

Atn1 Cas9-KO Strategy

Designer:

Huan Fan

Design Date:

2019-9-23

Project Overview

Project Name

Atxn1

Project type

Cas9-KO

Strain background

C57BL/6JGpt

Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *Atxn1* gene. The schematic diagram is as follows:



- The *Atxn1* gene has 6 transcripts. According to the structure of *Atxn1* gene, exon7 of *Atxn1-201* (ENSMUST00000091628.10) transcript is recommended as the knockout region. The region contains start codon ATG. Knock out the region will result in disruption of protein function.
- In this project we use CRISPR/Cas9 technology to modify *Atxn1* gene. The brief process is as follows: CRISPR/Cas9 system

- According to the existing MGI data, Mice homozygous for a knock-out allele exhibit decreased exploration, impaired spatial working memory, impaired coordination, and decreased paired-pulse facilitation.
- The *Atxn1* gene is located on the Chr13. 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)

Atxn1 ataxin 1 [Mus musculus (house mouse)]

Gene ID: 20238, updated on 2-Apr-2019

Summary



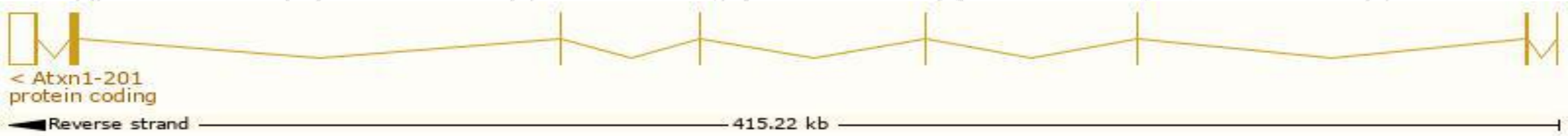
Official Symbol	Atxn1 provided by MGI
Official Full Name	ataxin 1 provided by MGI
Primary source	MGI:MGI:104783
See related	Ensembl:ENSMUSG00000046876
Gene type	protein coding
RefSeq status	VALIDATED
Organism	Mus musculus
Lineage	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Myomorpha; Muroidea; Muridae; Murinae; Mus; Mus
Also known as	2900016G23Rik, Atx1, C85907, Gm10786, Sca1
Expression	Ubiquitous expression in cortex adult (RPKM 5.7), frontal lobe adult (RPKM 4.8) and 28 other tissues See more
Orthologs	human all

Transcript information (Ensembl)

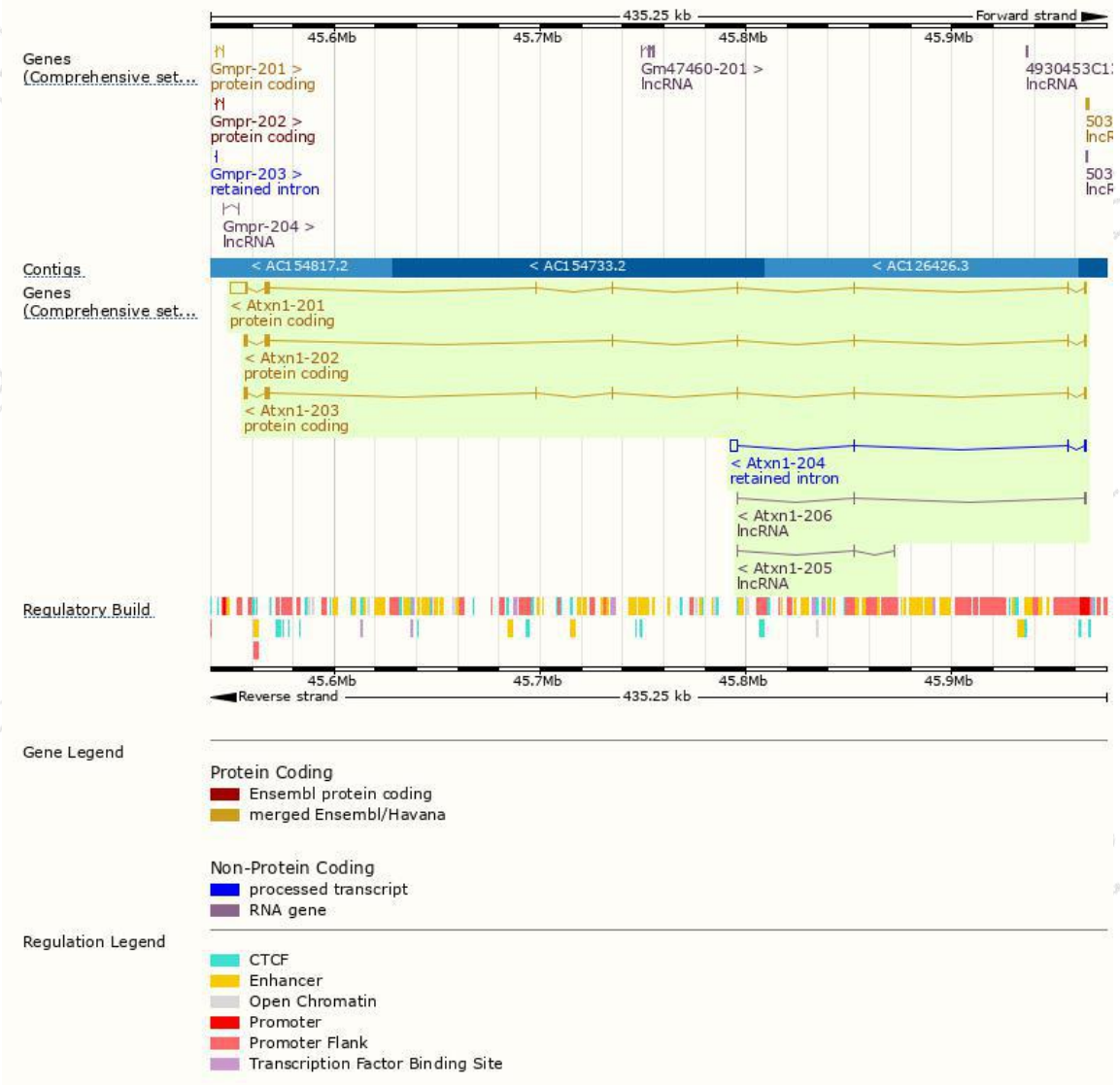
The gene has 6 transcripts,all transcripts are shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Atxn1-201	ENSMUST00000091628.10	10569	791aa	Protein coding	CCDS26483	P54254	TSL:1 GENCODE basic APPRIS P3
Atxn1-203	ENSMUST00000180110.8	3901	799aa	Protein coding	CCDS56877	J3QPR1	TSL:1 GENCODE basic APPRIS ALT2
Atxn1-202	ENSMUST00000167708.3	3751	791aa	Protein coding	CCDS26483	P54254	TSL:1 GENCODE basic APPRIS P3
Atxn1-206	ENSMUST00000222943.1	420	No protein	Processed transcript	-	-	TSL:2
Atxn1-205	ENSMUST00000222610.1	333	No protein	Processed transcript	-	-	TSL:3
Atxn1-204	ENSMUST00000221082.1	3753	No protein	Retained intron	-	-	TSL:1

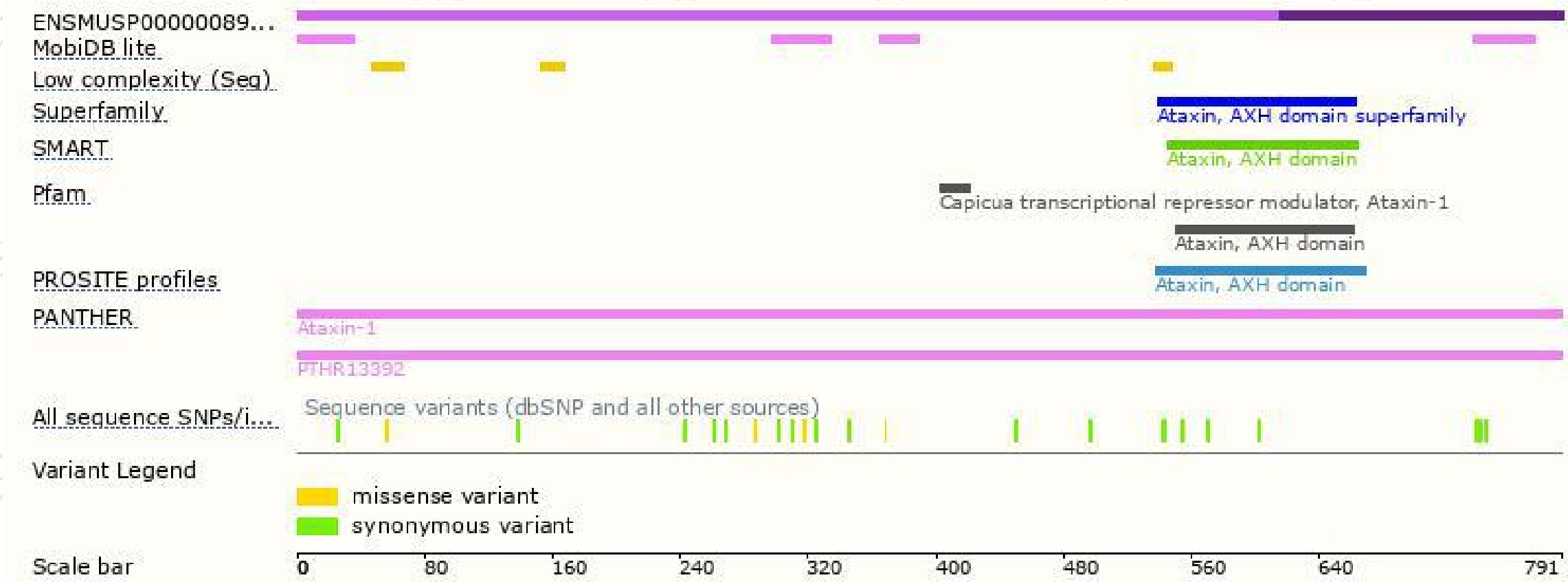
The strategy is based on the design of *Atxn1-201* transcript,The transcription is shown below



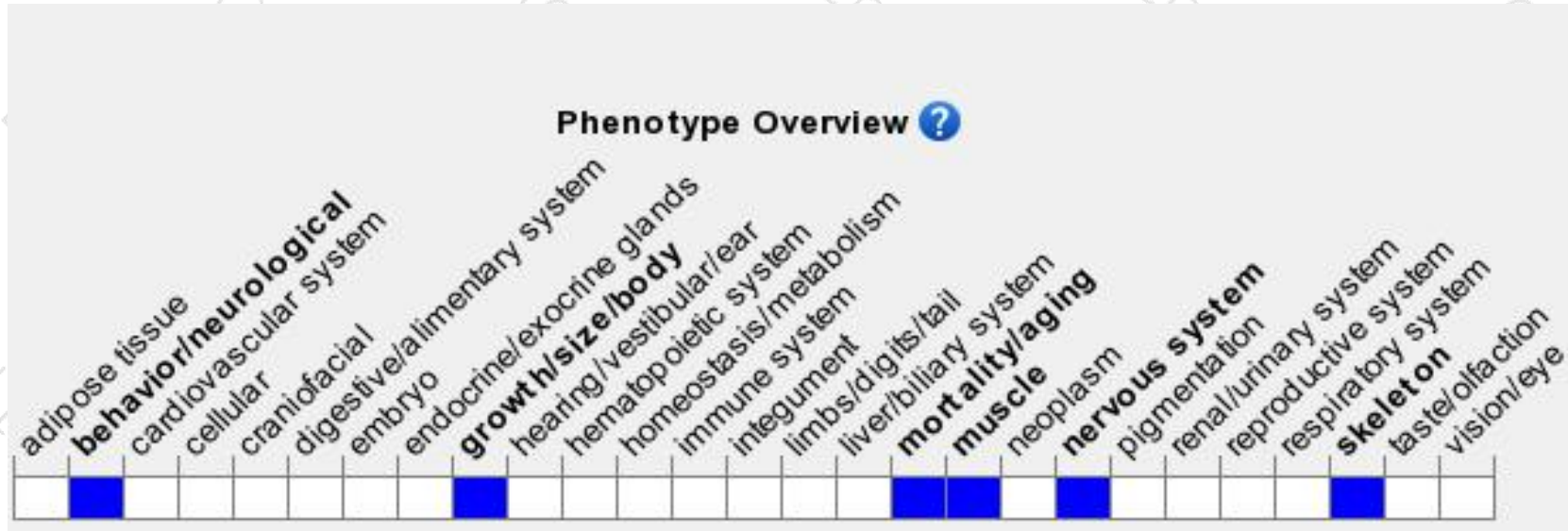
Genomic location distribution



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 decreased exploration, impaired spatial working memory, impaired coordination, and decreased paired-pulse facilitation.

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

Tel: 400-9660890

