Mef2a Cas9-KO Strategy

Designer: Huan Fan

Reviewer: Huan Wang

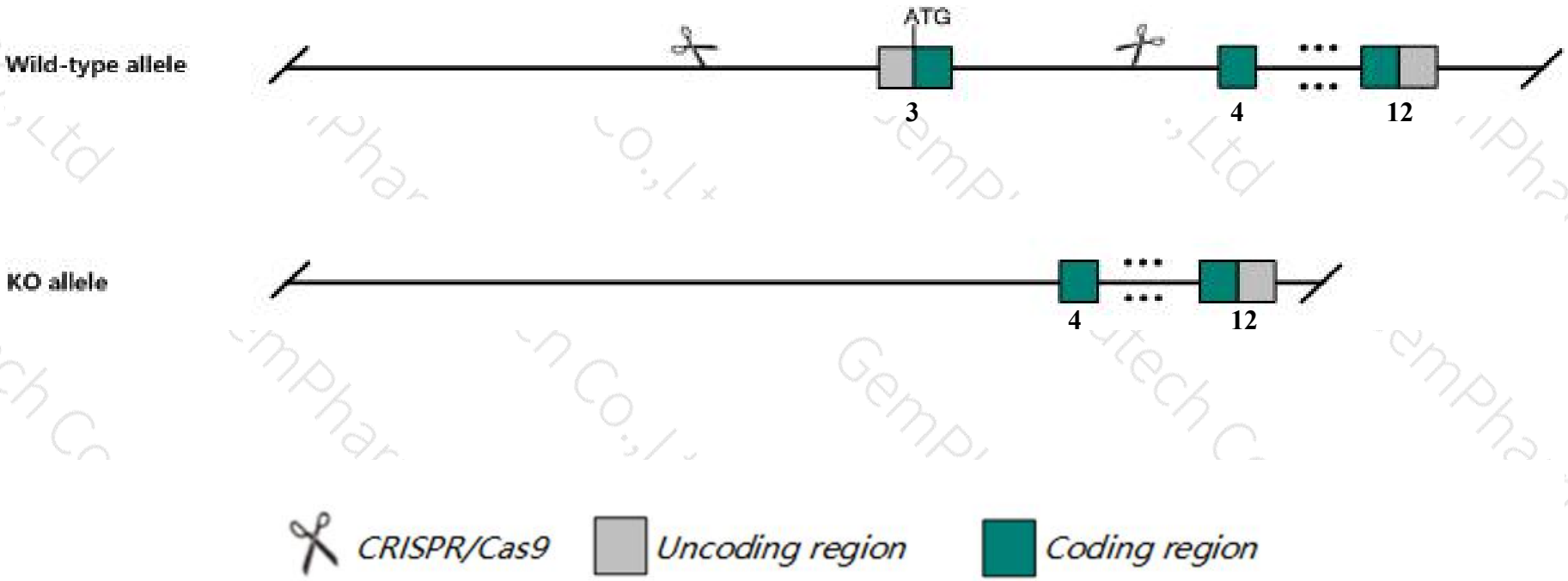
Design Date: 2019-12-11

Project Overview

Project Name	***Mef2a***
Project type	**Cas9-KO**
Strain background	**C57BL/6JGpt**

Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *Mef2a* gene. The schematic diagram is as follows:



Technical routes

➢ The *Mef2a* gene has 12 transcripts. According to the structure of *Mef2a* gene, exon3 of *Mef2a-208* (ENSMUST00000156690.7) transcript is recommended as the knockout region.The region contains start codon ATG. Knock out the region will result in disruption of protein function.

➢ In this project we use CRISPR/Cas9 technology to modify *Mef2a* gene. The brief process is as follows: CRISPR/Cas9 system

Notice

- According to the existing MGI data,Inactivation of this gene results in cardiac sudden death. Mice dying in the early postnatal period exhibit ventricular dilation, while mice dying in adulthood show a reduced number of mitochondria in the heart.
- Transcript *Mef2a-210* may not be affected.
- The *Mef2a* 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）

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Mef2a myocyte enhancer factor 2A [Mus musculus (house mouse)]

Gene ID: 17258, updated on 31-Jan-2019

Summary

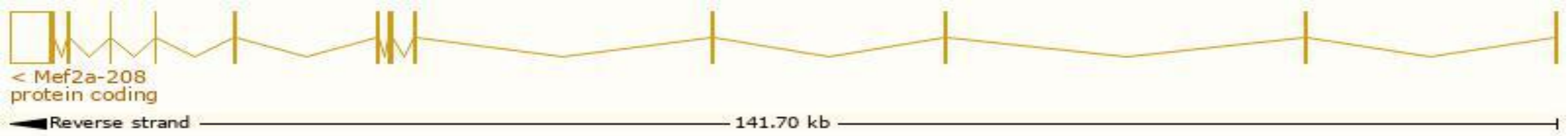
Official Symbol	Mef2a provided by MGI
Official Full Name	myocyte enhancer factor 2A provided byMGI
Primary source	MGI:MGI:99532
See related	Ensembl:ENSMUSG00000030557
Gene type	protein coding
RefSeq status	VALIDATED
Organism	Mus musculus
Lineage	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Myomorpha; Muroidea; Muridae; Murinae; Mus; Mus
Also known as	A430079H05Rik
Expression	Ubiquitous expression in heart adult (RPKM 19.7), frontal lobe adult (RPKM 17.9) and 28 other tissuesSee more
Orthologs	human all

Transcript information（Ensembl）

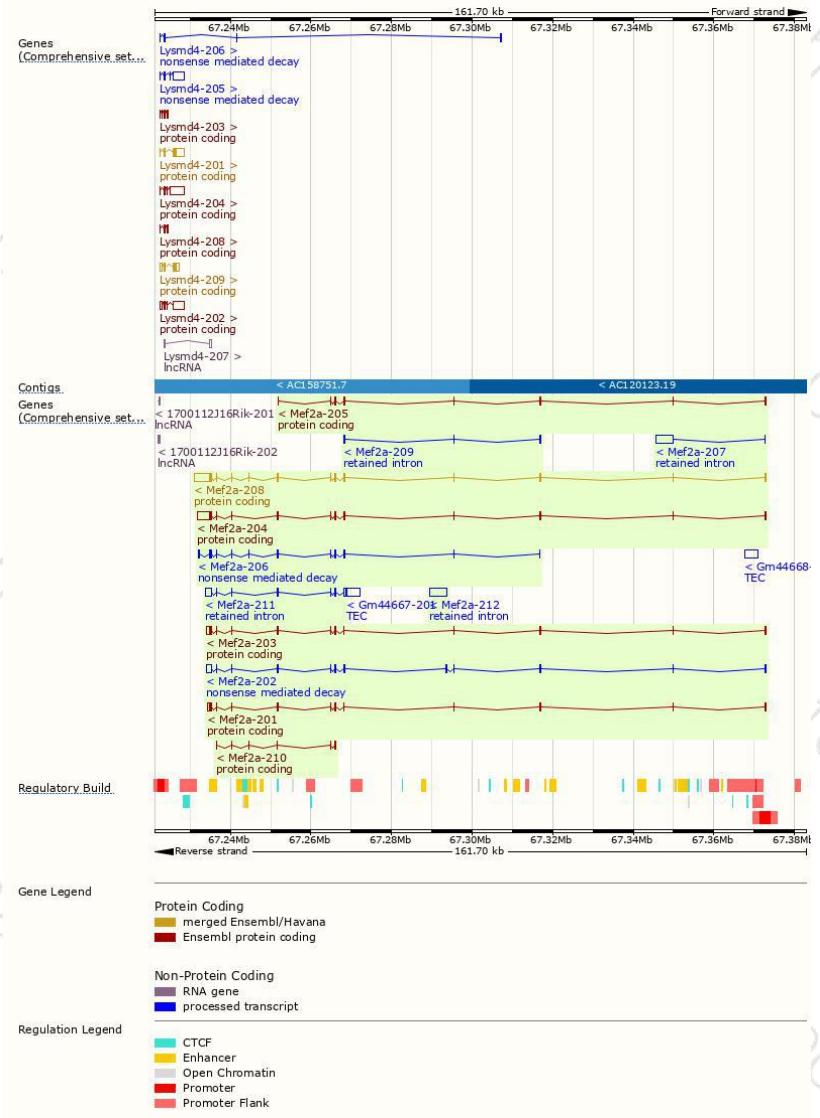
The gene has 12 transcripts,all transcripts are shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Mef2a-208	ENSMUST00000156690.7	5538	498aa	Protein coding	CCDS39981	Q60929	TSL:1 GENCODE basic
Mef2a-204	ENSMUST00000107476.7	4759	490aa	Protein coding	CCDS71980	Q60929	TSL:1 GENCODE basic
Mef2a-203	ENSMUST00000076325.11	2664	492aa	Protein coding	CCDS71979	Q60929	TSL:1 GENCODE basic APPRIS P1
Mef2a-201	ENSMUST00000032776.14	2476	492aa	Protein coding	CCDS71979	Q60929	TSL:1 GENCODE basic APPRIS P1
Mef2a-205	ENSMUST00000133074.1	1062	235aa	Protein coding	-	D3Z6M5	CDS 3' incomplete TSL:1
Mef2a-210	ENSMUST00000207715.1	631	210aa	Protein coding	-	A0A140LIL7	5' and 3' truncations in transcript evidence prevent annotation of the start and the end of the CDS. CDS 5' and 3' incomplete TSL:5
Mef2a-206	ENSMUST00000135493.7	1828	498aa	Nonsense mediated decay	CCDS39981	Q60929	TSL:1
Mef2a-202	ENSMUST00000072460.12	2677	100aa	Nonsense mediated decay	-	S4R2H4	TSL:1
Mef2a-207	ENSMUST00000144057.2	4445	No protein	Retained intron	-	-	TSL:2
Mef2a-212	ENSMUST00000208823.1	4259	No protein	Retained intron	-	-	TSL:NA
Mef2a-211	ENSMUST00000207794.1	2766	No protein	Retained intron	-	-	TSL:1
Mef2a-209	ENSMUST00000207486.1	625	No protein	Retained intron	-	-	TSL:2

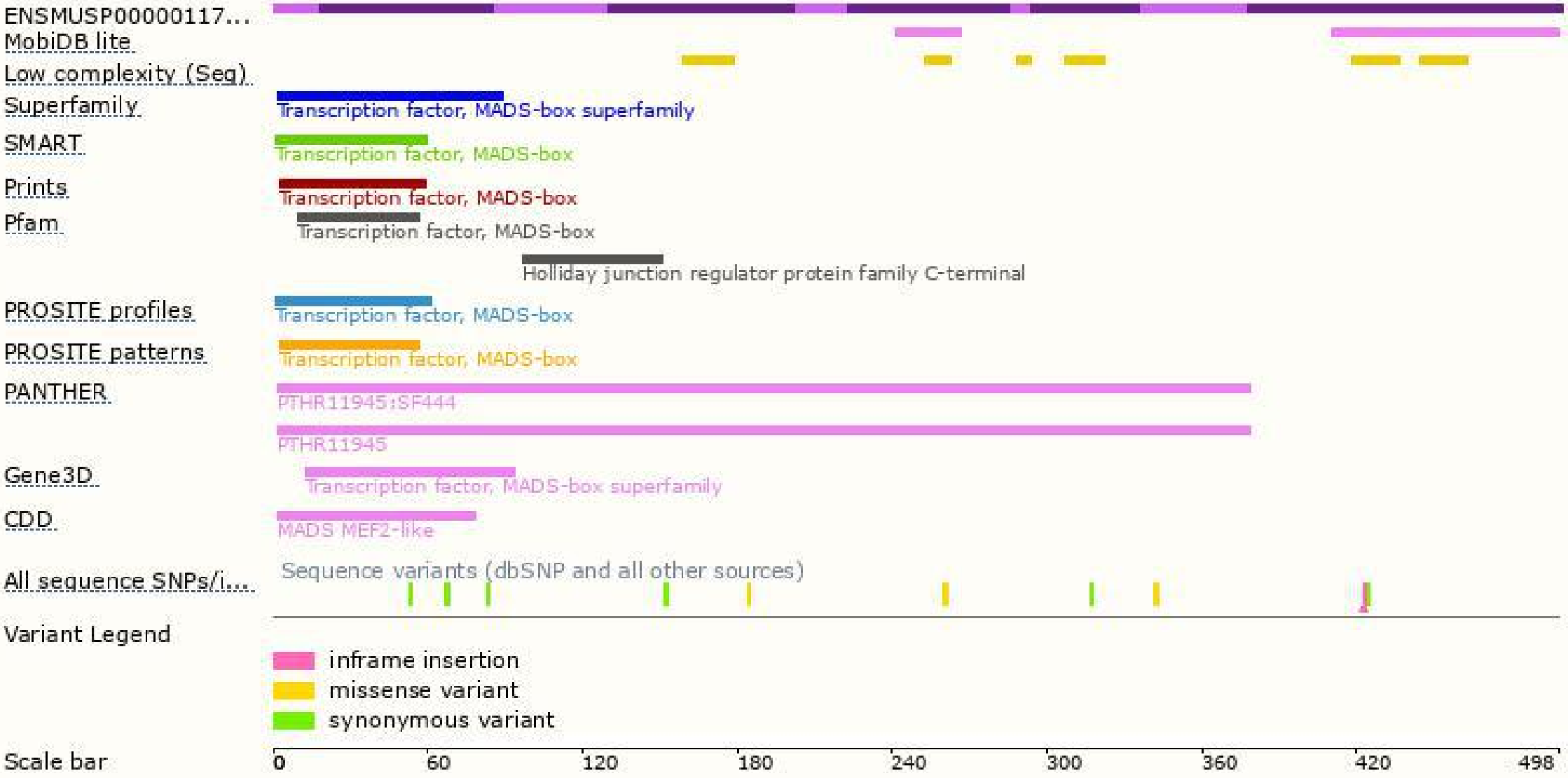
The strategy is based on the design of *Mef2a-208* transcript,The transcription is shown below



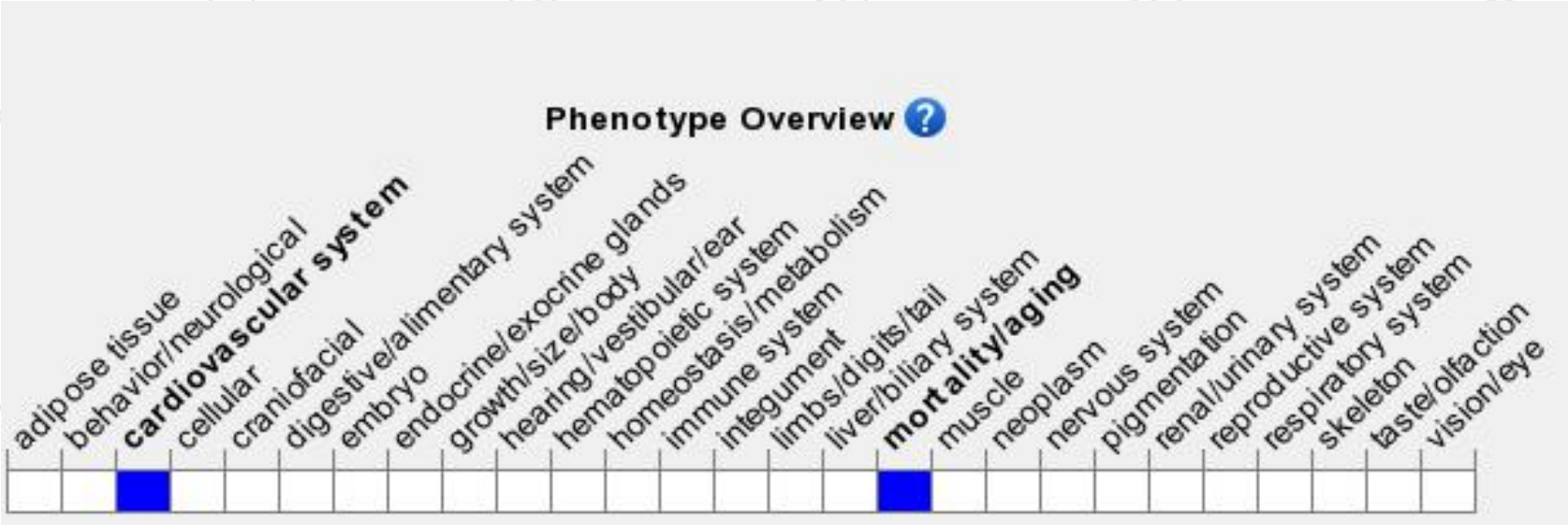
Genomic location distribution



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/).

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

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