Vav2 Cas9-CKO Strategy

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Project Overview

Project Name	***Vav2***
Project type	**Cas9-CKO**
Strain background	**C57BL/6JGpt**

Conditional Knockout strategy

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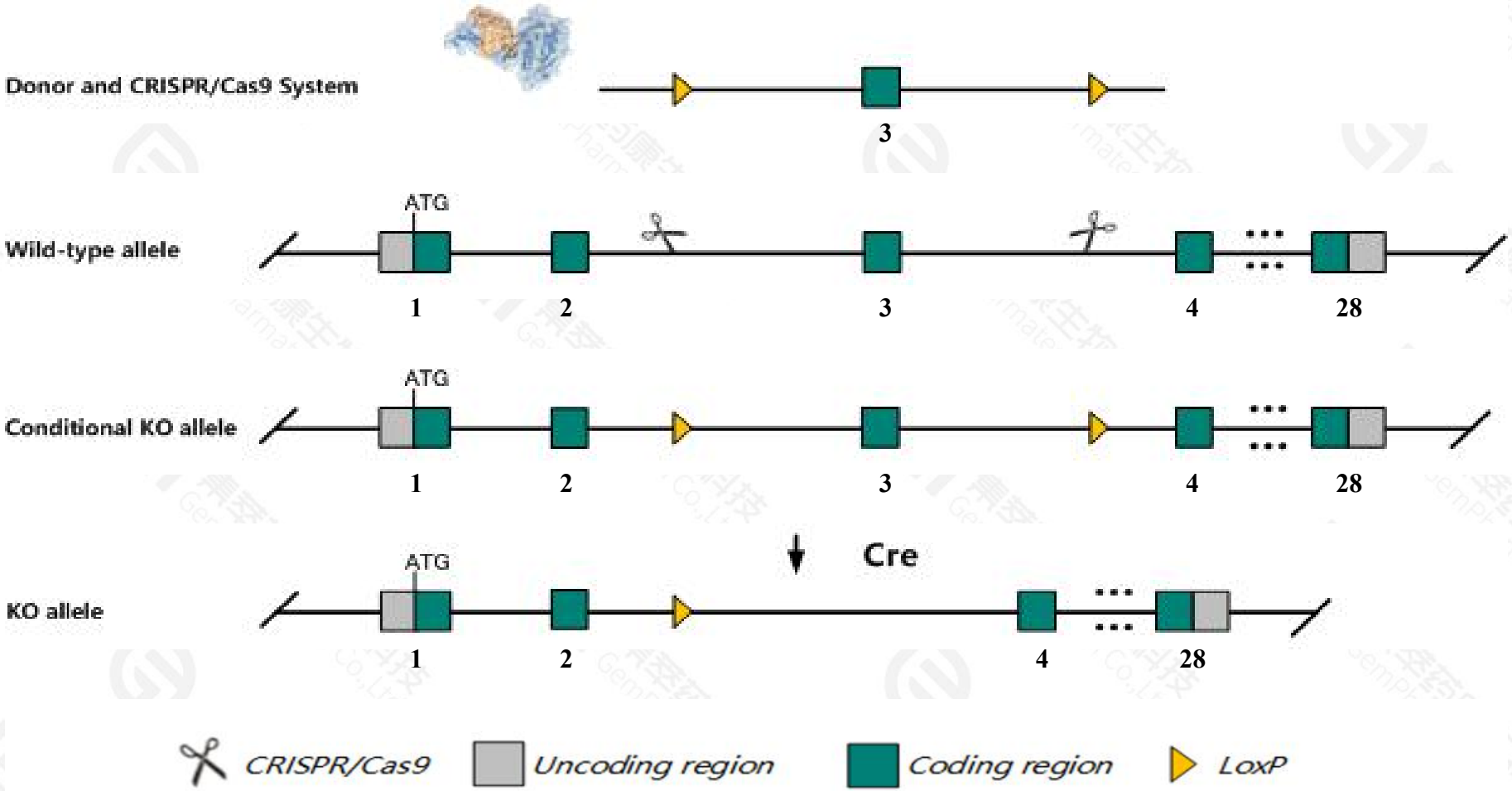
This model will use CRISPR/Cas9 technology to edit the *Vav2* gene. The schematic diagram is as follows:



Technical routes

➢ The *Vav2* gene has 7 transcripts. According to the structure of *Vav2* gene, exon3 of *Vav2-201*(ENSMUST00000056176.7) transcript is recommended as the knockout region.The region contains 59bp coding sequence. Knock out the region will result in disruption of protein function.

➢ In this project we use CRISPR/Cas9 technology to modify *Vav2* 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.

Notice

➢ According to the existing MGI data,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.

➢ 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 loxp insertion on gene transcription, RNA splicing and protein translation cannot be predicted at existing technological level.

Gene information（NCBI）

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

Gene ID: 22325, updated on 13-Mar-2020

Summary

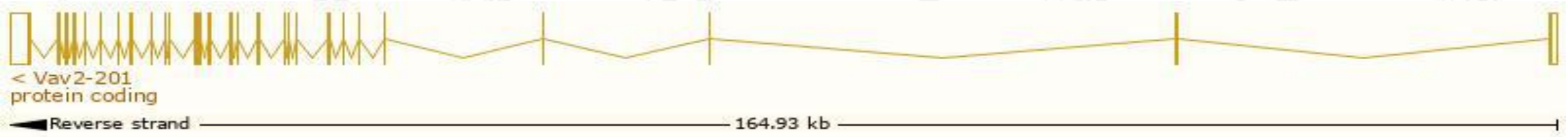
Official Symbol	Vav2 provided by MGI
Official Full Name	vav 2 oncogene provided by MGI
Primary source	MGI:MGI:102718
See related	Ensembl:ENSMUSG00000009621
Gene type	protein coding
RefSeq status	REVIEWED
Organism	Mus musculus
Lineage	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Myomorpha; Muroidea; Muridae; Murinae; Mus; Mus
Also known as	2810040F13Rik, AI847175, Vav-2
Summary	This gene encodes a member of the Vav family of Rho guanine nucleotide exchange factors. Vav family proteins are involved in the development and activation of lymphocytes, and the encoded protein may also be involved in angiogenesis. Disruption of this gene in mice is associated with heart, artery, and kidney defects, as well as tachycardia and hypertension. Alternative splicing results in multiple transcript variants. [provided by RefSeq, Dec 2015]
Expression	Ubiquitous expression in spleen adult (RPKM 23.7), duodenum adult (RPKM 17.4) and 28 other tissues See more
Orthologs	human all

Transcript information（Ensembl）

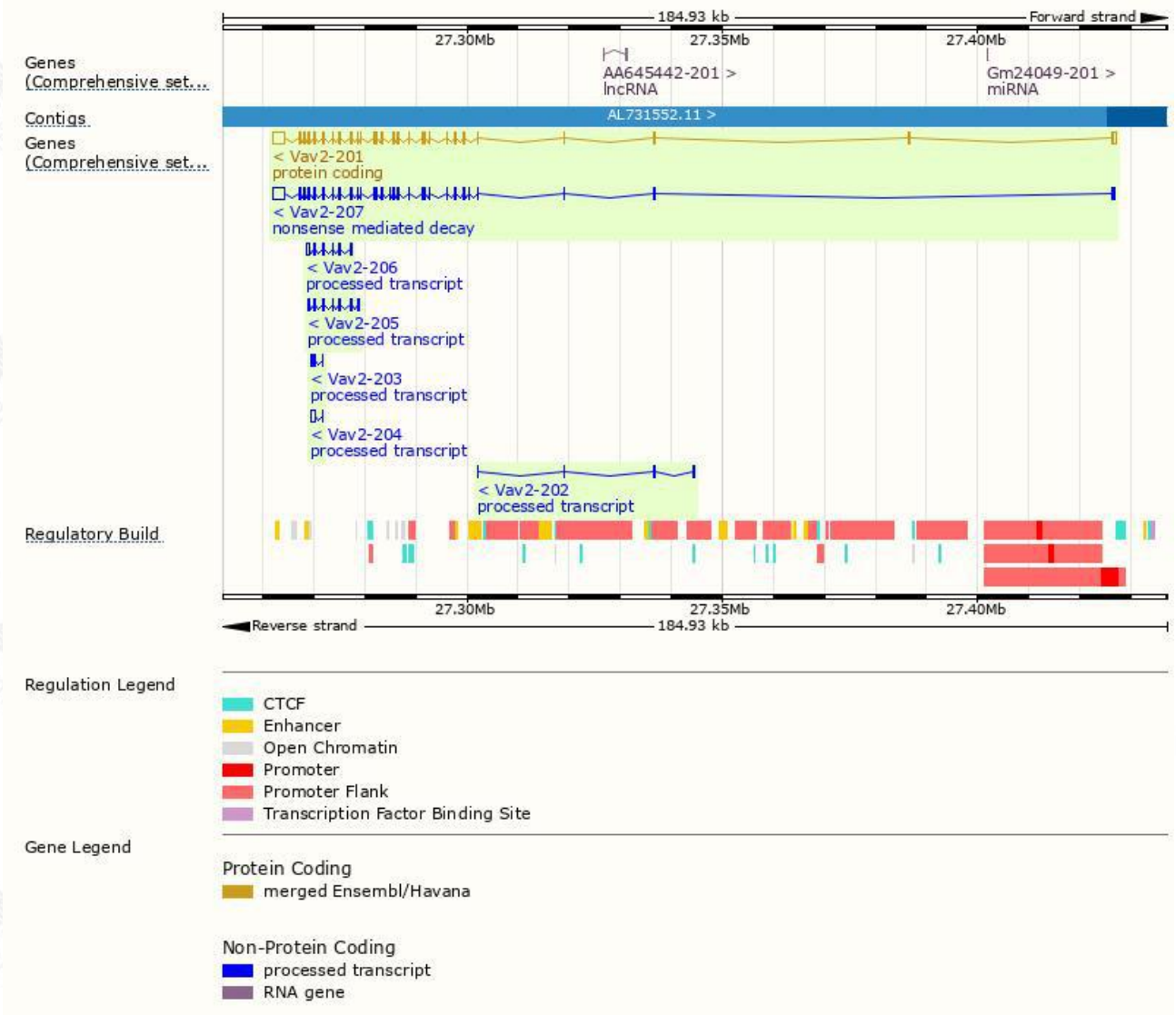
The gene has 7 transcripts,all transcripts are shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Vav2-201	ENSMUST00000056176.7	5221	868aa	Protein coding	CCDS15827	Q60992	TSL:1 GENCODE basic APPRIS is a system to annotate alternatively spliced transcripts based on a range of computational methods to identify the most functionally important transcript(s) of a gene. APPRIS P1
Vav2-207	ENSMUST00000185188.7	5098	829aa	Nonsense mediated decay	-	Q7TSI6	TSL:1
Vav2-206	ENSMUST00000149758.7	1027	No protein	Processed transcript	-	-	TSL:3
Vav2-205	ENSMUST00000148067.7	848	No protein	Processed transcript	-	-	TSL:3
Vav2-204	ENSMUST00000146843.1	659	No protein	Processed transcript	-	-	TSL:5
Vav2-202	ENSMUST00000132642.1	541	No protein	Processed transcript	-	-	TSL:3
Vav2-203	ENSMUST00000135584.1	276	No protein	Processed transcript	-	-	TSL:5

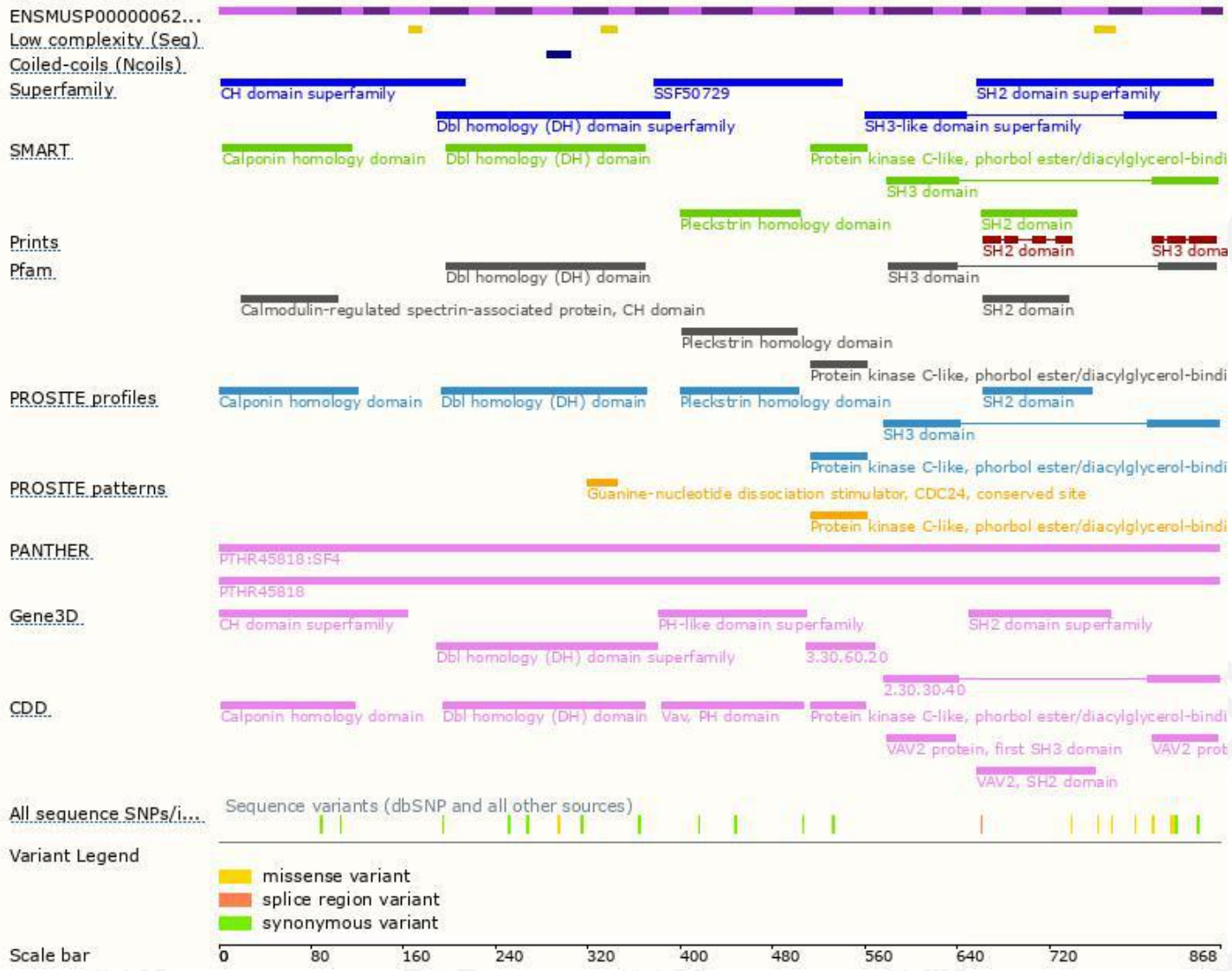
The strategy is based on the design of *Vav2-201* transcript,the transcription is shown below:



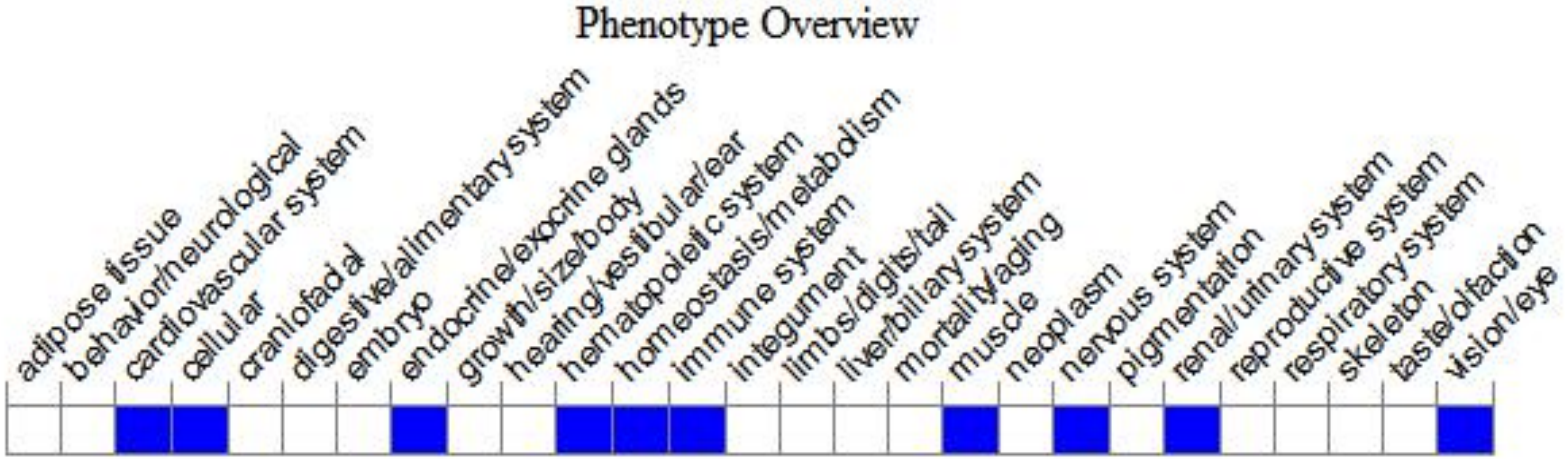
Genomic location distribution



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 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.

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