

Jup Cas9-KO Strategy

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Design Date:

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Project Overview



Project Name Jup

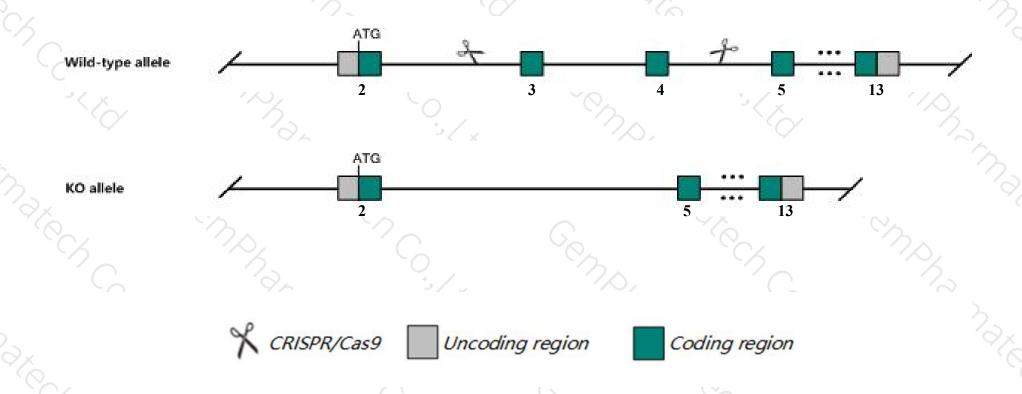
Project type Cas9-KO

Strain background C57BL/6JGpt

Knockout strategy



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



Technical routes



- > The *Jup* gene has 9 transcripts. According to the structure of *Jup* gene, exon3-exon4 of *Jup-201*(ENSMUST00000001592.14) transcript is recommended as the knockout region. The region contains 499bp coding sequence Knock out the region will result in disruption of protein function.
- ➤ In this project we use CRISPR/Cas9 technology to modify *Jup* gene. The brief process is as follows: CRISPR/Cas9 system w

Notice



- ➤ According to the existing MGI data, Homozygous null mutants die with severe heart defects at embryonic day 10.5-16, depending on genetic background. Mutants that survive to birth exhibit skin blistering and subcorneal acantholysis associated with reduced number of desmosomes.
- > The *Jup* gene is located on the Chr11. 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)



Jup junction plakoglobin [Mus musculus (house mouse)]

Gene ID: 16480, updated on 31-Jan-2019

Summary

☆ ?

Official Symbol Jup provided by MGI

Official Full Name junction plakoglobin provided by MGI

Primary source MGI:MGI:96650

See related Ensembl:ENSMUSG00000001552

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 Ctnng, D930025P04Rik, PG

Expression Broad expression in lung adult (RPKM 160.5), stomach adult (RPKM 151.6) and 23 other tissuesSee more

Orthologs human all

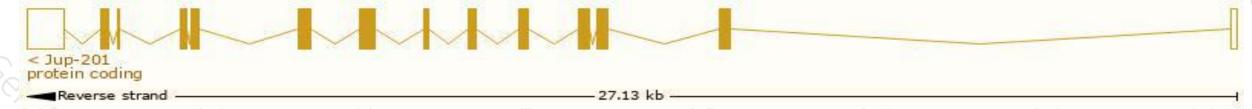
Transcript information (Ensembl)



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

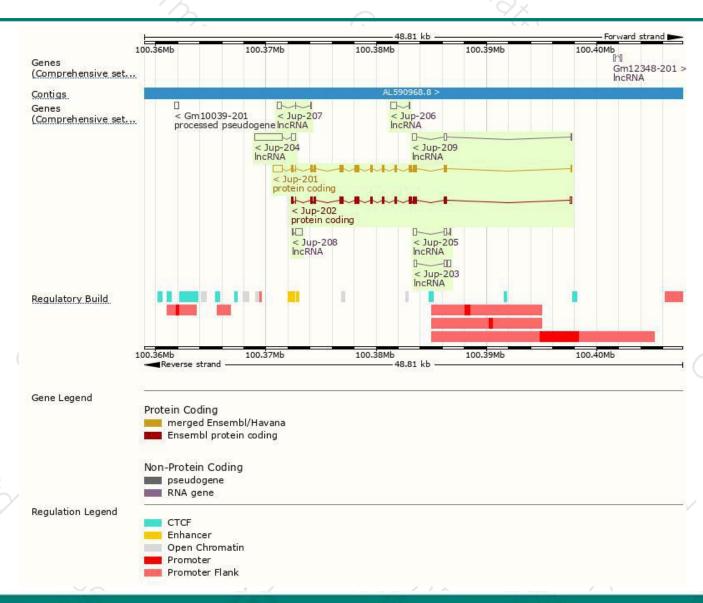
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Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Jup-201	ENSMUST00000001592.14	3205	<u>745aa</u>	Protein coding	CCDS25420	Q02257	TSL:1 GENCODE basic APPRIS P1
Jup-202	ENSMUST00000107403.1	2386	<u>745aa</u>	Protein coding	CCDS25420	Q02257	TSL:5 GENCODE basic APPRIS P1
Jup-204	ENSMUST00000124659.1	2913	No protein	IncRNA	(2)	- 2	TSL:2
Jup-208	ENSMUST00000152774.1	758	No protein	IncRNA	N23	72	TSL:2
Jup-203	ENSMUST00000123903.1	742	No protein	IncRNA	(5)	-	TSL:3
Jup-209	ENSMUST00000155746.7	684	No protein	IncRNA	686	-	TSL:2
Jup-206	ENSMUST00000149798.1	667	No protein	IncRNA	(2)		TSL:3
Jup-205	ENSMUST00000128268.7	502	No protein	IncRNA	N23	72	TSL:5
Jup-207	ENSMUST00000151476.1	441	No protein	IncRNA	11783	-	TSL:5

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



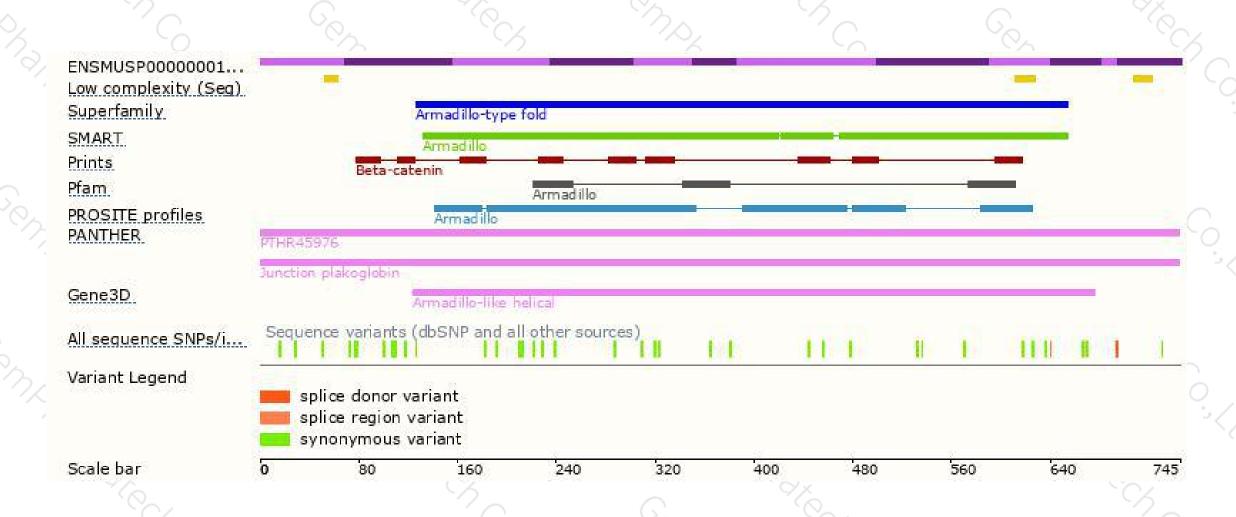
Genomic location distribution





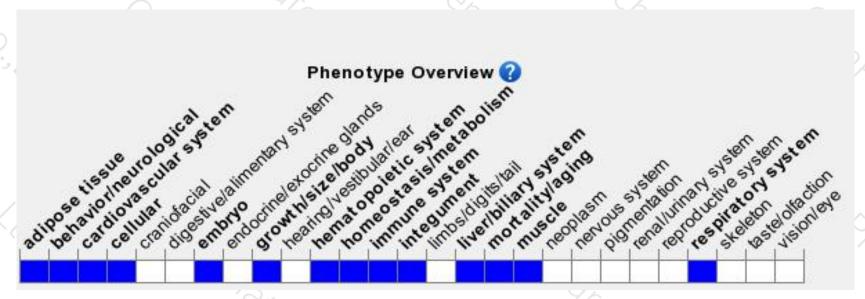
Protein domain





Mouse phenotype description(MGI)





Phenotypes affected by the gene are marked in blue.Data quoted from MGI database(http://www.informatics.jax.org/).

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





