Flvcr1 Cas9-CKO Strategy

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Project Overview

Project Name	***Flvcr1***
Project type	**Cas9-CKO**
Strain background	**C57BL/6JGpt**

Conditional Knockout strategy

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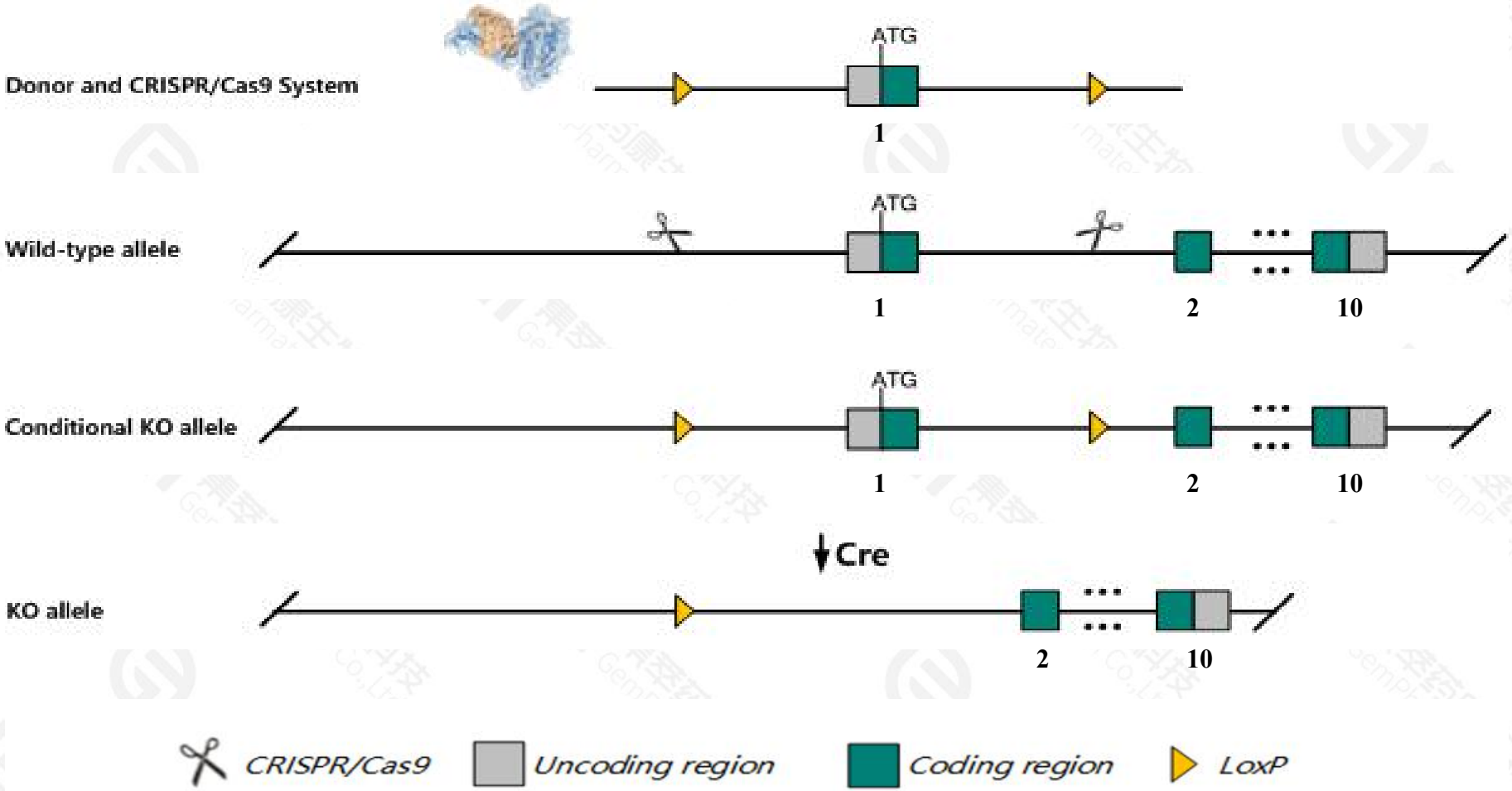
This model will use CRISPR/Cas9 technology to edit the *Flvcr1* gene. The schematic diagram is as follows:



Technical routes

➢ The *Flvcr1* gene has 6 transcripts. According to the structure of *Flvcr1* gene, exon1 of *Flvcr1-201*(ENSMUST00000085635.6) 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 *Flvcr1* 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 runting, cardiomegaly and splenomegaly, lack definitive erythropoiesis, develop severe hyperchromic macrocytic anemia and reticulocytopenia, and show craniofacial and limb defects and intrauterine lethality modulated by genetic background.

➢ The flox region contains functional region of the *A230020J21Rik* gene.Knockout the region may affect the function of *A230020J21Rik* gene.

➢ The *Flvcr1* gene is located on the Chr1. 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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Flvcr1 feline leukemia virus subgroup C cellular receptor 1 [Mus musculus (house mouse)]

Gene ID: 226844, updated on 17-Nov-2020

Summary

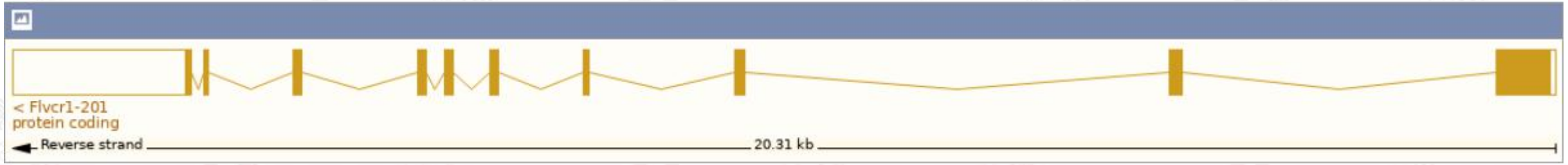
Official Symbol	Flvcr1 provided by MGI
Official Full Name	feline leukemia virus subgroup C cellular receptor 1 provided byMGI
Primary source	MGI:MGI:2444881
See related	Ensembl:ENSMUSG00000066595
Gene type	protein coding
RefSeq status	VALIDATED
Organism	Mus musculus
Lineage	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Myomorpha; Muroidea; Muridae; Murinae; Mus; Mus
Also known as	9630055N22Rik, FLVCR, Mfsd7, Mfsd7b
Expression	Ubiquitous expression in small intestine adult (RPKM 10.5), thymus adult (RPKM 9.2) and 28 other tissuesSee more
Orthologs	human all

Transcript information（Ensembl）

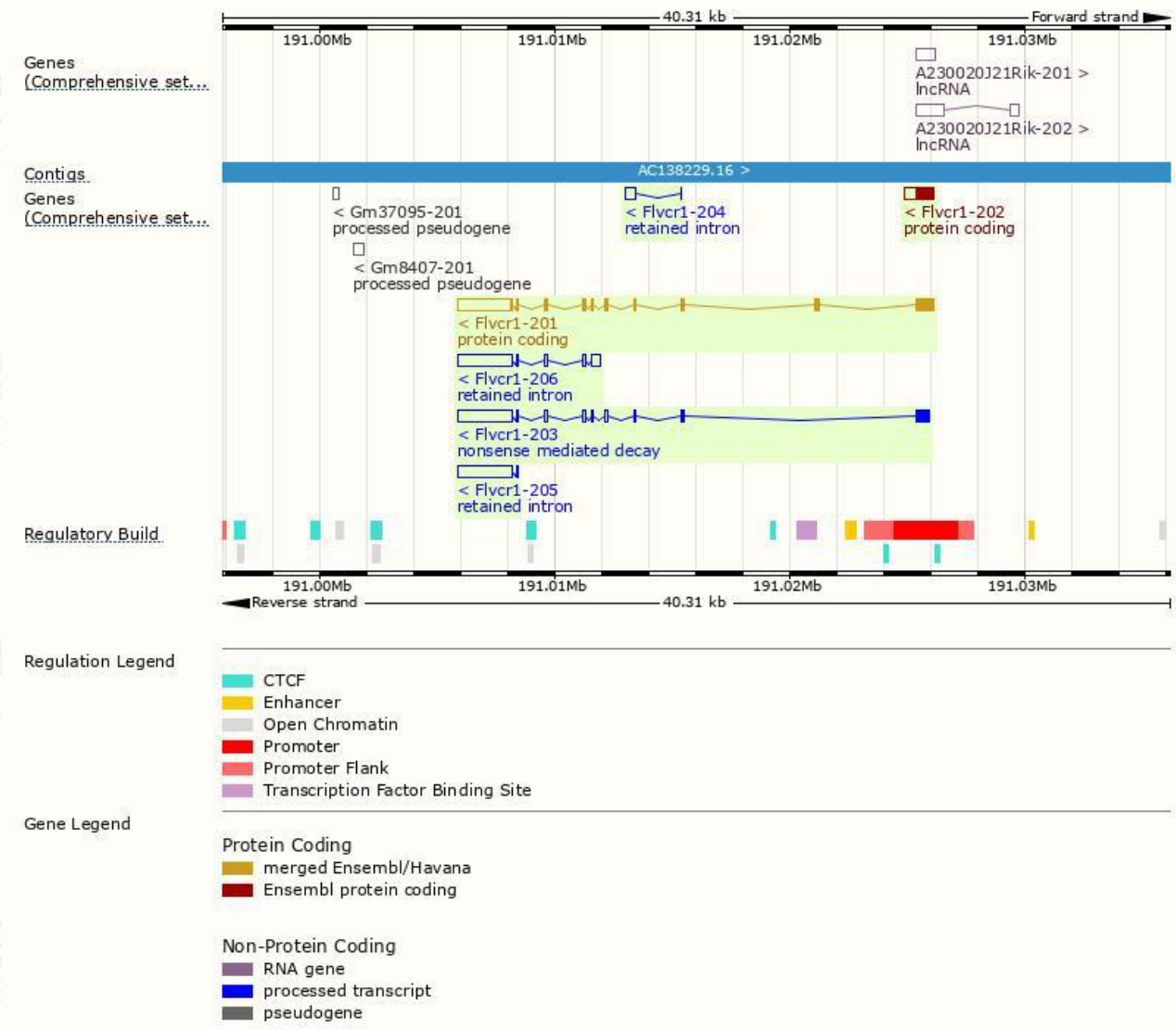
The gene has 6 transcripts,all transcripts are shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Flvcr1-201	ENSMUST00000085635.6	4040	560aa	Protein coding	CCDS35823		TSL:1 , GENCODE basic , APPRIS P1 ,
Flvcr1-202	ENSMUST00000191946.2	1216	246aa	Protein coding	CCDS83664		TSL:NA , GENCODE basic ,
Flvcr1-203	ENSMUST00000192666.2	3666	246aa	Nonsense mediated decay	-		CDS 5' incomplete , TSL:1 ,
Flvcr1-206	ENSMUST00000194917.6	3029	No protein	Retained intron	-		TSL:2 ,
Flvcr1-205	ENSMUST00000194589.2	2449	No protein	Retained intron	-		TSL:1 ,
Flvcr1-204	ENSMUST00000193399.2	490	No protein	Retained intron	-		TSL:3 ,

The strategy is based on the design of *Flvcr1-201* transcript,the transcription is shown below:

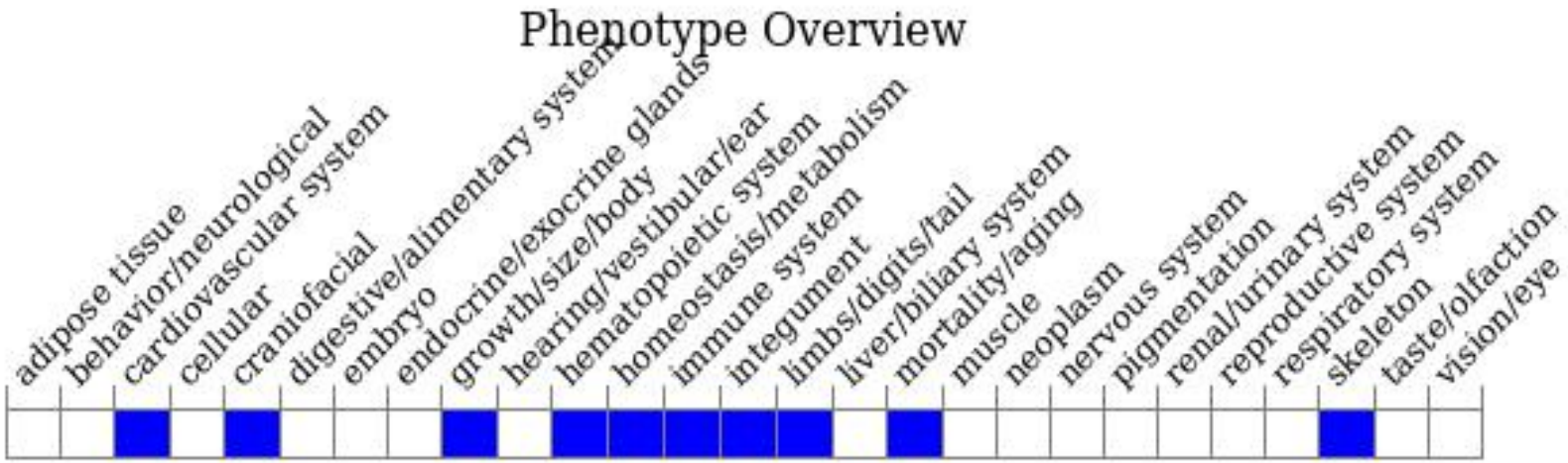


Genomic location distribution



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/).

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