

VAV2 Cas9-KO Strategy

Designer:

Bingxuan Li

Reviewer:

Huimin Su

Design Date:

2019-09-25

Project Overview

Project Name

VAV2

Project type

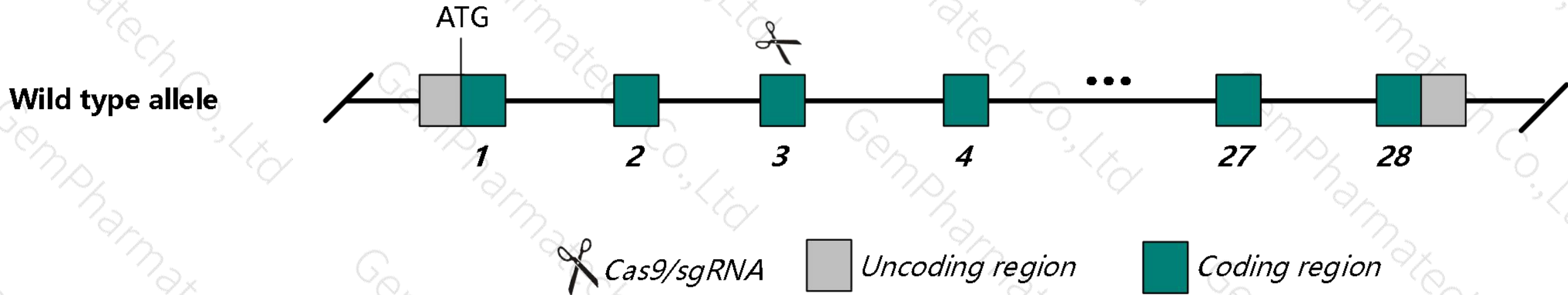
Cas9-KO

Strain background

C57BL/6N

Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *VAV2* gene. The schematic diagram is as follows:



- In this project we use CRISPR/Cas9 technology to modify *VAV2* gene. The brief process is as follows: sgRNA was transcribed in vitro. Cas9 and sgRNA were microinjected into the fertilized eggs of C57BL/6N 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/6N mice.

- According to the existing MGI data, mice homozygous for a knock-out allele exhibit partial postnatal lethality, growth retardation, small placenta, absent gastric milk in mice that die and abnormal placental.
- The *VAV2* 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)

Vav2 vav 2 oncogene [*Mus musculus* (house mouse)]

Gene ID: 22325, updated on 17-Mar-2015

Summary

Official Symbol Vav2 provided by [MGI](#)
Official Full Name vav 2 oncogene provided by [MGI](#)
Primary source [MGI:MGI:102718](#)
See related [Ensembl:ENSMUSG000000009621](#); [Vega:OTTMUSG00000012034](#)
Gene type protein coding
RefSeq status PROVISIONAL
Organism [Mus musculus](#)
Lineage Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi; Muroidea; Muridae; Murinae; Mus; Mus
Also known as A1847175; 2810040F13Rik
Orthologs [human](#) [all](#)

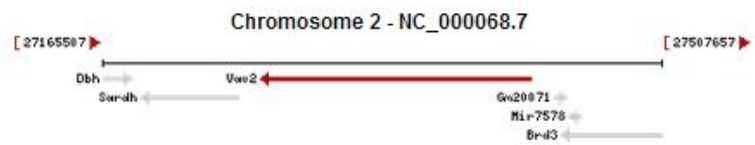
Genomic context

Location: 2 A3; 2 19.36 cM

See Vav2 in [Map](#)

Exon count: 30

Annotation release	Status	Assembly	Chr	Location
105	current	GRCm38.p3 (GCF_000001635.23)	2	NC_000068.7 (27262104..27427608, complement)
Build 37.2	previous assembly	MGSCv37 (GCF_000001635.18)	2	NC_000068.6 (27119155..27282345, complement)

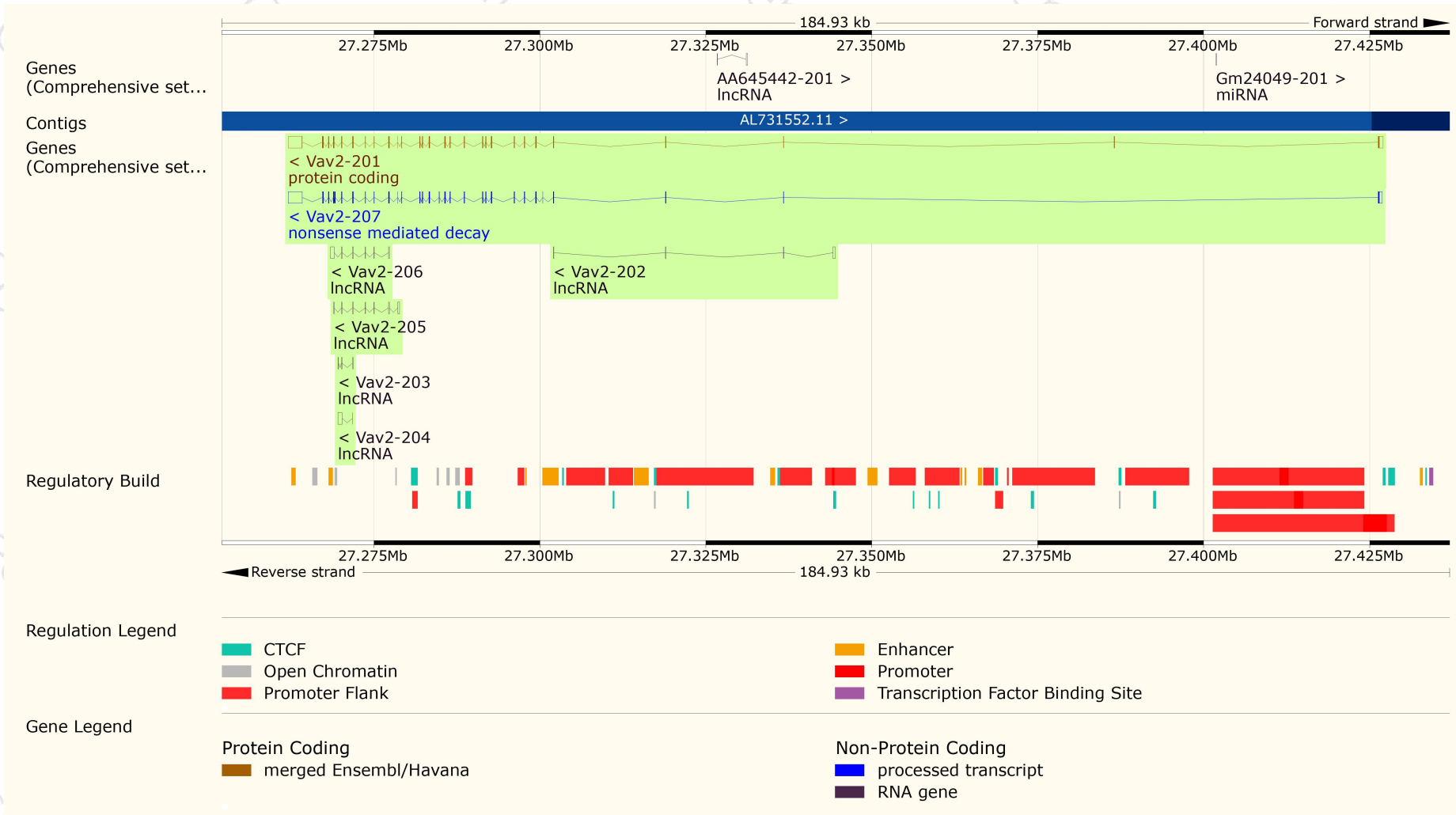


Transcript information (Ensembl)

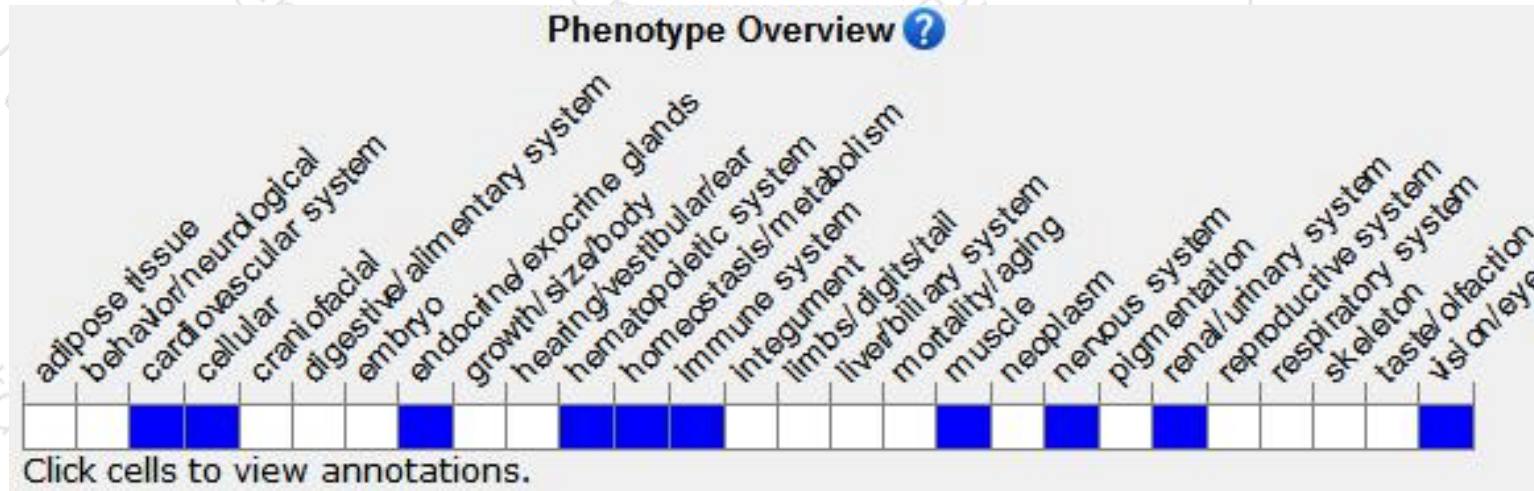
The gene has 7 transcripts,all transcripts are shown below:

Show/hide columns (1 hidden)							Filter	
Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags	
Vav2-201	ENSMUST00000056176.7	5221	868aa	Protein coding	CCDS15827	Q60992	TSL:1	GENCODE basic APPRIS P1
Vav2-207	ENSMUST00000185188.7	5098	829aa	Nonsense mediated decay	-	Q7TSI6	TSL:1	
Vav2-206	ENSMUST00000149758.7	1027	No protein	lncRNA	-	-	TSL:3	
Vav2-205	ENSMUST00000148067.7	848	No protein	lncRNA	-	-	TSL:3	
Vav2-204	ENSMUST00000146843.1	659	No protein	lncRNA	-	-	TSL:5	
Vav2-202	ENSMUST00000132642.1	541	No protein	lncRNA	-	-	TSL:3	
Vav2-203	ENSMUST00000135584.1	276	No protein	lncRNA	-	-	TSL:5	

Genomic location distribution



Mouse phenotype description(MGI)



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

Homozygous null mutants have defects in humoral immune response to type II thymus-independent antigens, in primary response to thymus-dependent antigens and inability to switch immunoglobulin class, form germinal centers and generate secondary responses.

If you have any questions, you are welcome to inquire.

Tel: 025-5864 1534

