Actl6a Cas9-KO Strategy

Designer: Daohua Xu
Reviewer: Huimin Su

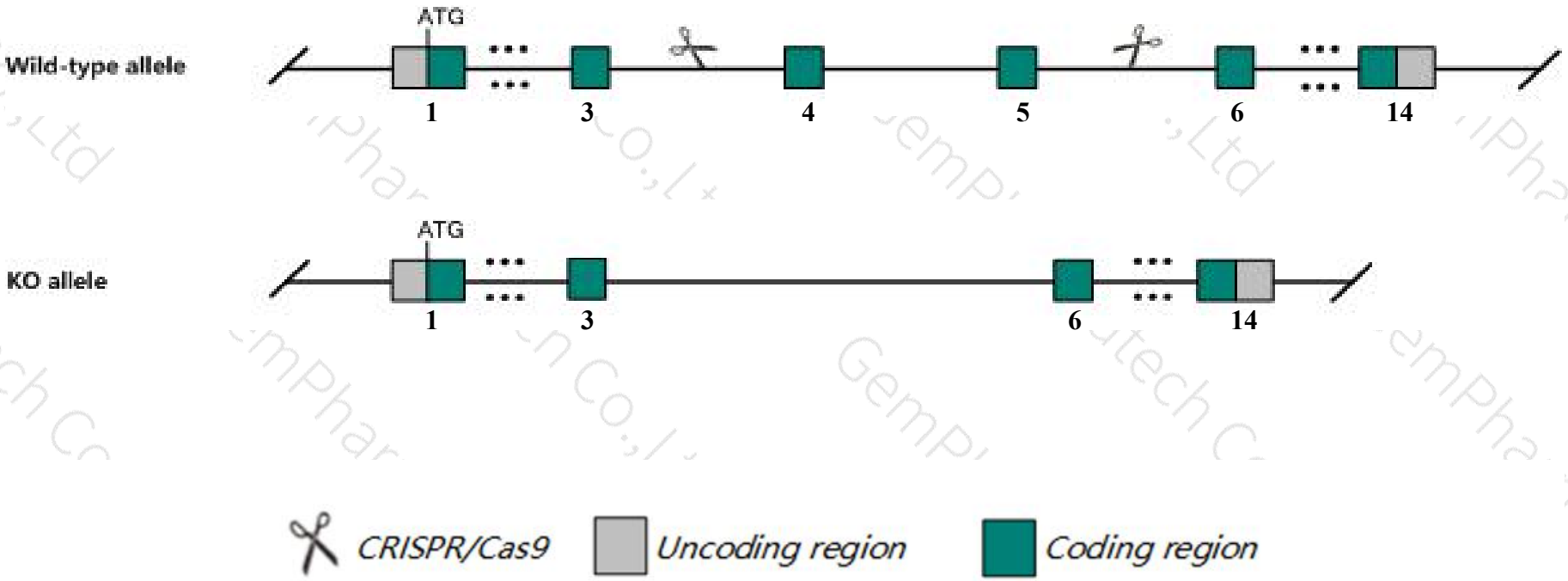
Design Date: 2019-11-26

Project Overview

Project Name	***Actl6a***
Project type	**Cas9-KO**
Strain background	**C57BL/6JGpt**

Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *Actl6a* gene. The schematic diagram is as follows:



Technical routes

➢ The *Actl6a* gene has 8 transcripts. According to the structure of *Actl6a* gene, exon4-exon5 of *Actl6a-201* (ENSMUST00000029214.13) transcript is recommended as the knockout region.The region contains 199bp coding sequence. Knock out the region will result in disruption of protein function.

➢ In this project we use CRISPR/Cas9 technology to modify *Actl6a* gene. The brief process is as follows: CRISPR/Cas9 system

Notice

➢ According to the existing MGI data,Mice homozygous for a knock-out allele exhibit embryonic lethality before E6.5. Mice homozygous for a conditional allele activated in hematopoietic cells exhibit bone marrow failure and premature death.

➢ The *Actl6a* gene is located on the Chr3. 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

Actl6a actin-like 6A [Mus musculus (house mouse)]

Gene ID: 56456, updated on 31-Jan-2019

Summary

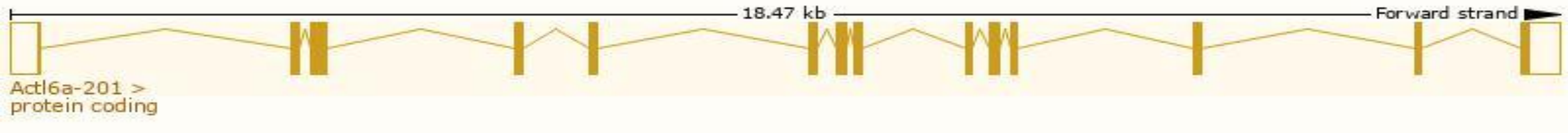
Official Symbol	Actl6a provided by MGI
Official Full Name	actin-like 6A provided byMGI
Primary source	MGI:MGI:1861453
See related	Ensembl:ENSMUSG00000027671
Gene type	protein coding
RefSeq status	VALIDATED
Organism	Mus musculus
Lineage	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Myomorpha; Muroidea; Muridae; Murinae; Mus; Mus
Also known as	2810432C06Rik, AI851094, ARP4, Actl6, Baf53a, C79802
Expression	Ubiquitous expression in CNS E11.5 (RPKM 32.3), liver E14 (RPKM 17.6) and 27 other tissuesSee more
Orthologs	human all

Transcript information（Ensembl）

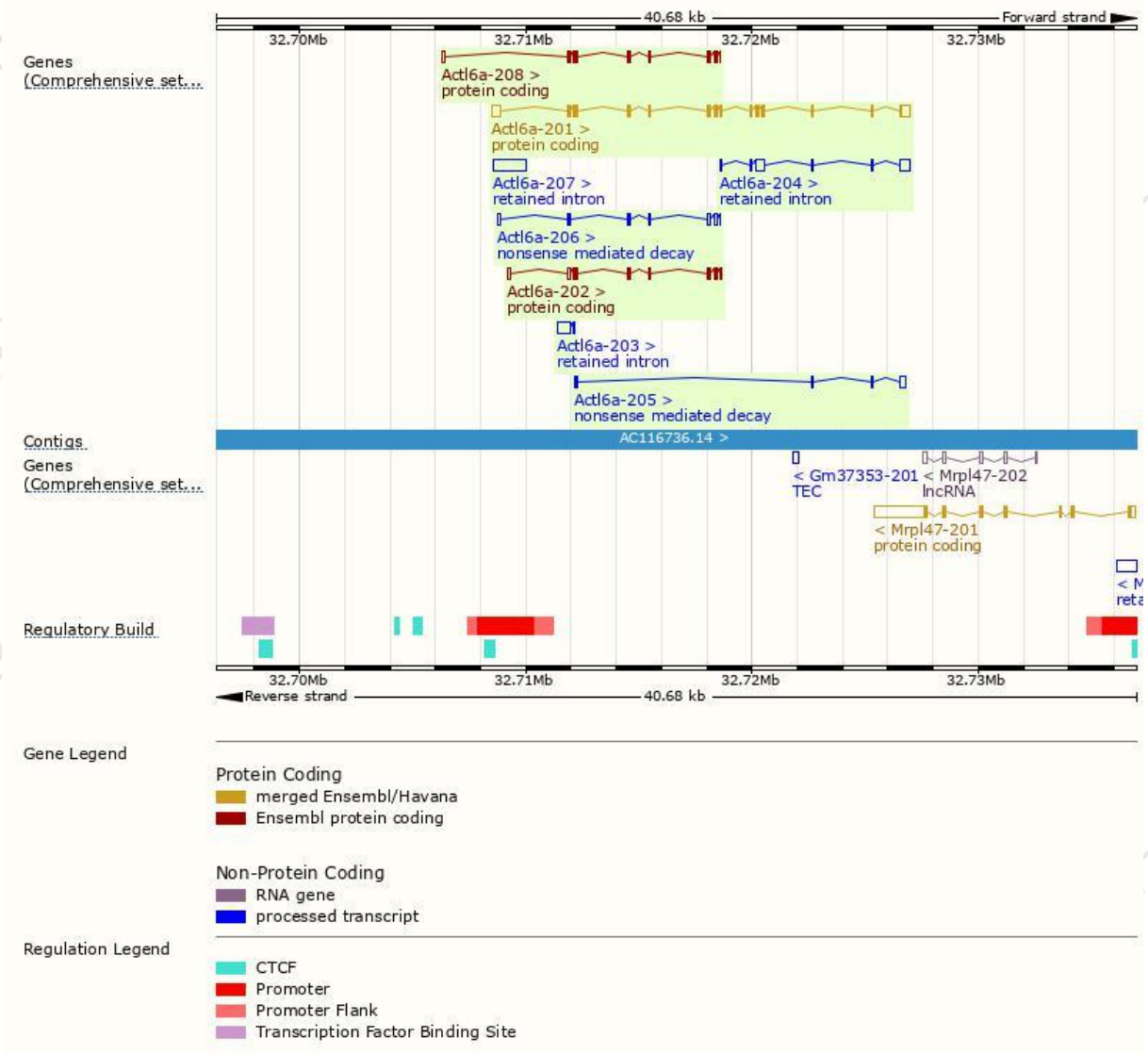
The gene has 8 transcripts,all transcripts are shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Actl6a-201	ENSMUST00000029214.13	2010	429aa	Protein coding	CCDS17298	Q505L1 Q9Z2N8	TSL:1 GENCODE basic APPRIS P1
Actl6a-202	ENSMUST00000126144.2	922	204aa	Protein coding	-	D3YVN1	CDS 3' incomplete TSL:5
Actl6a-208	ENSMUST00000194781.5	831	245aa	Protein coding	-	A0A0A6YWG8	CDS 3' incomplete TSL:5
Actl6a-206	ENSMUST00000193615.1	635	77aa	Nonsense mediated decay	-	A0A0A6YW15	TSL:3
Actl6a-205	ENSMUST00000193231.5	539	54aa	Nonsense mediated decay	-	A0A0A6YWR1	CDS 5' incomplete TSL:3
Actl6a-207	ENSMUST00000194226.1	1457	No protein	Retained intron	-	-	TSL:NA
Actl6a-204	ENSMUST00000153779.1	1112	No protein	Retained intron	-	-	TSL:3
Actl6a-203	ENSMUST00000135400.1	632	No protein	Retained intron	-	-	TSL:1

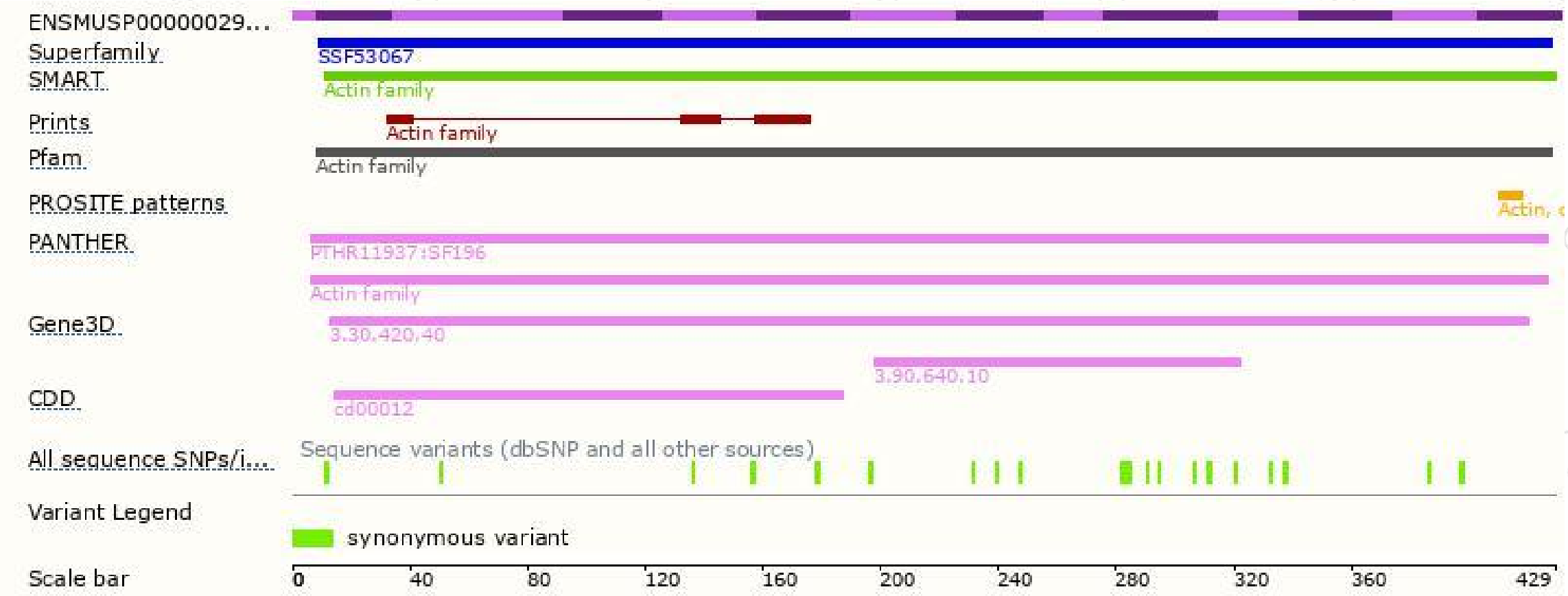
The strategy is based on the design of *Actl6a-201* transcript,The transcription is shown below



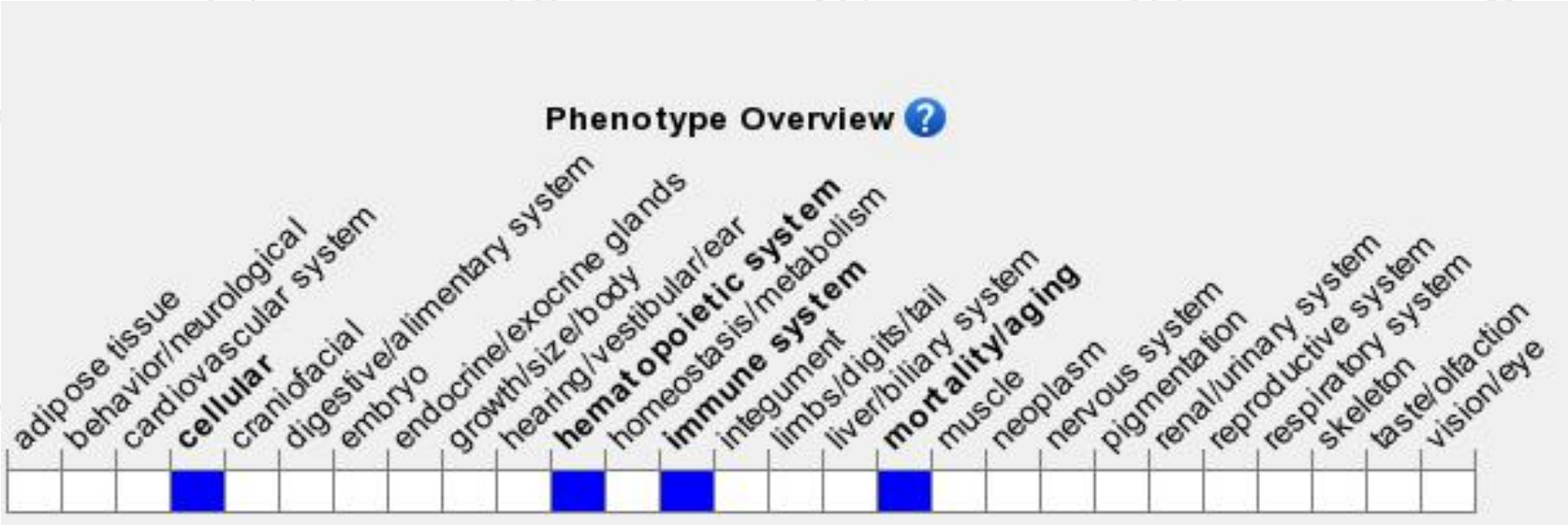
Genomic location distribution



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 knock-out allele exhibit embryonic lethality before E6.5. Mice homozygous for a conditional allele activated in hematopoietic cells exhibit bone marrow failure and premature death.

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