

Matr3 Cas9-KO Strategy

Designer:

Huan Wang

Reviewer:

Huan Fan

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Project Overview

Project Name

Matr3

Project type

Cas9-KO

Strain background

C57BL/6JGpt

Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *Matr3* gene. The schematic diagram is as follows:



- The *Matr3* gene has 18 transcripts. According to the structure of *Matr3* gene, exon2 of *Matr3-201* (ENSMUST00000166793.9) 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 *Matr3* gene. The brief process is as follows: CRISPR/Cas9 system

- According to the existing MGI data, Mice homozygous for a gene-trapped allele are early embryonic lethal. Heterozygotes show congenital heart defects including abnormal heart apex morphology, subaortic ventricular septal defects, double-outlet right ventricle, bicuspid aortic valve, aorta coarctation, and patent ductus arteriosus.
- The KO region contains functional region of the *Snhg4* gene. Knockout the region will affect the function of *Snhg4* gene.
- Transcript *Matr3-207,210,214,215* may not be affected.
- The *Matr3* gene is located on the Chr18. 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)

Matr3 matrin 3 [Mus musculus (house mouse)]

Gene ID: 17184, updated on 7-Apr-2019

Summary



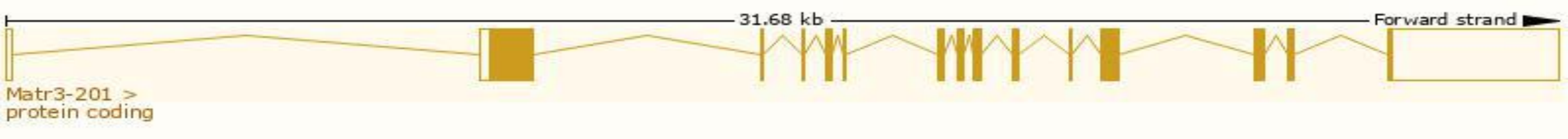
Official Symbol	Matr3 provided by MGI
Official Full Name	matrin 3 provided by MGI
Primary source	MGI:MGI:1298379
See related	Ensembl:ENSMUSG00000037236
Gene type	protein coding
RefSeq status	VALIDATED
Organism	Mus musculus
Lineage	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Myomorpha; Muroidea; Muridae; Murinae; Mus; Mus
Also known as	1110061A14Rik, 2810017I02Rik, AI841759, AW555618, D030046F20Rik, mKIAA0723
Expression	Broad expression in CNS E11.5 (RPKM 68.8), CNS E18 (RPKM 62.6) and 19 other tissues See more
Orthologs	human all

Transcript information (Ensembl)

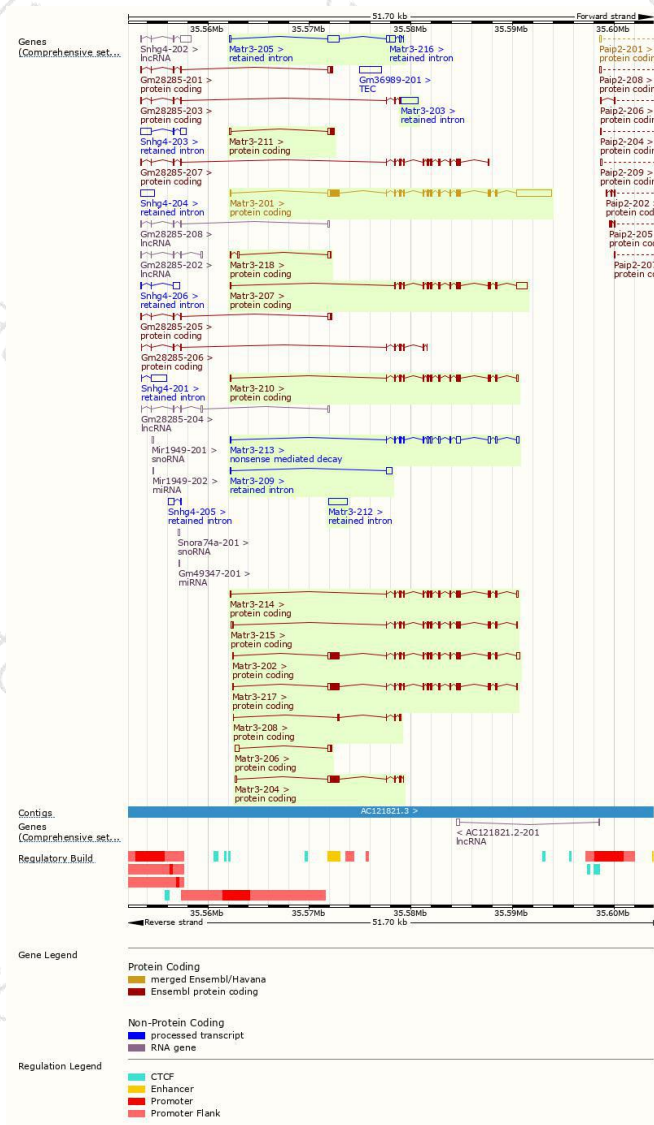
The gene has 18 transcripts,all transcripts are shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Matr3-201	ENSMUST00000166793.9	6262	846aa	Protein coding	CCDS29142	Q5BL18 Q8K310	TSL:1 GENCODE basic APPRIS P1
Matr3-202	ENSMUST00000235199.1	3107	846aa	Protein coding	CCDS29142	Q5BL18	GENCODE basic APPRIS P1
Matr3-217	ENSMUST00000237744.1	2845	846aa	Protein coding	CCDS29142	Q5BL18	GENCODE basic APPRIS P1
Matr3-207	ENSMUST00000235960.1	2638	508aa	Protein coding	-	A0A087WSP7	GENCODE basic
Matr3-215	ENSMUST00000237365.1	1951	558aa	Protein coding	-	A0A087WQZ1	GENCODE basic
Matr3-214	ENSMUST00000237061.1	1854	508aa	Protein coding	-	A0A087WSP7	GENCODE basic
Matr3-210	ENSMUST00000236507.1	1846	508aa	Protein coding	-	A0A087WSP7	GENCODE basic
Matr3-204	ENSMUST00000235581.1	1504	385aa	Protein coding	-	A0A087WSU2	CDS 3' incomplete
Matr3-206	ENSMUST00000235851.1	779	60aa	Protein coding	-	A0A087WNP3	CDS 3' incomplete
Matr3-211	ENSMUST00000236860.1	762	155aa	Protein coding	-	A0A087WQD6	CDS 3' incomplete
Matr3-218	ENSMUST00000237780.1	555	33aa	Protein coding	-	A0A087WQP4	CDS 3' incomplete
Matr3-208	ENSMUST00000236276.1	412	121aa	Protein coding	-	A0A087WNW7	CDS 3' incomplete
Matr3-213	ENSMUST00000237018.1	1888	91aa	Nonsense mediated decay	-	A0A087WSF8	
Matr3-212	ENSMUST00000237002.1	1781	No protein	Retained intron	-	-	
Matr3-203	ENSMUST00000235551.1	1700	No protein	Retained intron	-	-	
Matr3-205	ENSMUST00000235769.1	1567	No protein	Retained intron	-	-	
Matr3-216	ENSMUST00000237622.1	681	No protein	Retained intron	-	-	
Matr3-209	ENSMUST00000236327.1	625	No protein	Retained intron	-	-	

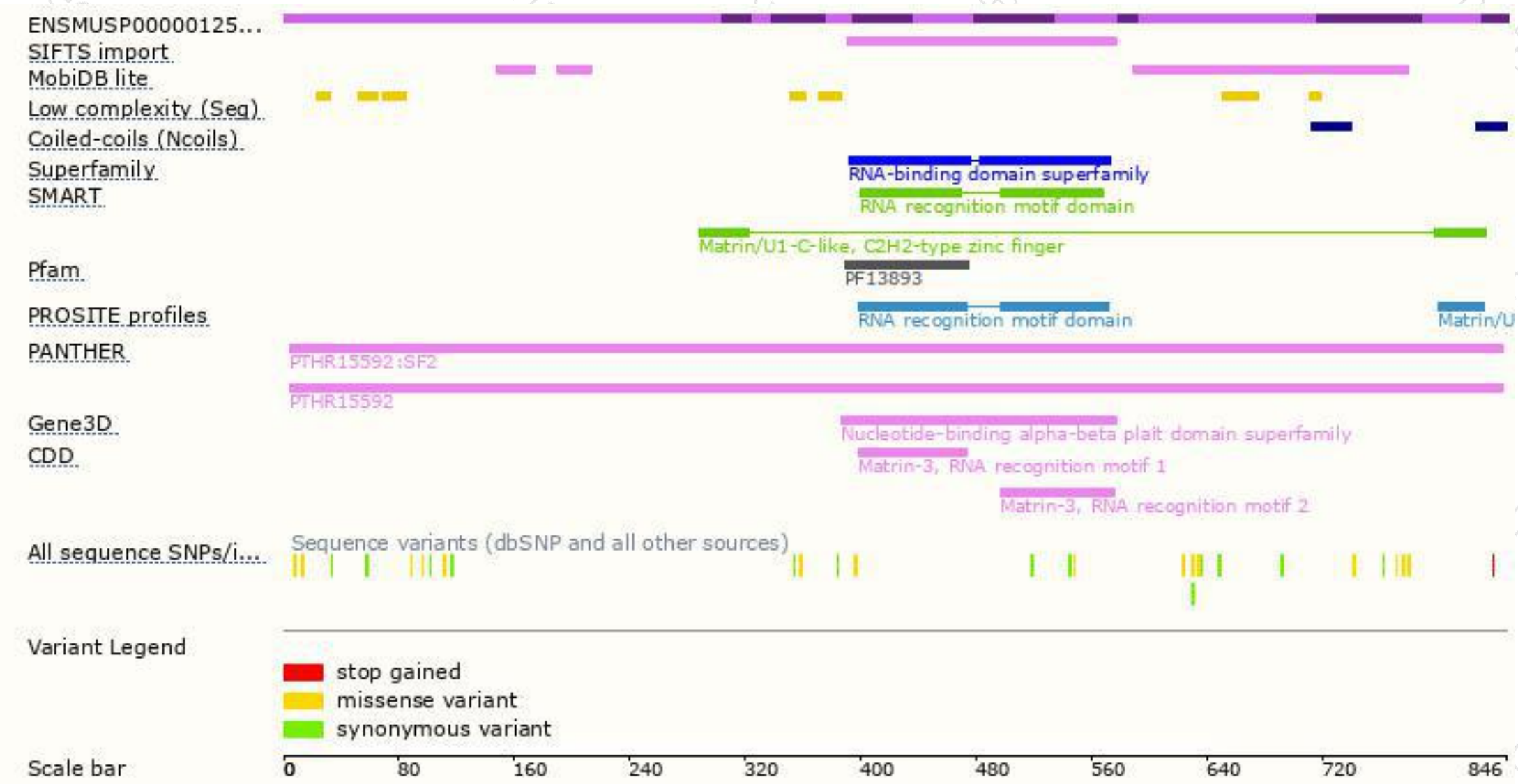
The strategy is based on the design of *Matr3-201* transcript,The transcription is shown below



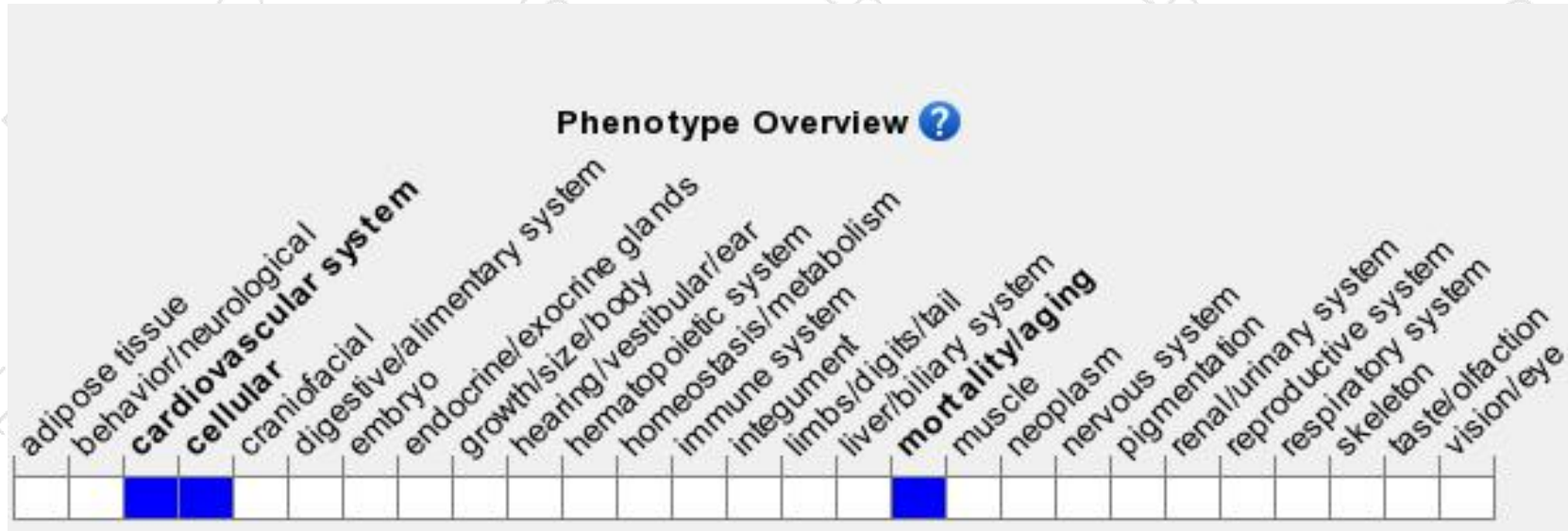
Genomic location distribution



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 a gene-trapped allele are early embryonic lethal.

Heterozygotes show congenital heart defects including abnormal heart apex morphology, subaortic ventricular septal defects, double-outlet right ventricle, bicuspid aortic valve, aorta coarctation, and patent ductus arteriosus.

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

Tel: 400-9660890

