

Aida Cas9-KO Strategy

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Project Overview



Project Name Aida

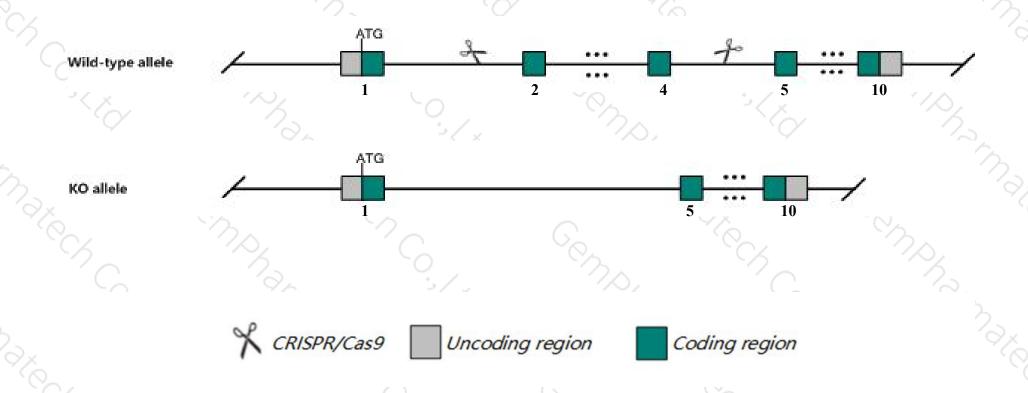
Project type Cas9-KO

Strain background C57BL/6JGpt

Knockout strategy



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



Technical routes



- ➤ The *Aida* gene has 9 transcripts. According to the structure of *Aida* gene, exon2-exon4 of *Aida-201* (ENSMUST00000109166.7) transcript is recommended as the knockout region. The region contains 179bp coding sequence. Knock out the region will result in disruption of protein function.
- ➤ In this project we use CRISPR/Cas9 technology to modify *Aida* gene. The brief process is as follows: CRISPR/Cas9 system v

Notice



- > The *Aida* 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)



Aida axin interactor, dorsalization associated [Mus musculus (house mouse)]

Gene ID: 108909, updated on 31-Jan-2019

Summary

☆ ?

Official Symbol Aida provided by MGI

Official Full Name axin interactor, dorsalization associated provided by MGI

Primary source MGI:MGI:1919737

See related Ensembl:ENSMUSG00000042901

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 2610208M17Rik, BC004835

Expression Ubiquitous expression in CNS E18 (RPKM 15.5), limb E14.5 (RPKM 15.1) and 28 other tissuesSee more

Orthologs <u>human</u> all

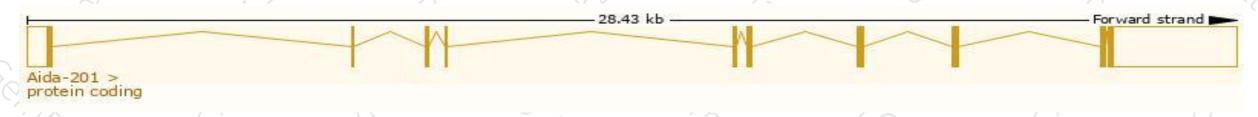
Transcript information (Ensembl)



The gene has 9 transcripts, all transcripts are shown below:

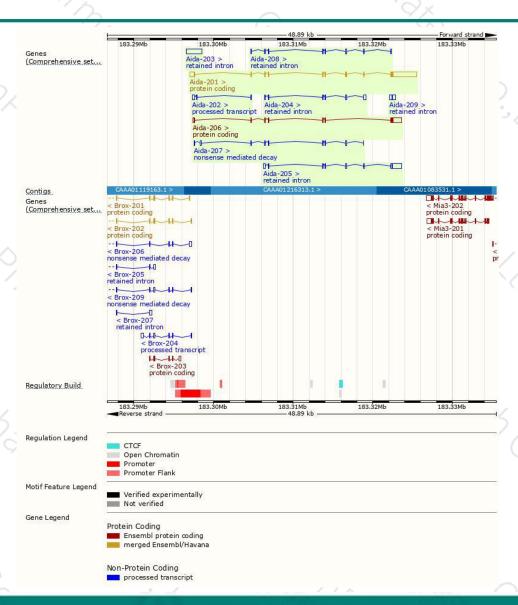
f in						
Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
ENSMUST00000109166.7	4279	305aa	Protein coding	CCDS56663	Q8C4Q6	TSL:1 GENCODE basic APPRIS P1
ENSMUST00000193625.1	1810	223aa	Protein coding	÷8	Q8C4Q6	TSL:3 GENCODE basic
ENSMUST00000193959.5	724	<u>21aa</u>	Nonsense mediated decay	20	A0A0A6YXT3	CDS 5' incomplete TSL:5
ENSMUST00000191782.1	426	No protein	Processed transcript	29	82	TSL:3
ENSMUST00000192252.1	1932	No protein	Retained intron	58		TSL:NA
ENSMUST00000193359.5	1894	No protein	Retained intron		. .	TSL:1
ENSMUST00000192293.1	710	No protein	Retained intron	20	12	TSL:2
ENSMUST00000194652.5	668	No protein	Retained intron	29	82	TSL:3
ENSMUST00000195268.1	626	No protein	Retained intron	5/	65	TSL:2
	ENSMUST00000193625.1 ENSMUST00000193959.5 ENSMUST00000191782.1 ENSMUST00000192252.1 ENSMUST00000193359.5 ENSMUST00000192293.1 ENSMUST00000194652.5	ENSMUST00000109166.7 4279 ENSMUST00000193625.1 1810 ENSMUST00000193959.5 724 ENSMUST00000191782.1 426 ENSMUST00000192252.1 1932 ENSMUST00000193359.5 1894 ENSMUST00000192293.1 710 ENSMUST00000194652.5 668	ENSMUST00000109166.7 4279 305aa ENSMUST00000193625.1 1810 223aa ENSMUST00000193959.5 724 21aa ENSMUST00000191782.1 426 No protein ENSMUST00000192252.1 1932 No protein ENSMUST00000193359.5 1894 No protein ENSMUST00000192293.1 710 No protein ENSMUST00000194652.5 668 No protein	ENSMUST00000109166.7 4279 305aa Protein coding ENSMUST00000193625.1 1810 223aa Protein coding ENSMUST00000193959.5 724 21aa Nonsense mediated decay ENSMUST00000191782.1 426 No protein Processed transcript ENSMUST00000192252.1 1932 No protein Retained intron ENSMUST00000193359.5 1894 No protein Retained intron ENSMUST00000192293.1 710 No protein Retained intron ENSMUST00000194652.5 668 No protein Retained intron	ENSMUST00000109166.7 4279 305aa Protein coding CCDS56663 ENSMUST00000193625.1 1810 223aa Protein coding - ENSMUST00000193959.5 724 21aa Nonsense mediated decay - ENSMUST00000191782.1 426 No protein Processed transcript - ENSMUST00000192252.1 1932 No protein Retained intron - ENSMUST00000193359.5 1894 No protein Retained intron - ENSMUST00000192293.1 710 No protein Retained intron - ENSMUST00000194652.5 668 No protein Retained intron -	ENSMUST00000109166.7 4279 305aa Protein coding CCDS56663 Q8C4Q6 ENSMUST00000193625.1 1810 223aa Protein coding - Q8C4Q6 ENSMUST00000193959.5 724 21aa Nonsense mediated decay - A0A0A6YXT3 ENSMUST00000191782.1 426 No protein Processed transcript - - ENSMUST00000192252.1 1932 No protein Retained intron - - ENSMUST00000193359.5 1894 No protein Retained intron - - ENSMUST00000192293.1 710 No protein Retained intron - - ENSMUST00000194652.5 668 No protein Retained intron - -

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



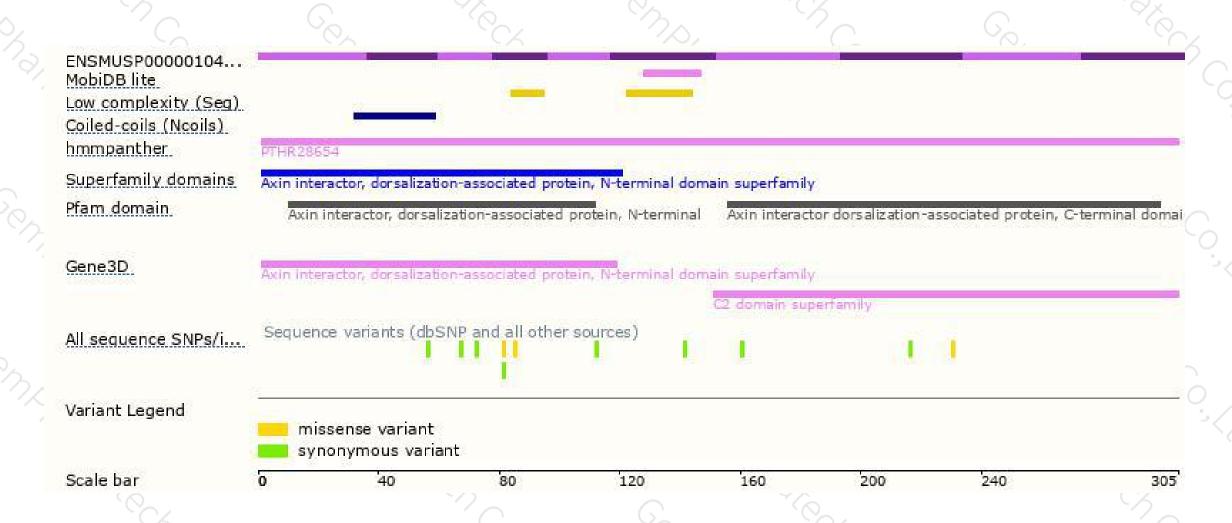
Genomic location distribution





Protein domain







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





