

# *Kcng2* Cas9-CKO Strategy

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**Reviewer: Yanhua Shen**

**Design Date: 2022-8-15**

# Project Overview

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**Project Name**

*Kcng2*

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**Project type**

**Cas9-CKO**

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**Strain background**

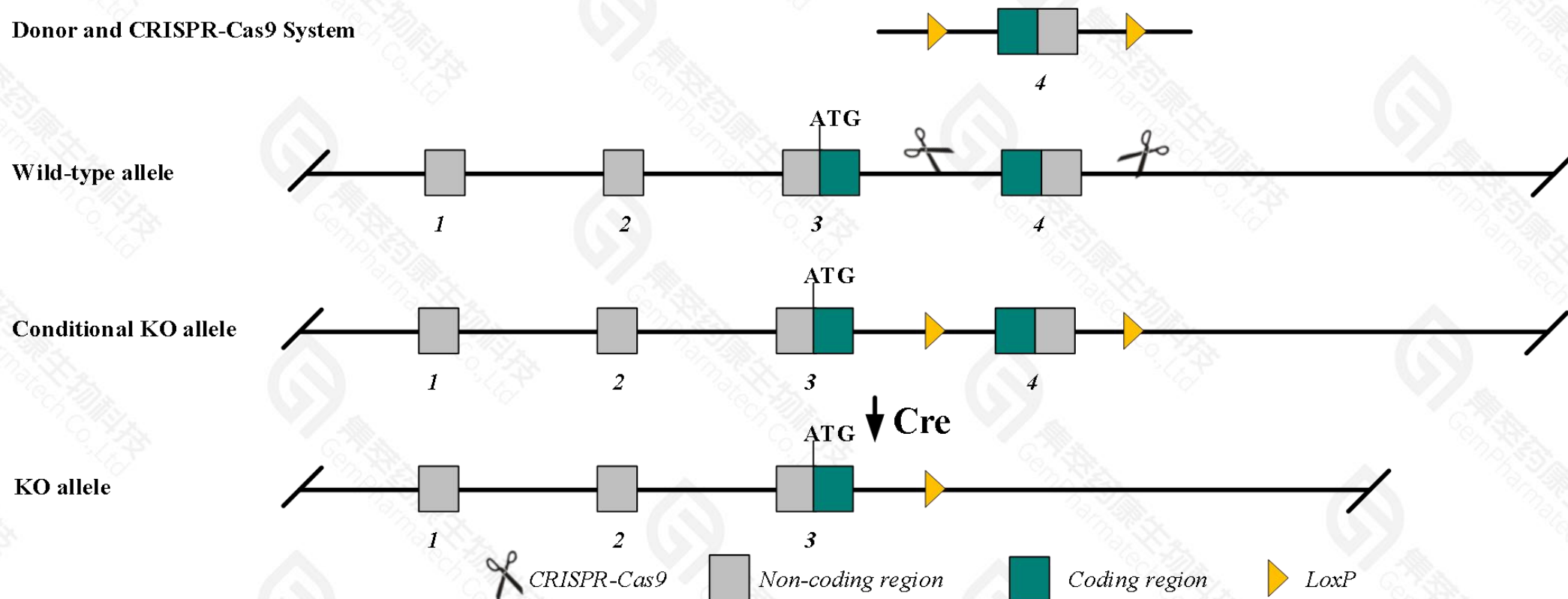
**C57BL/6JGpt**

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# Conditional Knockout strategy

This model will use CRISPR-Cas9 technology to edit the *Kcng2* gene. The schematic diagram is as follows:

Donor and CRISPR-Cas9 System



- The *Kcng2* gene has 3 transcripts. According to the structure of *Kcng2* gene, exon4 of *Kcng2-201*(ENSMUST00000077962.8) transcript is recommended as the knockout region. The region contains part of the coding sequence. Knock out the region will result in disruption of protein function.
- In this project we use CRISPR-Cas9 technology to modify *Kcng2* gene. The brief process is as follows: CRISPR-Cas9 system and Donor 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.
- The flox mice will be knocked out after mating with mice expressing Cre recombinase, resulting in the loss of function of the target gene in specific tissues and cell types.



- The KO region is close to *Slc66a2* gene. Knockout the region may affect the function of *Slc66a2* gene.
- The effect of *Kcng2-202* and *Kcng2-203* is unknown.
- The N-terminal of *Kcng2* gene will remain several amino acids, it may remain the partial function of *Kcng2* gene.
- The *Kcng2* gene is located on the Chr18. 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 loxp insertion on gene transcription, RNA splicing and protein translation cannot be predicted at existing technological level.

# Existing model information(MGI)

Kcng2 <sup>em1(IMPC)</sup> Bay		Your Input Welcome						
Endonuclease-mediated Allele Detail								
Nomenclature   Mutation origin   Mutation description   Expression   Phenotypes   Find Mice (IMSR)   References								
Nomenclature	Symbol: Kcng2 <sup>em1(IMPC)</sup> Bay Name: potassium voltage-gated channel, subfamily G, member 2; endonuclease-mediated mutation 1, Baylor College of Medicine MGI ID: MGI:6257602 Gene: Kcng2 Location: Chr18:80337761-80407469 bp, - strand Genetic Position: Chr18, 53.4 cM							
Mutation origin	Strain of Origin: C57BL/6N Project Collection: IMPC							
Mutation description	Allele Type: Endonuclease-mediated (Null/knockout) Mutation: Intragenic deletion Mutation details: This allele from IMPC was generated at Baylor College of Medicine by injecting CAS9 RNA and 2 guide sequences CCTAAGGAGGGGGCTGGCAATT, GTGGAGCACTCGCCCTATGGAGG, which resulted in a Exon Deletion. (J:265051) Inheritance: Not Specified							
Phenotypes	<div>Key: hm homozygous ht heterozygous tg involves transgenes <input checked="" type="checkbox"/> phenotype observed cn conditional genotype cx complex: &gt; 1 genome feature ot other: hemizygous, indeterminate, ... N normal phenotype</div> <div>Genotype/Background:<table><thead><tr><th>Allelic Composition</th><th>Genetic Background</th><th>Cell Line(s)</th></tr></thead><tbody><tr><td>hm1 Kcng2<sup>em1(IMPC)</sup>Bay/Kcng2<sup>em1(IMPC)</sup>Bay</td><td>C57BL/6N-Kcng2<sup>em1(IMPC)</sup>Bay/Bay</td><td></td></tr></tbody></table></div> <div>Phenotypes:<div><div>Affected Systems</div><div>show or hide all annotated terms</div><div><div>Sex: ♀ ♂</div><div>Source: ?</div><div>IMPC - BCM IMPC - BCM</div><div>behavior/neurological ▶ ✓ ✓</div><div>cardiovascular system ▶ ✓ ✓</div><div>growth/size/body ▶ ✓</div><div>homeostasis/metabolism ▶ ✓ ✓</div></div></div><div><a href="#">View</a> phenotypes and curated references for all genotypes (concatenated display).</div></div>		Allelic Composition	Genetic Background	Cell Line(s)	hm1 Kcng2 <sup>em1(IMPC)</sup> Bay/Kcng2 <sup>em1(IMPC)</sup> Bay	C57BL/6N-Kcng2 <sup>em1(IMPC)</sup> Bay/Bay	
Allelic Composition	Genetic Background	Cell Line(s)						
hm1 Kcng2 <sup>em1(IMPC)</sup> Bay/Kcng2 <sup>em1(IMPC)</sup> Bay	C57BL/6N-Kcng2 <sup>em1(IMPC)</sup> Bay/Bay							
Expression	In Structures Affected by this Mutation: 2 anatomical structures							
Find Mice (IMSR)	Mouse strains and cell lines available from the International Mouse Strain Resource (IMSR) Carrying this Mutation: Mouse Strains: 0 strains available Cell Lines: 0 lines available Carrying any Kcng2 Mutation: 5 strains or lines available							
References	Original: J:265051 MGI and IMPC, MGI Load of Endonuclease-Mediated Alleles (CRISPR) from the International Mouse Phenotyping Consortium (IMPC). Database Release. 2018;							

http://www.informatics.jax.org/allele/MGI:6257602

# Gene information (NCBI)

**Kcng2** potassium voltage-gated channel, subfamily G, member 2 [ *Mus musculus* (house mouse) ]

[Download Datasets](#)

Gene ID: 240444, updated on 13-Aug-2022

## Summary

**Official Symbol** Kcng2 provided by [MGI](#)

**Official Full Name** potassium voltage-gated channel, subfamily G, member 2 provided by [MGI](#)

**Primary source** [MGI:MGI:3694646](#)

**See related** [Ensembl:ENSMUSG00000059852](#) [AllianceGenome:MGI:3694646](#)

**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

**Summary** Predicted to enable voltage-gated potassium channel activity. Predicted to be involved in potassium ion transmembrane transport. Predicted to be part of voltage-gated potassium channel complex. Predicted to be integral component of membrane. Orthologous to human KCNG2 (potassium voltage-gated channel modifier subfamily G member 2). [provided by Alliance of Genome Resources, Apr 2022]

**Expression** Biased expression in heart adult (RPKM 41.8) and thymus adult (RPKM 2.3) [See more](#)

**Orthologs** [human](#) [all](#)

**NEW**

Try the new [Gene table](#)

Try the new [Transcript table](#)

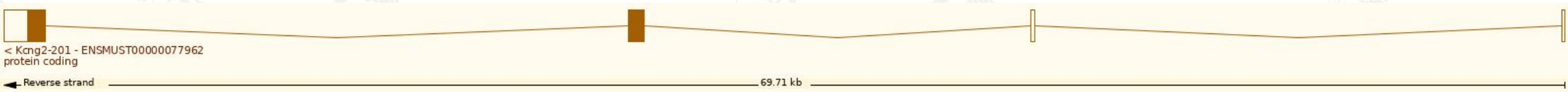


# Transcript information (Ensembl)

The gene has 3 transcripts,and the transcript is shown below:

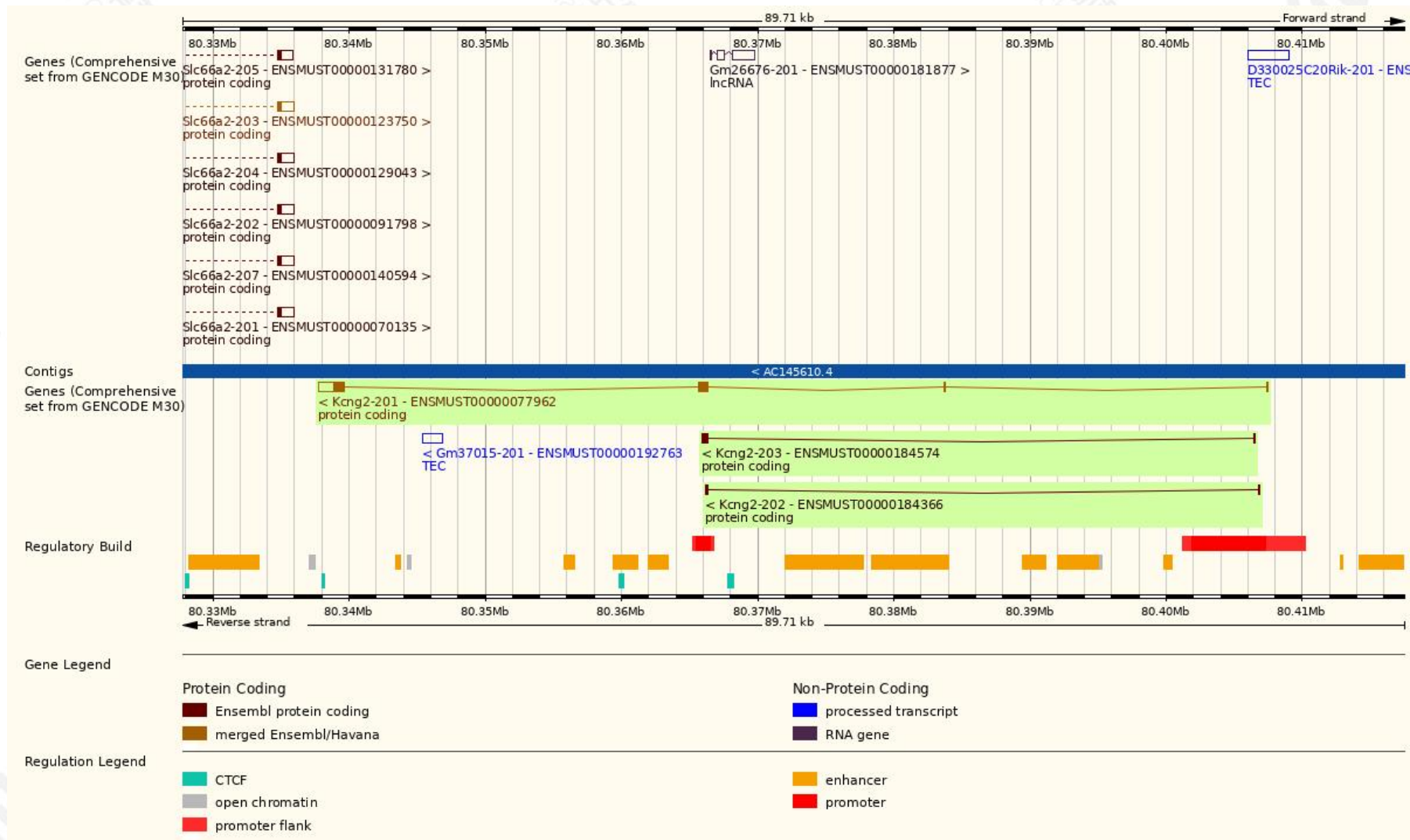
Transcript ID	Name	bp	Protein	Biotype	CCDS	UniProt Match	Flags
<a href="#">ENSMUST00000077962.8</a>	Kcng2-201	2813	<a href="#">480aa</a>	Protein coding	<a href="#">CCDS57127</a>	<a href="#">F7A6P6</a>	Ensembl Canonical GENCODE basic APPRIS P1 TSL:5
<a href="#">ENSMUST00000184366.2</a>	Kcng2-202	279	<a href="#">64aa</a>	Protein coding		<a href="#">V9GX03</a>	TSL:5 CDS 3' incomplete
<a href="#">ENSMUST00000184574.2</a>	Kcng2-203	616	<a href="#">152aa</a>	Protein coding		<a href="#">V9GXB3</a>	TSL:3 CDS 3' incomplete

The strategy is based on the design of *Kcng2-201* transcript,the transcription is shown below:

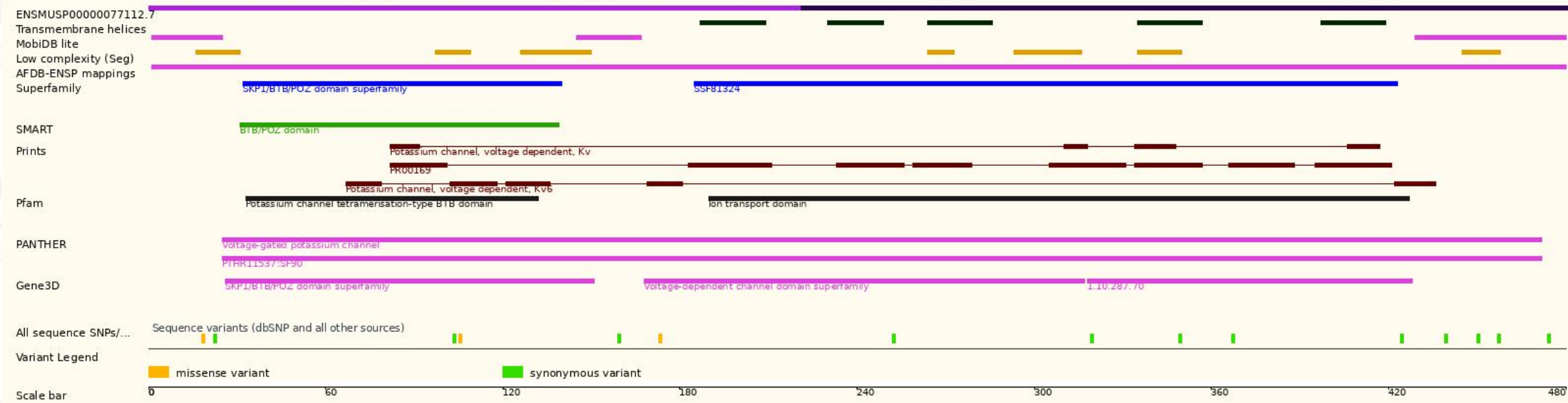




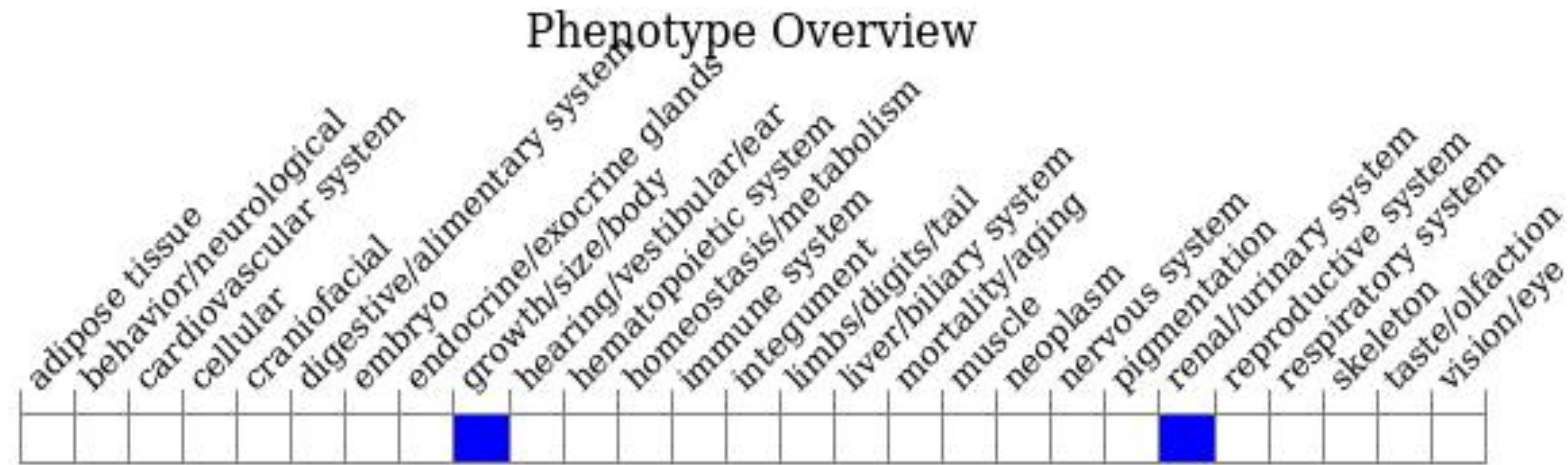
# Genomic location distribution



# 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/>).*



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