Mga Cas9-KO Strategy

Designer:Qiong Zhou

Project Overview

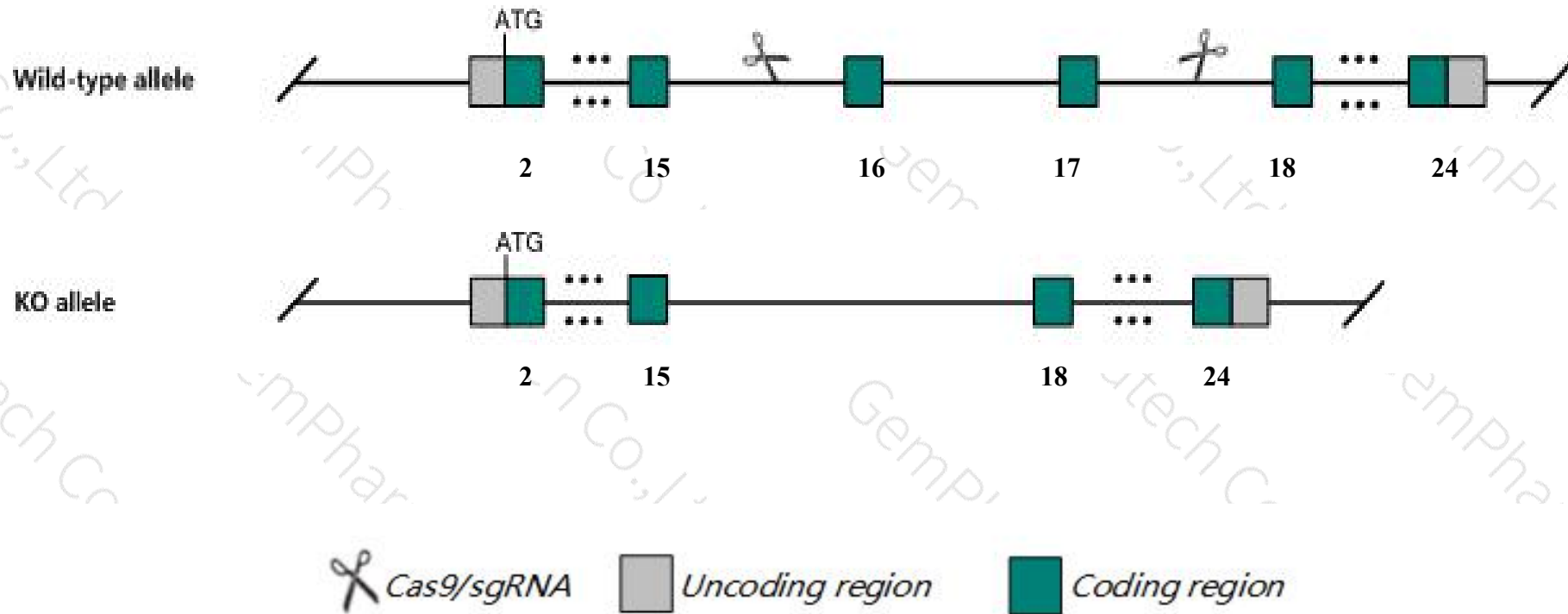|	
Project Name	*Mga*
Project type	**Cas9-KO**
Strain background	**C57BL/6J**

Knockout strategy

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

Technical routes

➢ The *Mga* gene has 15 transcripts. According to the structure of *Mga* gene, exon16-exon17 of *Mga-204* (ENSMUST00000110774.7) transcript is recommended as the knockout region.The region contains 1760bp coding sequence. Knock out the region will result in disruption of protein function.

➢ In this project we use CRISPR/Cas9 technology to modify *Mga* gene. The brief process is as follows: sgRNA was transcribed in vitro.Cas9 and sgRNA were microinjected into the fertilized eggs of C57BL/6J 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/6J mice.

Notice

➢ According to the existing MGI data,Embryos homozygous for a gene trap allele die shortly after implantation
  due to defective development of the inner cell mass (ICM) and the epiblast. ICM derivatives fail to
  develop past E4.5 and show increased apoptosis but no change in cell proliferation.

➢ The *Mga* gene is located on the Chr2. 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）

Mga MAX gene associated [Mus musculus (house mouse)]

Gene ID: 29808, updated on 31-Jan-2019

▲ Summary

|	
Official Symbol	Mga provided by MGI
Official Full Name	MAX gene associated provided by MGI
Primary source	MGI:MGI:1352483
See related	Ensembl:ENSMUSG00000033943
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	AV312082, C130042M01Rik, C80739, D030062C11Rik, Mad5
Expression	Ubiquitous expression in limb E14.5 (RPKM 3.0), CNS E11.5 (RPKM 2.8) and 26 other tissuesSee more
Orthologs	human all

Transcript information（Ensembl）

The gene has 15 transcripts,all transcripts are shown below:

| Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Mga-204	ENSMUST00000110774.7	13931	3042aa	Protein coding	CCDS38208	E9QLG3	TSL:5 GENCODE basic APPRIS P3
Mga-202	ENSMUST00000079934.11	13304	2833aa	Protein coding	CCDS50675	H7BX50	TSL:5 GENCODE basic APPRIS ALT2
Mga-203	ENSMUST00000110773.8	13577	2924aa	Protein coding	-	A2AWL7	TSL:5 GENCODE basic APPRIS ALT2
Mga-201	ENSMUST00000046717.12	11982	3003aa	Protein coding	-	A2AWL7	TSL:5 GENCODE basic APPRIS ALT2
Mga-215	ENSMUST00000156510.1	6995	2295aa	Protein coding	-	A2AWL7	CDS 3' incomplete TSL:1
Mga-206	ENSMUST00000129405.1	3317	No protein	Processed transcript	-	-	TSL:1
Mga-205	ENSMUST00000122889.1	2110	No protein	Processed transcript	-	-	TSL:1
Mga-209	ENSMUST00000138851.7	1264	No protein	Processed transcript	-	-	TSL:1
Mga-214	ENSMUST00000156074.1	864	No protein	Processed transcript	-	-	TSL:3
Mga-208	ENSMUST00000132054.1	739	No protein	Processed transcript	-	-	TSL:3
Mga-213	ENSMUST00000152148.1	739	No protein	Processed transcript	-	-	TSL:3
Mga-212	ENSMUST00000151074.1	649	No protein	Processed transcript	-	-	TSL:3
Mga-210	ENSMUST00000141776.7	2763	No protein	Retained intron	-	-	TSL:1
Mga-207	ENSMUST00000131396.1	985	No protein	Retained intron	-	-	TSL:2
Mga-211	ENSMUST00000150742.1	825	No protein	Retained intron	-	-	TSL:2

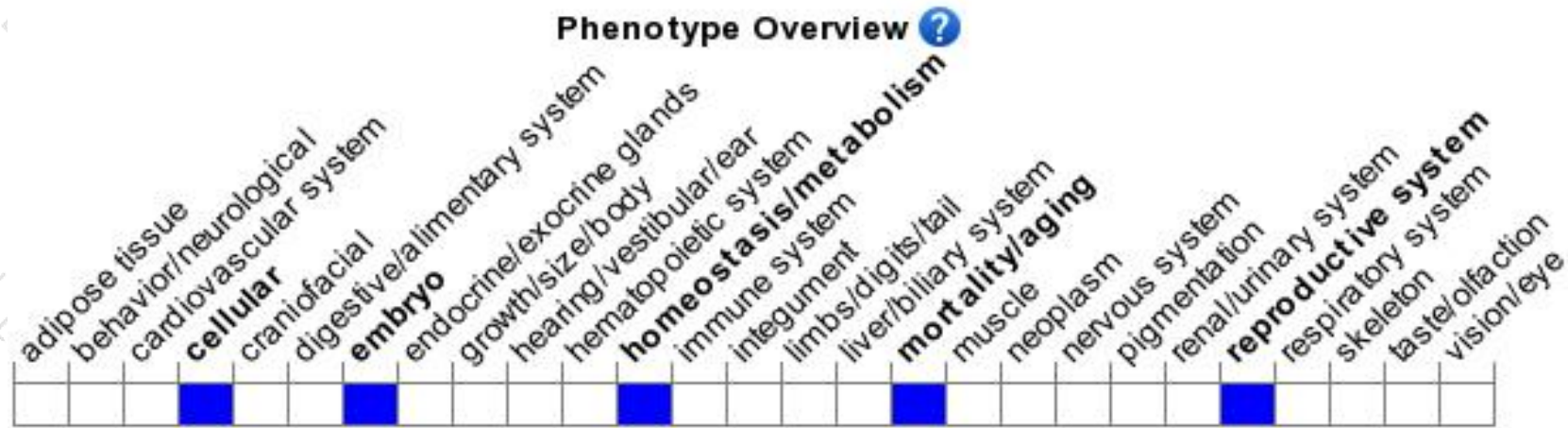The strategy is based on the design of *Mga-204* transcript,The transcription is shown below
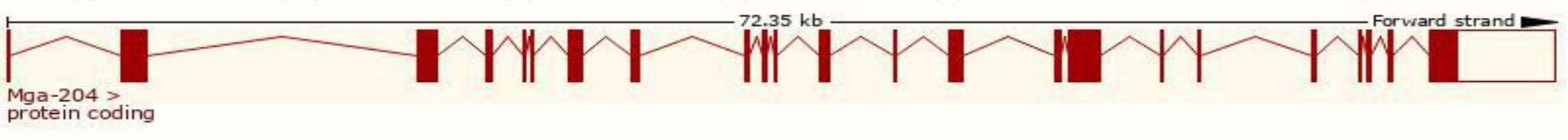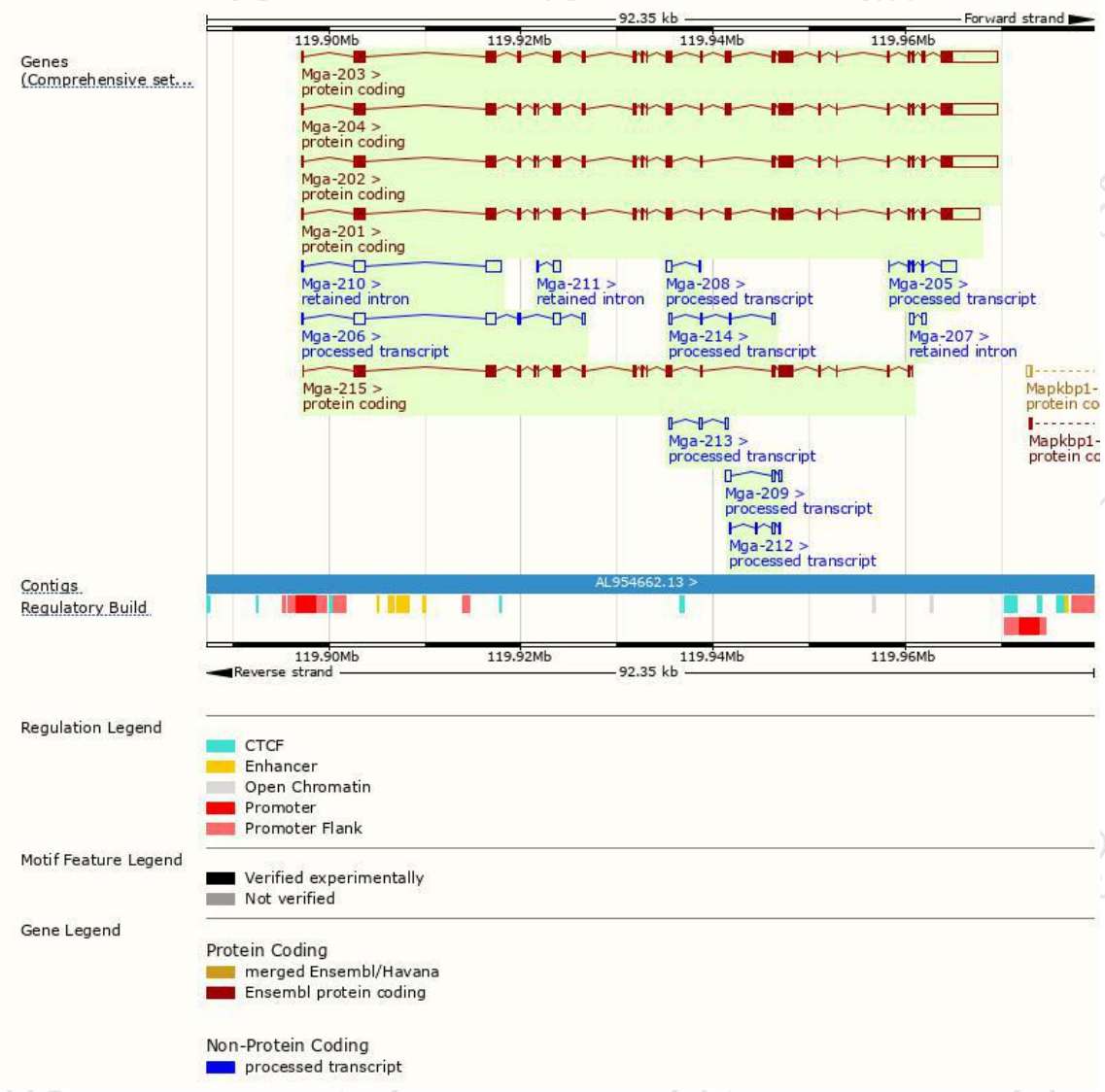
Protein domain
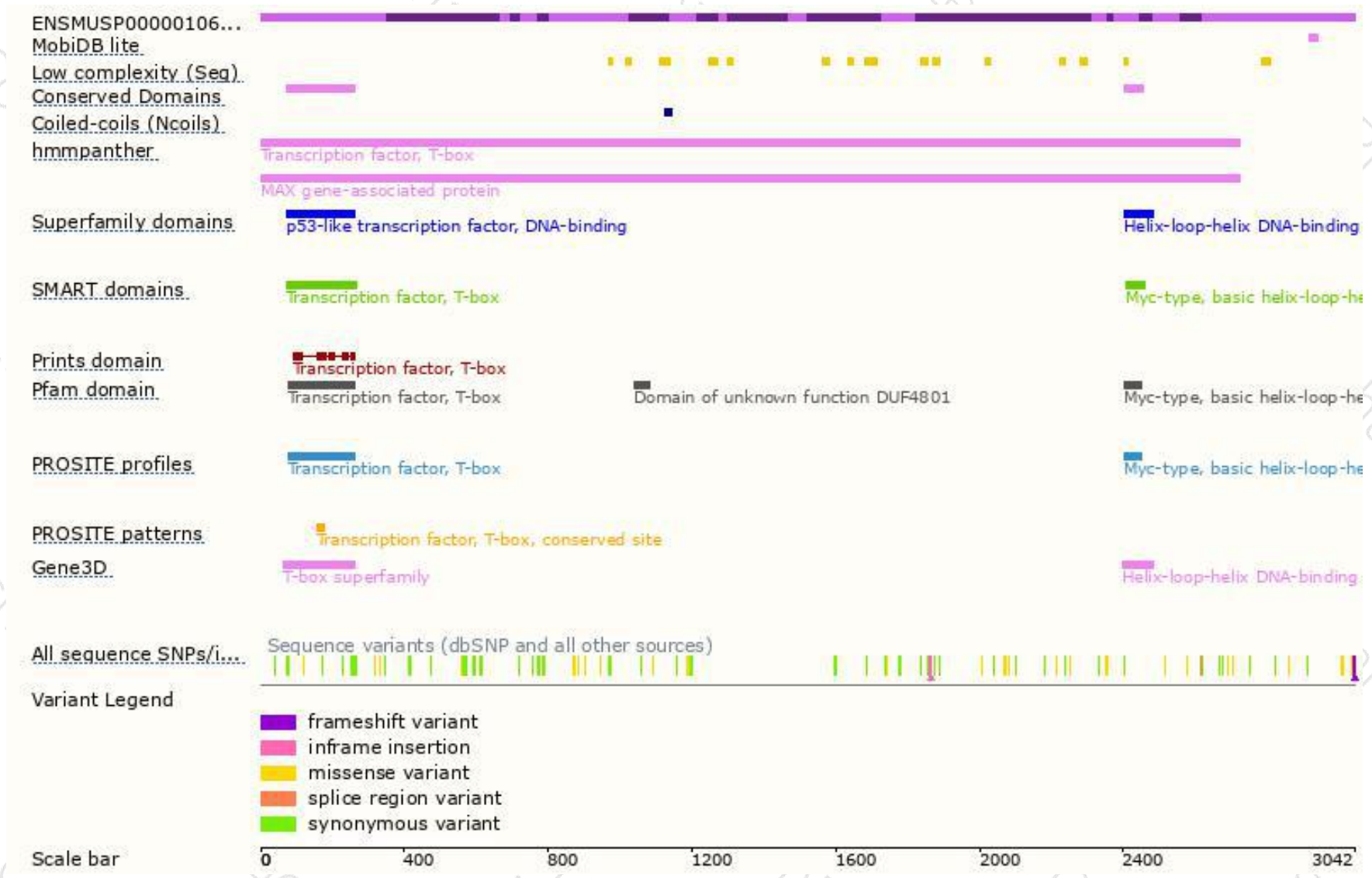
Mouse phenotype description(MGI)

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,Embryos homozygous for a gene trap allele die shortly after implantation due to defective development of the inner cell mass (ICM) and the epiblast. ICM derivatives fail to develop past E4.5 and show increased apoptosis but no change in cell proliferation.

If you have any questions, you are welcome to inquire.
Tel: 025-5864 1534

集萃药康生物科技
GemPharmatech Co.,Ltd