

Mef2c Cas9-KO Strategy

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Reviewer:

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Project Overview

Project Name

Mef2c

Project type

Cas9-KO

Strain background

C57BL/6JGpt

Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *Mef2c* gene. The schematic diagram is as follows:



- The *Mef2c* gene has 31 transcripts. According to the structure of *Mef2c* gene, exon3-exon5 of *Mef2c-212* (ENSMUST00000197146.4) transcript is recommended as the knockout region. The region contains 535bp coding sequence. Knock out the region will result in disruption of protein function.
- In this project we use CRISPR/Cas9 technology to modify *Mef2c* gene. The brief process is as follows: CRISPR/Cas9 system

- According to the existing MGI data, Mice homozygous for disruptions in this gene have cardiovascular abnormalities and die as embryos.
- The *Mef2c* gene is located on the Chr13. 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)

Mef2c myocyte enhancer factor 2C [*Mus musculus* (house mouse)]

Gene ID: 17260, updated on 3-Sep-2019

Summary

| | |
|---------------------------|---|
| Official Symbol | Mef2c provided by MGI |
| Official Full Name | myocyte enhancer factor 2C provided by MGI |
| Primary source | MGI:MGI:99458 |
| See related | Ensembl:ENSMUSG000000005583 |
| 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 | Mef2; AV011172; 5430401D19Rik; 9930028G15Rik |
| Expression | Biased expression in cortex adult (RPKM 49.3), frontal lobe adult (RPKM 37.4) and 11 other tissues See more |
| Orthologs | human all |

Transcript information (Ensembl)

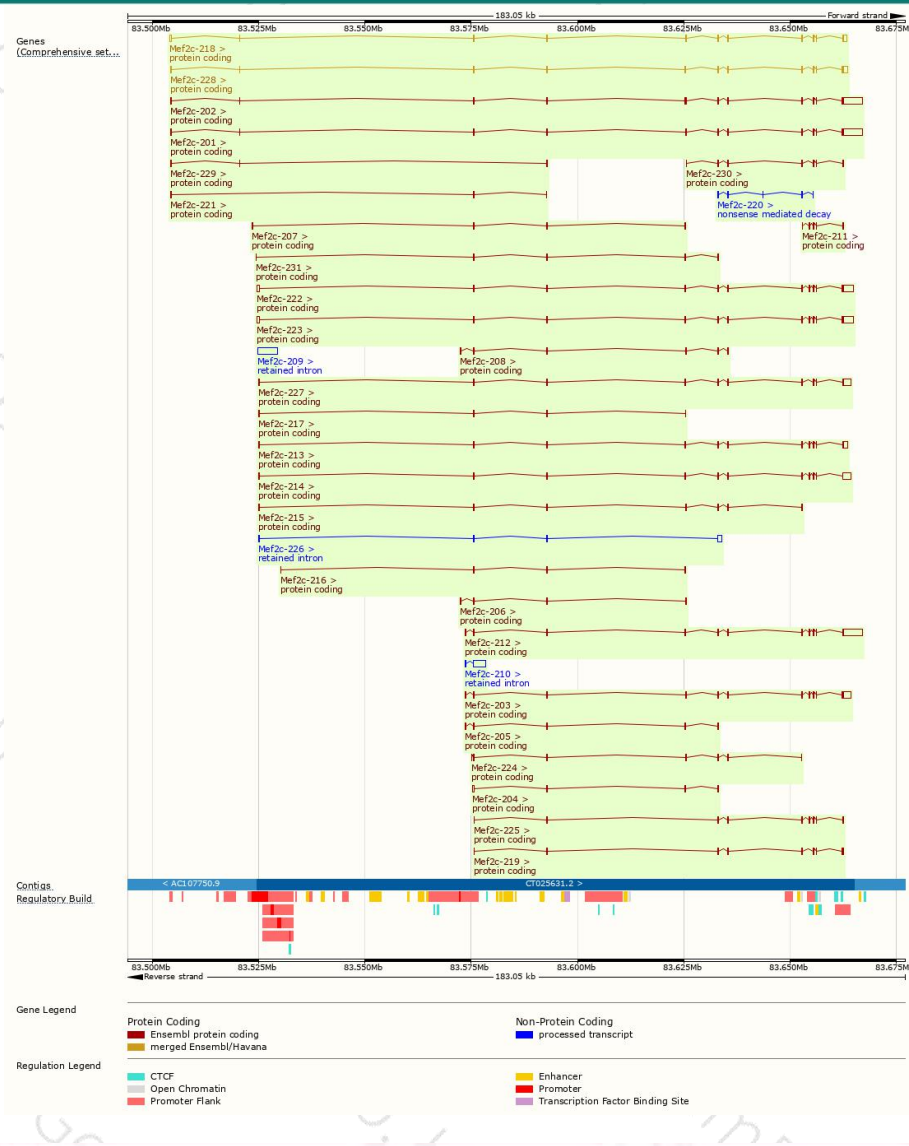
The gene has 31 transcripts,all transcripts are shown below:

| Name | Transcript ID | bp | Protein | Biotype | CCDS | UniProt | Flags |
|-----------|----------------------|------|------------|-------------------------|-----------------------------|---|---------------------------------|
| Mef2c-212 | ENSMUST00000197146.4 | 6088 | 442aa | Protein coding | CCDS84043.2 | Q8CFN5 | TSL:1 GENCODE basic |
| Mef2c-222 | ENSMUST00000199019.4 | 4441 | 474aa | Protein coding | CCDS84042.2 | Q8CFN5 | TSL:5 GENCODE basic |
| Mef2c-223 | ENSMUST00000199105.4 | 4361 | 474aa | Protein coding | CCDS84042.2 | Q8CFN5 | TSL:5 GENCODE basic |
| Mef2c-203 | ENSMUST00000185052.5 | 3556 | 472aa | Protein coding | CCDS84045.2 | Q8CFN5 | TSL:1 GENCODE basic APPRIS ALT1 |
| Mef2c-227 | ENSMUST00000199432.4 | 3498 | 434aa | Protein coding | CCDS84044.2 | A0A0G2JEC2 | TSL:1 GENCODE basic |
| Mef2c-228 | ENSMUST00000199450.4 | 2862 | 466aa | Protein coding | CCDS49320.2 | Q3V1B5 Q8CFN5 | TSL:1 GENCODE basic |
| Mef2c-213 | ENSMUST00000197681.4 | 2753 | 442aa | Protein coding | CCDS84043.2 | Q8CFN5 | TSL:5 GENCODE basic |
| Mef2c-218 | ENSMUST00000198199.4 | 2589 | 432aa | Protein coding | CCDS26664.2 | Q8CFN5 | TSL:1 GENCODE basic APPRIS P3 |
| Mef2c-202 | ENSMUST00000163888.7 | 6277 | 484aa | Protein coding | - | A0A0H2UH28 | TSL:5 GENCODE basic |
| Mef2c-201 | ENSMUST0000005722.13 | 6217 | 464aa | Protein coding | - | A0A0H2UKB6 | TSL:5 GENCODE basic APPRIS ALT1 |
| Mef2c-214 | ENSMUST00000197722.4 | 3517 | 400aa | Protein coding | - | A0A0G2JDQ1 | TSL:5 GENCODE basic |
| Mef2c-219 | ENSMUST00000198217.4 | 1257 | 418aa | Protein coding | - | A0A0G2JDT0 | TSL:5 GENCODE basic |
| Mef2c-225 | ENSMUST00000199210.4 | 1185 | 394aa | Protein coding | - | A0A0G2JE18 | TSL:5 GENCODE basic |
| Mef2c-215 | ENSMUST00000197938.4 | 1060 | 242aa | Protein coding | - | A0A0G2JF17 | CDS 3' incomplete TSL:5 |
| Mef2c-230 | ENSMUST00000200138.4 | 1011 | 249aa | Protein coding | - | A0A0G2JEC3 | CDS 5' incomplete TSL:5 |
| Mef2c-204 | ENSMUST00000195904.4 | 976 | 169aa | Protein coding | - | A0A0G2JFX2 | CDS 3' incomplete TSL:3 |
| Mef2c-208 | ENSMUST00000196730.4 | 913 | 205aa | Protein coding | - | A0A0G2JFX1 | CDS 3' incomplete TSL:5 |
| Mef2c-205 | ENSMUST00000195984.4 | 873 | 194aa | Protein coding | - | A0A0G2JGL3 | CDS 3' incomplete TSL:3 |
| Mef2c-224 | ENSMUST00000199167.4 | 854 | 227aa | Protein coding | - | A0A0G2JES4 | CDS 3' incomplete TSL:5 |
| Mef2c-211 | ENSMUST00000197145.1 | 724 | 152aa | Protein coding | - | A0A0G2JE38 | CDS 5' incomplete TSL:5 |
| Mef2c-231 | ENSMUST00000200394.4 | 702 | 161aa | Protein coding | - | A0A0G2JGK3 | CDS 3' incomplete TSL:5 |
| Mef2c-217 | ENSMUST00000198069.4 | 689 | 108aa | Protein coding | - | A0A0G2JFS4 | CDS 3' incomplete TSL:5 |
| Mef2c-206 | ENSMUST00000196207.4 | 623 | 120aa | Protein coding | - | A0A0G2JFL7 | CDS 3' incomplete TSL:5 |
| Mef2c-207 | ENSMUST00000196493.4 | 609 | 129aa | Protein coding | - | A0A0G2JET3 | CDS 3' incomplete TSL:5 |
| Mef2c-216 | ENSMUST00000198064.4 | 556 | 126aa | Protein coding | - | A0A0G2JDK0 | CDS 3' incomplete TSL:5 |
| Mef2c-221 | ENSMUST00000198916.4 | 363 | 29aa | Protein coding | - | A0A0G2JFM7 | CDS 3' incomplete TSL:3 |
| Mef2c-229 | ENSMUST00000200123.4 | 332 | 23aa | Protein coding | - | A0A0G2JEM8 | CDS 3' incomplete TSL:3 |
| Mef2c-229 | ENSMUST00000200123.4 | 332 | 23aa | Protein coding | - | A0A0G2JEM8 | CDS 3' incomplete TSL:3 |
| Mef2c-220 | ENSMUST00000198360.1 | 546 | 80aa | Nonsense mediated decay | - | A0A0G2JF80 | CDS 5' incomplete TSL:2 |
| Mef2c-209 | ENSMUST00000196832.1 | 4553 | No protein | Retained intron | - | - | TSL:NA |
| Mef2c-210 | ENSMUST00000197022.1 | 3032 | No protein | Retained intron | - | - | TSL:1 |
| Mef2c-226 | ENSMUST00000199262.1 | 1391 | No protein | Retained intron | - | - | TSL:1 |

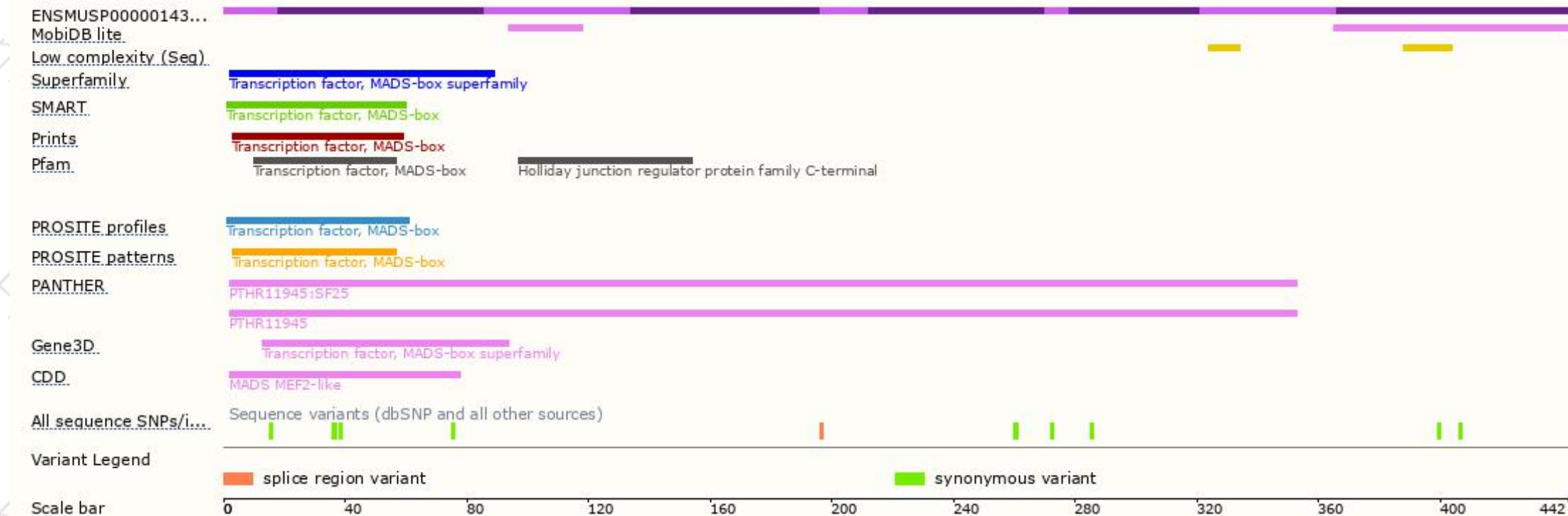
The strategy is based on the design of *Mef2c-212* transcript,The transcription is shown below



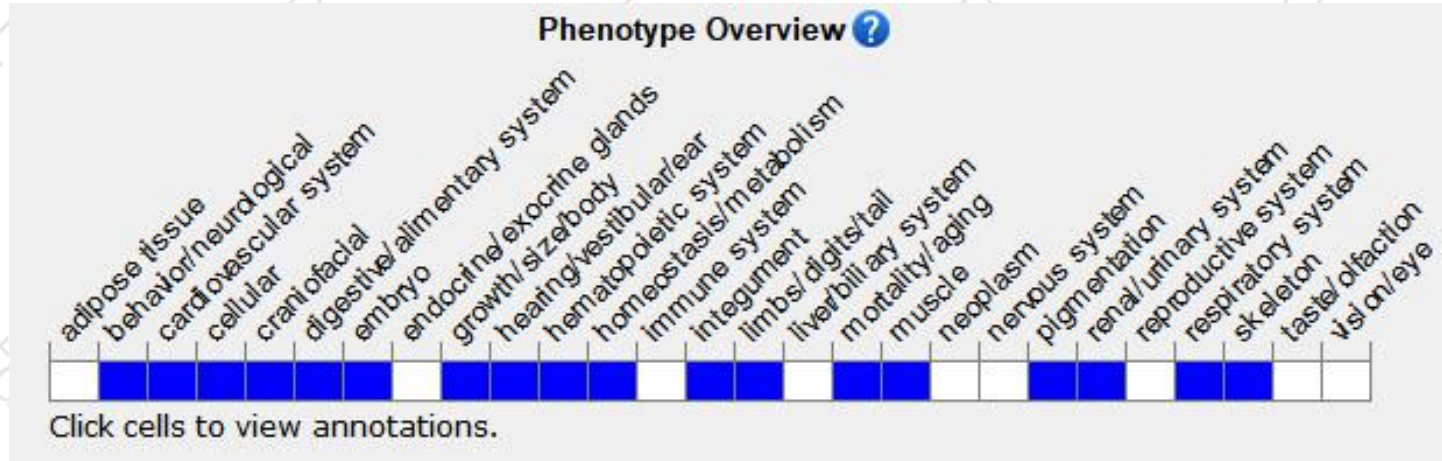
Genomic location distribution



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 disruptions in this gene have cardiovascular abnormalities and die as embryos.

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

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