Kcnq1 Cas9-KO Strategy

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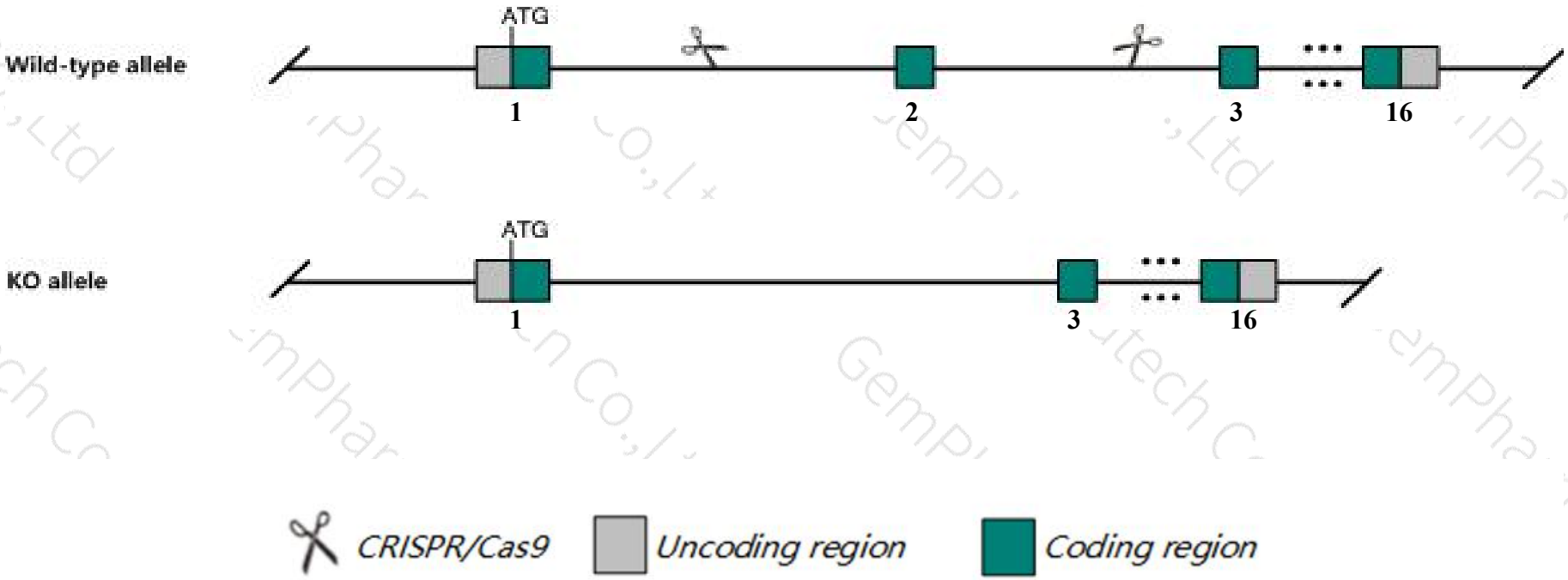
Project Overview

Project Name	***Kcnq1***
Project type	**Cas9-KO**
Strain background	**C57BL/6JGpt**

Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *Kcnq1* gene. The schematic diagram is as follows:



Technical routes

➢ The *Kcnq1* gene has 7 transcripts. According to the structure of *Kcnq1* gene, exon2 of *Kcnq1-201* (ENSMUST00000009689.10) transcript is recommended as the knockout region.The region contains 91bp coding sequence. Knock out the region will result in disruption of protein function.

➢ In this project we use CRISPR/Cas9 technology to modify *Kcnq1* gene. The brief process is as follows: CRISPR/Cas9 system

Notice

- According to the existing MGI data,Homozygous targeted null or spontaneous mutants show circling and head-tossing behavior and are deaf with inner ear dysmorphology. Paternal inheritance of a deletion of an imprinted control region within an intron of this gene results in small body size.

- The *Kcnq1* gene is located on the Chr7. 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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Kcnq1 potassium voltage-gated channel, subfamily Q, member 1 [Mus musculus (house mouse)]

Gene ID: 16535, updated on 31-Jan-2019

Summary

Official Symbol	Kcnq1 provided by MGI
Official Full Name	potassium voltage-gated channel, subfamily Q, member 1 provided by MGI
Primary source	MGI:MGI:108083
See related	Ensembl:ENSMUSG00000009545
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	AW559127, KVLQT1, Kcna9
Expression	Biased expression in large intestine adult (RPKM 20.0), colon adult (RPKM 19.5) and 10 other tissues See more
Orthologs	human all

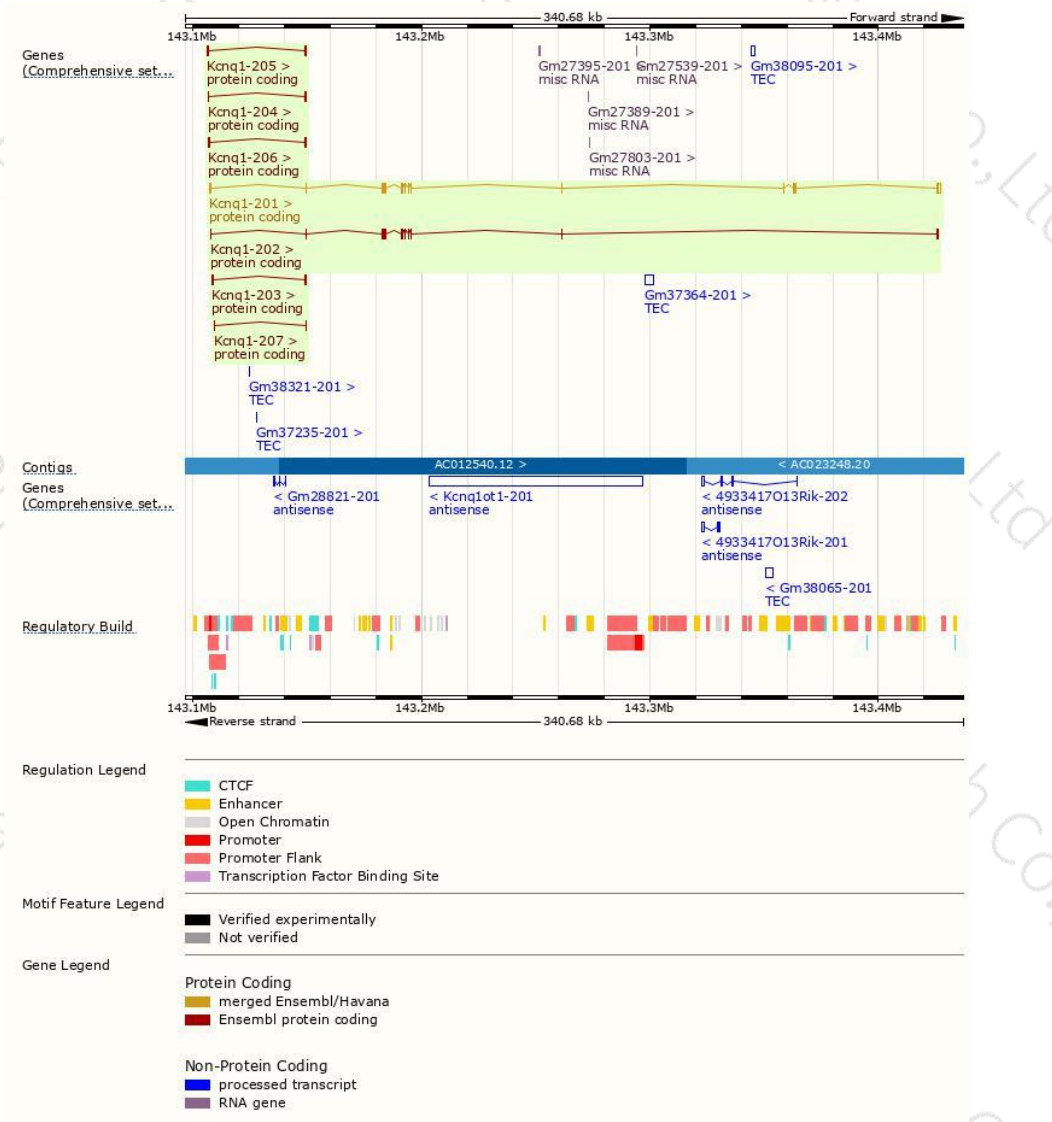
Transcript information（Ensembl）

The gene has 7 transcripts,all transcripts are shown below:

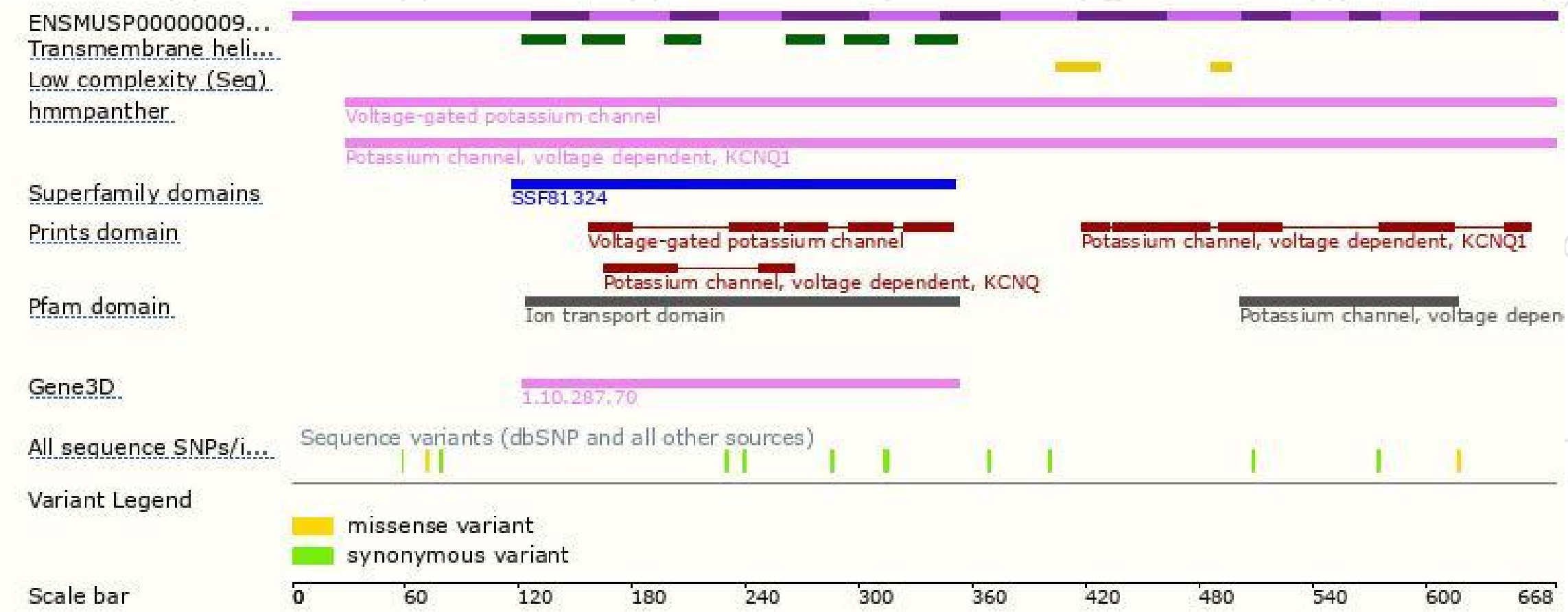
Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Kcnq1-201	ENSMUST00000009689.10	3029	668aa	Protein coding	CCDS22039	P97414	TSL:1 GENCODE basic APPRIS P1
Kcnq1-202	ENSMUST00000185383.1	1535	440aa	Protein coding	-	A0A087WNY7	TSL:1 GENCODE basic
Kcnq1-203	ENSMUST00000186284.6	490	77aa	Protein coding	-	A0A087WQE3	CDS 3' incomplete TSL:1
Kcnq1-206	ENSMUST00000186798.1	294	49aa	Protein coding	-	A0A087WPJ2	CDS 3' incomplete TSL:1
Kcnq1-207	ENSMUST00000187213.1	282	39aa	Protein coding	-	A0A087WPA8	CDS 3' incomplete TSL:1
Kcnq1-204	ENSMUST00000186288.6	196	30aa	Protein coding	-	A0A087WRU8	CDS 3' incomplete TSL:1
Kcnq1-205	ENSMUST00000186488.6	182	60aa	Protein coding	-	A0A087WRK7	CDS 3' incomplete TSL:1

The strategy is based on the design of *Kcnq1-201* transcript,The transcription is shown below

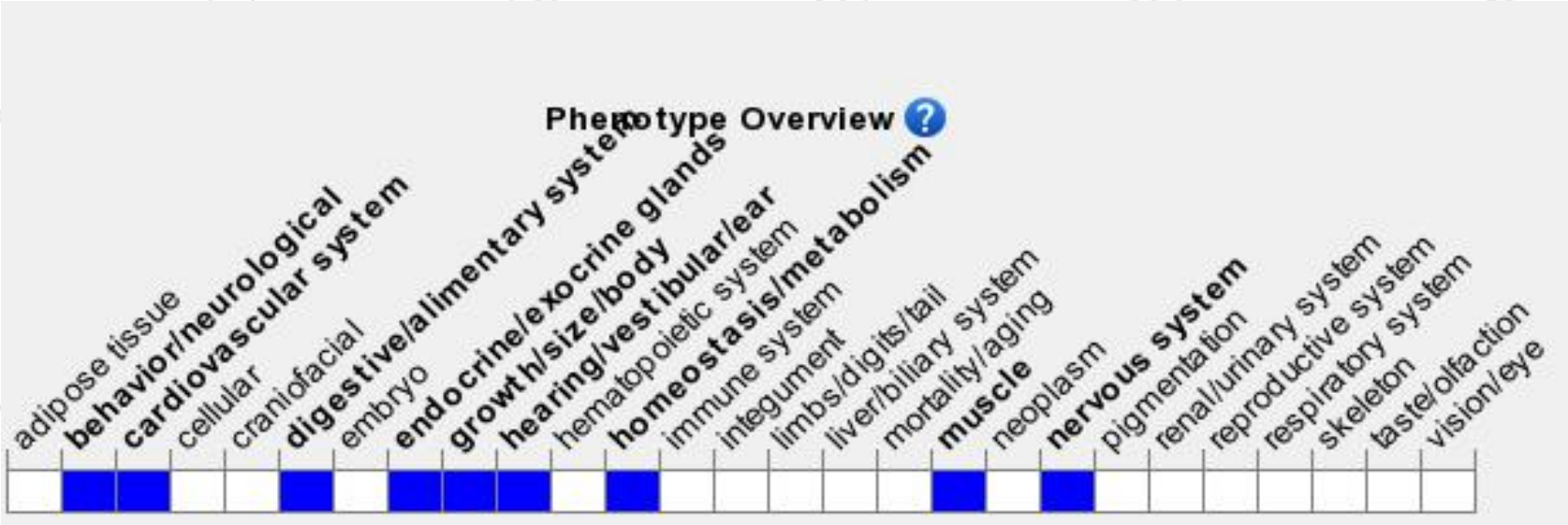
Genomic location distribution



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/).

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

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