

Astn2 Cas9-KO Strategy

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Project Overview

Project Name

Astn2

Project type

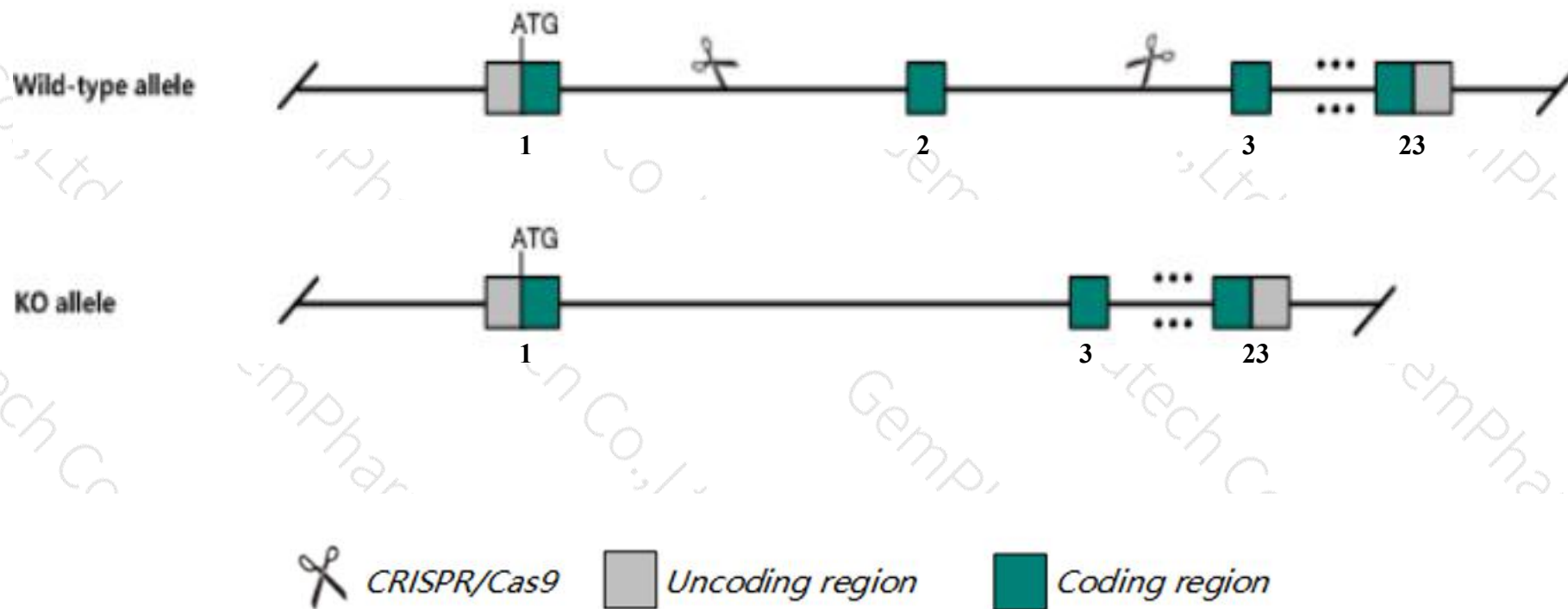
Cas9-KO

Strain background

C57BL/6JGpt

Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *Astn2* gene. The schematic diagram is as follows:



- The *Astn2* gene has 2 transcripts. According to the structure of *Astn2* gene, exon2 of *Astn2-201* (ENSMUST00000068214.10) transcript is recommended as the knockout region. The region contains 188bp coding sequence. Knock out the region will result in disruption of protein function.
- In this project we use CRISPR/Cas9 technology to modify *Astn2* gene. The brief process is as follows: CRISPR/Cas9 system

- The *Astn2* gene is located on the Chr4. 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)

Astn2 astrotactin 2 [Mus musculus (house mouse)]

Gene ID: 56079, updated on 13-Mar-2020

Summary



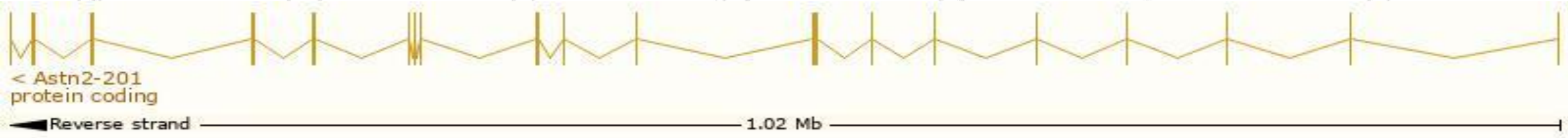
Official Symbol	Astn2 provided by MGI
Official Full Name	astrotactin 2 provided by MGI
Primary source	MGI:MGI:1889277
See related	Ensembl:ENSMUSG00000028373
Gene type	protein coding
RefSeq status	VALIDATED
Organism	Mus musculus
Lineage	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Myomorpha; Muroidea; Muridae; Murinae; Mus; Mus
Also known as	1d8, Astn1, bM452J22.1
Expression	Biased expression in cerebellum adult (RPKM 12.4), cortex adult (RPKM 4.1) and 12 other tissues See more
Orthologs	human all

Transcript information (Ensembl)

The gene has 2 transcripts,all transcripts are shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Astn2-201	ENSMUST00000068214.10	4959	1352aa	Protein coding	CCDS18269	Q80Z10	TSL:5 APPRIS is a system to annotate alternatively spliced transcripts based on a range of computational methods to identify the most functionally important transcript(s) of a gene. APPRIS P4
Astn2-202	ENSMUST00000084496.2	4675	1300aa	Protein coding	CCDS18268	Q80Z10	TSL:5 GENCODE basic APPRIS is a system to annotate alternatively spliced transcripts based on a range of computational methods to identify the most functionally important transcript(s) of a gene. APPRIS ALT2

The strategy is based on the design of *Astn2-201* transcript,The transcription is shown below



Genomic location distribution



Protein domain



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

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