

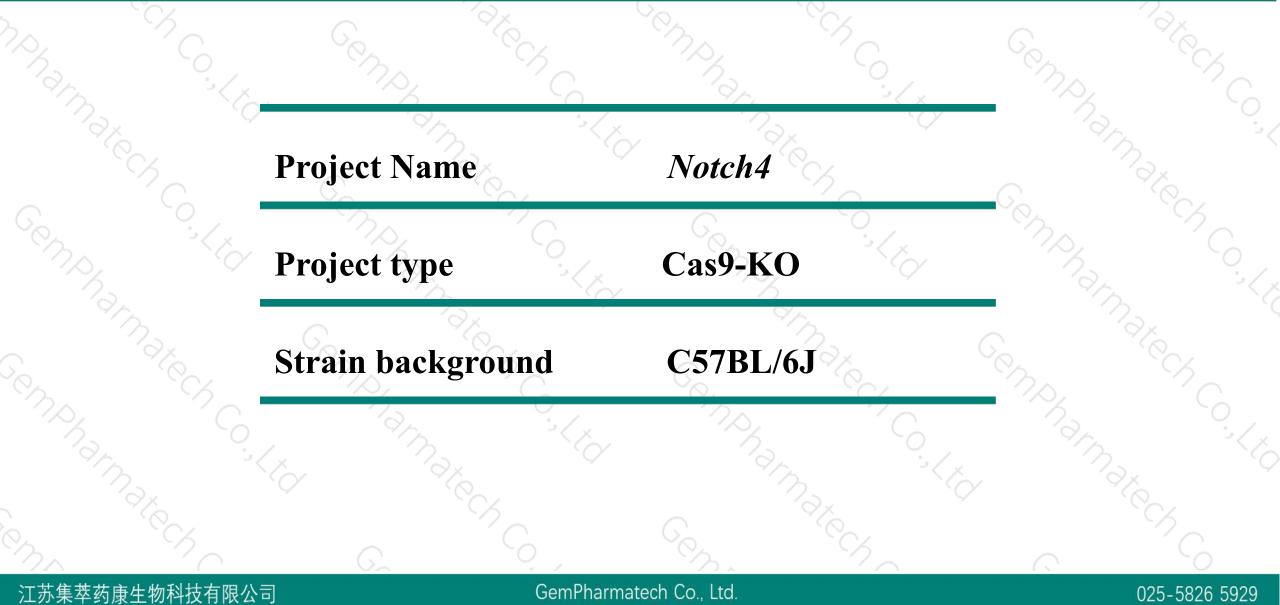
Notch4 Cas9-KO Strategy

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Designer: Huan Fan Design Date: 2019-8-23

Project Overview

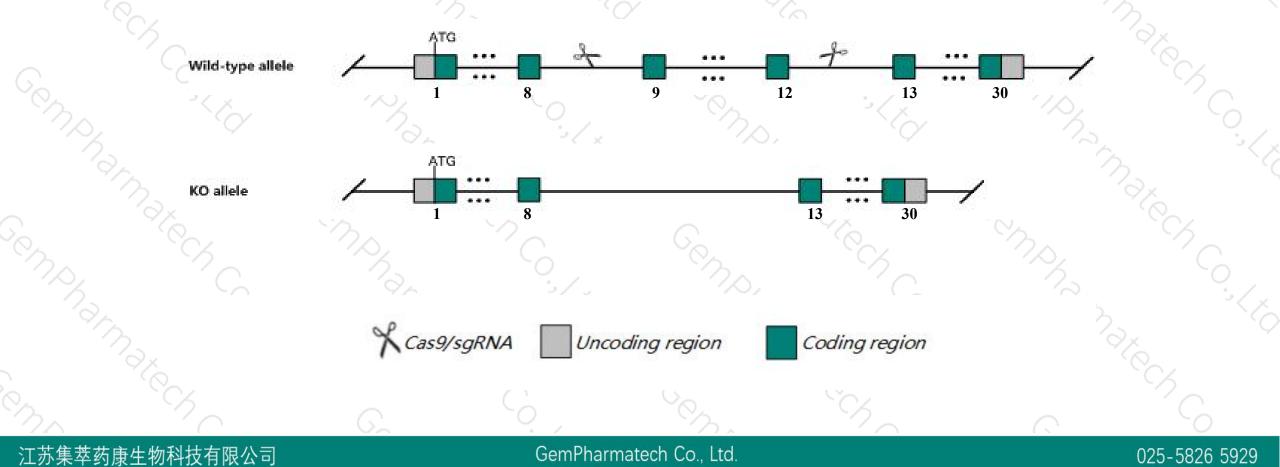




Knockout strategy



This model will use CRISPR/Cas9 technology to edit the Notch4 gene. The schematic diagram is as follows:





- The Notch4 gene has 12 transcripts. According to the structure of Notch4 gene, exon9-exon12 of Notch4-201 (ENSMUST00000015612.13) transcript is recommended as the knockout region. The region contains 511bp coding sequence. Knock out the region will result in disruption of protein function.
- In this project we use CRISPR/Cas9 technology to modify *Notch4* gene. The brief process is as follows: sgRNA was transcribed in vitro.Cas9 and sgRNA were microinjected into the fertilized eggs of C57BL/6J mice.Fertilized eggs were transplanted to obtain positive F0 mice which were confirmed by PCR and sequencing. A stable F1 generation mouse model was obtained by mating positive F0 generation mice with C57BL/6J mice.

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- According to the existing MGI data, Mice homozygous for a knock-out allele are viable and fertile but exhibit a slight delay in postnatal retinal angiogenesis.
- The Notch4 gene is located on the Chr17. 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.

Notice

Gene information (NCBI)



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Notch4 notch 4 [Mus musculus (house mouse)]

Gene ID: 18132, updated on 31-Jan-2019

Summary

Official SymbolNotch4 provided by MGIOfficial Full Namenotch 4 provided by MGIPrimary sourceMGI:MGI:107471See relatedEnsembl:ENSMUSG0000015468Gene typeprotein codingRefSeq statusVALIDATEDOrganismMus musculusLineageEukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Golires; Rodentia; Myomorpha;
Muroidea; Murinae; Mus; MusAlso knownasInt-3, Int3, N4ExpressionBiased expression in lung adult (RPKM 37.2), adrenal adult (RPKM 14.3) and 14 other tissuesSee more
human all

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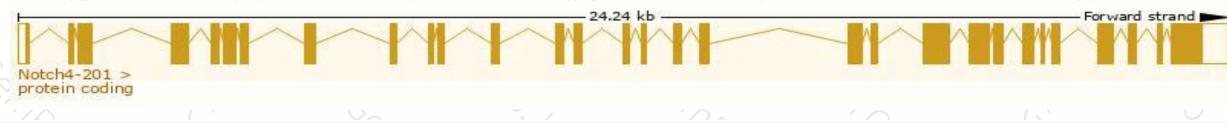
Transcript information (Ensembl)



Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Notch4-201	ENSMUST00000015612.13	6591	<u>1964aa</u>	Protein coding	CCDS28647	A2CG28	TSL:1 GENCODE basic APPRIS P1
Notch4-211	ENSMUST00000173389.7	6380	<u>978aa</u>	Nonsense mediated decay	-8	<u>G3UX69</u>	TSL:1
Notch4-208	ENSMUST00000151867.1	804	<u>43aa</u>	Nonsense mediated decay	-	G3UZH3	CDS 5' incomplete TSL:5
Notch4-207	ENSMUST00000151654.7	733	<u>43aa</u>	Nonsense mediated decay	22	G3UZH3	CDS 5' incomplete TSL:5
Notch4-210	ENSMUST00000156724.1	619	No protein	Processed transcript	5	65	TSL:2
lotch4-212	ENSMUST00000174707.1	451	No protein	Processed transcript	-5	87	TSL:3
Notch4-203	ENSMUST00000126950.1	356	No protein	Processed transcript	<u>-</u>	34	TSL:3
Notch4-202	ENSMUST00000126702.1	247	No protein	Processed transcript	24	8 <u>4</u>	TSL:5
lotch4-204	ENSMUST00000128314.1	796	No protein	Retained intron	5	65	TSL:3
Notch4-206	ENSMUST00000150441.1	642	No protein	Retained intron	-5	87	TSL:5
Notch4-205	ENSMUST00000141768.1	598	No protein	Retained intron	<u>.</u>	34	TSL:2
Notch4-209	ENSMUST00000152714.1	352	No protein	Retained intron	2	ė <u>.</u>	TSL:3

The gene has 12 transcripts, all transcripts are shown below:

The strategy is based on the design of Notch4-201 transcript, The transcription is shown below



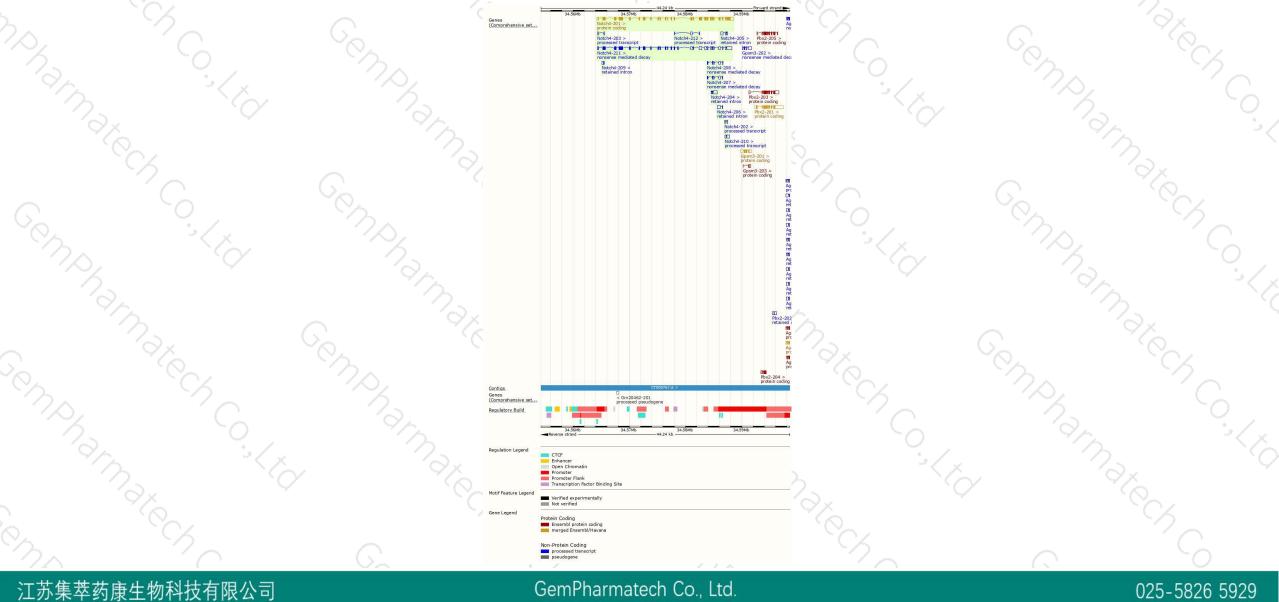
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Genomic location distribution





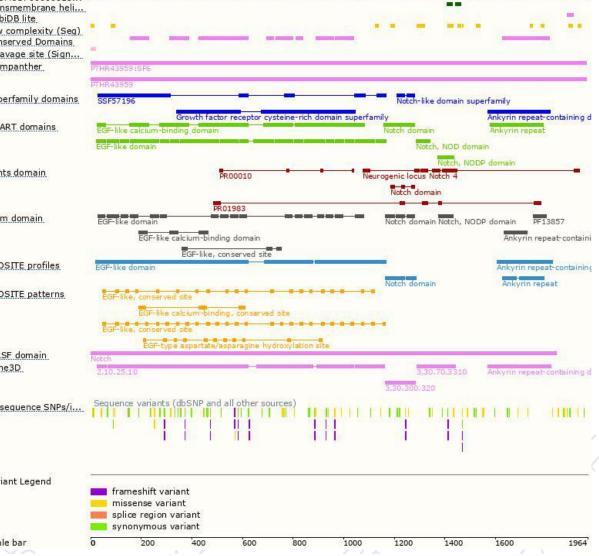
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Protein domain



ENSMUSP00000015... Transmembrane heli... MobiDB lite Low complexity (Seg) Conserved Domains Cleavage site (Sign... hmmpanther PTHR43959:SF6 FTHR4395 Superfamily domains SSF57196 SMART domains EGF-like calcium-binding domain EGF-like domain Prints domain Pfam domain EGE-like domain PROSITE profiles GF-like domain PROSITE patterns EGF-like, conserved site PIRSF domain Gene3D 2.10.25.10 All sequence SNPs/i... Variant Legend 📕 frameshift variant missense variant splice region variant 🗾 synonymous variant Scale bar 200 400



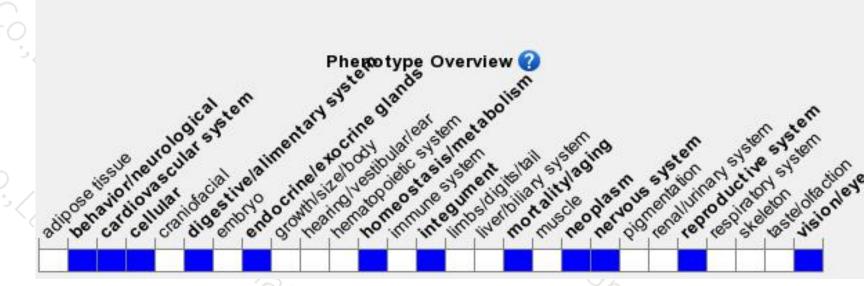
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Mouse phenotype description(MGI)





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

According to the existing MGI data, Mice homozygous for a knock-out allele are viable and fertile but exhibit a slight delay in postnatal retinal angiogenesis.



If you have any questions, you are welcome to inquire. Tel: 025-5864 1534



