



# **Fgf16 Cas9-KO Strategy**

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**Reviewer:**

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**Design Date:**

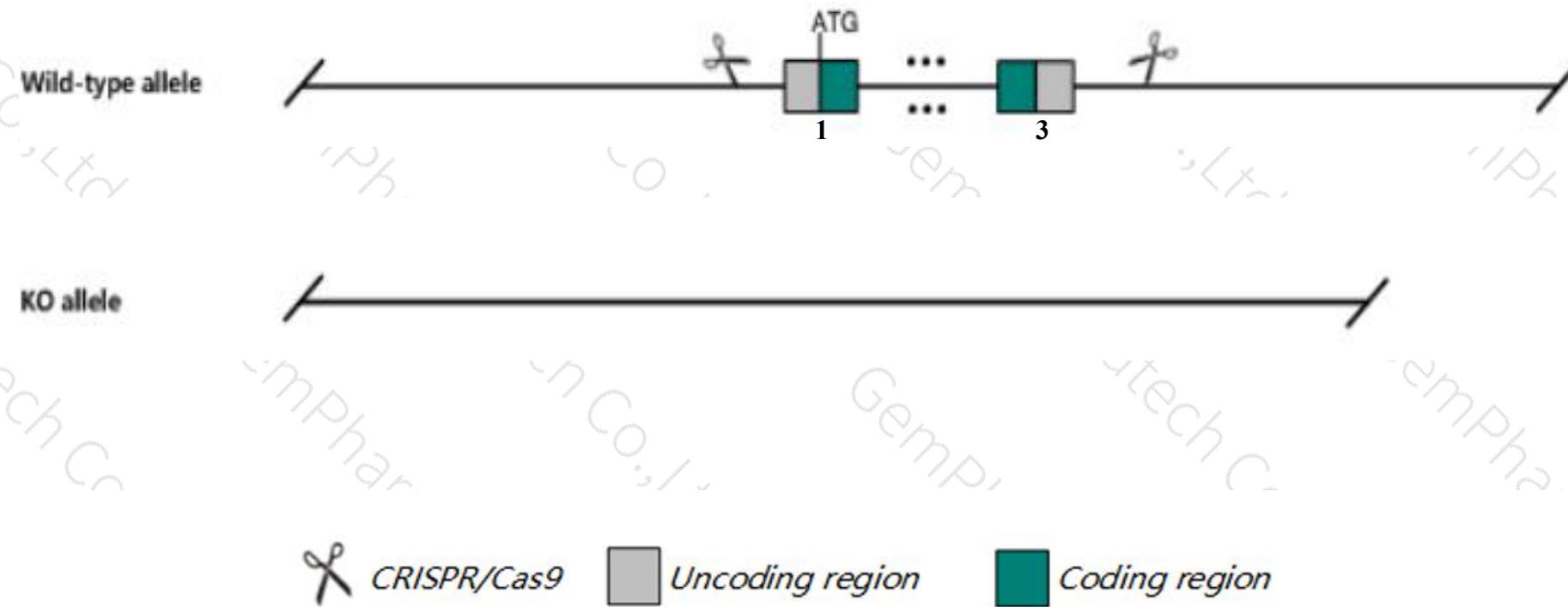
**2020-4-18**

# Project Overview

<b>Project Name</b>	<i>Fgf16</i>
<b>Project type</b>	Cas9-KO
<b>Strain background</b>	C57BL/6JGpt

# Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *Fgf16* gene. The schematic diagram is as follows:



# Technical routes

- The *Fgf16* gene has 1 transcript. According to the structure of *Fgf16* gene, exon1-exon3 of *Fgf16-201* (ENSMUST00000033581.3) transcript is recommended as the knockout region. The region contains all of the coding sequence. Knock out the region will result in disruption of protein function.
- In this project we use CRISPR/Cas9 technology to modify *Fgf16* gene. The brief process is as follows: CRISPR/Cas9 system



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# Notice

- According to the existing MGI data, males hemizygous for one null allele show reduced fetal cardiomyocyte proliferation and postnatal cardiomyocyte numbers. males hemizygous for another null allele die in midgestation with craniofacial and heart defects including cardiac hemorrhage, chamber dilation, thin walls and poor trabeculation.
- The *Fgf16* 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 the gene knockout on gene transcription, RNA splicing and protein translation cannot be predicted at the existing technology level.



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# Gene information (NCBI)

## Fgf16 fibroblast growth factor 16 [Mus musculus (house mouse)]

Gene ID: 80903, updated on 13-Mar-2020

### Summary



**Official Symbol** Fgf16 provided by [MGI](#)

**Official Full Name** fibroblast growth factor 16 provided by [MGI](#)

**Primary source** [MGI:MGI:1931627](#)

**See related** [Ensembl:ENSMUSG00000031230](#)

**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

**Expression** Biased expression in heart adult (RPKM 1.9), frontal lobe adult (RPKM 0.4) and 4 other tissues [See more](#)

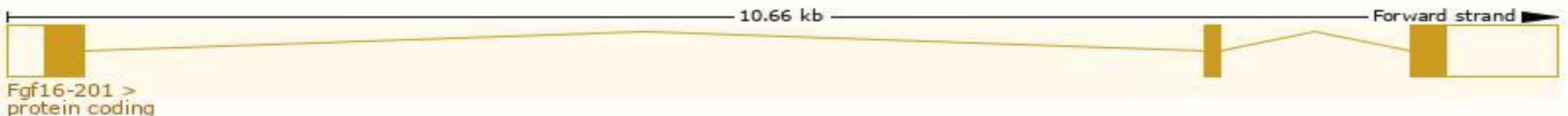
**Orthologs** [human](#) [all](#)

# Transcript information (Ensembl)

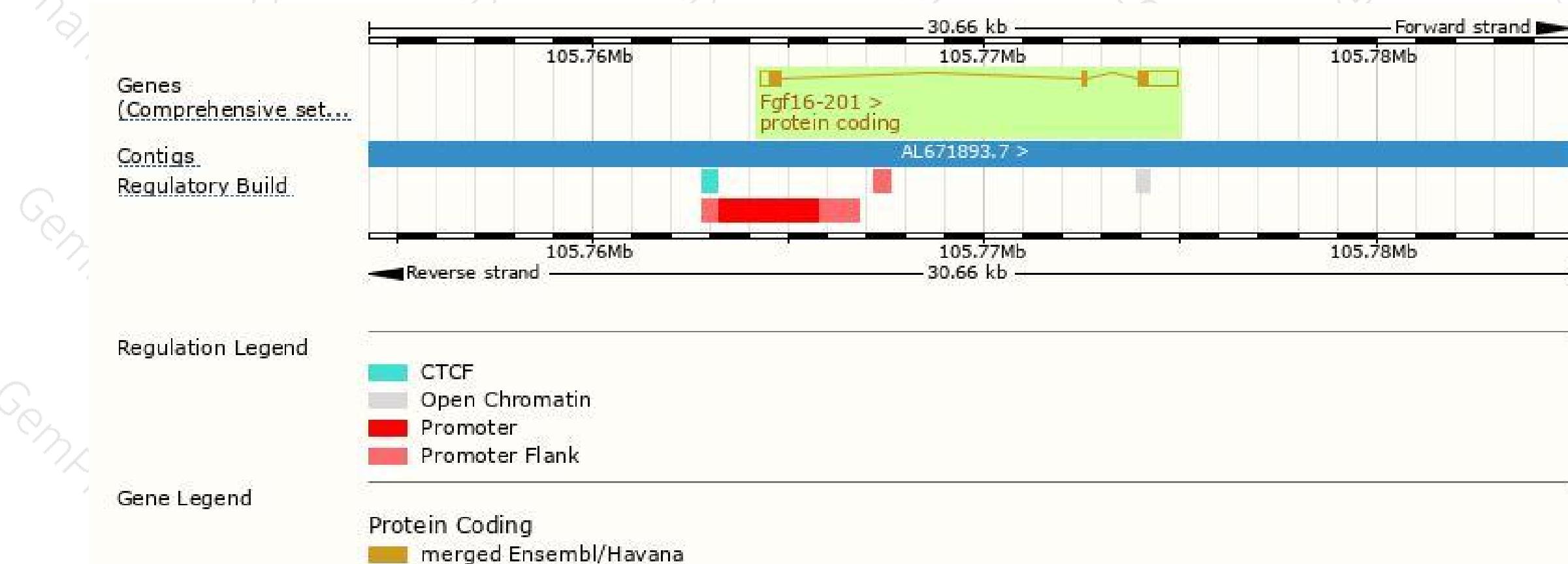
The gene has 1 transcript, and the transcript is shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Fgf16-201	<a href="#">ENSMUST00000033581.3</a>	1645	<a href="#">207aa</a>	Protein coding	<a href="#">CCDS30336</a>	<a href="#">Q9ESL8</a>	TSL:1 GENCODE basic APPRIS P1

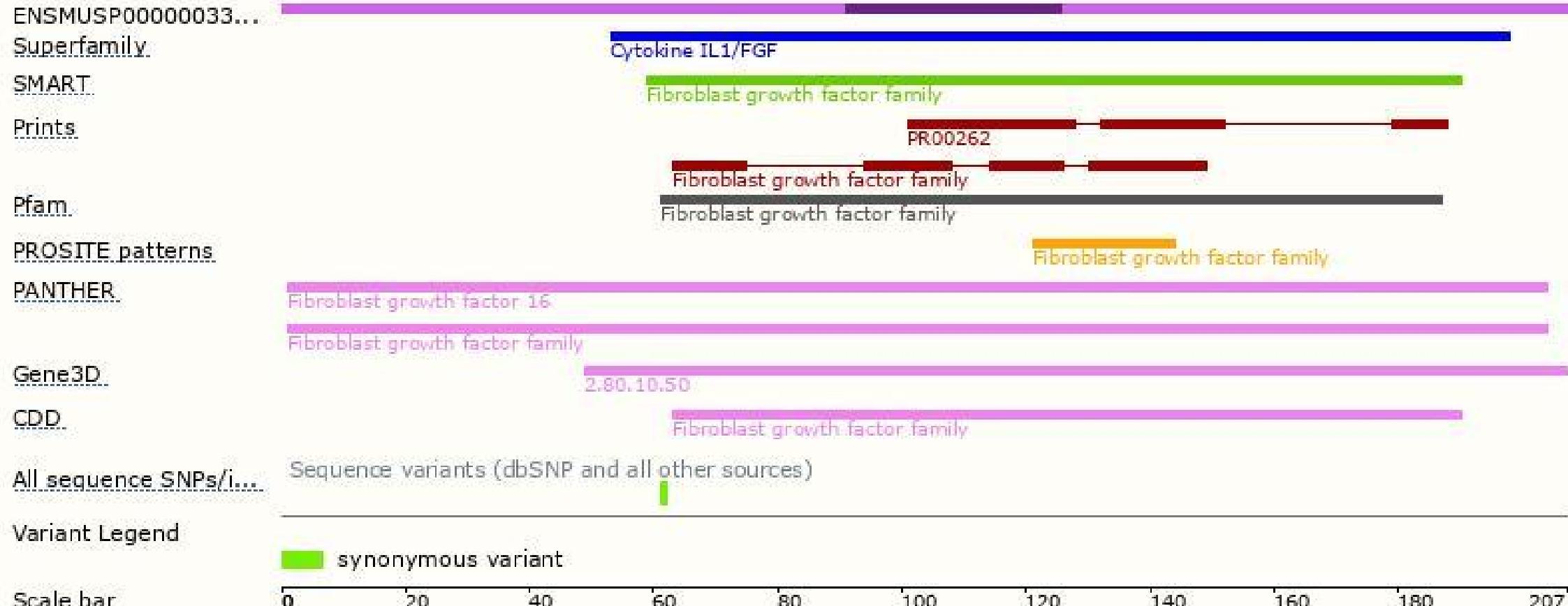
The strategy is based on the design of *Fgf16-201* transcript. The transcription is shown below



# Genomic location distribution



# Protein domain

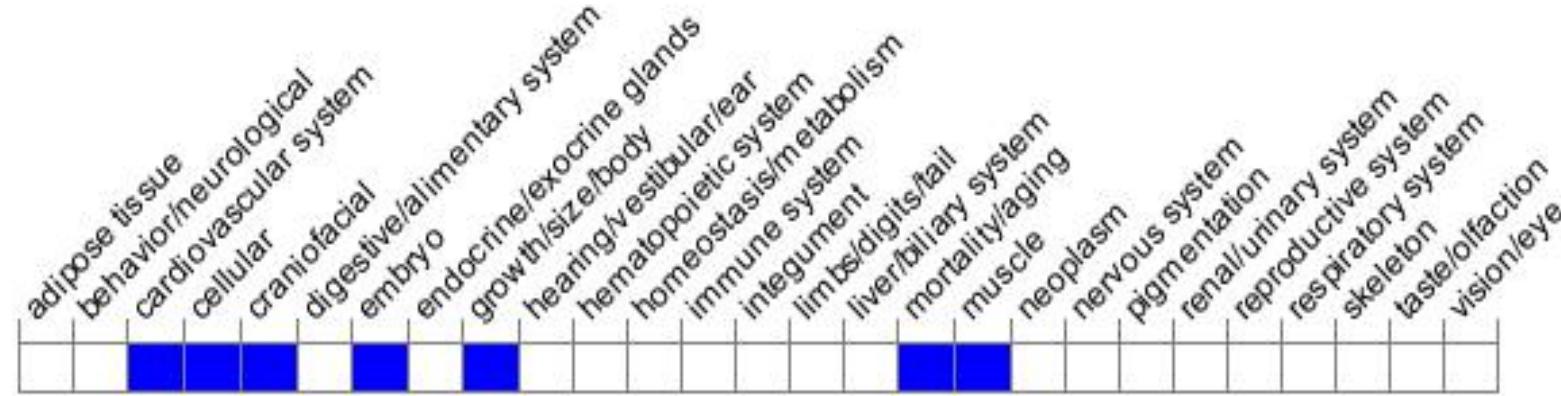




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# Mouse phenotype description(MGI )

Phenotype Overview



*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 hemizygous for one null allele show reduced fetal cardiomyocyte proliferation and postnatal cardiomyocyte numbers. Males hemizygous for another null allele die in midgestation with craniofacial and heart defects including cardiac hemorrhage, chamber dilation, thin walls and poor trabeculation.



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

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