

Adam11 Cas9-KO Strategy

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Project Overview

Project Name

Adam11

Project type

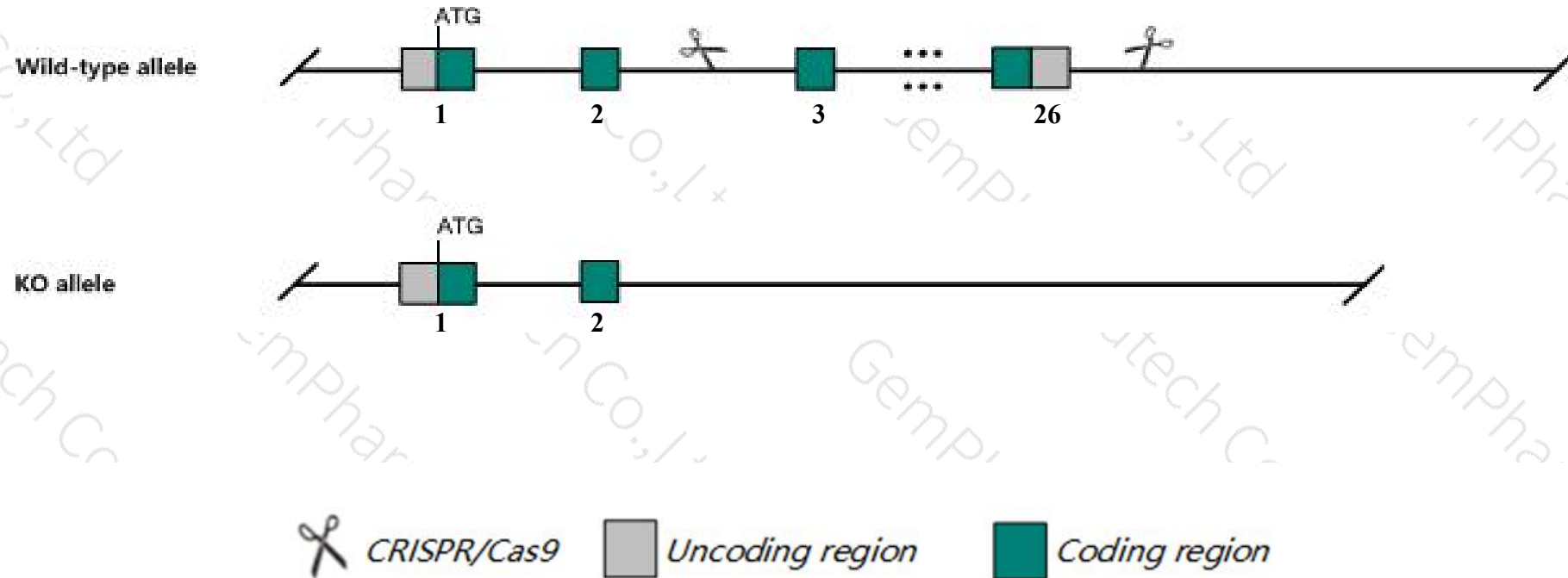
Cas9-KO

Strain background

C57BL/6JGpt

Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *Adam11* gene. The schematic diagram is as follows:



- The *Adam11* gene has 9 transcripts. According to the structure of *Adam11* gene, exon3-exon26 of *Adam11-201* (ENSMUST00000068150.6) transcript is recommended as the knockout region. The region contains most of the coding sequence. Knock out the region will result in disruption of protein function.
- In this project we use CRISPR/Cas9 technology to modify *Adam11* gene. The brief process is as follows: CRISPR/Cas9 system

- According to the existing MGI data, mice homozygous for a targeted disruption of this gene are viable and overtly normal but show impaired hippocampus-dependent spatial learning and cerebellum-dependent motor coordination when tested using water maze and rotating rod tasks.
- The *Adam11* gene is located on the Chr11. 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)

Adam11 a disintegrin and metallopeptidase domain 11 [*Mus musculus* (house mouse)]

Gene ID: 11488, updated on 12-Aug-2019

Summary

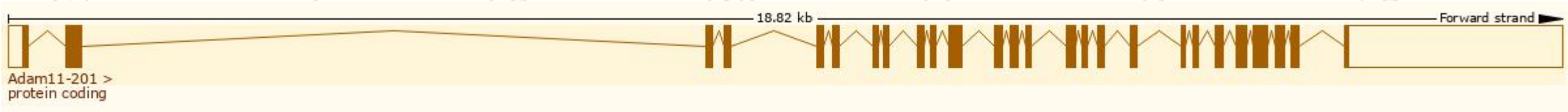
Official Symbol	Adam11 provided by MGI
Official Full Name	a disintegrin and metallopeptidase domain 11 provided by MGI
Primary source	MGI:MGI:1098667
See related	Ensembl:ENSMUSG000000020926
Gene type	protein coding
RefSeq status	REVIEWED
Organism	Mus musculus
Lineage	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Myomorpha; Muroidea; Muridae; Murinae; Mus; Mus
Also known as	Mdc; AW060611
Summary	This gene encodes a member of a disintegrin and metalloprotease (ADAM) family of endoproteases that play important roles in various biological processes including cell signaling, adhesion and migration. The encoded preproprotein undergoes proteolytic processing to generate a mature, functional protein. The protein encoded by this gene is believed to lack metalloproteinase activity due to the lack of a critical catalytic motif. Mice lacking the encoded protein exhibit defects in spatial learning, motor coordination and altered perception of pain. Alternative splicing results in multiple transcript variants encoding different isoforms that may undergo similar processing. [provided by RefSeq, May 2016]
Expression	Broad expression in cerebellum adult (RPKM 47.6), cortex adult (RPKM 21.6) and 15 other tissues See more
Orthologs	human all

Transcript information (Ensembl)

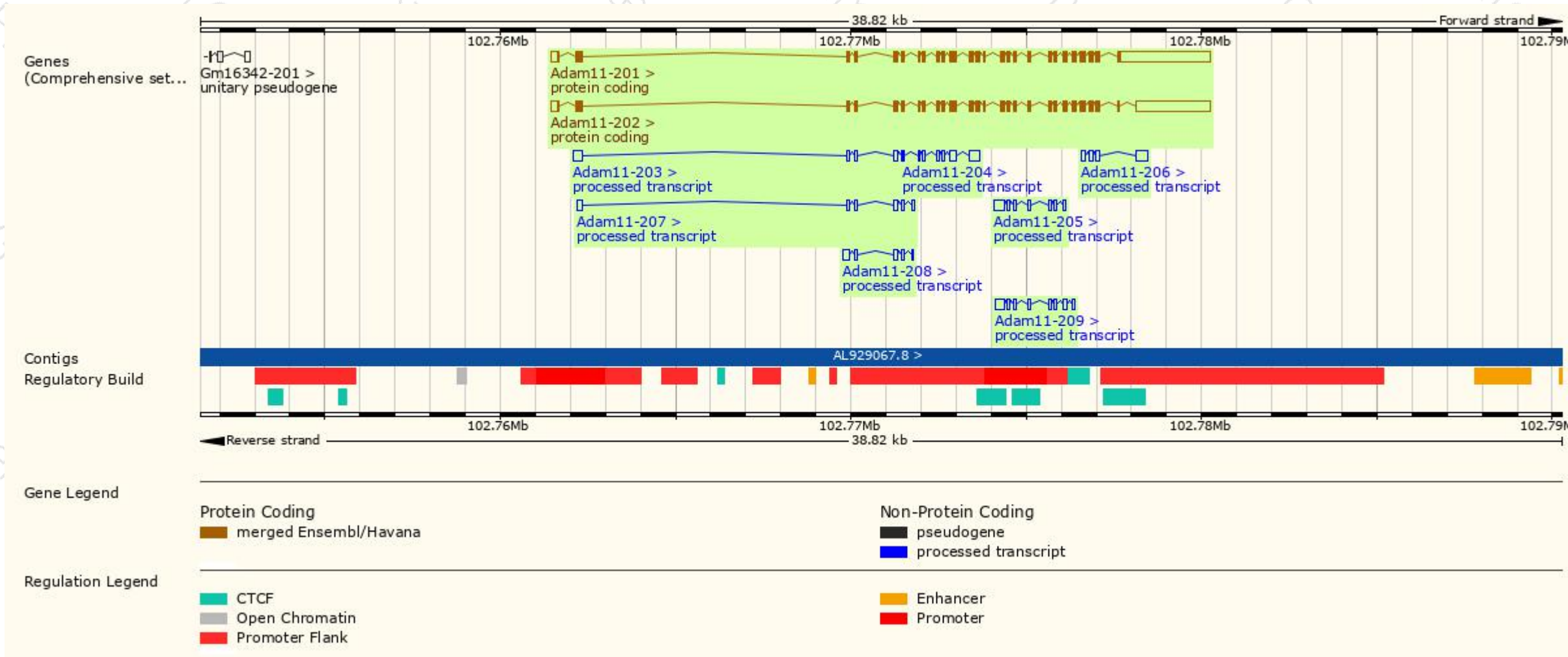
The gene has 9 transcripts,all transcripts are shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Adam11-201	ENSMUST00000068150.6	5102	778aa	Protein coding	CCDS48946	Q7TQG7	TSL:1 GENCODE basic APPRIS ALT2
Adam11-202	ENSMUST00000103081.9	4620	773aa	Protein coding	CCDS25503	Q9R1V4	TSL:1 GENCODE basic APPRIS P3
Adam11-209	ENSMUST00000143269.1	788	No protein	Processed transcript	-	-	TSL:5
Adam11-204	ENSMUST00000126024.1	746	No protein	Processed transcript	-	-	TSL:5
Adam11-205	ENSMUST00000134296.7	705	No protein	Processed transcript	-	-	TSL:3
Adam11-206	ENSMUST00000135513.1	687	No protein	Processed transcript	-	-	TSL:5
Adam11-207	ENSMUST00000141563.7	551	No protein	Processed transcript	-	-	TSL:3
Adam11-203	ENSMUST00000124879.7	514	No protein	Processed transcript	-	-	TSL:5
Adam11-208	ENSMUST00000142912.1	464	No protein	Processed transcript	-	-	TSL:5

The strategy is based on the design of *Adam11-201* transcript, the transcription is shown below:



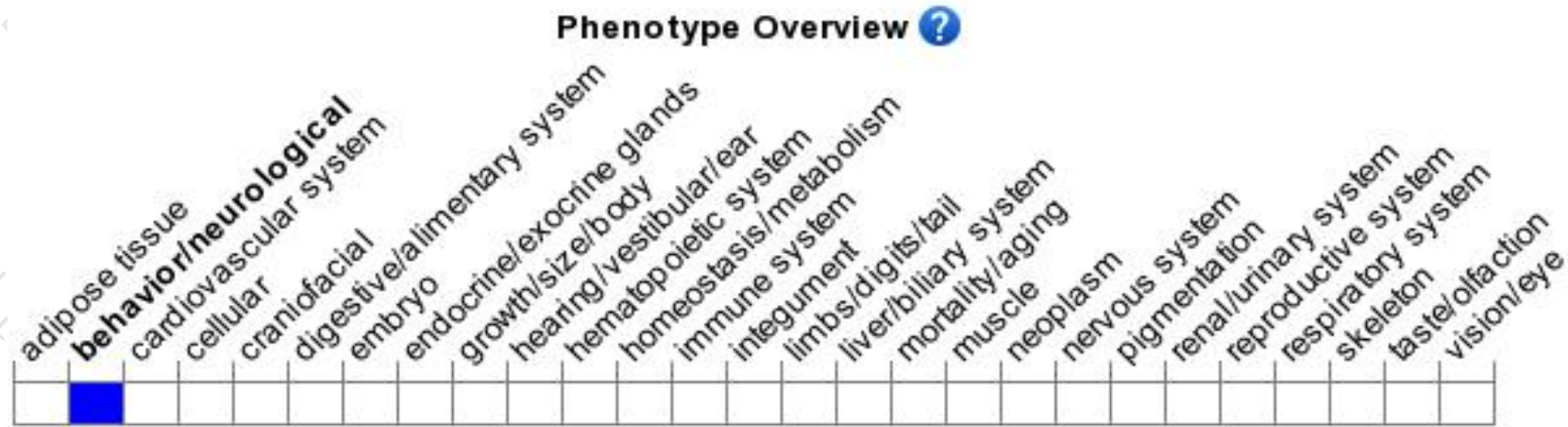
Genomic location distribution



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 targeted disruption of this gene are viable and overtly normal but show impaired hippocampus-dependent spatial learning and cerebellum-dependent motor coordination when tested using water maze and rotating rod tasks.

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

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