

Calcr1 Cas9-KO Strategy

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Project Overview

Project Name

Calcr1

Project type

Cas9-KO

Strain background

C57BL/6JGpt

Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *Calcr1* gene. The schematic diagram is as follows:



- The *Calcr1* gene has 3 transcripts. According to the structure of *Calcr1* gene, exon6-exon9 of *Calcr1-201* (ENSMUST00000074262.8) transcript is recommended as the knockout region. The region contains 446bp coding sequence. Knock out the region will result in disruption of protein function.
- In this project we use CRISPR/Cas9 technology to modify *Calcr1* gene. The brief process is as follows: CRISPR/Cas9 system

- According to the existing MGI data, Homozygous mutation of this gene results in lethality between E13.5-E14.5, hydrops fetalis and cardiovascular defects such as thin vascular smooth muscle walls and small, disorganized hearts resulting from a decrease in cell proliferation and an increase in apoptosis.
- The *Calcr1* 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)

Calcr1 calcitonin receptor-like [Mus musculus (house mouse)]

Gene ID: 54598, updated on 31-Jan-2019

Summary



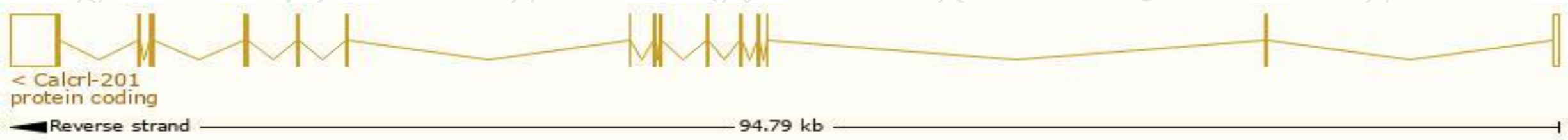
Official Symbol	Calcr1 provided by MGI
Official Full Name	calcitonin receptor-like provided by MGI
Primary source	MGI:MGI:1926944
See related	Ensembl:ENSMUSG00000059588
Gene type	protein coding
RefSeq status	VALIDATED
Organism	Mus musculus
Lineage	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Myomorpha; Muroidea; Muridae; Murinae; Mus; Mus
Also known as	AV071593, CRLR
Expression	Biased expression in lung adult (RPKM 53.6), bladder adult (RPKM 7.2) and 3 other tissues See more
Orthologs	human all

Transcript information (Ensembl)

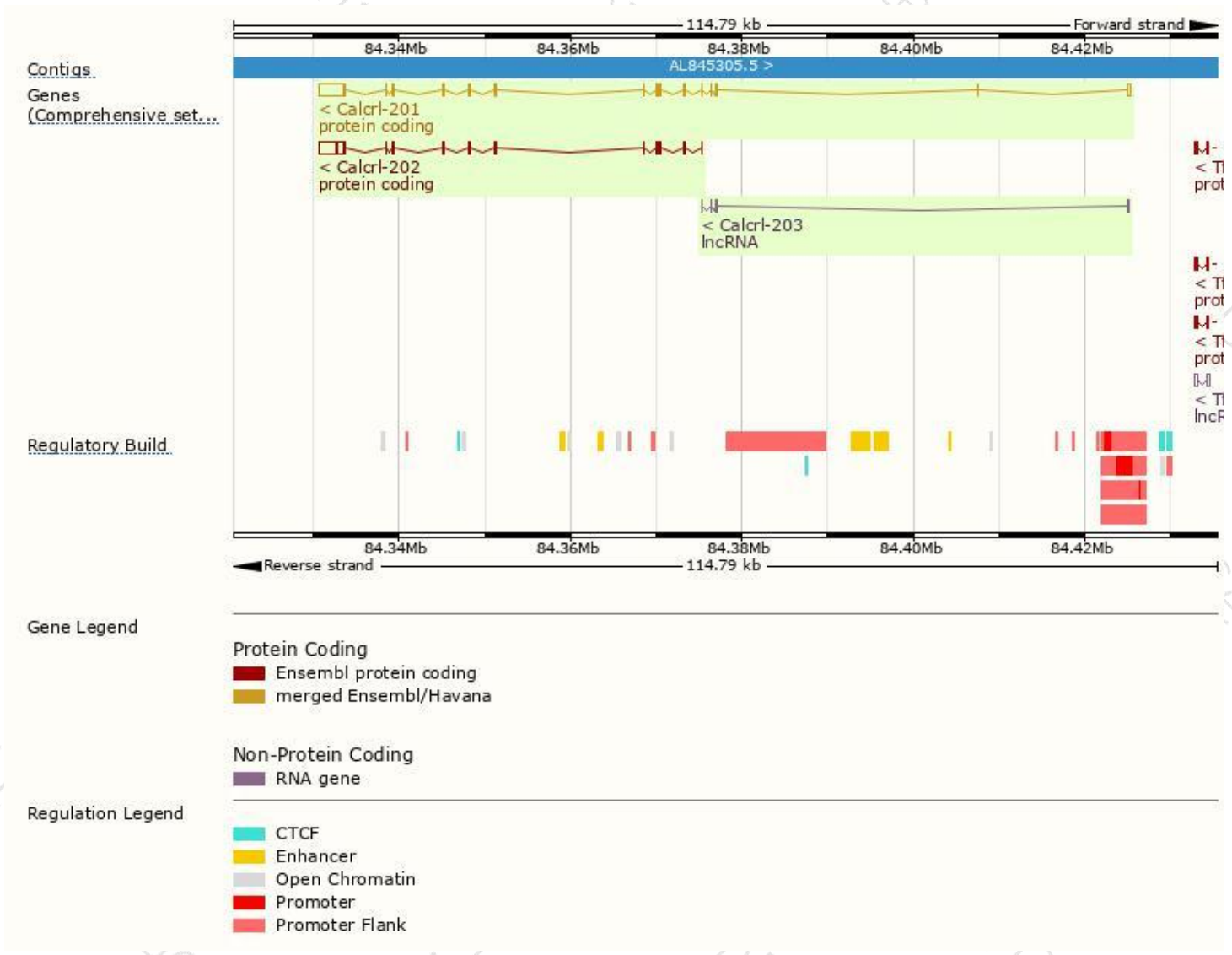
The gene has 3 transcripts,all transcripts are shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Calcr1-201	ENSMUST00000074262.8	4882	463aa	Protein coding	CCDS16184	A2AR99 Q9R1W5	TSL:1 GENCODE basic APPRIS P1
Calcr1-202	ENSMUST00000099944.3	3973	463aa	Protein coding	CCDS16184	A2AR99 Q9R1W5	TSL:1 GENCODE basic APPRIS P1
Calcr1-203	ENSMUST00000151295.1	500	No protein	lncRNA	-	-	TSL:5

The strategy is based on the design of *Calcr1-201* transcript,The transcription is shown below



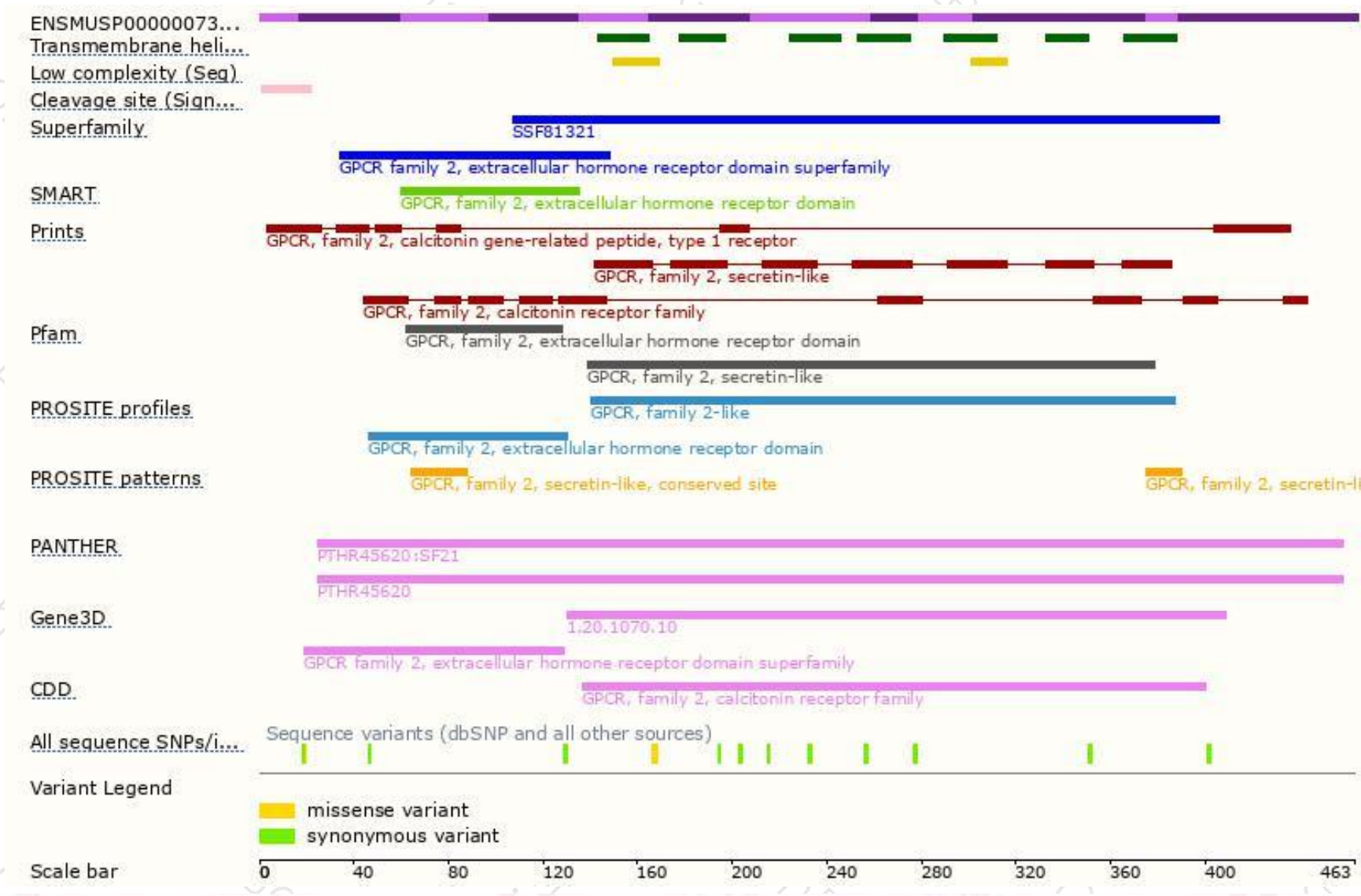
Genomic location distribution



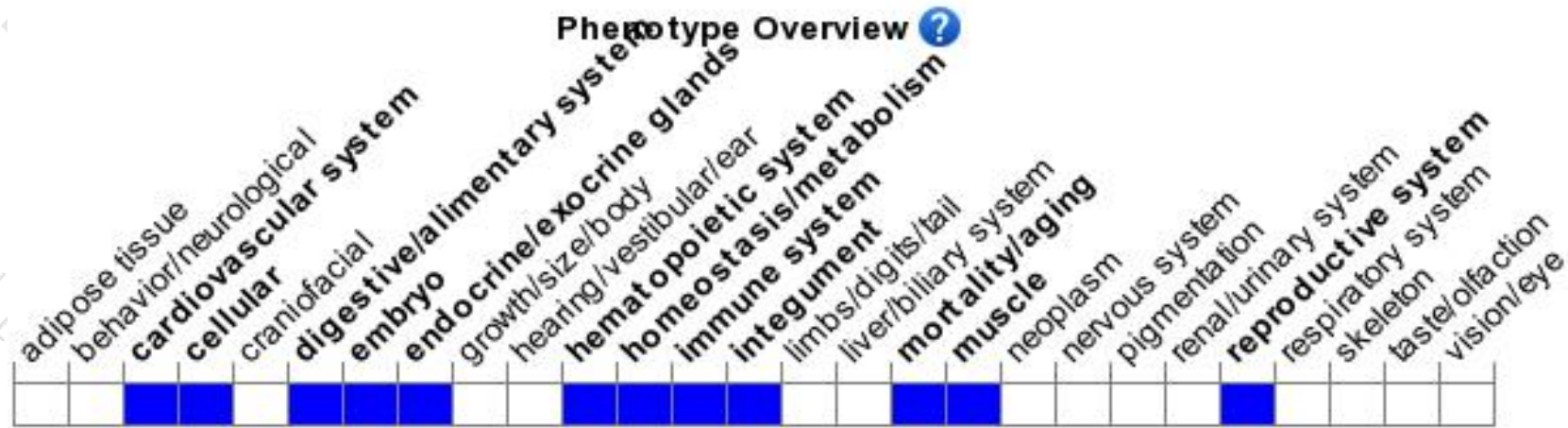
Protein domain



集萃药康
GemPharmatech



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, Homozygous mutation of this gene results in lethality between E13.5-E14.5, hydrops fetalis and cardiovascular defects such as thin vascular smooth muscle walls and small, disorganized hearts resulting from a decrease in cell proliferation and an increase in apoptosis.

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

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