Fgf13 Cas9-CKO Strategy

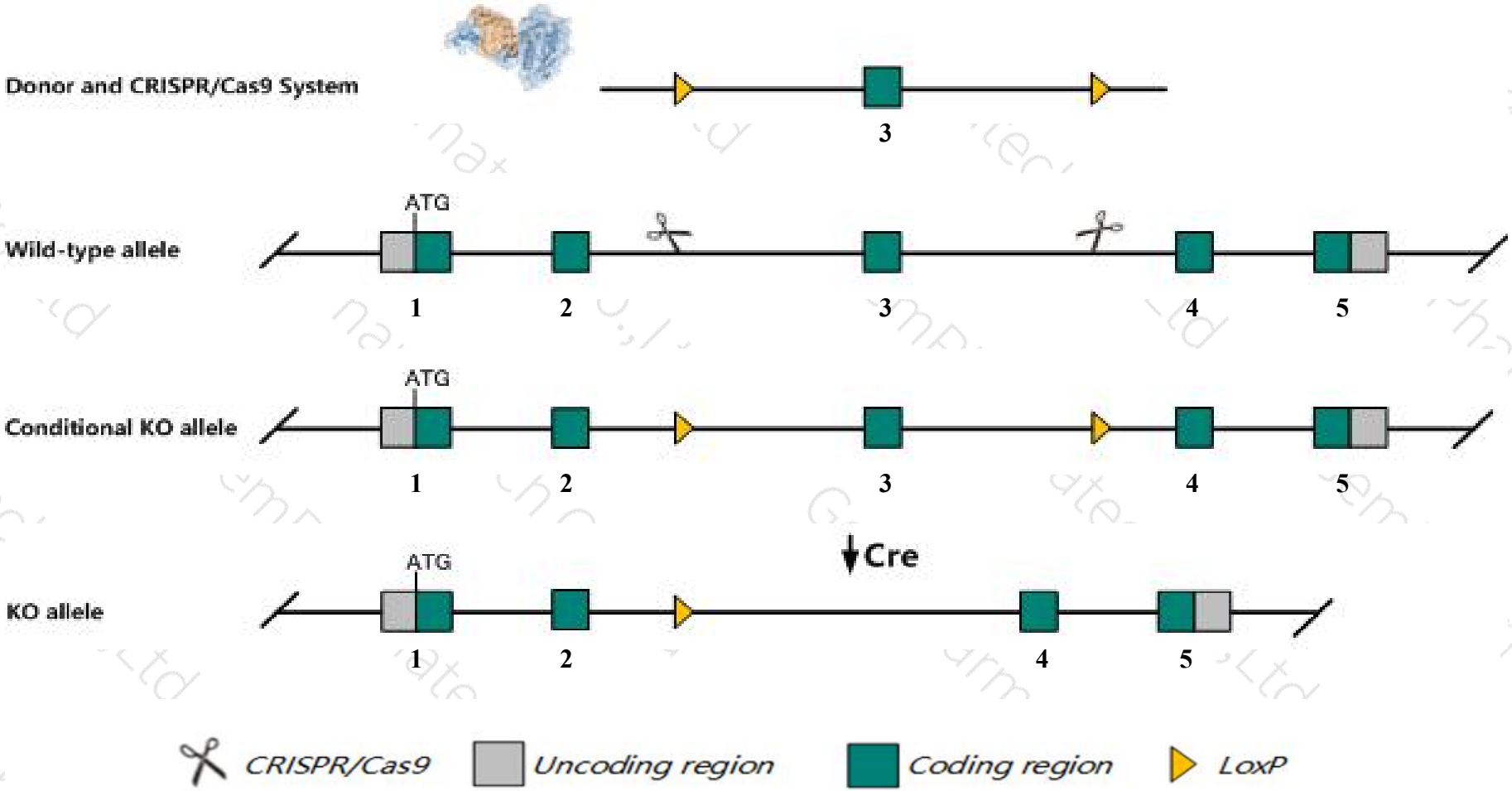
Designer: Huan Wang
Reviewer: Huan Fan
Design Date: 2020-4-23

Project Overview

Project Name	***Fgf13***
Project type	**Cas9-CKO**
Strain background	**C57BL/6JGpt**

Conditional Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *Fgf13* gene. The schematic diagram is as follows:



Technical routes

- The *Fgf13* gene has 9 transcripts. According to the structure of *Fgf13* gene, exon3 of *Fgf13-201* (ENSMUST00000033473.11) transcript is recommended as the knockout region.The region contains 104bp coding sequence. Knock out the region will result in disruption of protein function.

- In this project we use CRISPR/Cas9 technology to modify *Fgf13* 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,males hemizgyous for a null allele die by e12.5. heterozyous females for this allele develop spontaneous seizures and have increased susceptibility to hyperthermia-induced seizures and epilepsy.
- Some amino acids will remain at the N-terminus and some functions may be retained.
- Transcript *Fgf13-205,Fgf13-206, Fgf13-208* may not be affected.
- The *Fgf13* gene is located on the ChrX. 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）

集萃药康 GemPharmatech

Fgf13 fibroblast growth factor 13 [Mus musculus (house mouse)]

Gene ID: 14168, updated on 13-Mar-2020

Summary

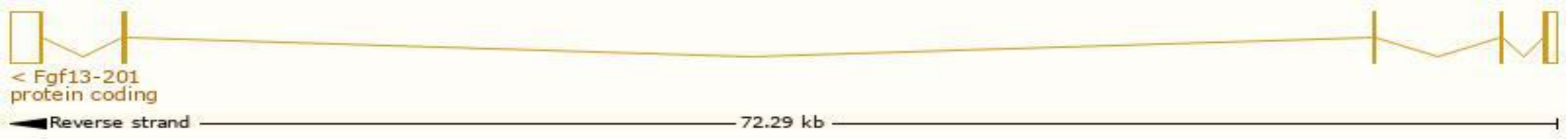
Official Symbol	Fgf13 provided by MGI
Official Full Name	fibroblast growth factor 13 provided by MGI
Primary source	MGI:MGI:109178
See related	Ensembl:ENSMUSG00000031137
Gene type	protein coding
RefSeq status	VALIDATED
Organism	Mus musculus
Lineage	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Myomorpha; Muroidea; Muridae; Murinae; Mus; Mus
Also known as	Fhf2
Expression	Biased expression in CNS E18 (RPKM 22.7), frontal lobe adult (RPKM 16.1) and 11 other tissues See more
Orthologs	human all

Transcript information（Ensembl）

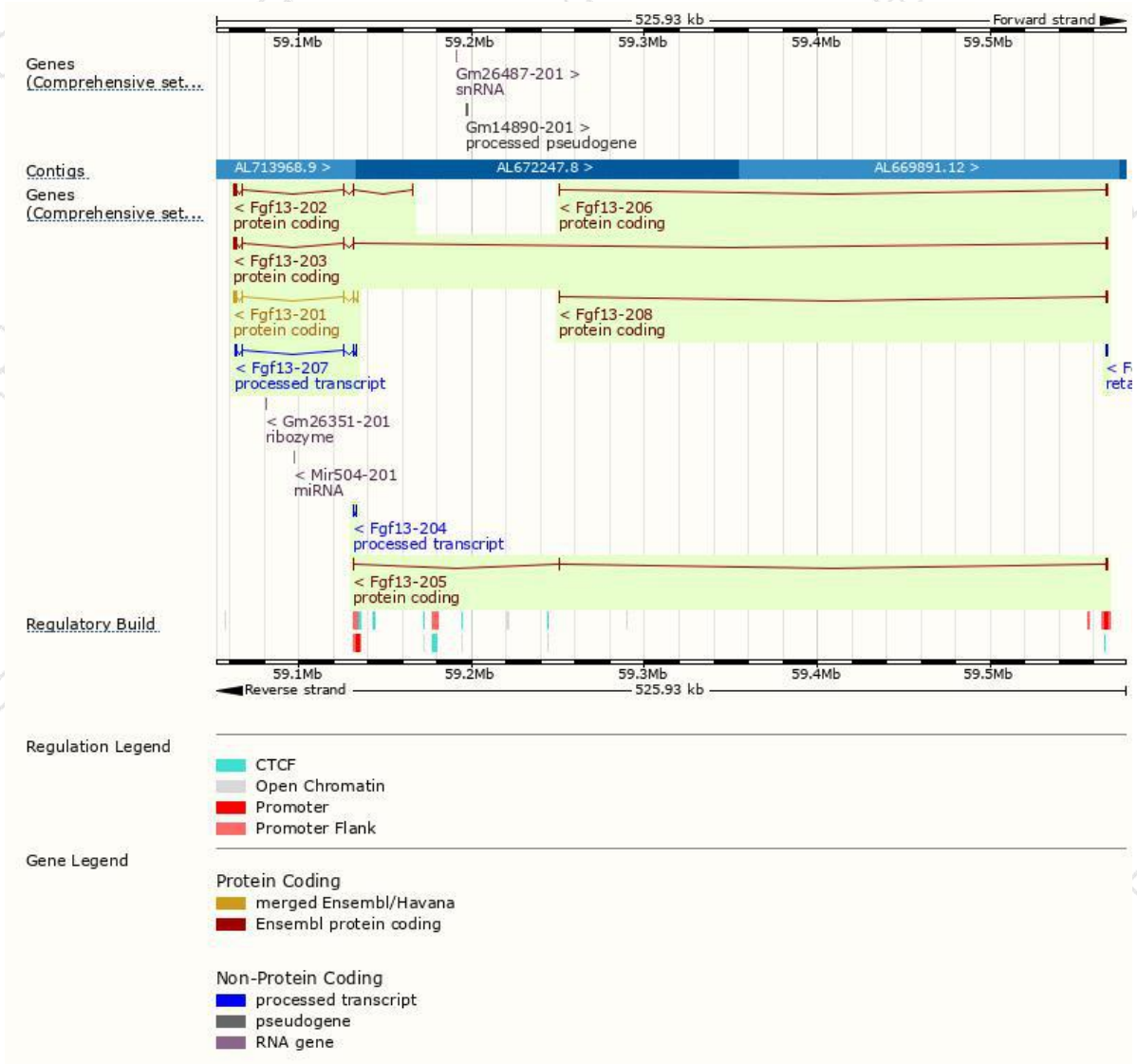
The gene has 9 transcripts,all transcripts are shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Fgf13-201	ENSMUST00000033473.11	2499	245aa	Protein coding	CCDS30157	P70377	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 P3
Fgf13-202	ENSMUST00000119306.1	2091	192aa	Protein coding	CCDS72383	P70377	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 ALT1
Fgf13-203	ENSMUST00000119833.7	2237	187aa	Protein coding	-	B1AU20	TSL:5 GENCODE basic
Fgf13-208	ENSMUST00000145767.1	617	43aa	Protein coding	-	B1AU22	CDS 3' incomplete TSL:2
Fgf13-205	ENSMUST00000124402.1	575	97aa	Protein coding	-	A0A067XG51	CDS 3' incomplete TSL:2
Fgf13-206	ENSMUST00000131319.7	456	69aa	Protein coding	-	B1AU23	CDS 3' incomplete TSL:3
Fgf13-207	ENSMUST00000138503.1	666	No protein	Processed transcript	-	-	TSL:3
Fgf13-204	ENSMUST00000123660.1	151	No protein	Processed transcript	-	-	TSL:1
Fgf13-209	ENSMUST00000150413.1	600	No protein	Retained intron	-	-	TSL:3

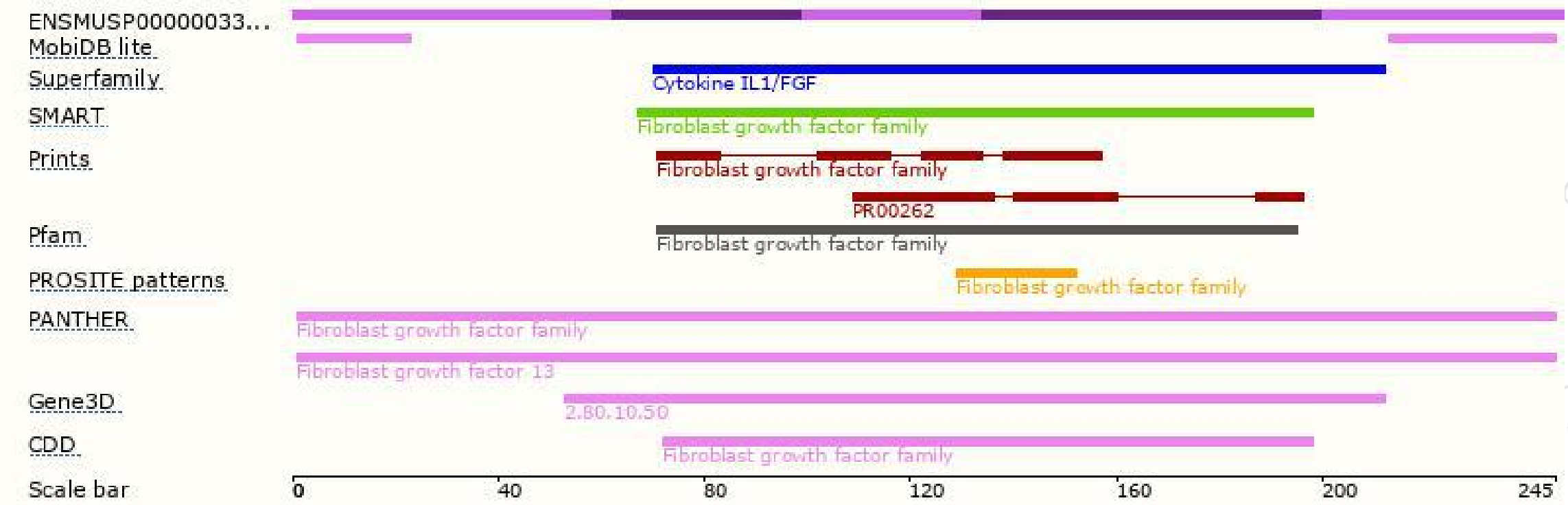
The strategy is based on the design of *Fgf13-201* transcript,the transcription is shown below:



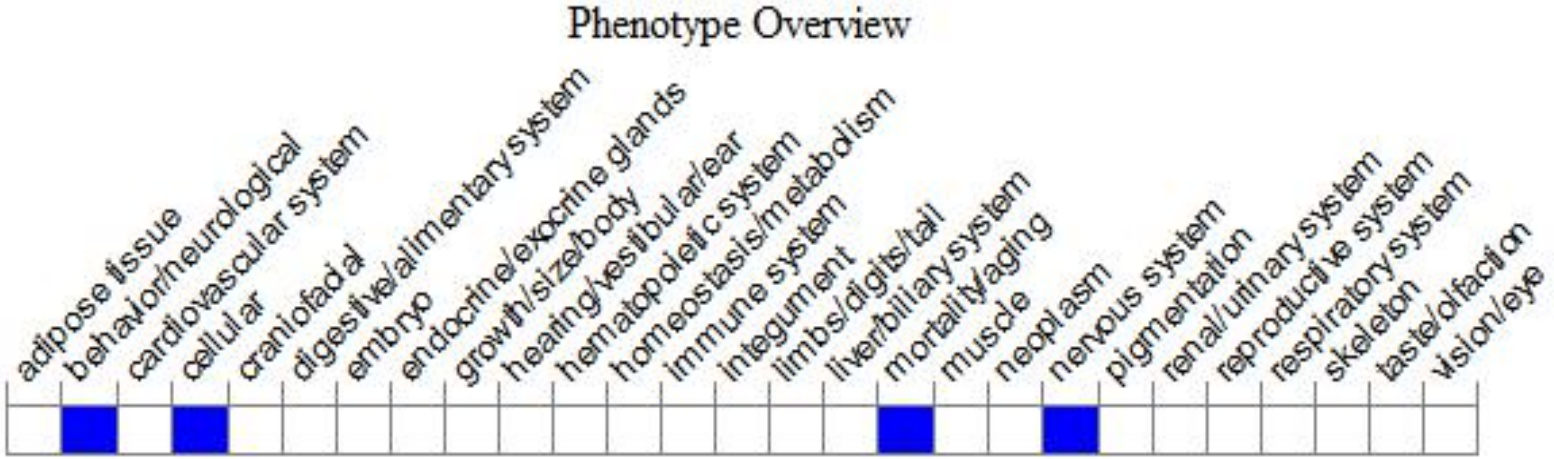
Genomic location distribution



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,males hemizgyous for a null allele die by E12.5. Heterozyous females for this allele develop spontaneous seizures and have increased susceptibility to hyperthermia-induced seizures and epilepsy.

集萃药康
GemPharmatech

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

Tel: 400-9660890

集萃药康生物科技
GemPharmatech Co.,Ltd