

# ***Kcnq4* Cas9-KO Strategy**

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**Reviewer:**

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# Project Overview

**Project Name**

***Kcnq4***

**Project type**

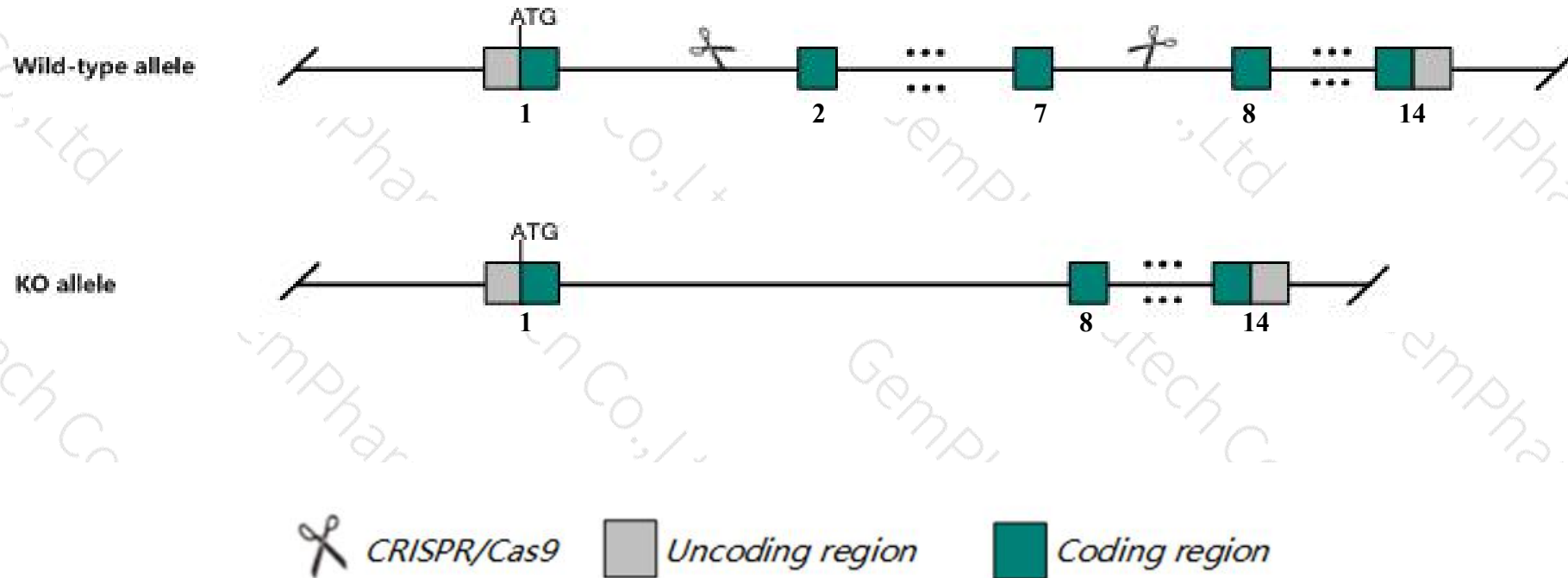
**Cas9-KO**

**Strain background**

**C57BL/6JGpt**

# Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *Kcnq4* gene. The schematic diagram is as follows:



- The *Kcnq4* gene has 2 transcripts. According to the structure of *Kcnq4* gene, exon2-exon7 of *Kcnq4-201* (ENSMUST00000030376.7) transcript is recommended as the knockout region. The region contains 727bp coding sequence. Knock out the region will result in disruption of protein function.
- In this project we use CRISPR/Cas9 technology to modify *Kcnq4* gene. The brief process is as follows: CRISPR/Cas9 system

- According to the existing MGI data, Mice that are either homozygous for a knock-out allele or homozygous for a dominant negative knock-in allele exhibit a slowly progressive hearing loss due to chronic depolarization and subsequent degeneration of cochlear outer hair cells.
- The *Kcnq4* gene is located on the Chr4. 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)

## Kcnq4 potassium voltage-gated channel, subfamily Q, member 4 [Mus musculus (house mouse)]

Gene ID: 60613, updated on 5-Mar-2019

### Summary



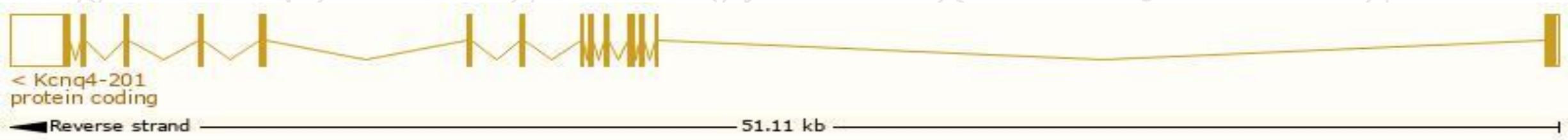
<b>Official Symbol</b>	Kcnq4 provided by <a href="#">MGI</a>
<b>Official Full Name</b>	potassium voltage-gated channel, subfamily Q, member 4 provided by <a href="#">MGI</a>
<b>Primary source</b>	<a href="#">MGI:MGI:1926803</a>
<b>See related</b>	<a href="#">Ensembl:ENSMUSG00000028631</a>
<b>Gene type</b>	protein coding
<b>RefSeq status</b>	VALIDATED
<b>Organism</b>	<a href="#">Mus musculus</a>
<b>Lineage</b>	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Myomorpha; Muroidea; Muridae; Murinae; Mus; Mus
<b>Expression</b>	Broad expression in subcutaneous fat pad adult (RPKM 8.4), mammary gland adult (RPKM 7.6) and 22 other tissues <a href="#">See more</a>
<b>Orthologs</b>	<a href="#">human</a> <a href="#">all</a>

# Transcript information (Ensembl)

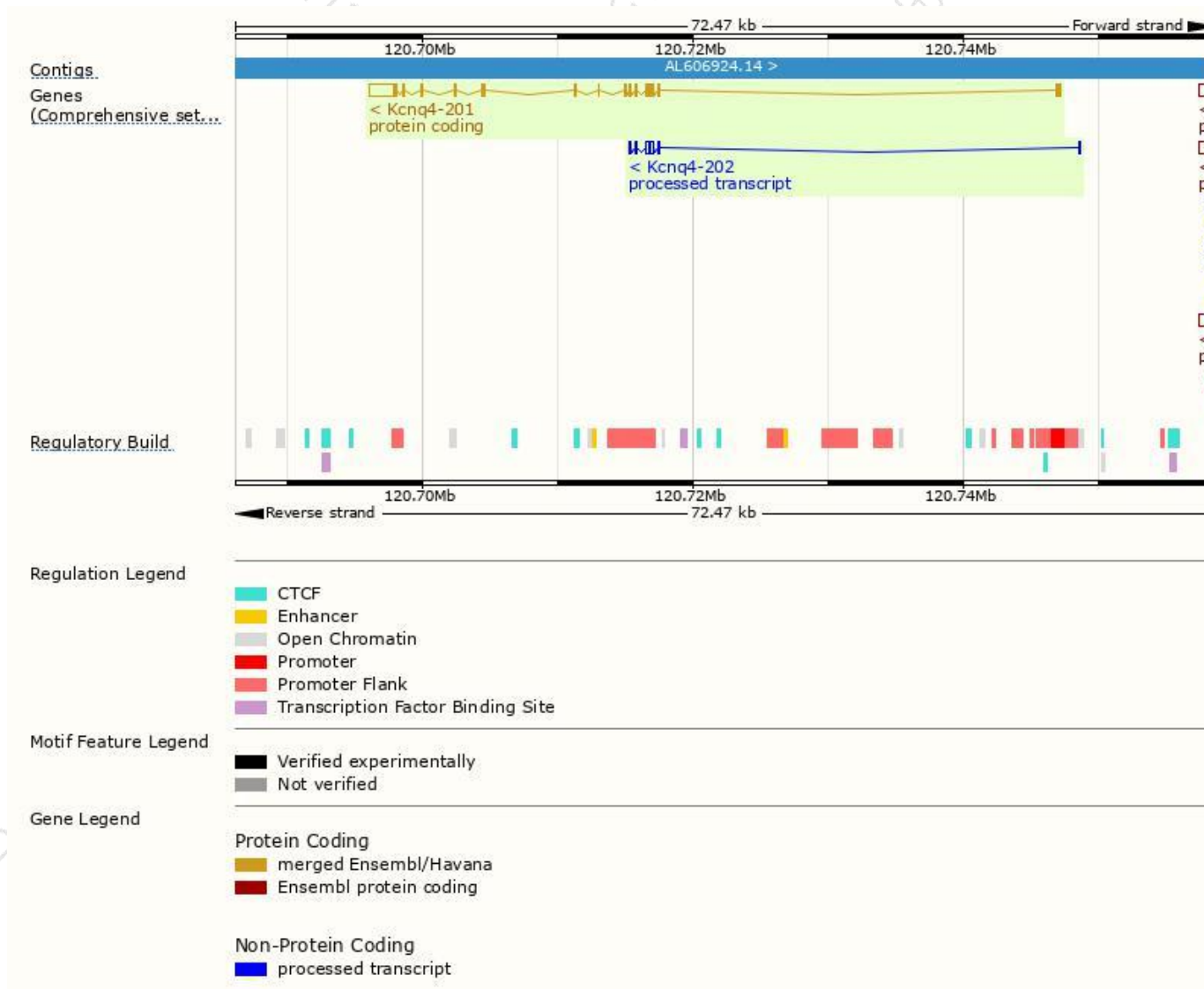
The gene has 2 transcripts,all transcripts are shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Kcnq4-201	<a href="#">ENSMUST00000030376.7</a>	3919	<a href="#">696aa</a>	Protein coding	<a href="#">CCDS38865</a>	<a href="#">Q9JK97</a>	TSL:5 GENCODE basic APPRIS P1
Kcnq4-202	<a href="#">ENSMUST00000129478.1</a>	736	No protein	Processed transcript	-	-	TSL:3

The strategy is based on the design of *Kcnq4-201* transcript,The transcription is shown below

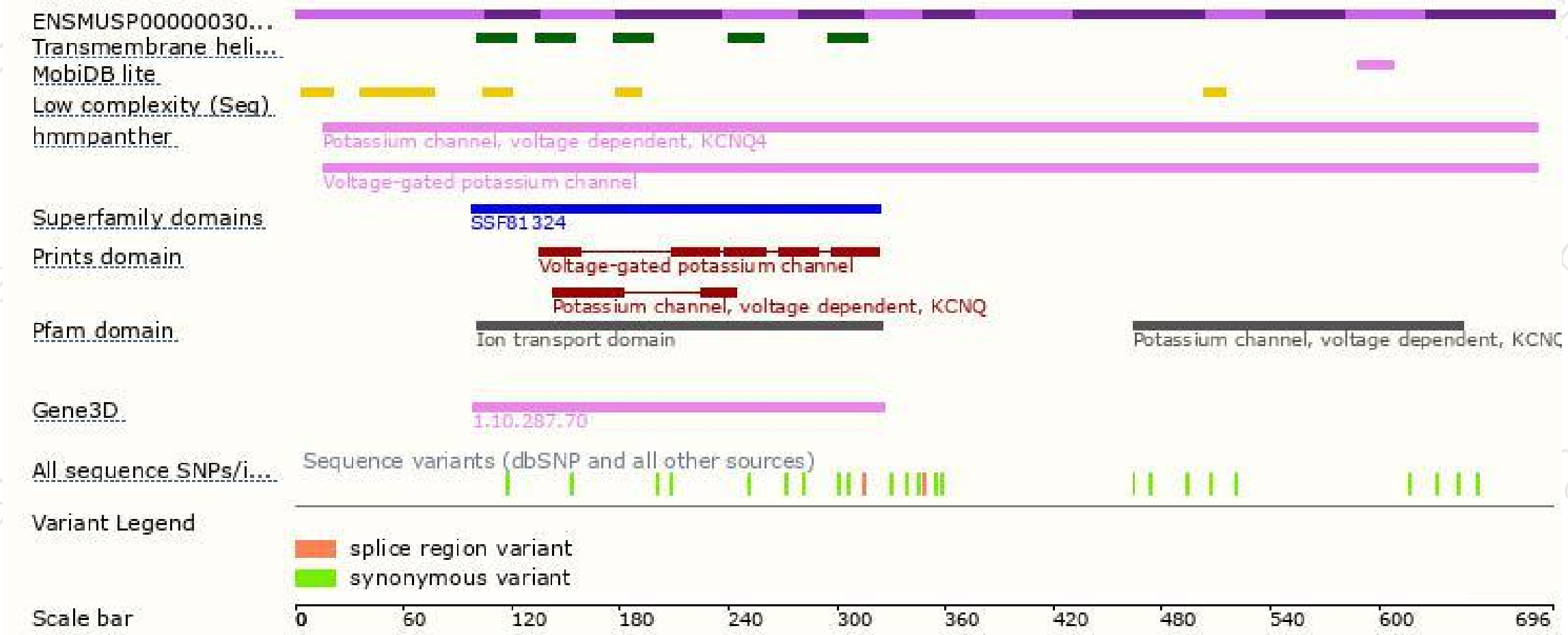


# Genomic location distribution

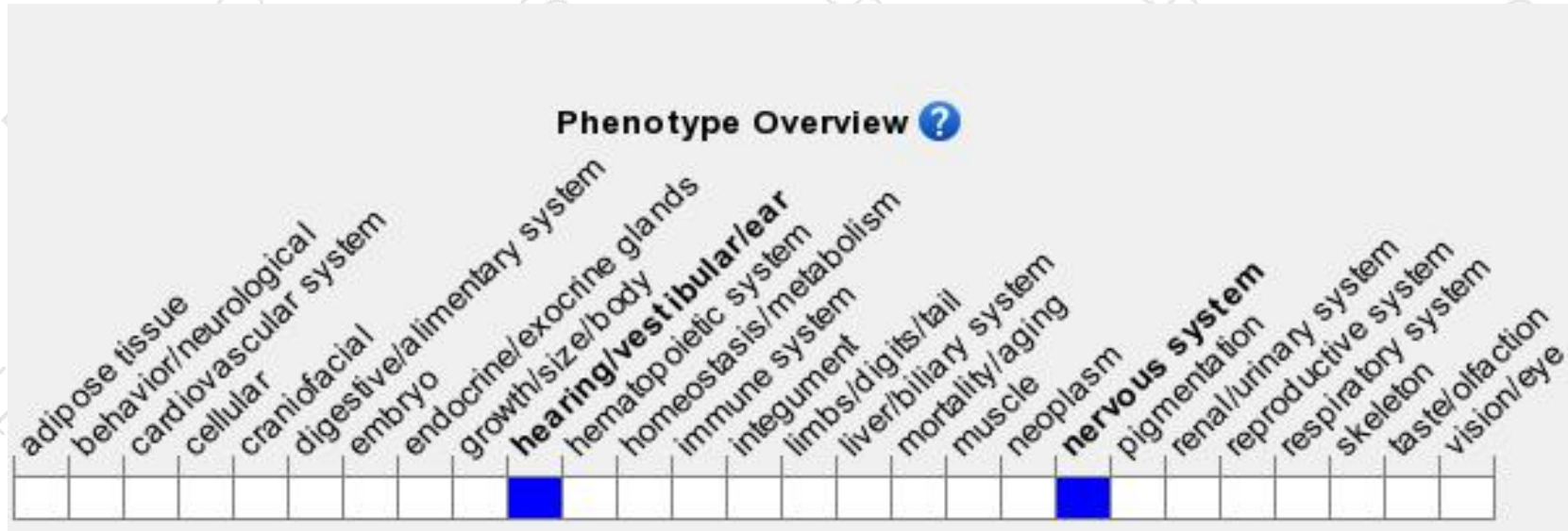




# Protein domain



# 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 that are either homozygous for a knock-out allele or homozygous for a dominant negative knock-in allele exhibit a slowly progressive hearing loss due to chronic depolarization and subsequent degeneration of cochlear outer hair cells.

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

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