

Atn2 Cas9-KO Strategy

Designer: Xiaojing Li
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Reviewer: Jia Yu

Project Overview

Project Name

Atxn2

Project type

Cas9-KO

Strain background

C57BL/6JGpt

Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *Atxn2* gene. The schematic diagram is as follows:



- The *Atxn2* gene has 20 transcripts. According to the structure of *Atxn2* gene, exon3-exon5 of *Atxn2-201* (ENSMUST00000051950.13) transcript is recommended as the knockout region. The region contains 283bp coding sequence. Knock out the region will result in disruption of protein function.
- In this project we use CRISPR/Cas9 technology to modify *Atxn2* gene. The brief process is as follows: CRISPR/Cas9 system

- According to the existing MGI data, Homozygous mice exhibit an enlarged fat pad, hepatic steatosis and enlarged seminal vesicles. A mild defect in motor learning is seen, but no other notable behavioral or neurological defects are detectable.
- The *Atxn2* gene is located on the Chr5. 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)

Atxn2 ataxin 2 [Mus musculus (house mouse)]

Gene ID: 20239, updated on 31-Jan-2019

Summary



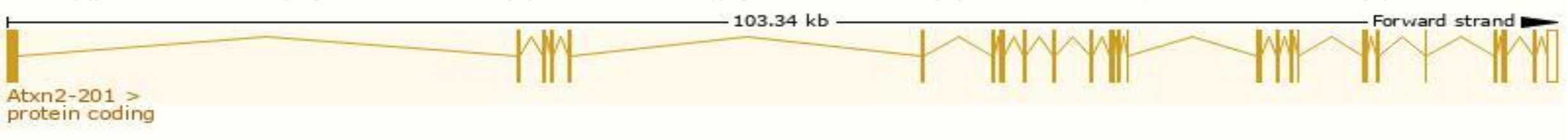
| | |
|---------------------------|---|
| Official Symbol | Atxn2 provided by MGI |
| Official Full Name | ataxin 2 provided by MGI |
| Primary source | MGI:MGI:1277223 |
| See related | Ensembl:ENSMUSG00000042605 |
| Gene type | protein coding |
| RefSeq status | VALIDATED |
| Organism | Mus musculus |
| Lineage | Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Myomorpha; Muroidea; Muridae; Murinae; Mus; Mus |
| Also known as | 9630045M23Rik, ATX2, AW544490, Sca2 |
| Expression | Ubiquitous expression in adrenal adult (RPKM 15.1), testis adult (RPKM 13.0) and 28 other tissues See more |
| Orthologs | human all |

Transcript information（Ensembl）

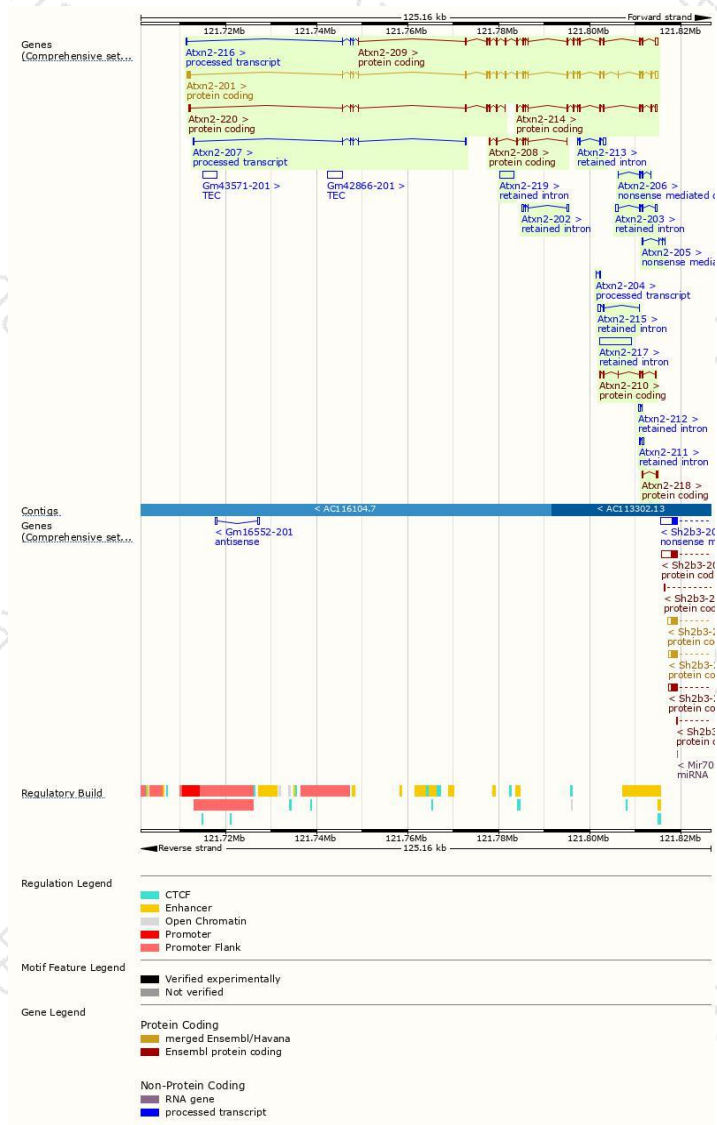
The gene has 20 transcripts,all transcripts are shown below:

| Name | Transcript ID | bp | Protein | Biotype | CCDS | UniProt | Flags |
|-----------|---------------------------------------|------|------------------------|-------------------------|---------------------------|----------------------------|---|
| Atxn2-201 | ENSMUST00000051950.13 | 4472 | 1286aa | Protein coding | CCDS39250 | E9QM77 | TSL:1 GENCODE basic APPRIS P1 |
| Atxn2-209 | ENSMUST00000161064.7 | 3294 | 929aa | Protein coding | - | F6U2C2 | CDS 5' incomplete TSL:5 |
| Atxn2-214 | ENSMUST00000162327.7 | 2343 | 662aa | Protein coding | - | F6V8M6 | CDS 5' incomplete TSL:5 |
| Atxn2-220 | ENSMUST00000225761.1 | 1434 | 402aa | Protein coding | - | A0A286YDU2 | CDS 3' incomplete |
| Atxn2-208 | ENSMUST00000160821.5 | 990 | 330aa | Protein coding | - | F7B6X4 | 5' and 3' truncations in transcript evidence prevent annotation of the start and the end of the CDS. CDS 5' and 3' incomplete TSL:5 |
| Atxn2-210 | ENSMUST00000161159.7 | 891 | 234aa | Protein coding | - | F6UTV7 | CDS 5' incomplete TSL:3 |
| Atxn2-218 | ENSMUST00000199864.1 | 412 | 64aa | Protein coding | - | A0A0G2JF15 | CDS 5' incomplete TSL:3 |
| Atxn2-206 | ENSMUST00000160462.1 | 397 | 65aa | Nonsense mediated decay | - | F6U209 | CDS 5' incomplete TSL:5 |
| Atxn2-205 | ENSMUST00000160220.1 | 388 | 96aa | Nonsense mediated decay | - | F6U2Q5 | CDS 5' incomplete TSL:3 |
| Atxn2-207 | ENSMUST00000160813.1 | 497 | No protein | Processed transcript | - | - | TSL:3 |
| Atxn2-216 | ENSMUST00000162611.7 | 461 | No protein | Processed transcript | - | - | TSL:3 |
| Atxn2-204 | ENSMUST00000160093.1 | 240 | No protein | Processed transcript | - | - | TSL:3 |
| Atxn2-217 | ENSMUST00000199451.1 | 6946 | No protein | Retained intron | - | - | TSL:NA |
| Atxn2-219 | ENSMUST00000200499.1 | 3131 | No protein | Retained intron | - | - | TSL:NA |
| Atxn2-203 | ENSMUST00000159928.1 | 1468 | No protein | Retained intron | - | - | TSL:5 |
| Atxn2-202 | ENSMUST00000159828.1 | 1003 | No protein | Retained intron | - | - | TSL:2 |
| Atxn2-213 | ENSMUST00000161872.7 | 755 | No protein | Retained intron | - | - | TSL:5 |
| Atxn2-215 | ENSMUST00000162459.1 | 754 | No protein | Retained intron | - | - | TSL:3 |
| Atxn2-211 | ENSMUST00000161433.1 | 578 | No protein | Retained intron | - | - | TSL:2 |
| Atxn2-212 | ENSMUST00000161836.1 | 482 | No protein | Retained intron | - | - | TSL:2 |

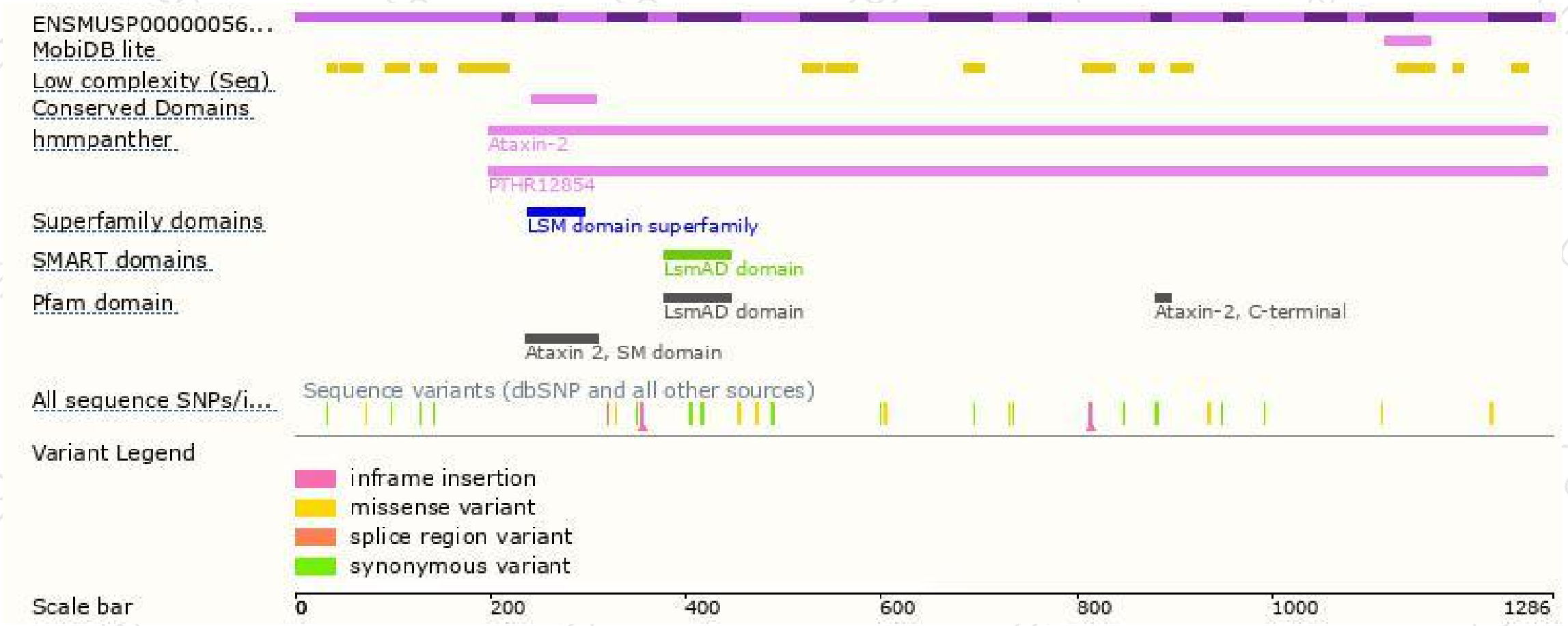
The strategy is based on the design of *Atxn2-201* transcript,The transcription is shown below



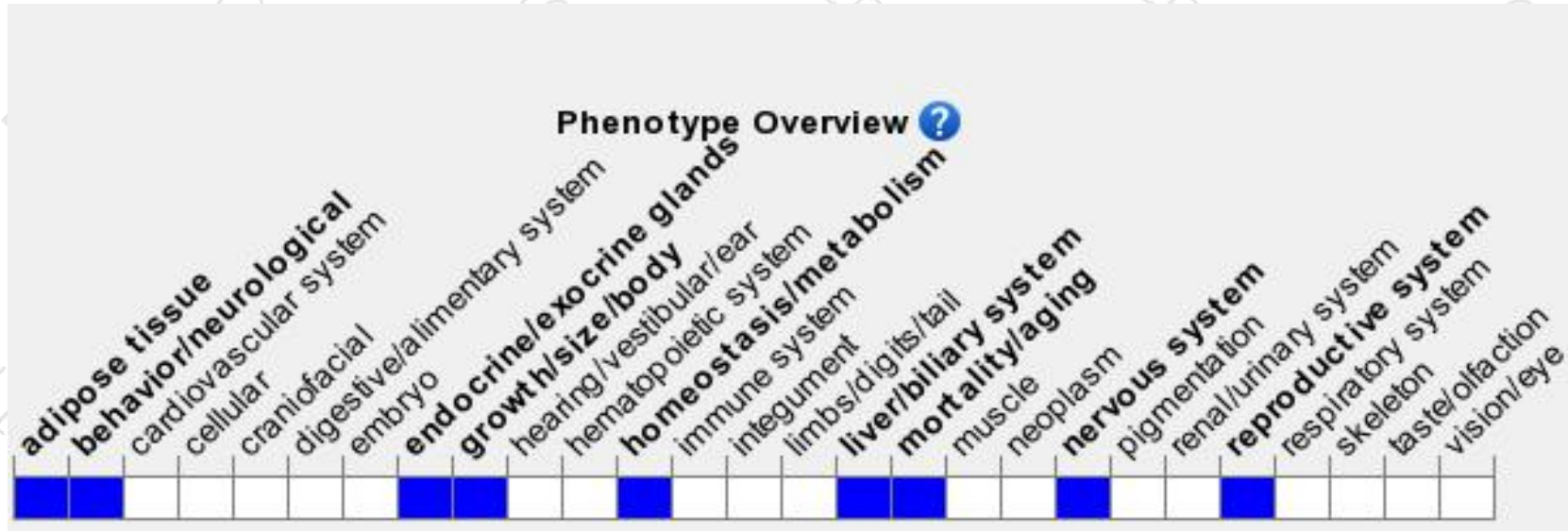
Genomic location distribution



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/>).

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

Tel: 400-9660890

