

Vnn1 Cas9-KO Strategy

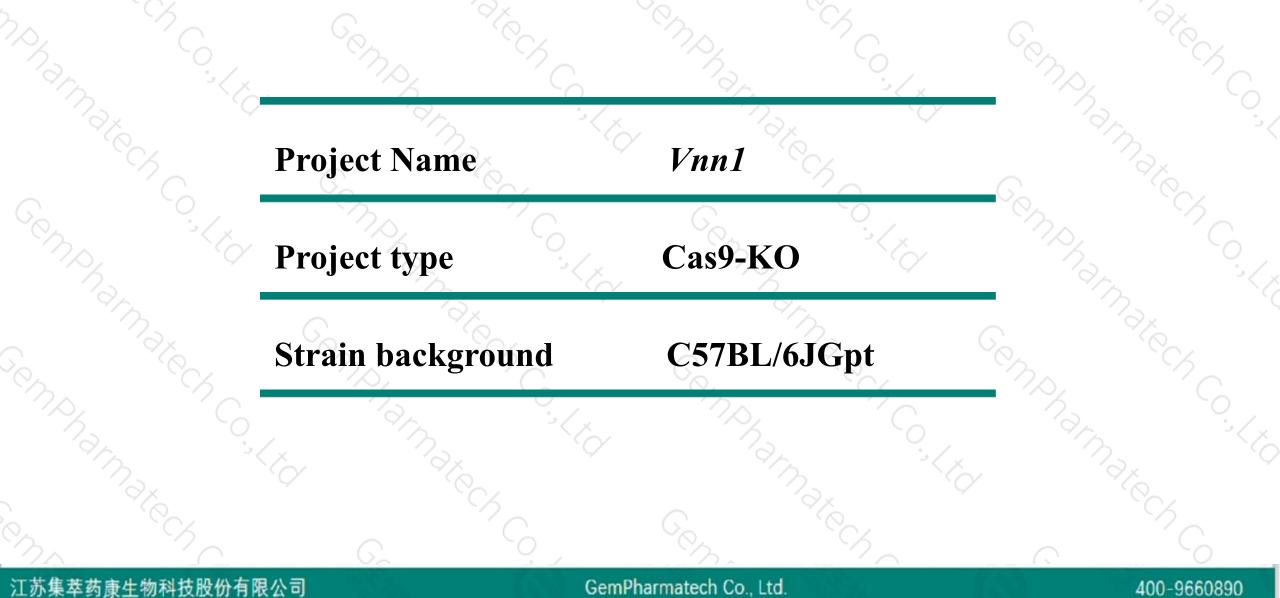
Designer: Reviewer: Design Date:

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Yang Zeng Huimin Su 2019-12-23

Project Overview

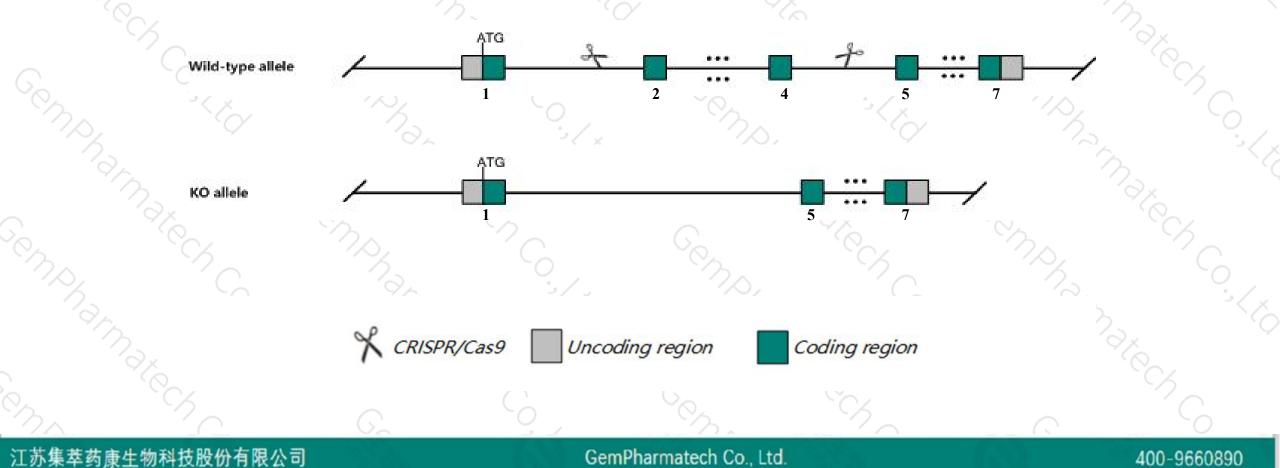




Knockout strategy



This model will use CRISPR/Cas9 technology to edit the *Vnn1* gene. The schematic diagram is as follows:





- The Vnn1 gene has 2 transcripts. According to the structure of Vnn1 gene, exon2-exon4 of Vnn1-201 (ENSMUST00000041416.7) transcript is recommended as the knockout region. The region contains 616bp coding sequence. Knock out the region will result in disruption of protein function.
- > In this project we use CRISPR/Cas9 technology to modify *Vnn1* gene. The brief process is as follows: CRISPR/Cas9 system we

- According to the existing MGI data, Mice homozygous for disruptions of this gene develop normally and so no abnormalities in the maturation of lymphoid organs. However, membrane bound pantetheinase is absent in livers and kidneys resulting in an absence of cysteamine in these organs.
- The Vnn1 gene is located on the Chr10. 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)



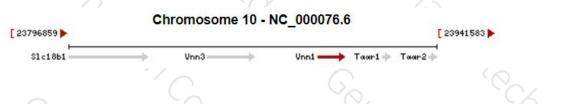
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Vnn1 vanin 1 [Mus musculus (house mouse)]

Gene ID: 22361, updated on 26-Nov-2019

Summary

Official Symbol Vnn1 provided by MGI Official Full Name vanin 1 provided by MGI **Primary source** MGI:MGI:108395 Ensembl:ENSMUSG0000037440 See related protein coding Gene type RefSeg status VALIDATED Organism Mus musculus Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Myomorpha; Lineage Muroidea; Muridae; Murinae; Mus; Mus Also known as V-1 Biased expression in large intestine adult (RPKM 31.3), placenta adult (RPKM 24.5) and 8 other tissues See more Expression Orthologs human all



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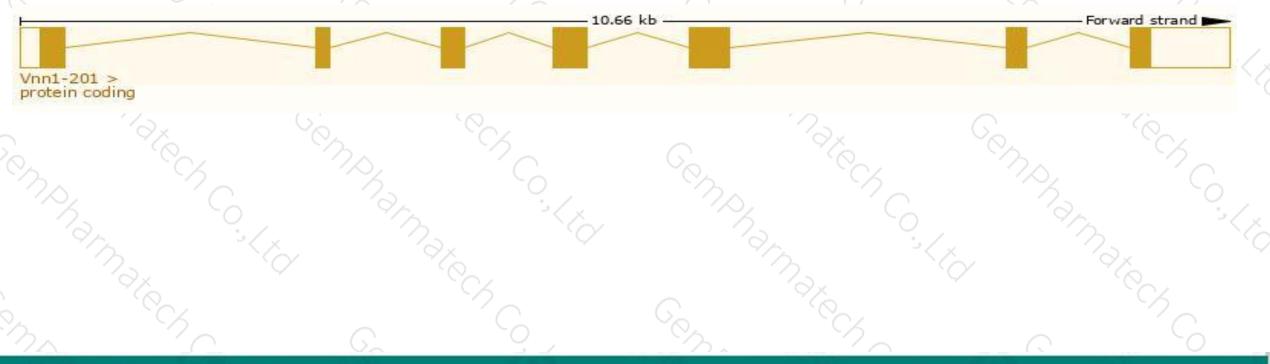
Transcript information (Ensembl)



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

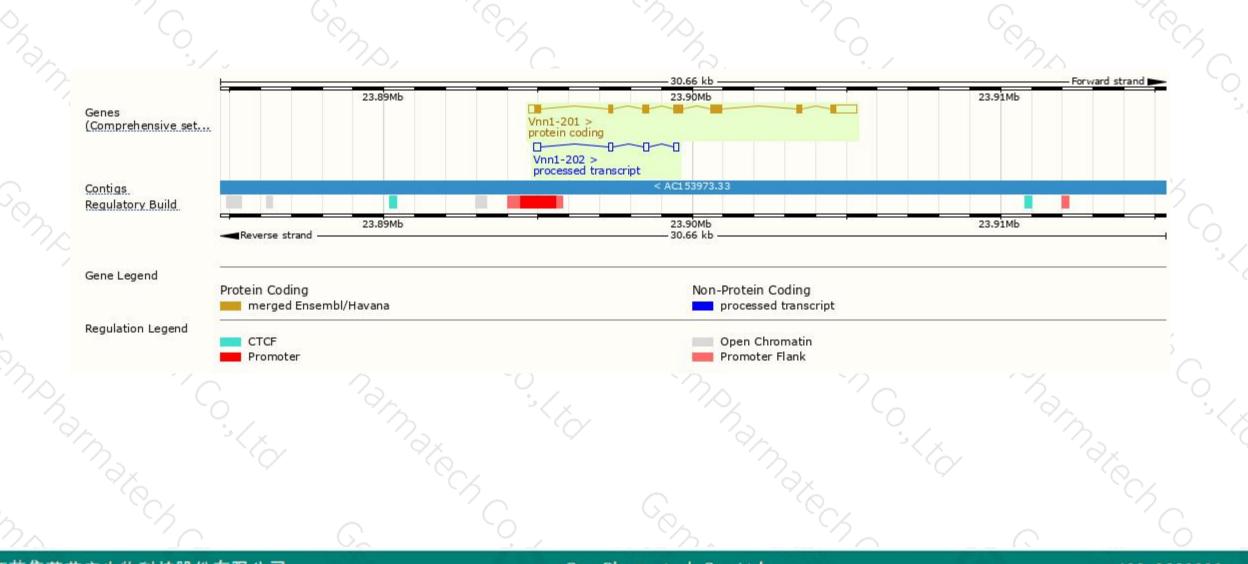
Name 🖕	Transcript ID 💧	bp 🍦	Protein 🖕	Translation ID	Biotype 💧	CCDS 🍦	UniProt 🖕	Flags 🖕		
Vnn1-201	ENSMUST0000041416.7	2416	<u>512aa</u>	ENSMUSP00000040599.7	Protein coding	<u>CCDS35868</u> 译	<u>Q9Z0K8</u> ₽	TSL:1	GENCODE basic	APPRIS P1
Vnn1-202	ENSMUST00000219254.1	717	No protein	2	IncRNA	2)	1940		TSL:3	

The strategy is based on the design of *Vnn1-201* transcript, The transcription is shown below



Genomic location distribution





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Protein domain

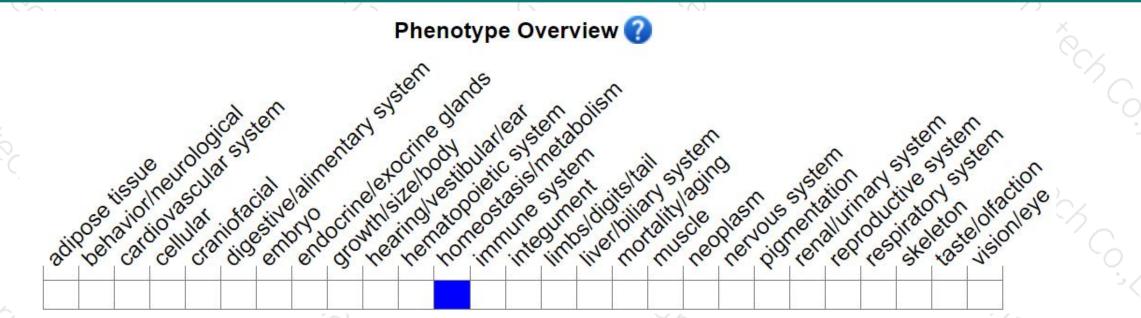


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	PROSITE profiles	Carbon	-nitrogen hydrolase							
	PIRSF	Biotinidase-like, eu	karyotic					3		
	PANTHER	Biotinidase/VNN far	mily							
$\gamma_{\mathcal{O}}$	Gene3D	PTHR10609:SF16	gen hydrolase superfan	nio -				0		
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Mouse 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 disruptions of this gene develop normally and so no abnormalities in the maturation of lymphoid organs. However, membrane bound pantetheinase is absent in livers and kidneys resulting in an absence of cysteamine in these organs.

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



