

Atoh7 Cas9-KO Strategy

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Project Overview

Project Name

Atoh7

Project type

Cas9-KO

Strain background

C57BL/6JGpt

Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *Atoh7* gene. The schematic diagram is as follows:



- The *Atoh7* gene has 2 transcripts. According to the structure of *Atoh7* gene, exon1 of *Atoh7-201* (ENSMUST00000044059.4) transcript is recommended as the knockout region. The region contains all 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 *Atoh7* gene. The brief process is as follows: CRISPR/Cas9 system

- According to the existing MGI data, Homozygous mutation of this gene results in impaired differentiation of retinal ganglion cells resulting in an increase of amacrine cells. Mice show impaired optic nerve formation and one allele shows loss of circadian photoentrainment.
- *Gm38063* gene will be deleted together in this strategy.
- The *Atoh7* gene is located on the Chr10. 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)

Atoh7 atonal bHLH transcription factor 7 [*Mus musculus* (house mouse)]

Gene ID: 53404, updated on 5-Nov-2019

Summary

- Official Symbol Atoh7 provided by [MGI](#)
- Official Full Name atonal bHLH transcription factor 7 provided by [MGI](#)
- Primary source [MGI:MGI:1355553](#)
- See related [Ensembl:ENSMUSG00000036816](#)
- 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 Math5; bHLHa13
- Expression Biased expression in cerebellum adult (RPKM 1.7), cortex adult (RPKM 0.3) and 4 other tissues [See more](#)
- Orthologs [human](#) [all](#)

Genomic context

Location: 10 B4; 10 32.54 cM

See Atoh7 in [Genome Data Viewer](#)

Exon count: 1

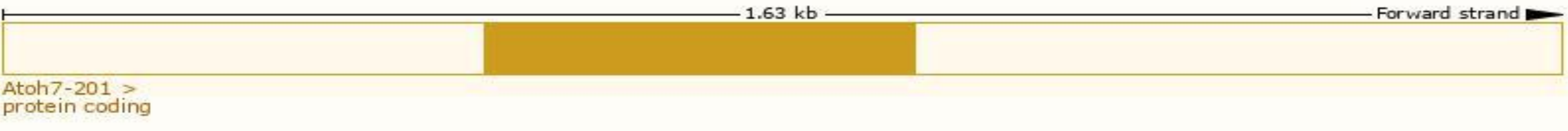
Annotation release	Status	Assembly	Chr	Location
108	current	GRCm38.p6 (GCF_000001635.26)	10	NC_000076.6 (63099785..63101280)
Build 37.2	previous assembly	MGSCv37 (GCF_000001635.18)	10	NC_000076.5 (62562904..62563353)

Transcript information (Ensembl)

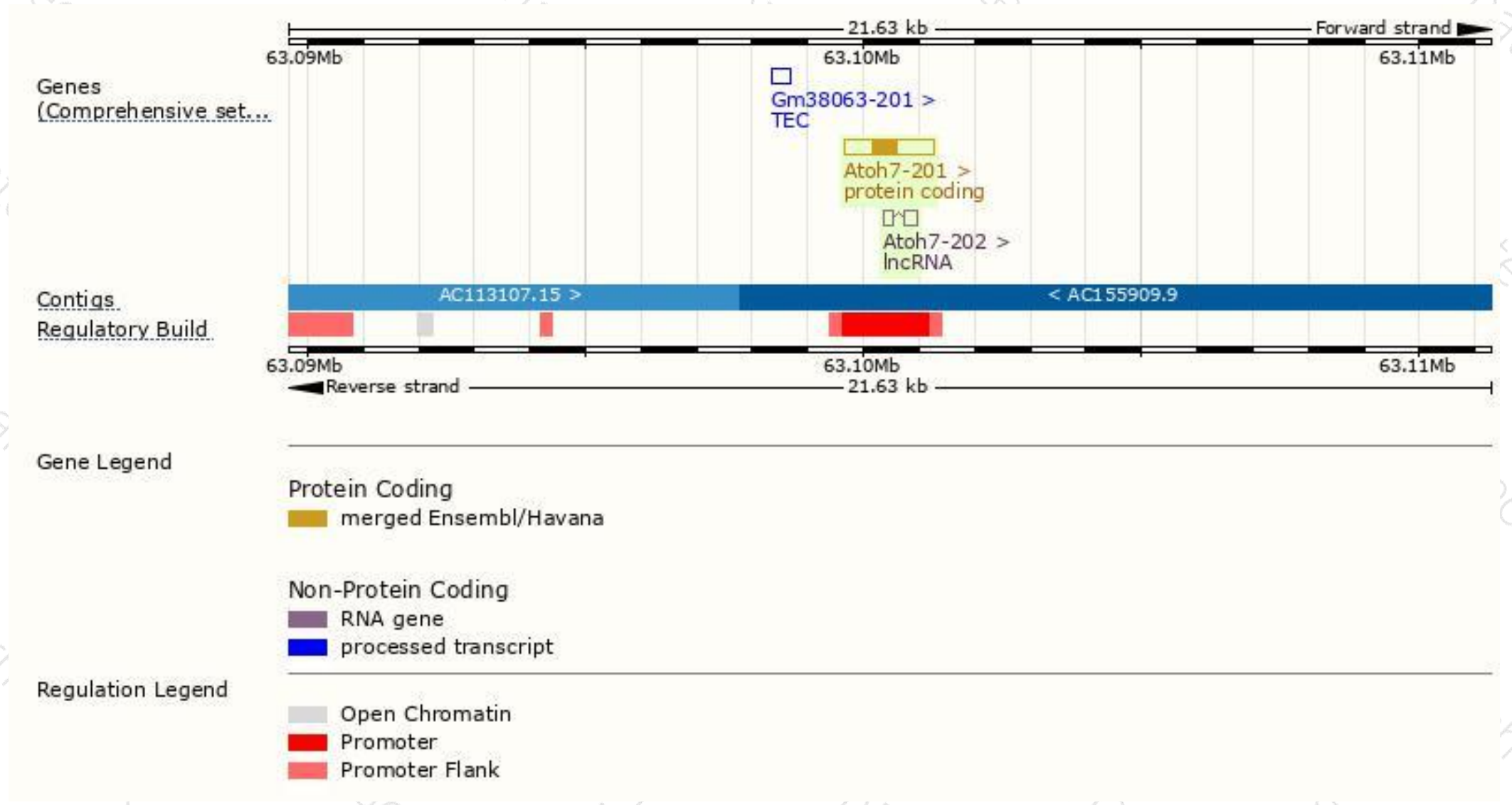
The gene has 2 transcripts,all transcripts are shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Atoh7-201	ENSMUST00000044059.4	1629	149aa	Protein coding	CCDS23896	Q9Z2E5	TSL:NA GENCODE basic APPRIS P1
Atoh7-202	ENSMUST00000219964.1	416	No protein	lncRNA	-	-	TSL:1

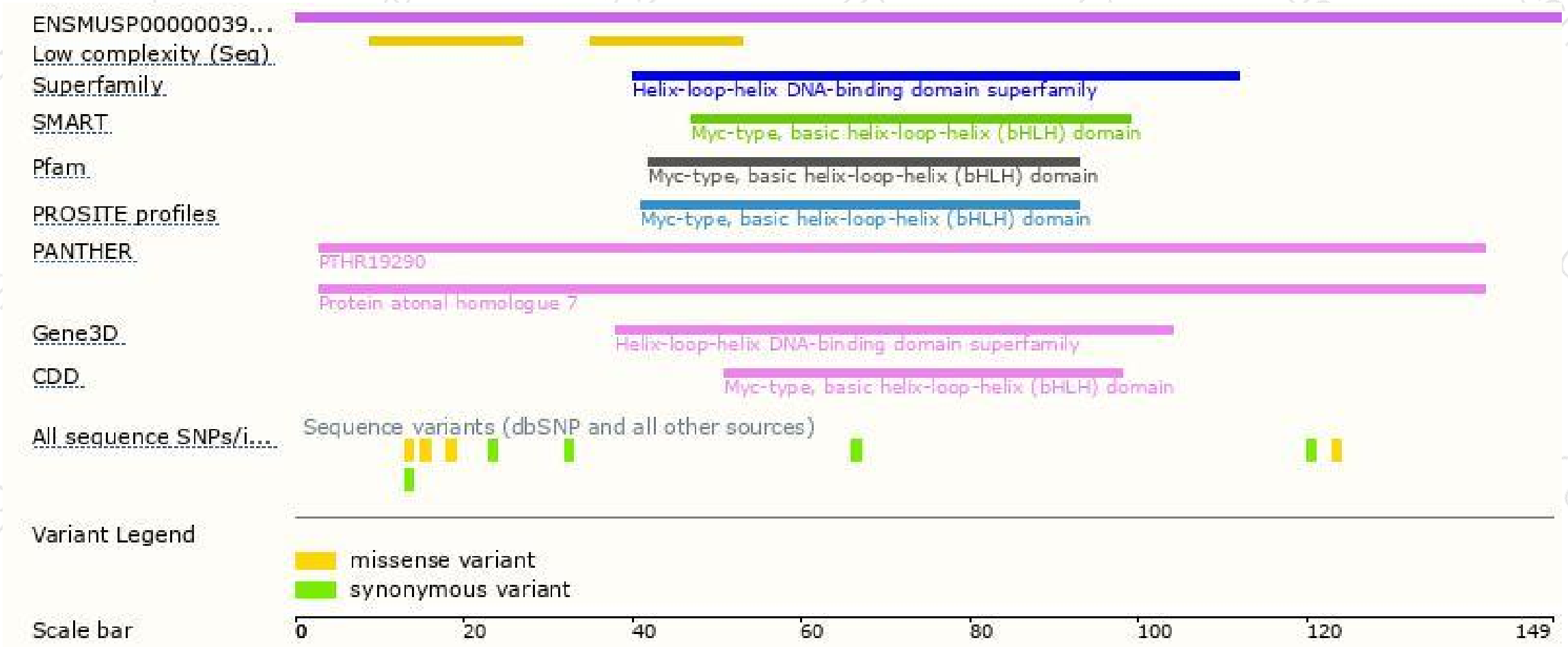
The strategy is based on the design of *Atoh7-201* transcript,The transcription is shown below



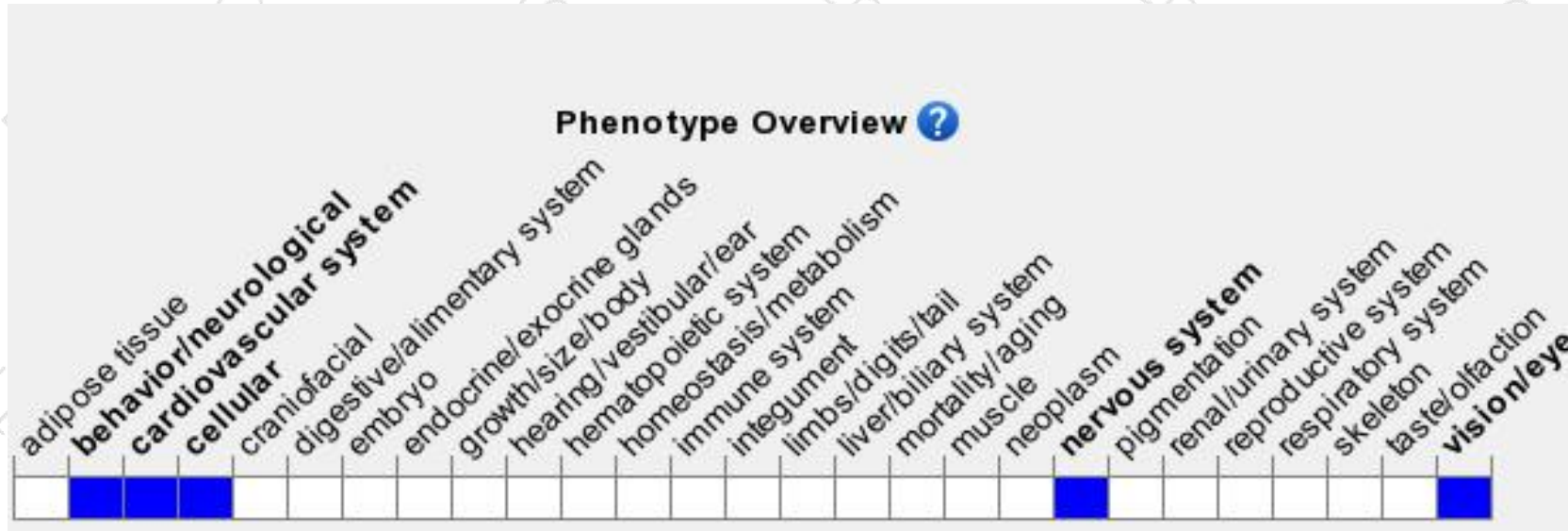
Genomic location distribution



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, Homozygous mutation of this gene results in impaired differentiation of retinal ganglion cells resulting in an increase of amacrine cells. Mice show impaired optic nerve formation and one allele shows loss of circadian photoentrainment.

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

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