

Mef2c Cas9-CKO Strategy

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Design Date:

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Project Overview

Project Name

Mef2c

Project type

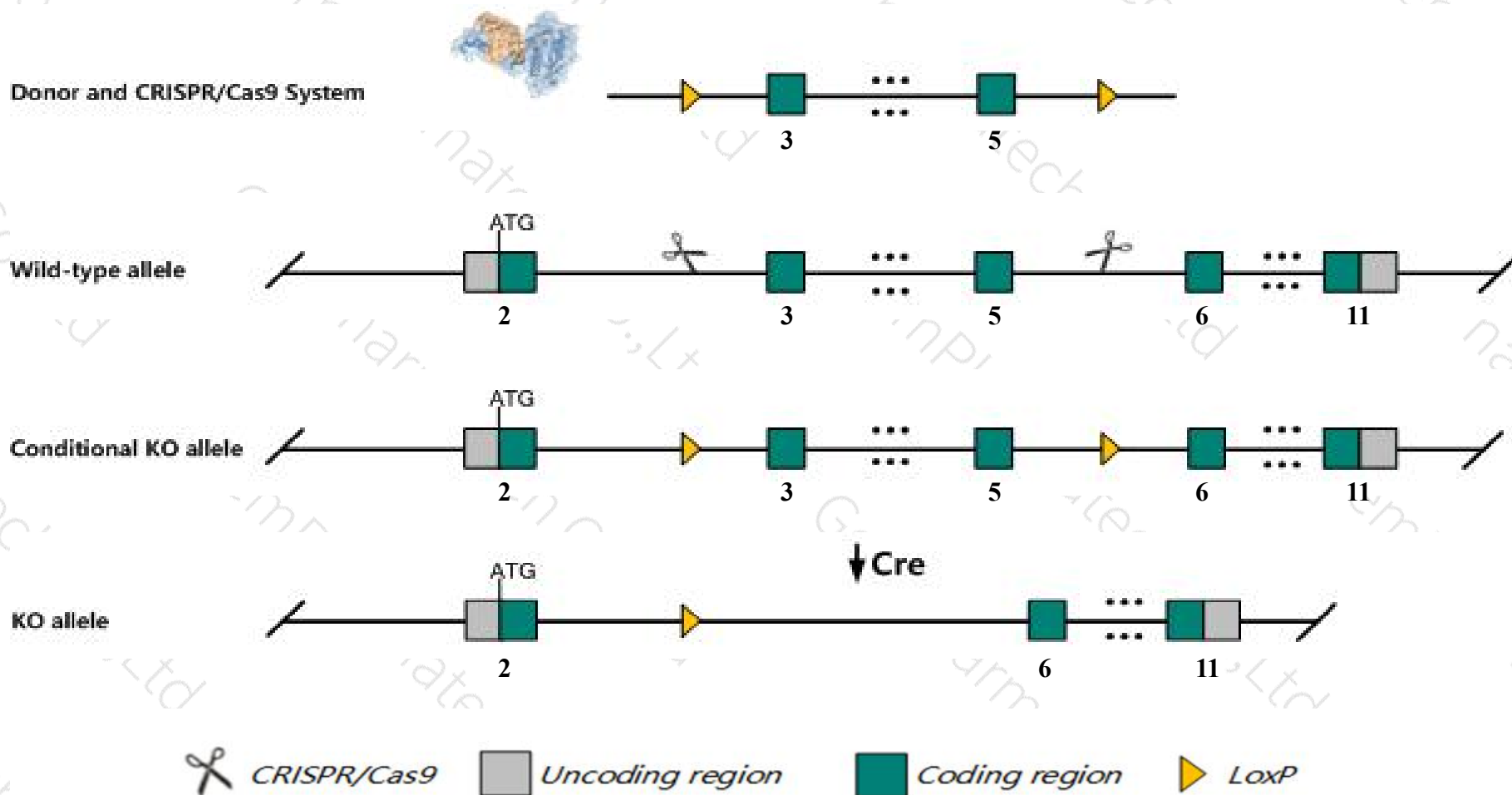
Cas9-CKO

Strain background

C57BL/6JGpt

Conditional Knockout strategy

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



Technical routes

- 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 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.

- 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 loxp insertion on gene transcription, RNA splicing and protein translation cannot be predicted at existing technological 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:ENSMUSG00000005583
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)

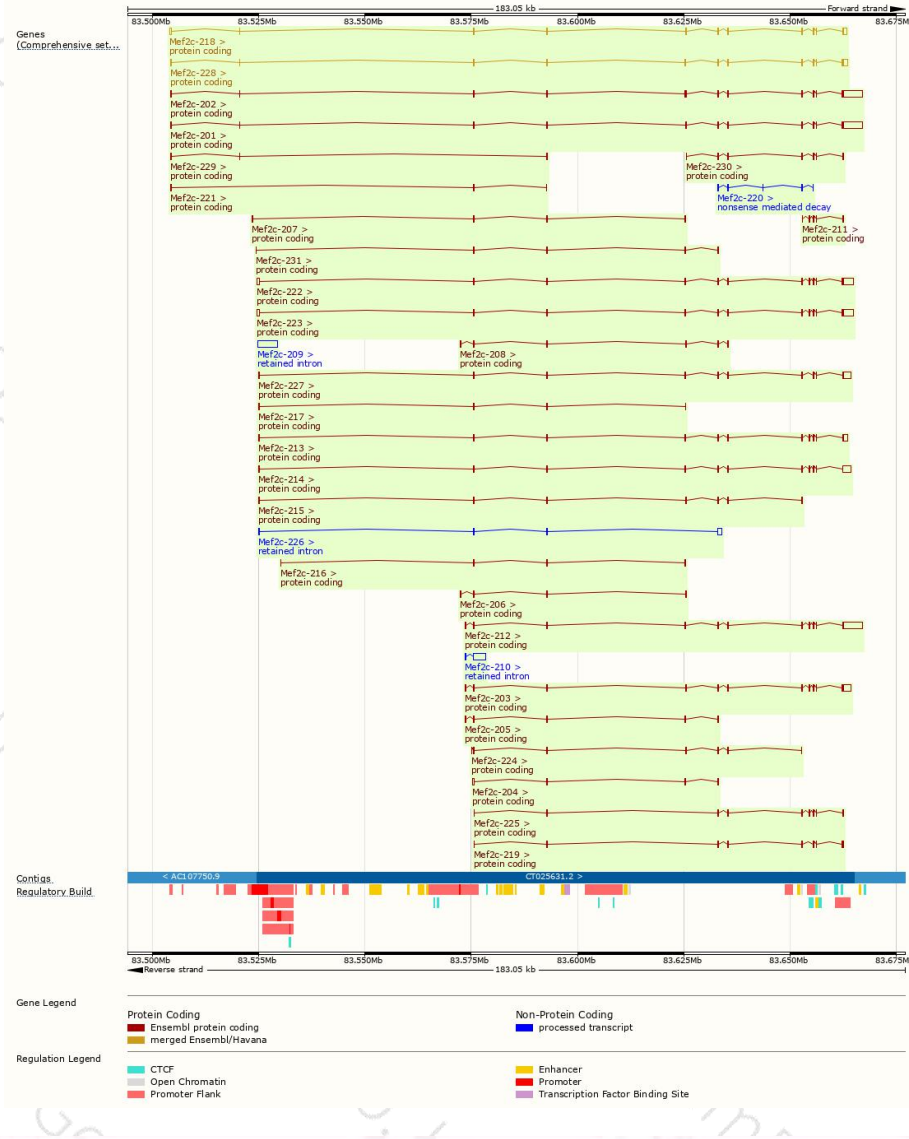
The gene has 31 transcripts,all transcripts are shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Mef2c-212	ENSMUST00000197146.4	6088	442aa	Protein coding	CCDS84043.2	Q8CFN5.2	TSL:1 GENCODE basic
Mef2c-222	ENSMUST00000199019.4	4441	474aa	Protein coding	CCDS84042.2	Q8CFN5.2	TSL:5 GENCODE basic
Mef2c-223	ENSMUST00000199105.4	4361	474aa	Protein coding	CCDS84042.2	Q8CFN5.2	TSL:5 GENCODE basic
Mef2c-203	ENSMUST00000185052.5	3556	472aa	Protein coding	CCDS84045.2	Q8CFN5.2	TSL:1 GENCODE basic APPRIS ALT1
Mef2c-227	ENSMUST00000199432.4	3498	434aa	Protein coding	CCDS84044.2	A0A0G2JEC2.2	TSL:1 GENCODE basic
Mef2c-228	ENSMUST00000199450.4	2862	466aa	Protein coding	CCDS49320.2	Q3V1B5.2 Q8CFN5.2	TSL:1 GENCODE basic
Mef2c-213	ENSMUST00000197681.4	2753	442aa	Protein coding	CCDS84043.2	Q8CFN5.2	TSL:5 GENCODE basic
Mef2c-218	ENSMUST00000198199.4	2589	432aa	Protein coding	CCDS26664.2	Q8CFN5.2	TSL:1 GENCODE basic APPRIS P3
Mef2c-202	ENSMUST00000163888.7	6277	484aa	Protein coding	-	A0A0H2UH28.2	TSL:5 GENCODE basic
Mef2c-201	ENSMUST0000005722.13	6217	464aa	Protein coding	-	A0A0H2UKB6.2	TSL:5 GENCODE basic APPRIS ALT1
Mef2c-214	ENSMUST00000197722.4	3517	400aa	Protein coding	-	A0A0G2JDQ1.2	TSL:5 GENCODE basic
Mef2c-219	ENSMUST00000198217.4	1257	418aa	Protein coding	-	A0A0G2JDT0.2	TSL:5 GENCODE basic
Mef2c-225	ENSMUST00000199210.4	1185	394aa	Protein coding	-	A0A0G2JE18.2	TSL:5 GENCODE basic
Mef2c-215	ENSMUST00000197938.4	1060	242aa	Protein coding	-	A0A0G2JF17.2	CDS 3' incomplete TSL:5
Mef2c-230	ENSMUST00000200138.4	1011	249aa	Protein coding	-	A0A0G2JEC3.2	CDS 5' incomplete TSL:5
Mef2c-204	ENSMUST00000195904.4	976	169aa	Protein coding	-	A0A0G2JFX2.2	CDS 3' incomplete TSL:3
Mef2c-208	ENSMUST00000196730.4	913	205aa	Protein coding	-	A0A0G2JFX1.2	CDS 3' incomplete TSL:5
Mef2c-205	ENSMUST00000195984.4	873	194aa	Protein coding	-	A0A0G2JGL3.2	CDS 3' incomplete TSL:3
Mef2c-224	ENSMUST00000199167.4	854	227aa	Protein coding	-	A0A0G2JES4.2	CDS 3' incomplete TSL:5
Mef2c-211	ENSMUST00000197145.1	724	152aa	Protein coding	-	A0A0G2JE38.2	CDS 5' incomplete TSL:5
Mef2c-231	ENSMUST00000200394.4	702	161aa	Protein coding	-	A0A0G2JGK3.2	CDS 3' incomplete TSL:5
Mef2c-217	ENSMUST00000198069.4	689	108aa	Protein coding	-	A0A0G2JFS4.2	CDS 3' incomplete TSL:5
Mef2c-206	ENSMUST00000196207.4	623	120aa	Protein coding	-	A0A0G2JFL7.2	CDS 3' incomplete TSL:5
Mef2c-207	ENSMUST00000196493.4	609	129aa	Protein coding	-	A0A0G2JET3.2	CDS 3' incomplete TSL:5
Mef2c-216	ENSMUST00000198064.4	556	126aa	Protein coding	-	A0A0G2JDK0.2	CDS 3' incomplete TSL:5
Mef2c-221	ENSMUST00000198916.4	363	29aa	Protein coding	-	A0A0G2JFM7.2	CDS 3' incomplete TSL:3
Mef2c-229	ENSMUST00000200123.4	332	23aa	Protein coding	-	A0A0G2JEM8.2	CDS 3' incomplete TSL:3
Mef2c-229	ENSMUST00000200123.4	332	23aa	Protein coding	-	A0A0G2JFM8.2	CDS 3' incomplete TSL:3
Mef2c-220	ENSMUST00000198360.1	546	80aa	Nonsense mediated decay	-	A0A0G2JF80.2	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

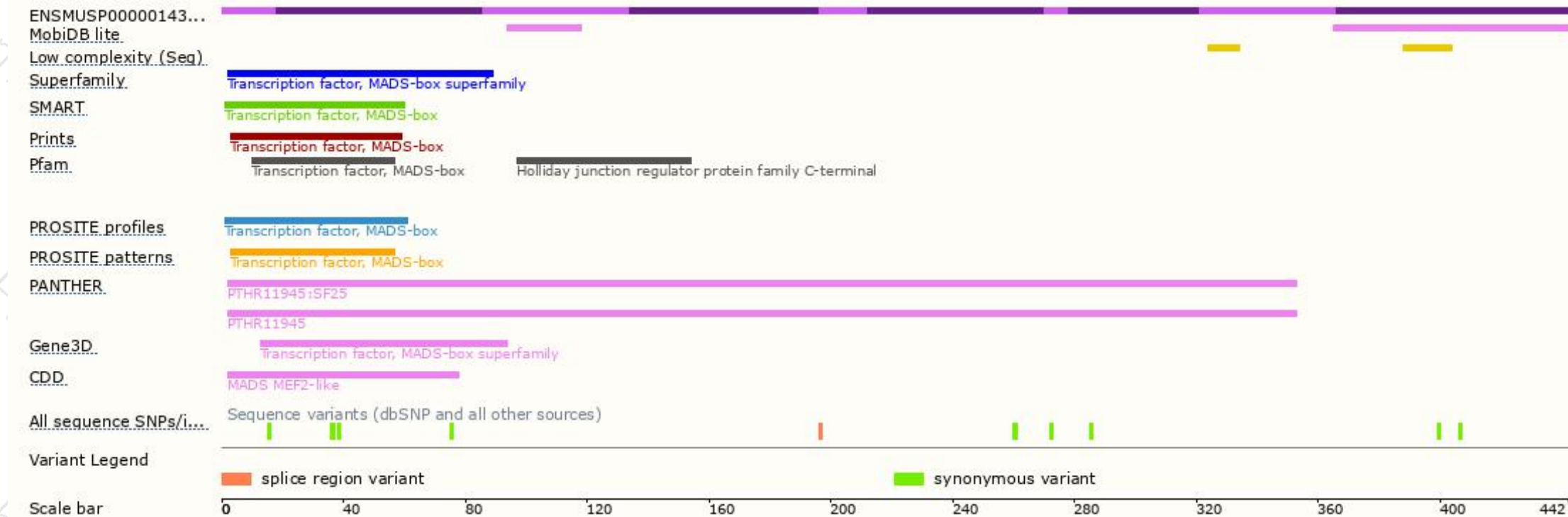
The strategy is based on the design of *Mef2c-212* transcript,The transcription is shown below



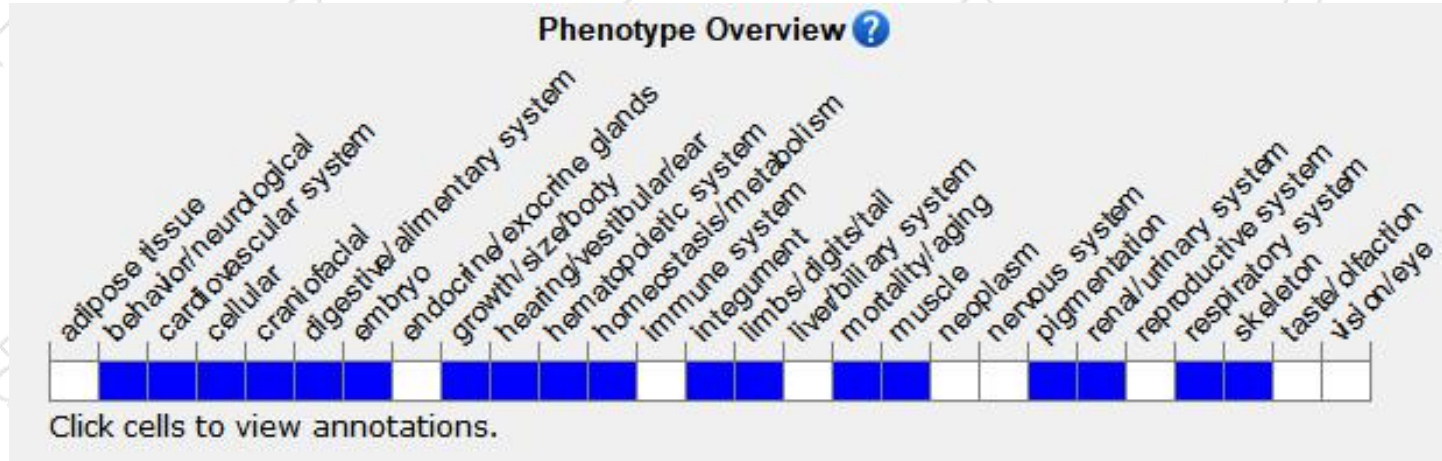
Genomic location distribution



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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