Iqgap1 Cas9-KO Strategy

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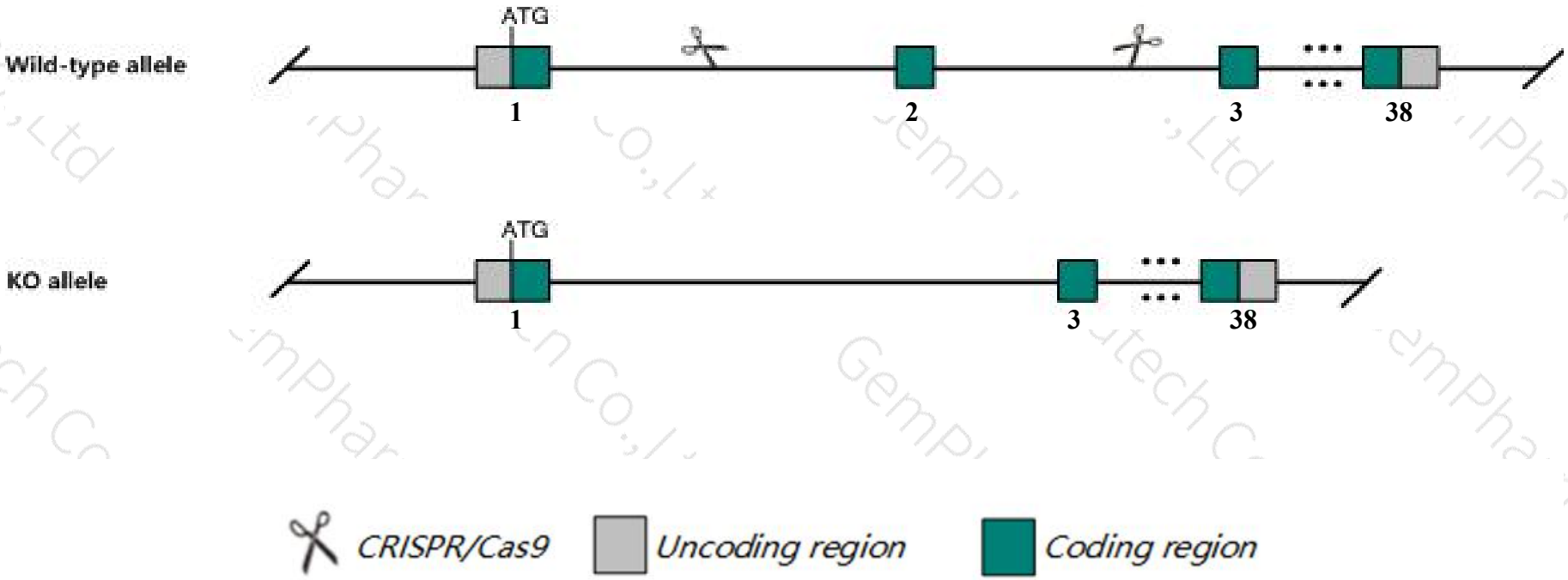
Project Overview

Project Name	***Iqgap1***
Project type	**Cas9-KO**
Strain background	**C57BL/6JGpt**

Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *Iqgap1* gene. The schematic diagram is as follows:



Technical routes

➢ The *Iqgap1* gene has 8 transcripts. According to the structure of *Iqgap1* gene, exon2 of *Iqgap1-201* (ENSMUST00000167377.2) 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 *Iqgap1* gene. The brief process is as follows: CRISPR/Cas9 systen

Notice

- According to the existing MGI data,Homozygotes for a targeted null allele exhibit a late-onset gastric hyperplasia.
- Transcript *Iqgap1*-203&205 may not be affected.
- The *Iqgap1* 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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Iqgap1 IQ motif containing GTPase activating protein 1 [*Mus musculus* (house mouse)]

Gene ID: 29875, updated on 21-Aug-2019

Summary

Official Symbol	Iqgap1 provided by MGI
Official Full Name	IQ motif containing GTPase activating protein 1 provided by MGI
Primary source	MGI:MGI:1352757
See related	Ensembl:ENSMUSG00000030536
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	AA682088; mKIAA0051; D7Ertd237e; D7Ertd257e
Expression	Ubiquitous expression in lung adult (RPKM 47.3), spleen adult (RPKM 27.7) and 27 other tissues See more
Orthologs	human all

Genomic context

Location: 7 D3; 7 45.68 cM

See Iqgap1 in Genome Data Viewer

Exon count: 41

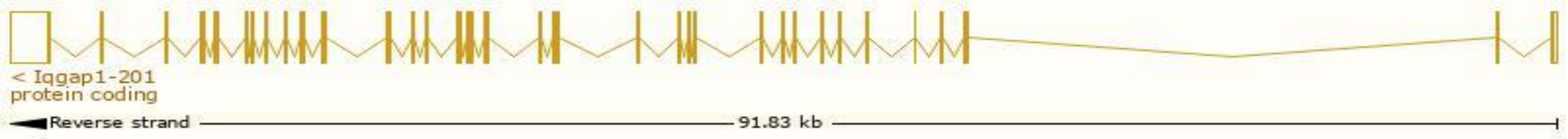
Annotation release	Status	Assembly	Chr	Location
108	current	GRCm38.p6 (GCF_000001635.26)	7	NC_000073.6 (80711583..80815549, complement)
Build 37.2	previous assembly	MGSCv37 (GCF_000001635.18)	7	NC_000073.5 (87856469..87948217, complement)

Transcript information（Ensembl）

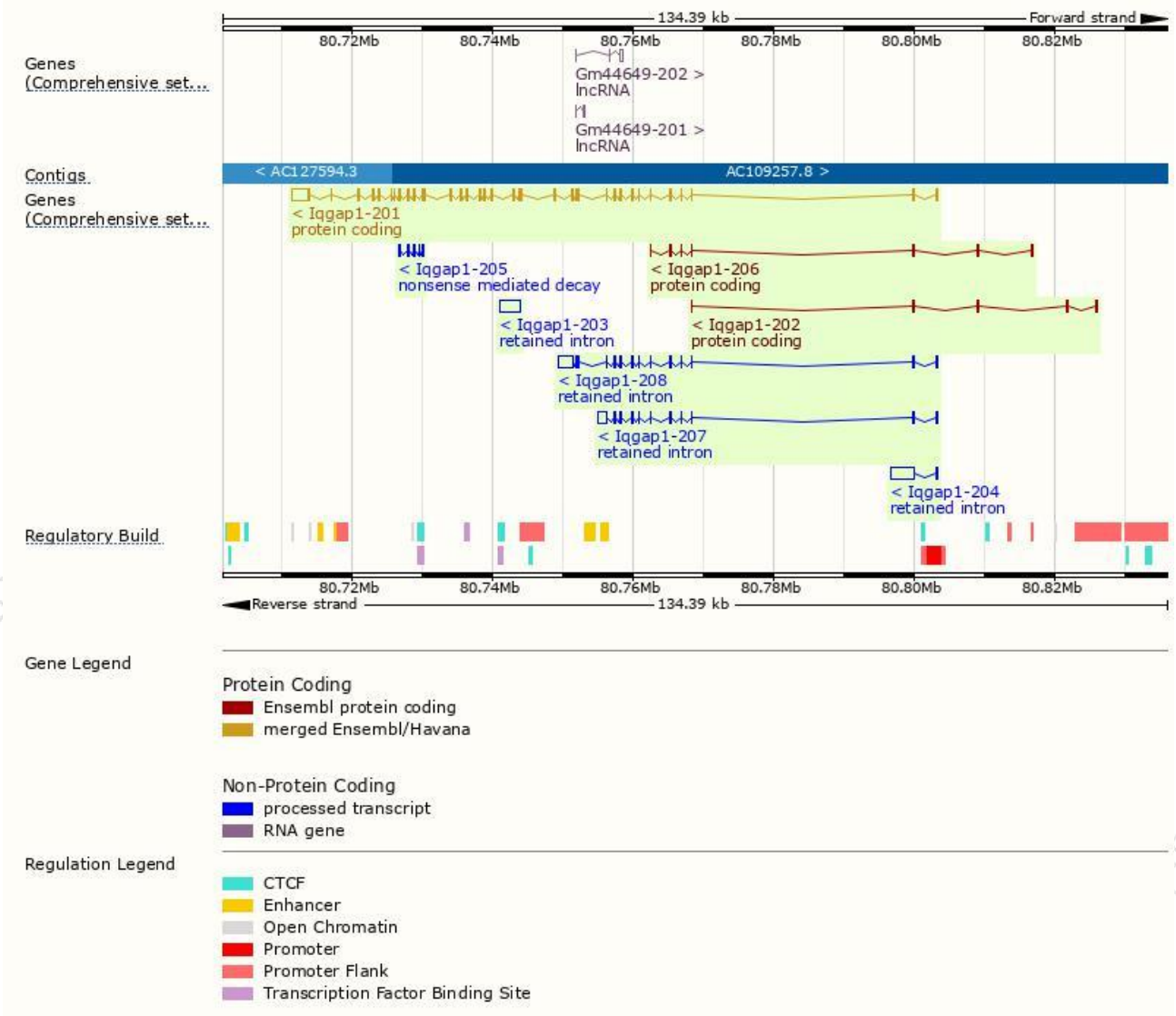
The gene has 8 transcripts,all transcripts are shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Iqgap1-201	ENSMUST00000167377.2	7444	1657aa	Protein coding	CCDS40001	Q9JKF1	TSL:1 GENCODE basic APPRIS P1
Iqgap1-206	ENSMUST00000205813.1	560	186aa	Protein coding	-	A0A0U1RNG5	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
Iqgap1-202	ENSMUST00000205304.1	484	101aa	Protein coding	-	A0A0U1RPU3	CDS 3' incomplete TSL:3
Iqgap1-205	ENSMUST00000205606.1	569	37aa	Nonsense mediated decay	-	A0A0U1RPI2	CDS 5' incomplete TSL:5
Iqgap1-208	ENSMUST00000206149.1	3629	No protein	Retained intron	-	-	TSL:1
Iqgap1-204	ENSMUST00000205540.1	3367	No protein	Retained intron	-	-	TSL:1
Iqgap1-203	ENSMUST00000205383.1	2803	No protein	Retained intron	-	-	TSL:NA
Iqgap1-207	ENSMUST00000205824.1	2307	No protein	Retained intron	-	-	TSL:1

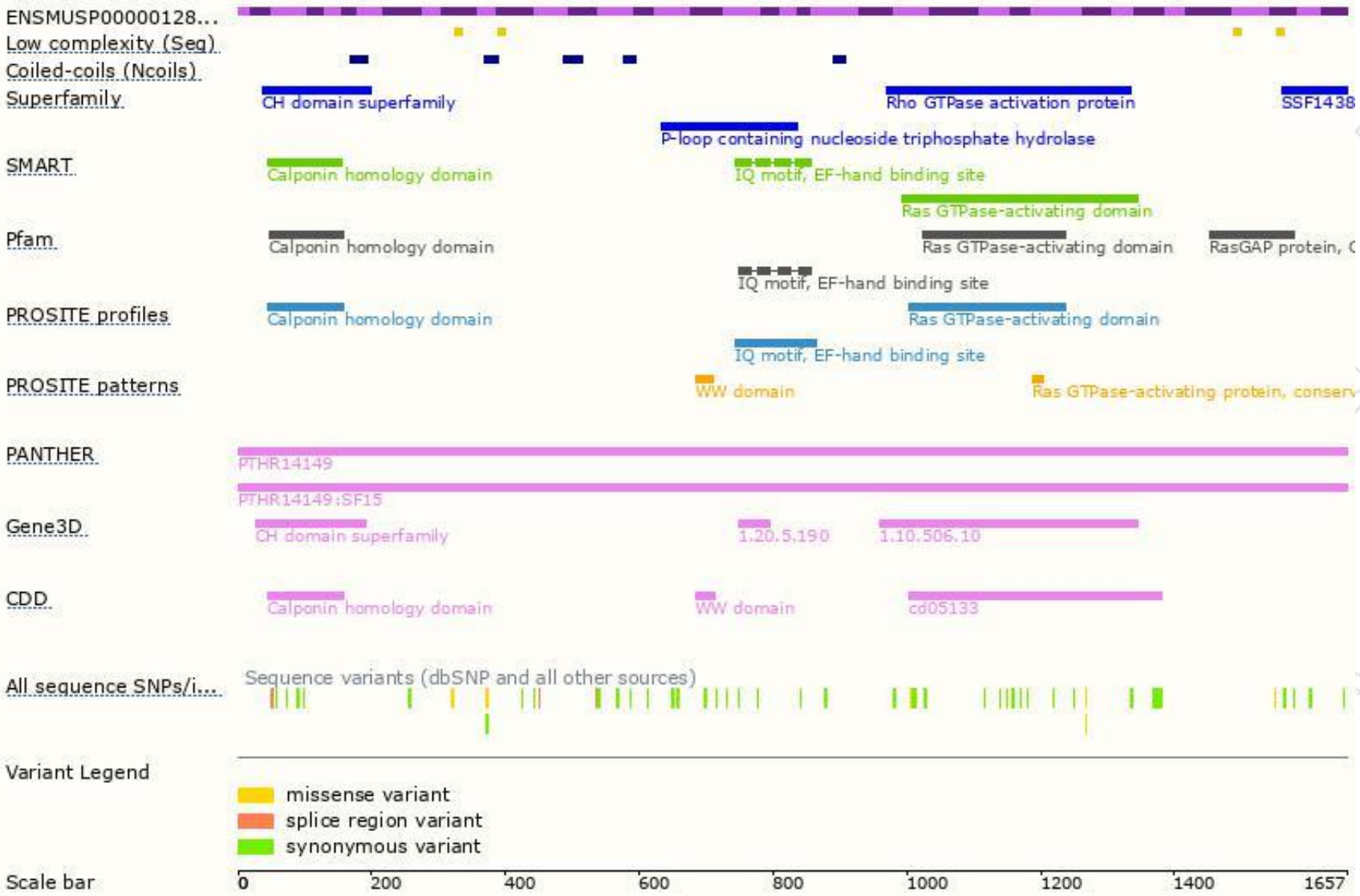
The strategy is based on the design of *Iqgap1-201* transcript,The transcription is shown below



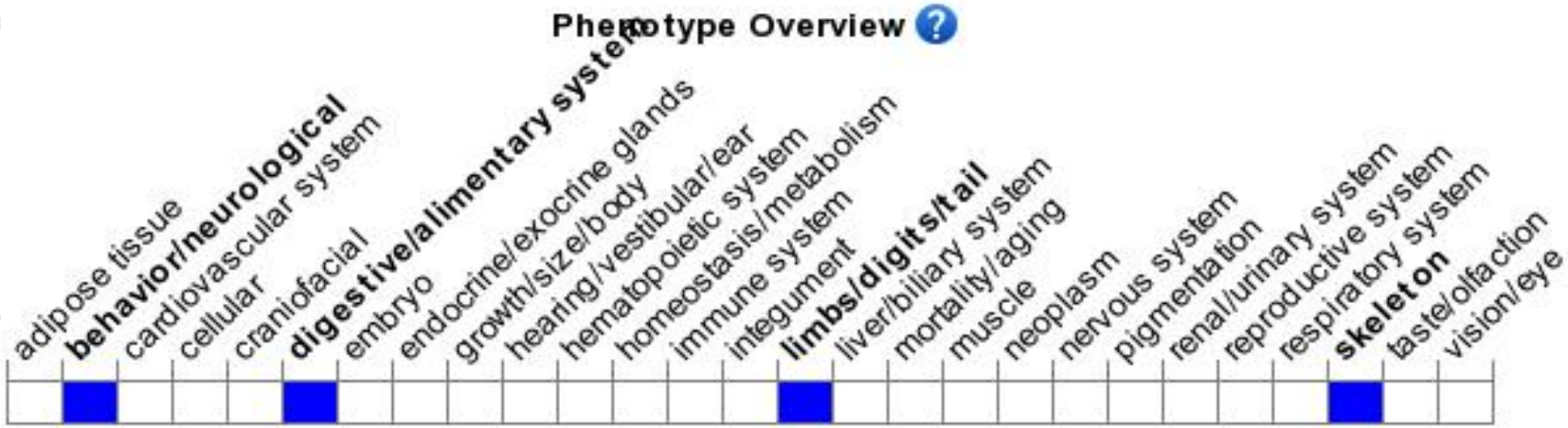
Genomic location distribution



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,Homozygotes for a targeted null allele exhibit a late-onset gastric hyperplasia.

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

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