

Flrt3 Cas9-KO Strategy

Designer: JiaYu

Reviewer: Xiaojing Li

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Project Overview

Project Name

Flrt3

Project type

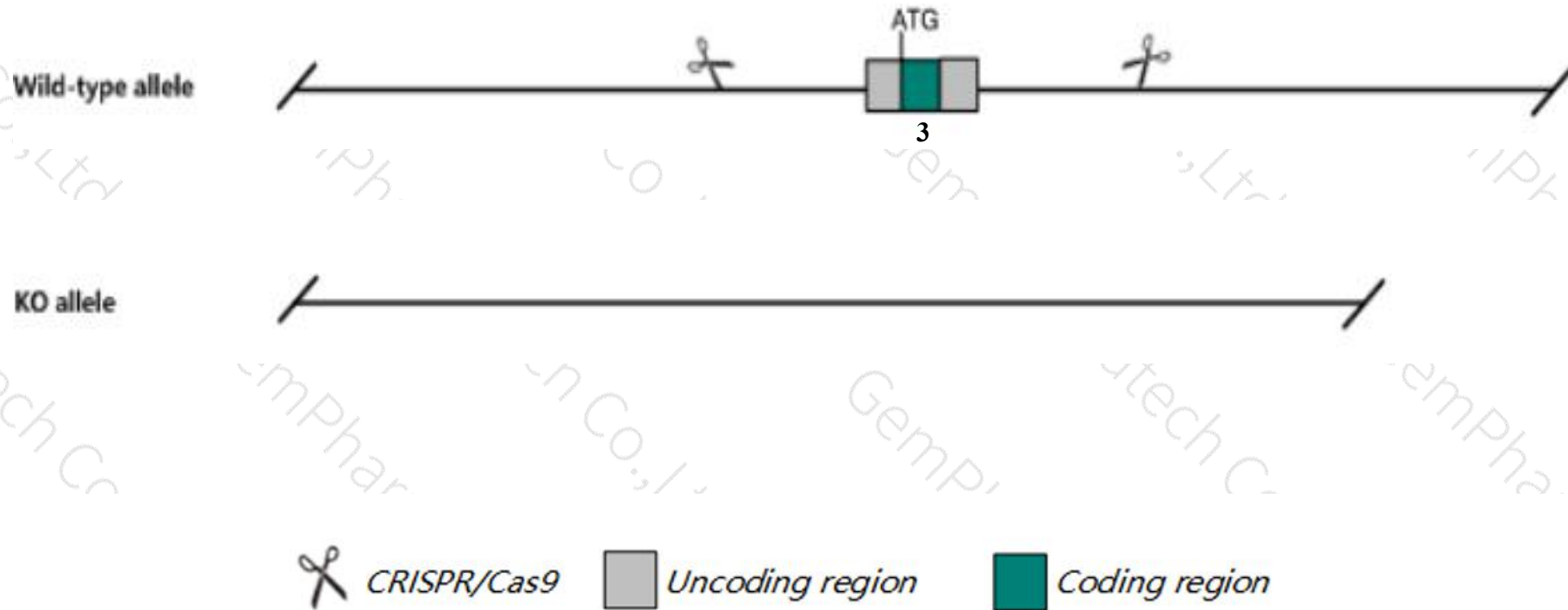
Cas9-KO

Strain background

C57BL/6JGpt

Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *Flrt3* gene. The schematic diagram is as follows:



Technical routes

- The *Flrt3* gene has 3 transcripts. According to the structure of *Flrt3* gene, exon3 of *Flrt3*-202(ENSMUST00000110057.2) transcript is recommended as the knockout region. The region contains all of the coding sequence. Knock out the region will result in disruption of protein function.
- In this project we use CRISPR/Cas9 technology to modify *Flrt3* gene. The brief process is as follows: CRISPR/Cas9 system 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.

- According to the existing MGI data, mice homozygous for a null allele exhibit embryonic lethality during organogenesis, abnormal embryonic tissue development, disrupted head formation, cardia bifida and abnormal ventral wall closure.
- The KO region contains functional region of the *Flrt3* gene. Knockout the region may affect the function of *Macrod2* gene.
- The *Flrt3* 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 the gene knockout on gene transcription, RNA splicing and protein translation cannot be predicted at the existing technology level.

Gene information (NCBI)

Flrt3 fibronectin leucine rich transmembrane protein 3 [Mus musculus (house mouse)]

Gene ID: 71436, updated on 13-Mar-2020

Summary



Official Symbol [Flrt3](#) provided by [MGI](#)

Official Full Name [fibronectin leucine rich transmembrane protein 3](#) provided by [MGI](#)

Primary source [MGI:MGI:1918686](#)

See related [Ensembl:ENSMUSG00000051379](#)

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 [5530600M07Rik](#), [C430047I10Rik](#), [mKIAA1469](#)

Expression Broad expression in CNS E11.5 (RPKM 7.2), bladder adult (RPKM 5.0) and 16 other tissues [See more](#)

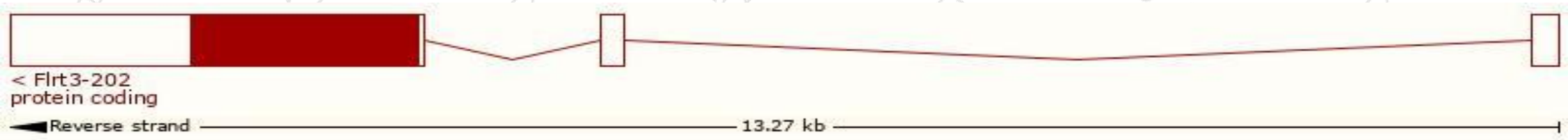
Orthologs [human](#) [all](#)

Transcript information (Ensembl)

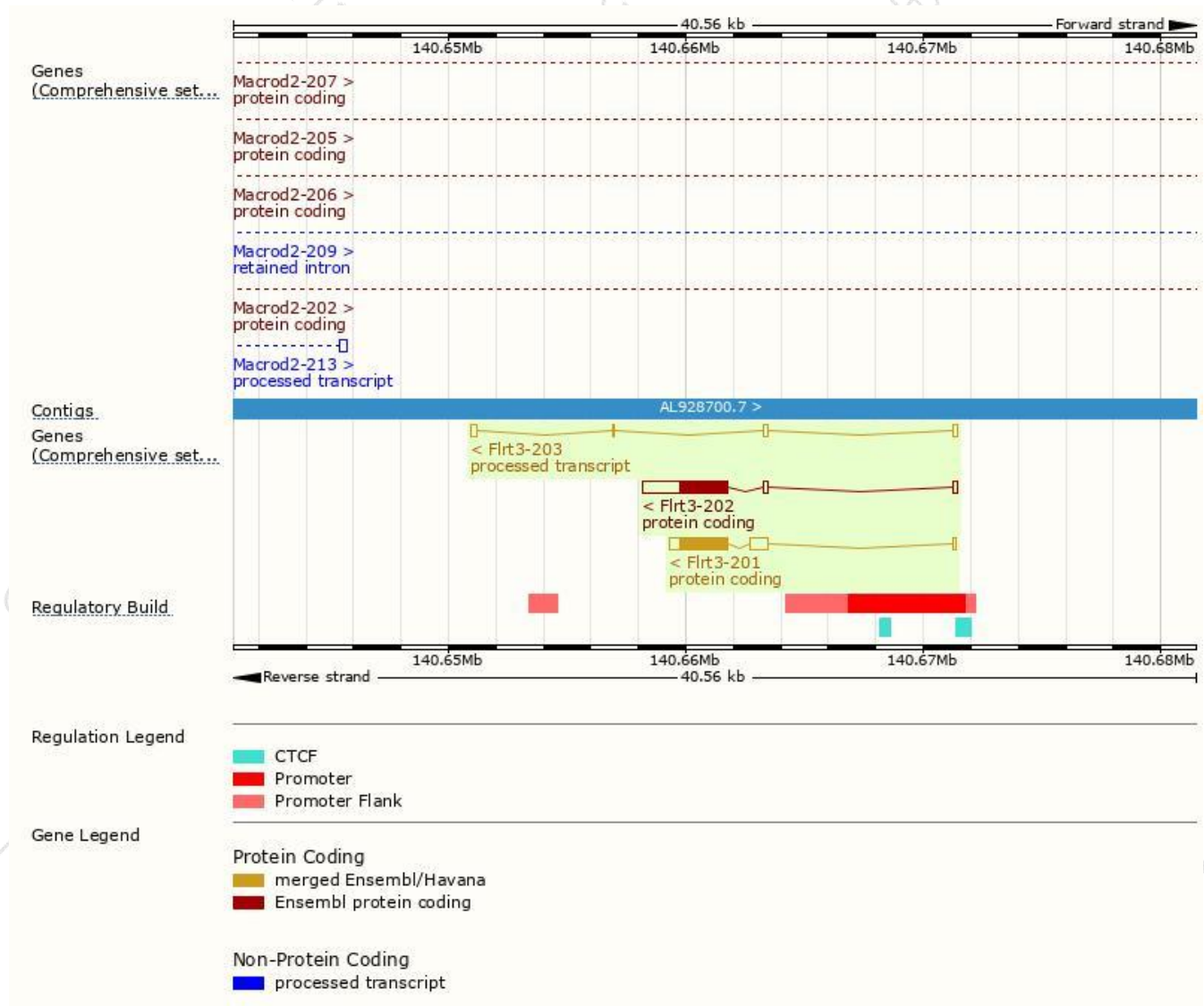
The gene has 3 transcripts,all transcripts are shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Flrt3-202	ENSMUST00000110057.2	3977	649aa	Protein coding	CCDS16806	Q8BGT1	TSL:1 GENCODE basic APPRIS P1
Flrt3-201	ENSMUST00000056760.3	3334	649aa	Protein coding	CCDS16806	Q8BGT1	TSL:1 GENCODE basic APPRIS P1
Flrt3-203	ENSMUST00000172544.7	739	No protein	Processed transcript	-	-	TSL:1

The strategy is based on the design of *Flrt3-202* transcript,the transcription is shown below:



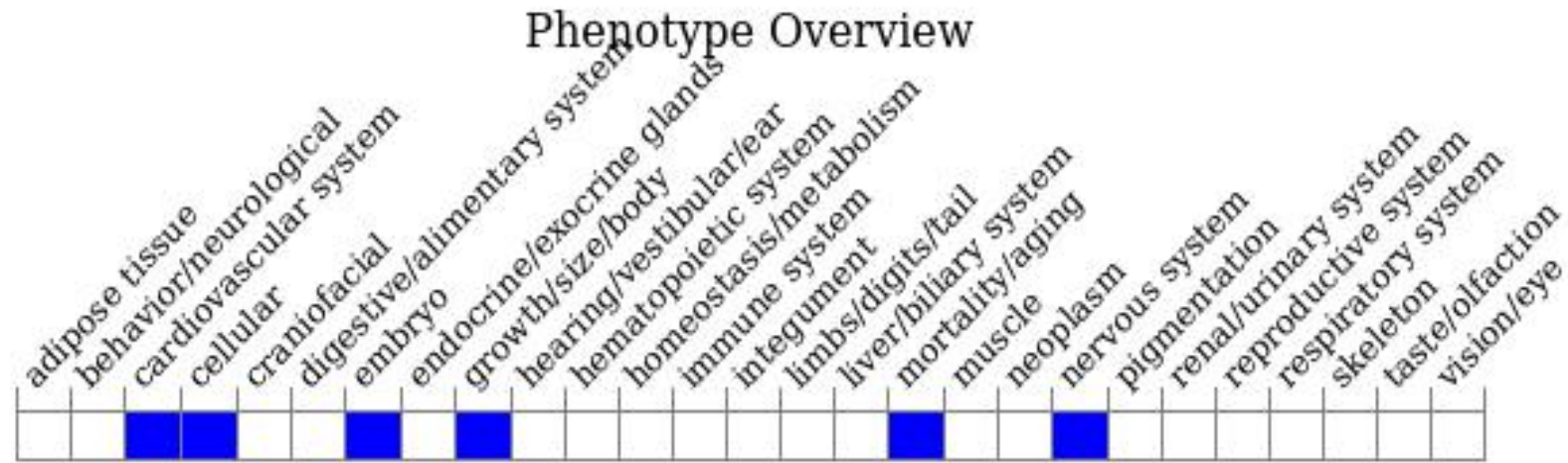
Genomic location distribution



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/>).

According to the existing MGI data, mice homozygous for a null allele exhibit embryonic lethality during organogenesis, abnormal embryonic tissue development, disrupted head formation, cardia bifida and abnormal ventral wall closure.

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

Tel: 400-9660890

