# *Kcnq2* Cas9-KO Strategy

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**Design Date:** 2019-7-18

# Project Overview

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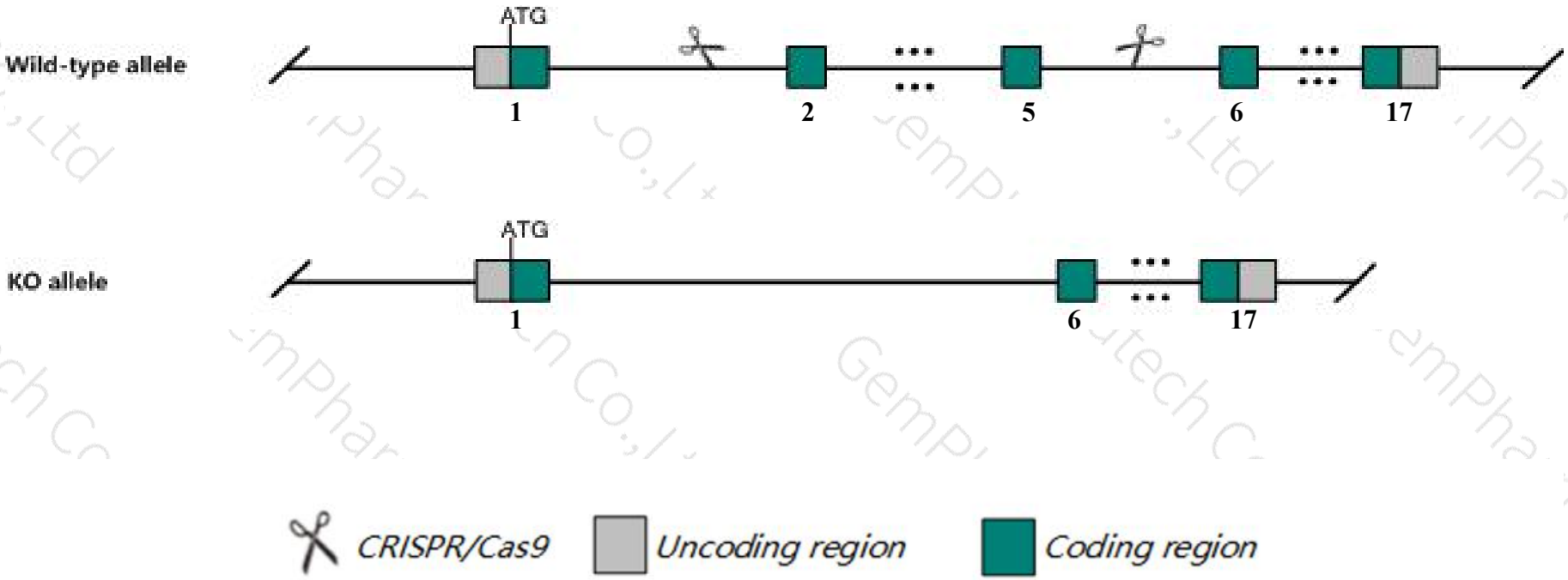
|---|---|
| **Project Name** | ***Kcnq2*** |
| **Project type** | **Cas9-KO** |
| **Strain background** | **C57BL/6JGpt** |

# Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *Kcnq2* gene. The schematic diagram is as follows:



# Technical routes

➢ The *Kcnq2* gene has 21 transcripts. According to the structure of *Kcnq2* gene, exon2-exon5 of *Kcnq2-217* (ENSMUST00000149964.8) transcript is recommended as the knockout region.The region contains 520bp coding sequence. Knock out the region will result in disruption of protein function.

➢ In this project we use CRISPR/Cas9 technology to modify *Kcnq2* gene. The brief process is as follows: CRISPR/Cas9 system

# Notice

- According to the existing MGI data,Mice homozygous for a null mutation die perinatally with pulmonary atelectasis. Heterozygous mice exhibit a hypersensitivity to the epileptic inducer pentylenetetrazole. Mice homozygous for a knock-in allele exhibit spontaneous seizures and premature death.

- The *Kcnq2* gene is located on the Chr2. 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）

集萃药康 GemPharmatech

## Kcnq2 potassium voltage-gated channel, subfamily Q, member 2 [Mus musculus (house mouse)]

Gene ID: 16536, updated on 16-Feb-2019

### Summary

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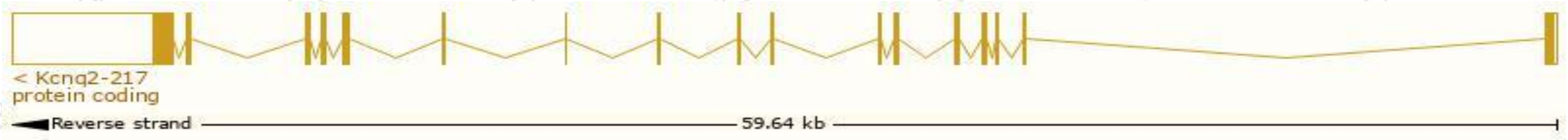
|---|---|
| **Official Symbol** | Kcnq2 provided by MGI |
| **Official Full Name** | potassium voltage-gated channel, subfamily Q, member 2 provided by MGI |
| **Primary source** | MGI:MGI:1309503 |
| **See related** | Ensembl:ENSMUSG00000016346 |
| **Gene type** | protein coding |
| **RefSeq status** | 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** | HNSPC, KQT2, Nmf134 |
| **Expression** | Biased expression in cortex adult (RPKM 26.0), frontal lobe adult (RPKM 26.0) and 5 other tissues See more |
| **Orthologs** | human all |

# Transcript information（Ensembl）

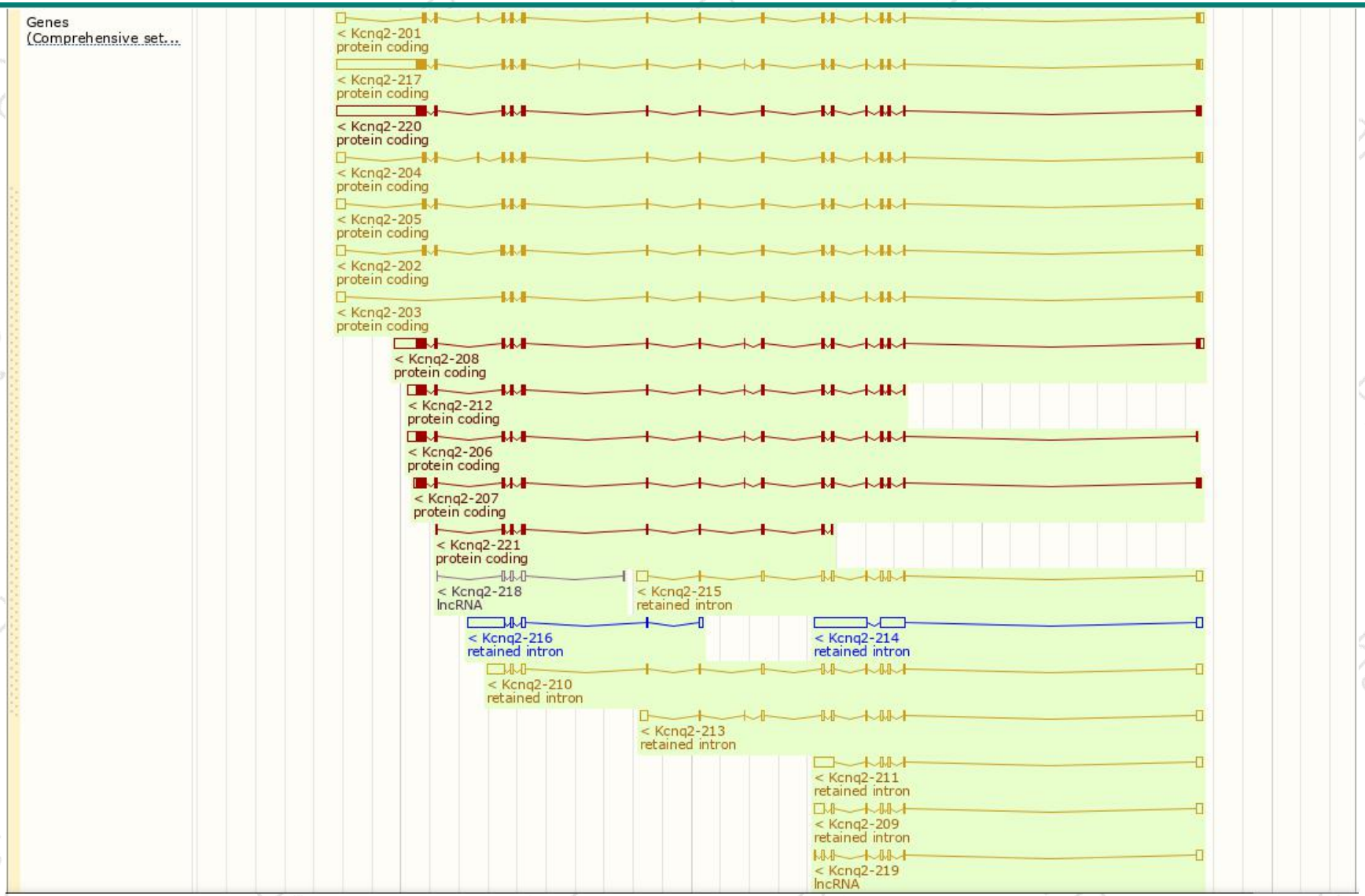
The gene has 21 transcripts,all transcripts are shown below:

| Name | Transcript ID | bp | Protein | Biotype | CCDS | UniProt | Flags |
|---|---|---|---|---|---|---|---|
| Kcnq2-217 | ENSMUST00000149964.8 | 8209 | 870aa | Protein coding | CCDS17198 | B7ZBV9 | TSL:1 GENCODE basic APPRIS P2 |
| Kcnq2-201 | ENSMUST00000016491.13 | 3067 | 759aa | Protein coding | CCDS17193 | B7ZBV4 | TSL:1 GENCODE basic |
| Kcnq2-202 | ENSMUST00000049792.14 | 2920 | 754aa | Protein coding | CCDS17194 | B7ZBV6 | TSL:1 GENCODE basic |
| Kcnq2-204 | ENSMUST00000103047.9 | 2899 | 747aa | Protein coding | CCDS17195 | B7ZBV8 | TSL:1 GENCODE basic |
| Kcnq2-205 | ENSMUST00000103048.9 | 2827 | 723aa | Protein coding | CCDS17196 | B7ZBV7 | TSL:1 GENCODE basic |
| Kcnq2-203 | ENSMUST00000081528.12 | 2382 | 570aa | Protein coding | CCDS17197 | B7ZBV5 | TSL:1 GENCODE basic |
| Kcnq2-220 | ENSMUST00000197015.4 | 8031 | 842aa | Protein coding | - | A0A0G2JFQ2 | TSL:5 GENCODE basic APPRIS ALT2 |
| Kcnq2-208 | ENSMUST00000103051.8 | 4200 | 852aa | Protein coding | - | B7ZBW1 | TSL:5 GENCODE basic APPRIS ALT2 |
| Kcnq2-206 | ENSMUST00000103049.9 | 2936 | 795aa | Protein coding | - | F6UC55 | CDS 5' incomplete TSL:1 |
| Kcnq2-212 | ENSMUST00000129695.7 | 2735 | 726aa | Protein coding | - | B7ZBV3 | CDS 5' incomplete TSL:1 |
| Kcnq2-207 | ENSMUST00000103050.9 | 2713 | 839aa | Protein coding | - | B7ZBW2 | TSL:5 GENCODE basic APPRIS ALT2 |
| Kcnq2-221 | ENSMUST00000197599.1 | 855 | 285aa | Protein coding | - | A0A0G2JGA6 | CDS 5' and 3' incomplete TSL:5 |
| Kcnq2-214 | ENSMUST00000140789.1 | 5796 | No protein | Retained intron | - | - | TSL:2 |
| Kcnq2-216 | ENSMUST00000145861.7 | 3131 | No protein | Retained intron | - | - | TSL:1 |
| Kcnq2-210 | ENSMUST00000129073.7 | 2758 | No protein | Retained intron | - | - | TSL:2 |
| Kcnq2-211 | ENSMUST00000129361.2 | 2243 | No protein | Retained intron | - | - | TSL:2 |
| Kcnq2-215 | ENSMUST00000144592.7 | 2011 | No protein | Retained intron | - | - | TSL:2 |
| Kcnq2-213 | ENSMUST00000139458.7 | 1816 | No protein | Retained intron | - | - | TSL:2 |
| Kcnq2-209 | ENSMUST00000123336.7 | 1686 | No protein | Retained intron | - | - | TSL:2 |
| Kcnq2-219 | ENSMUST00000154164.7 | 1226 | No protein | lncRNA | - | - | TSL:2 |
| Kcnq2-218 | ENSMUST00000152099.6 | 513 | No protein | lncRNA | - | - | TSL:5 |

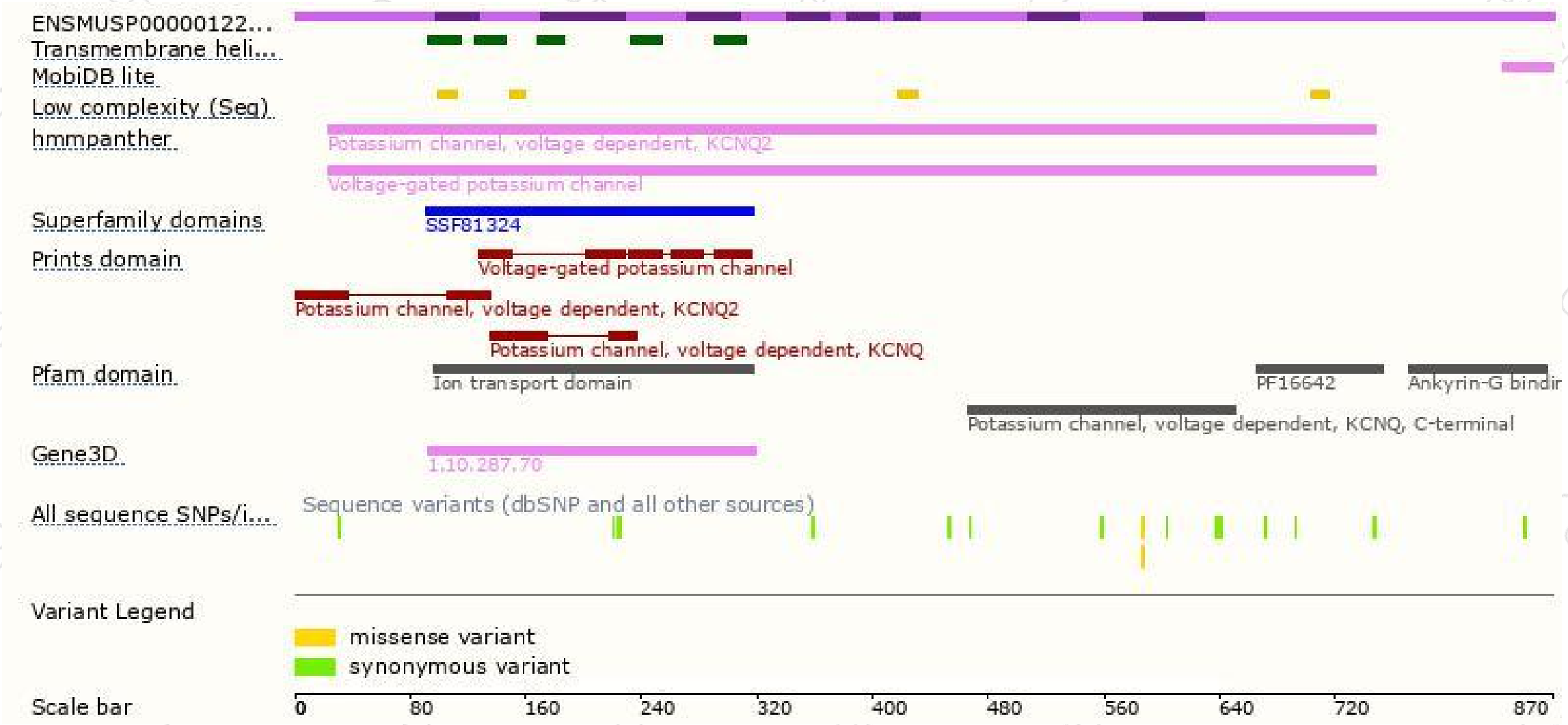
The strategy is based on the design of *Kcnq2-217* transcript,The transcription is shown below



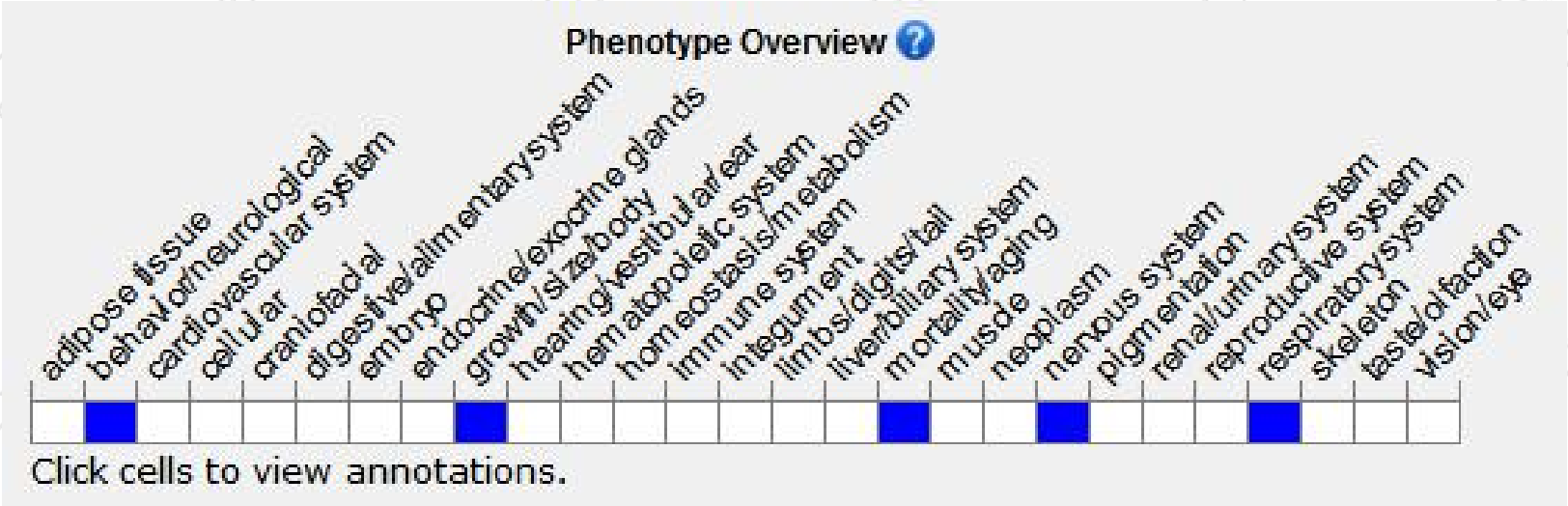
# Genomic location distribution



# 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 null mutation die perinatally with pulmonary atelectasis. Heterozygous mice exhibit a hypersensitivity to the epileptic inducer pentylenetetrazole. Mice homozygous for a knock-in allele exhibit spontaneous seizures and premature death.

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

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