

Parvg Cas9-CKO Strategy

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Project Overview

Project Name

Parvg

Project type

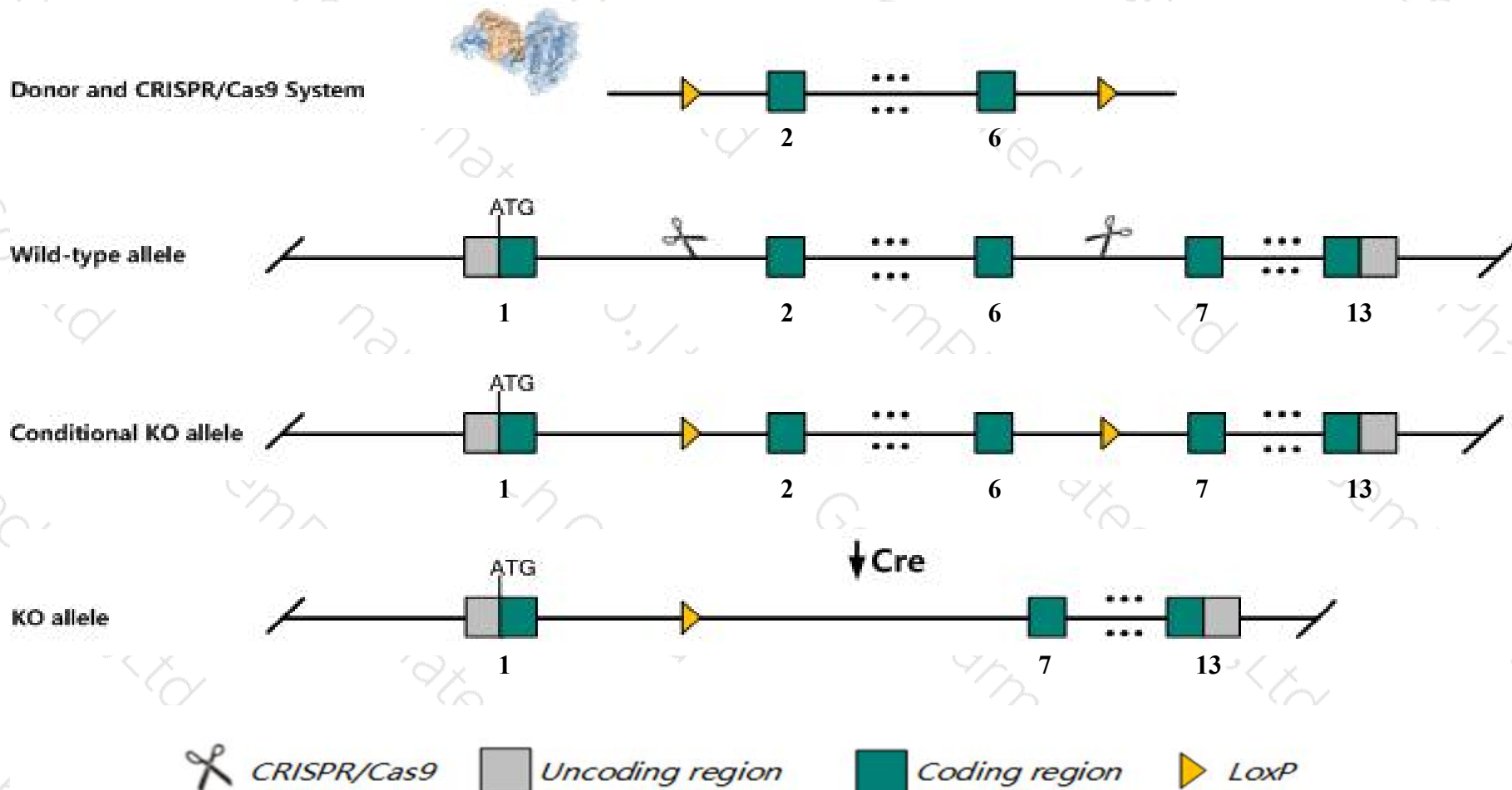
Cas9-CKO

Strain background

C57BL/6J

Conditional Knockout strategy

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



- The *Parvg* gene has 7 transcripts. According to the structure of *Parvg* gene, exon2-exon6 of *Parvg*-207 (ENSMUST00000163667.1) transcript is recommended as the knockout region. The region contains 521bp coding sequence. Knock out the region will result in disruption of protein function.
- In this project we use CRISPR/Cas9 technology to modify *Parvg* gene. The brief process is as follows: CRISPR/Cas9 system and Donor were microinjected into the fertilized eggs of C57BL/6J 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/6J 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 null mice are viable and fertile with a normal life span and normal immune cell development and function.
- The *Parvg* gene is located on the Chr15. 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)

Parvg parvin, gamma [Mus musculus (house mouse)]

Gene ID: 64099, updated on 13-Mar-2020

Summary



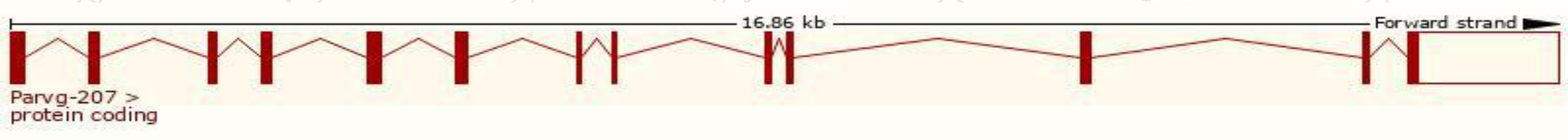
Official Symbol	Parvg provided by MGI
Official Full Name	parvin, gamma provided by MGI
Primary source	MGI:MGI:2158329
See related	Ensembl:ENSMUSG00000022439
Gene type	protein coding
RefSeq status	VALIDATED
Organism	Mus musculus
Lineage	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Myomorpha; Muroidea; Muridae; Murinae; Mus; Mus
Also known as	AI413459
Expression	Biased expression in thymus adult (RPKM 40.8), spleen adult (RPKM 24.7) and 6 other tissues See more
Orthologs	human all

Transcript information (Ensembl)

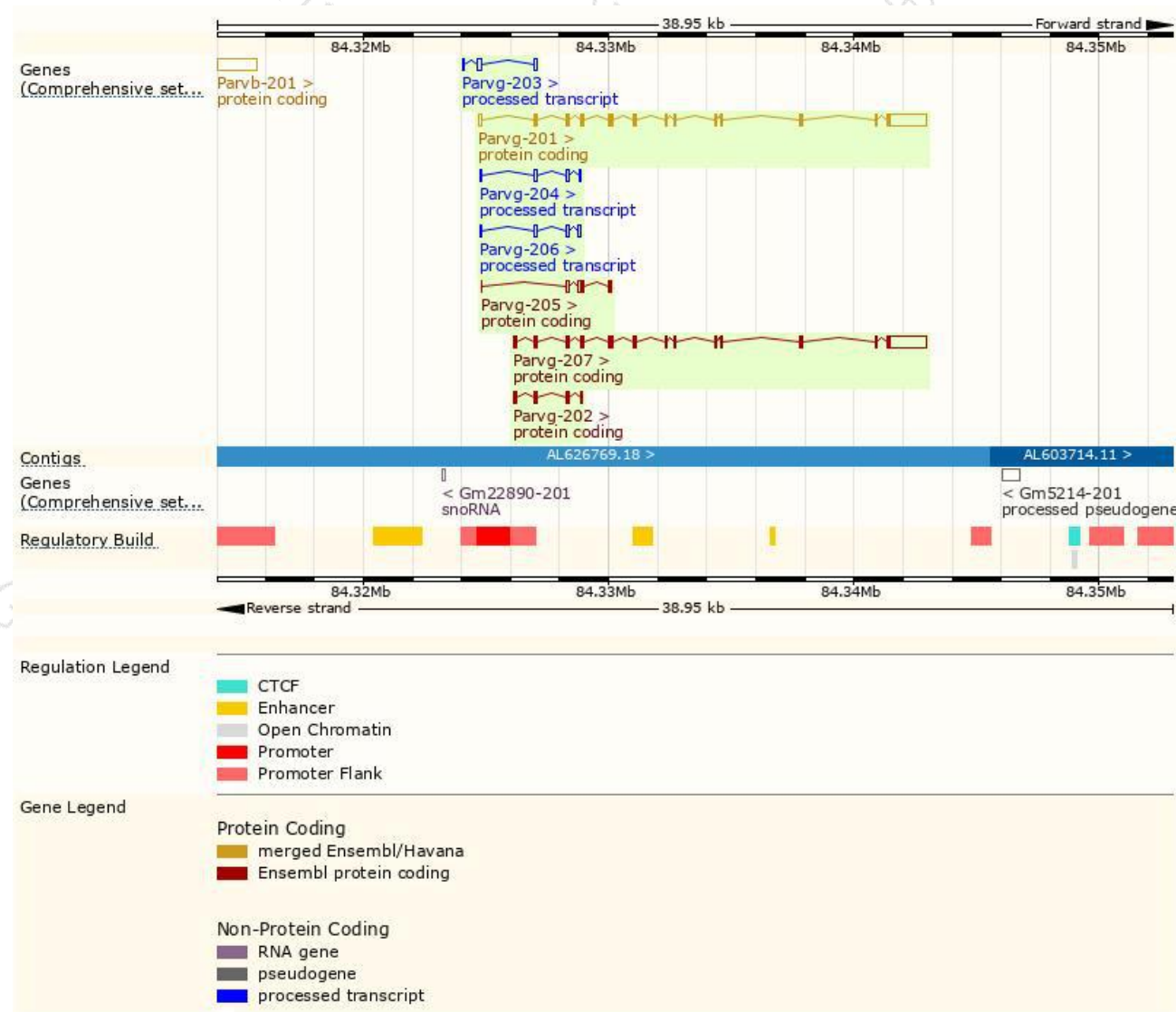
The gene has 7 transcripts,all transcripts are shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Parvg-207	ENSMUST00000163667.1	2700	384aa	Protein coding	CCDS49686	E9PYG5	TSL:5 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 ALT2
Parvg-201	ENSMUST00000023074.8	2619	331aa	Protein coding	CCDS27710	Q9ERD8	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 P3
Parvg-202	ENSMUST00000125928.7	381	122aa	Protein coding	-	A6PW97	CDS 3' incomplete TSL:2
Parvg-205	ENSMUST00000145809.1	380	56aa	Protein coding	-	A0A2I3BS32	CDS 3' incomplete TSL:3
Parvg-204	ENSMUST00000139235.7	363	No protein	Processed transcript	-	-	TSL:3
Parvg-203	ENSMUST00000127551.1	351	No protein	Processed transcript	-	-	TSL:3
Parvg-206	ENSMUST00000151072.7	346	No protein	Processed transcript	-	-	TSL:3

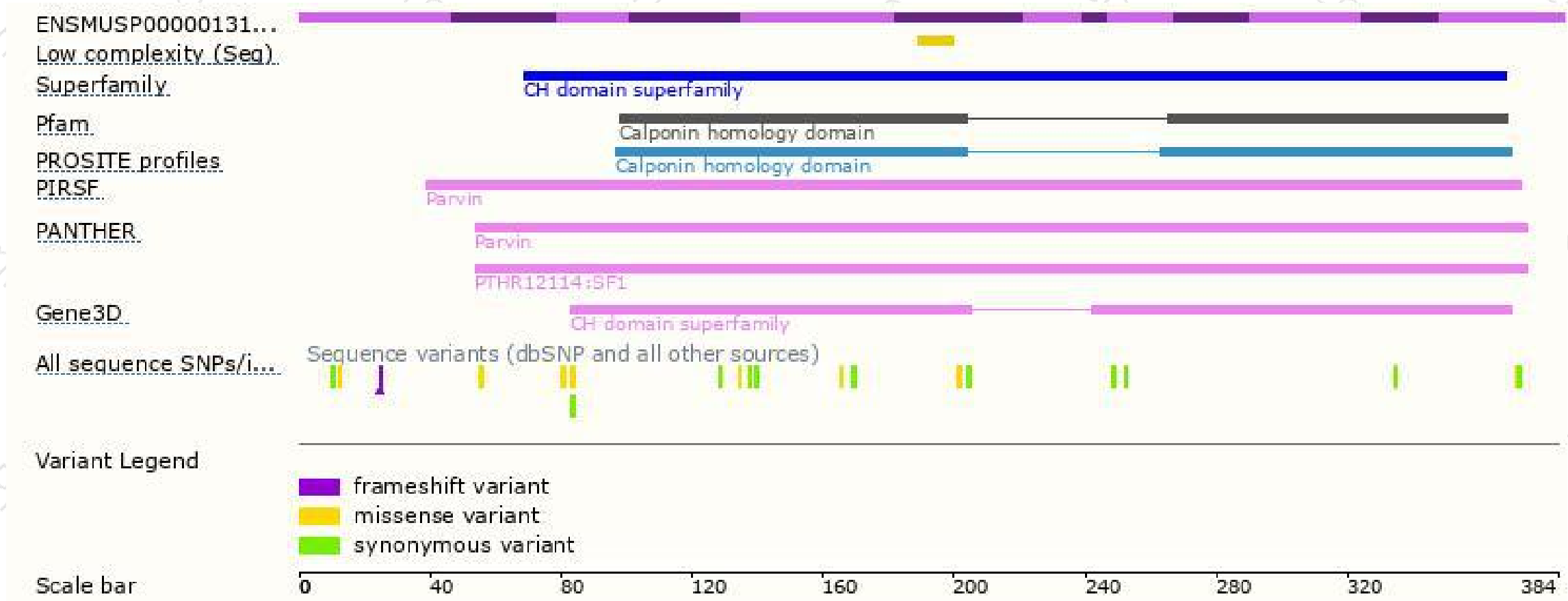
The strategy is based on the design of *Parvg-207* transcript,the transcription is shown below:



Genomic location distribution



Protein domain



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

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