

# *Fgfr2* Cas9-KO Strategy

**Designer:** Jinling Wang

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# Project Overview



**Project Name**

***Fgfr2***

**Project type**

**Cas9-KO**

**Strain background**

**C57BL/6JGpt**

# Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *Fgfr2* gene. The schematic diagram is as follows:



- The *Fgfr2* gene has 27 transcripts. According to the structure of *Fgfr2* gene, exon3 of *Fgfr2-211* (ENSMUST00000120187.8) transcript is recommended as the knockout region. The region contains 170bp coding sequence. Knock out the region will result in disruption of protein function.
- In this project we use CRISPR/Cas9 technology to modify *Fgfr2* gene. The brief process is as follows: CRISPR/Cas9 system

- According to the existing MGI data, Mice homozygous for null mutations die as embryos. Isoform IIIb deficient mutants die at birth with defects in multiple organs and tissues. Isoform IIIc deficient mutants have defects in osteoblast and chondrocyte lineages, producing dwarfism.
- The *Fgfr2* gene is located on the Chr7. 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)

## Fgfr2 fibroblast growth factor receptor 2 [Mus musculus (house mouse)]

Gene ID: 14183, updated on 9-Apr-2019

### Summary



<b>Official Symbol</b>	Fgfr2 provided by <a href="#">MGI</a>
<b>Official Full Name</b>	fibroblast growth factor receptor 2 provided by <a href="#">MGI</a>
<b>Primary source</b>	<a href="#">MGI:MGI:95523</a>
<b>See related</b>	<a href="#">Ensembl:ENSMUSG00000030849</a>
<b>Gene type</b>	protein coding
<b>RefSeq status</b>	VALIDATED
<b>Organism</b>	<a href="#">Mus musculus</a>
<b>Lineage</b>	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Myomorpha; Muroidea; Muridae; Murinae; Mus; Mus
<b>Also known as</b>	AU043015, AW556123, Bek, Fgfr-2, Fgfr-7, Fgfr7, KGFR, KGFRTr, sv5
<b>Expression</b>	Ubiquitous expression in limb E14.5 (RPKM 15.2), lung adult (RPKM 13.2) and 25 other tissues <a href="#">See more</a>
<b>Orthologs</b>	<a href="#">human</a> <a href="#">all</a>

# Transcript information (Ensembl)

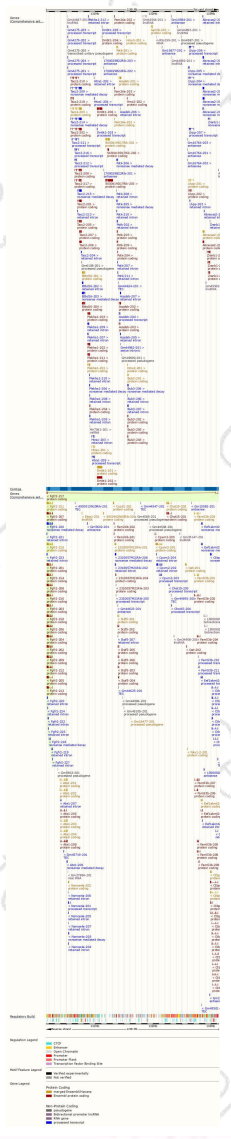
The gene has 27 transcripts, all transcripts are shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Fgfr2-211	ENSMUST00000120187.8	4311	726aa	Protein coding	CCDS52412	E9Q7C7	TSL1 GENCODE basic APPRIS ALT1
Fgfr2-207	ENSMUST00000117672.7	4223	723aa	Protein coding	CCDS85431	E9Q5C2	TSL1 GENCODE basic APPRIS ALT1
Fgfr2-215	ENSMUST00000122054.7	3323	840aa	Protein coding	CCDS52413	E9QK53	TSL1 GENCODE basic APPRIS P4
Fgfr2-208	ENSMUST00000117858.7	2563	813aa	Protein coding	-	E9PX67	CDS 5' incomplete TSL1
Fgfr2-204	ENSMUST00000117691.7	2469	822aa	Protein coding	-	E9Q7E8	CDS 5' incomplete TSL1
Fgfr2-202	ENSMUST00000117089.7	2463	820aa	Protein coding	-	E9PVJ6	CDS 5' incomplete TSL1
Fgfr2-209	ENSMUST00000119260.7	2460	818aa	Protein coding	-	E9Q7TQ	CDS 5' incomplete TSL1
Fgfr2-217	ENSMUST00000124096.7	2425	182aa	Protein coding	-	F2Z480	TSL5 GENCODE basic
Fgfr2-208	ENSMUST00000118296.7	2296	724aa	Protein coding	-	E9PXV8	CDS 5' incomplete TSL1
Fgfr2-214	ENSMUST00000121080.7	2218	698aa	Protein coding	-	E9PX88	CDS 5' incomplete TSL1
Fgfr2-216	ENSMUST00000122446.7	2212	696aa	Protein coding	-	E9Q5C3	CDS 5' incomplete TSL1
Fgfr2-201	ENSMUST00000117073.1	2209	695aa	Protein coding	-	E9PX60	CDS 5' incomplete TSL1
Fgfr2-210	ENSMUST00000120141.7	2196	731aa	Protein coding	-	E9Q708	CDS 5' incomplete TSL1
Fgfr2-212	ENSMUST00000120715.7	2130	709aa	Protein coding	-	D3Z5M8	CDS 5' incomplete TSL5
Fgfr2-203	ENSMUST00000117357.7	2118	705aa	Protein coding	-	E9PX90	CDS 5' incomplete TSL1
Fgfr2-213	ENSMUST00000121084.7	1830	609aa	Protein coding	-	E9Q700	CDS 5' incomplete TSL1
Fgfr2-205	ENSMUST00000117754.7	1827	608aa	Protein coding	-	E9Q7E8	CDS 5' incomplete TSL1
Fgfr2-228	ENSMUST00000153166.7	4429	334aa	Nonsense mediated decay	-	D6RJK6	TSL1
Fgfr2-218	ENSMUST00000127091.1	665	61aa	Nonsense mediated decay	-	F7BDU9	CDS 5' incomplete TSL2
Fgfr2-227	ENSMUST00000208644.1	3981	No protein	Retained intron	-	-	TSLNA
Fgfr2-219	ENSMUST00000129103.1	1265	No protein	Retained intron	-	-	TSL1
Fgfr2-223	ENSMUST00000138264.1	957	No protein	Retained intron	-	-	TSL5
Fgfr2-222	ENSMUST00000133806.1	953	No protein	Retained intron	-	-	TSL2
Fgfr2-221	ENSMUST00000130557.1	790	No protein	Retained intron	-	-	TSL2
Fgfr2-220	ENSMUST00000129542.1	719	No protein	Retained intron	-	-	TSL2
Fgfr2-225	ENSMUST00000148675.1	656	No protein	Retained intron	-	-	TSL2
Fgfr2-224	ENSMUST00000147859.1	335	No protein	Retained intron	-	-	TSL2

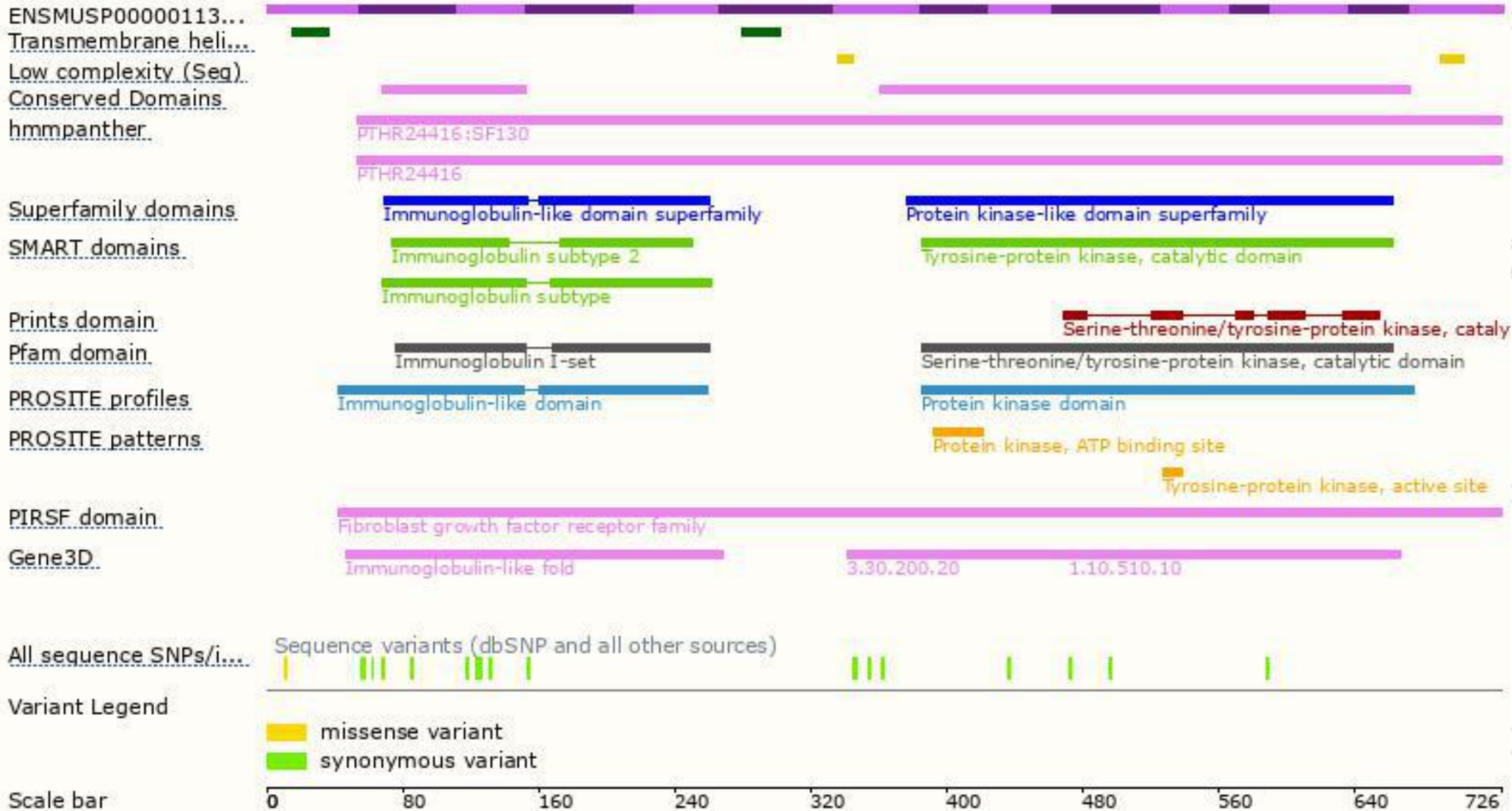
The strategy is based on the design of *Fgfr2-211* transcript, The transcription is shown below



# 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, Mice homozygous for null mutations die as embryos. Isoform IIIb deficient mutants die at birth with defects in multiple organs and tissues. Isoform IIIc deficient mutants have defects in osteoblast and chondrocyte lineages, producing dwarfism.

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

Tel: 400-9660890

