

Actr3 Cas9-KO Strategy

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Reviewer:

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Project Overview

Project Name

Actr3

Project type

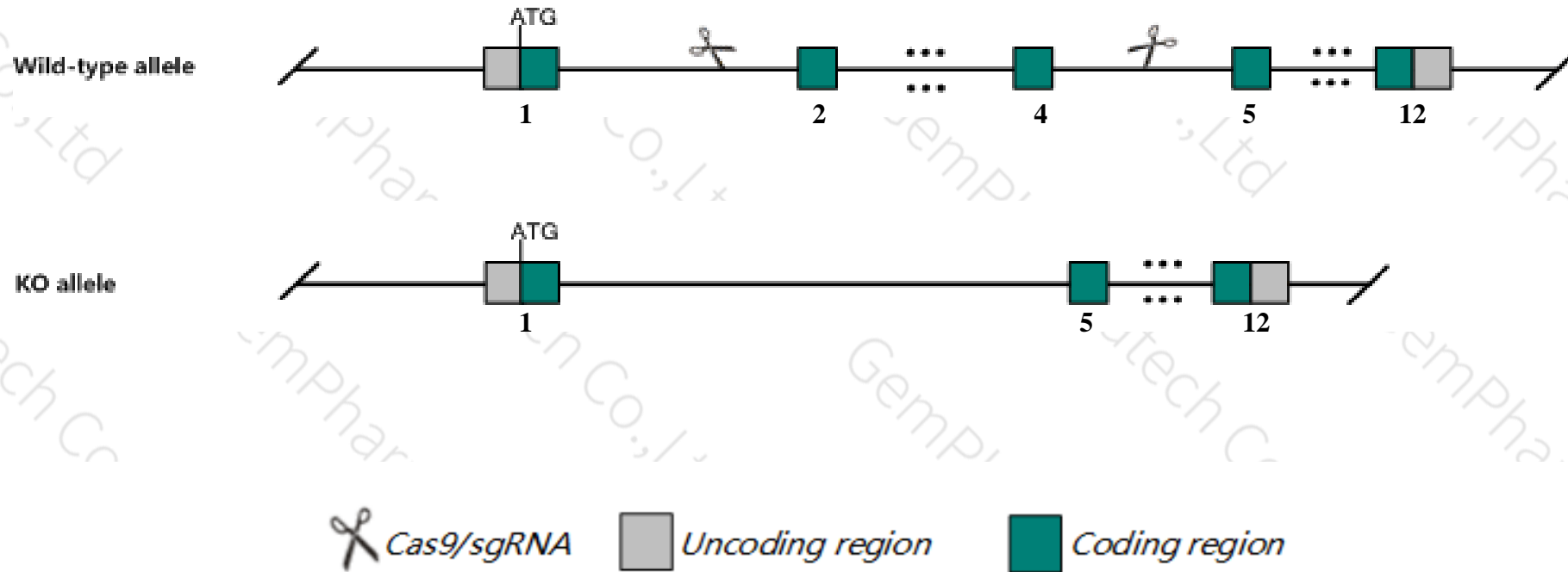
Cas9-KO

Strain background

C57BL/6JGpt

Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *Actr3* gene. The schematic diagram is as follows:



- The *Actr3* gene has 12 transcripts. According to the structure of *Actr3* gene, exon2-exon4 of *Actr3*-202 (ENSMUST00000178474.7) transcript is recommended as the knockout region. The region contains 292bp coding sequence. Knock out the region will result in disruption of protein function.
- In this project we use CRISPR/Cas9 technology to modify *Actr3* gene. The brief process is as follows: sgRNA was transcribed in vitro. Cas9 and sgRNA 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.

- According to the existing MGI data, Mice homozygous for a null allele die prior to E4.5 and exhibit abnormal embryogenesis.
- The *Actr3* gene is located on the Chr1. 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.

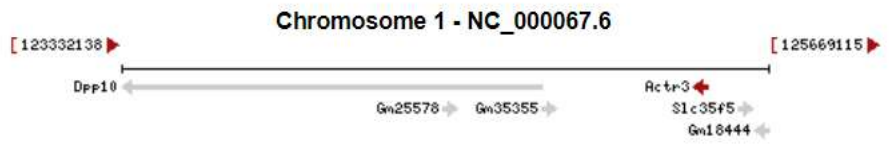
Gene information (NCBI)

Actr3 ARP3 actin-related protein 3 [*Mus musculus* (house mouse)]

Gene ID: 74117, updated on 10-Sep-2019

Summary

- Official Symbol** Actr3 provided by MGI
- Official Full Name** ARP3 actin-related protein 3 provided by MGI
- Primary source** [MGI:MGI:1921367](#)
- See related** [Ensembl:ENSMUSG00000026341](#)
- 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** Arp3; 1200003A09Rik
- Expression** Ubiquitous expression in placenta adult (RPKM 60.4), CNS E14 (RPKM 36.5) and 28 other tissues [See more](#)
- Orthologs** [human](#) [all](#)

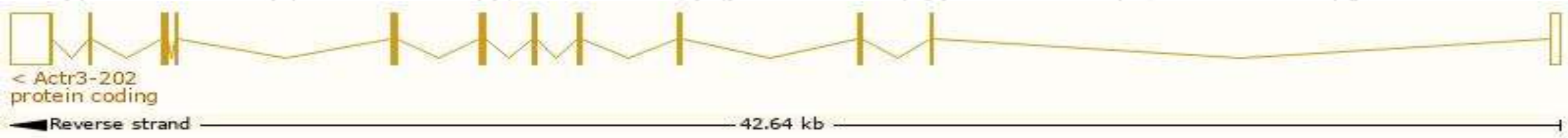


Transcript information (Ensembl)

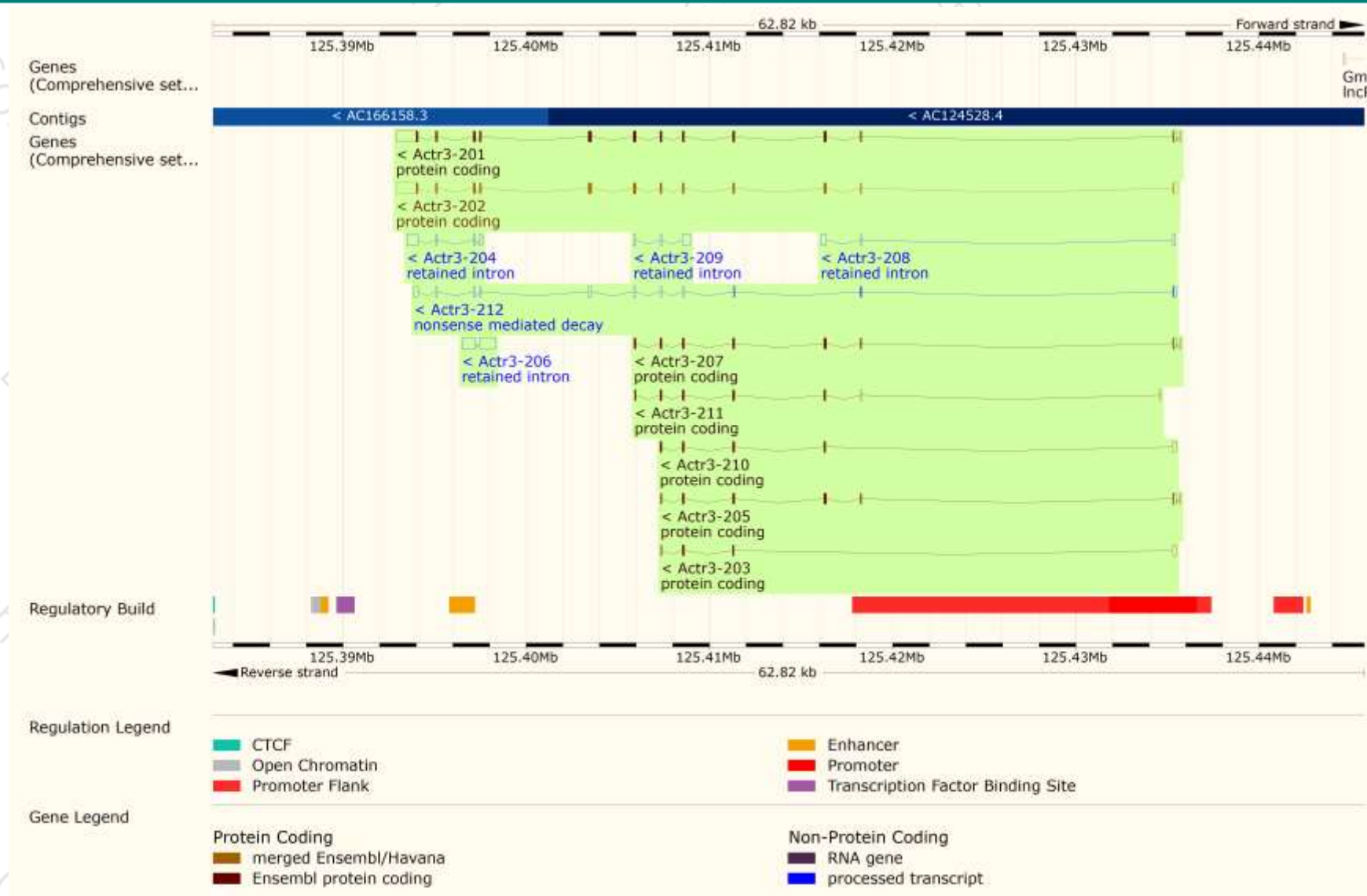
The gene has 12 transcripts,all transcripts are shown below:

Name	Transcript ID	bp	Protein	Translation ID	Biotype	CCDS	UniProt	Flags
Actr3-202	ENSMUST00000178474.7	2565	418aa	ENSMUSP00000137503.1	Protein coding	CCDS15242	Q3ULF7 Q99JY9	TSL:1 Gencode basic APPRIS P1
Actr3-201	ENSMUST00000027579.16	2554	418aa	ENSMUSP00000027579.10	Protein coding	CCDS15242	Q3ULF7 Q99JY9	TSL:5 Gencode basic APPRIS P1
Actr3-207	ENSMUST00000188497.6	856	216aa	ENSMUSP00000140535.1	Protein coding	-	A0A087WRA1	CDS 3' incomplete TSL:3
Actr3-205	ENSMUST00000187460.6	667	161aa	ENSMUSP00000140000.1	Protein coding	-	A0A087WQ14	CDS 3' incomplete TSL:2
Actr3-211	ENSMUST00000191544.6	654	155aa	ENSMUSP00000139674.1	Protein coding	-	A0A087WP86	CDS 3' incomplete TSL:3
Actr3-210	ENSMUST00000191004.6	610	129aa	ENSMUSP00000140953.1	Protein coding	-	A0A087WS98	CDS 3' incomplete TSL:5
Actr3-203	ENSMUST00000185280.1	435	70aa	ENSMUSP00000140082.1	Protein coding	-	A0A087WQ83	CDS 3' incomplete TSL:5
Actr3-212	ENSMUST00000191578.6	1390	41aa	ENSMUSP00000139886.1	Nonsense mediated decay	-	A0A087WPR6	TSL:5
Actr3-206	ENSMUST00000188362.1	1609	No protein	-	Retained intron	-	-	TSL:2
Actr3-204	ENSMUST00000186008.6	978	No protein	-	Retained intron	-	-	TSL:2
Actr3-209	ENSMUST00000189192.1	658	No protein	-	Retained intron	-	-	TSL:2
Actr3-208	ENSMUST00000188827.1	517	No protein	-	Retained intron	-	-	TSL:2

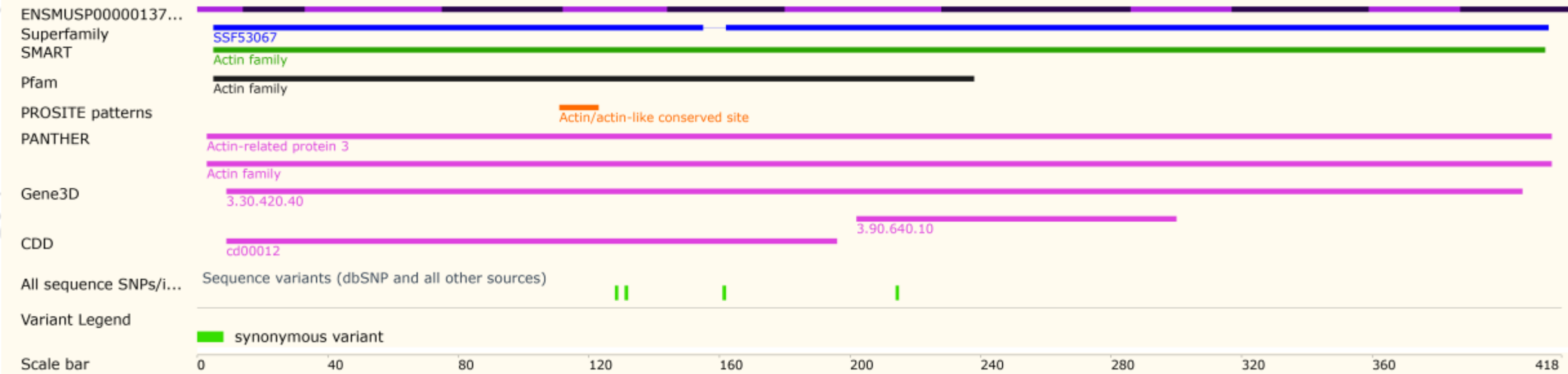
The strategy is based on the design of *Actr3-202* transcript,The transcription is shown below



Genomic location distribution

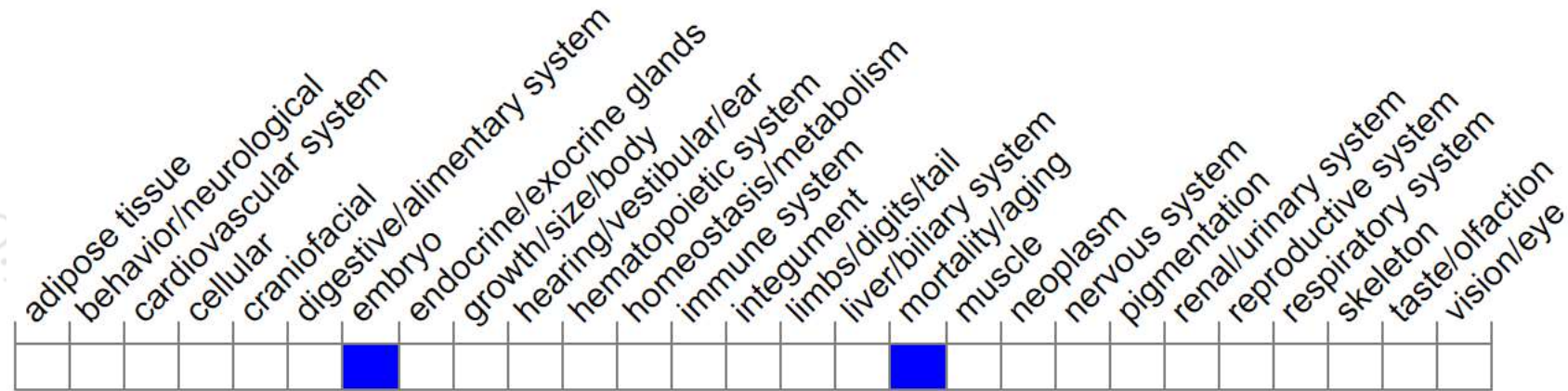


Protein domain



Mouse phenotype description(MGI)

Phenotype Overview ?



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 null allele die prior to E4.5 and exhibit abnormal embryogenesis.

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

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