Morf4l1 Cas9-KO Strategy

Designer: Huan Wang

Reviewer: Huan Fan

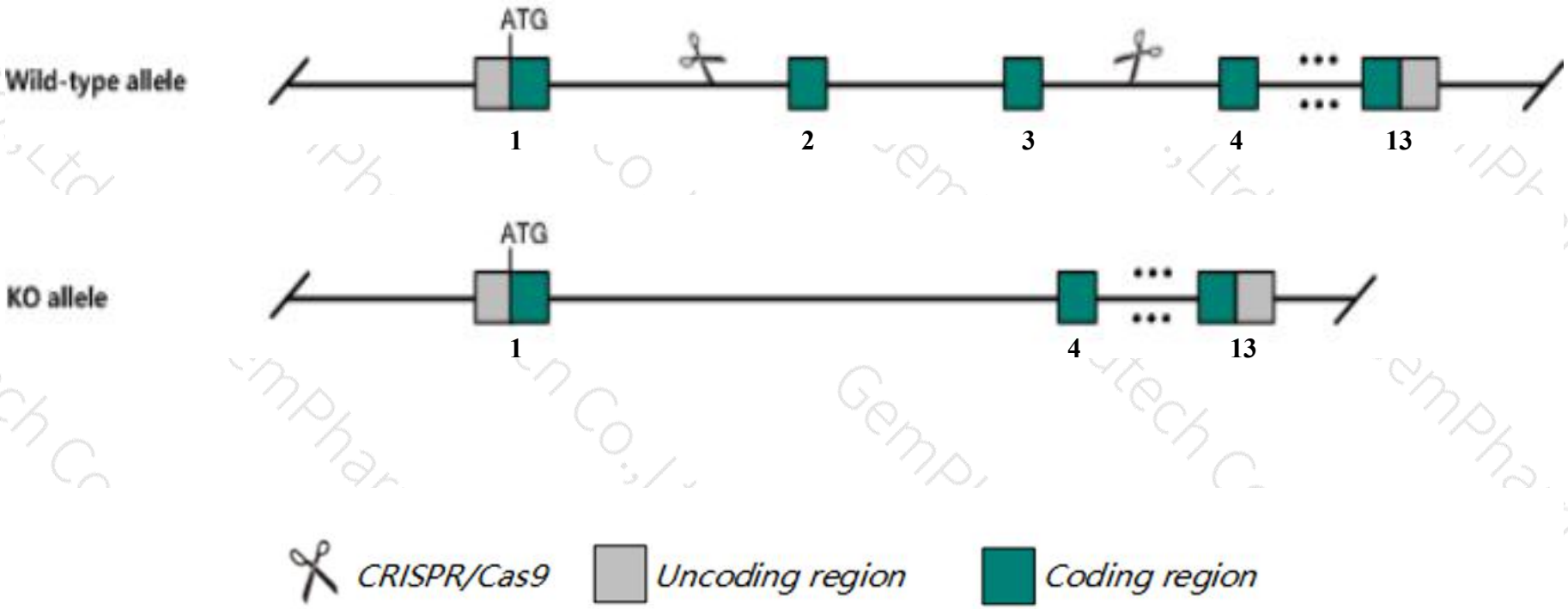
Design Date: 2020-5-26

Project Overview

Project Name	***Morf4l1***
Project type	**Cas9-KO**
Strain background	**C57BL/6JGpt**

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 syste

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 the gene knockout on gene transcription, RNA splicing and protein translation cannot be predicted at the existing technology level.

Gene information（NCBI）

集萃药康 GemPharmatech

Morf4l1 mortality factor 4 like 1 [Mus musculus (house mouse)]

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

Summary

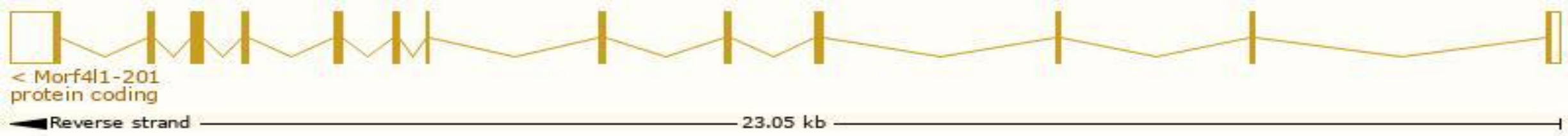
Official Symbol	Morf4l1 provided by MGI
Official Full Name	mortality factor 4 like 1 provided byMGI
Primary source	MGI:MGI:1096551
See related	Ensembl:ENSMUSG00000062270
Gene type	protein coding
RefSeq status	VALIDATED
Organism	Mus musculus
Lineage	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; 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	human all

Transcript information（Ensembl）

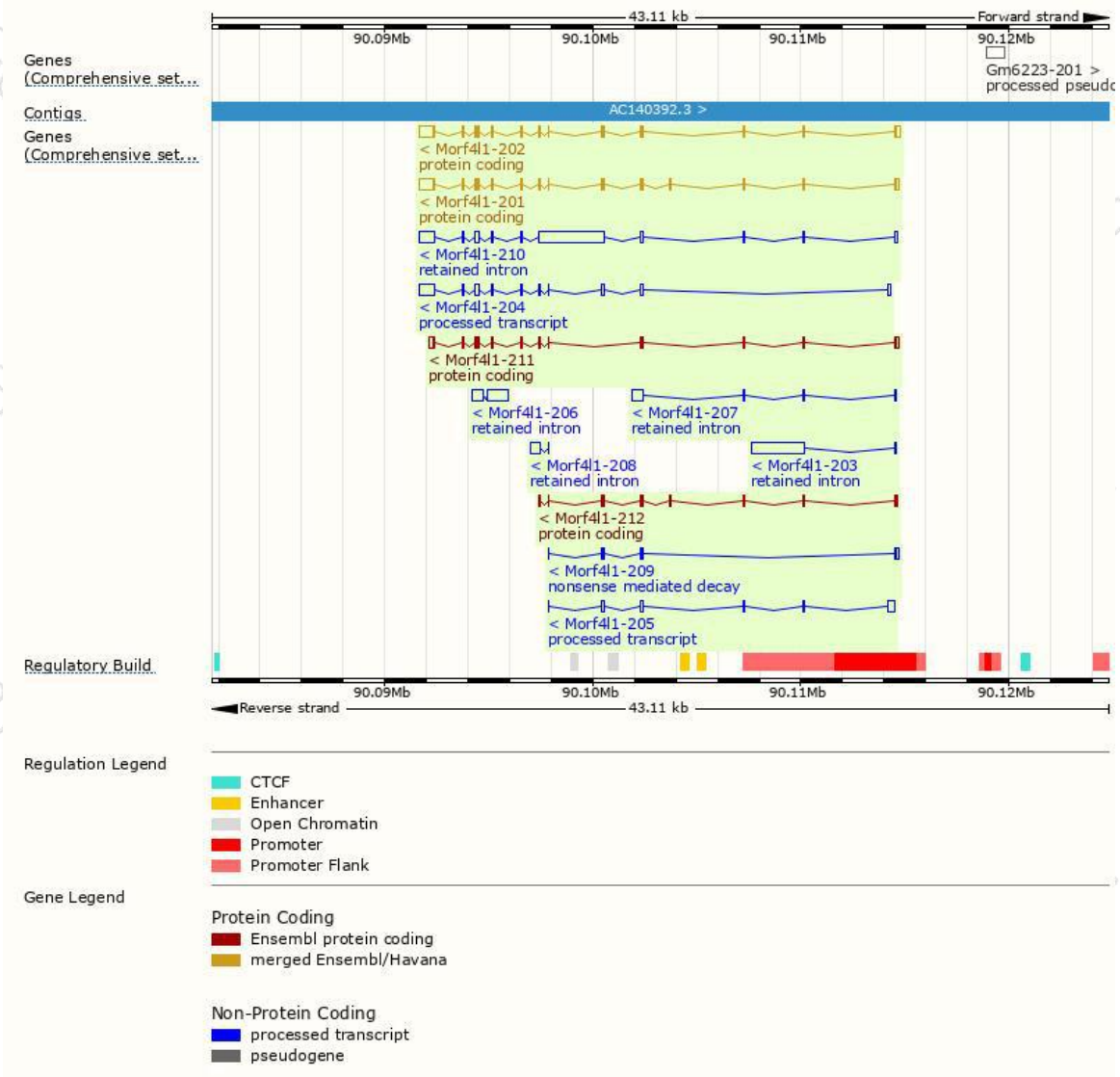
The gene has 12 transcripts,all transcripts are shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Morf4l1-201	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
Morf4l1-202	ENSMUST00000169860.7	1824	323aa	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 ALT1
Morf4l1-211	ENSMUST00000191189.6	1223	296aa	Protein coding	-	A0A087WQB0	TSL:5 GENCODE basic
Morf4l1-212	ENSMUST00000191353.1	600	172aa	Protein coding	-	A0A087WQ34	CDS 3' incomplete TSL:3
Morf4l1-209	ENSMUST00000190345.1	335	50aa	Nonsense mediated decay	-	A0A087WSL1	TSL:5
Morf4l1-204	ENSMUST00000187771.7	1540	No protein	Processed transcript	-	-	TSL:5
Morf4l1-205	ENSMUST00000188905.6	603	No protein	Processed transcript	-	-	TSL:5
Morf4l1-210	ENSMUST00000190377.6	4640	No protein	Retained intron	-	-	TSL:1
Morf4l1-203	ENSMUST00000185433.1	2584	No protein	Retained intron	-	-	TSL:1
Morf4l1-206	ENSMUST00000189089.1	1536	No protein	Retained intron	-	-	TSL:5
Morf4l1-207	ENSMUST00000189241.1	666	No protein	Retained intron	-	-	TSL:1
Morf4l1-208	ENSMUST00000189420.1	504	No protein	Retained intron	-	-	TSL:2

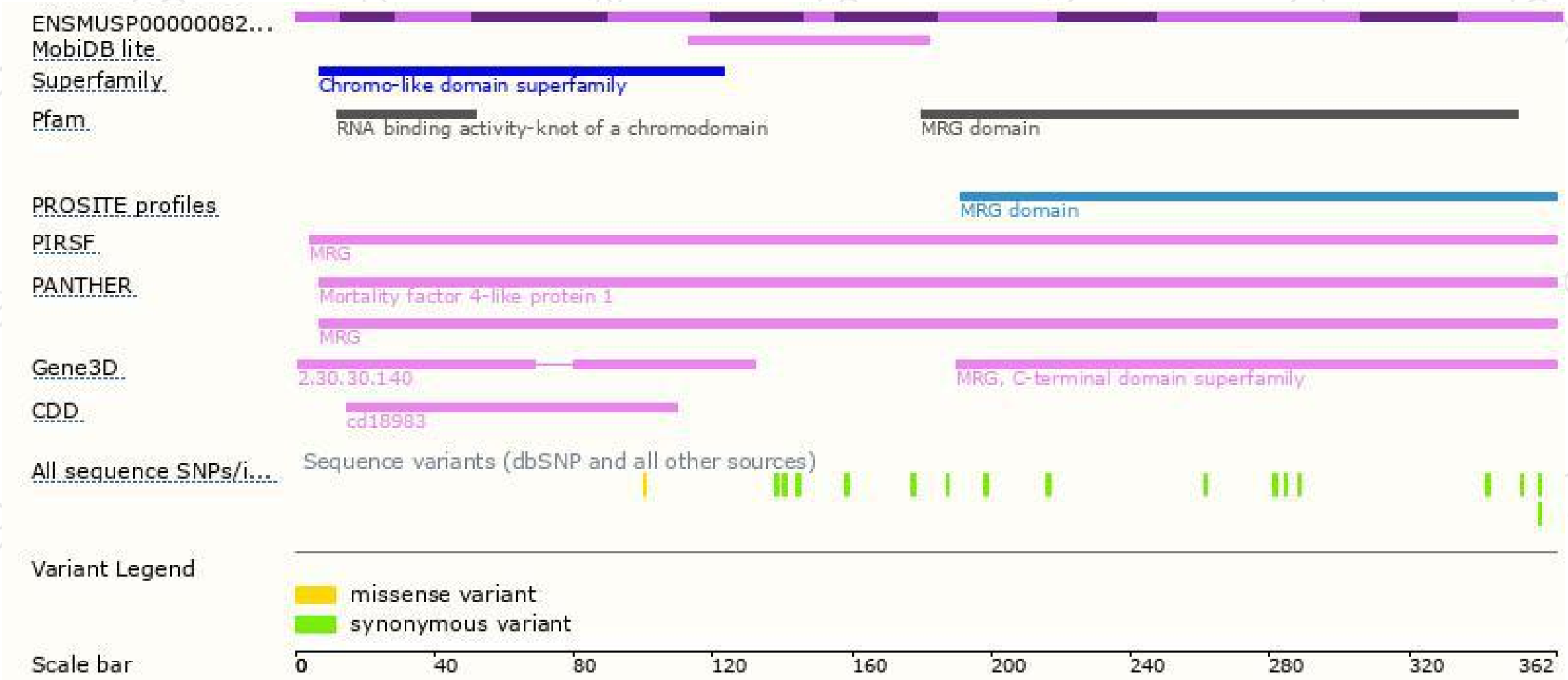
The strategy is based on the design of *Morf4l1-201* transcript,the transcription is shown below:



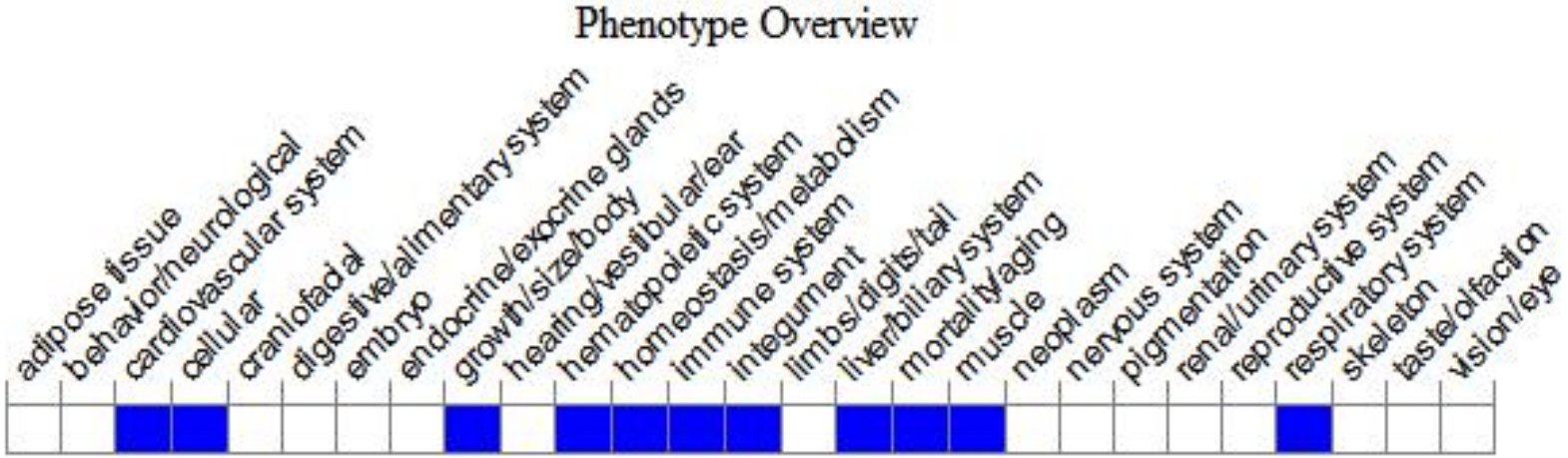
Genomic location distribution



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.

集萃药康
GemPharmatech

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

Tel: 400-9660890

集萃药康生物科技
GemPharmatech Co.,Ltd