

Egfr4 Cas9-KO Strategy

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Project Overview



Project Name

Fgfr4

Project type

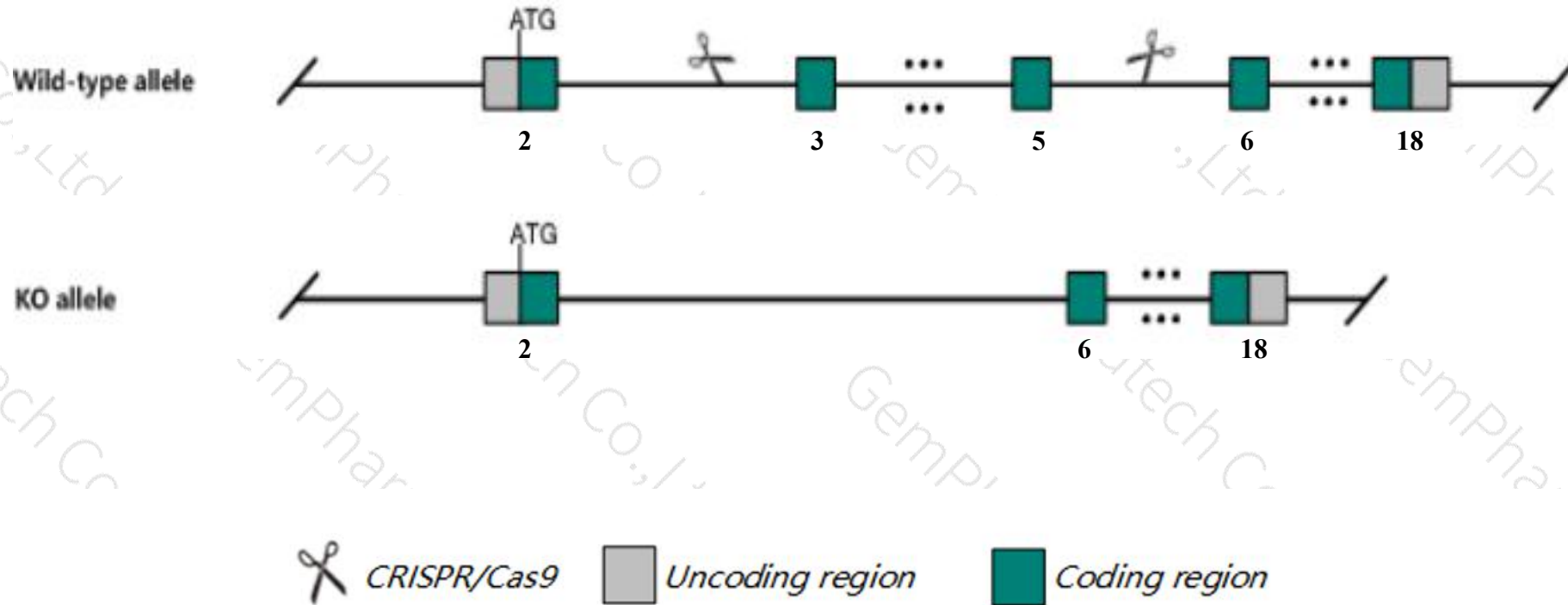
Cas9-KO

Strain background

C57BL/6JGpt

Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *Fgfr4* gene. The schematic diagram is as follows:



- The *Fgfr4* gene has 3 transcripts. According to the structure of *Fgfr4* gene, exon3-exon5 of *Fgfr4-201*(ENSMUST00000005452.5) transcript is recommended as the knockout region. The region contains 512bp coding sequence. Knock out the region will result in disruption of protein function.
- In this project we use CRISPR/Cas9 technology to modify *Fgfr4* 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, homozygotes for a targeted mutation are viable, healthy and overtly normal, except for a 10% weight reduction at weaning. Mice doubly homozygous for disruptions of *Fgfr3* and *Fgfr4* show novel phenotypes not seen in either single mutant, including dwarfism and defective respiratory alveogenesis.
- The *Fgfr4* gene is located on the Chr13. 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)

Fgfr4 fibroblast growth factor receptor 4 [Mus musculus (house mouse)]

Gene ID: 14186, updated on 13-Mar-2020

Summary



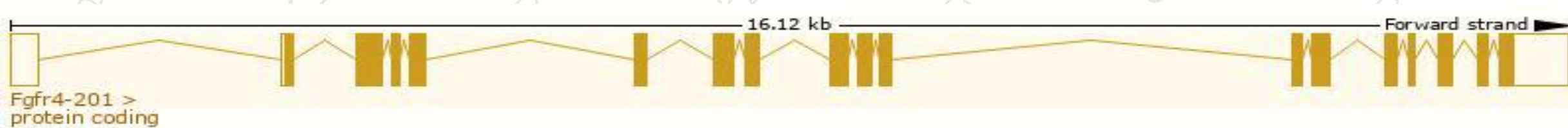
Official Symbol	Fgfr4 provided by MGI
Official Full Name	fibroblast growth factor receptor 4 provided by MGI
Primary source	MGI:MGI:95525
See related	Ensembl:ENSMUSG000000005320
Gene type	protein coding
RefSeq status	VALIDATED
Organism	Mus musculus
Lineage	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Myomorpha; Muroidea; Muridae; Murinae; Mus; Mus
Also known as	Fgfr-4
Expression	Biased expression in adrenal adult (RPKM 26.0), lung adult (RPKM 20.3) and 14 other tissues See more
Orthologs	human all

Transcript information (Ensembl)

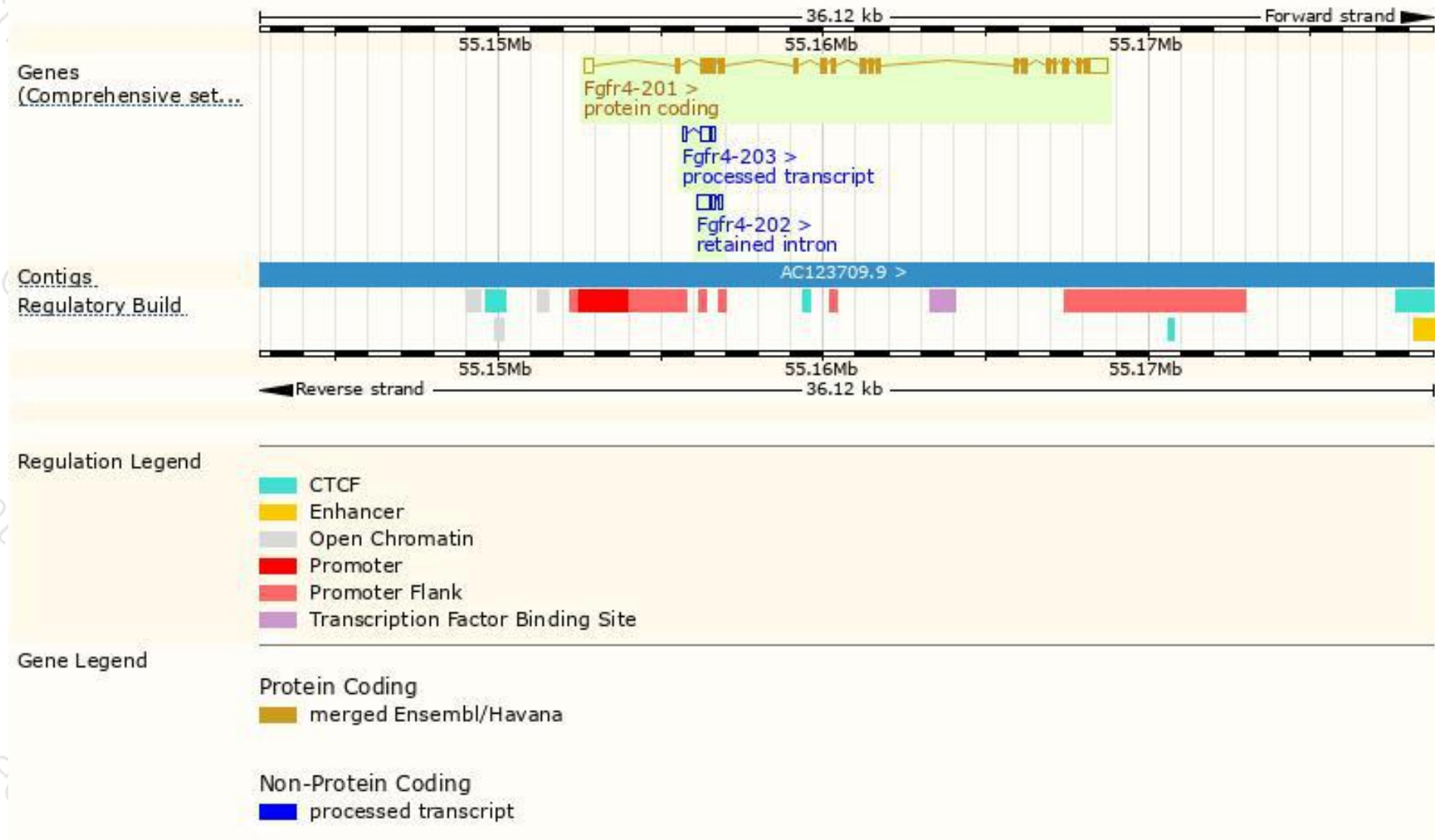
The gene has 3 transcripts, all transcripts are shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Fgfr4-201	ENSMUST0000005452.5	3324	799aa	Protein coding	CCDS26540	A0A0R4IZY3	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 P1
Fgfr4-203	ENSMUST00000162967.1	438	No protein	Processed transcript	-	-	TSL:3
Fgfr4-202	ENSMUST00000162167.1	590	No protein	Retained intron	-	-	TSL:3

The strategy is based on the design of *Fgfr4-201* transcript, the transcription is shown below:



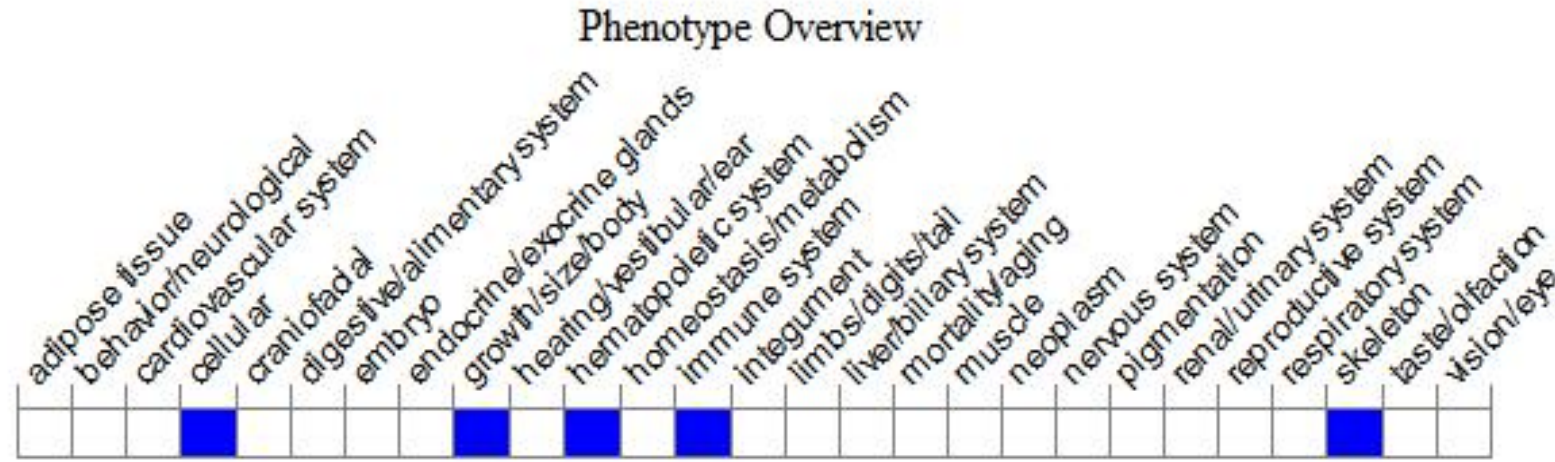
Genomic location distribution



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/>).

According to the existing MGI data, homozygotes for a targeted mutation are viable, healthy and overtly normal, except for a 10% weight reduction at weaning. Mice doubly homozygous for disruptions of Fgfr3 and Fgfr4 show novel phenotypes not seen in either single mutant, including dwarfism and defective respiratory alveogenesis.

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

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