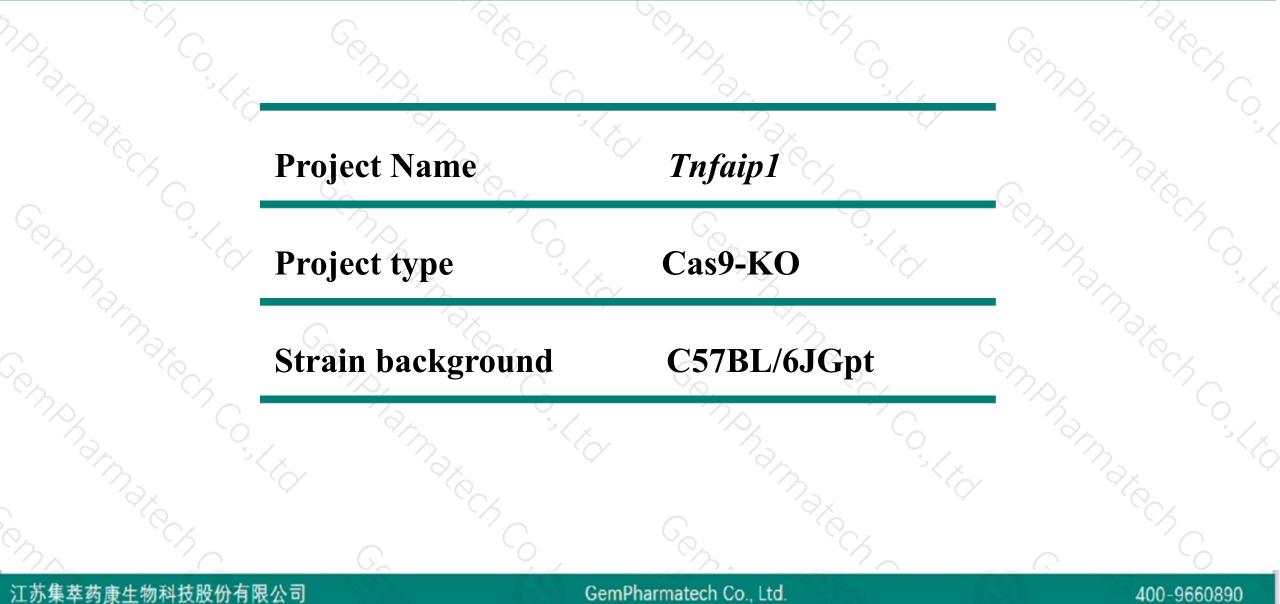


Tnfaip1 Cas9-KO Strategy

Designer:Xueting Zhang Reviewer:Yanhua Shen Date:2020-02-11

Project Overview

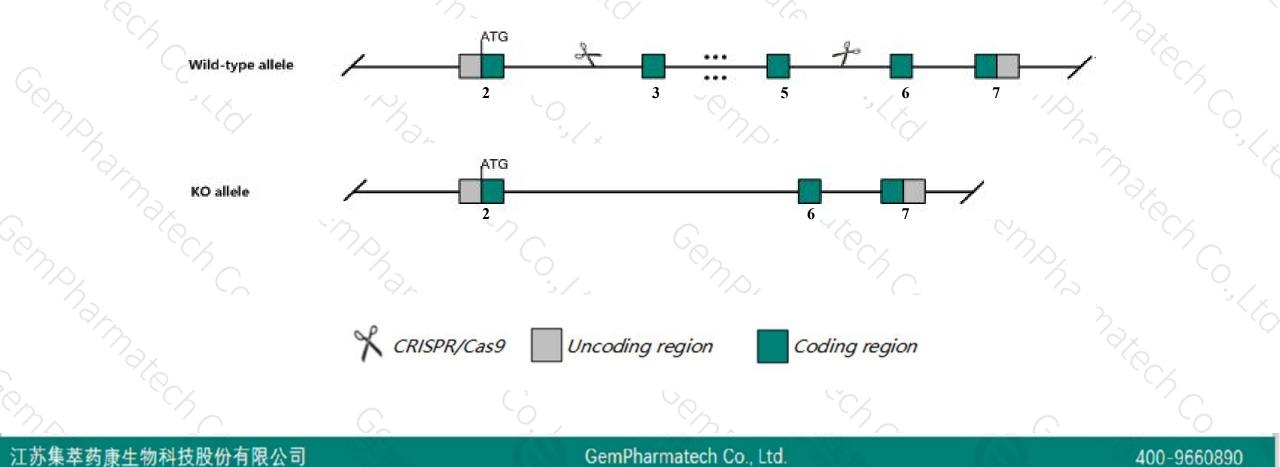




Knockout strategy



This model will use CRISPR/Cas9 technology to edit the *Tnfaip1* gene. The schematic diagram is as follows:





- The *Tnfaip1* gene has 2 transcripts. According to the structure of *Tnfaip1* gene, exon3-exon5 of *Tnfaip1-202* (ENSMUST00000108277.2) transcript is recommended as the knockout region. The region contains 313bp coding sequence. Knock out the region will result in disruption of protein function.
- > In this project we use CRISPR/Cas9 technology to modify *Tnfaip1* gene. The brief process is as follows: CRISPR/Cas9 system



- The floxed region is near to the N-terminal of *Ift20* gene, this strategy may influence the regulatory function of the N-terminal of *Ift20* gene.

The *Tnfaip1* 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)



Infaip1 tumor necrosis factor, alpha-induced protein 1 (endothelial) [Mus musculus (house mouse)] Gene ID: 21927, updated on 10-Oct-2019 Summary \$? Official Symbol Tnfaip1 provided by MGI Official Full Name tumor necrosis factor, alpha-induced protein 1 (endothelial) provided by MGI Primary source MGI:MGI:104961 See related Ensembl:ENSMUSG00000017615 Gene type protein coding RefSeg 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 Edp1; Edp-1; Tnfip1; Bacurd2 Expression Ubiquitous expression in lung adult (RPKM 35.5), large intestine adult (RPKM 31.2) and 28 other tissues See more Orthologs human all Genomic context ☆ ?

Location: 11 B5; 11 46.74 cM

Exon count: 7

See Tnfaip1 in Genome Data Viewer

Annotation release	Status	Assembly	Chr	Location
108	current	GRCm38.p6 (GCF_000001635.26)	11	NC_000077.6 (7852285078536270, complement)
Build 37.2	previous assembly	MGSCv37 (GCF_000001635.18)	11	NC_000077.5 (7833635278349762, complement)

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Transcript information (Ensembl)



The gene has 2 transcripts, all transcripts are shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Tnfaip1-202	ENSMUST00000108277.2	3768	<u>316aa</u>	Protein coding	CCDS25110	<u>070479</u>	TSL:1 GENCODE basic APPRIS P1
Tnfaip1-201	ENSMUST00000017759.8	3720	<u>316aa</u>	Protein coding	CCDS25110	070479	TSL:1 GENCODE basic APPRIS P1

The strategy is based on the design of *Tnfaip1-202* transcript, The transcription is shown below

< Tnfaip1-202 protein coding

Reverse strand

- 13.48 kb --

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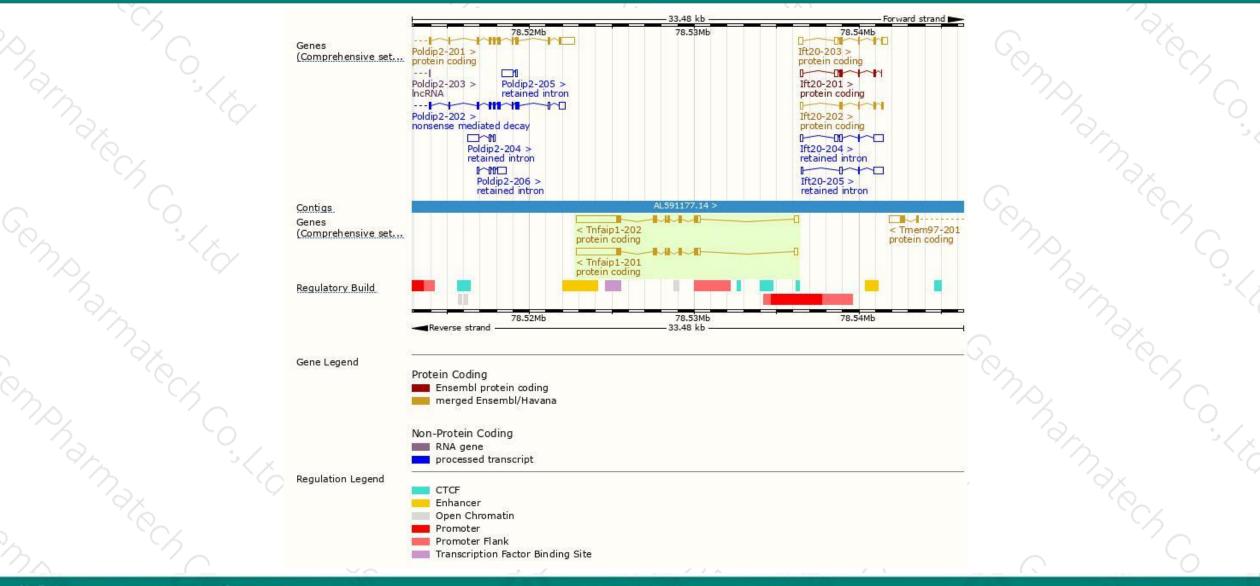
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Genomic location distribution



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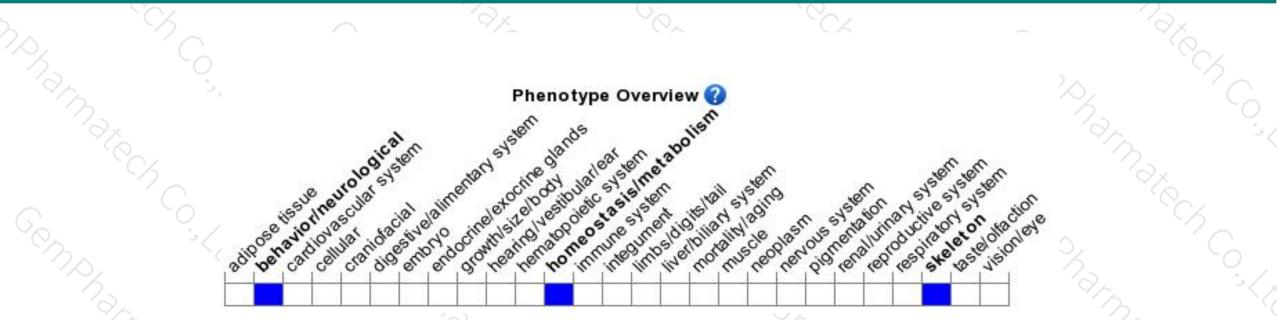
Protein domain



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\sim	Pfam	Potassium channel tetramerisation-type BTB domain								
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		PTHR11145:SF17								240
	Gene3D	3.30.710.10								
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	Variant Legend	synonymous val	riant						<u> </u>) ''
	Scale bar	o 40	80	120	160	200	240		316	
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Mouse phenotype description(MGI)





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



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



