001E11Rik, Rines
Expression	Broad expression in genital fat pad adult (RPKM 6.2), CNS E18 (RPKM 4.7) and 15 other tissues See more
Orthologs	human all

Transcript information（Ensembl）

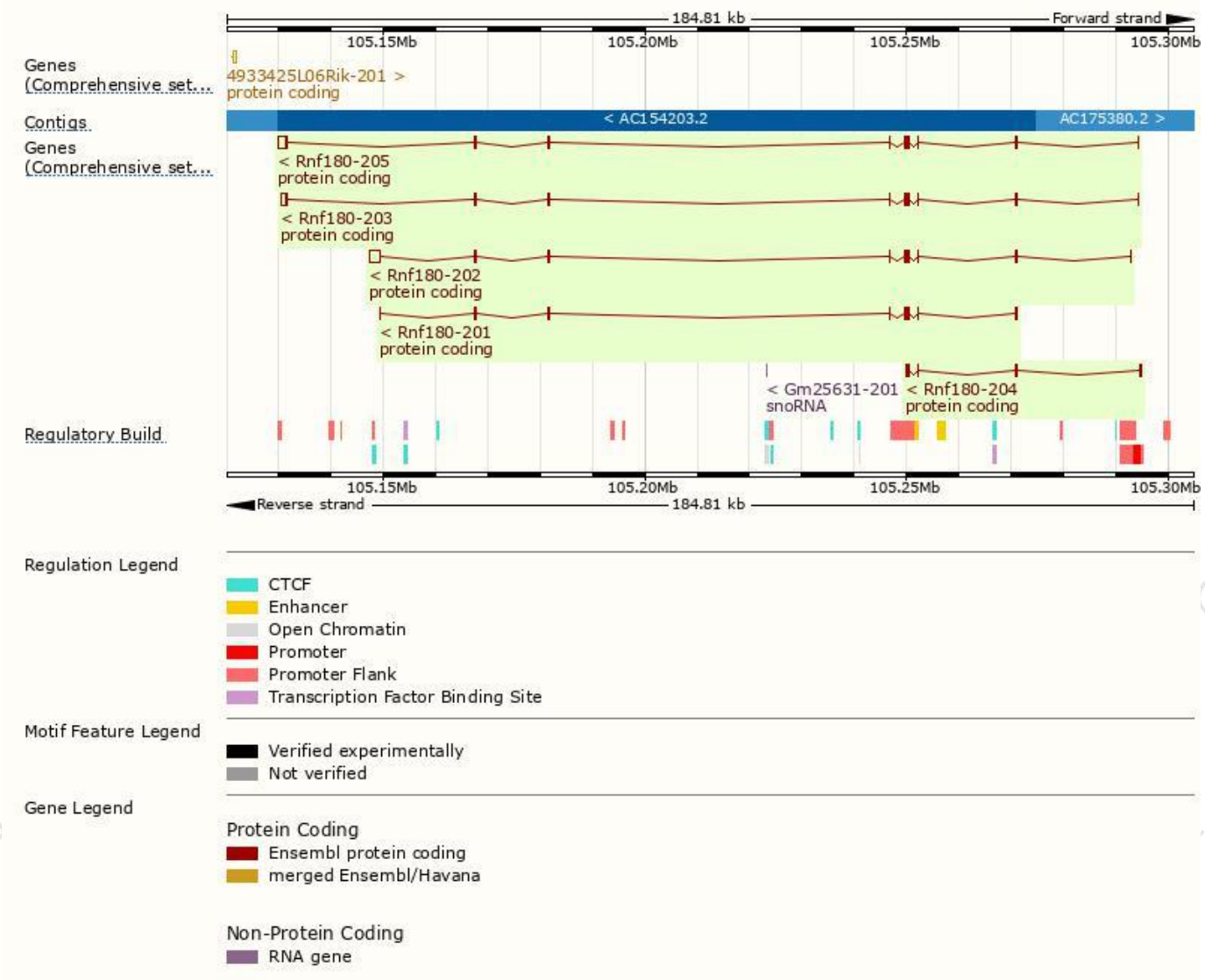
The gene has 5 transcripts,all transcripts are shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Rnf180-202	ENSMUST00000224011.1	3785	575aa	Protein coding	CCDS36775	Q3U827	GENCODE basic APPRIS P2
Rnf180-201	ENSMUST00000069686.6	1728	575aa	Protein coding	CCDS36775	Q3U827	TSL:5 GENCODE basic APPRIS P2
Rnf180-205	ENSMUST00000226044.1	3279	591aa	Protein coding	-	Q3U827	GENCODE basic APPRIS ALT2
Rnf180-203	ENSMUST00000224662.1	2734	592aa	Protein coding	-	Q3U827	GENCODE basic APPRIS ALT2
Rnf180-204	ENSMUST00000224749.1	1017	317aa	Protein coding	-	A0A286YCL6	CDS 3' incomplete

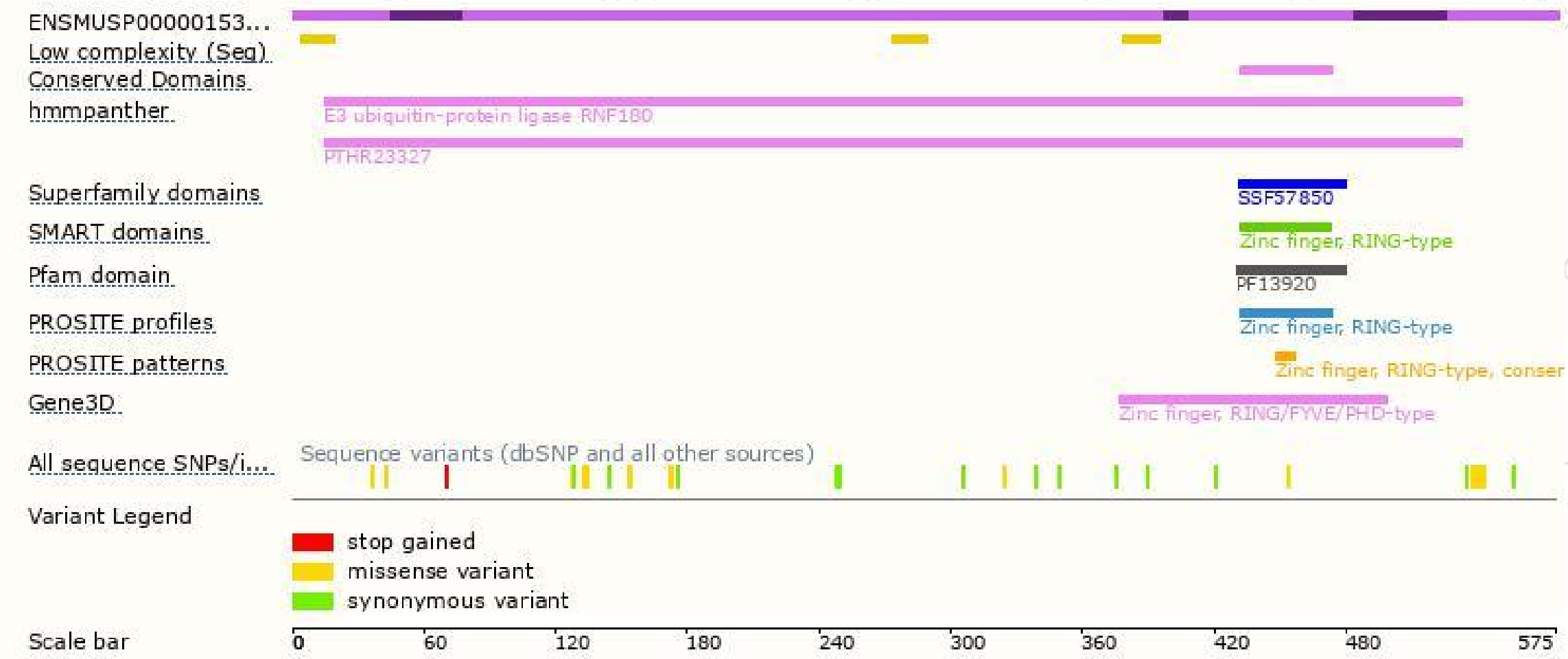
The strategy is based on the design of *Rnf180-202* transcript,The transcription is shown below



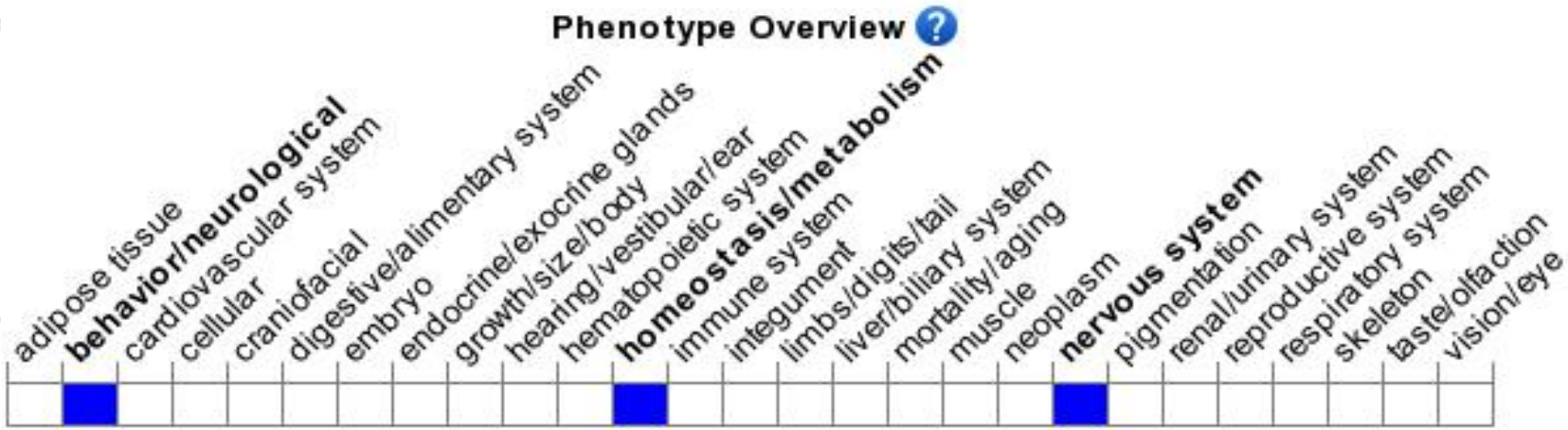
Genomic location distribution



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/).

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

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