

Fgfr3 Cas9-CKO Strategy

Designer: Jinling Wang

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Project Overview

Project Name

Fgfr3

Project type

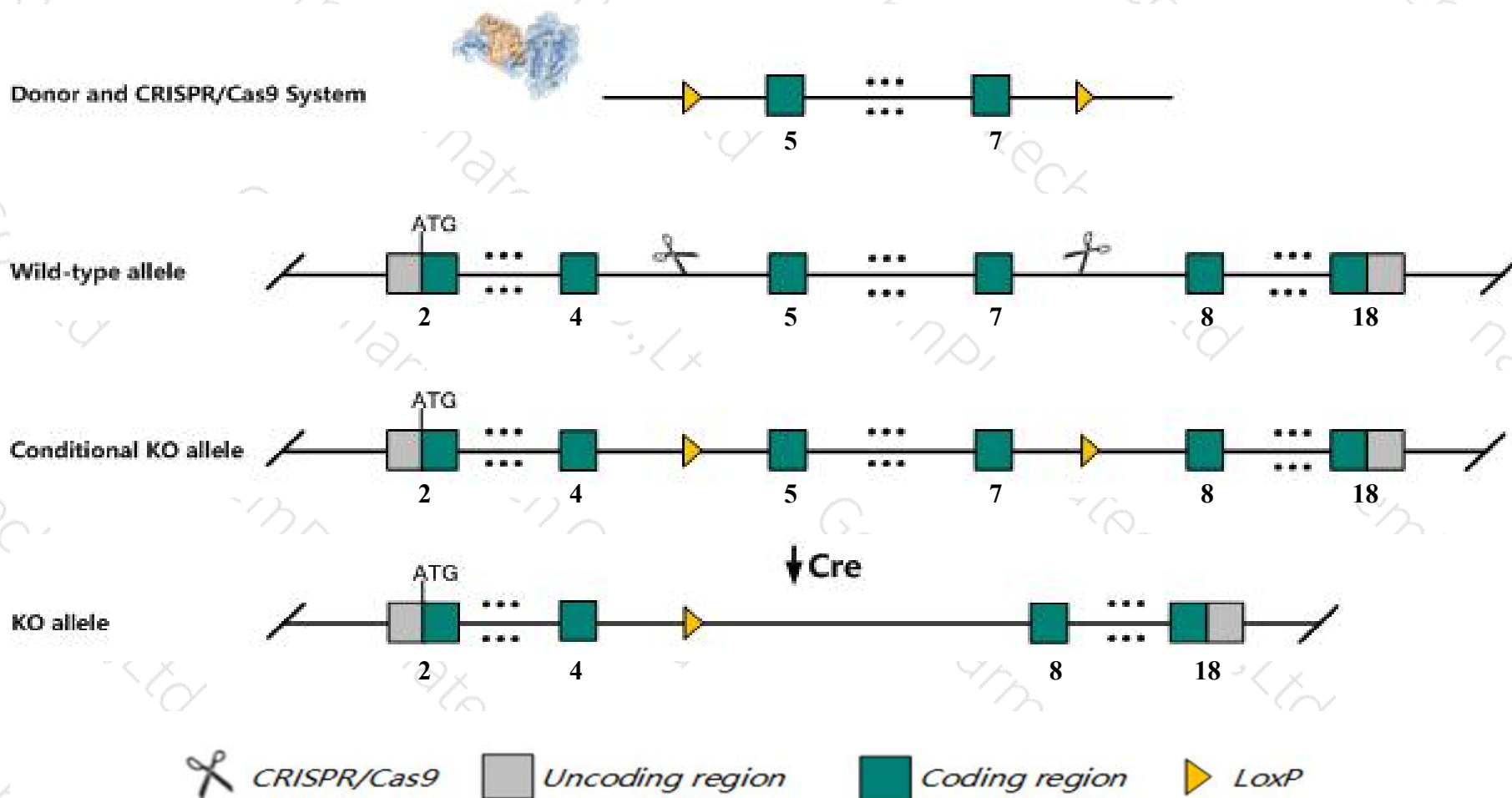
Cas9-CKO

Strain background

C57BL/6JGpt

Conditional Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *Fgfr3* gene. The schematic diagram is as follows:



- The *Fgfr3* gene has 17 transcripts. According to the structure of *Fgfr3* gene, exon5-exon7 of *Fgfr3-210* (ENSMUST00000169212.8) transcript is recommended as the knockout region. The region contains 485bp coding sequence. Knock out the region will result in disruption of protein function.
- In this project we use CRISPR/Cas9 technology to modify *Fgfr3* 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.

- According to the existing MGI data, Mutant alleles generally cause skeletal deformities, with some causing decreased body size, premature death, or hearing loss due to developmental defects of the ear.
- The *Fgfr3* gene is located on the Chr5. 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)

Fgfr3 fibroblast growth factor receptor 3 [Mus musculus (house mouse)]

Gene ID: 14184, updated on 25-Mar-2019

Summary

Official Symbol	Fgfr3 provided by MGI
Official Full Name	fibroblast growth factor receptor 3 provided by MGI
Primary source	MGI:MGI:95524
See related	Ensembl:ENSMUSG00000054252
Gene type	protein coding
RefSeq status	REVIEWED
Organism	Mus musculus
Lineage	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Myomorpha; Muroidea; Muridae; Murinae; Mus; Mus
Also known as	CD333, FR3, Fgfr-3, Fig-2, HBGFR, Mfr3, sam3
Summary	This gene encodes a member of the fibroblast growth factor receptor family. Members of this family are highly conserved proteins that differ from one another in their ligand affinities and tissue distribution. A representative protein consists of an extracellular region composed of three immunoglobulin-like domains, a single hydrophobic membrane-spanning segment, and a cytoplasmic tyrosine kinase domain. The extracellular portion of the protein interacts with fibroblast growth factors, setting in motion a cascade of downstream signals, ultimately influencing mitogenesis and differentiation. This family member binds acidic and basic fibroblast growth hormone and plays a role in bone development and maintenance. Mutations in this gene may be associated with craniosynostosis and multiple types of skeletal dysplasia. A pseudogene of this gene is located on chromosome 1. Alternatively spliced transcript variants encoding multiple isoforms have been observed for this gene. [provided by RefSeq, Apr 2011]
Expression	Broad expression in lung adult (RPKM 46.0), limb E14.5 (RPKM 23.9) and 21 other tissues See more
Orthologs	human all

Transcript information (Ensembl)

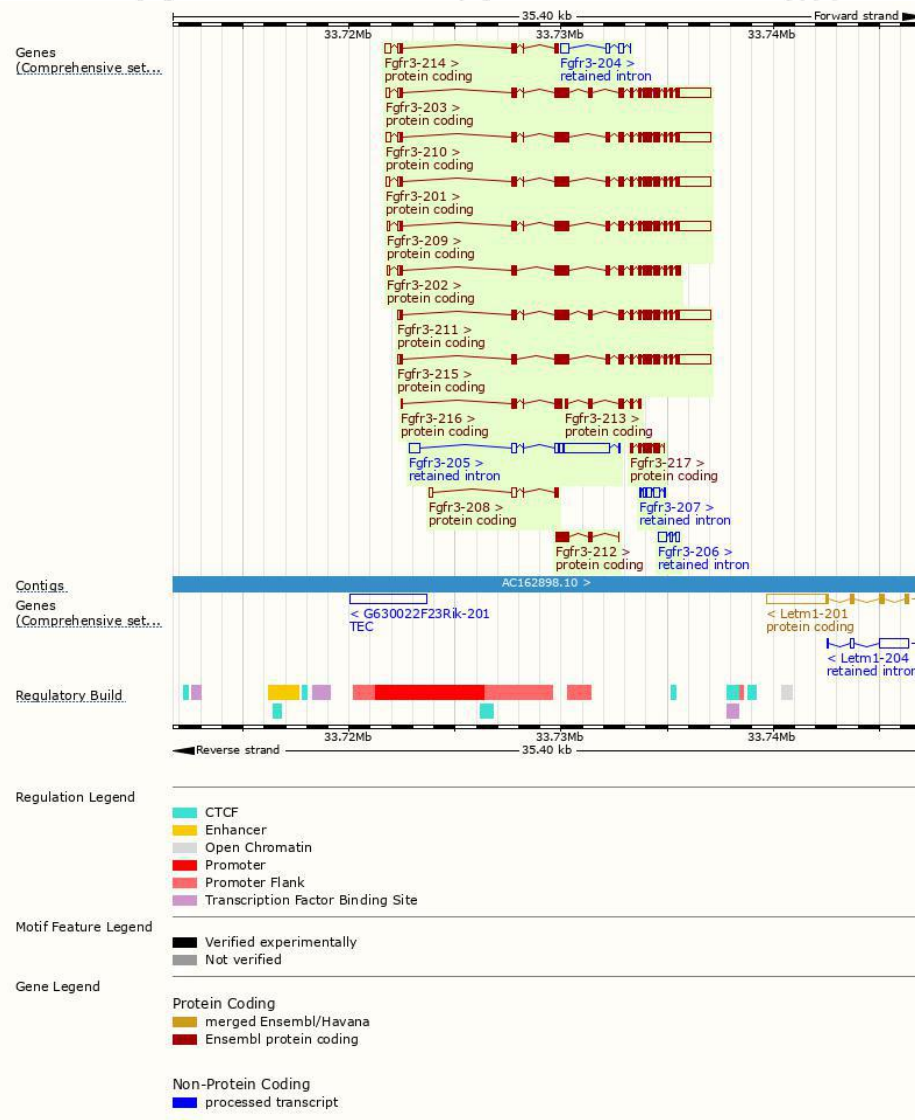
The gene has 17 transcripts, all transcripts are shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Fgfr3-210	ENSMUST00000169212.8	4245	800aa	Protein coding	CCDS51465	Q7TSI8	TSL:1 GENCODE basic APPRIS P4
Fgfr3-201	ENSMUST00000067150.13	4218	800aa	Protein coding	CCDS51465	Q7TSI8	TSL:1 GENCODE basic APPRIS P4
Fgfr3-209	ENSMUST00000164207.9	4150	801aa	Protein coding	CCDS57335	F6TK14	TSL:1 GENCODE basic APPRIS ALT2
Fgfr3-215	ENSMUST00000202138.3	3960	782aa	Protein coding	CCDS51466	Q61563	TSL:1 GENCODE basic APPRIS ALT2
Fgfr3-202	ENSMUST00000087820.7	2630	782aa	Protein coding	CCDS51466	Q61563	TSL:5 GENCODE basic APPRIS ALT2
Fgfr3-203	ENSMUST00000114411.8	4225	802aa	Protein coding	-	E9QNJ9	TSL:5 GENCODE basic APPRIS ALT2
Fgfr3-211	ENSMUST00000171509.8	4020	802aa	Protein coding	-	E9QNJ9	TSL:5 GENCODE basic APPRIS ALT2
Fgfr3-214	ENSMUST00000201437.3	968	194aa	Protein coding	-	A0A0J9YUX1	CDS 3' incomplete TSL:3
Fgfr3-217	ENSMUST00000202791.2	780	260aa	Protein coding	-	A0A0J9YTQ5	5' and 3' truncations in transcript evidence prevent annotation of the start and the end of the CDS. CDS 5' and 3' incomplete TSL:2
Fgfr3-213	ENSMUST00000201295.1	668	222aa	Protein coding	-	A0A0J9YUB8	5' and 3' truncations in transcript evidence prevent annotation of the start and the end of the CDS. CDS 5' and 3' incomplete TSL:5
Fgfr3-208	ENSMUST00000155002.2	650	47aa	Protein coding	-	D3Z7U5	CDS 3' incomplete TSL:3
Fgfr3-216	ENSMUST00000202182.1	648	216aa	Protein coding	-	A0A0J9YU04	5' and 3' truncations in transcript evidence prevent annotation of the start and the end of the CDS. CDS 5' and 3' incomplete TSL:3
Fgfr3-212	ENSMUST00000181298.4	601	200aa	Protein coding	-	A0A0J9YU20	5' and 3' truncations in transcript evidence prevent annotation of the start and the end of the CDS. CDS 5' and 3' incomplete TSL:5
Fgfr3-205	ENSMUST00000134610.7	3316	No protein	Retained intron	-	-	TSL:2
Fgfr3-204	ENSMUST00000132724.1	737	No protein	Retained intron	-	-	TSL:3
Fgfr3-207	ENSMUST00000152661.1	732	No protein	Retained intron	-	-	TSL:3
Fgfr3-206	ENSMUST00000142860.1	641	No protein	Retained intron	-	-	TSL:2

The strategy is based on the design of *Fgfr3-210* transcript, The transcription is shown below



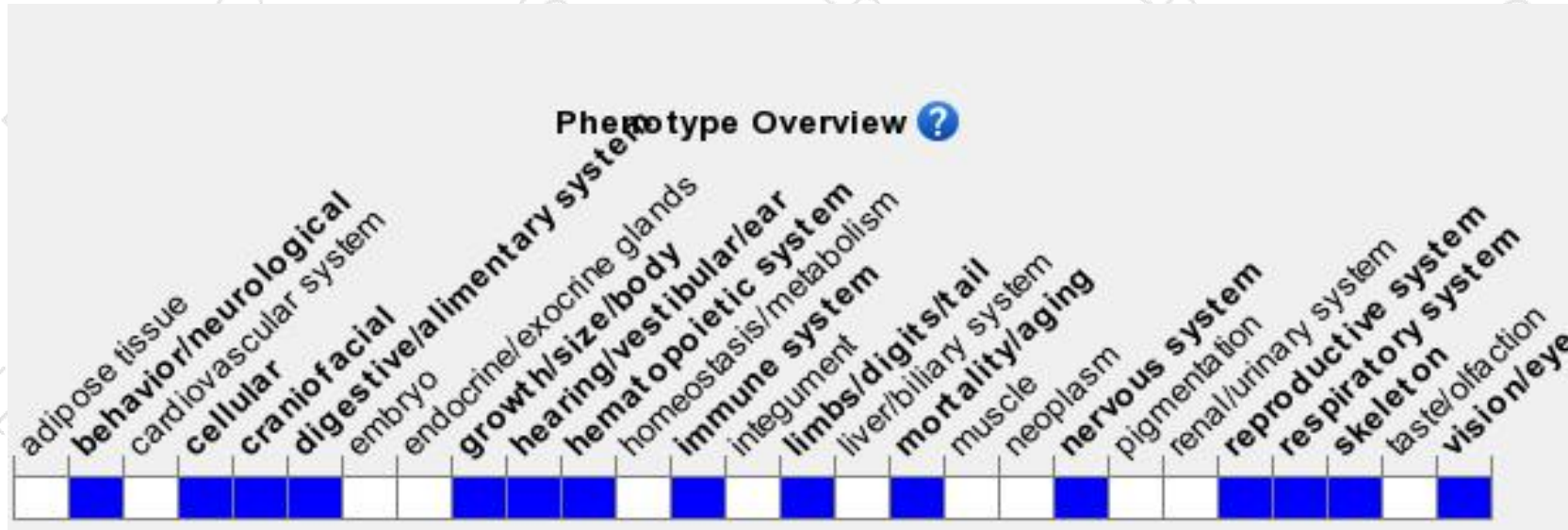
Genomic location distribution



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, Mutant alleles generally cause skeletal deformities, with some causing decreased body size, premature death, or hearing loss due to developmental defects of the ear.

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

Tel: 400-9660890

