

Foxk2 Cas9-CKO Strategy

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Project Overview

Project Name

Foxk2

Project type

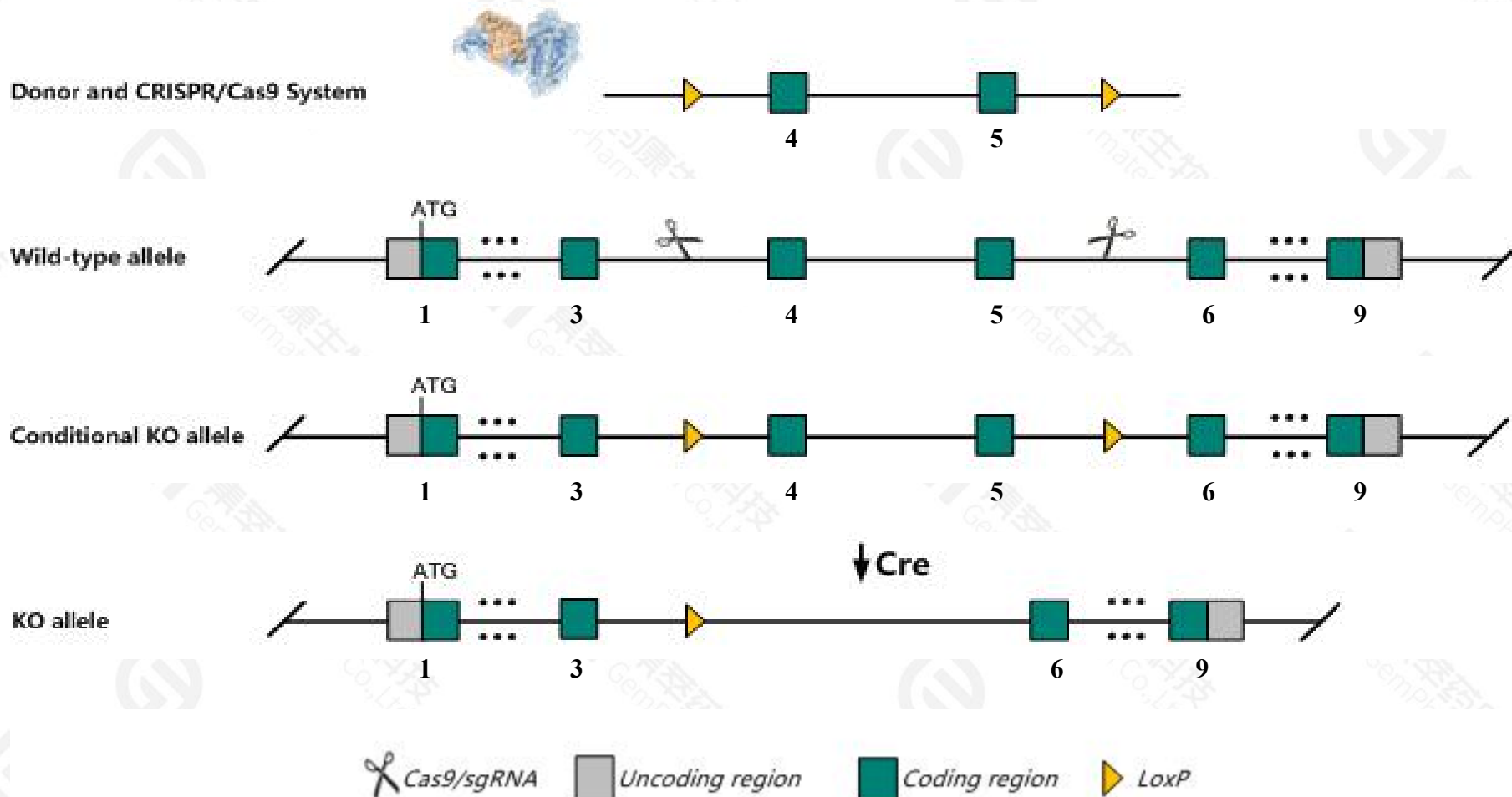
Cas9-CKO

Strain background

C57BL/6JGpt

Conditional Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *Foxk2* gene. The schematic diagram is as follows:



Technical routes

- The *Foxk2* gene has 3 transcripts. According to the structure of *Foxk2* gene, exon4-exon5 of *Foxk2*-201(ENSMUST00000106113.2) transcript is recommended as the knockout region. The region contains 341bp coding sequence. Knock out the region will result in disruption of protein function.
- In this project we use CRISPR/Cas9 technology to modify *Foxk2* gene. The brief process is as follows: sgRNA was transcribed in vitro, donor was constructed. Cas9, sgRNA 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 was 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 *Foxk2* gene is located on the Chr11. 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)

Foxk2 forkhead box K2 [Mus musculus (house mouse)]

Gene ID: 68837, updated on 13-Dec-2020

Summary



Official Symbol Foxk2 provided by [MGI](#)

Official Full Name forkhead box K2 provided by [MGI](#)

Primary source [MGI:MGI:1916087](#)

See related [Ensembl:ENSMUSG00000039275](#)

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 1110054H05Rik, 5730434B08Rik, 6230415M23Rik, ILF, Il, Ilf1

Expression Ubiquitous expression in whole brain E14.5 (RPKM 17.4), ovary adult (RPKM 17.3) and 28 other tissues [See more](#)

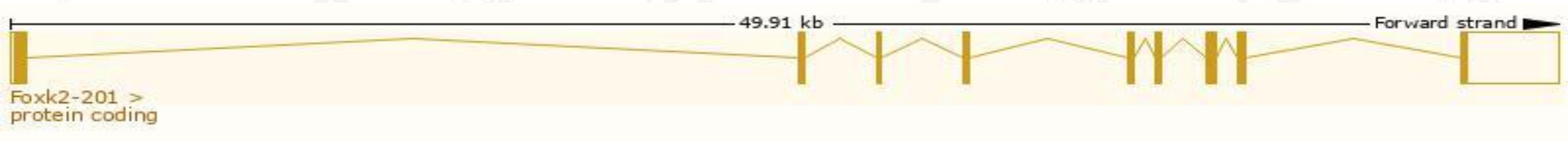
Orthologs [human](#) [all](#)

Transcript information (Ensembl)

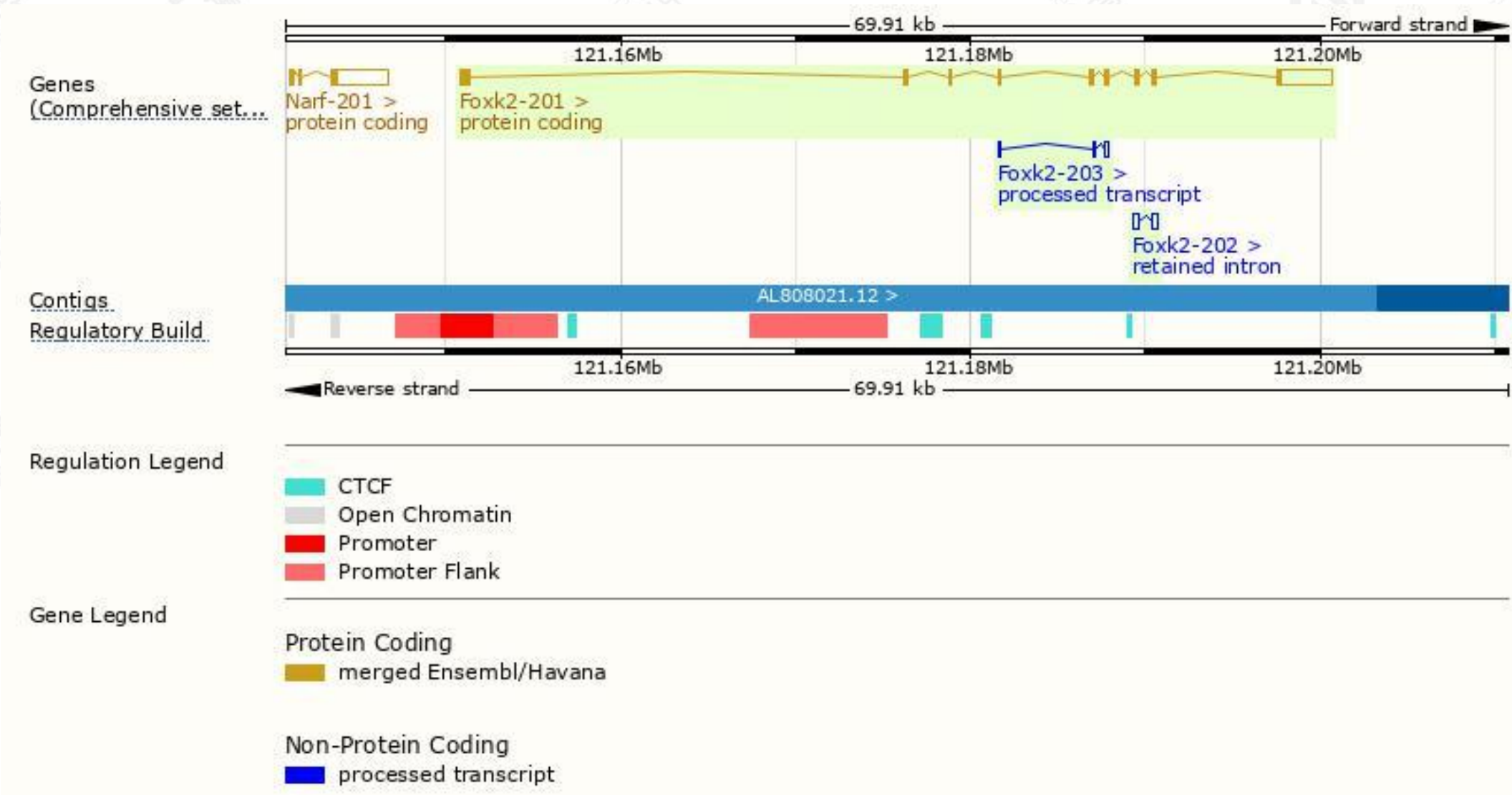
The gene has 3 transcripts,all transcripts are shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Foxk2-201	ENSMUST00000106113.2	5029	651aa	Protein coding	CCDS36393		TSL:1 , GENCODE basic , APPRIS P1 ,
Foxk2-203	ENSMUST00000153579.2	452	No protein	Processed transcript	-		TSL:5 ,
Foxk2-202	ENSMUST00000151492.2	607	No protein	Retained intron	-		TSL:2 ,

The strategy is based on the design of *Foxk2-201* transcript,the transcription is shown below:



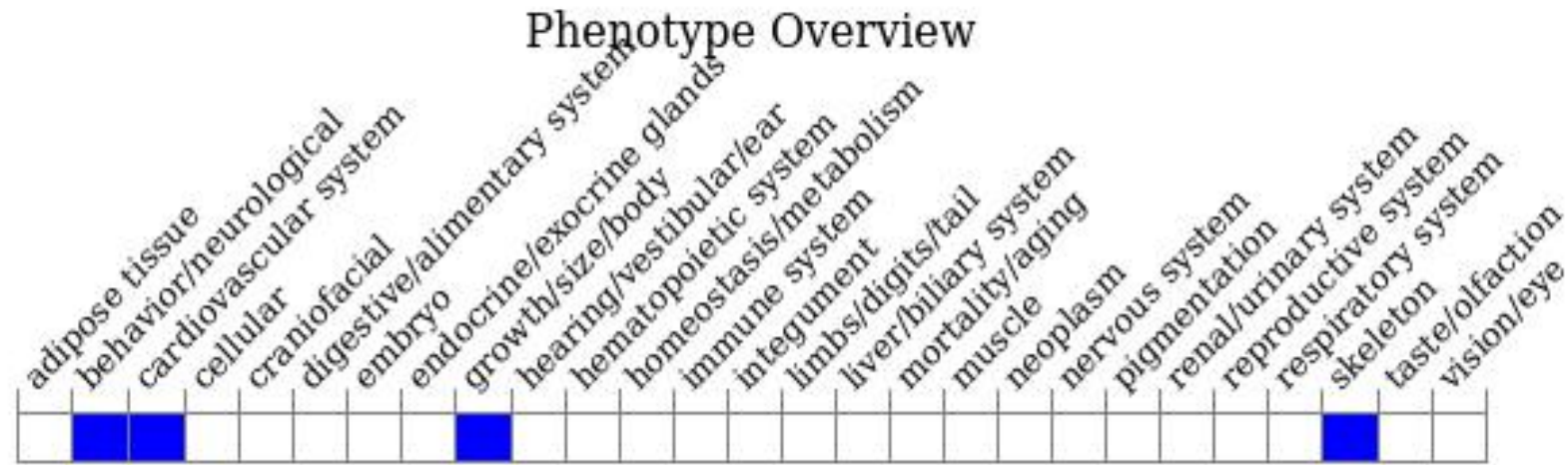
Genomic location distribution



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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