Vgll2 Cas9-CKO Strategy

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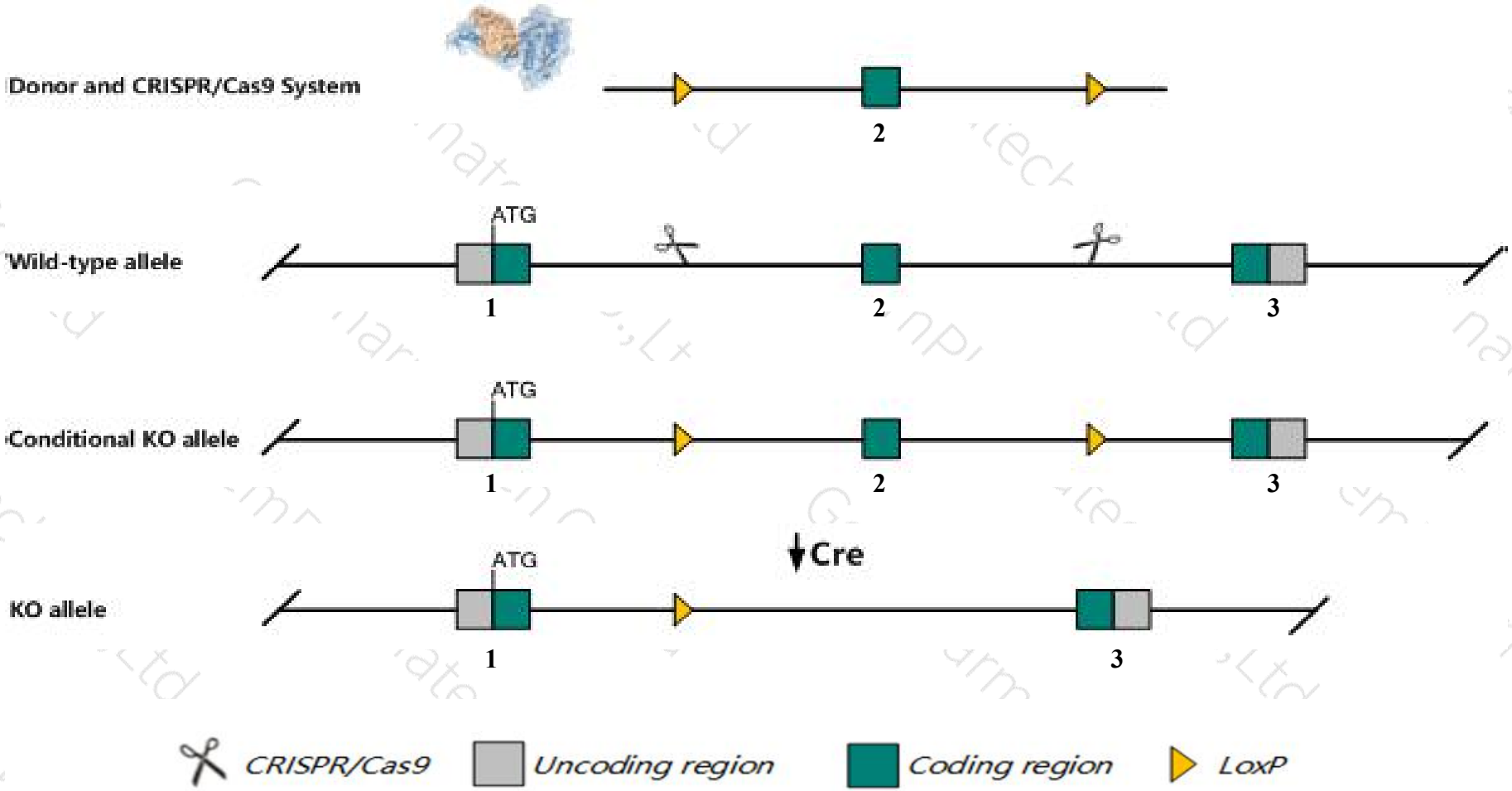
Project Overview

Project Name	***Vgll2***
Project type	**Cas9-CKO**
Strain background	**C57BL/6JGpt**

Conditional Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *Vgll2* gene. The schematic diagram is as follows:



Technical routes

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- The *Vgll2* gene has 2 transcripts. According to the structure of *Vgll2* gene, exon2 of *Vgll2-202* (ENSMUST00000163017.9) transcript is recommended as the knockout region.The region contains 307bp coding sequence. Knock out the region will result in disruption of protein function.

- In this project we use CRISPR/Cas9 technology to modify *Vgll2* 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,Mice homozygous for a knock-out allele exhibit abnormal skeletal muscle fiber type ratio and impaired exercise endurance.
- The floxed region is near to the N-terminal of *Gm24084* gene,this strategy may influence the regulatory function of the N-terminal of *Gm24084* gene.
- The *Vgll2* 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 loxp insertion on gene transcription, RNA splicing and protein translation cannot be predicted at existing technological level.

Gene information （NCBI）

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Vgll2 vestigial like family member 2 [*Mus musculus* (house mouse)]

Gene ID: 215031, updated on 27-Aug-2019

Summary

Official Symbol	Vgll2 provided by MGI
Official Full Name	vestigial like family member 2 provided by MGI
Primary source	MGI:MGI:2447460
See related	Ensembl:ENSMUSG00000049641
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	Vito1; vgl-2; VITO-1; C130057C21Rik
Summary	This gene is a member of the Vestigial-like (Vgl) gene family and is upregulated during muscle differentiation. The product of this gene interacts with and modifies the DNA-binding properties of the transcription factor, TEF-1, and is important for muscle tissue development. Reduced expression of this gene leads to a reduction in the terminal differentiation of muscle cells. Alternate splicing results in multiple protein isoforms. [provided by RefSeq, Jul 2014]
Expression	Biased expression in limb E14.5 (RPKM 21.9), mammary gland adult (RPKM 2.2) and 2 other tissues See more
Orthologs	human all

Genomic context

Location: 10; 10 B3

See Vgll2 in Genome Data Viewer

Exon count: 3

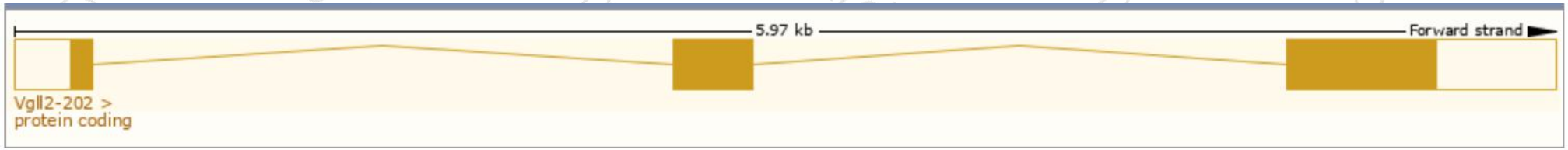
Annotation release	Status	Assembly	Chr	Location
108	current	GRCm38.p6 (GCF_000001635.26)	10	NC_000076.6 (52022502..52028471)
Build 37.2	previous assembly	MGSCv37 (GCF_000001635.18)	10	NC_000076.5 (51742492..51748277)

Transcript information（Ensembl）

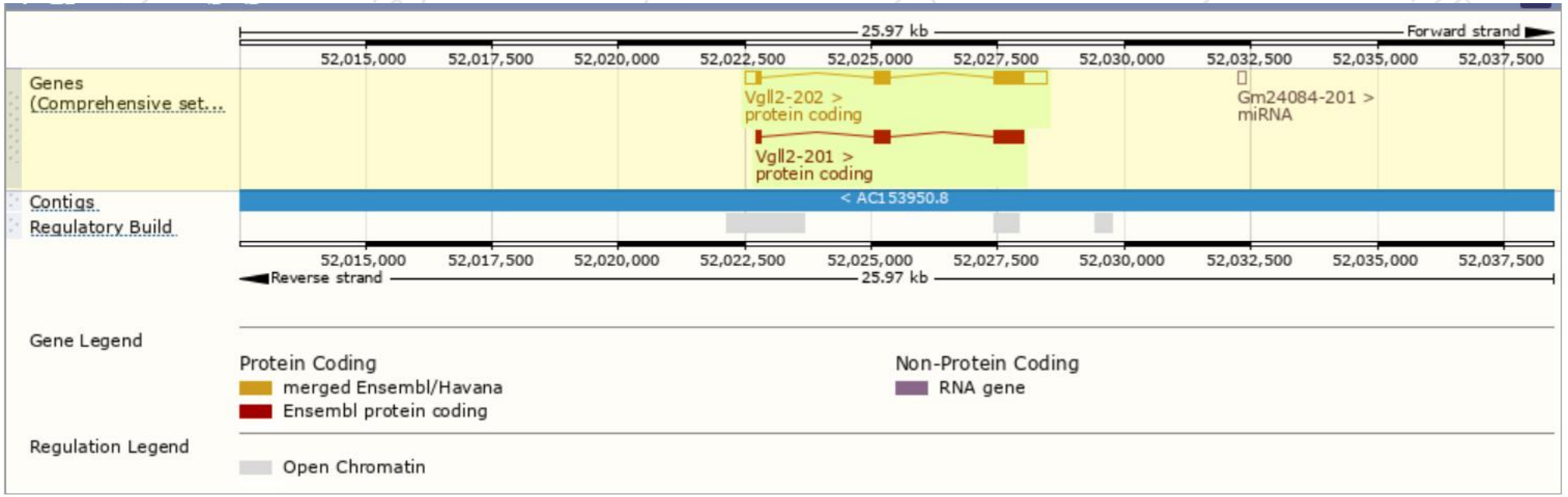
The gene has 2 transcripts,all transcripts are shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Vgll2-202	ENSMUST00000163017.9	1650	322aa	Protein coding	CCDS23837	Q8BGW8	TSL:1 GENCODE basic APPRIS P3
Vgll2-201	ENSMUST00000058347.5	966	321aa	Protein coding	CCDS78812	A0A0R4J0M3	TSL:1 GENCODE basic APPRIS ALT2

The strategy is based on the design of *Vgll2-202* transcript,The transcription is shown below

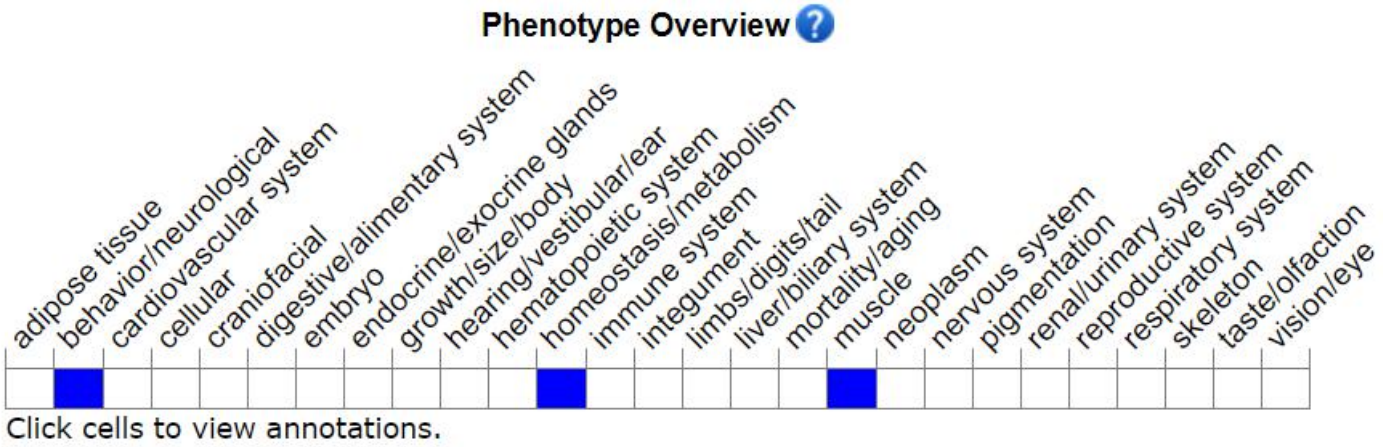


Genomic location distribution



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/).

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

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