

***Flvcr2* Cas9-CKO Strategy**

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Project Overview

Project Name

Flvcr2

Project type

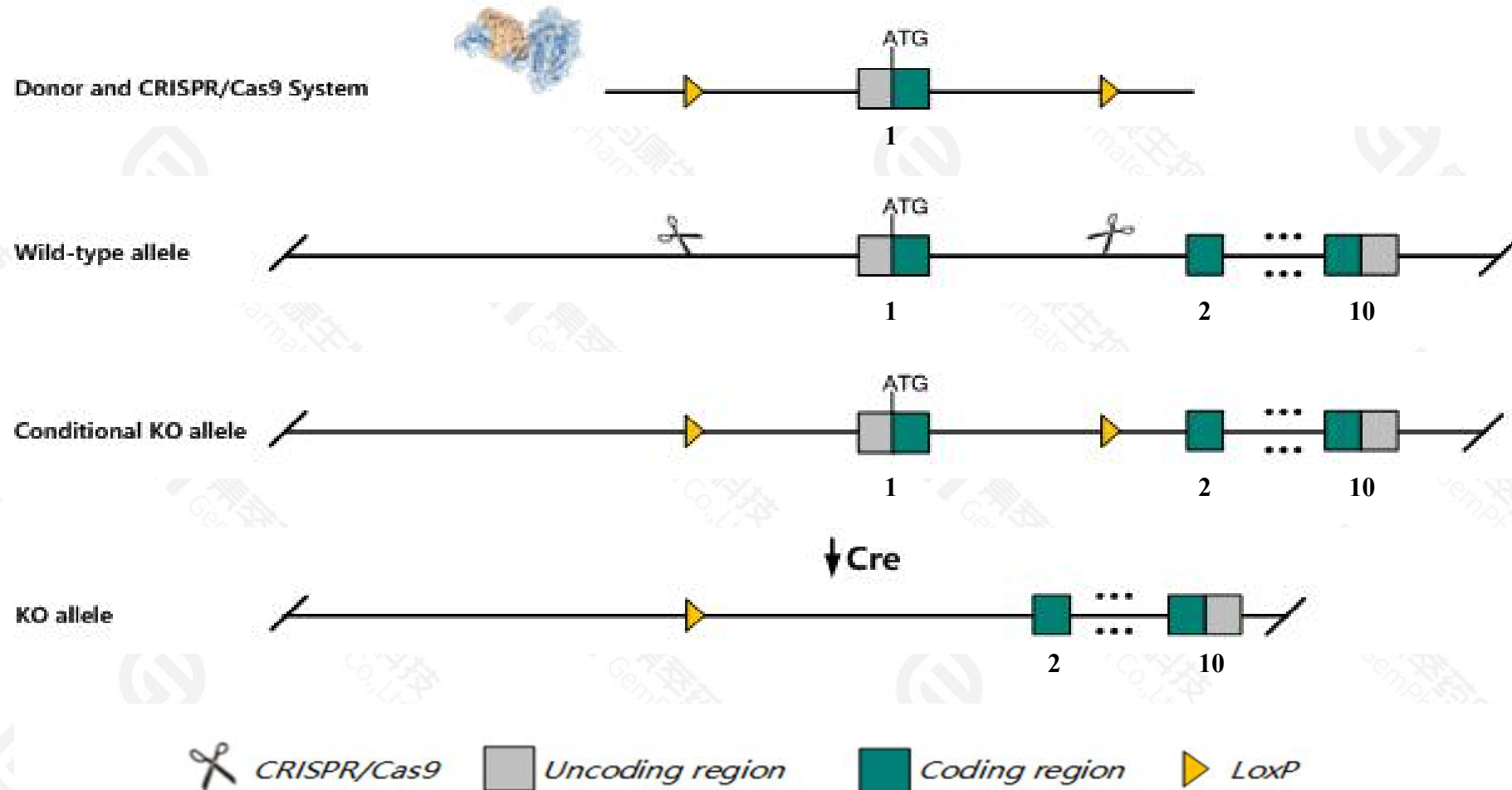
Cas9-CKO

Strain background

C57BL/6JGpt

Conditional Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *Flvcr2* gene. The schematic diagram is as follows:



Technical routes

- The *Flvcr2* gene has 2 transcripts. According to the structure of *Flvcr2* gene, exon1 of *Flvcr2*-201(ENSMUST00000040461.4) transcript is recommended as the knockout region. The region contains start codon ATG. Knock out the region will result in disruption of protein function.
- In this project we use CRISPR/Cas9 technology to modify *Flvcr2* 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.

- The *Flvcr2* gene is located on the Chr12. 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)

Flvcr2 feline leukemia virus subgroup C cellular receptor 2 [Mus musculus (house mouse)]

Gene ID: 217721, updated on 2-Mar-2021

Summary



Official Symbol Flvcr2 provided by [MGI](#)

Official Full Name feline leukemia virus subgroup C cellular receptor 2 provided by [MGI](#)

Primary source [MGI:MGI:2384974](#)

See related [Ensembl:ENSMUSG00000034258](#)

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 CCT, Mfsd7, Mfsd7c

Expression Broad expression in testis adult (RPKM 19.4), placenta adult (RPKM 12.9) and 17 other tissues [See more](#)

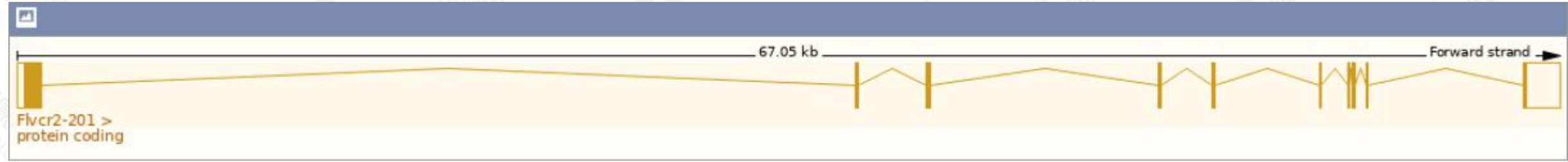
Orthologs [human](#) [all](#)

Transcript information (Ensembl)

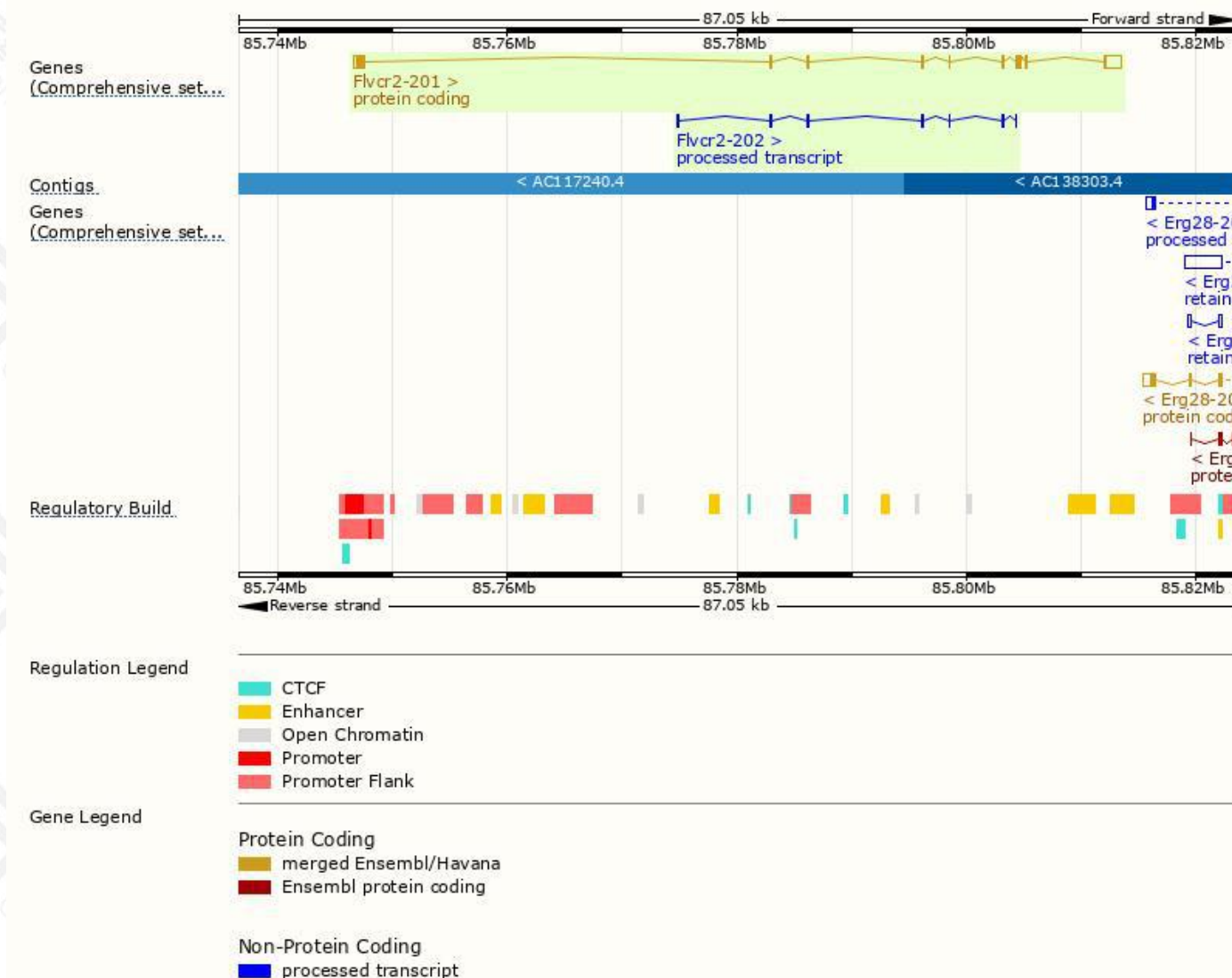
The gene has 2 transcripts,all transcripts are shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Flvcr2-201	ENSMUST00000040461.4	3435	551aa	Protein coding	CCDS26062		TSL:1 , GENCODE basic , APPRIS P1 ,
Flvcr2-202	ENSMUST00000221585.2	642	No protein	Processed transcript	-		TSL:5 ,

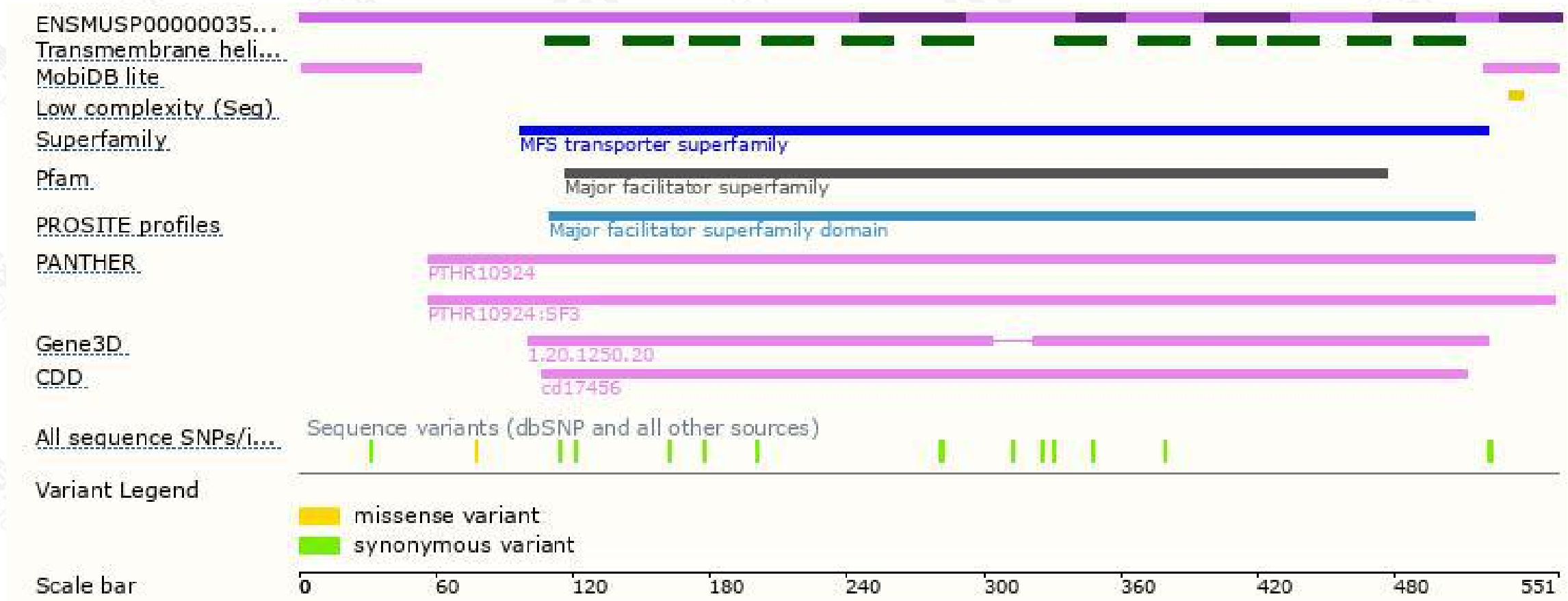
The strategy is based on the design of *Flvcr2-201* transcript,the transcription is shown below:



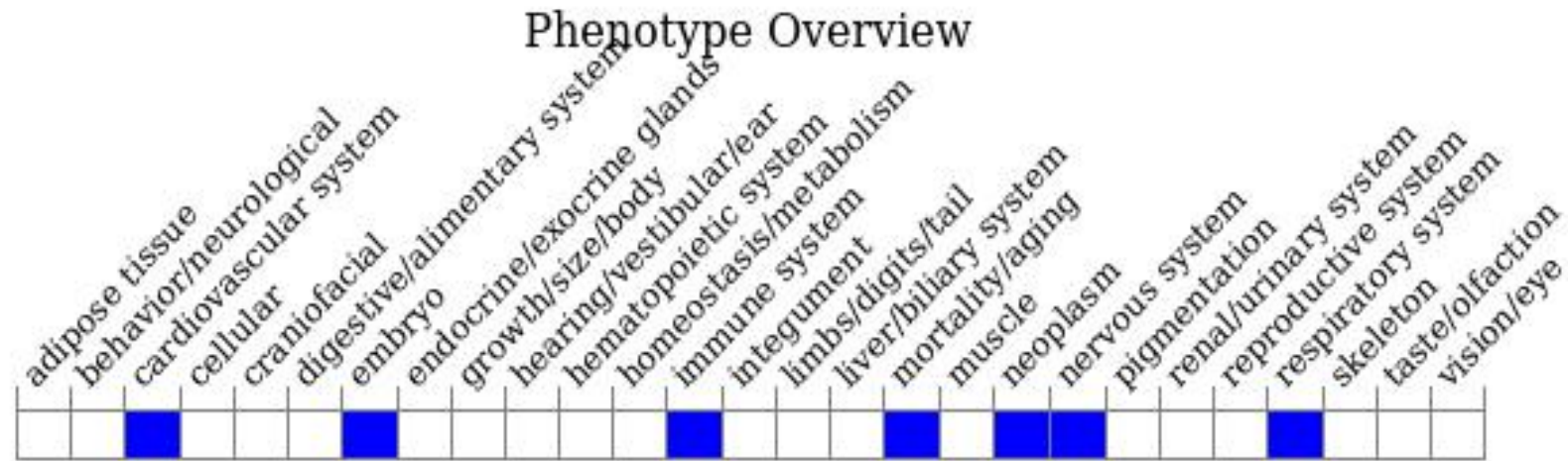
Genomic location distribution



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/>).

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