

Vav3 Cas9-CKO Strategy

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Reviewer:

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Design Date:

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Project Overview

Project Name

Vav3

Project type

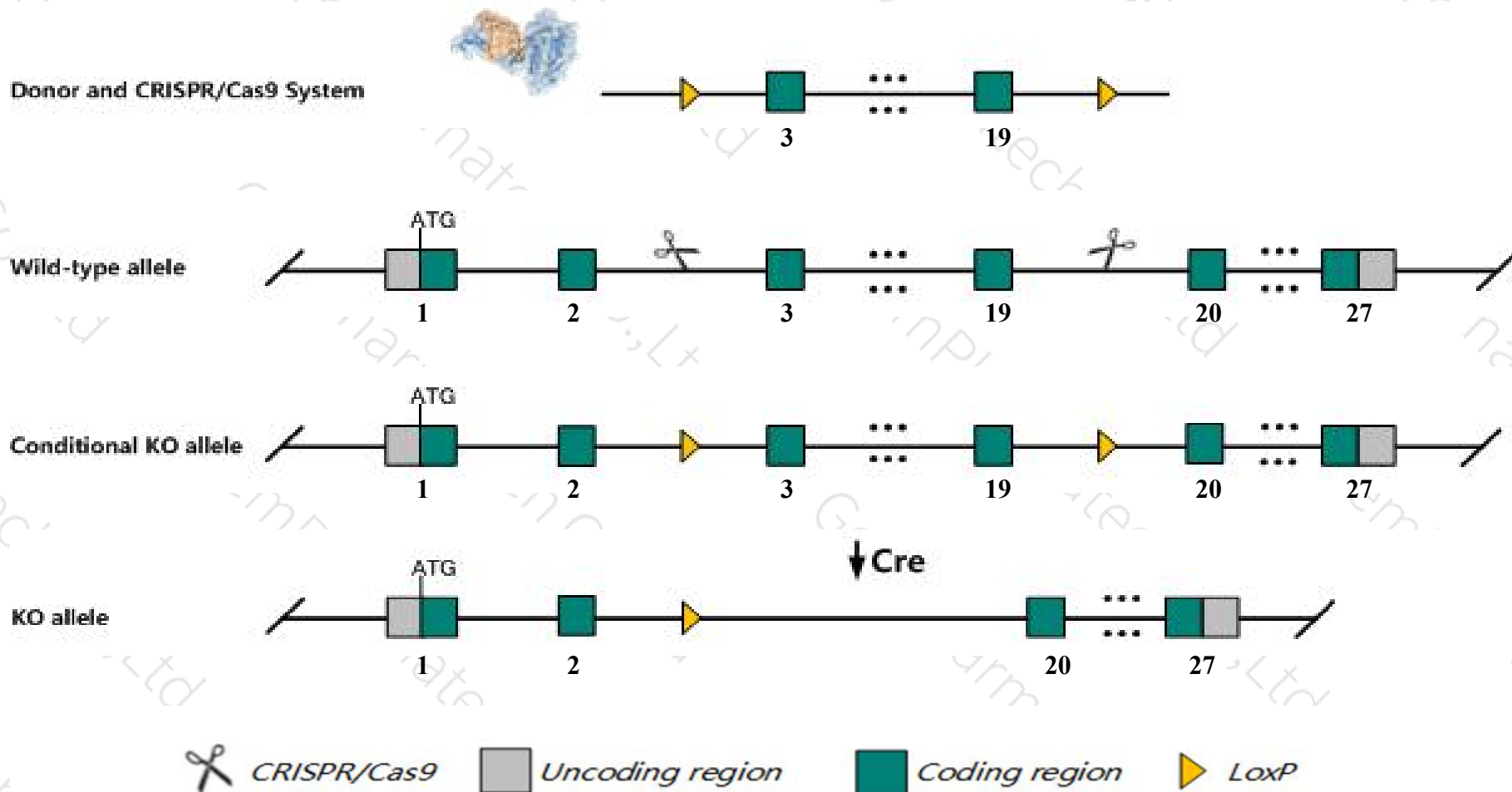
Cas9-CKO

Strain background

C57BL/6JGpt

Conditional Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *Vav3* gene. The schematic diagram is as follows:



Technical routes

- The *Vav3* gene has 6 transcripts. According to the structure of *Vav3* gene, exon3-exon19 of *Vav3-201* (ENSMUST00000046864.13) transcript is recommended as the knockout region. The region contains 1456bp coding sequence. Knock out the region will result in disruption of protein function.
- In this project we use CRISPR/Cas9 technology to modify *Vav3* gene. The brief process is as follows: CRISPR/Cas9 system and Donor were microinjected into the fertilized eggs of C57BL/6JGpt 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/6JGpt mice.
- The flox mice will be knocked out after mating with mice expressing Cre recombinase, resulting in the loss of function of the target gene in specific tissues and cell types.

- According to the existing MGI data, Homozygous mutation of this gene results in tachycardia, systemic arterial hypertension, cardiovascular remodeling, hyperactivity of sympathetic neurons and thus high catecholamine levels, and increased levels of kidney-related hormones.
- The *Vav3* gene is located on the Chr3. 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 loxp insertion on gene transcription, RNA splicing and protein translation cannot be predicted at existing technological level.

Gene information (NCBI)

Vav3 vav 3 oncogene [*Mus musculus* (house mouse)]

Gene ID: 57257, updated on 22-Oct-2019

Summary

Official Symbol Vav3 provided by [MGI](#)
Official Full Name vav 3 oncogene provided by [MGI](#)
Primary source [MGI:MGI:1888518](#)
See related [Ensembl:ENSMUSG00000033721](#)
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 Idd18.1; AA986410; A530094I06Rik
Expression Ubiquitous expression in whole brain E14.5 (RPKM 2.7), CNS E14 (RPKM 2.5) and 27 other tissues [See more](#)
Orthologs [human](#) [all](#)

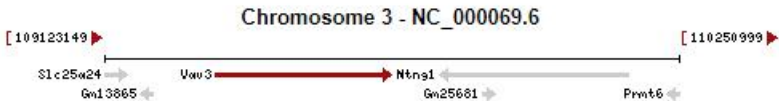
Genomic context

Location: 3; 3 F3

See Vav3 in [Genome Data Viewer](#)

Exon count: 28

Annotation release	Status	Assembly	Chr	Location
108	current	GRCm38.p6 (GCF_000001635.26)	3	NC_000069.6 (109340317..109685694)
Build 37.2	previous assembly	MGSCv37 (GCF_000001635.18)	3	NC_000069.5 (109143601..109488612)

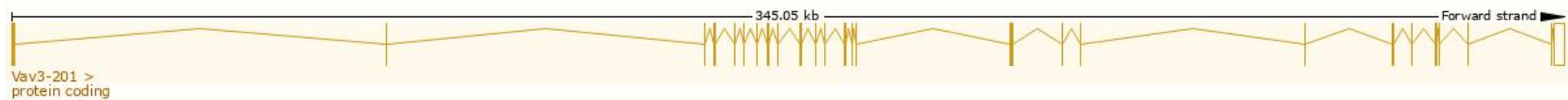


Transcript information (Ensembl)

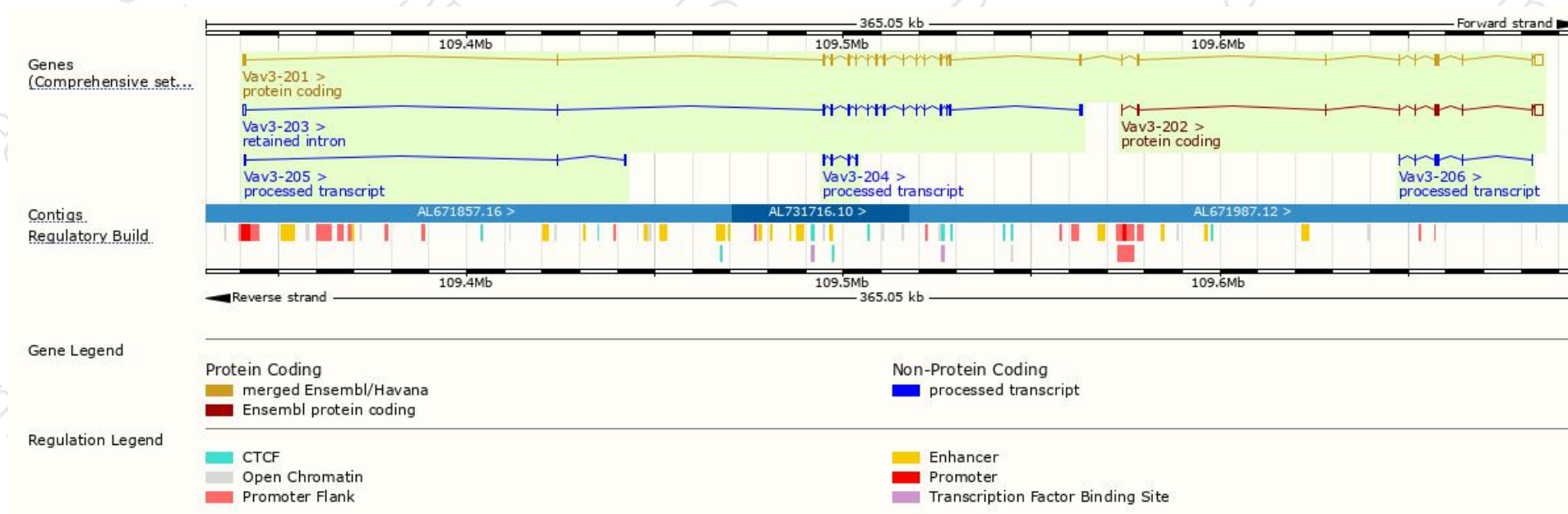
The gene has 6 transcripts,all transcripts are shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Vav3-201	ENSMUST00000046864.13	5019	847aa	Protein coding	CCDS17773	Q9R0C8	TSL:1 GENCODE basic APPRIS P1
Vav3-202	ENSMUST00000106576.2	3123	287aa	Protein coding	CCDS59650	Q9R0C8	TSL:1 GENCODE basic
Vav3-206	ENSMUST00000148866.1	579	No protein	Processed transcript	-	-	TSL:3
Vav3-204	ENSMUST00000128033.1	515	No protein	Processed transcript	-	-	TSL:3
Vav3-205	ENSMUST00000137871.1	465	No protein	Processed transcript	-	-	TSL:1
Vav3-203	ENSMUST00000126179.7	2398	No protein	Retained intron	-	-	TSL:1

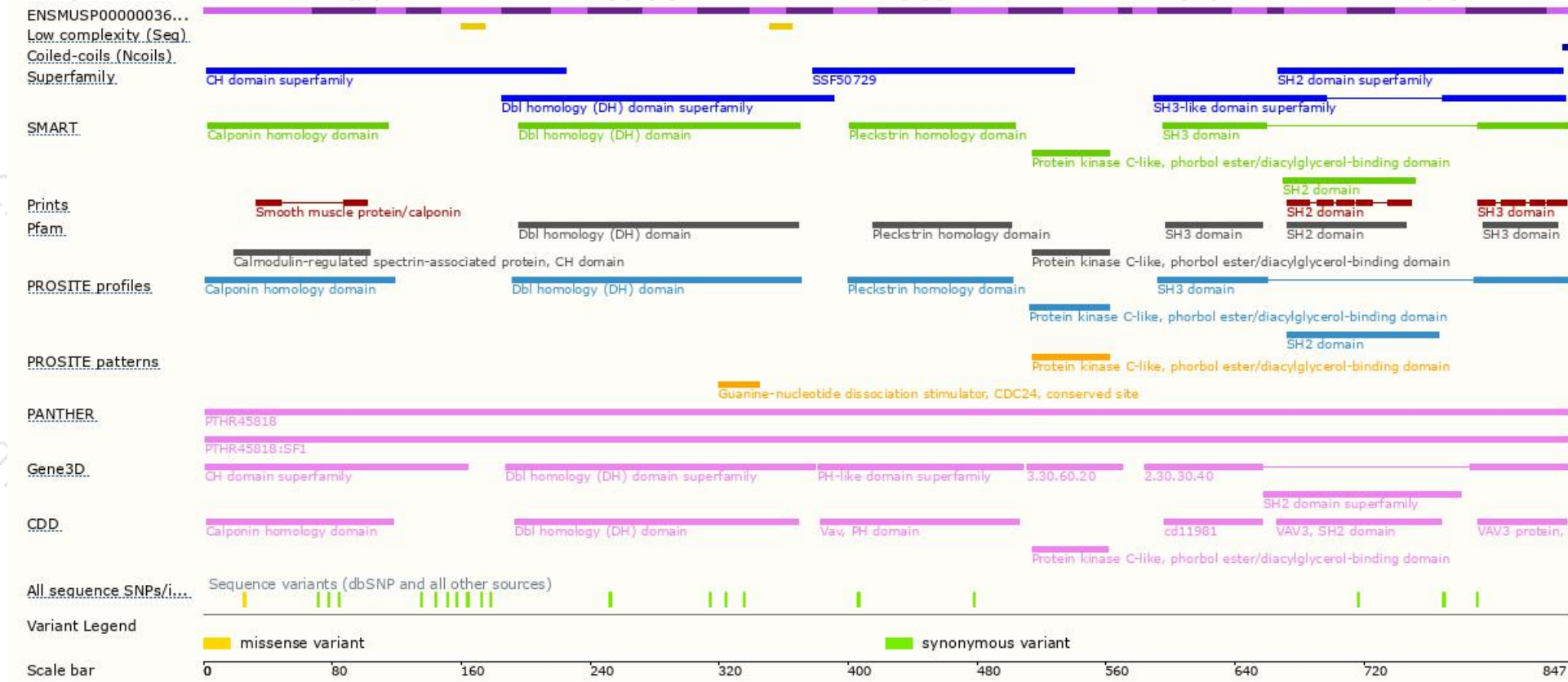
The strategy is based on the design of *Vav3-201* transcript,The transcription is shown below



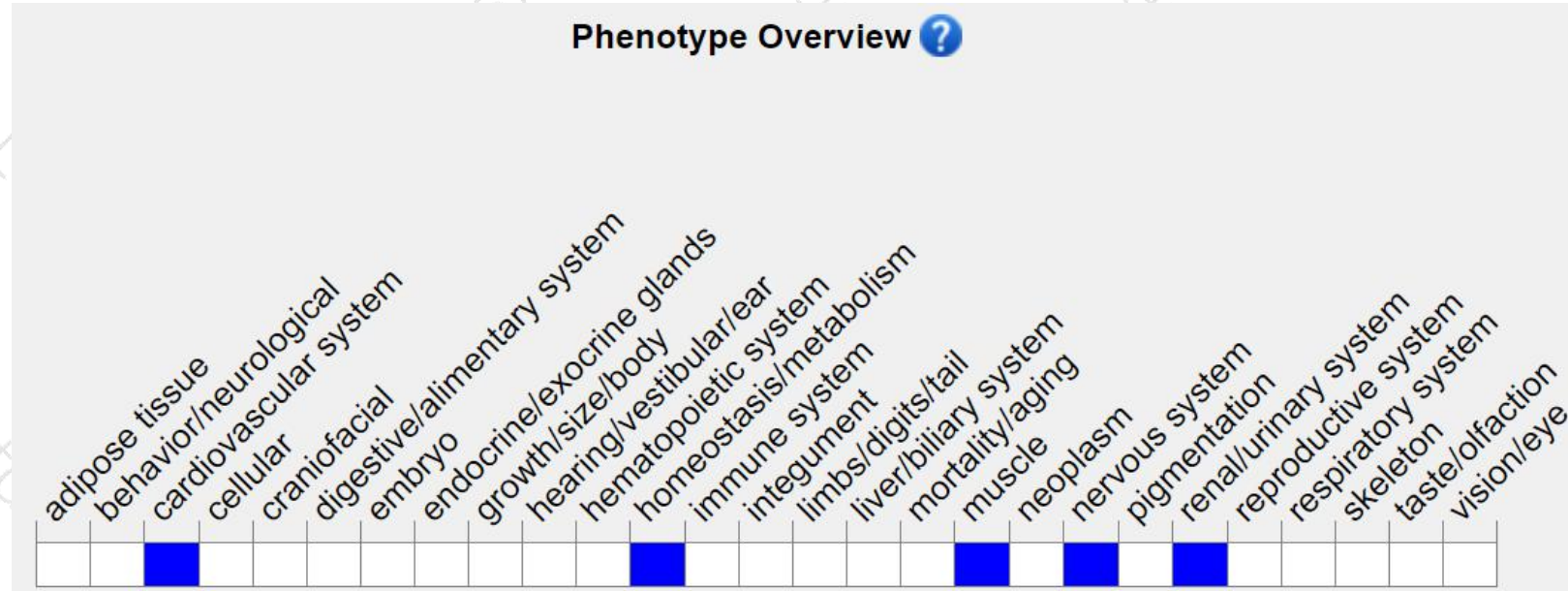
Genomic location distribution



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/>).

According to the existing MGI data, Homozygous mutation of this gene results in tachycardia, systemic arterial hypertension, cardiovascular remodeling, hyperactivity of sympathetic neurons and thus high catecholamine levels, and increased levels of kidney-related hormones.

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

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