

***Kcnh5* Cas9-KO Strategy**

Designer:Fengjuan Wang

Reviewer:Yu Li

Design Date:2019-10-24

Project Overview

Project Name

Kcnh5

Project type

Cas9-KO

Strain background

C57BL/6JGpt

Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *Kcnh5* gene. The schematic diagram is as follows:



- The *Kcnh5* gene has 1 transcript. According to the structure of *Kcnh5* gene, exon2 of *Kcnh5-201* (ENSMUST00000042299.3) transcript is recommended as the knockout region. The region contains 124bp coding sequence. Knock out the region will result in disruption of protein function.
- In this project we use CRISPR/Cas9 technology to modify *Kcnh5* gene. The brief process is as follows: gRNA was transcribed in vitro. Cas9 and gRNA 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 targeted gene disruption display thigmotaxis and abnormal startle reflex.
- The *Kcnh5* 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)

Kcnh5 potassium voltage-gated channel, subfamily H (eag-related), member 5 [Mus musculus (house mouse)]

Gene ID: 238271, updated on 31-Jan-2019

Summary



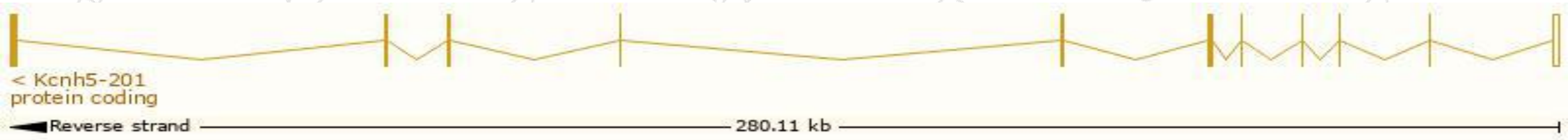
| | |
|---------------------------|---|
| Official Symbol | Kcnh5 provided by MGI |
| Official Full Name | potassium voltage-gated channel, subfamily H (eag-related), member 5 provided by MGI |
| Primary source | MGI:MGI:3584508 |
| See related | Ensembl:ENSMUSG000000034402 |
| Gene type | protein coding |
| 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 | Eag2 |
| Expression | Biased expression in cortex adult (RPKM 2.7), frontal lobe adult (RPKM 1.7) and 4 other tissues See more |
| Orthologs | human all |

Transcript information (Ensembl)

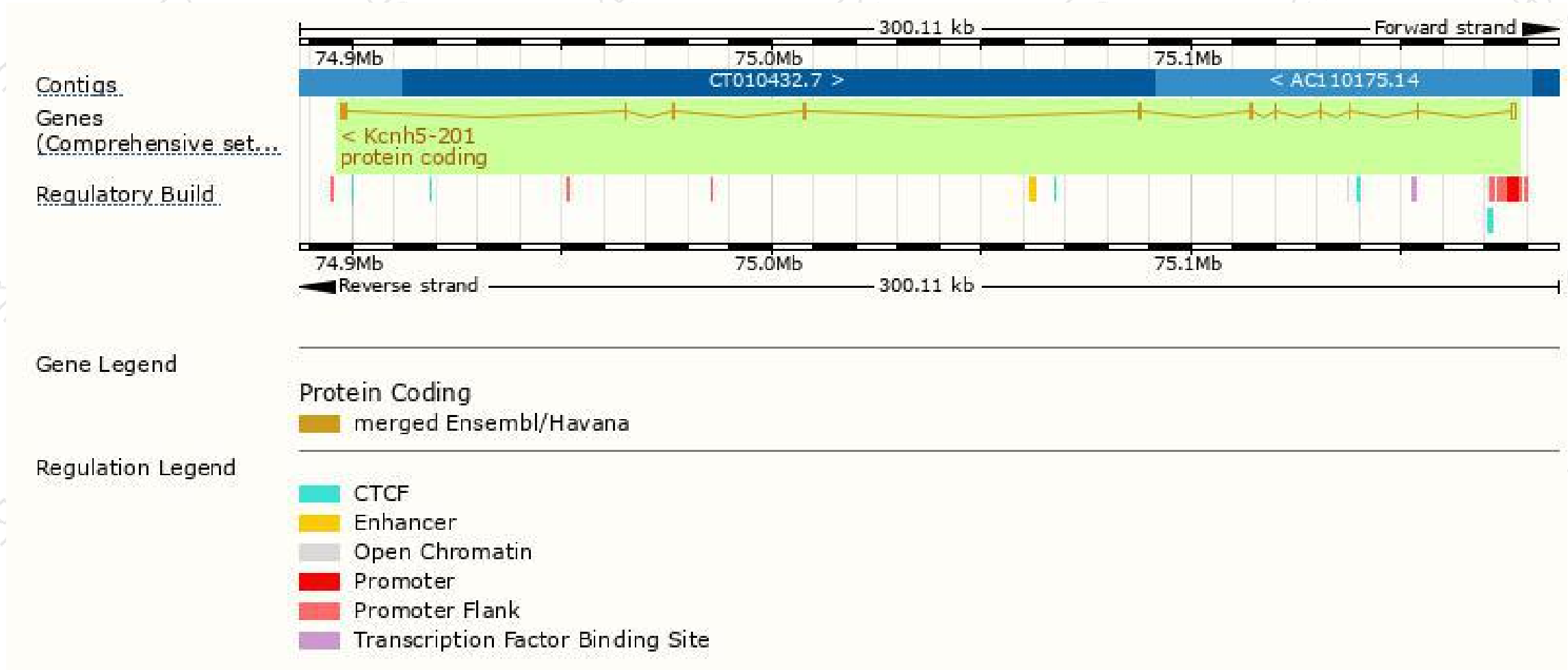
The gene has 1 transcript, and the transcript is shown below:

| Name | Transcript ID | bp | Protein | Biotype | CCDS | UniProt | Flags |
|-----------|--------------------------------------|------|-----------------------|----------------|---------------------------|------------------------|-------------------------------|
| Kcnh5-201 | ENSMUST00000042299.3 | 4058 | 988aa | Protein coding | CCDS25980 | Q920E3 | TSL:1 GENCODE basic APPRIS P1 |

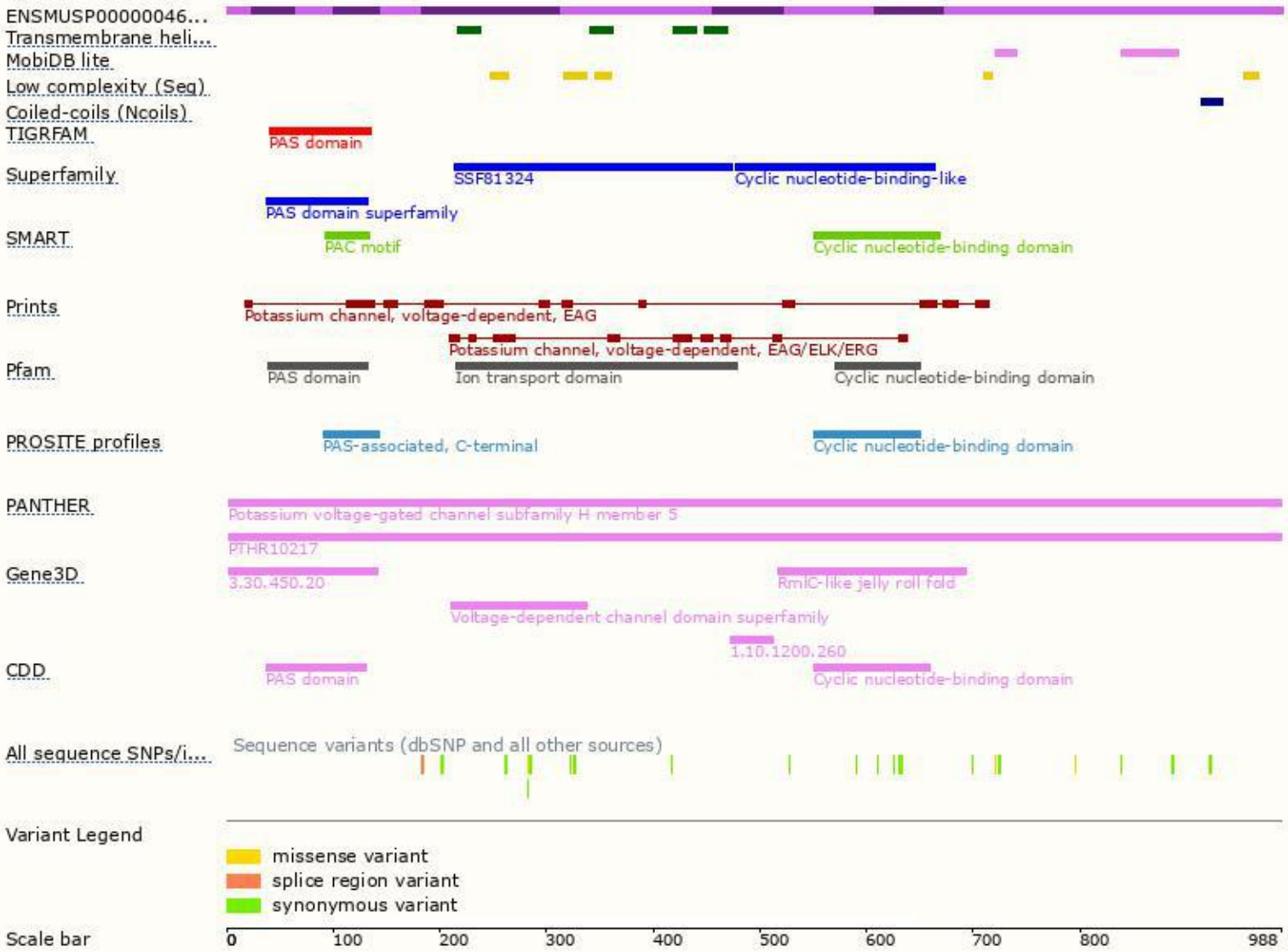
The strategy is based on the design of *Kcnh5-201* transcript, The transcription is shown below



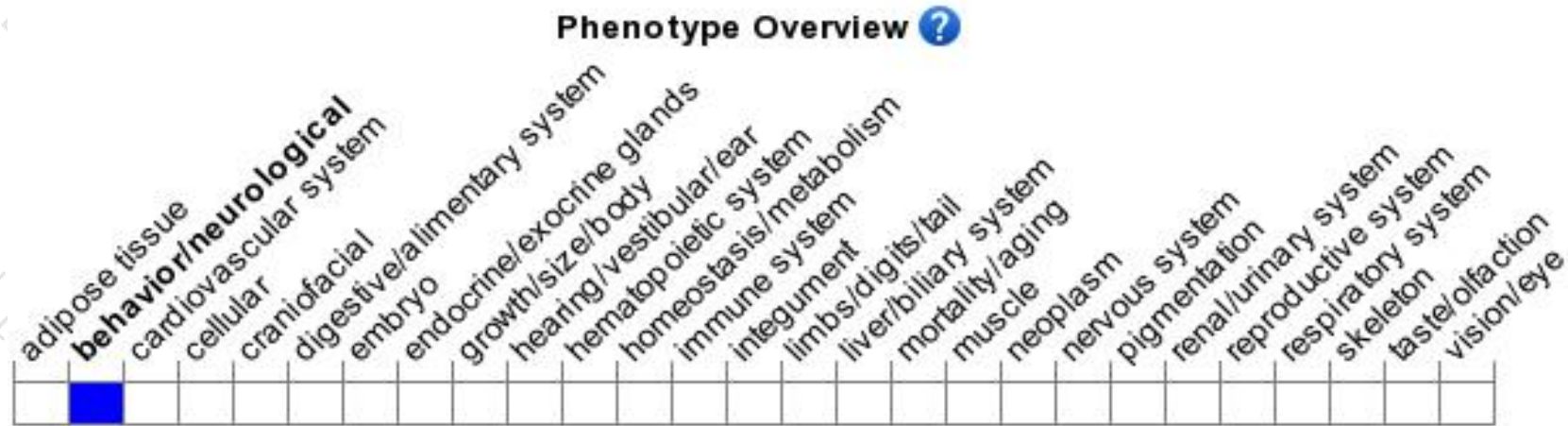
Genomic location distribution



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, Mice homozygous for a targeted gene disruption display thigmotaxis and abnormal startle reflex.

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

Tel: 400-9660890

