

Itga8 Cas9-KO Strategy

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Reviewer:

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Project Overview



Project Name Itga8

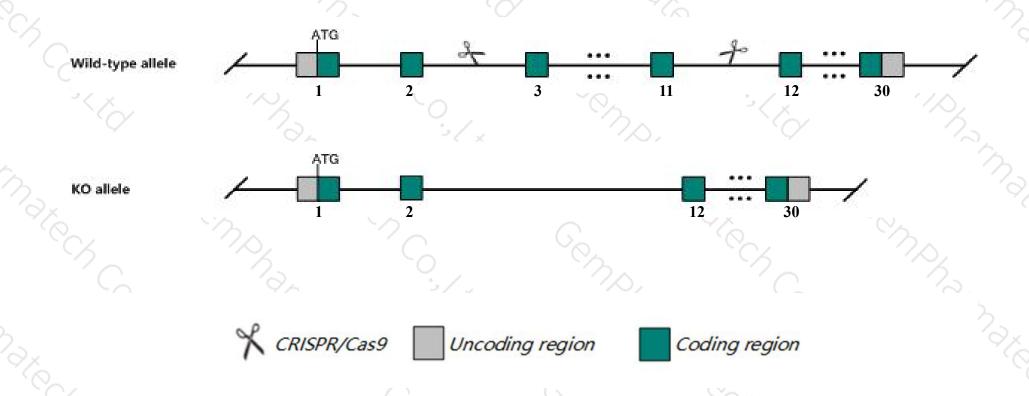
Project type Cas9-KO

Strain background C57BL/6JGpt

Knockout strategy



This model will use CRISPR/Cas9 technology to edit the *Itga8* gene. The schematic diagram is as follows:



Technical routes



- ➤ The *Itga8* gene has 7 transcripts. According to the structure of *Itga8* gene, exon3-exon11 of *Itga8-201*(ENSMUST00000028106.10) transcript is recommended as the knockout region. The region contains 658bp coding sequence Knock out the region will result in disruption of protein function.
- > In this project we use CRISPR/Cas9 technology to modify *Itga8* gene. The brief process is as follows: CRISPR/Cas9 system

Notice



- ➤ According to the existing MGI data, Mice homozygous for disruptions in this gene usually die by the end of the second day after birth. Those that do survive have reduced kidneys and abnormal steriocilia in the inner ear.
- > Transcripts 202,203 may not be affected.
- ➤ The effect of transcript 205 is unknown.
- The *Itga8* 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)



Itga8 integrin alpha 8 [Mus musculus (house mouse)]

Gene ID: 241226, updated on 12-Aug-2019

Summary

☆ ?

Official Symbol Itga8 provided by MGI

Official Full Name integrin alpha 8 provided by MGI

Primary source MGI:MGI:109442

See related Ensembl: ENSMUSG00000026768

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 Al447669

Summary This gene encodes a member of the integrin family of cell surface proteins that mediate cellular interactions with the extracellular matrix

and other cells. The encoded protein undergoes proteolytic processing to generate the disulfide-linked heterodimeric alpha subunit which, in turn associates with a beta subunit to form the functional integrin receptor. Mice lacking the encoded protein mostly die after birth due to kidney defects, but some of animals that survive exhibit defects in the sensory hair cells of the inner ear. [provided by

RefSeq, Aug 2016]

Expression Biased expression in lung adult (RPKM 16.4), bladder adult (RPKM 4.7) and 14 other tissues See more

Orthologs human all

Genomic context

☆ ?

Location: 2 A1; 2 9.12 cM

See Itga8 in Genome Data Viewer

Exon count: 33

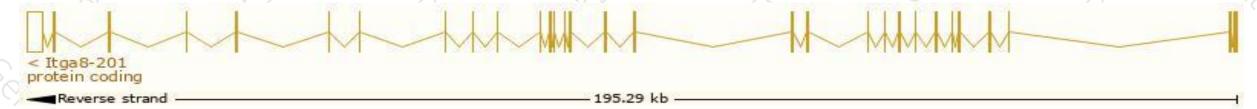
Transcript information (Ensembl)



The gene has 7 transcripts, all transcripts are shown below:

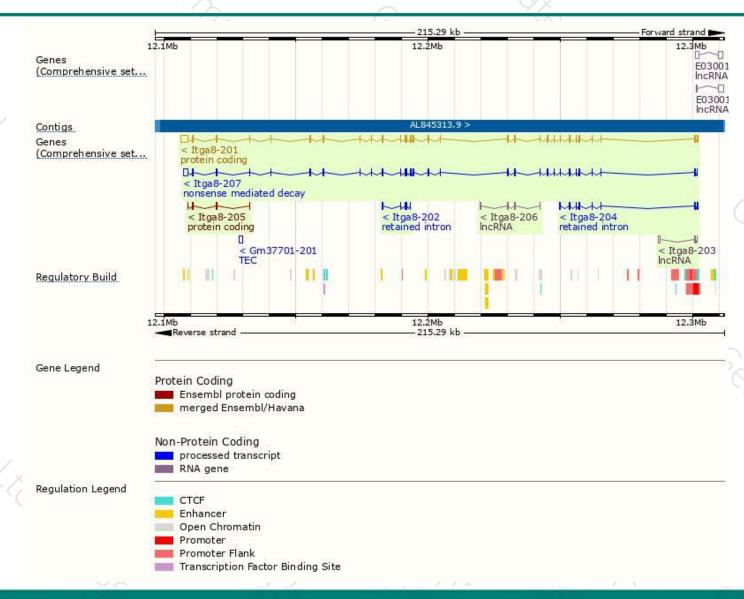
Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
ENSMUST00000028106.10	5812	<u>1062aa</u>	Protein coding	CCDS15689	A2ARA8	TSL:1 GENCODE basic APPRIS P1
ENSMUST00000148055.1	491	<u>133aa</u>	Protein coding	-	G3UYV5	CDS 5' incomplete TSL:5
ENSMUST00000172791.7	4948	<u>590aa</u>	Nonsense mediated decay	4	G3UYN5	TSL:1
ENSMUST00000141477.7	1265	No protein	Retained intron	70	2	TSL:1
ENSMUST00000129370.1	488	No protein	Retained intron	-		TSL:3
ENSMUST00000172716.2	924	No protein	IncRNA			TSL:3
ENSMUST00000130548.2	885	No protein	IncRNA	-	-	TSL:5
	ENSMUST00000148055.1 ENSMUST00000172791.7 ENSMUST00000141477.7 ENSMUST00000129370.1 ENSMUST00000172716.2	ENSMUST000000148055.1 491 ENSMUST00000172791.7 4948 ENSMUST00000141477.7 1265 ENSMUST00000129370.1 488 ENSMUST00000172716.2 924	ENSMUST00000028106.10 5812 1062aa ENSMUST00000148055.1 491 133aa ENSMUST00000172791.7 4948 590aa ENSMUST00000141477.7 1265 No protein ENSMUST00000129370.1 488 No protein ENSMUST00000172716.2 924 No protein	ENSMUST00000028106.10 5812 1062aa Protein coding ENSMUST00000148055.1 491 133aa Protein coding ENSMUST00000172791.7 4948 590aa Nonsense mediated decay ENSMUST00000141477.7 1265 No protein Retained intron ENSMUST00000129370.1 488 No protein Retained intron ENSMUST00000172716.2 924 No protein IncRNA	ENSMUST00000028106.10 5812 1062aa Protein coding CCDS15689 ENSMUST00000148055.1 491 133aa Protein coding - ENSMUST00000172791.7 4948 590aa Nonsense mediated decay - ENSMUST00000141477.7 1265 No protein Retained intron - ENSMUST00000129370.1 488 No protein Retained intron - ENSMUST00000172716.2 924 No protein IncRNA -	ENSMUST00000028106.10 5812 1062aa Protein coding CCDS15689 A2ARA8 ENSMUST00000148055.1 491 133aa Protein coding - G3UYV5 ENSMUST00000172791.7 4948 590aa Nonsense mediated decay - G3UYN5 ENSMUST00000141477.7 1265 No protein Retained intron - - ENSMUST00000129370.1 488 No protein Retained intron - - ENSMUST00000172716.2 924 No protein IncRNA - -

The strategy is based on the design of *Itga8-201* transcript, The transcription is shown below



Genomic location distribution





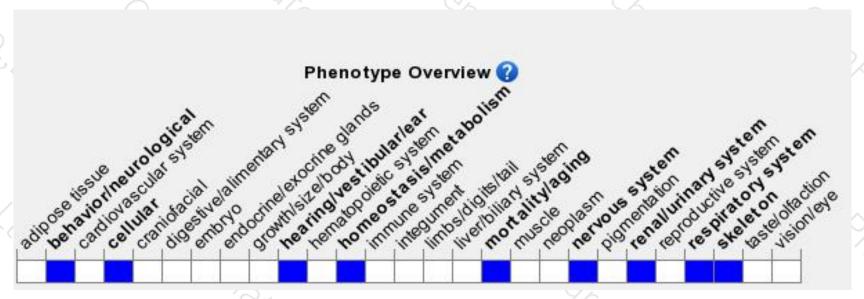
Protein domain





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 disruptions in this gene usually die by the end of the second day after birth. Those that do survive have reduced kidneys and abnormal steriocilia in the inner ear.



If you have any questions, you are welcome to inquire. Tel: 400-9660890





