Fgfr1 Cas9-CKO Strategy

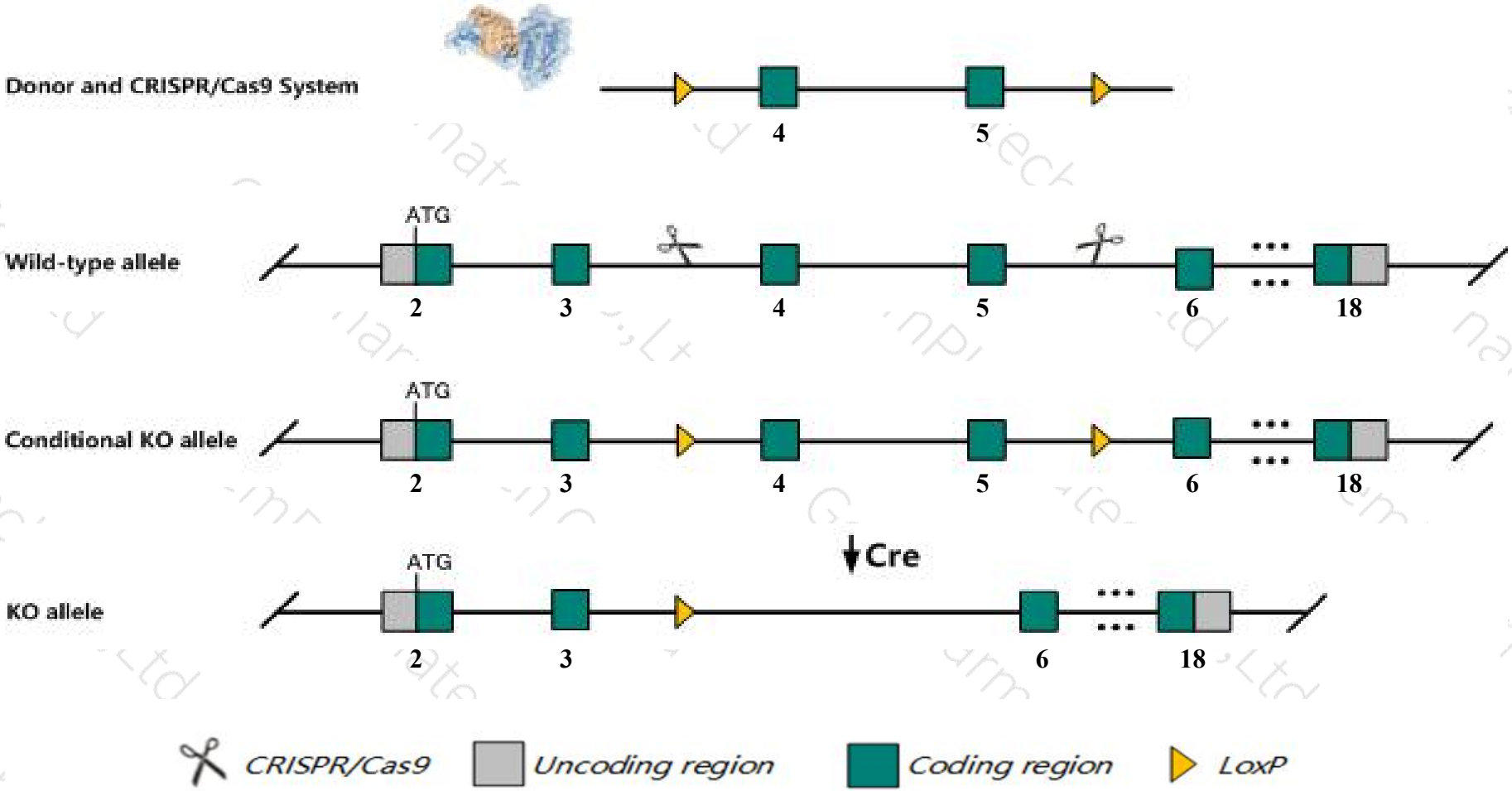
Designer: Jinling Wang
Reviewer：Shilei Zhu
Date: 2020/1/6

Project Overview

Project Name	***Fgfr1***
Project type	**Cas9-CKO**
Strain background	**C57BL/6JGpt**

Conditional Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *Fgfr1* gene. The schematic diagram is as follows:



Technical routes

- The *Fgfr1* gene has 19 transcripts. According to the structure of *Fgfr1* gene, exon4-exon5 of *Fgfr1-201* (ENSMUST00000084027.12) transcript is recommended as the knockout region.The region contains 263bp coding sequence. Knock out the region will result in disruption of protein function.

- In this project we use CRISPR/Cas9 technology to modify *Fgfr1* 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,Homozygotes for targeted null mutations die around gastrulation and show defective patterning of axial structures. Hypomorphic and selectively ablated mutations exhibit a wide range of abnormalities affecting diverse structures.

➢ The *Fgfr1* gene is located on the Chr8. 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

Fgfr1 fibroblast growth factor receptor 1 [Mus musculus (house mouse)]

Gene ID: 14182, updated on 26-Feb-2019

Summary

Official Symbol	Fgfr1 provided by MGI
Official Full Name	fibroblast growth factor receptor 1 provided byMGI
Primary source	MGI:MGI:95522
See related	Ensembl:ENSMUSG00000031565
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	AW208770, Eask, FGFR-I, FLG, Fgfr-1, Flt-2, Fr1, Hspy, MFR, bFGF-R-1, c-fgr
Expression	Broad expression in limb E14.5 (RPKM 38.2), adrenal adult (RPKM 35.4) and 23 other tissuesSee more
Orthologs	human all

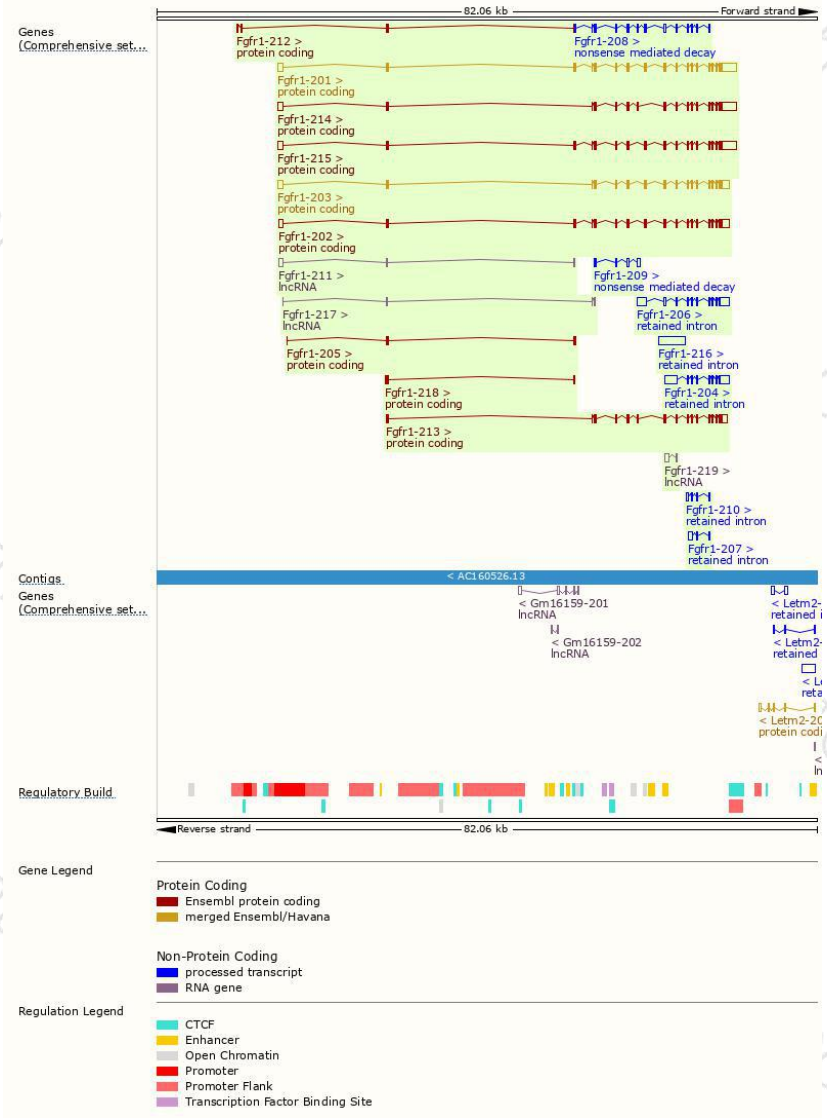
Transcript information（Ensembl）

The gene has 19 transcripts,all transcripts are shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Fgfr1-201	ENSMUST00000084027.12	5025	822aa	Protein coding	CCDS52526	P16092	TSL:5 GENCODE basic APPRIS P3
Fgfr1-202	ENSMUST00000117179.8	4046	820aa	Protein coding	CCDS57614	P16092 Q8CIM9	TSL:1 GENCODE basic APPRIS ALT1
Fgfr1-203	ENSMUST00000119398.9	3789	733aa	Protein coding	CCDS40304	P16092	TSL:1 GENCODE basic
Fgfr1-215	ENSMUST00000179592.7	5041	833aa	Protein coding	-	J3QN85	TSL:5 GENCODE basic
Fgfr1-214	ENSMUST00000178276.7	4741	733aa	Protein coding	-	P16092	TSL:5 GENCODE basic
Fgfr1-213	ENSMUST00000167764.1	2915	733aa	Protein coding	-	P16092	TSL:1 GENCODE basic
Fgfr1-205	ENSMUST00000124228.1	488	104aa	Protein coding	-	D3Z4V6	CDS 3' incomplete TSL:3
Fgfr1-212	ENSMUST00000155564.7	453	50aa	Protein coding	-	D3YW77	CDS 3' incomplete TSL:3
Fgfr1-218	ENSMUST00000210846.1	385	86aa	Protein coding	-	A0A1B0GSQ7	CDS 3' incomplete TSL:2
Fgfr1-208	ENSMUST00000138104.8	1903	300aa	Nonsense mediated decay	-	A0A1B0GSZ6	CDS 5' incomplete TSL:5
Fgfr1-209	ENSMUST00000138455.1	826	47aa	Nonsense mediated decay	-	A0A1B0GSD9	CDS 5' incomplete TSL:3
Fgfr1-204	ENSMUST00000120106.8	3386	No protein	Retained intron	-	-	TSL:1
Fgfr1-206	ENSMUST00000126118.8	3332	No protein	Retained intron	-	-	TSL:1
Fgfr1-216	ENSMUST00000210504.1	3324	No protein	Retained intron	-	-	TSL:NA
Fgfr1-207	ENSMUST00000133936.1	840	No protein	Retained intron	-	-	TSL:5
Fgfr1-210	ENSMUST00000145218.7	635	No protein	Retained intron	-	-	TSL:3
Fgfr1-211	ENSMUST00000148322.1	734	No protein	lncRNA	-	-	TSL:3
Fgfr1-219	ENSMUST00000211419.1	599	No protein	lncRNA	-	-	TSL:3
Fgfr1-217	ENSMUST00000210778.1	381	No protein	lncRNA	-	-	TSL:3

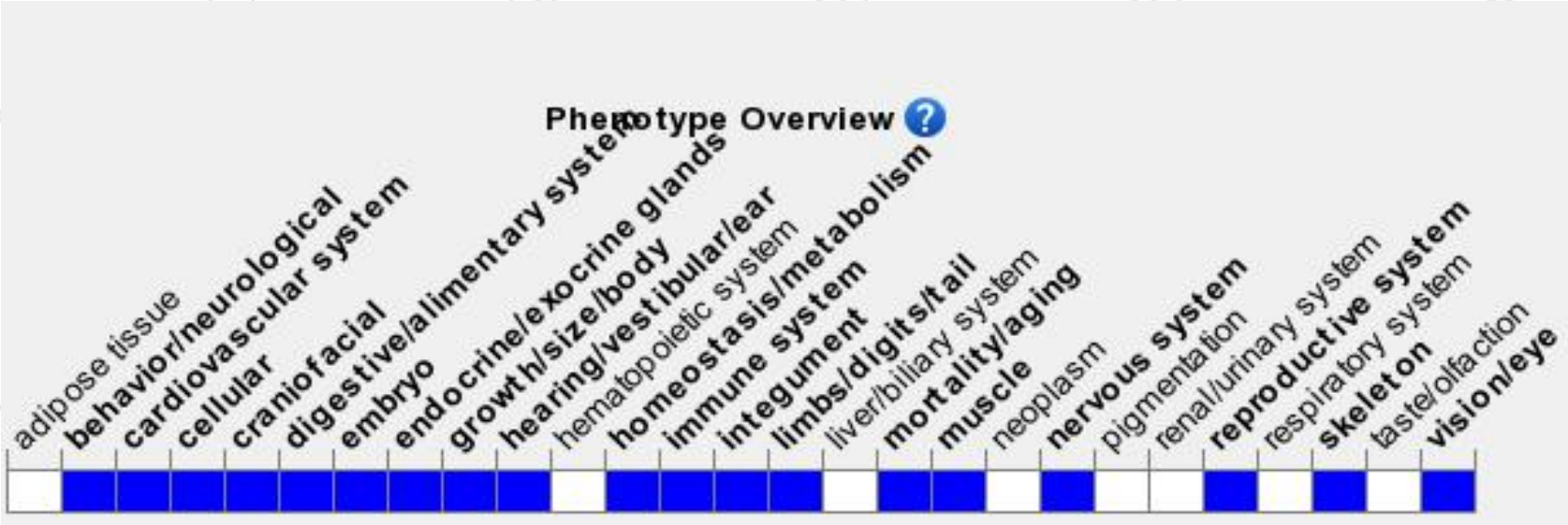
The strategy is based on the design of *Fgfr1-201* transcript,The transcription is shown below

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 targeted null mutations die around gastrulation and show defective patterning of axial structures. Hypomorphic and selectively ablated mutations exhibit a wide range of abnormalities affecting diverse structures.

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