

# Atxn713 Cas9-KO Strategy

**Designer: Jinling Wang** 

Reviewer: Fengjuan Wang

**Design Date: 2018-10-17** 

# **Project Overview**



**Project Name** 

Atxn7l3

**Project type** 

Cas9-KO

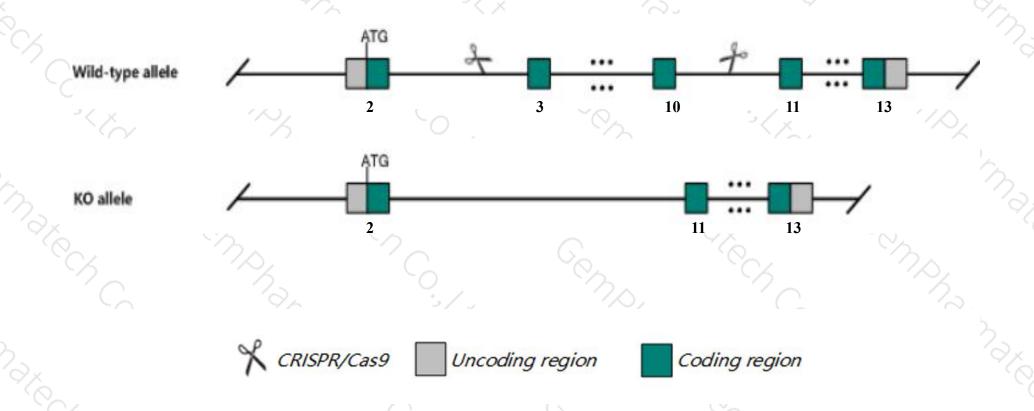
Strain background

C57BL/6JGpt

# **Knockout strategy**



This model will use CRISPR/Cas9 technology to edit the *Atxn7l3* gene. The schematic diagram is as follows:



### **Technical routes**



- The *Atxn713* gene has 6 transcripts. According to the structure of *Atxn713* gene, exon3-exon10 of *Atxn713-201*(ENSMUST00000073234.8) transcript is recommended as the knockout region. The region contains 614bp coding sequence. Knock out the region will result in disruption of protein function.
- ➤ In this project we use CRISPR/Cas9 technology to modify *Atxn713* gene. The brief process is as follows: CRISPR/Cas9 system were microinjected into the fertilized eggs of C57BL/6JGpt mice. Fertilized eggs were transplanted to obtain positive F0 mice which were confirmed by PCR and sequencing. A stable F1 generation mouse model was obtained by mating positive F0 generation mice with C57BL/6JGpt mice.

### **Notice**



- > According to the existing MGI data, mouse embryonic stem cells homozygous for a knock-out allele exhibit strikingly increased H2B monoubiquitination (H2Bub) levels and fail to show loss of global H2Bub following inhibition of transcriptional elongation.
- > The Intron2 and Intron10 are only 306bp and 234bp,loxp insertion may affect mRNA splicing.
- > The Atxn7l3 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)



#### Atxn7l3 ataxin 7-like 3 [Mus musculus (house mouse)]

Gene ID: 217218, updated on 13-Mar-2020

#### Summary

☆ ?

Official Symbol Atxn7l3 provided by MGI

Official Full Name ataxin 7-like 3 provided by MGI

Primary source MGI:MGI:3036270

See related Ensembl:ENSMUSG00000059995

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 E030022H21Rik

Expression Ubiquitous expression in cortex adult (RPKM 32.3), whole brain E14.5 (RPKM 28.1) and 28 other tissuesSee more

Orthologs <u>human all</u>

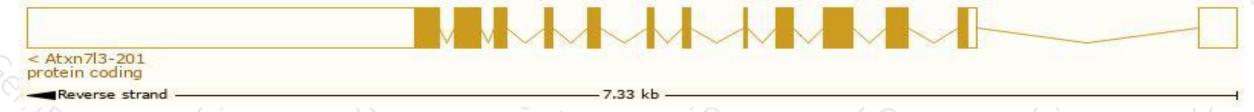
# Transcript information (Ensembl)



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

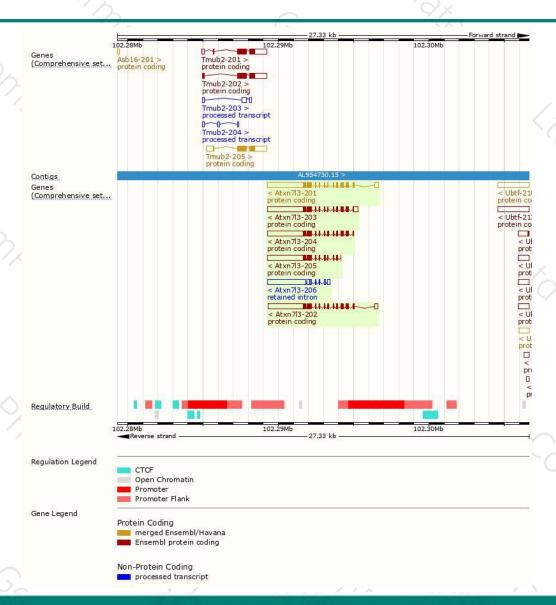
Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Atxn7l3-203	ENSMUST00000107134.7	3712	<u>347aa</u>	Protein coding	CCDS48941	A2AWT3	TSL:5 GENCODE basic APPRIS ALT1
Atxn7l3-202	ENSMUST00000107132.2	3706	<u>354aa</u>	Protein coding	CCDS48942	A2AWT3	TSL:5 GENCODE basic APPRIS P4
Atxn7l3-201	ENSMUST00000073234.8	3688	<u>347aa</u>	Protein coding	CCD548941	A2AWT3	TSL:1 GENCODE basic APPRIS ALT1
Atxn7l3-204	ENSMUST00000137387.7	3408	350aa	Protein coding	=	Z4YN62	CDS 5' incomplete TSL:5
Atxn7l3-205	ENSMUST00000141516.7	3130	<u>258aa</u>	Protein coding	#	F6RCN9	CDS 5' incomplete TSL:5
Atxn7l3-206	ENSMUST00000145484.1	3102	No protein	Retained intron	5	-	TSL:1

The strategy is based on the design of *Atxn7l3-201* transcript, the transcription is shown below:



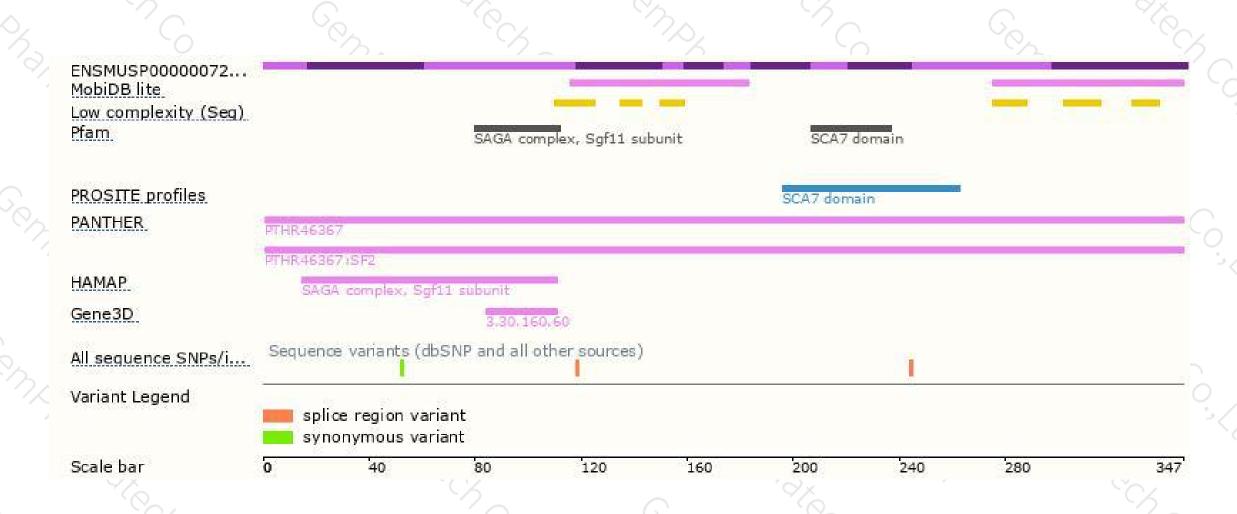
### Genomic location distribution





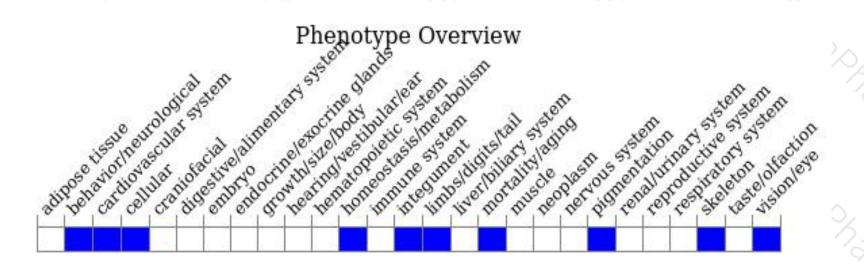
### Protein domain





## 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, mouse embryonic stem cells homozygous for a knock-out allele exhibit strikingly increased H2B monoubiquitination (H2Bub) levels and fail to show loss of global H2Bub following inhibition of transcriptional elongation.



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





