

Itfg2 Cas9-KO Strategy

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Project Overview

Project Name

Itfg2

Project type

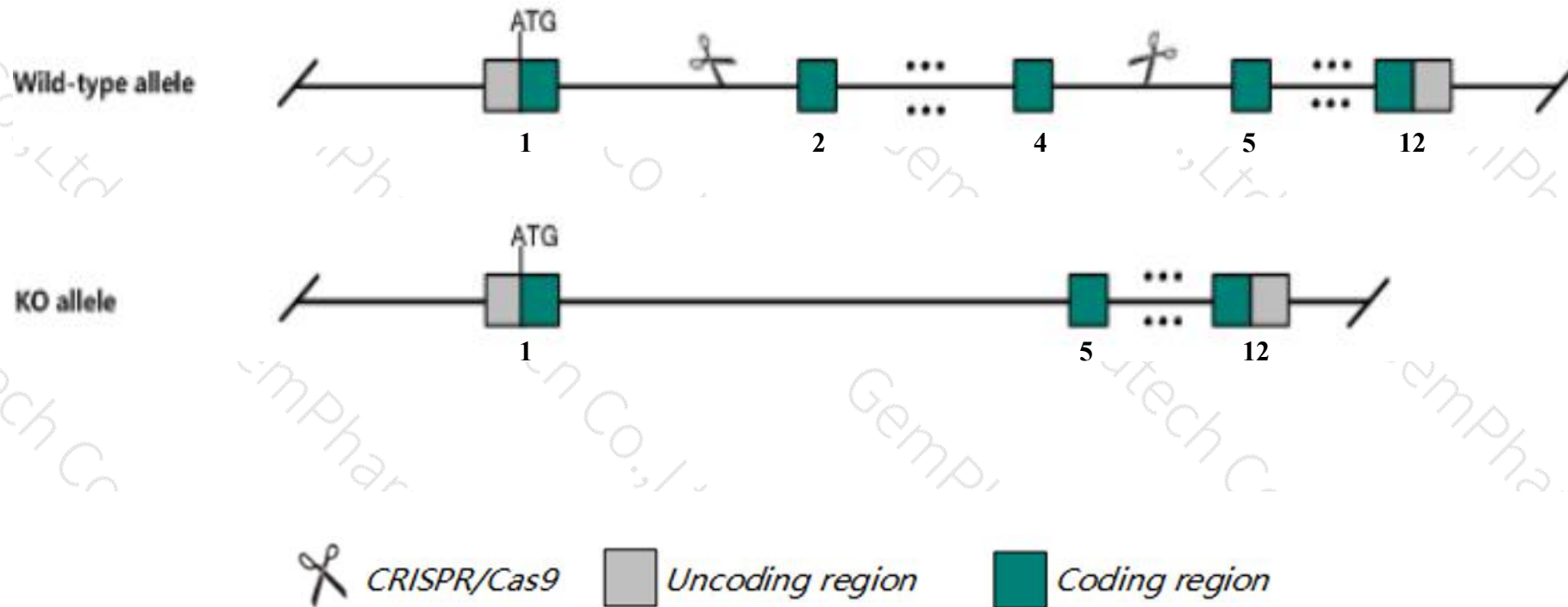
Cas9-KO

Strain background

C57BL/6JGpt

Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *Itfg2* gene. The schematic diagram is as follows:



- The *Itfg2* gene has 10 transcripts. According to the structure of *Itfg2* gene, exon2-exon4 of *Itfg2-201* (ENSMUST00000001559.10) transcript is recommended as the knockout region. The region contains 307bp coding sequence. Knock out the region will result in disruption of protein function.
- In this project we use CRISPR/Cas9 technology to modify *Itfg2* gene. The brief process is as follows: CRISPR/Cas9 system v

- According to the existing MGI data, Mice homozygous for a gene trap allele exhibit abnormal B cell differentiation.
- The KO region contains functional region of the *Nrip2* gene. Knockout the region may affect the function of *Nrip2* gene.
- The *Itfg2* gene is located on the Chr6. 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)

Itfg2 integrin alpha FG-GAP repeat containing 2 [Mus musculus (house mouse)]

Gene ID: 101142, updated on 31-Jan-2019

Summary



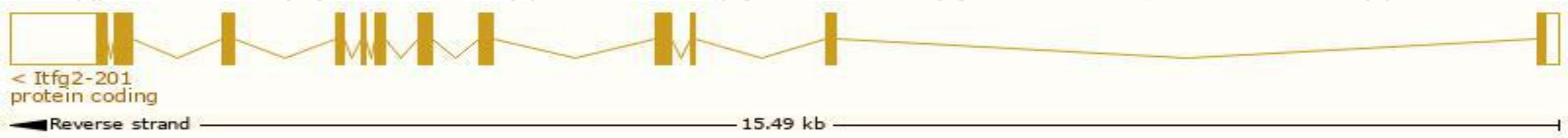
Official Symbol	Itfg2 provided by MGI
Official Full Name	integrin alpha FG-GAP repeat containing 2 provided by MGI
Primary source	MGI:MGI:1915450
See related	Ensembl:ENSMUSG000000001518
Gene type	protein coding
RefSeq status	PROVISIONAL
Organism	Mus musculus
Lineage	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Myomorpha; Muroidea; Muridae; Murinae; Mus; Mus
Also known as	2700050P07Rik, AI646725
Expression	Ubiquitous expression in cerebellum adult (RPKM 9.9), limb E14.5 (RPKM 8.4) and 28 other tissues See more
Orthologs	human all

Transcript information (Ensembl)

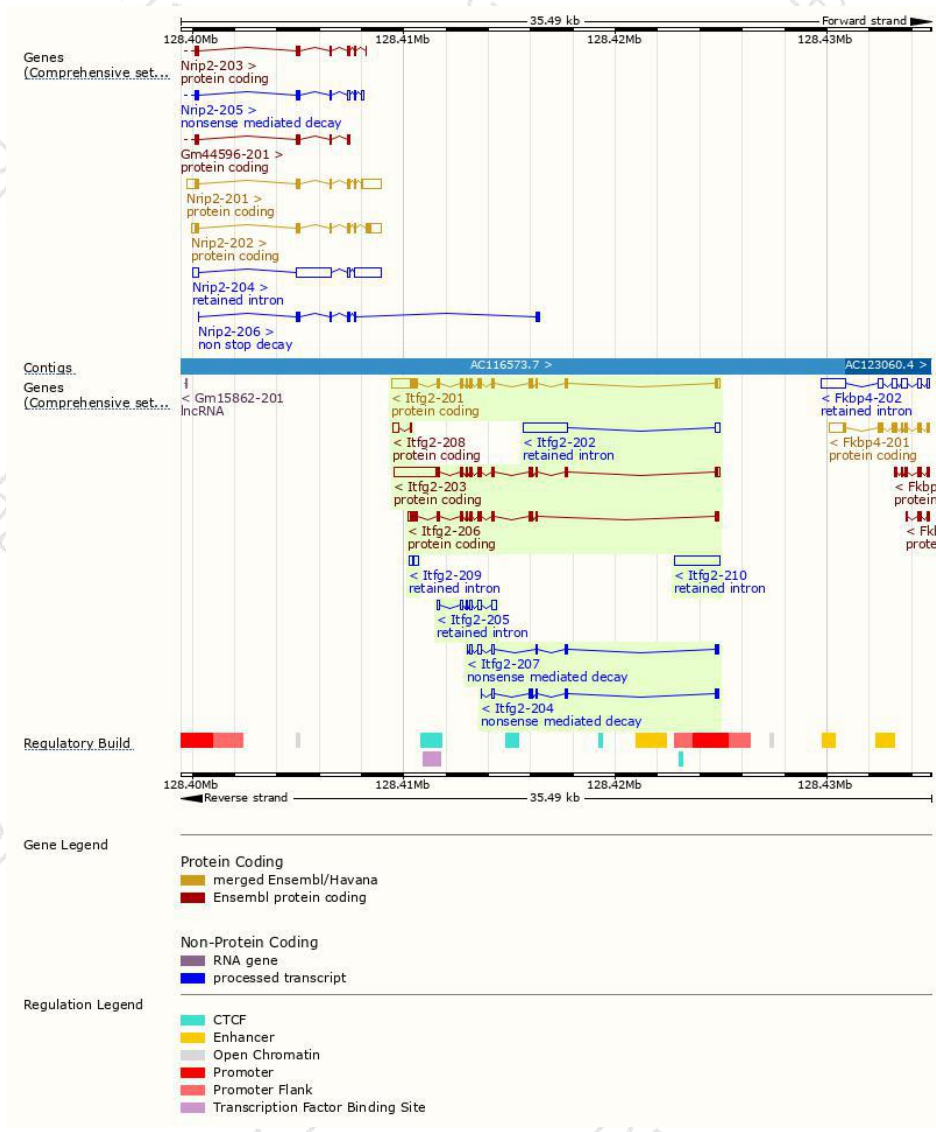
The gene has 10 transcripts,all transcripts are shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Itfg2-201	ENSMUST00000001559.10	2320	443aa	Protein coding	CCDS20572	Q91WI7	TSL:1 GENCODE basic APPRIS P1
Itfg2-203	ENSMUST00000142615.3	3191	358aa	Protein coding	-	Q3TWL5	TSL:1 GENCODE basic
Itfg2-206	ENSMUST00000203374.2	1394	411aa	Protein coding	-	A0A0N4SW06	TSL:5 GENCODE basic
Itfg2-208	ENSMUST00000203984.1	338	22aa	Protein coding	-	A0A0N4SUV5	CDS 5' incomplete TSL:2
Itfg2-207	ENSMUST00000203853.2	724	87aa	Nonsense mediated decay	-	A0A0N4SVX2	TSL:5
Itfg2-204	ENSMUST00000203026.1	655	136aa	Nonsense mediated decay	-	A0A0N4SW62	TSL:3
Itfg2-202	ENSMUST00000133994.1	2296	No protein	Retained intron	-	-	TSL:1
Itfg2-210	ENSMUST00000204467.1	2135	No protein	Retained intron	-	-	TSL:NA
Itfg2-205	ENSMUST00000203195.2	723	No protein	Retained intron	-	-	TSL:3
Itfg2-209	ENSMUST00000204362.1	353	No protein	Retained intron	-	-	TSL:2

The strategy is based on the design of *Itfg2-201* transcript,The transcription is shown below



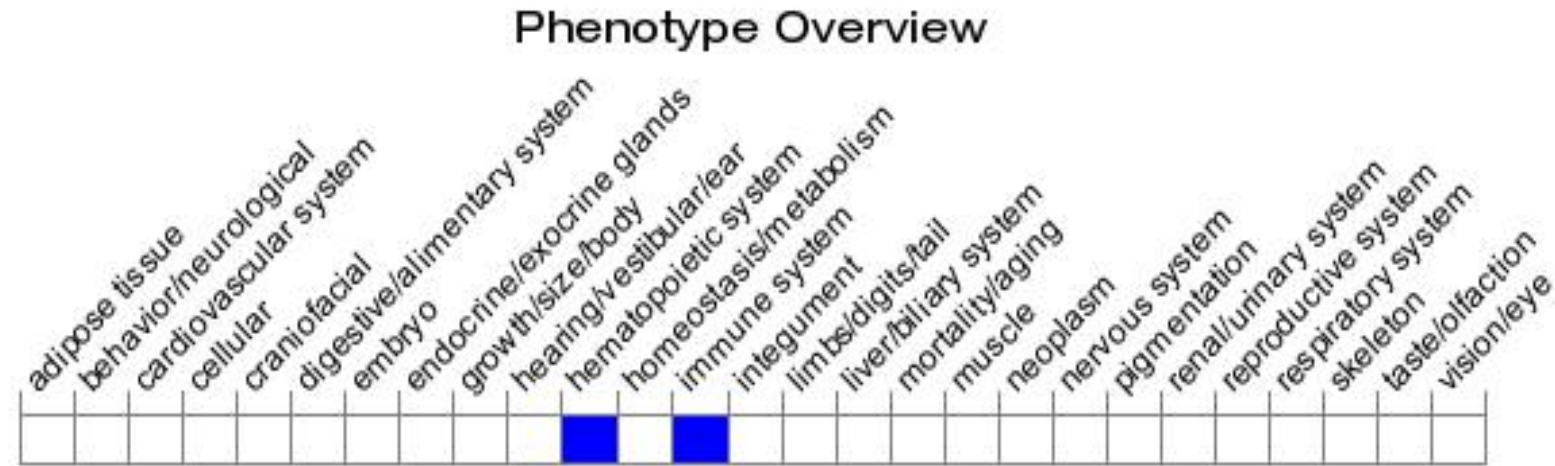
Genomic location distribution



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 gene trap allele exhibit abnormal B cell differentiation.

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

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