

***Kcnk13* Cas9-KO Strategy**

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Project Overview

Project Name

Kcnk13

Project type

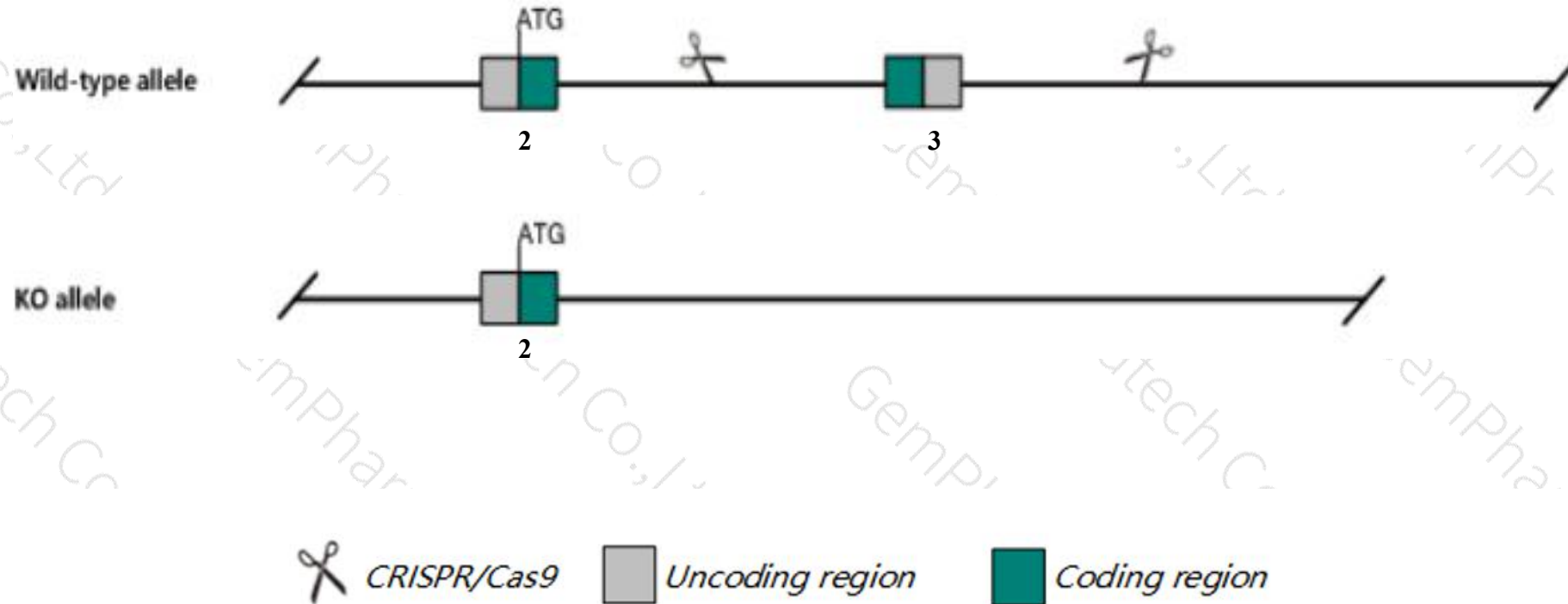
Cas9-KO

Strain background

C57BL/6JGpt

Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *Kcnk13* gene. The schematic diagram is as follows:



- The *Kcnk13* gene has 4 transcripts. According to the structure of *Kcnk13* gene, exon3 of *Kcnk13*-201(ENSMUST00000049788.8) transcript is recommended as the knockout region. The region contains 884bp coding sequence. Knock out the region will result in disruption of protein function.
- In this project we use CRISPR/Cas9 technology to modify *Kcnk13* 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, homozygous knockout reduces the surveillance activity of microglial cells in the brain.
- The *Kcnk13* gene is located on the Chr12. 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)

Kcnk13 potassium channel, subfamily K, member 13 [Mus musculus (house mouse)]

Gene ID: 217826, updated on 13-Mar-2020

Summary



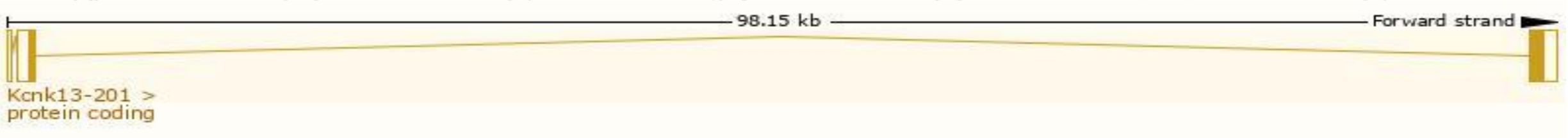
Official Symbol	Kcnk13 provided by MGI
Official Full Name	potassium channel, subfamily K, member 13 provided by MGI
Primary source	MGI:MGI:2384976
See related	Ensembl:ENSMUSG00000045404
Gene type	protein coding
RefSeq status	VALIDATED
Organism	Mus musculus
Lineage	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Myomorpha; Muroidea; Muridae; Murinae; Mus; Mus
Also known as	BB085247, F730021E22Rik, Gm1570, Gm1685
Expression	Broad expression in cerebellum adult (RPKM 2.1), frontal lobe adult (RPKM 1.7) and 24 other tissues See more
Orthologs	human all

Transcript information (Ensembl)

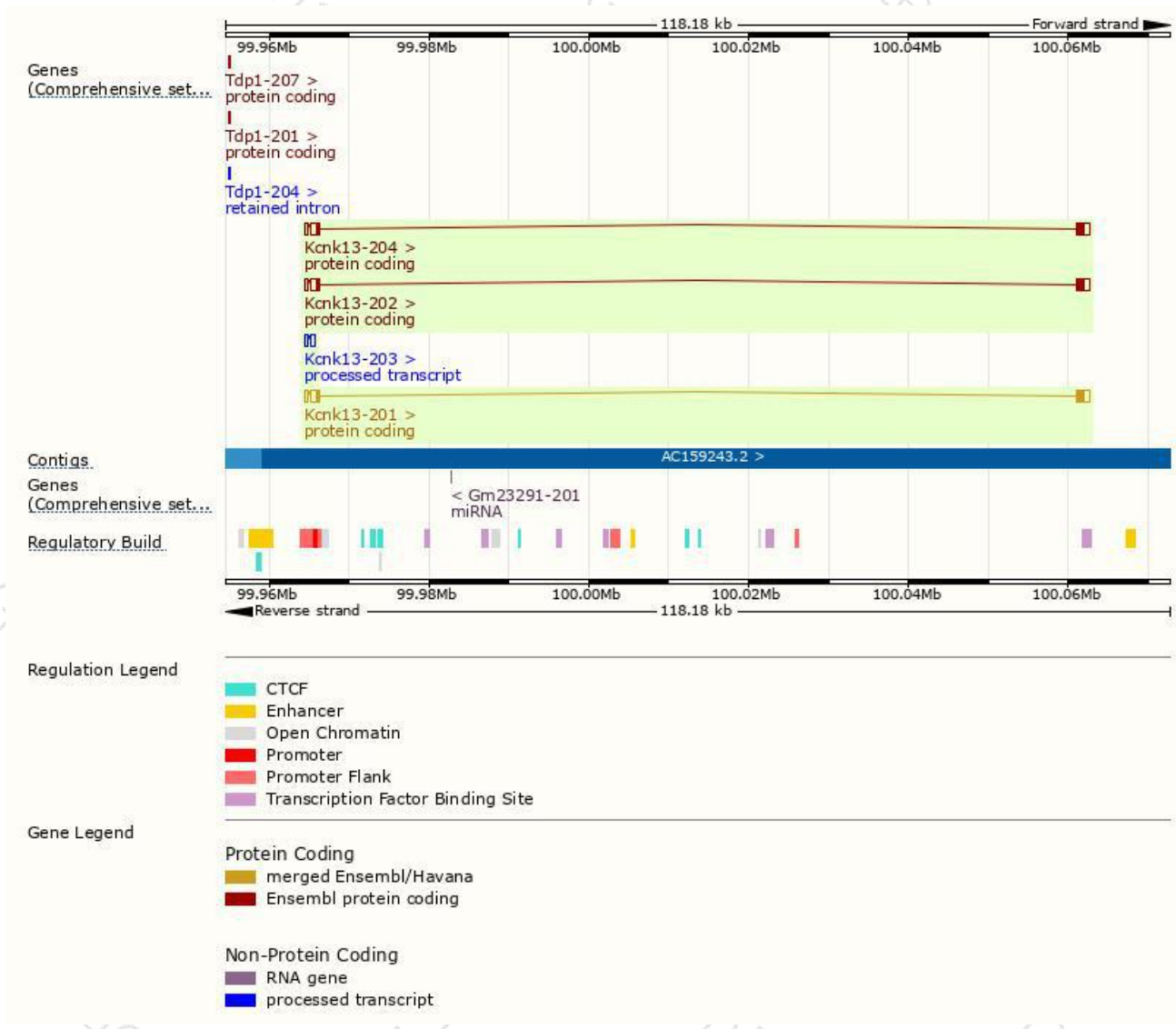
The gene has 4 transcripts,all transcripts are shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Kcnk13-201	ENSMUST00000049788.8	3078	405aa	Protein coding	CCDS26106	Q3TYG8 Q8R1P5	TSL:1 GENCODE basic APPRIS P1
Kcnk13-204	ENSMUST00000177549.7	3075	405aa	Protein coding	CCDS26106	Q3TYG8 Q8R1P5	TSL:5 GENCODE basic APPRIS P1
Kcnk13-202	ENSMUST00000160413.7	3061	405aa	Protein coding	CCDS26106	Q3TYG8 Q8R1P5	TSL:1 GENCODE basic APPRIS P1
Kcnk13-203	ENSMUST00000162221.2	834	No protein	Processed transcript	-	-	TSL:2

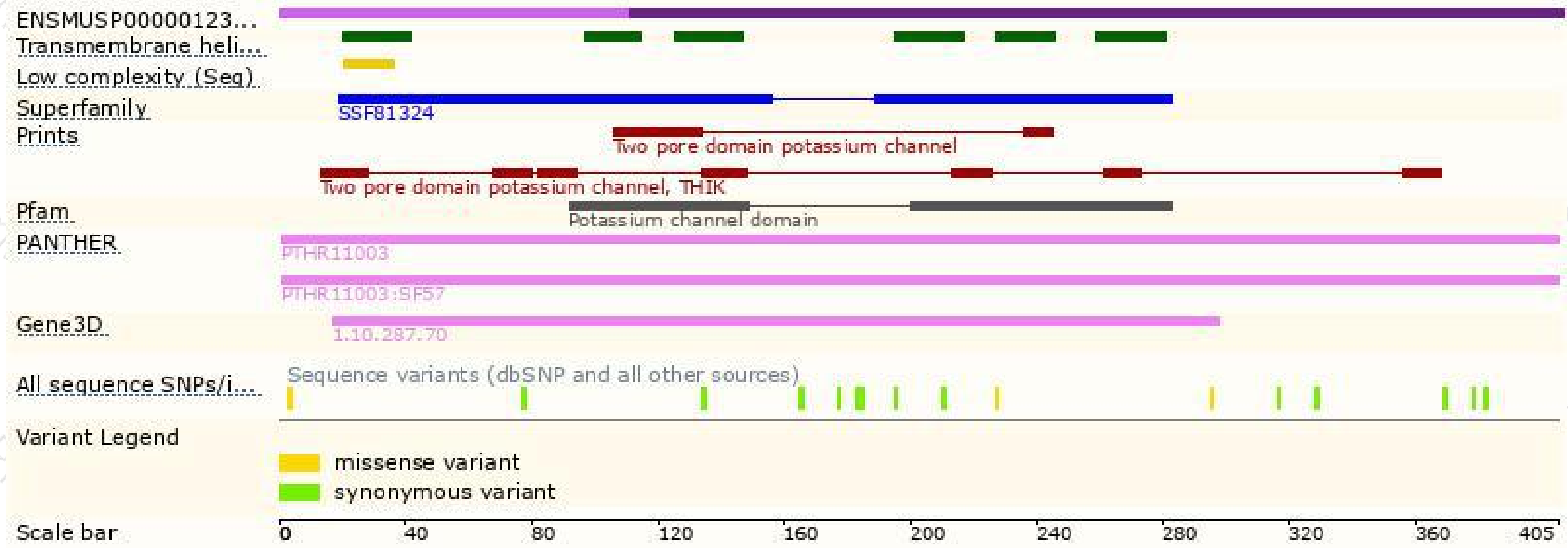
The strategy is based on the design of *Kcnk13-201* transcript,the transcription is shown below:



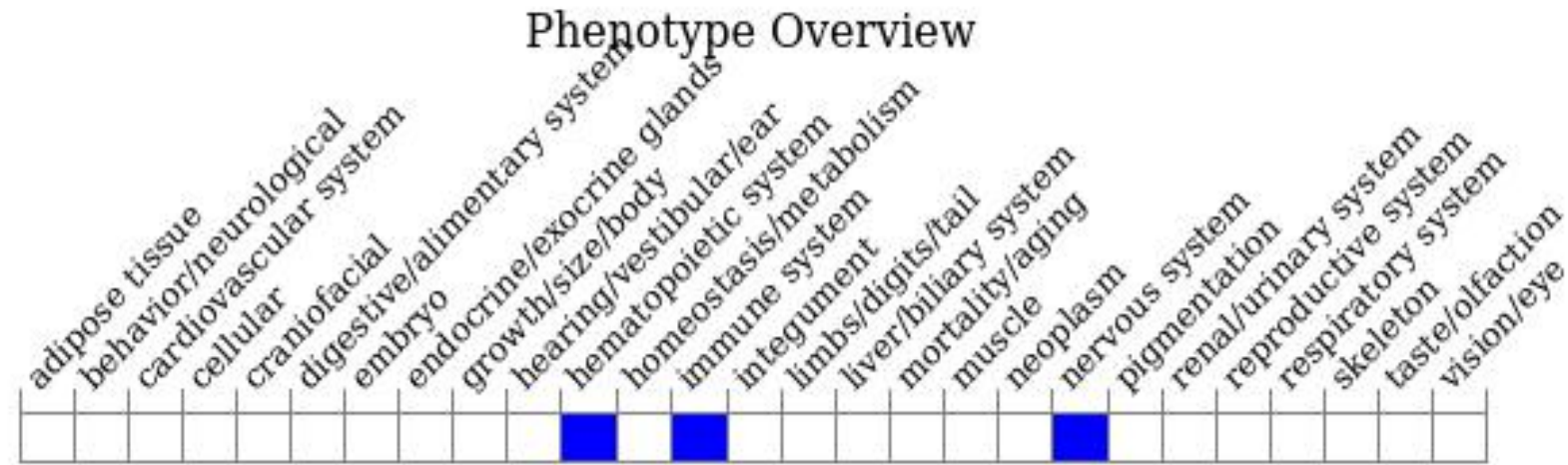
Genomic location distribution



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, homozygous knockout reduces the surveillance activity of microglial cells in the brain.

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

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