

Iqgap2 Cas9-KO Strategy

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Project Overview

Project Name

Iqgap2

Project type

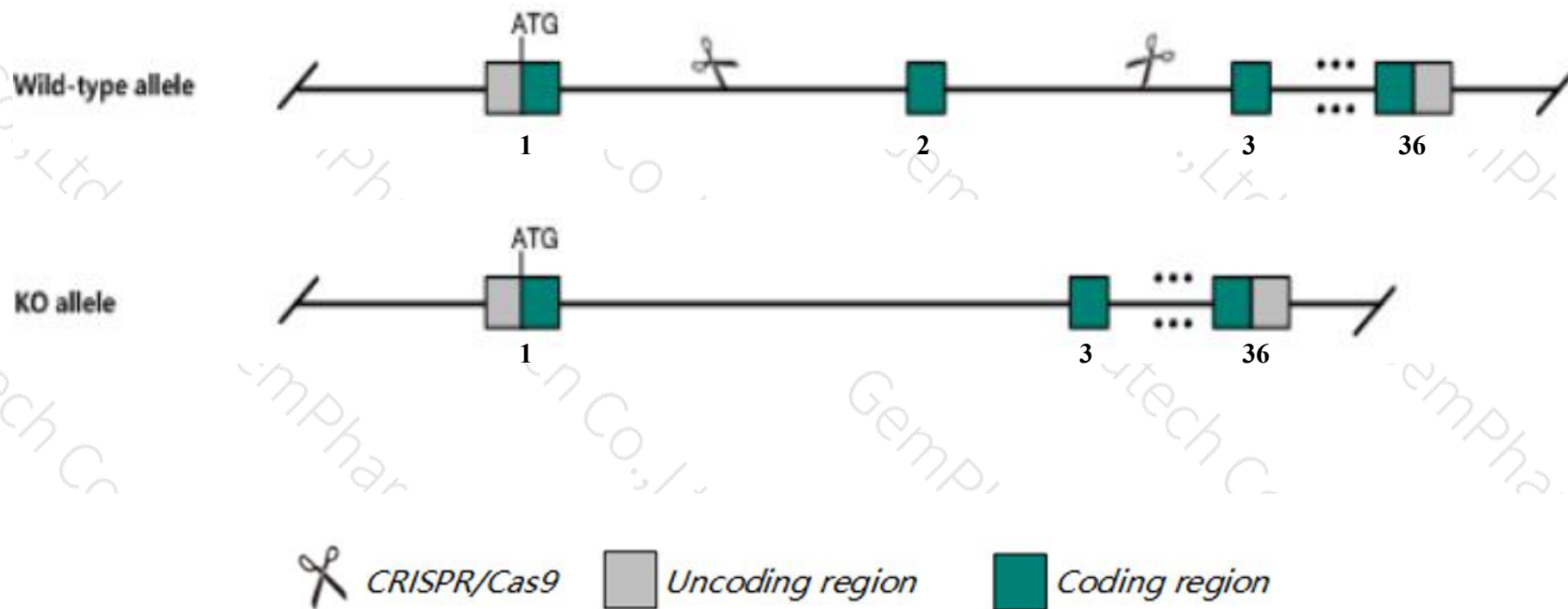
Cas9-KO

Strain background

C57BL/6JGpt

Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *Iqgap2* gene. The schematic diagram is as follows:



- The *Iqgap2* gene has 9 transcripts. According to the structure of *Iqgap2* gene, exon2 of *Iqgap2*-201(ENSMUST00000068603.7) transcript is recommended as the knockout region. The region contains 100bp coding sequence. Knock out the region will result in disruption of protein function.
- In this project we use CRISPR/Cas9 technology to modify *Iqgap2* gene. The brief process is as follows: CRISPR/Cas9 system 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.

- According to the existing MGI data, mice homozygous for a null mutation display reduced survival with increased incidence of hepatocellular carcinomas, increased hepatocyte apoptosis, and hepatocyte mitochondrial abnormalities.
- The *Iqgap2* gene is located on the Chr13. 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)

Iqgap2 IQ motif containing GTPase activating protein 2 [*Mus musculus* (house mouse)]

Gene ID: 544963, updated on 26-Jun-2020

Summary

Official Symbol	Iqgap2 provided by MGI
Official Full Name	IQ motif containing GTPase activating protein 2 provided by MGI
Primary source	MGI:MGI:2449975
See related	Ensembl:ENSMUSG00000021676
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	AI788777; A630053O10; 4933417J23Rik
Expression	Broad expression in placenta adult (RPKM 18.9), liver E18 (RPKM 15.9) and 25 other tissues See more
Orthologs	human all

Transcript information (Ensembl)

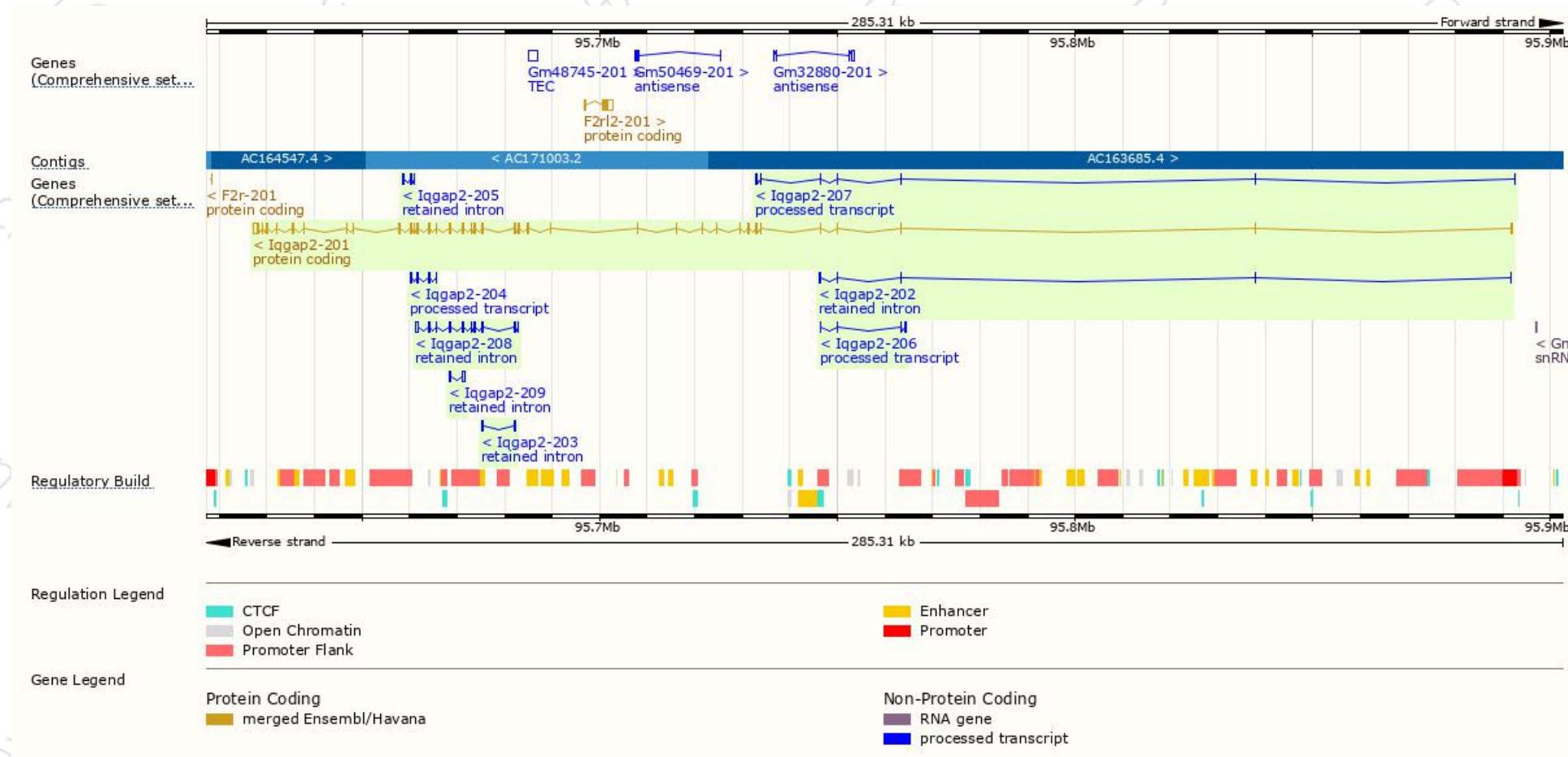
The gene has 9 transcripts,all transcripts are shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Iqgap2-201	ENSMUST00000068603.7	5847	1575aa	Protein coding	CCDS36753	Q3UQ44	TSL:1 GENCODE basic APPRIS P1
Iqgap2-204	ENSMUST00000238392.1	628	No protein	Processed transcript	-	-	-
Iqgap2-207	ENSMUST00000238515.1	599	No protein	Processed transcript	-	-	-
Iqgap2-206	ENSMUST00000238496.1	540	No protein	Processed transcript	-	-	-
Iqgap2-208	ENSMUST00000238595.1	1499	No protein	Retained intron	-	-	-
Iqgap2-205	ENSMUST00000238404.1	681	No protein	Retained intron	-	-	-
Iqgap2-202	ENSMUST00000238261.1	632	No protein	Retained intron	-	-	-
Iqgap2-209	ENSMUST00000238783.1	382	No protein	Retained intron	-	-	-
Iqgap2-203	ENSMUST00000238263.1	277	No protein	Retained intron	-	-	-

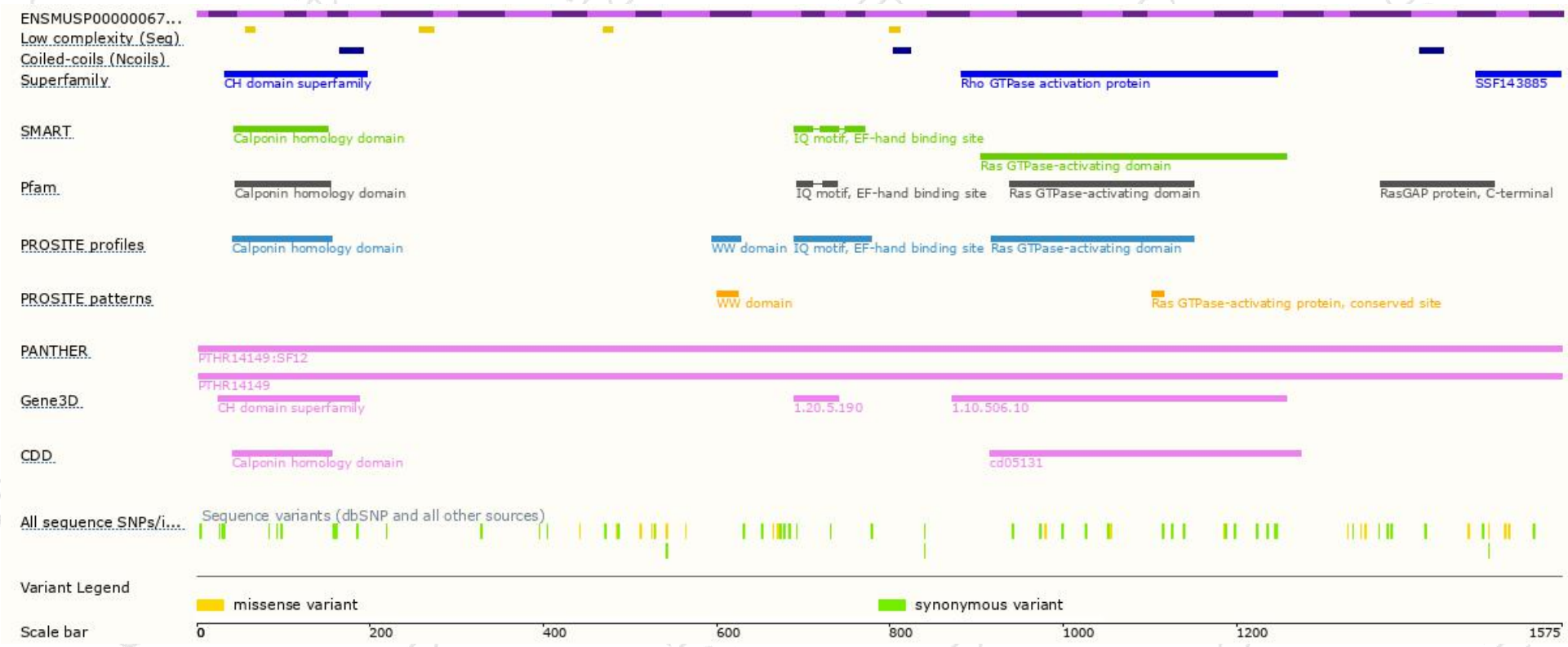
The strategy is based on the design of *Iqgap2-201* transcript,the transcription is shown below:



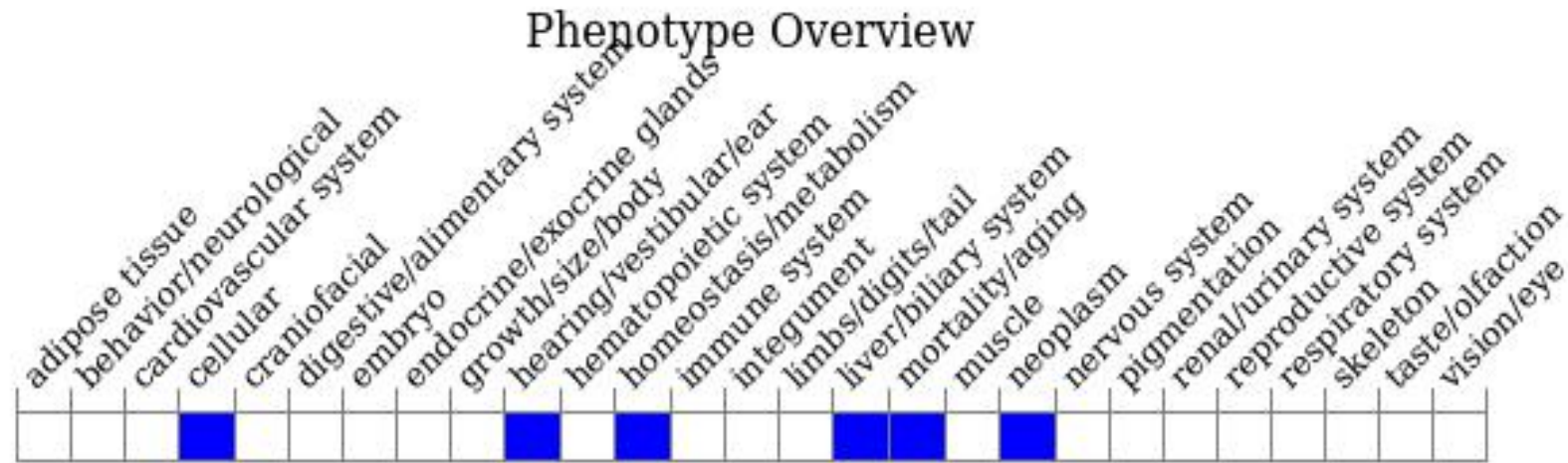
Genomic location distribution



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/>).

According to the existing MGI data, mice homozygous for a null mutation display reduced survival with increased incidence of hepatocellular carcinomas, increased hepatocyte apoptosis, and hepatocyte mitochondrial abnormalities.

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

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