Fgf8 Cas9-KO Strategy

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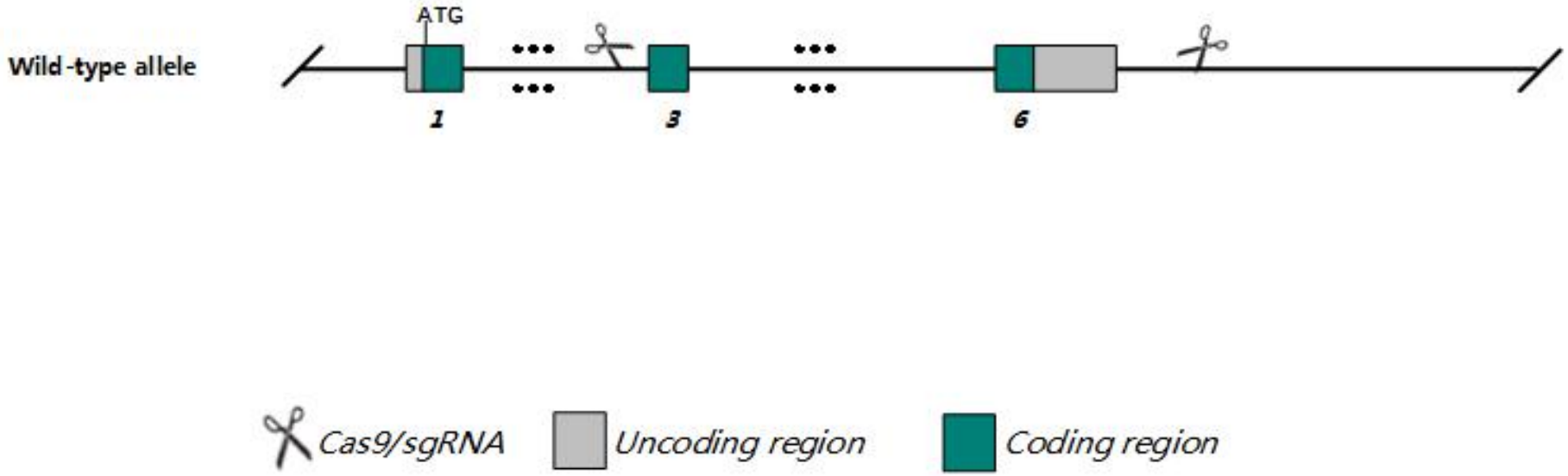
Project Overview

Project Name	***Fgf8***
Project type	**Cas9-KO**
Strain background	**C57BL/6JGpt**

Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *Fgf8* gene. The schematic diagram is as follows:



Technical routes

➢ The *Fgf8* gene has 6 transcripts. According to the structure of *Fgf8* gene, exon3 of *Fgf8-201* (ENSMUST00000026240.13) transcript is recommended as the knockout region.The region contains most 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 *Fgf8* gene. The brief process is as follows: CRISPR/Cas9 system v

Notice

- According to the existing MGI data,Homozygotes for targeted mutations exhibit cardiovascular defects (including abnormal left-right axis determination), impaired limb, thymic, and craniofacial development, and prenatal or early postnatal lethality.

- The *Fgf8* gene is located on the Chr19. 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）

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Fgf8 fibroblast growth factor 8 [Mus musculus (house mouse)]

Gene ID: 14179, updated on 19-Mar-2019

Summary

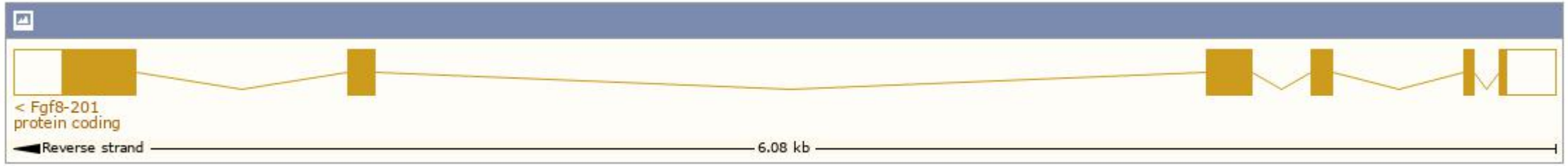
Official Symbol	Fgf8 provided by MGI
Official Full Name	fibroblast growth factor 8 provided byMGI
Primary source	MGI:MGI:99604
See related	Ensembl:ENSMUSG00000025219
Gene type	protein coding
RefSeq status	VALIDATED
Organism	Mus musculus
Lineage	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Myomorpha; Muroidea; Muridae; Murinae; Mus; Mus
Also known as	Aigf, Fgf-8
Expression	Biased expression in CNS E11.5 (RPKM 1.9), ovary adult (RPKM 1.5) and 5 other tissuesSee more
Orthologs	human all

Transcript information（Ensembl）

The gene has 6 transcripts,all transcripts are shown below:

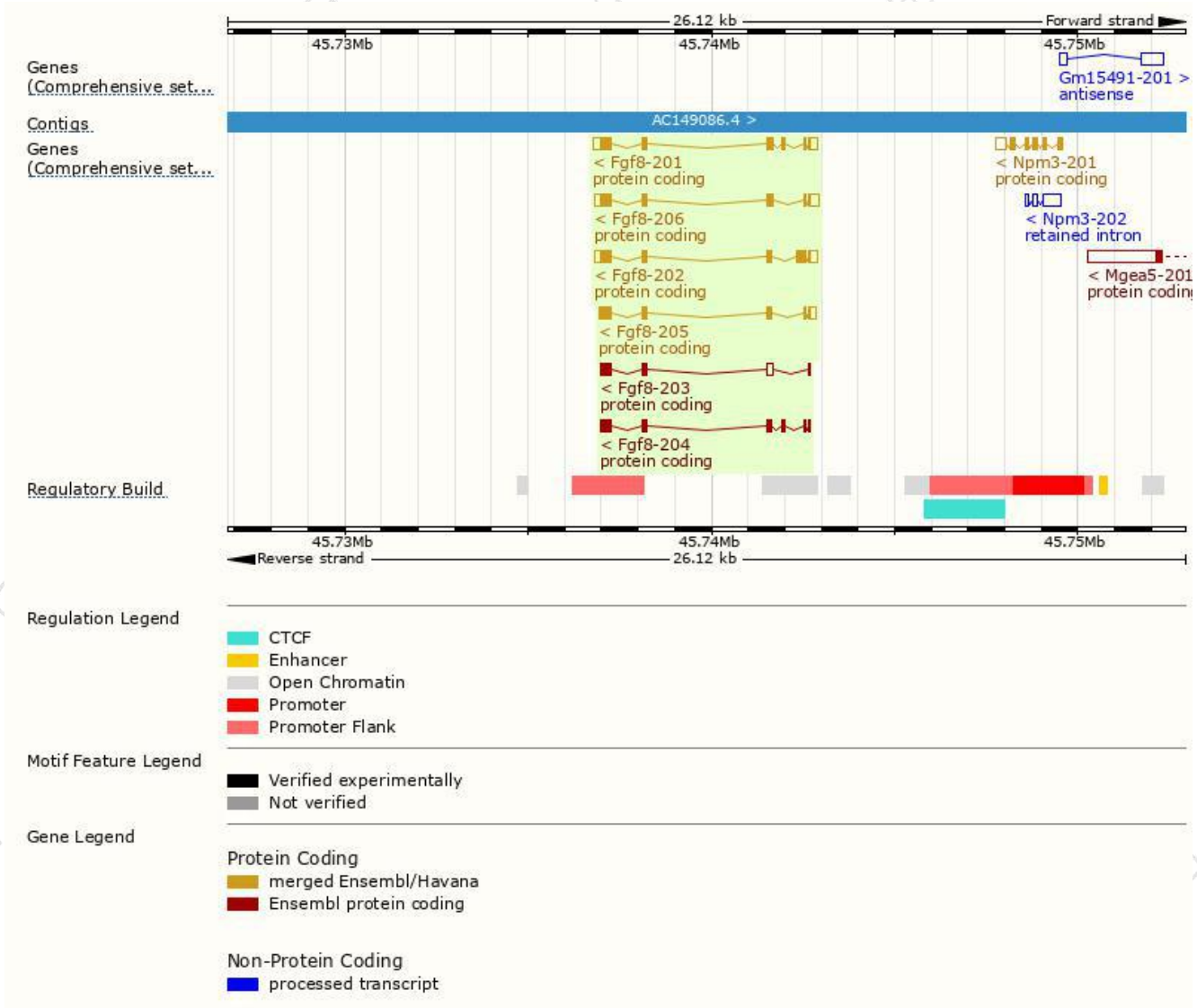
Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Fgf8-202	ENSMUST00000026241.11	1168	268aa	Protein coding	CCDS29864	P37237	TSL:1 GENCODE basic
Fgf8-201	ENSMUST00000026240.13	1117	244aa	Protein coding	CCDS50452	Q80ZL6	TSL:1 GENCODE basic APPRIS P4
Fgf8-206	ENSMUST00000111928.7	1056	215aa	Protein coding	CCDS50451	P37237 Q3V279	TSL:1 GENCODE basic APPRIS ALT2
Fgf8-205	ENSMUST00000111927.7	843	204aa	Protein coding	CCDS50450	P37237	TSL:1 GENCODE basic APPRIS ALT1
Fgf8-204	ENSMUST00000111925.1	702	233aa	Protein coding	-	D3Z207	TSL:5 GENCODE basic APPRIS ALT2
Fgf8-203	ENSMUST00000111924.7	630	140aa	Protein coding	-	D3Z208	TSL:5 GENCODE basic

The strategy is based on the design of *Fgf8-201* transcript,The transcription is shown below

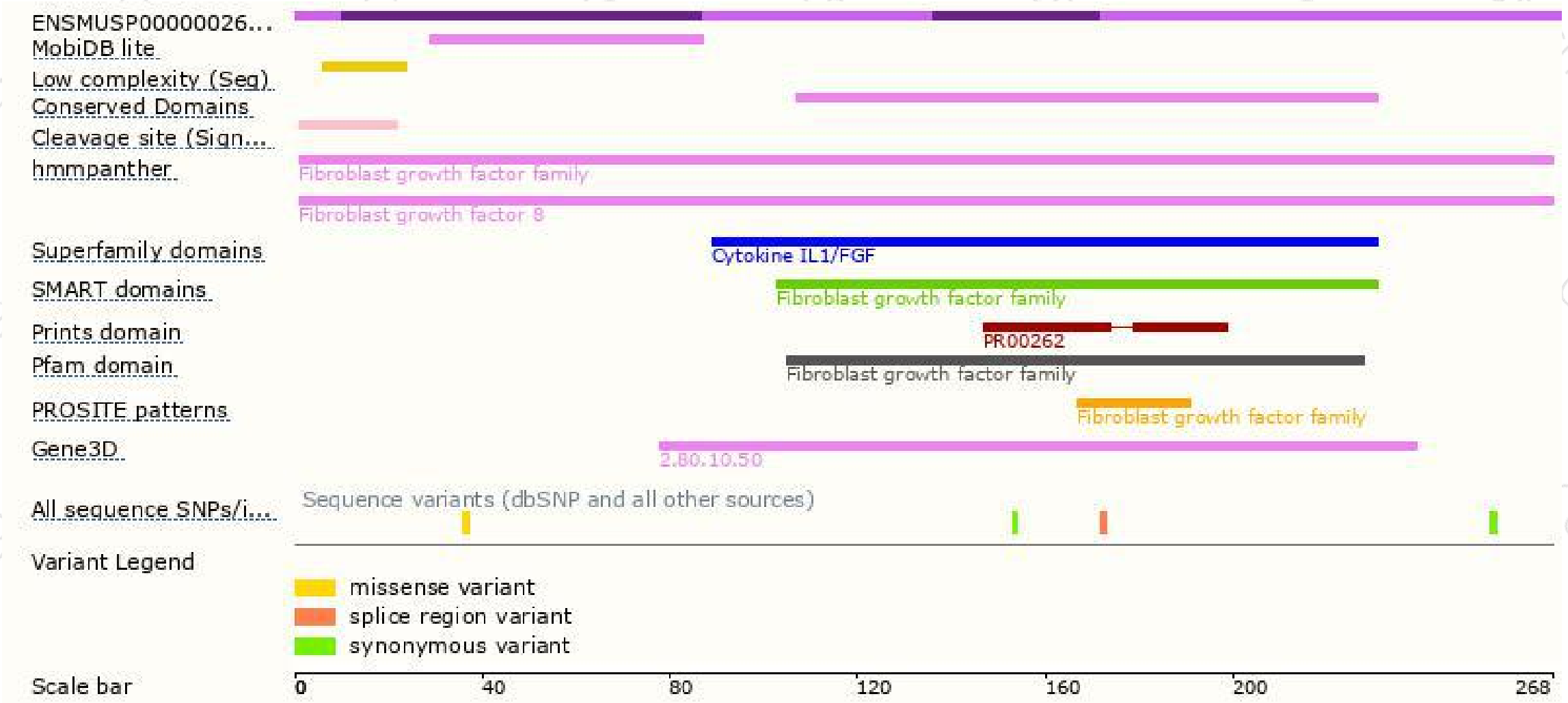


Statistics Exons: 6, Coding exons: 6, Transcript length: 1,117 bps, Translation length: 244 residues

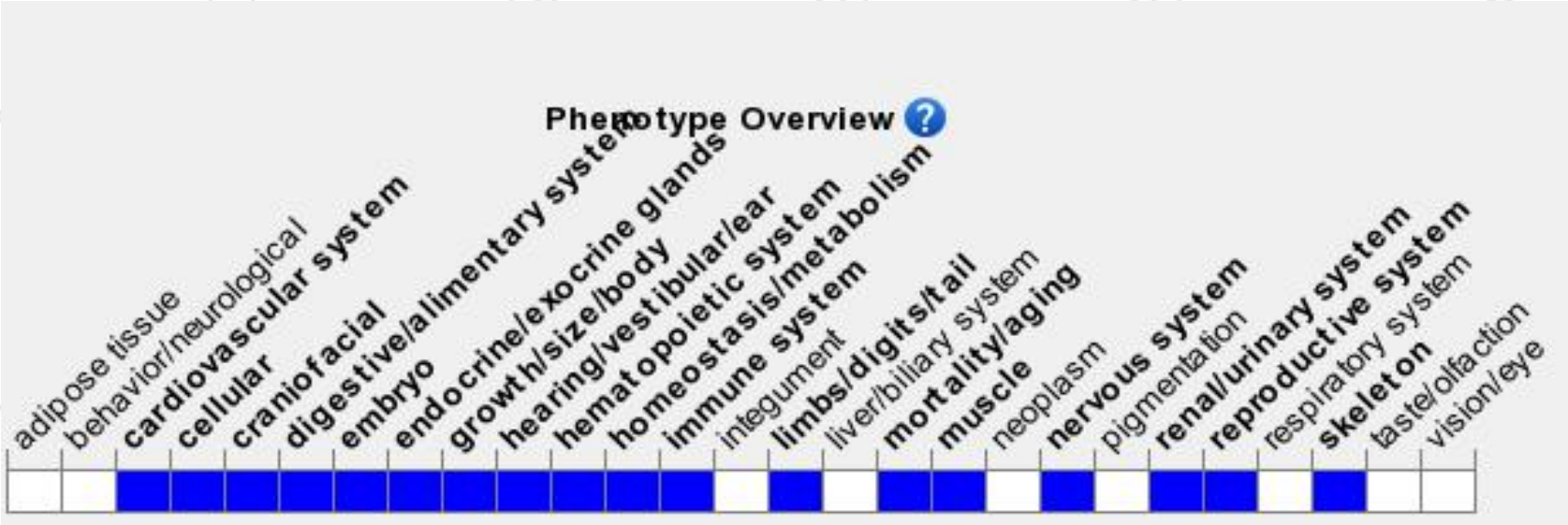
Genomic location distribution



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/).

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

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