Kcnip2 Cas9-CKO Strategy

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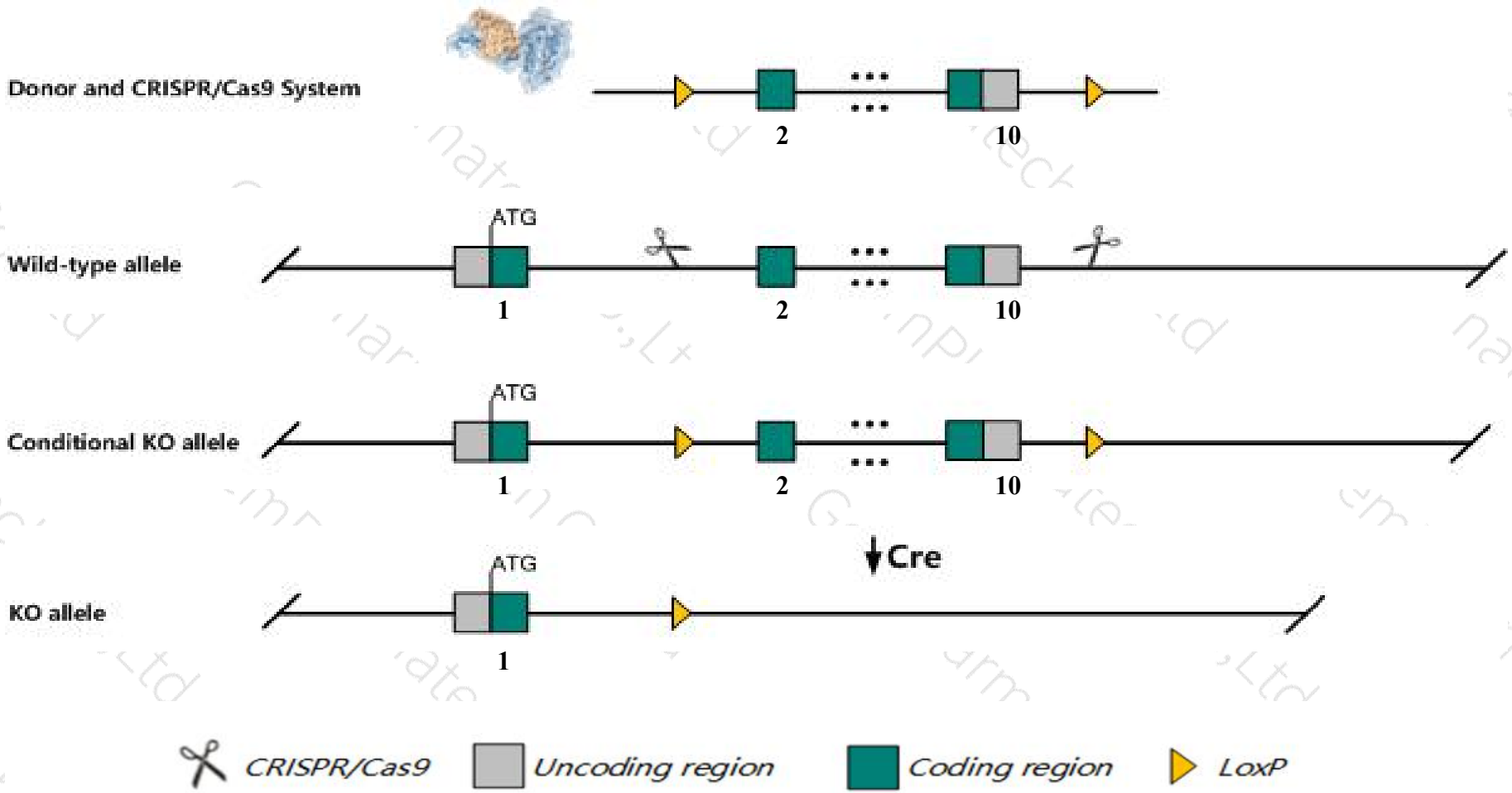
Project Overview

Project Name	***Kcnip2***
Project type	**Cas9-CKO**
Strain background	**C57BL/6JGpt**

Conditional Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *Kcnip2* gene. The schematic diagram is as follows:



Technical routes

➢ The *Kcnip2* gene has 10 transcripts. According to the structure of *Kcnip2* gene, exon2-exon10 of *Kcnip2-209* (ENSMUST00000162528.8) transcript is recommended as the knockout region.The region contains most 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 *Kcnip2* 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.

Notice

- According to the existing MGI data,Mice homozygous for disruptions in this gene are susceptible to induced cardiac arrhythmias but are otherwise normal.
- The floxed region is near to the N-terminal of *Oga* gene,this strategy may influence the regulatory function of the N-terminal of Oga gene.
- The *Kcnip2* gene is located on the Chr19. 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.

Gene information （NCBI）

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Kcnip2 Kv channel-interacting protein 2 [*Mus musculus* (house mouse)]

Gene ID: 80906, updated on 7-Oct-2019

Summary

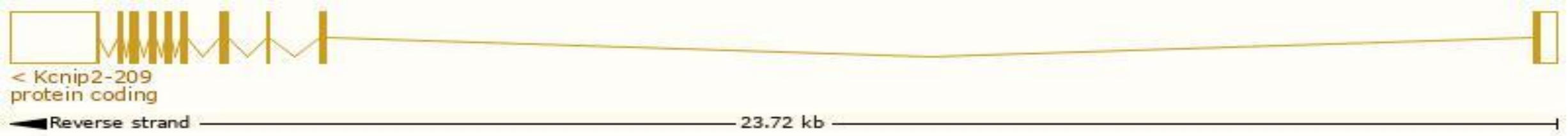
Official Symbol	Kcnip2 provided by MGI
Official Full Name	Kv channel-interacting protein 2 provided by MGI
Primary source	MGI:MGI:2135916
See related	Ensembl:ENSMUSG00000025221
Gene type	protein coding
RefSeq status	REVIEWED
Organism	Mus musculus
Lineage	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Myomorpha; Muroidea; Muridae; Murinae; Mus; Mus
Also known as	KChIP2
Summary	This gene encodes a member of the voltage-gated potassium channel-interacting protein (KCNIP) family. KCNIP family members are small calcium binding proteins that commonly exhibit unique variation at their N-termini, and which modulate A-type potassium channels. This gene is predominantly expressed in the adult heart, and to a lesser extent in the brain. Disruption of this gene is associated with susceptibility to cardiac arrhythmias and lack of transient outward potassium current in ventricular myocytes, and downregulated expression is associated with cardiac hypertrophy. The encoded protein has also been implicated as a repressor of immune response. Alternative splicing results in multiple transcript variants. [provided by RefSeq, Feb 2013]
Expression	Biased expression in heart adult (RPKM 60.6), cortex adult (RPKM 30.5) and 5 other tissues See more
Orthologs	human all

Transcript information（Ensembl）

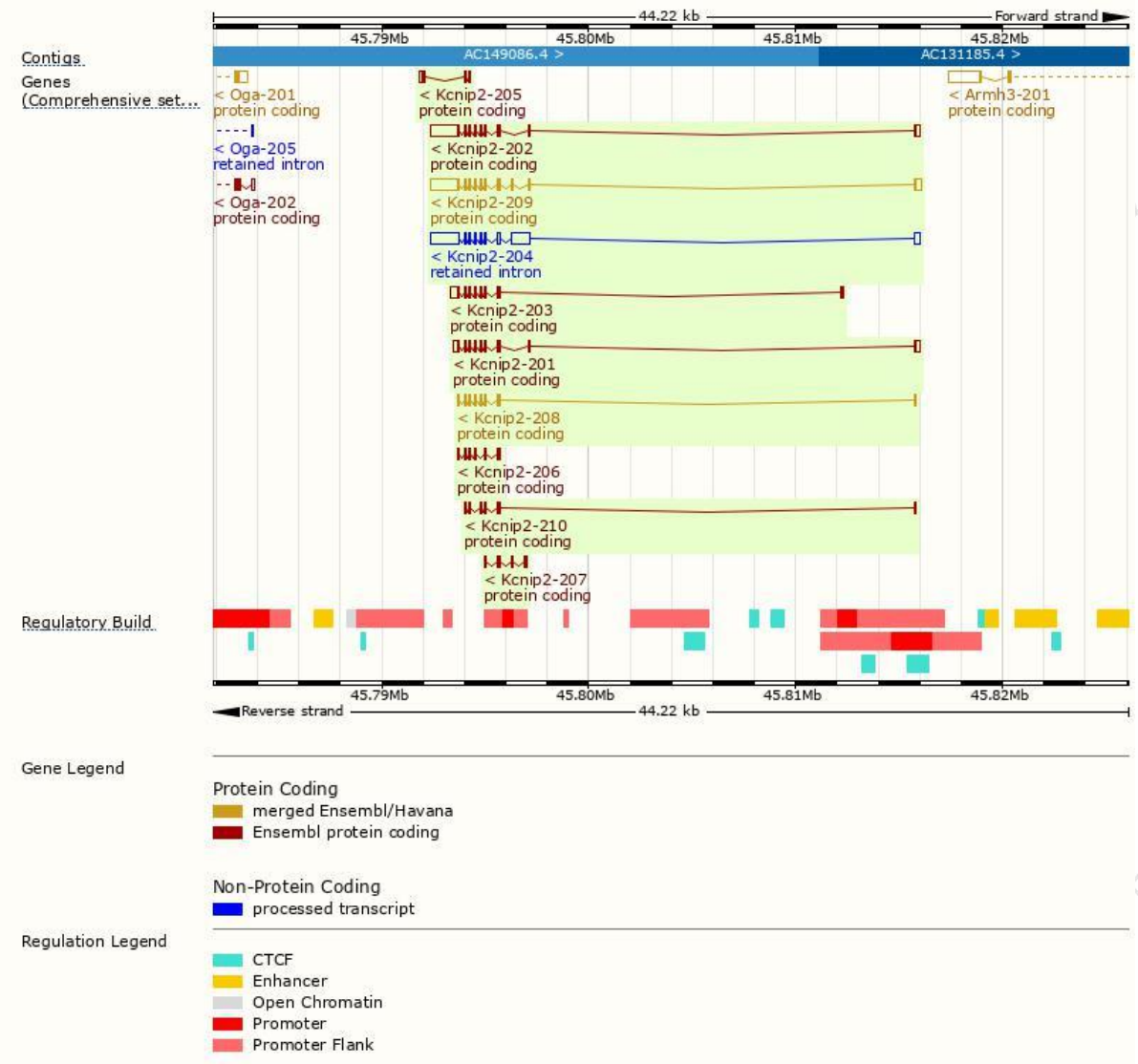
The gene has 10 transcripts,all transcripts are shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Kcnip2-209	ENSMUST00000162528.8	2395	270aa	Protein coding	CCDS38004	Q3YAB3	TSL:1 GENCODE basic APPRIS ALT1
Kcnip2-202	ENSMUST00000079431.9	2302	252aa	Protein coding	CCDS50453	Q3YAB2	TSL:1 GENCODE basic APPRIS ALT1
Kcnip2-203	ENSMUST00000086993.10	1005	225aa	Protein coding	CCDS70955	Q3YAA4 Q9JJ69	TSL:1 GENCODE basic APPRIS ALT1
Kcnip2-208	ENSMUST00000161886.8	693	220aa	Protein coding	CCDS29868	Q3YAB1	TSL:1 GENCODE basic APPRIS P3
Kcnip2-201	ENSMUST00000026247.12	1203	252aa	Protein coding	-	E9QNK8	TSL:5 GENCODE basic APPRIS ALT1
Kcnip2-206	ENSMUST00000159245.7	519	172aa	Protein coding	-	F6TBA6	CDS 5' incomplete TSL:5
Kcnip2-210	ENSMUST00000162661.8	517	172aa	Protein coding	-	E0CX94	CDS 3' incomplete TSL:5
Kcnip2-205	ENSMUST00000159210.8	383	95aa	Protein coding	-	E0CXC0	CDS 5' incomplete TSL:3
Kcnip2-207	ENSMUST00000159446.1	375	125aa	Protein coding	-	F7BWB2	5' and 3' truncations in transcript evidence prevent annotation of the start and the end of the CDS. CDS 5' and 3' incomplete TSL:3
Kcnip2-204	ENSMUST00000111906.1	3114	No protein	Retained intron	-	-	TSL:2

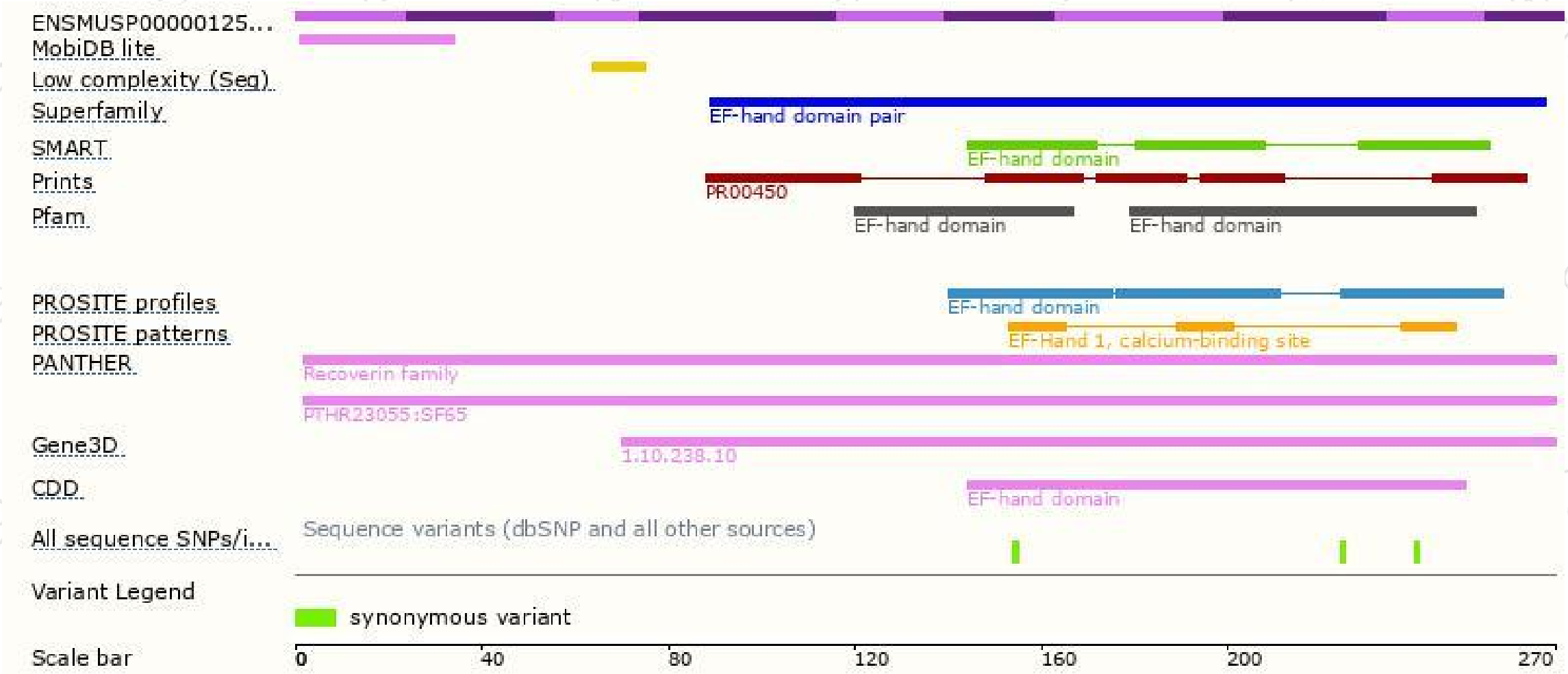
The strategy is based on the design of *Kcnip2-209* transcript,The transcription is shown below



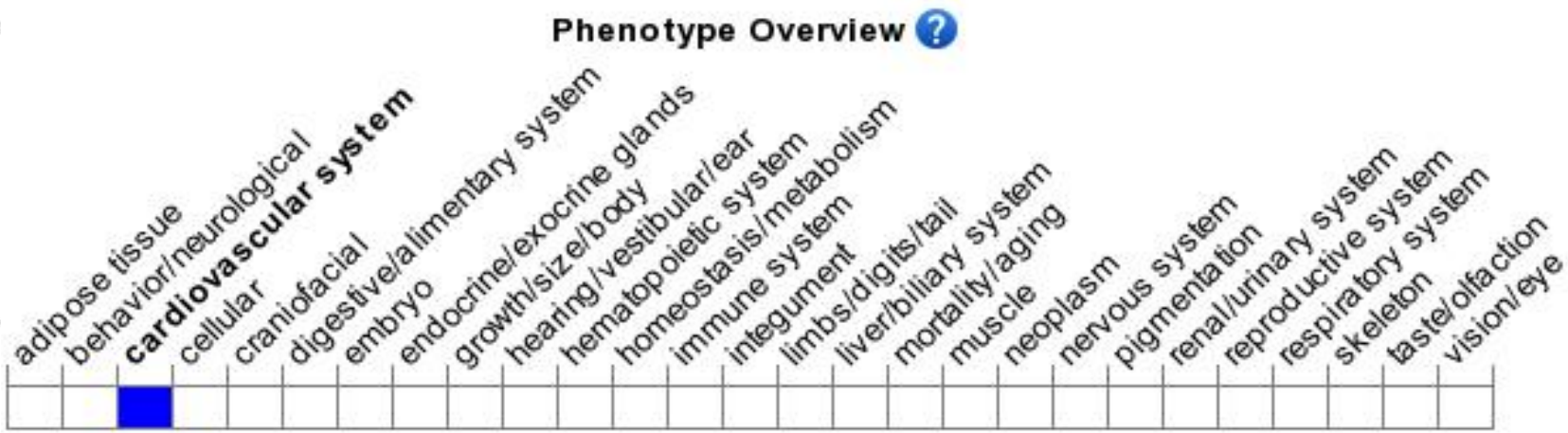
Genomic location distribution



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 disruptions in this gene are susceptible to induced cardiac arrhythmias but are otherwise normal.

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

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