

Morf411 Cas9-CKO Strategy

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Project Overview



Project Name

Morf4l1

Project type

Cas9-CKO

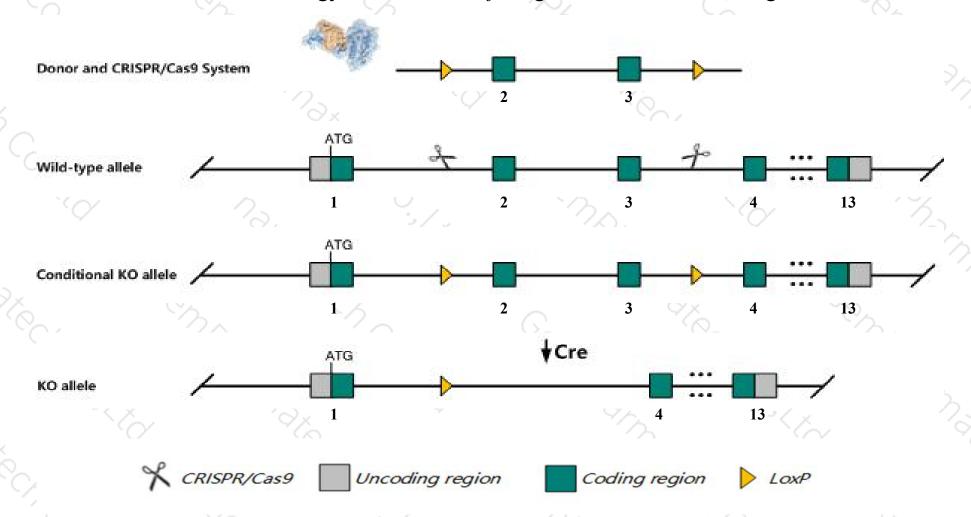
Strain background

C57BL/6JGpt

Conditional Knockout strategy



This model will use CRISPR/Cas9 technology to edit the *Morf4l1* gene. The schematic diagram is as follows:



Technical routes



- The *Morf4l1* gene has 12 transcripts. According to the structure of *Morf4l1* gene, exon2-exon3 of *Morf4l1-201* (ENSMUST00000085248.11) transcript is recommended as the knockout region. The region contains 115bp coding sequence. Knock out the region will result in disruption of protein function.
- In this project we use CRISPR/Cas9 technology to modify *Morf4l1* 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.

Notice



- ➤ According to the existing MGI data,homozygous null mice display perinatal lethality, cardiac hypertrophy, reduced alveolar space, decreased cell proliferation, congestion of the liver, lung, and spleen, skin edema, and thin skin.
- The *Morf4l1* gene is located on the Chr9. 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)



Morf4I1 mortality factor 4 like 1 [Mus musculus (house mouse)]

Gene ID: 21761, updated on 13-Mar-2020

Summary

☆ ?

Official Symbol Morf4I1 provided by MGI

Official Full Name mortality factor 4 like 1 provided by MGI

Primary source MGI:MGI:1096551

See related Ensembl:ENSMUSG00000062270

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 MORFRG15, MRG15, TEG-189, Tex189, mKIAA4002

Expression Broad expression in testis adult (RPKM 222.1), CNS E11.5 (RPKM 158.1) and 24 other tissuesSee more

Orthologs <u>human all</u>

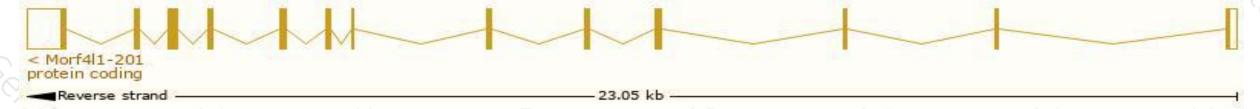
Transcript information (Ensembl)



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

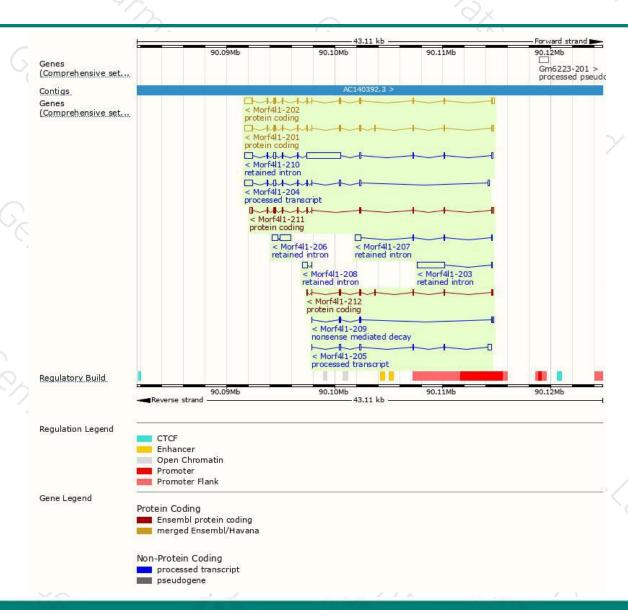
Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Morf4I1-201	ENSMUST00000085248.11	1882	362aa	Protein coding	CCDS23400	P60762	TSL:1 GENCODE basic APPRIS is a system to annotate alternatively spliced transcripts based on a range of computational methods to identify the most functionally important transcript(s) of a gene. APPRIS P3
Morf4I1-202	ENSMUST00000169860.7	1824	<u>323aa</u>	Protein coding	CCDS52885	P60762 Q569V4	TSL:1 GENCODE basic APPRIS is a system to annotate alternatively spliced transcripts based on a range of computational methods to identify the most functionally important transcript(s) of a gene. APPRIS ALT
Morf4I1-211	ENSMUST00000191189.6	1223	296aa	Protein coding	-	A0A087WQB0	TSL:5 GENCODE basic
Morf4I1-212	ENSMUST00000191353.1	600	<u>172aa</u>	Protein coding		A0A087WQ34	CDS 3' incomplete TSL:3
Morf4I1-209	ENSMUST00000190345.1	335	<u>50aa</u>	Nonsense mediated decay		A0A087WSL1	TSL:5
Morf4I1-204	ENSMUST00000187771.7	1540	No protein	Processed transcript	-		TSL:5
Morf4I1-205	ENSMUST00000188905.6	603	No protein	Processed transcript	-	-	TSL:5
Morf4I1-210	ENSMUST00000190377.6	4640	No protein	Retained intron	-	-	TSL:1
Morf4I1-203	ENSMUST00000185433.1	2584	No protein	Retained intron		-	TSL:1
Morf4I1-206	ENSMUST00000189089.1	1536	No protein	Retained intron			TSL:5
Morf4I1-207	ENSMUST00000189241.1	666	No protein	Retained intron	-	-	TSL:1
Morf4I1-208	ENSMUST00000189420.1	504	No protein	Retained intron	2	120	TSL:2

The strategy is based on the design of *Morf4l1-201* transcript, the transcription is shown below:



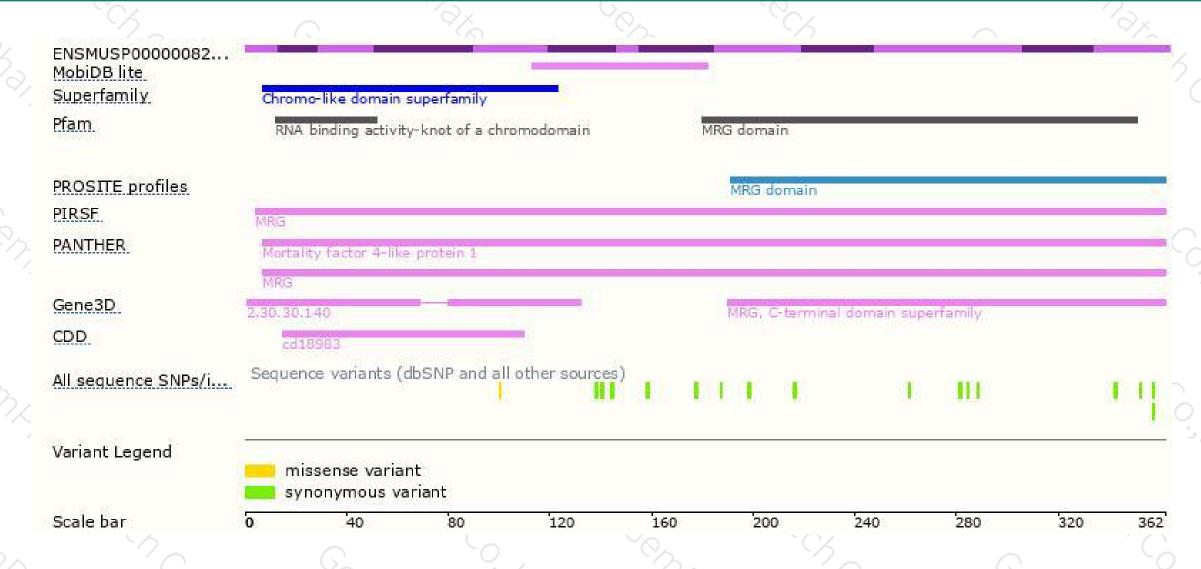
Genomic location distribution





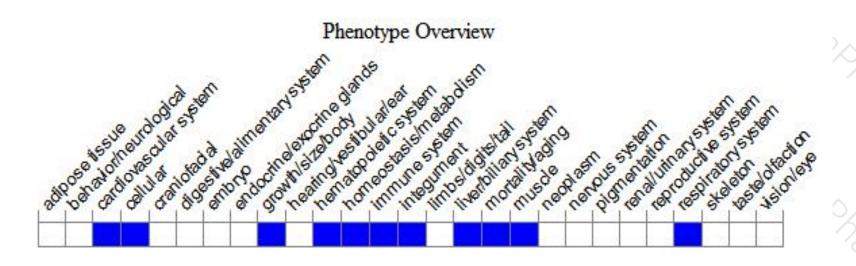
Protein domain





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, homozygous null mice display perinatal lethality, cardiac hypertrophy, reduced alveolar space, decreased cell proliferation, congestion of the liver, lung, and spleen, skin edema, and thin skin.



If you have any questions, you are welcome to inquire. Tel: 400-9660890





